Article title: Accumulation of miRNAs differentially modulated by drought is affected by grafting in grapevine

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Supplementary material

Table S1. Stem loop primers used in this study for miRNA-specific RT-PCR assay. The last eight bases at 3’ of each primer are highlighted to indicate the region complementary to the miRNA sequence.

Primer description	**Type of miRNA**	**Stem-loop primer sequence (5’-3’)**
Stem Vvi-miR156b,c,d	conserved	CGCAGTTACTTCGAGAGAGAGAGAGAGACGAAGTAACTGCG**GTGCTCAC**
Stem Vvi-miR159c	conserved	CGCAGTTACTTCGAGAGAGAGAGAGAGACGAAGTAACTGCG**TAGAGCTC**
Stem Vvi-miR393a	conserved	CGCAGTTACTTCGAGAGAGAGAGAGAGACGAAGTAACTGCG**GATCAATG**
Stem Vvi-miR396c,d	conserved	CGCAGTTACTTCGAGAGAGAGAGAGAGACGAAGTAACTGCG**CAGTTCAA**
Stem Vvi-miR3624	known	CGCAGTTACTTCGAGAGAGAGAGAGAGACGAAGTAACTGCG**AGTAGTAT**
Stem n_22	novel	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGAC**AAATGAAA***
Stem n_47	novel	CGCAGTTACTTCGAGAGAGAGAGAGAGACGAAGTAACTGCG**GGAATGGG**
Stem n_231	novel	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGAC**GGAGGAAT***
Stem n_479	novel	CGCAGTTACTTCGAGAGAGAGAGAGAGACGAAGTAACTGCG**GGAATGGG**
Stem n_520	novel	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGAC**GATGACAG***
Stem n_622	novel	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGAC**GCTGACAG***
Stem n_55	novel	CGCAGTTACTTCGAGAGAGAGAGAGAGACGAAGTAACTGCG**CTATCAAT**
Stem n_191	novel	CGCAGTTACTTCGAGAGAGAGAGAGAGACGAAGTAACTGCG**TGCAGGTG**
Stem n_312	novel	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGAC**CATGTGAT***
Stem n_327	novel	CGCAGTTACTTCGAGAGAGAGAGAGAGACGAAGTAACTGCG**TGTGCTCT**
Stem n_337	novel	CGCAGTTACTTCGAGAGAGAGAGAGAGACGAAGTAACTGCG**TCTTATCC**
Stem n_346	novel	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGAC**GGTCCCCC***

* from Chen et al. (2005)

Table S2. Oligonucleotides used in this study for RT-qPCR analysis of miRNAs and related target transcripts.

