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Table2.1. List of miRNAs that are involved in seed germination & dormancy.

miRNAs	Targets of miRNA	Upregulation ↑ ()	Downregulation ↓ ()	Seed germination related function	References
miR395	ATP Sulfurylases (<i>APS1</i> , <i>APS3</i> , <i>APS4</i>); Sulfate transporter (<i>SULTR2:1</i>)	↑ (<i>APS1</i> , <i>APS4</i> , <i>SULTR2:1</i> by miR395c)	↓ (<i>APS1</i> , <i>APS4</i> , <i>SULTR2:1</i> by miR395c and <i>APS3</i> by miR395e)	Regulatory effects on seed germination under salt & dehydration stress conditions	Kim et al, (2010b).
miR402	<i>DML3</i> (<i>DEMETER-LIKE protein 3</i>)		↓	Regulatory effect on seed germination & seedling growth under salt, dehydration & cold stress conditions	Kim et al, (2010a)
miR417	Unknown	Unknown	Unknown	Plays a role as a negative regulator of seed germination in <i>Arabidopsis thaliana</i> under salt stress condition.	Jung and kang, 2007
miR160	<i>ARF10</i> , <i>ARF16</i> , <i>ARF17</i>		↓ (<i>ARF10</i>)	<i>ARF10</i> mutant show up regulation of ABA responsive genes during germination	Liu et al, 2007
miR159	<i>MYB33</i> , <i>MYB65</i> , <i>MYB101</i>	↑ (<i>MYB33</i> , <i>MYB101</i>)		<i>MYB33</i> & <i>MYB101</i> are the positive regulators of ABA signalling during seed dormancy & germination.	Reyes & Chua, 2007
miR165/166	<i>PHB</i> , <i>PHV</i> , <i>REV</i> etc.	Unknown	Unknown	Maintain the auxin signal during seed development & maturation .So could	Huang et al, 2013

				have role in seed germination & dormancy also.	
miR164	<i>NAC1, CUC1/CUC2</i>	Unknown	Unknown	Maintain the auxin signal during seed development & maturation.	Huang et al, 2013
miR167	<i>ARF6, ARF8</i>	Unknown	Unknown	Maintain the auxin signal during seed development & maturation.	Huang et al, 2013;
miR156	<i>SPL 3, 4, 5</i>		↓	Seed development & maturation.	Huang et al, 2013; Li et al, 2013
miR172	<i>AP2</i>	↑		Seed development & maturation.	Huang et al, 2013; Li et al, 2013
miR158	Unknown	Unknown	Unknown	Seed development & maturation.	Huang et al, 2013

(The first five miRNAs in the grey shaded region of the table are also involved in mediating the stress response signals during germination)

Table 4.1.1. List of miRNAs differentially expressed in *Arabidopsis* seeds in imbibed seeds compare to dry seed (0 hr imbibitions) in a miRNA microarray analysis.

Probe ID	P value	Fold change	Regulation
ath-miR165a_st	0.031280305	1.89	up
ath-miR165b_st	0.03036148	1.85	up
ath-miR172a_st	0.008049283	-2.95	down
ath-miR390b_st	0.026625743	-1.68	down
ath-miR160a_st	0.03898194	-1.34	down
ath-miR156h_st	0.013480782	1.36	up
ath-miR157a_st	0.02468334	-1.45	down
ath-miR157c_st	0.032628458	1.36	up
ath-miR157d_st	0.04986837	-1.53	down
ath-miR164a_st	0.027664782	-2.04	down
ath-miR169b_st	0.00931509	-2.39	down
ath-miR161.1_st	0.021728164	1.32	up
ath-miR399a_st	0.017388277	-1.66	down

ath-miR399b_st	0.00114095	-6.97	down
ath-miR399c_st	0.034463275	-4.65	down
ath-miR824_st	0.00269617	-1.66	down
ath-miR834_st	0.009251686	-3.06	down
ath-miR854a_st	0.019733708	-4.12	down
ath-miR2112-5p_st	0.005841855	-1.20	down

Table 4.2.1. The locus-ID and descriptions of the candidate validated targets of known miRNAs during *Arabidopsis* seed germination.

Serial no.	miRNA	Target gene no.(Locus ID)	Description of the target gene	Target annotation	Validated by
1	165/166	AT2G34710	Homeobox-leucine zipper protein PHB	PHB	qRT-PCR
2		AT1G30490	Homeobox-leucine zipper protein PHV	PHV	qRT-PCR
3		AT4G32880	Homeobox-leucine zipper protein ATHB-8	ATHB-8	qRT-PCR
4		AT1G52150	Homeobox-leucine zipper protein ATHB-15	ATHB-15	qRT-PCR
5	172	AT4G36920	APETALA2	AP2	qRT-PCR
6		AT2G28550	Target of early activation tagged(EAT)1	TOE1	qRT-PCR
7		AT5G60120	Target of early activation tagged(EAT)2	TOE2	qRT-PCR
8		AT5G67180	Target of early activation tagged(EAT)3	TOE3	qRT-PCR
9	390	AT5G62000	Auxin response factor 2	ARF2	qRT-PCR

