Table 1 Suppl. Information on tested TaMIRs and specific primers used for a TaMIRs expression analysis (Ta - annealing temperature).

Name of TaMIRs	Accession number	Forward primer 5´- 3´	Reverse primer 5´- 3´	Product length [bp]	Ta [°C]
TaMIR156	MI0016450	CGGCAAGAGGGAGAGAGAGA	GGCGTTTTGGGAAGGTGTATGT	223	53
TaMIR159a	MI0006170	GGTTCCCACTATCCTATC CC A	TGCAGAGCTCCCTTCAATCCA	112	53
TaMIR159b	MI0006171	AAAAAGGGGTGTTGCTGTG	ATGCAGAGCTCCCTTCAATCC	238	51
TaMIR160	MI0006172	GATATGCCTGGCTCCCTGTATG	AGACGGTCATGCTTGGCTCCTC	103	54
TaMIR164	MI0006173	GGTGGAGAAGCAGGGCACGT	GGTGGAGAAGAAAGGCACAT	156	53
TaMIR167	MI0006174	CTGCCCAAGGGAACGAGTGA	AGAAGTAGTTGAGCCCAACG	108	53
TaMIR174	MI0006175	GATGTTGGCTCGACTCACTCAG	CTGAGATATTGGCACGGCTCA	89	54
TaMIR399	MI0006176	CGTGTGTGAATCACAGGGC	GGGCAATTTCCTTTGGCA	125	53
TaMIR408	MI0006177	AAGGGATGAGGCAAGCAACAAAA	GGAGGGGAGCCAGGGAAGAG	119	58
TaMIR414	None	CCTTGCCCTCCTCAGTATC	GCTGGTGAAGAAGCACTCT	232	53
TaMIR444	MI0006178	CAAGGCGCAAAATTAATAGAAGAT	ACCTGCCAGTAGATGAAAACA	310	50
TaMIR841	MI0016310	CCCAACTGAGTGCGAAGAAG	CCCGAGCAACTTGAAAGTGT	254	53
TaMIR855	MI0016331	CCACCCGAAACATACCACTC	CCCTTTGTCCGACTCCTTTT	168	53
TaMIR857	MI0016335	GCGGTTGGTAACACTTATAG	GGTTACAAGCCCACAGTTA	162	53
TaMIR1117	MI0006179	AAAATGGGACCTTTAGTACC	GCGACTAAAGCTCCTCCCT	113	46
TaMIR1118	MI0006180	AAGCACGTGGATAGAGGAAG	CGAACCAAACATAAAAAAAAGG	139	46
TaMIR1119	MI0006181	AGCGTCAGCGTGTGAGGCG	CGCATAGCACTCCCACTCC	158	55
TaMIR1120	MI0006182	GGGCAGGTACTCCCTCCGT	GTGATTCAGGAGCTGGGAA	109	51
TaMIR1121	MI0006183	TATATATGTACTCCCTCTGT	TACAGTACTCCCTCCGTAA	98	44
TaMIR1122	MI0006184	CTCCCTCCGTCCCAAAAA	ACGAAGTAAAATGAGTGAATCTA	211	48
TaMIR1123	MI0006185	CCAGGTCTCATATAAATCAGGT	AATTCTATGAGACCAGGTCTCA	196	48
TaMIR1124	MI0006186	ATTACATGACTCAAAGGAACG	AGTACCGAGTCTAGCTTCC	129	48
TaMIR1125	MI0006187	TTTGGCCGTAAATTTAACCA	GACCGGTAAATTTAACCAAC	138	46
TaMIR1126	MI0006188	GTACTCTCTCCGTTCCTAAA	ATACTCCCTCCGTTTCTAA	164	55
TaMIR1127	MI0006189	ACATTAGATCTCAACTAC	ATCCACATTAGAATATACTCCC	149	43
TaMIR1128	MI0006190	ATATGAGAGCATGGGTGAG	ACATAAACGCCAAGCCAGAA	190	48
TaMIR1129	MI0006191	GCCATTCAGCCAGAAGAA	ATGGTGGACGGAGGGAGTT	269	51
TaMIR1130	MI0006192	AAATGTCTTATACTCCCTCC	CGTTGCAAATACTACCACTC	122	46
TaMIR1131	MI0006193	CATTAGTACCGGTTCGTGG	CCCAGACTGACAACATCC	91	47
TaMIR1132	MI0006194	TACTCCCTCCGTTTCACAAT	TACTCCTTCCGTTCCATAAT	154	47
TaMIR1133	MI0006195	ACTTCTTAGTGATAGTGGTCA	TAGCAACTTCAGTGAGTATATC	180	48
TaMIR1134	MI0006196	ACGCGTCCGGCATTCTTCT	TACATGTTGTTGCAGCTGCA	178	53
TaMIR1135	MI0006197	CTACTCCCTCCATTCGGAA	TACTCCCTCCGTTCGGAAT	108	50
TaMIR1136	MI0006198	TACTCCCTCCGTTCCGAAT	TACTCCCTCCGTTTCAAATT	107	48
TaMIR1137	MI0006199	CACGATGACGACGATTAGA	GATTTTCCTTATCACTAGCAA	148	43
TaMIR1138	MI0006200	ATCTTGTATAGGTCTGTCTA	CAGTTTGTTTAATTCACATCTAG	189	43
TaMIR1139	MI0006201	GCCACAGTGGAGAGTAACAT	AGTGGGAGTAACTTCAATAGT	216	48
TaMIR1216	None	CCGACCCTCAGCAAGAACAAT	CGCCTACCCTGGTGTCAAG	223	53
tubulin	U76558	AGAACACTGTTGTAAGGCTCAAC	GAGCTTTACTGC CTCGAACATGG	526	53

Table 2 Suppl. Target genes subjected to an expression analysis and the corresponding specific primers.