Gene description	Gene ID (miRBase V.22 or VVGDB 12X V1)	Primer	Primer sequence (5'-3')	Product size (bp)
Vvi-miR156b,c,d	MI0006486- MI0006487- MI0006488	Forward	ACAGAAGAGAGTGAGCACCG	61
		Reverse A[a]	CGCAGTTACTTCGAGAGAGAGA	
Vvi-miR159c	MI0006495	Forward	GGATTGAAGGGAGCTCTACG	62
		Reverse A[a]	CGCAGTTACTTCGAGAGAGAGA	
Vvi-miR393a	MI0007952	Forward	CCAAAGGGATCGCATTG	61
		Reverse A[a]	CGCAGTTACTTCGAGAGAGAGA	
Vvi-miR396c,d	MI0007955- MI0006571	Forward	TTCCACAGCTTTCTTGAACTG	62
		Reverse A[a]	CGCAGTTACTTCGAGAGAGAGA	
Vvi-miR3624	MI0016017	Forward	TCAGGGCAGCAGCATACTAC	62
		Reverse A[a]	CGCAGTTACTTCGAGAGAGAGA	
novel 22 (n_22)		Forward	GCGTAGACCATGCATTTTCA	64
		Reverse B[b]	GTCGTATCCAGTGCAGGGT	
novel 47 (n_47)		Forward	TTCCCAATGCCGCCCA	63
		Reverse A[a]	CGCAGTTACTTCGAGAGAGAGA	
novel 231 (n_231)		Forward	GCCAAGAAGCACATTCCTCC	65
		Reverse B[b]	GTCGTATCCAGTGCAGGGT	
novel 479 (n_479)		Forward	TCTTACCAACACCTCCCATTCC	63
		Reverse A[a]	CGCAGTTACTTCGAGAGAGAGA	
novel 520 (n_520)		Forward	GCCGGCTCTCTAGACTTCTGT	65
		Reverse B[b]	GTCGTATCCAGTGCAGGGT	
novel 622 (n_622)		Forward	CGCTCATTTCTCTTTCTGTCA	66
		Reverse B[b]	GTCGTATCCAGTGCAGGGT	
novel 55 (n_55)		Forward	ATTCTTATCGATTGATAGCGCAG	59
		Reverse A[a]	CGCAGTTACTTCGAGAGAGAGA	
novel 191 (n_191)		Forward	GACTTAGGAAGAATGCACC	64
		Reverse A[a]	CGCAGTTACTTCGAGAGAGAGA	
novel 312 (n_312)		Forward	GGAGTGACCTGAGAATCA	66
		Reverse B[b]	GTCGTATCCAGTGCAGGGT	
novel 327 (n_327)		Forward	TTGACAAAGAGAGAGAGCACAC	62
		Reverse A[a]	CGCAGTTACTTCGAGAGAGAGA	
novel 337 (n_337)		Forward	TGTTTGGTTAGTGATGGGATAAG	65
		Reverse A[a]	CGCAGTTACTTCGAGAGAGAGA	
novel 346 (n_346)		Forward	CTGGAAGCCGATGGGG	65
		Reverse B[b]	GTCGTATCCAGTGCAGGGT	

[a, b] Reverse A and B primers were the universal reverse primers respectively used for amplifying cDNA samples obtained using either the stem loop primer designed in this study or the stem loop primer by Chen et al. (2005) (see Table S1).

Table S2. Continued.

