SUPPLEMENTAL MATERIAL

Supplemental Figures

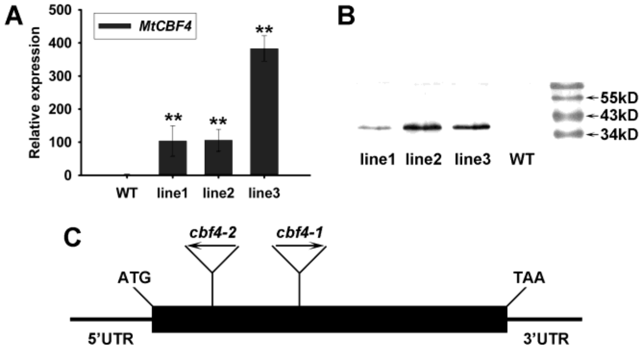

Figure S1. qRT-PCR and western blot analysis of Pro35S:MtCBF4 transgenic *M. truncatula* plants. (A) qRT-PCR analysis of *MtCBF4* expression in wild-type (WT) and Pro35S:MtCBF4:3xFLAG *M. truncatula* plants (T1 generation). The *MtActin* gene was used as a reference gene. Data represent the mean and SD for three independent replicates (Kruskal-Wallis non-parametric test, $^{**}P < 0.01$, $^{*}P < 0.05$). (B) Western blot analysis of Pro35S:MtCBF4:3xFLAG transgenic *M. truncatula* plants (T1 generation). An anti-FLAG antibody was used. (C) The *Tnt1* insertion sites in the *MtCBF4* gene are indicated for *cbf4-1* and *cbf4-2* mutant alleles.

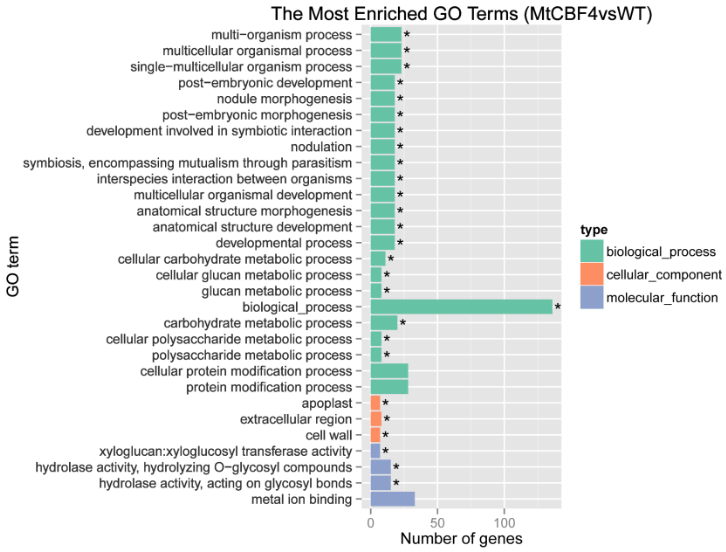

Figure S2. Functional category enrichment analysis of differentially expressed genes based on GO terms.

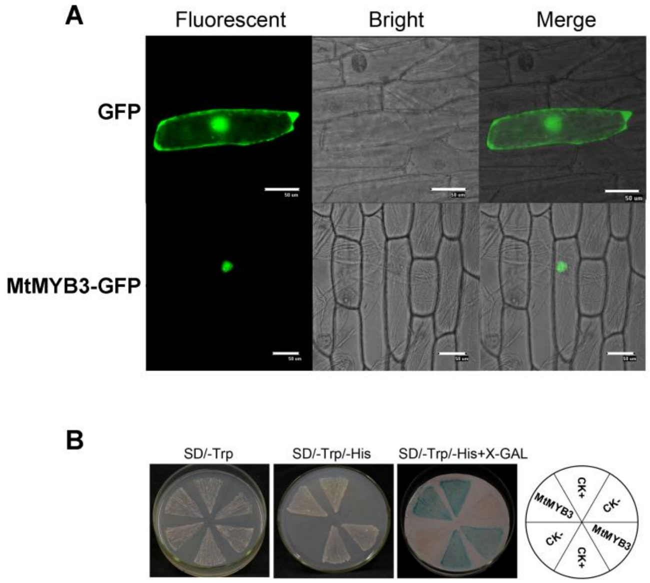

Figure S3. **Subcellular localization and transcriptional activation analysis of MtMYB3.** (A) Subcellular localization of MtMYB3. A Pro35S:MtMYB3:GFP construct was bombarded into onion epidermal cells with DNA-coated gold particles, and GFP expression was visualized after 16 h. Cells expressing GFP alone were used as control. Bars = 50 μm. (B) Transcriptional activation analysis of MtMYB3 in yeast. Yeast cells transformed with pBD GAL4-MtMYB3 (MtMYB3), pBD GAL4 empty vector (CK-, negative control), and pGAL4 vector (CK+, positive control) were grown on a SD/-Trp medium, or on a SD/-Trp/-His selective medium with or without X-GAL.