Name of target gene	Accession number	Interacted by TaMIR	Primers	Product length [bp]	Ta [°C]
Squamosa promoter-binding-like protein 16	AL810223	TaMIR156	Forward: 5´-ATGCGCTTCTGCCAACAGTGCA Reverse: 5´-AGAGCACAGTCTGAGTCCA	490	53
ORF1 protein	TC395266	TaMIR408	Forward: 5´- GCTTAACGACGGATCATCATC Reverse: 5´- TGGAGCGCTTAAATCCCAGT	476	53
DEAD/DEAH box helicase	CK214996	TaMIR1119	Forward: 5´- ATTGGTTGACTCAGCATCACC Reverse: 5´- AATACAAGAAGGGCAATGGCC	588	53
Major facilitator family transporter	TC441451	TaMIR1129	Forward: 5´-CCGCTCTATAGCTTTGCTTT Reverse: 5´-AATTGATTGGGTGAGATGAG	199	54
Calmodulin-like protein	BE516586	TaMIR1133	Forward: 5´- CTGATATATACTTCCTCCGTCC Reverse: 5´- ACGGCGAGCTCGATTTCCA	287	53
Endo-1,4-beta-glucanase	TC399881	TaMIR1136	Forward: 5´-GGACAAGTGGCTTATTCTGA Reverse: 5´-TCAGAATAAGCCACTTGTCC	448	53
Transcription factor Myb1	TC397585	TaMIR1139	Forward: 5´-GGGTGAGGATGATCTTGTGTT Reverse: 5´-CCCGATGCAGTTCAGTGGAA	486	54
Protein translation factor SUI1 homolog	TC405470	TaMIR1120	Forward: 5´-GAACTATGTGCATGTGCGTGT Reverse: 5´-CATACAAACCATGTTGAAGGAC	449	54
Catalase-1	TC372427	TaMIR1121	Forward: 5´-GACGACAAGCTGCTGCAGA Reverse: 5´-TCGGACAGGGGATCGATCAT	487	54
WRKY DNA binding domain	TC379745	TaMIR1123	Forward: 5´-CCAGACCTAGACGACAACC Reverse: 5´-GGCGGTCATCGCAAGTAAA	512	54
Receptor-like protein kinase	TC402631	TaMIR1134	Forward: 5´-AAGCACACCATGTGACGCG Reverse: 5´-AGGAGTAGACTGGACAACAC	530	54

Table 3 Suppl. Target genes regulated by drought-responsive and tissue-predominant TaMIRs. Un-pairing base pairs between TaMIR and the corresponding target gene are shown in *red*. The target genes highlighted by *blue* were randomly selected to an expression analysis under conditions of normal growth and of drought stress.

Name of TaMIRs	TaMIR sequence (3’ to 5’)	Tentative consensus (TC) hit	Score between TaMIR and TC	Pairing position sequence of TC to TaMIR (5’-3’)	Putative function of target gene
TaMIR156 (15)	ugacagaagagagugagcaca	TC453361	1.0	miRNA 21 ACACGAGUGAGAGAAGACAGU 1 Target 338 UGUGCUCUCUCUCUUCUGUCA 358	*Teosinte glume architecture 1*
		AL810223	1.0	miRNA 21 ACACGAGUGAGAGAAGACAGU 1 Target 522 UGUGCUCUCUCUCUUCUGUCA 542	*Squamosa promoter-binding-like protein 16*
		TC409846	1.0	miRNA 20 CACGAGUGAGAGAAGACAGU 1 Target 596 GUGCUCUCUCUCUUCUGUCA 615	*Isoform 2 of Q6H509*
		CK196549	1.0	miRNA 21 ACACGAGUGAGAGAAGACAGU 1 Target 194 UGUGCUCUCUCUCUUCUGUCA 214	*Squamosa promoter-binding-like protein 2*
		TC420438	2.0	miRNA 20 CACGAGUGAGAGAAGACAGU 1 Target 699 AUGCUCCCUCUCUUCUGUCA 718	*Chromosome chr19 scaffold_4*
		TC441570	2.0	miRNA 20 CACGAGUGAGAGAAGACAGU 1 Target 56 AUGCUCCCUCUCUUCUGUCA 75	*Alr2394 protein*
		TC384445	2.0	miRNA 20 CACGAGUGAGAGAAGACAGU 1 Target 532 AUGCUCUCUCUCUUCUGUCA 551	*Squamosa promoter-binding-like protein 3*
		TC412204	2.0	miRNA 20 CACGAGUGAGAGAAGACAGU 1 Target 210 AUGCUCUCUCUCUUCUGUCA 229	*Squamosa promoter-binding-like protein 11*
		DR739383	2.5	miRNA 21 ACACGAGUGAGAGAAGACAGU 1 Target 439 UGUGCUCCUUUUCUUUUGUCA 459	*Glycosyl/glycerophosphate transferase*
		TC373290	3.0	miRNA 21 ACACGAGUGAGAGAAGACAGU 1 Target 465 UUUGCUCACUCUUUGCUGUCA 485	*Chromosome undetermined SCAF8211*
		TC372857	3.0	miRNA 21 ACACGAGUGAGAGAAGACAGU 1 Target 66 UGUGCUCGCCCUUCUCUGUCA 86	Annotation not available