Gene description	Gene ID (miRBase V.22 or VVGDB 12X V1)	Primer	Primer sequence (5’-3’)	Product size (bp)
Metal ion binding protein (VvMetallothionein)	VIT_00s0194g00340	Forward	GCTGAGGGTTGATCTTGAGTG	92
		Reverse	CAAAGAAAGCCTGGTCTCGT	
Growth Regulating Factor-like 1 (VvGRL1-like)	VIT_00s0494g00010	Forward	CTATCAACCCACACCTTCTGC	97
		Reverse	CCCTCTAACCCCAGCAAAA	
Auxin signalling f-box 2 (VvAUXIN F-BOX 2)	VIT_14s0068g01330	Forward	CAGGTTGAAGAGAATGGTGGT	104
		Reverse	TGGTAAACCCTTCACAGCTG	
Constans-like protein 5 (VvCONSTANS-like)	VIT_04s0008g07340	Forward	GTCGATGGATCCAAAGCTTC	100
		Reverse	CACCAATGGAGCTTGAACACT	
Topless related protein (VvTOPLESS-like)	VIT_09s0002g08370	Forward	TGCAGTTTCCTCACCTCAAA	99
		Reverse	CTGGATTTGGCCTTGGATT	
GATA transcription factor 26-like (VvGATA26-like)	VIT_00s0287g00040	Forward	GAAGGGTGATTATGAAGGCAG	104
		Reverse	AAGAGAGCCACCATCAGGA	
MYB transcription factor (VvMYB-like)	VIT_19s0090g00590	Forward	TCTCTATCCCTCTTCGACCC	96
		Reverse	GTCACCCGATCGCTTGTA	
Calmodulin binding protein MLO 16 (VvMLO16)	VIT_12s0035g00260	Forward	CCATTCATCTCTTTTCAACAGC	118
		Reverse	TTTGGGGGAATGTTAGTGTC	
Disease resistance protein NBS-LRR (VvNBS-LRR)	VIT_09s0096g00830	Forward	GGATGATCGGCTTATATGGGT	107
		Reverse	GGCCCAAATTACGACATCA	
Polyphenol oxidase, chloroplastic-like (VvPolyoxC)	VIT_00s0480g00100	Forward	CATTGCGCCTATTGCCA	98
		Reverse	CACGTGTTGTATTGGTTGGC	
NBS-LRR defence protein RPS5-like (VvRPS5)	VIT_09s0002g04950	Forward	GGGTGGGAATTATGGTATTGTA	99
		Reverse	CTCAAAGTCATTGGATGTTGC	
Zinc Finger protein (VvZinc)	VIT_06s0004g06440	Forward	GGGGAAGAGAAAGCCATCAT	100
		Reverse	GGTTCAATTCCTTCTCCTTCTG	
Hexose transporter HT5 (VvHT5)	VIT_05s0020g03140	Forward	CCCTGTTGTTAATGGAAGTGAC	92
		Reverse	CCTCCCCATACACCACTAATC	
CBL interacting protein kinase 13 (VvCIPK13)	VIT_13s0067g02480	Forward	GATAAGGCCAGCACTCAAGG	101
		Reverse	CCTGCAGTTCTTGATATGGTTC	
Squamosa Promoter binding protein-Like 6 (VvSPL6)	VIT_01s0011g00130	Forward	GAACTGAGGACTGCACTGG	109
		Reverse	AGTCCTGCGATTGAGCTGA	
Small Nuclear RNA U6 (VvU6)	VIT_06s0009g02760	Forward	ACAGAGAAGATTAGCATGGC	58
		Reverse	ACCATTTCTCGATTTGTGC	
Ubiquitin (VvUBI)	VIT_16s0098g01190 Perrone et al. 2012	Forward	TCTGAGGCTTCGTGGTGGTA	99
		Reverse	AGGCGTGCATAACATTTGCG	
Actin (*VvACT1*)	VIT_04s0044g00580 Perrone et al. 2012	Forward	GCCCCTCGTCTGTGACAATG	101
		Reverse	CCTTGGCCGACCCACAATA	

Table S3. Conserved and known miRNAs identified by high-throughput SOLiD sequencing in *Vitis vinifera* cv. Cabernet Sauvignon (CS) and M4 root (R) and leaf (L) samples upon irrigated (IRR) and drought stress (DS) conditions. The relative number of reads was calculated by dividing the number of reads of each miRNA with the total number of reads obtained for each cDNA library (see the Methods section for further details).

miRbase ID	**miRNA synonyms**	**miRNA family**	**RELATIVE NUMBER OF READS**							
			CS auto-grafted plants				**M4 auto-grafted plants**			
			IRR L	**IRR R**	**DS L**	**DS R**	**IRR L**	**IRR R**	**DS L**	**DS R**
vvi-miR156b	vvi-miR156c|vvi-miR156d	miR156	496	880	655	1894	528	551	936	752
vvi-miR156e			0	109	0	0	4	9	0	2
vvi-miR156f	vvi-miR156g|vvi-miR156i		4363	400	758	2027	1651	492	602	2688
vvi-miR159a		miR159	0	101	0	59	1	37	28	3
vvi-miR159c			20088	41022	12976	49683	15970	45946	18164	50821
vvi-miR160a	vvi-miR160b	miR160	161	299	221	547	175	145	245	127
vvi-miR160c	vvi-miR160d|vvi-miR160e		1644	2615	1617	3595	1864	1678	2424	676
vvi-miR162		miR162	31101	12696	32202	21483	21361	11915	10352	24036
vvi-miR164a	vvi-miR164c|vvi-miR164d	miR164	5233	3208	9534	5341	7767	3088	1332	1739
vvi-miR164b			105	44	57	0	300	15	11	78
vvi-miR166a	vvi-miR166b	miR166	372	1211	564	725	1043	1143	1187	701
vvi-miR166c	vvi-miR166d|vvi-miR166e|vvi-miR166f|vvi-miR166g|vvi-miR166h		22532	60207	73810	41427	76829	58087	28974	54561
vvi-miR167a		miR167	421	246	100	547	203	89	535	655
vvi-miR167b	vvi-miR167d|vvi-miR167e		20211	6429	8962	9173	14204	4086	6057	11469
vvi-miR167c			2199	3567	1420	12561	1332	5997	20421	1124
vvi-miR168		miR168	8391	8043	4258	4572	6599	5528	1231	2477
vvi-miR169a	vvi-miR169c|vvi-miR169j|vvi-miR169k|vvi-miR169s|vvi-miR169w	miR169	644	1283	690	459	928	1644	1237	1190
vvi-miR169b	vvi-miR169h		124	24	149	30	165	18	67	208
vvi-miR169d			1131	2341	721	1835	2776	5225	7550	2595
vvi-miR169e			449	32	175	118	104	82	28	214
vvi-miR169f	vvi-miR169g		14631	428	12854	3196	11894	545	1399	18096