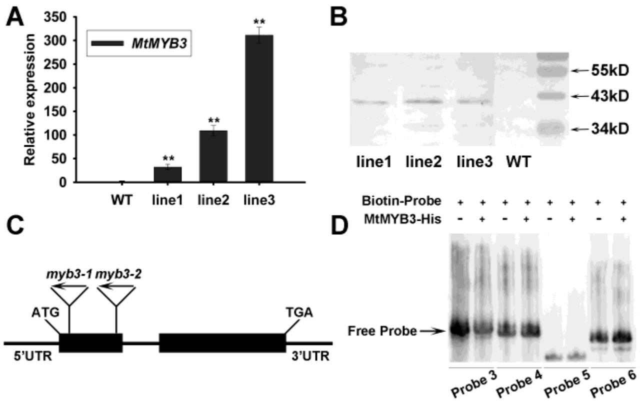

Figure S4. qRT-PCR and western blot analysis of Pro35S:MtMYB3 transgenic *M. truncatula* plants. (A) qRT-PCR analysis of *MtMYB3* expression in wild-type (WT) and Pro35S:MtMYB3:3xFLAG *M. truncatula* plants (T1 generation). The *MtActin* gene was used as a reference gene. Data represent the mean and SD for three independent replicates (Kruskal-Wallis non-parametric test, $^{**}P < 0.01$, $^{*}P < 0.05$).(B) Western blot analysis of Pro35S:MtMYB3:3xFLAG transgenic *M. truncatula* plants (T1 generation). (C) The *Tnt1* insertion sites in the *MtMYB3* gene are indicated for *myb3-1* and *myb3-2* mutant alleles. (D) EMSA assay for MtMYB3 interaction with MYB *cis*-elements from the promoter of *MtCBF4* except probe 1 and 2 (shown in Fig. 4A), corresponding to probes 3 to 6.

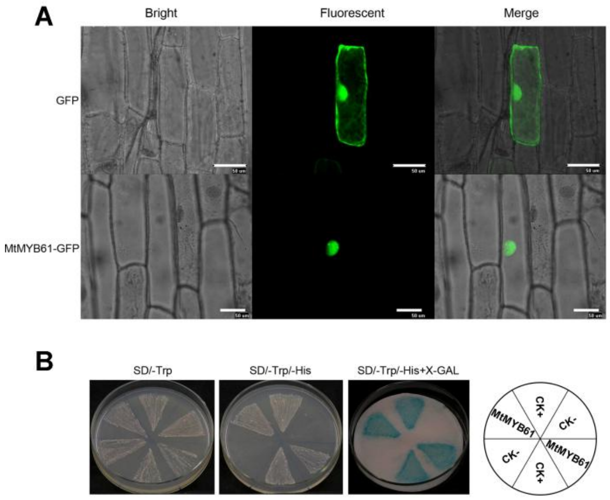

Figure S5. Subcellular localization and transcriptional activation analysis of MtMYB61. (A) Subcellular localization of MtMYB61-GFP. A Pro35S:MtMYB61:GFP construct was bombarded into onion epidermal cells with DNA-coated gold particles, and GFP expression was visualized after 16 h. Cells expressing GFP alone were used as control. Bars = 50 μm. (B) Transcriptional activation analysis of MtMYB61 in yeast. Yeast cells transformed with pBD GAL4-MtMYB61 (MtMYB61), pBD GAL4 empty vector (CK-, negative control), and pGAL4 vector (CK+, positive control) were grown on a SD/-Trp medium, or on a SD/-Trp/-His selective medium with or without X-GAL.

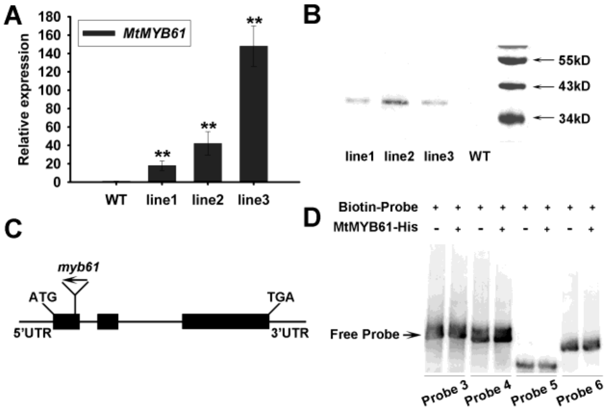

Figure S6. qRT-PCR and western blot analysis of Pro35S:MtMYB61 transgenic *M. truncatula* plants. (A) qRT-PCR analysis of *MtMYB61* expression in wild type (WT) and Pro35S:MtMYB61:3xFLAG *M. truncatula* plants (T1 generation). The *MtActin* gene was used as a reference gene. Data represent the mean and SD for three independent replicates (Kruskal-Wallis non-parametric test, **P < 0.01, *P < 0.05). (B) Western blot analysis of Pro35S:MtMYB61:3xFLAG transgenic *M. truncatula* plants (T1 generation). (C) The *Tnt1* insertion site in the *MtMYB61* gene is indicated for the *myb61* mutant allele. (D) EMSA assay for MtMYB61 interaction with MYB *cis*-elements from the promoter of *MtCBF4* except probe 1 and 2 (shown in Fig. 10A), corresponding to probes 3 to 6.