TaMIR408 (1)	cugcacugccucuucccuggc	CA741955	3.0	miRNA 20 CACGAGUGAGAGAAGACAGU 1 Target 174 AUACUCACUUUCUUUUGUCA 193	*Cytochrome P450*
		TC390294	3.0	miRNA 20 CACGAGUGAGAGAAGACAGU 1 Target 634 UUGUUCAAUCUCUUCUGUCG 653	*Cob(I) alamin adenolsyl transferase*
		TC460639	3.0	miRNA 21 ACACGAGUGAGAGAAGACAGU 1 Target 764 UGUGCUACCUCUCUUUUGUUA 784	*Annotation not available*
		TC398965	3.0	miRNA 21 ACACGAGUGAGAGAAGACAGU 1 Target 358 UGUGUUGGCUCUCUUCUGUUG 378	*Predicted permease*
		TC395266	3.0	miRNA 21 CGGUCCCUUCUCCGUCACGUC 1 Target 107 GCCGGGGGGGGGUAGUGUAG127	*ORF1 protein*
TaMIR1119 (21)	uggcacggcgugaugcugagucag	CA635649	0.0	miRNA 24 GACUGAGUCGUAGUGCGGCACGGU 1 Target 243 CUGACUCAGCAUCACGCCGUGCCA 266	*placenta cDNA clone*
		CK195785	0.0	miRNA 24 GACUGAGUCGUAGUGCGGCACGGU 1 Target 251 CUGACUCAGCAUCACGCCGUGCCA 274	Annotation not available
		TC439372	0.0	miRNA 24 GACUGAGUCGUAGUGCGGCACGGU 1 Target 251 CUGACUCAGCAUCACGCCGUGCCA 274	*LigA*
		TC450314	0.0	miRNA 24 GACUGAGUCGUAGUGCGGCACGGU 1 Target 274 CUGACUCAGCAUCACGCCGUGCCA 297	*162345 protein*
		CA636098	0.0	miRNA 24 GACUGAGUCGUAGUGCGGCACGGU 1 Target 251 CUGACUCAGCAUCACGCCGUGCCA 274	*AGAP006112-PA*
		CA610772	0.0	miRNA 24 GACUGAGUCGUAGUGCGGCACGGU	*Methylenetetrahydrofolate reductase*

		1 Target 220 CUGACUCAGCAUCACGCCGUGCCA 243	
TC377097	0.0	miRNA 24 GACUGAGUCGUAGUGCGGCACGGU 1 Target 503 CUGACUCAGCAUCACGCCGUGCCA 526	*Fibroin 1*
TC379547	0.0	miRNA 24 GACUGAGUCGUAGUGCGGCACGGU 1 Target 429 CUGACUCAGCAUCACGCCGUGCCA 452	*Fibroin 1*
TC396004	0.0	miRNA 24 GACUGAGUCGUAGUGCGGCACGGU 1 Target 377 CUGACUCAGCAUCACGCCGUGCCA 400	*Fibroin 3*
CA630409	1.0	miRNA 24 GACUGAGUCGUAGUGCGGCACGGU 1 Target 215 CUGGCUGAGCAUCACGCCGUGCCA 238	*Predicted protein*
CK214996	1.0	miRNA 24 GACUGAGUCGUAGUGCGGCACGGU 1 Target 252 UUGACUCAGCAUCACCCCGUGCCA 275	*DEAD/DEAH box helicase*
CK215346	1.0	miRNA 24 GACUGAGUCGUAGUGCGGCACGGU 1 Target 219 CUGACUAAGCAUCACGCCGUGCCA 242	*Fibroin heavy chain*
CA633293	1.0	miRNA 24 GACUGAGUCGUAGUGCGGCACGGU 1 Target 200 CUGACUGAGCAUCACGCCGUGCCA 223	*AFR161Cp*
TC442230	1.0	miRNA 24 GACUGAGUCGUAGUGCGGCACGGU 1 Target 220 CUGACUAAGCAUCACGCCGUGCCA 243	Annotation not available

		CA635234	1.0	miRNA 24 GACUGAGUCGUAGUGCGGCACGGU 1 Target 201 CUGGCUGAGCAUCACGCCGUGCCA 224	*Os03g0718400 protein*
		CK199678	1.0	miRNA 24 GACUGAGUCGUAGUGCGGCACGGU 1 Target 217 CUGACUGAGCAUCACGCCGUGCCA 240	Annotation not available
		CA663170	1.0	miRNA 24 GACUGAGUCGUAGUGCGGCACGGU 1 Target 192 CUGGCUGAGCAUCACGCCGUGCCA 215	*Os02g0265100 protein*
		TC443826	1.0	miRNA 24 GACUGAGUCGUAGUGCGGCACGGU 1 Target 226 CUGGCUGAGCAUCACGCCGUGCCA 249	*Predicted protein*
		CK194409	1.0	miRNA 24 GACUGAGUCGUAGUGCGGCACGGU 1 Target 213 CUGACUGAGCAUCACGCCGUGCCA 236	*Periplasmic protein TonB*
		TC382412	1.0	miRNA 24 GACUGAGUCGUAGUGCGGCACGGU 1 Target 275 CUGACUGAGCAUCACGCCGUGCCA 298	Annotation not available
		TC441495	1.0	miRNA 24 GACUGAGUCGUAGUGCGGCACGGU 1 Target 226 CUGACUGAGCAUCACGCCGUGCCA 249	*Predicted protein*
TaMIR1129 (2)	cagcgagccagcggagaccggcag	BQ244248	2.5	miRNA 20 GCCAGAGGCGACCGAGCGAC 1 Target 407 UGGUUUCUGUUGGUUCGCUG 426	*Molybdenum cofactor sulfurase protein-like*
		TC441451	3.0	miRNA 22 CGGCCA-GAGGCGACCGAGCGAC 1 Target 58 GCUGGUGCUCUGCUGGCUUGCUG 80	*Major facilitator family transporter*
TaMIR1133	cauauacucccuccgu	TC418799	0.0	miRNA 22	*SJCHGC07048 protein*