Table S3. Continued.

miRBase ID	**miRNA synonyms**	**miRNA family**	**RELATIVE NUMBER OF READS**							
			CS auto-grafted plants				**M4 auto-grafted plants**			
			IRR L	**IRR R**	**DS L**	**DS R**	**IRR L**	**IRR R**	**DS L**	**DS R**
vvi-miR169l		miR169	180	113	94	44	70	51	11	132
vvi-miR169m	vvi-miR169n|vvi-miR169p|vvi-miR169q		237	182	144	192	150	91	22	289
vvi-miR169o			289	36	141	74	108	4	6	196
vvi-miR169r	vvi-miR169u		129	186	51	74	54	221	139	255
vvi-miR169t			42	44	10	30	63	79	39	153
vvi-miR169v			93	65	29	44	311	218	306	310
vvi-miR171a	vvi-miR171c|vvi-miR171d|vvi-miR171i	miR171	1722	3749	612	6939	625	5003	7149	248
vvi-miR171f			4	133	3	0	14	111	84	4
vvi-miR172c		miR172	75	743	74	163	82	837	1131	25
vvi-miR172d			1323	2103	2225	1391	1642	3617	2401	1348
vvi-miR390		miR390	137	117	134	59	211	196	178	53
vvi-miR393a	vvi-miR393b	miR393	121	0	114	98	107	1	90	10
vvi-miR394a	vvi-miR394c	miR394	139	202	154	385	78	113	184	73
vvi-miR394b			138	198	153	370	76	113	184	73
vvi-miR395a	vvi-miR395b|vvi-miR395c|vvi-miR395d|vvi-miR395e|vvi-miR395f|vvi-miR395g|vvi-miR395h|vvi-miR395i|vvi-miR395j|vvi-miR395k|vvi-miR395l|vvi-miR395m	miR395	1791	73	733	621	583	47	150	262
vvi-miR396a		miR396	8601	7966	2245	8197	3184	5239	5193	4183
vvi-miR396b			3761	4580	893	3817	1082	3322	2435	1527

Table S3. Continued.