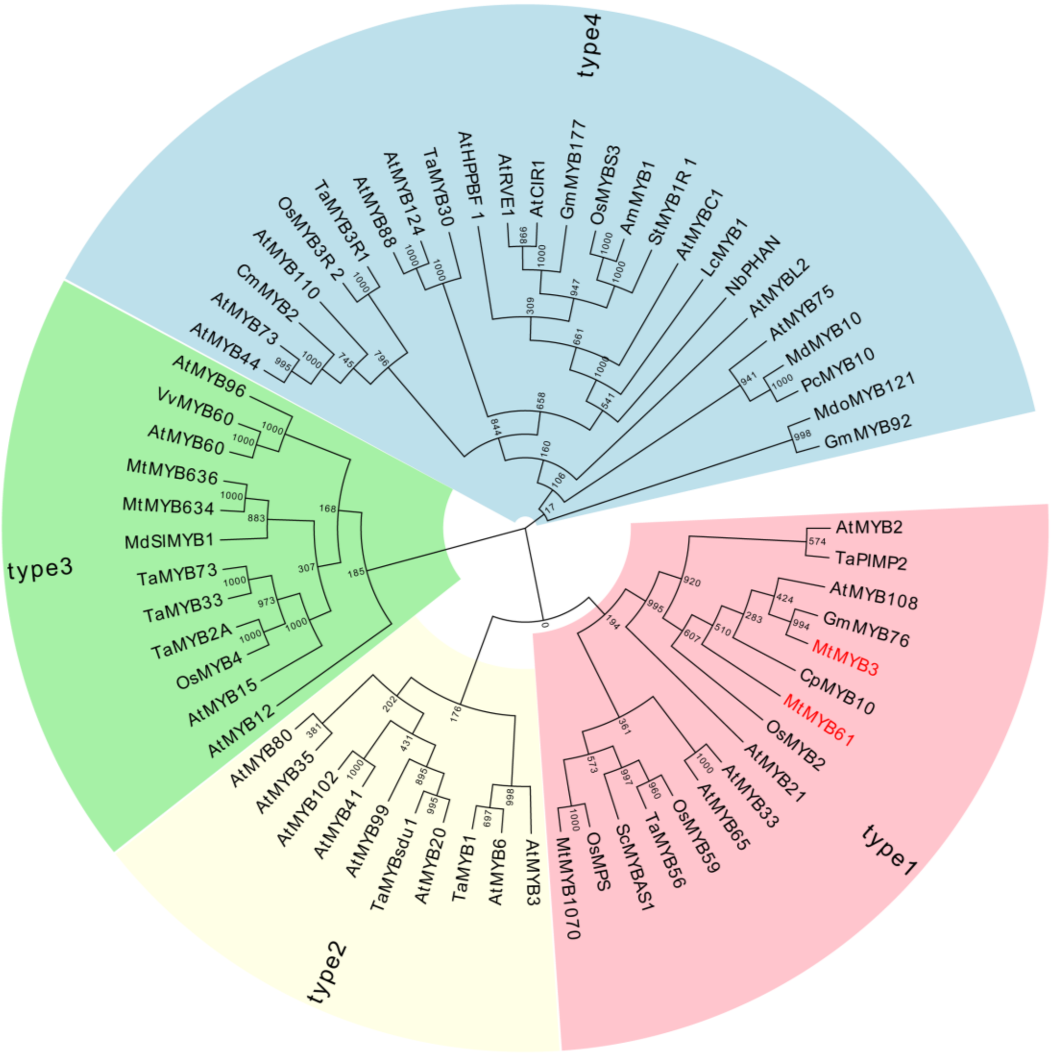

Figure S7. Phylogenetic analysis of selected MYB transcription factors involved in abiotic stress from *Arabidopsis thaliana*, *Malus domestica*, *Oryza sativa*, *Triticum aestivum*, *Nicotiana benthamiana*, *Vitis vinifera*, *Solanum tuberosum*, *Chrysanthemum*, *Glycine max*, *Avicennia marina*, *Leymus chinensis*, *Pyrus communis*, *Craterostigma plantagineum*, *Saccharum officinarum* and *Medicago truncatula*.

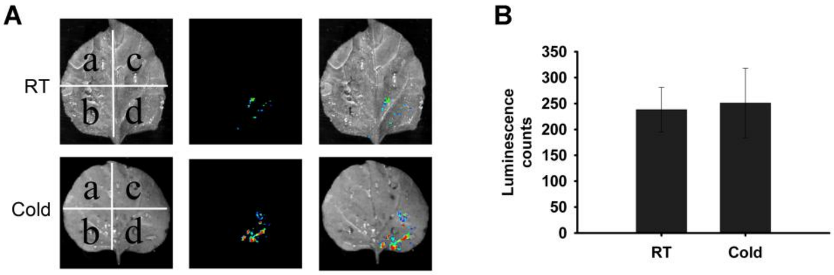

Figure S8. Cold does not affect the interaction between MtMYB3 and MtMYB61. (A) Tobacco leaves were co-transformed with the vector cLUC and the control vector nLUC (1), MtMYB3:cLUC and nLUC (2), MtMYB61:nLUC and cLUC (3), or MtMYB61:nLUC and MtMYB3:cLUC (4). Leaves were maintained at 4°C for 2h (Cold) or at Room Temperature (RT) before imaging. (B) Quantification of the luciferase activity. The mean values and SD were calculated from the results of three replicated experiments. No significant difference between RT and Cold conditions was detected.

Supplemental Table

Supplemental Table 1. List of differentially expressed genes between WT and 35S:MtCBF4 transgenic plants.