(14)	ccgaaa			AAAGCCUGCCUCCCUCAUAUAC 1 Target 449 UUUCGGACGGAGGGAGUAUAUG 470	
		TC407624	0.0	miRNA 22 AAAGCCUGCCUCCCUCAUAUAC 1 Target 597 UUUCGGACGGAGGGAGUAUAUG 618	Annotation not available
		TC374916	1.0	miRNA 22 AAAGCCUGCCUCCCUCAUAUAC 1 Target 1413 UUUCGGACGGAGGGAGUAUAUC 1434	*Os04g0211700 protein*
		TC440867	1.0	miRNA 22 AAAGCCUGCCUCCCUCAUAUAC 1 Target 249 UUCCGGACGGAGGGAGUAUAUG 270	*Expressed protein*
		CD898129	1.0	miRNA 22 AAAGCCUGCCUCCCUCAUAUAC 1 Target 62 UUUGGGACGGAGGGAGUAUAUG 83	Annotation not available
		BE516586	1.0	miRNA 22 AAAGCCUGCCUCCCUCAUAUAC 1 Target 154 UUUCGGACGGAGGGAGUAUAUA 175	*Calmodulin-like protein*
		GH731872	1.0	miRNA 22 AAAGCCUGCCUCCCUCAUAUAC 1 Target 292 UUUGGGACGGAGGGAGUAUAUG 313	Annotation not available
		TC368568	1.5	miRNA 21 AAGCCUGCCUCCCUCAUAUAC 1 Target 2825 UUUGGACGGAGGGAGUAUAUU 2845	*SET domain protein*
		CJ798548	1.5	miRNA 22 AAAGCCUGCCUCCCUCAUAUAC 1 Target 478 UUUCGGACGGAGGGAGUAUUUG 499	Annotation not available
		BQ838905	1.5	miRNA 22 AAAGCCUGCCUCCCUCAUAUAC 1 Target 14 UUUCGGACGGAGGGAGUACAUG 35	*Early nodulin protein*
		TC393163	2.0	miRNA 22 AAAGCCUGCCUCCCUCAUAUAC 1 Target 409 UUUCGAACGGAGGGAGUAUAUU 430	*Annotation not available*

		TC405193	2.0	miRNA 22 AAAGCCUGCCUCCCUCAUAUAC 1 Target 610 UUUUGGACGGAGGGAGUAGAUG 631	*Os05g0556100 protein*
		CJ868699	2.0	miRNA 22 AAAGCCUGCCUCCCUCAUAUAC 1 Target 622 UUCCGGACGGAGGGAGUAUAUA 643	*NADH-ubiquinone/plastoquinone oxidoreductase, chain 6*
		TC407900	2.5	miRNA 22 AAAGCCUGCCUCCCUCAUAUAC 1 Target 12 UUUCGGACGGAGGGAGCAUAUA 33	Annotation not available
TaMIR1136 (1)	uugucgcagguauggauguaucua	TC399881	1.0	miRNA 23 UCUAUGUAGGUAUGGACGCUGUU 1 Target 631 AGAUACAUCCAUACGUGCGACAA 653	*Endo-1,4-beta-glucanase*
TaMIR1139 (7)	agaguaacauacacuaguaaca	TC449025	1.5	miRNA 22 ACAAUGAUCACAUACAAUGAGA 1 Target 15 UGUUACUAGUGUAUGUUACUAU 36	Annotation not available
		CJ636238	2.0	miRNA 21 CAAUGAUCACAUACAAUGAGA 1 Target 368 GUAACUAGUCUAUGUUACUCU 388	*Glycine cleavage system H protein, mitochondrial precursor*
		TC384616	2.5	miRNA 20 AAUGAUCACAUACAAUGAGA 1 Target 1430 UUGCUACUGUAUGUUAUUUU 1449	*Chromosome undetermined scaffold_52*
		TC397135	2.5	miRNA 22 ACAAUGAUCACAUACAAUGAGA 1 Target 365 UCUUGUUGGUGUAUGUUACUCA 386	Annotation not available
		TC400227	2.5	miRNA 22 ACAAUGAUCACAUACAAUGAGA 1 Target 583 UCUUGUUGGUGUAUGUUACUCA 604	*Ribonuclease III*
		CB412183	3.0	miRNA 22 ACAAUGAUCACAUACAAUGAGA 1 Target 356 UGUUACUAGUGUGUGUUGUUUG 377	*Chloride peroxidase*
		TC397585	3.0	miRNA 22 ACAAUGAUCACAUACAAUGAGA 1 Target 1458 UGUUACUAGUCUAAGUUACUCC 1479	*Transcription factor Myb1*

TaMIR1120 (6)	acauucuuauauuaugagacggag	TC405470	0.0	miRNA 20 CAGAGUAUUAUAUUCUUACA 1 Target 1 GUCUCAUAAUAUAAGAAUGU 20	*Protein translation factor SUI1 homolog*
		CJ572772	1.5	miRNA 24 GAGGCAGAGUAUUAUAUUCUUACA 1 Target 60 CUCUGUCCCAUAAUAUAAGAGUGU 83	*OJ000126_13.4 protein*
		TC393660	2.0	miRNA 24 GAGGCAGAGUAUUAUAUUCUUACA 1 Target 838 CUCUGUCUCAUAAUAUAAGAGCGU 861	*Os01g0588700 protein*
		BE516383	2.0	miRNA 24 GAGGCAGAGUAUUAUAUUCUUACA 1 Target 95 CUCUGUUUCAUAAUAUAAAAAUGU 118	*Os03g0188500 protein*
		TC402657	2.5	miRNA 24 GAGGCAGAGUAUUAUAUUCUUACA 1 Target 108 CUCCGUCCCAUAAUAUAAGAACGU 131	*Glyceraldehyde-3-phosphate dehydrogenase*
		TC449066	2.5	miRNA 24 GAGGCAGAGUAUUAUAUUCUUACA 1 Target 806 CUCCGUCCCAUAAUAUAAGAUUGU 829	*S-adenosylmethionine decarboxylase proenzyme*
TaMIR1121 (5)	aguagugaucuaaacgcucuua	CA696517	0.0	miRNA 22 AUUCUCGCAAAUCUAGUGAUGA 1 Target 100 UAAGAGCGUUUAGAUCACUACU 121	Annotation not available
		TC372427	0.5	miRNA 22 AUUCUCGCAAAUCUAGUGAUGA 1 Target 1431 UAAGAGCGUUUAGAUCACUAUU 1452	*Catalase-1*
		TC377671	0.5	miRNA 22 AUUCUCGCAAAUCUAGUGAUGA 1 Target 1218 UAAGAGUGUUUAGAUCACUACU 1239	*Os01g0916300 protein*
		TC426178	1.0	miRNA 22 AUUCUCGCAAAUCUAGUGAUGA 1 Target 401	*Chromosome undetermined SCAF15013*