miRBase ID	miRNA synonyms	miRNA family	RELATIVE NUMBER OF READS							
			CS auto-grafted plants				M4 auto-grafted plants			
			IRR L	IRR R	DS L	DS R	IRR L	IRR R	DS L	DS R
vvi-miR396c	vvi-miR396d	miR396	144836	232688	72230	105492	80946	165154	109141	102958
vvi-miR397a		miR397	7589	11316	13457	7546	3047	34615	21953	2443
vvi-miR398a		miR398	5051	3313	3261	2382	3338	5033	3460	814
vvi-miR398b	vvi-miR398c		3190	1768	5070	2811	1336	2443	3705	1045
vvi-miR399a	vvi-miR399h	miR399	5744	589	22259	1997	1445	189	1777	4370
vvi-miR399b	vvi-miR399c		8547	1340	4642	1879	899	821	1471	2327
vvi-miR399e			140	24	1387	133	137	26	106	403
vvi-miR399g			835	137	3475	562	404	40	273	628
vvi-miR399i			22730	2740	24647	8138	4215	825	2925	7393
vvi-miR403a	vvi-miR403b|vvi-miR403c|vvi-miR403d|vvi-miR403e|vvi-miR403f	miR403	919	916	647	2382	1201	806	1705	1316
vvi-miR408		miR408	4368	1760	5076	2841	3556	1492	1878	2229
vvi-miR447b		miR447	261	73	29	30	0	0	0	1
vvi-miR477		miR477	141	254	47	89	39	191	357	143
vvi-miR479		miR479	18	307	24	252	121	60	123	58
vvi-miR482		miR482	23727	54517	15415	83121	13602	72937	111270	7367
vvi-miR535a	vvi-miR535b|vvi-miR535c	miR535	49634	15662	43924	31367	62976	9561	13216	53725
vvi-miR828a		miR828	256	65	260	118	130	37	50	249
vvi-miR2111		miR2111	298	484	149	829	236	366	318	259
vvi-miR2950		miR2950	1053	1445	418	621	378	992	412	1233
vvi-miR3623		miR3623	11311	7058	6072	8626	7456	7727	11105	9254
vvi-miR3624		miR3624	15787	20202	15396	22208	78452	50916	66388	64638

Table S3. Continued.

miRBase ID	miRNA synonyms	miRNA family	RELATIVE NUMBER OF READS							
			CS auto-grafted plants				M4 auto-grafted plants			
			IRR L	IRR R	DS L	DS R	IRR L	IRR R	DS L	DS R
vvi-miR3626		miR3626	333	359	66	163	0	0	33	0
vvi-miR3629a	vvi-miR3629b|vvi-miR3629c	miR3629	17	0	21	15	208	1	33	43
vvi-miR3631a	vvi-miR3631b|vvi-miR3631c|vvi-miR3631d	miR3631	29	52	15	148	24	45	28	12
vvi-miR3632		miR3632	1333	3220	1248	4350	1480	4159	5700	1635
vvi-miR3633a		miR3633	31	157	49	266	3	233	50	7
vvi-miR3634		miR3634	14537	13019	5860	7442	12245	14546	12877	13288
vvi-miR3636		miR3636	369	428	257	577	1813	2021	2078	987
vvi-miR3637		miR3637	72	149	93	296	271	239	518	99
vvi-miR3638		miR3638	80	77	303	281	117	48	0	60
vvi-miR3639		miR3639	1	0	0	0	151	100	279	121
vvi-miR3640		miR3640	54	186	50	266	233	409	813	176

Table S4. Putative novel miRNAs identified by high-throughput SOLiD sequencing in CS and M4 root (R) and leaf (L) samples upon irrigated (IRR) and drought stress (DS) conditions. The relative number of reads was calculated by dividing the number of reads of each miRNA with the total number of reads obtained for each cDNA library (see the Methods section for further details).

novel miRNA ID	Chr	Start	End	Strand	5’-3’ Sequence	Lenght (nt)	Hairpin length (nt)	Hairpin minimum free energy (ΔG kcal mol^{-1})	RELATIVE NUMBER OF READS							
									CS auto-grafted plants				M4 auto-grafted plants			
									IRR L	IRR R	DS L	DS R	IRR L	IRR R	DS L	DS R
n_ 22	5	6841977	6841996	-	TAGACCATGCATTTTCATTT	20	111	-28.90	0	104	783	47	871	905	258	1432
n_ 47	4	19755493	19755514	-	TTTTCCCAATGCCGCCCATTCC	22	173	-71.80	25795	15911	8323	8114	5177	9260	5318	12422
n_ 55	4	22814922	22814939	+	ATTCTTATCGATTGATAG	18	146	-37.30	0	0	0	126	0	0	0	0
n_ 96	2	17923804	17923822	+	TTAGATTACATTAGTAAGT	19	101	-23.30	0	0	155	0	84	6	0	0
n_ 107	Un	11734039	11734059	+	GTGCTCTCTCTCGCTGTCATA	21	146	-55.90	227	0	136	0	0	0	0	0
n_ 135	7	15077651	15077669	-	CCGGGTAGATATGTTCGGA	19	101	-38.00	0	62	0	126	0	29	150	0
n_ 191	Un	42448872	42448894	+	GACTTAGGAAGAATGCACCTGCA	23	163	-86.20	109	0	0	0	0	0	0	0
n_ 221	5	24742194	24742215	-	TTTTGTTGCTGGTCATCTAGTC	22	149	-52.60	580	17	0	94	103	0	0	0
n_ 231	3	17003585	17003605	+	TGCCAAGAAGCACATTCCTCC	21	81	-67.00	0	0	0	5630	0	26609	0	0
n_ 284	14	27330868	27330887	-	ATATATCTGACATACTAATT	20	108	-27.80	6	109	7	94	11	75	107	21
n_ 290	2	855711	855731	-	AGAGCTTTCTTCAGTCCACTC	21	212	-80.10	6	0	0	0	14	0	112	0
n_ 306	8	22308239	22308259	+	ATGTATTTGAGGGAAAGCAAA	21	153	-61.40	103	0	5	0	0	13	0	27