Up-regulated genes in MtCBF4 overexpressing lines	
Gene ID	**Annotation**
AC233660_22	-//-
Medtr1g092630	-//-
Medtr2g014050	sp|Q8SVY9|Y3G1_ENCCU Uncharacterized protein ECU03_1610 OS=Encephalitozoon cuniculi (strain GB-M1) GN=ECU03_1610 PE=1 SV=1//3.38195e-07
Medtr4g058610	-//-
Medtr4g115940	-//-
Medtr6g044390	sp|Q9STX9|TIP51_ARATH Probable aquaporin TIP5-1 OS=Arabidopsis thaliana GN=TIP5-1 PE=2 SV=1//2.81001e-35
Medtr1g101600	sp|Q9M0L0|DRE1A_ARATH Dehydration-responsive element-binding protein 1A OS=Arabidopsis thaliana GN=DREB1A PE=1 SV=2//1.39545e-59
Medtr4g035490	sp|Q9C809|B3GT8_ARATH Probable beta-1,3-galactosyltransferase 8 OS=Arabidopsis thaliana GN=B3GALT8 PE=2 SV=1//0
Medtr1g071850	sp|Q9S7C9|ESCA_ARATH Putative DNA-binding protein ESCAROLA OS=Arabidopsis thaliana GN=ESC PE=2 SV=1//4.82879e-09
Medtr8g005450	-//-
Medtr8g055900	-//-
Medtr7g109740	-//-
Medtr1g080340	sp|Q8W595|SUVR4_ARATH Histone-lysine N-methyltransferase SUVR4 OS=Arabidopsis thaliana GN=SUVR4 PE=2 SV=2//7.73706e-18
Medtr4g078690	sp|P98205|ALA2_ARATH Phospholipid-transporting ATPase 2 OS=Arabidopsis

	thaliana GN=ALA2 PE=1 SV=1//2.14139e-10
Medtr7g111460	-//-
Medtr3g116870	-//-
Medtr1g080080	-//-
Medtr4g082900	-//-
Medtr7g098760	sp|Q76CU2|PDR1_TOBAC Pleiotropic drug resistance protein 1 OS=Nicotiana tabacum GN=PDR1 PE=2 SV=1//6.33562e-08
Medtr8g094120	-//-
Medtr8g036590	-//-
Medtr3g030400	-//-
Medtr3g085150	-//-
Medtr8g077530	-//-
Medtr5g054560	sp|P49690|RL23_ARATH 60S ribosomal protein L23 OS=Arabidopsis thaliana GN=RPL23A PE=2 SV=3//1.15195e-13
AC233112_1016	-//-
Medtr4g012390	-//-
Medtr3g041540	sp|Q9FT70|RQL4B_ARATH ATP-dependent DNA helicase Q-like 4B OS=Arabidopsis thaliana GN=RECQL4B PE=2 SV=1//5.1528e-09
Medtr1g015480	sp|Q9SMY8|FBL15_ARATH F-box/LRR-repeat protein 15 OS=Arabidopsis thaliana GN=FBL15 PE=1 SV=2//0
Medtr2g086350	-//-
Medtr2g018710	-//-
Medtr5g040970	-//-
Medtr7g073430	sp|Q9LY00|WRK70_ARATH Probable WRKY transcription factor 70 OS=Arabidopsis thaliana GN=WRKY70 PE=2 SV=1//2.06495e-10
Medtr7g093820	sp|P13240|DR206_PEA Disease resistance response protein 206 OS=Pisum sativum GN=PI206 PE=2 SV=2//7.96129e-10

Medtr5g093210	-//-
Medtr1g082310	sp|Q8RXC8|RBK2_ARATH Receptor-like cytosolic serine/threonine-protein kinase RBK2 OS=Arabidopsis thaliana GN=RBK2 PE=1 SV=1//7.23689e-08
Medtr7g025130	-//-
Medtr2g008430	sp|Q9ZQI7|ALD1_ARATH Aminotransferase ALD1 OS=Arabidopsis thaliana GN=ALD1 PE=2 SV=2//0
Medtr6g008650	sp|O49858|C82A3_SOYBN Cytochrome P450 82A3 OS=Glycine max GN=CYP82A3 PE=2 SV=1//0
Medtr3g030540	sp|Q9SFB7|QRT2_ARATH Polygalacturonase QRT2 OS=Arabidopsis thaliana GN=QRT2 PE=1 SV=2//9.67049e-132
AC233679_12	-//-
Medtr3g100270	sp|O95239|KIF4A_HUMAN Chromosome-associated kinesin KIF4A OS=Homo sapiens GN=KIF4A PE=1 SV=3//2.11929e-09
Medtr4g082880	-//-
Medtr1g043930	sp|Q9SX31|PERK9_ARATH Proline-rich receptor-like protein kinase PERK9 OS=Arabidopsis thaliana GN=PERK9 PE=2 SV=1//1.73124e-15
AC235674_16	sp|Q04980|LTI65_ARATH Low-temperature-induced 65 kDa protein OS=Arabidopsis thaliana GN=LTI65 PE=2 SV=2//1.17211e-08
Medtr4g128580	sp|Q38910|XTH23_ARATH Probable xyloglucan endotransglucosylase/hydrolase protein 23 OS=Arabidopsis thaliana GN=XTH23 PE=2 SV=1//1.38281e-141
Medtr1g075030	-//-
Medtr5g047070	sp|Q9SCZ4|FERON_ARATH Receptor-like protein kinase FERONIA OS=Arabidopsis thaliana GN=FER PE=1 SV=1//1.01907e-160
Medtr2g009840	sp|Q6Z6W2|MAD57_ORYSJ MADS-box transcription factor 57 OS=Oryza sativa subsp. japonica GN=MADS57 PE=2 SV=2//8.23177e-32
Medtr8g014760	sp|C0LGD6|Y1570_ARATH Probable LRR receptor-like serine/threonine-protein