10		AT2G33860	Auxin response factor 3	ARF3	qRT-PCR
11		AT5G60450	Auxin response factor 4	ARF4	qRT-PCR
12	160	AT2G28350	Auxin response factor 10	ARF10	qRT-PCR
		AT4G30080	Auxin response factor 16	ARF16	qRT-PCR
13		AT1G77850	Auxin response factor 17	ARF17	qRT-PCR
14	156/157	AT2G33810	Squamosa promoter binding protein-like 3	SPL3	qRT-PCR
15	156/157	AT2G42200	Squamosa promoter binding protein-like 9	SPL9	qRT-PCR
16		AT1G27370	Squamosa promoter binding protein-like 10	SPL10	qRT-PCR

17	164	AT3G15170	Cup-shaped cotyledon1(ANAC054, Arabidopsis NAC domain containing protein 54).	CUC1	qRT-PCR
18		AT5G53950	Cup-shaped cotyledon2(ANAC098, Arabidopsis NAC domain containing protein 98).	CUC2	qRT-PCR
19		AT1G56010	NAC domain proteins(ANAC022, Arabidopsis NAC domain containing protein 22).	NAC1	qRT-PCR
20	169	AT1G17590	Nuclear factor Y, subunit A8	NF-YA8	qRT-PCR
21		AT1G54160	Nuclear factor Y, subunit A5	NF-YA5	qRT-PCR
22	161	AT5G16640	Pentatricopeptide repeat (PPR) superfamily protein	(PPR) superfamily protein	qRT-PCR
23	399	AT2G33770	Phosphate 2	PHO2	qRT-PCR
24	824	AT3G57230	AGAMOUS-like 16	AGL16	qRT-PCR
25	834	AT4G00930	COP1-interacting protein 4.1	CIP4.1	qRT-PCR
26	854	AT5G05100	Single-stranded nucleic acid binding R3H protein	R3H	qRT-PCR

Table-A1. List of primers for stem loop qRT-PCR used in this study.

Serial no.	Name of the Primers	Sequence of the primers
1	ath-miR165/166-F	GTACTCGGACCAGGCTTCA
2	ath-miR165/166-SL	GTC GTA TCC AGT GCA GGG TCC GAG GTA TTC GCA CTG GAT ACG AC GGGGGA
3	ath-miR172(a/b)F	CGGCGAGAATCTTGATGATG
4	ath-miR172(a/b)-SL	GTC GTA TCC AGT GCA GGG TCC GAG GTA TTC GCA CTG GAT ACG AC ATGCAG
5	ath-miR390b-F	GCGTAAGCTCAGGAGGGAT
6	ath-miR390b-SL	GTC GTA TCC AGT GCA GGG TCC GAG GTA TTC GCA CTG GAT ACG ACGGCGCT
7	ath-miR160a	ACTGCCTGGCTCCCTGT
8	160a-SL	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACT GGCA
9	ath-miR156h-F	GCGTGGTGACAGAAGAAAGA
10	ath-miR156h-SL	GTC GTA TCC AGT GCA GGG TCC GAG GTA TTC GCA CTG GAT ACG AC GTGCTC
11	ath-miR157(a/c/d)-F	GCGTCGTTGACAGAAGATAGA
12	ath-miR157(a/c/d)-SL	GTC GTA TCC AGT GCA GGG TCC GAG GTA TTC GCA CTG GAT ACG AC GTGCTC
13	ath-miR164a	GCTAATGGAGAAGCAGGGCA
14	164a-SL	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACT GCAC
15	ath-miR169b	GCGTACAGCCAAGGATGACT
16	169b-SL	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACC CGGC
17	ath-miR161-F	GCTCGCTGAAAGTGACTACAT
18	ath-miR161-SL	GTC GTA TCC AGT GCA GGG TCC GAG GTA TTC GCA CTG GAT ACG AC ACCCCG
19	ath-miR399a-F	GCGATGCCAAAGGAGATTT

20	ath-miR399a-SL	GTC GTA TCC AGT GCA GGG TCC GAG GTA TTC GCA CTG GAT ACG AC CAGGGC
21	ath-miR399(b/c)F	ACGC TGCCAAAGGAGAGTT
22	ath-miR824-F	CTGCGCTAGACCATTTGTGAG
23	ath-miR824-SL	GTC GTA TCC AGT GCA GGG TCC GAG GTA TTC GCA CTG GAT ACG AC TCCCTT
24	ath-miR834-F	GTCGTGGTAGCAGTAGCGG
25	ath-miR834-SL	GTC GTA TCC AGT GCA GGG TCC GAG GTA TTC GCA CTG GAT ACG AC TTACCA
26	ath-miR854(a/b)-F	GCGTCAGATGAGGATAGGGAG
27	ath-miR854-SL	GTC GTA TCC AGT GCA GGG TCC GAG GTA TTC GCA CTG GAT ACG AC CTCCTC
28	ath-miR2112-5p-F	GCTTAGCGCAAATGCGGA