TaMIR1123 (8)	uccgugagaccuggucucauaga			UAAGAGCGUUUAGAUCACUACC 422	
		CV774411	1.0	miRNA 22 AUUCUCGCAAAUCUAGUGAUGA 1 Target 381 UAAGAGCGUUUAGAUUGCUACU 402	Annotation not available
		CJ724067	2.0	miRNA 23 AGAUACUCUGGUCCAGAGUGCCU 1 Target 634 UCUAUGAGACCAGGUCUCNCGGG 656	Annotation not available
		TC379745	2.0	miRNA 20 UACUCUGGUCCAGAGUGCCU 1 Target 539 GUGAAACUAGGUCUCACGGA 558	*WRKY DNA binding domain*
		TC371699	2.5	miRNA 23 AGAUACUCUGGUCCAGAGUGCCU 1 Target 2560 UGUAUGAGACCGGGUCUCAUAGA 2582	*Lipoxygenase*
		TC398465	2.5	miRNA 20 UACUCUGGUCCAGAGUGCCU 1 Target 943 GUGAAACUAGGUCUCGCGGA 962	*WRKY DNA binding domain*
		CA616203	3.0	miRNA 23 AGAUACUCUGGUCCAGAGUGCCU 1 Target 434 UGUUUGAGGCCAGAUCUCAUGGA 456	*O-methyltransferase family protein*
		TC411782	3.0	miRNA 20 UACUCUGGUCCAGAGUGCCU 1 Target 115 GUGAAGCUAGGUCUCGCGGA 134	*Cell division membrane protein*
		TC373584	3.0	miRNA 20 UACUCUGGUCCAGAGUGCCU 1 Target 471 AUGAGUUCAGGUCUCUCGGA 490	*Os01g0708900 protein*
		TC446694	3.0	miRNA 20 UACUCUGGUCCAGAGUGCCU 1 Target 248 GUGAAGCUAGGUCUCGCGGA 267	*WRKY DNA binding domain*
TaMIR1134 (14)	caacaacaacaagaagaagaagau	TC445329	0.0	miRNA 23 AGAAGAAGAAGAACAACAACAAC 1 Target 30 UCUUCUUCUUCUUGUUGUUGUUG 52	*Chromosome chr8 scaffold_106*
		TC400842	1.0	miRNA 23 AGAAGAAGAAGAACAACAACAAC 1 Target 554 UUUUCUUCUUAUUGUUGUUGUUG 576	*Isopentenyl pyrophosphate isomerase IDI2*

CD454365	1.0	miRNA 23 AGAAGAAGAAGAACAACAACAAC 1 Target 181 UCUUCUUCUUAUUGUUGUUGUUG 203	*Predicted protein*
CN011842	1.5	miRNA 22 GAAGAAGAAGAACAACAACAAC 1 Target 115 UUUUUUUUUUUUGUUGUUGUUG 136	Annotation not available
CA698436	2.0	miRNA 23 AGAAGAAGAAGAACAACAACAAC 1 Target 99 UCUUCUGCUUCUUGUUGUUGUUU 121	*Expressed protein*
TC443552	2.5	miRNA 24 UAGAAGAAGAAGAACAACAACAAC 1 Target 80 AUCUUCAUCUUUUUGUUGUUGUUU 103	*LigA*
TC416929	2.5	miRNA 24 UAGAAGAAGAAGAACAACAACAAC 1 Target 753 AUCUUUUACUUCUUAUUGUUGUUG 776	*Protein arginine N-methyltransferase*
CJ696481	2.5	miRNA 23 AGAAGAAGAAGAACAACAACAAC 1 Target 149 UUUUCUUCUUCUUGUUCUUGUUC 171	*Serine carboxypeptidase 1 precursor*
TC402631	2.5	miRNA 23 AGAAGAAGAAGAACAACAACAAC 1 Target 348 UCUUCUUCUUCUUGGUGGUGUUG 370	*Receptor-like protein kinase*
TC372437	2.5	miRNA 24 UAGAAGAAGAAGAACAACAACAAC 1 Target 78 GUGUUCUUCUUCUUGUUGUUGUCU 101	*Chlorophyll a/b binding protein precursor*
TC400050	2.5	miRNA 23 AGAAGAAGAAGAACAACAACAAC 1 Target 16 UCUUCUUCUUCUUCUUCUUGUUG 38	*Chromosome chr4 scaffold_6*
CK203449	3.0	miRNA 24 UAGAAGAAGAAGAA-CAACAACAAC 1 Target 471	*EF-hand Ca*$^{2+}$*-binding protein CCD1*

			AUCUUCUUCUUCUUCGUUGUUGUUU 495	
	TC405965	3.0	miRNA 24 UAGAAGAAGAAGAACAACA-ACAAC 1 Target 802 AUUUUCUUCUUUUUGUUGUGUGUUG 826	*Thioredoxin*
	TC378909	3.0	miRNA 24 UAGAAGAAGAAGAACAACAACAAC 1 Target 1020 AUUUUUGUUUUCUUGUUGUUGUUU 1043	*Phosphatidylinositol-4-phosphate 5-kinase 1*

Table 4 Suppl. Function groups of target genes regulated by drought-responsible TaMIRs.