	kinase At1g05700 OS=Arabidopsis thaliana GN=At1g05700 PE=2 SV=1//0
Medtr3g086440	sp|Q94BZ1|ZIFL1_ARATH Protein ZINC INDUCED FACILITATOR-LIKE 1 OS=Arabidopsis thaliana GN=ZIFL1 PE=2 SV=1//7.17673e-169
Medtr4g054920	sp|O81117|C94A1_VICSA Cytochrome P450 94A1 OS=Vicia sativa GN=CYP94A1 PE=2 SV=2//7.89216e-131
Medtr2g014760	sp|Q9SGP6|GRXC9_ARATH Glutaredoxin-C9 OS=Arabidopsis thaliana GN=GRXC9 PE=1 SV=1//7.89273e-39
Medtr3g077870	sp|Q9ZUD9|SRO2_ARATH Probable inactive poly [ADP-ribose] polymerase SRO2 OS=Arabidopsis thaliana GN=SRO2 PE=1 SV=1//1.13472e-59
Medtr8g079360	sp|Q9FKZ1|DRL42_ARATH Probable disease resistance protein At5g66900 OS=Arabidopsis thaliana GN=At5g66900 PE=2 SV=1//8.26087e-119
Medtr7g111380	sp|Q0DKW8|LTI6B_ORYSJ Hydrophobic protein LTI6B OS=Oryza sativa subsp. japonica GN=LTI6B PE=2 SV=1//4.56312e-14
Medtr5g037610	sp|Q40392|TMVRN_NICGU TMV resistance protein N OS=Nicotiana glutinosa GN=N PE=1 SV=1//1.55164e-42
Medtr5g064360	-//-
Medtr5g083500	-//-
Medtr3g028490	-//-
AC233682_15	-//-
Medtr4g068520	sp|O23164|CRPM4_ARATH Cold-regulated 413 plasma membrane protein 4 OS=Arabidopsis thaliana GN=At4g37220 PE=2 SV=2//2.25242e-37
Medtr8g041820	sp|O64774|Y1146_ARATH G-type lectin S-receptor-like serine/threonine-protein kinase At1g61460 OS=Arabidopsis thaliana GN=At1g61460 PE=2 SV=4//4.62315e-34
Medtr1g075230	-//-
Medtr5g063080	sp|Q6ZGP8|TPP4_ORYSJ Probable trehalose-phosphate phosphatase 4 OS=Oryza sativa subsp. japonica GN=TPP4 PE=2 SV=1//6.9355e-102

Medtr5g087080	sp|Q9C9H7|RLP12_ARATH Receptor-like protein 12 OS=Arabidopsis thaliana GN=RLP12 PE=2 SV=2//9.33685e-08
Medtr8g038100	sp|P08688|ALB2_PEA Albumin-2 OS=Pisum sativum PE=2 SV=1//2.46384e-81
Medtr6g045200	sp|Q9FLV9|SLAH3_ARATH S-type anion channel SLAH3 OS=Arabidopsis thaliana GN=SLAH3 PE=1 SV=1//0
Medtr5g062370	sp|Q9SGZ5|BXL7_ARATH Probable beta-D-xylosidase 7 OS=Arabidopsis thaliana GN=BXL7 PE=2 SV=2//1.50151e-07
Medtr8g013610	sp|Q9SXB8|Y1133_ARATH G-type lectin S-receptor-like serine/threonine-protein kinase At1g11330 OS=Arabidopsis thaliana GN=At1g11330 PE=1 SV=3//8.49967e-12
Medtr3g101260	-//-
Medtr2g011210	sp|O81906|B120_ARATH G-type lectin S-receptor-like serine/threonine-protein kinase B120 OS=Arabidopsis thaliana GN=B120 PE=1 SV=1//6.94318e-16
Medtr2g089140	sp|Q8LDW9|XTH9_ARATH Xyloglucan endotransglucosylase/hydrolase protein 9 OS=Arabidopsis thaliana GN=XTH9 PE=2 SV=2//3.1067e-64
Medtr1g045610	sp|Q9LK95|MYB21_ARATH Transcription factor MYB21 OS=Arabidopsis thaliana GN=MYB21 PE=1 SV=1//3.89015e-15
Medtr3g084630	sp|P35694|BRU1_SOYBN Brassinosteroid-regulated protein BRU1 OS=Glycine max PE=2 SV=1//1.94135e-37
Medtr5g035980	sp|Q8YRI1|YY46_NOSS1 Uncharacterized WD repeat-containing protein alr3466 OS=Nostoc sp. (strain PCC 7120 / UTEX 2576) GN=alr3466 PE=4 SV=1//1.34363e-13
Medtr7g086340	-//-
Medtr8g037670	sp|P08688|ALB2_PEA Albumin-2 OS=Pisum sativum PE=2 SV=1//3.13971e-84
Medtr4g082990	sp|Q96558|UGDH_SOYBN UDP-glucose 6-dehydrogenase OS=Glycine max PE=2 SV=1//7.24654e-90
Medtr2g088000	sp|Q9C519|WRKY6_ARATH WRKY transcription factor 6 OS=Arabidopsis