29	ath-miR2112-5p-SL	GTC GTA TCC AGT GCA GGG TCC GAG GTA TTC GCA CTG GAT ACG ACACATTG
30	Universal reverse primer (UVRP)	GTG CAG GGT CCG AGG T
31	ath-Actin7-F	GGT CGT ACA ACC GGT ATT GT
32	ath-Actin7-R	GAT AGC ATG TGG AAG TGA GAA

Table-A2. List of primers for validation of miRNA targets used in this study by qRT-PCR.

Serial no.	Name of the Primers	Sequence of the primers
1	PHB-F	GGACTCCTTTCTATAGCAGAGGAGG
2	PHB -R	AAAGTTTGAAGAAGGTGGCCAG
3	PHV -F	TTGCGGAGGAGACCTTGGCG
4	PHV-R	GATAGTACCACCATTTCAGTG
5	ATHB8-F	AACACCACTTGACCCCTCAACATCAG
6	ATHB8-R	CACGCAACCAACAAGGCTTATCC

7	ATHB15-F	ATTGGCATCTCAAAATCCTCAGAGA
8	ATHB15-R	GGCAACACGTTTCATAACTTCAACAGC
9	ARF10- F	TGGCGAGTCCATGTGTTATC
10	ARF10 - R	TGTAAGTGTGTTACCGGTGT
11	ARF16 -F	TCAAGCCCGTTAAGCTCTGT
12	ARF16 -R	GGTGGTCTATTCAAGTAGTAATGGTG
13	ARF17-F	CCTCAAAGTGGACTGTCTAGTGC
14	ARF17 -R	GGTGAATAGCTGGGGAGGAT
15	ARF 2-F	TCCTGAGGCTAATCAAGACGA
16	ARF 2-R	GGAGGCTGTCGAGACATATC
17	ARF 3-F	CAACACTTGTTCGGATGGTG
18	ARF 3-R	CCCACACCAAATGTTCTCT
19	ARF 4-F	ATACTACCCACCCGGAAC
20	ARF 4-R	TGAGACTGCATCGCAAATC
21	SPL3 -F	GGAAAAGCACAAGTACTAAAG
22	SPL3 -R	TGTCGTAGGTTTAGCAGATAGC
23	SPL9 -F	CACTAAACTAGAGAGCTACAAGGG
24	SPL9 -R	GAAGAAGCTCGCCATGTAT
25	SPL10 -F	CATATTTGCTGATGGATTGG
26	SPL10 -R	GTGTTTGATCCCTTGTGAATC
27	AP2-F	TCGACGAACCAAGTGTGAC
28	AP2-R	CAGCCAATTTTGTGAGGAGT
29	TOE1-F	AAACAAGCGCCGTGAGAC
30	TOE1-R	TAACCACGTGTTGCATTGTC
31	TOE2-F	CATGATCAGTCCAGTGGTG
32	TOE2-R	CTGATTCAGATTGACGAAGG

33	TOE3-F	TAGCAATGATGACGACGACT
34	TOE3-R	GATGATGAATCAGGGACGAG
35	NAC1-F	ACTTTGACCAAGAACCCTCTTC
36	NAC1-R	CTGAGTTGGTTAGGTTTCGAGTT
37	CUC1-F	GCAATTGCTCCGATCATCAATAC
38	CUC1-R	GAGCGGGAAGGAATGTATGAA
39	CUC2-F	ACCAACACAACCGTCACA
40	CUC2-R	AGTTAACGTCTAAGCCCAAGG
41	NF-YA8-F	CGGTGGAATCTGGTAATGTGT

42	NF-YA8-R	CTGGACAAAGCGTGTGAAATAAG
43	NF-YA5-F	TCCGGAGACTGGTGATGATA
44	NF-YA5-R	GAGATTGTAGAGGATATGAAAGCAAAG
45	PPR-F	GCTACTCGAATGGTAAGCTGTAT
46	PPR-R	CCTCTGAAACCCTTCCTTCTTT
47	PHO2-F	AAGTGAAGTTTCTCCCGTTAGG
48	PHO2-R	GGAACCCAAGATGTGATTGGA
49	AGL16-F	AGAGGTCGAGGGTGTGAAA
50	AGL16-R	GGACATGTTCGTTTCGAGGTATC
51	CIP4.1-F	GTGAGTTGACATCTACTCCAGTTAC
52	CIP4.1-R	GTGCTCCGTTTATCTCGTTCA
53	R3H-F	TTCAACAGCCCTAGCAGTTC
54	R3H-R	CCACCACTTCAGTCTCATTCT