Functional group	Name of target gene	Accession number	Interacted by TaMIR
Signal transduction (2)	*Periplasmic protein TonB*	CK194409	TaMIR1119
	Calmodulin-like protein	BE516586	TaMIR1133
Transcriptional regulation (6)	*Squamosa promoter-binding-like protein 16*	AL810223	TaMIR156
	Squamosa promoter-binding-like protein 2	CK196549	TaMIR156
	Squamosa promoter-binding-like protein 3	TC384445	TaMIR156
	Squamosa promoter-binding-like protein 11	TC412204	TaMIR156
	SET domain protein	TC368568	TaMIR1133
	Transcription factor Myb1	TC397585	TaMIR1139
RNA metabolism (2)	*DEAD/DEAH box helicase*	CK214996	TaMIR1119
	Ribonuclease III	TC400227	TaMIR1139
Primary metabolism (3)	*Cob(I) alamin adenolsyl transferase*	TC390294	TaMIR156
	Methylenetetrahydrofolate reductase	CA610772	TaMIR1119
	NADH-ubiquinone/plastoquinone oxidoreductase	CJ868699	TaMIR1133
Secondary metabolism (8)	*Glycosyl/glycerophosphate transferase*	DR739383	TaMIR156
	Cytochrome P450	CA741955	TaMIR156
	Fibroin 1	TC377097	TaMIR1119
	Fibroin 2	TC379547	TaMIR1119
	Fibroin 3	TC396004	TaMIR1119
	Fibroin heavy chain	CK215346	TaMIR1119
	Endo-1,4-beta-glucanase	TC399881	TaMIR1136
	Glycine cleavage system H protein, mitochondrial ursor	CJ636238	TaMIR1139

Trafficking (2)	*Predicted permease permease*	TC398965	TaMIR156
	Major facilitator family transporter	TC441451	TaMIR1129
Development (2)	*Teosinte glume architecture 1*	TC453361	TaMIR156
	Early nodulin protein	BQ838905	TaMIR1133
Defense response (2)	*Molybdenum cofactor sulfurase protein-like*	BQ244248	TaMIR1129
	Chloride peroxidase	CB412183	TaMIR1139
Unknown function (21)	*Isoform 2 of Q6H509*	TC409846	TaMIR156
	Chromosome chr19 scaffold_4	TC420438	TaMIR156
	Alr2394 protein	TC441570	TaMIR156
	Chromosome undetermined SCAF8211	TC373290	TaMIR156
	ORF1 protein	TC395266	TaMIR408
	placenta cDNA clone	CA635649	TaMIR1119
	LigA	TC439372	TaMIR1119
	162345 protein	TC450314	TaMIR1119
	AGAP006112-PA	CA636098	TaMIR1119
	Predicted protein	CA630409	TaMIR1119
	AFR161Cp	CA633293	TaMIR1119
	Os03g0718400 protein	CA635234	TaMIR1119
	Os02g0265100 protein	CA663170	TaMIR1119
	Predicted protein	TC443826	TaMIR1119
	Predicted protein	TC441495	TaMIR1119
	SJCHGC07048 protein	TC418799	TaMIR1133

	Os04g0211700 protein	TC374916	TaMIR1133
	Expressed protein	TC440867	TaMIR1133
	Os05g0556100 protein	TC405193	TaMIR1133
	Chromosome undetermined scaffold_52	TC384616	TaMIR1139
	162345 protein	TC450314	TaMIR1119
To be annotated (13)	Annotation not available	TC372857	TaMIR156
	Annotation not available	TC460639	TaMIR156
	Annotation not available	CK195785	TaMIR1119
	Annotation not available	TC442230	TaMIR1119
	Annotation not available	CK199678	TaMIR1119
	Annotation not available	TC382412	TaMIR1119
	Annotation not available	TC407624	TaMIR1133
	Annotation not available	CD898129	TaMIR1133
	Annotation not available	GH731872	TaMIR1133
	Annotation not available	CJ798548	TaMIR1133
	Annotation not available	TC393163	TaMIR1133
	Annotation not available	TC449025	TaMIR1139
	Annotation not available	TC397135	TaMIR1139

Table 5 Suppl. Function groups of target genes regulated by tissue-predominant TaMIRs.

Functional group	Name of target gene	Accession number	Interacted by TaMIR
Signal transdustion (3)	*Receptor-like protein kinase*	TC402631	TaMIR1134
	EF-hand Ca^{2+}-binding protein CCD1	CK203449	TaMIR1134
	Phosphatidylinositol-4-phosphate 5-kinase 1	TC378909	TaMIR1134
Transcriptional regulation (4)	*Protein translation factor SUI1 homolog*	TC405470	TaMIR1120
	WRKY DNA binding domain	TC379745	TaMIR1123
	WRKY DNA binding domain	TC398465	TaMIR1123
	WRKY DNA binding domain	TC446694	TaMIR1123
Post-translational modification (2)	*Protein arginine N-methyltransferase*	TC416929	TaMIR1134
	Thioredoxin	TC405965	TaMIR1134
Protein degradation (1)	*Serine carboxypeptidase*	CJ696481	TaMIR1134
Primary metabolism (3)	*Glyceraldehyde-3-phosphate dehydrogenase*	TC402657	TaMIR1120
	Lipoxygenase	TC371699	TaMIR1123
	Chlorophyll a/b binding protein precursor	TC372437	TaMIR1134
Secondary metabolism (3)	*S-adenosylmethionine decarboxylase proenzyme*	TC449066	TaMIR1120
	O-methyltransferase family protein	CA616203	TaMIR1123
	Isopentenyl pyrophosphate isomerase IDI2	TC400842	TaMIR1134
Development (1)	*Cell division membrane protein*	TC411782	TaMIR1123
Defense response (1)	*Catalase-1*	TC372427	TaMIR1121
Unknown function (11)	*OJ000126_13.4 protein*	CJ572772	TaMIR1120
	Os01g0588700 protein	TC393660	TaMIR1120
	Os03g0188500 protein	BE516383	TaMIR1120
	Os01g0916300 protein	TC377671	TaMIR1121
	Chromosome undetermined SCAF15013	TC426178	TaMIR1121
	Os01g0708900 protein	TC373584	TaMIR1123

	Chromosome chr8 scaffold_106	TC445329	TaMIR1134
	Predicted protein	CD454365	TaMIR1134
	Expressed protein	CA698436	TaMIR1134
	LigA	TC443552	TaMIR1134
	Chromosome chr4 scaffold_6	TC400050	TaMIR1134
To be annotated (4)	Annotation not available	CA696517	TaMIR1121
	Annotation not available	CV774411	TaMIR1121
	Annotation not available	CJ724067	TaMIR1123
	Annotation not available	CN011842	TaMIR1134