	thaliana GN=WRKY6 PE=1 SV=1//3.75511e-88
Medtr7g111350	sp|Q9ZNS6|RCI2B_ARATH Hydrophobic protein RCI2B OS=Arabidopsis thaliana GN=RCI2B PE=2 SV=1//6.52392e-25
Medtr3g008920	sp|P49173|NIP1_NICAL Probable aquaporin NIP-type OS=Nicotiana alata PE=2 SV=1//2.7168e-104
Medtr1g104890	sp|Q8GYA4|CRK10_ARATH Cysteine-rich receptor-like protein kinase 10 OS=Arabidopsis thaliana GN=CRK10 PE=1 SV=3//1.53087e-11
AC151738_9	sp|Q40392|TMVRN_NICGU TMV resistance protein N OS=Nicotiana glutinosa GN=N PE=1 SV=1//2.50303e-84
Medtr5g074600	sp|B6VJS4|ROMT_VITVI Trans-resveratrol di-O-methyltransferase OS=Vitis vinifera GN=ROMT PE=1 SV=2//2.02706e-137
Medtr4g100950	sp|F4JMI5|GUX7_ARATH Putative glucuronosyltransferase PGSIP7 OS=Arabidopsis thaliana GN=PGSIP7 PE=3 SV=1//6.50111e-18
Medtr1g025250	sp|Q93X17|SNAK2_SOLTU Snakin-2 OS=Solanum tuberosum GN=SN2 PE=1 SV=1//3.5008e-24
Medtr1g081240	sp|O23969|SF21_HELAN Pollen-specific protein SF21 OS=Helianthus annuus GN=SF21 PE=2 SV=1//5.41644e-08
Medtr5g014090	sp|Q9FUR2|IP5P2_ARATH Type I inositol 1,4,5-trisphosphate 5-phosphatase 2 OS=Arabidopsis thaliana GN=IP5P2 PE=1 SV=2//0
Medtr1g031520	sp|Q9FID6|Y5392_ARATH Probable receptor-like protein kinase At5g39020 OS=Arabidopsis thaliana GN=At5g39020 PE=2 SV=1//6.5193e-91
Medtr8g091390	sp|P24792|ASO_CUCMA L-ascorbate oxidase OS=Cucurbita maxima GN=AAO PE=1 SV=2//0
CU651566_11	sp|Q9Y7K5|YGI3_SCHPO Uncharacterized WD repeat-containing protein C2A9.03 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=SPBC2A9.03 PE=2 SV=2//1.37559e-40
Medtr5g070490	sp|Q7XA42|RGA1_SOLBU Putative disease resistance protein RGA1

	OS=Solanum bulbocastanum GN=RGA1 PE=2 SV=2//0
Medtr6g025680	-//-
Medtr3g041560	sp|Q9C7S5|PSYR1_ARATH Tyrosine-sulfated glycopeptide receptor 1 OS=Arabidopsis thaliana GN=PSYR1 PE=2 SV=1//1.58416e-48
Medtr3g077630	-//-
Medtr7g111770	-//-
Medtr5g062650	sp|Q9SGZ5|BXL7_ARATH Probable beta-D-xylosidase 7 OS=Arabidopsis thaliana GN=BXL7 PE=2 SV=2//0
Medtr5g070480	sp|Q0WNJ6|CLAH1_ARATH Clathrin heavy chain 1 OS=Arabidopsis thaliana GN=CHC1 PE=1 SV=1//6.02121e-09
Medtr4g124320	-//-
AC235674_10	sp|C0LGQ5|GSO1_ARATH LRR receptor-like serine/threonine-protein kinase GSO1 OS=Arabidopsis thaliana GN=GSO1 PE=2 SV=1//1.00512e-26
Medtr4g063240	sp|Q9LQQ4|H2B1_ARATH Histone H2B.1 OS=Arabidopsis thaliana GN=At1g07790 PE=1 SV=3//1.80431e-59
Medtr6g031090	sp|Q9SSA7|GLIP5_ARATH GDSL esterase/lipase 5 OS=Arabidopsis thaliana GN=GLIP5 PE=2 SV=2//2.32255e-07
Medtr6g021900	-//-
Medtr5g010830	sp|Q9SIA3|MATE6_ARATH MATE efflux family protein 6 OS=Arabidopsis thaliana GN=DTXL2 PE=2 SV=2//9.89743e-79
Medtr1g098140	sp|P30075|CHS4_MEDSA Chalcone synthase 4 OS=Medicago sativa GN=CHS4 PE=2 SV=2//0
Medtr7g073380	sp|Q9LY00|WRK70_ARATH Probable WRKY transcription factor 70 OS=Arabidopsis thaliana GN=WRKY70 PE=2 SV=1//5.07013e-11
Medtr3g028470	-//-
Medtr1g014320	sp|P93338|GAPN_NICPL NADP-dependent glyceraldehyde-3-phosphate dehydrogenase OS=Nicotiana plumbaginifolia GN=GAPN PE=2