Table S4. Continued.

novel miRNA ID	Chr	Start	End	Strand	5’-3’ Sequence	Lenght (nt)	Hairpin length (nt)	Hairpin minimum free energy (ΔG kcal mol^{-1})	RELATIVE NUMBER OF READS							
									CS auto-grafted plants				M4 auto-grafted plants			
									IRR L	IRR R	DS L	DS R	IRR L	IRR R	DS L	DS R
n_ 312	6	15575591	15575612	+	GGAGTGACCTGAGAATCACATG	22	157	-72.80	0	0	0	0	94	0	0	0
n_ 315	11	1504204	1504224	-	GCTTACTCCCTATCTGTCACC	21	110	-47.20	0	584	0	55	0	315	50	0
n_ 327	Un	11820804	11820824	+	TTGACAAAGAGAGAGAGCACA	21	117	-52.90	0	0	0	0	202	9	0	0
n_ 337	1	21550133	21550156	-	TGTTTGGTTAGTGATGGGATAAGA	24	90	-36.30	0	0	0	131	0	0	0	0
n_ 346	6	19950755	19950775	-	GCTGGAAGCCGATGGGGGACC	21	145	-59.10	0	0	241	0	0	0	0	0
n_ 401	14	26463744	26463765	+	CCTCTCTCTTCTCCTGTCAACA	22	95	-43.90	180	26	109	0	0	27	11	0
n_ 416	12	10940324	10940342	+	CCTTGCAAAATTTTCGCCA	19	151	-67.70	0	0	0	68	0	0	142	4
n_ 471	9	21822451	21822474	+	AGTATATTTGCATCAAATTTGTCA	24	166	-60.00	90	60	50	113	21	32	0	36
n_ 479	1	3865640	3865661	+	TCTTACCAACACCTCCCATTCC	22	156	-55.80	107728	43575	54805	33779	49632	51423	28463	46827
n_ 520	17	3046335	3046355	-	GCTCTCTAGACTTCTGTCATC	21	101	-48.10	4257	269	1188	581	3156	320	671	3030
n_ 529	1	21550134	21550157	-	ATGTTTGGTTAGTGATGGGATAAG	24	90	-36.30	47	177	9	0	0	0	0	3
n_ 532	6	8159628	8159648	+	CGCTATCTATCCTGAGTTTCA	21	153	-65.00	540	294	151	92	88	232	96	101
n_ 579	8	19949276	19949297	-	CACATATAATTTTTTCCCGTCA	22	156	-47.90	124	141	56	0	87	42	65	93

Table S4. Continued.