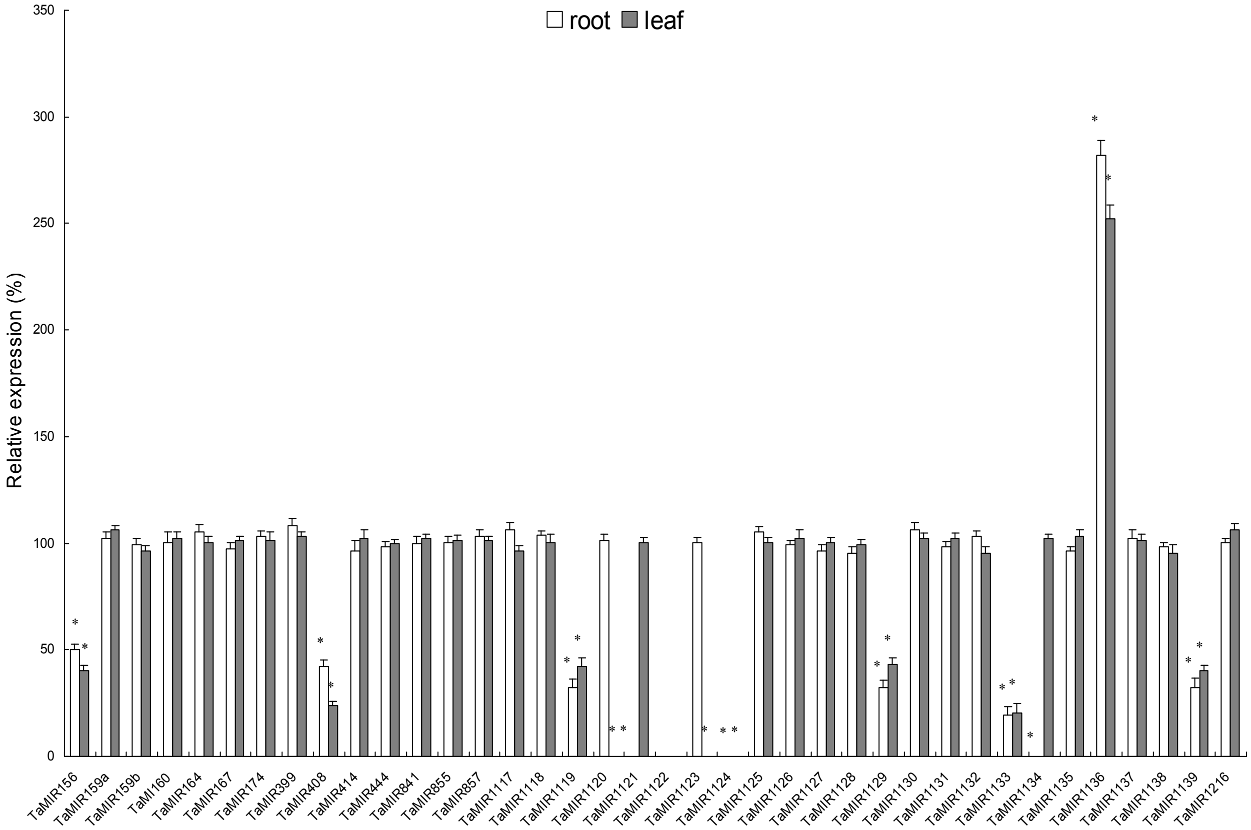

Fig. 1 Suppl. Expression patterns of TaMIRs in roots and leaves under conditions of normal growth and of drought stress. The relative expressions are expressed by ratios between the expression levels under the drought stress conditions with those under the normal growth conditions. The *bars* represent SEs of three independent assays of qPCR, and the symbol * stands for significance of differences at $P \leq 0.01$.

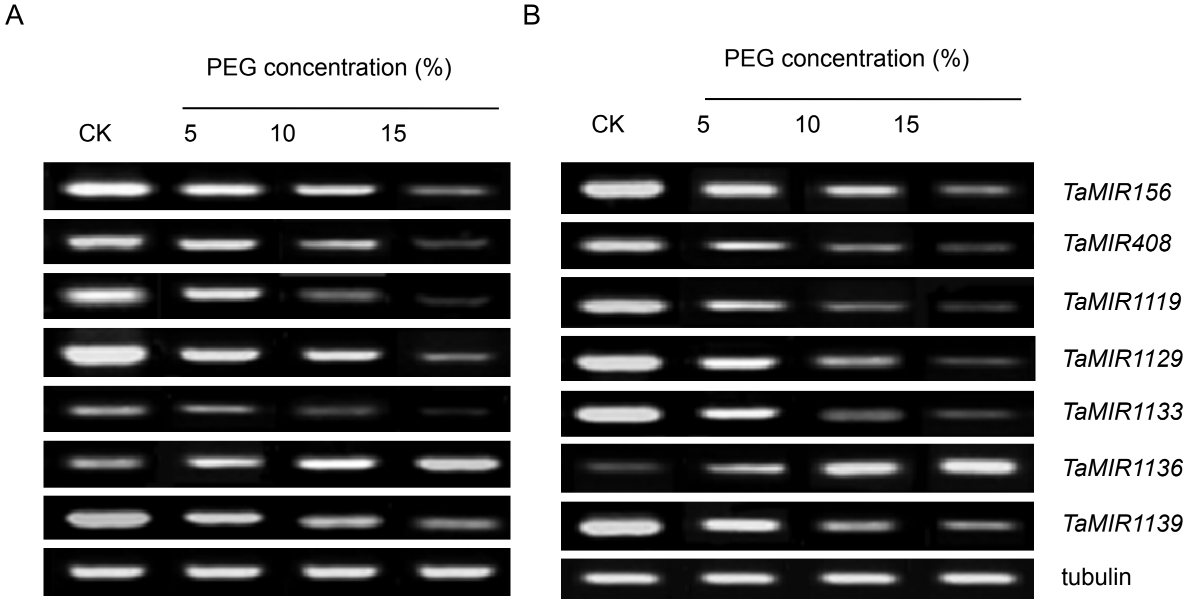

Fig. 2 Suppl. Expression patterns of drought-responsive TaMIRs in roots and leaves detected by semiquantative RT-PCR under conditions of normal growth and various drought stresses (*A* - roots, *B* - leaves; CK - the control group (normal growth conditions).