	SV=1//1.09825e-13
Medtr4g094010	sp|Q8RXN0|AB11G_ARATH ABC transporter G family member 11 OS=Arabidopsis thaliana GN=ABCG11 PE=1 SV=1//0
Medtr1g098460	sp|Q70II3|EF110_ARATH Ethylene-responsive transcription factor ERF110 OS=Arabidopsis thaliana GN=ERF110 PE=2 SV=2//9.60079e-16
Medtr2g033820	sp|Q9FGZ4|WRK48_ARATH Probable WRKY transcription factor 48 OS=Arabidopsis thaliana GN=WRKY48 PE=2 SV=1//5.05395e-14
Medtr3g055380	sp|Q9XGY6|WAXS1_SIMCH Long-chain-alcohol O-fatty-acyltransferase OS=Simmondsia chinensis PE=1 SV=1//4.44066e-81
Medtr1g031650	-//-
Medtr5g062320	sp|Q9SGZ5|BXL7_ARATH Probable beta-D-xylosidase 7 OS=Arabidopsis thaliana GN=BXL7 PE=2 SV=2//1.89419e-07
Medtr2g042900	sp|Q9S7M2|TI10B_ARATH Protein TIFY 10B OS=Arabidopsis thaliana GN=TIFY10B PE=1 SV=1//1.66914e-33
Medtr1g090150	sp|Q9FQA3|GST23_MAIZE Glutathione transferase GST 23 OS=Zea mays PE=2 SV=1//5.9693e-66
Medtr5g023730	sp|F4HUK6|AAE1_ARATH Probable acyl-activating enzyme 1, peroxisomal OS=Arabidopsis thaliana GN=AAE1 PE=2 SV=1//2.18497e-174
Medtr6g088450	sp|Q8VZ80|PLT5_ARATH Polyol transporter 5 OS=Arabidopsis thaliana GN=PLT5 PE=1 SV=2//2.73902e-68
Medtr2g100490	sp|Q8S3D2|BH087_ARATH Transcription factor bHLH87 OS=Arabidopsis thaliana GN=BHLH87 PE=2 SV=1//1.5934e-63
Medtr7g089860	sp|O80669|SIB2_ARATH Sigma factor binding protein 2, chloroplastic OS=Arabidopsis thaliana GN=SIB2 PE=2 SV=1//2.66375e-08
Medtr3g064370	sp|Q8H191|PAO4_ARATH Probable polyamine oxidase 4 OS=Arabidopsis thaliana GN=PAO4 PE=1 SV=1//1.58298e-08
Medtr4g076640	-//-

Medtr8g069320	-//-
Medtr8g092590	sp|Q94JQ6|CESA6_ARATH Cellulose synthase A catalytic subunit 6 [UDP-forming] OS=Arabidopsis thaliana GN=CESA6 PE=1 SV=2//3.14126e-06
Medtr5g088990	-//-
Medtr8g069280	-//-
Medtr3g107730	sp|Q9SUU1|BOR7_ARATH Probable boron transporter 7 OS=Arabidopsis thaliana GN=BOR7 PE=2 SV=3//8.80234e-12
Medtr2g101590	sp|Q9M817|PTR6_ARATH Probable peptide transporter At1g52190 OS=Arabidopsis thaliana GN=At1g52190 PE=1 SV=1//0
Medtr6g072250	sp|Q40392|TMVRN_NICGU TMV resistance protein N OS=Nicotiana glutinosa GN=N PE=1 SV=1//2.4066e-07
Medtr7g093530	sp|Q38910|XTH23_ARATH Probable xyloglucan endotransglucosylase/hydrolase protein 23 OS=Arabidopsis thaliana GN=XTH23 PE=2 SV=1//7.38481e-149
Medtr7g023560	sp|Q9SLD4|ZAT11_ARATH Zinc finger protein ZAT11 OS=Arabidopsis thaliana GN=ZAT11 PE=2 SV=1//5.78802e-30
Medtr2g007960	sp|Q6J163|5NG4_PINTA Auxin-induced protein 5NG4 OS=Pinus taeda PE=2 SV=1//1.79172e-06
Medtr1g025950	sp|Q7XWU3|CADH6_ORYSJ Probable cinnamyl alcohol dehydrogenase 6 OS=Oryza sativa subsp. japonica GN=CAD6 PE=2 SV=2//8.10059e-173
Medtr6g007980	-//-
Medtr8g061110	sp|Q9LW83|CE101_ARATH G-type lectin S-receptor-like serine/threonine-protein kinase CES101 OS=Arabidopsis thaliana GN=CES101 PE=2 SV=2//7.7766e-07
Medtr2g069420	-//-
Medtr2g062410	-//-
Medtr6g086120	sp|Q9LHF1|LRX4_ARATH Leucine-rich repeat extensin-like protein 4