novel miRNA ID	**Chr**	**Start**	**End**	**Strand**	**5’-3’ Sequence**	**Lenght (nt)**	**Hairpin length (nt)**	**Hairpin minimum free energy (ΔG kcal mol^{-1})**	**RELATIVE NUMBER OF READS**							
									CS auto-grafted plants				**M4 auto-grafted plants**			
									IRR L	**IRR R**	**DS L**	**DS R**	**IRR L**	**IRR R**	**DS L**	**DS R**
n_ 581	5	6820787	6820808	-	TTACACAGAGAGATGACGGTGG	22	99	-49.20	0	222	35	0	41	376	90	65
n_ 622	4	5357009	5357030	-	GCTCATTTCTCTTTCTGTCAGC	22	116	-58.90	2241	11817	1342	5846	4374	5757	6809	3918
n_ 710	17	5927890	5927911	+	TCCCAGGAGAGATGGCACCTGC	22	149	-62.90	3156	69	1311	378	1027	81	20	1349

Table S5. Target transcripts of the novel candidate miRNAs analysed in this study. For each novel miRNA, the related target genes with the corresponding description and functional annotation are reported.

Novel miRNA ID	Target Gene ID (VvGDB 12X V1 CRIBI)	Gene Description	GO Functional Category
n_22	VIT_12s0035g00260	Calmodulin binding protein (MLO16)	Stress response
n_47	VIT_09s0096g00830	NBS-LRR defense protein	Stress response
n_231	VIT_00s0480g00100	Polyphenol oxidase, chloroplastic-like	Secondary metabolism
n_479	VIT_09s0002g04950	NBS-LRR defense protein RPS5-like	Stress response
	VIT_11s0037g01270	NBS-LRR defense protein	Stress response
n_520	VIT_06s0004g06440	zinc finger domain transcription factor	Regulation of transcription
n_622	VIT_05s0020g03140	Hexose transporter (HT5)	Sugar transport
	VIT_03s0038g00720	NADH dehydrogenase	Energy metabolism
n_191	VIT_13s0067g02480	CBL interacting protein kinase 13 (CIPK13)	ABA-mediated signaling pathway
n_327	VIT_01s0011g00130	Squamosa Promoter binding protein-Like 6 (SPL6)	Regulation of transcription (SBP family)
	VIT_01s0010g03710	Squamosa Promoter binding protein-Like 12 (SPL12)	Regulation of transcription (SBP family)
n_346	VIT_06s0009g03800	Uncharacterized protein: PHD finger transcription factor	Regulation of transcription (DDT family)
	VIT_08s0007g06560	putative serine/threonine kinase	Signaling pathway
n_55	VIT_12s0059g00450	Uncharacterized protein: DNA topoisomerase I	Nucleic acid metabolism
	VIT_04s0023g01900	Uncharacterized protein: AAA-type ATPase	Transport

Table S6. Target transcripts of the conserved/known miRNAs analysed in this study. For each conserved or known miRNA, the related target genes are reported with the corresponding description, functional annotation and reference.

miRNA ID (miRBase v.22)	Target Gene ID (VvGDB 12X V1 CRIBI)	Gene Description	GO Functional Category	Reference[a]
miR156b,c,d	VIT_04s0008g07340	Zinc finger protein CONSTANS 5-like (CONSTANS like)	Development	*Pantaleo et al., 2010*
miR393a	VIT_14s0068g01330	Auxin responsive factor TIR1-like	Auxin-mediated signalling pathway	*Belli Kullan et al., 2015*
miR396c,d	VIT_00s0494g00010	Growth regulating factor 1 like (GRL1 like)	Regulation of transcription (GRF family)	*Belli Kullan et al., 2015;*
miR3624	VIT_00s0194g00340	Metallothionein	Cellular homeostasis and Stress response	*Carra et al., 2009; Pantaleo et al., 2010*
miR159c	VIT_00s0287g00040	GATA transcription factor 26-like (GATA)	Regulation of transcription (C2C2-GATA family)	*Pantaleo et al., 2010*
	VIT_09s0002g08370	Topless-related protein 1 (TPR1)	Auxin-mediated signaling pathway	
	VIT_19s0090g00590	Myb-like transcription factor (MYB)	Regulation of transcription (MYB family)	

[a] scientific works where the target genes were *in silico* predicted and/or validated by either degradome or 5’RACE technique.