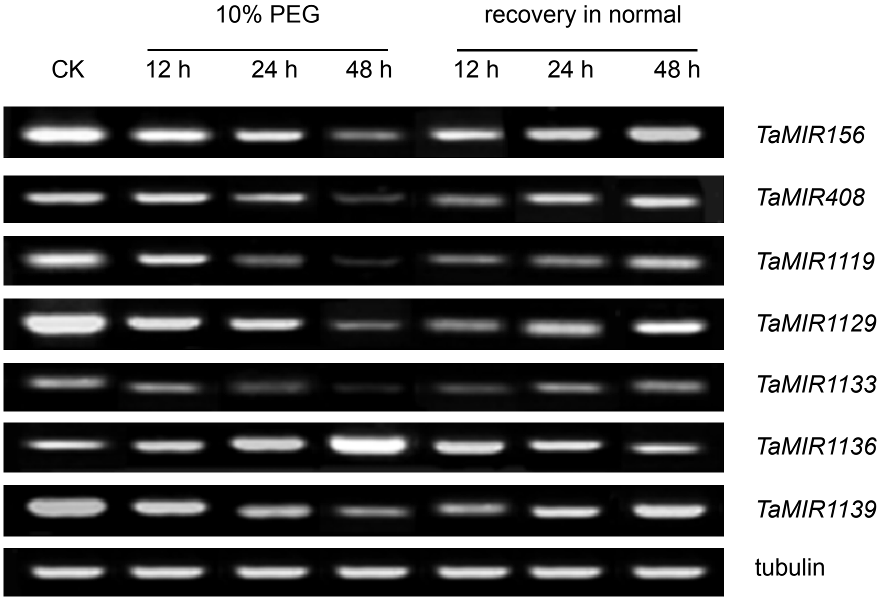

Fig. 3 Suppl. Expression patterns of drought-responsive TaMIRs in roots and leaves detected by semiquantative RT-PCR across regimes of drought induction and normal growth recovery (CK - the control group (normal growth condition).

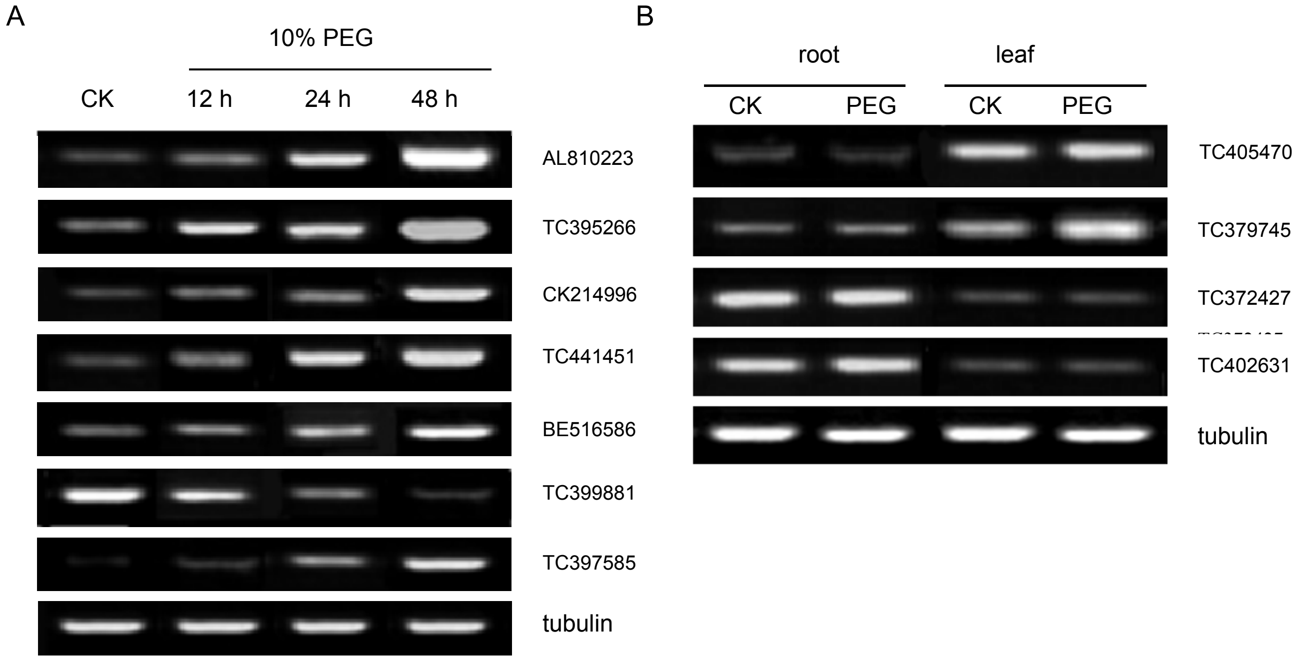

Fig. 4 Suppl. Expression patterns of target genes regulated by drought-responsive and tissue-predominat TaMIRs and detected by semiquantitative RT-PCR (*A* - expression patterns of target genes regulated by drought-responsible TaMIRs at different times of drought induction; *B* - expression patterns of target genes regulated by root- and leaf-predominant TaMIRs. In ***A***: AL810223 (*squamosa promoter-binding-like protein 16*), TC395266 (*ORF1 protein*), CK214996 (*DEAD/DEAH box helicase*), TC441451 (*major facilitator family transporter*), BE516586 (*calmodulin-like protein*), TC399881 (*endo-1,4-beta-glucanase*), TC397585 (*transcription factor Myb1*). In *B*: CK and PEG stand for normal growth conditions and a drought stress, respectively. R/L stands for root divided by leaf. TC405470 (*protein translation factor SUI1 homolog*), TC372427 (*catalase-1*), TC379745 (*WRKY DNA binding domain*), and TC402631 (*receptor-like protein kinase*).