	OS=Arabidopsis thaliana GN=LRX4 PE=1 SV=1//0
Medtr3g019490	sp|O81832|Y4729_ARATH G-type lectin S-receptor-like serine/threonine-protein kinase At4g27290 OS=Arabidopsis thaliana GN=At4g27290 PE=2 SV=4//7.10829e-10
Medtr2g011170	sp|O81905|SD18_ARATH Receptor-like serine/threonine-protein kinase SD1-8 OS=Arabidopsis thaliana GN=SD18 PE=1 SV=1//0
Medtr5g018270	sp|P29162|ASOL_TOBAC L-ascorbate oxidase homolog OS=Nicotiana tabacum PE=2 SV=1//0
Medtr2g039780	sp|A2BW76|EFTS_PROM5 Elongation factor Ts OS=Prochlorococcus marinus (strain MIT 9515) GN=tsf PE=3 SV=1//1.8968e-52
Medtr5g036080	sp|P29136|MEP1_SOYBN Metalloendoproteinase 1 OS=Glycine max PE=1 SV=2//4.47403e-41
Medtr6g072310	sp|Q40392|TMVRN_NICGU TMV resistance protein N OS=Nicotiana glutinosa GN=N PE=1 SV=1//1.56301e-127
Medtr4g062330	sp|O35250|EXOC7_MOUSE Exocyst complex component 7 OS=Mus musculus GN=Exoc7 PE=1 SV=2//6.91472e-08
Medtr2g039770	sp|Q40392|TMVRN_NICGU TMV resistance protein N OS=Nicotiana glutinosa GN=N PE=1 SV=1//9.34088e-130
Medtr4g123990	sp|Q9FWX7|AB11B_ARATH ABC transporter B family member 11 OS=Arabidopsis thaliana GN=ABCB11 PE=2 SV=1//0
Medtr7g091200	sp|Q7XA42|RGA1_SOLBU Putative disease resistance protein RGA1 OS=Solanum bulbocastanum GN=RGA1 PE=2 SV=2//3.60056e-11
Medtr5g010730	sp|Q9FPR3|EDR1_ARATH Serine/threonine-protein kinase EDR1 OS=Arabidopsis thaliana GN=EDR1 PE=1 SV=1//1.73452e-26
Medtr7g038520	sp|Q40392|TMVRN_NICGU TMV resistance protein N OS=Nicotiana glutinosa GN=N PE=1 SV=1//8.94211e-34
Medtr8g104490	-//-

Medtr1g075480	sp|Q86TV6|TTC7B_HUMAN Tetratricopeptide repeat protein 7B OS=Homo sapiens GN=TTC7B PE=1 SV=3//4.64624e-13
Medtr2g088080	sp|Q00624|ASOL_BRANA L-ascorbate oxidase homolog OS=Brassica napus GN=Bp10 PE=2 SV=1//1.52559e-176
Medtr5g031310	sp|Q9ZRF1|MTDH_FRAAN Probable mannitol dehydrogenase OS=Fragaria ananassa GN=CAD PE=2 SV=1//2.8403e-14
Medtr3g094970	-//-
Medtr8g083150	sp|O23262|RLF32_ARATH Protein RALF-like 32 OS=Arabidopsis thaliana GN=RALFL32 PE=3 SV=1//1.38064e-22
Medtr3g049970	sp|Q9MB73|LGT_CITUN Limonoid UDP-glucosyltransferase OS=Citrus unshiu PE=2 SV=1//0
Medtr4g093580	sp|Q964D8|BUP1_DICDI Beta-ureidopropionase OS=Dictyostelium discoideum GN=pyd3 PE=1 SV=1//1.15546e-12
Medtr7g090420	-//-
Medtr3g008500	sp|O64896|TPPA_ARATH Trehalose-phosphate phosphatase A OS=Arabidopsis thaliana GN=TPPA PE=1 SV=1//1.53468e-17
Medtr5g029370	sp|Q9STM3|REF6_ARATH Lysine-specific demethylase REF6 OS=Arabidopsis thaliana GN=REF6 PE=1 SV=1//1.74015e-65
Medtr3g079340	-//-
Medtr1g097900	sp|P30075|CHS4_MEDSA Chalcone synthase 4 OS=Medicago sativa GN=CHS4 PE=2 SV=2//0
Medtr1g102240	-//-
Medtr1g019340	sp|Q9Y2H1|ST38L_HUMAN Serine/threonine-protein kinase 38-like OS=Homo sapiens GN=STK38L PE=1 SV=3//4.28874e-145
Medtr7g075910	sp|P93733|PLDB1_ARATH Phospholipase D beta 1 OS=Arabidopsis thaliana GN=PLDBETA1 PE=2 SV=4//0
Medtr2g012990	-//-

Medtr1g102360	sp|Q9STJ8|Y4539_ARATH Receptor-like serine/threonine-protein kinase At4g25390 OS=Arabidopsis thaliana GN=At4g25390 PE=1 SV=1//4.64923e-31
Medtr5g069600	sp|Q9FIL7|CRCK1_ARATH Calmodulin-binding receptor-like cytoplasmic kinase 1 OS=Arabidopsis thaliana GN=CRCK1 PE=1 SV=1//7.14883e-11
Medtr7g117890	sp|Q681N2|PUB15_ARATH U-box domain-containing protein 15 OS=Arabidopsis thaliana GN=PUB15 PE=2 SV=2//5.29736e-19
Medtr3g031220	sp|Q8S8P5|WRK33_ARATH Probable WRKY transcription factor 33 OS=Arabidopsis thaliana GN=WRKY33 PE=1 SV=2//3.04476e-16
Medtr5g062430	sp|Q9SGZ5|BXL7_ARATH Probable beta-D-xylosidase 7 OS=Arabidopsis thaliana GN=BXL7 PE=2 SV=2//0
Medtr3g084510	sp|P43298|TMK1_ARATH Probable receptor protein kinase TMK1 OS=Arabidopsis thaliana GN=TMK1 PE=2 SV=1//2.31987e-60
Medtr7g084250	sp|Q9LX66|HERK_ARATH Receptor-like protein kinase HERK 1 OS=Arabidopsis thaliana GN=HERK1 PE=1 SV=1//4.56205e-17
Medtr3g088970	sp|Q9SZX3|ASSY_ARATH Argininosuccinate synthase, chloroplastic OS=Arabidopsis thaliana GN=At4g24830 PE=2 SV=3//2.18452e-138
CU633465_13	sp|Q38909|XTH28_ARATH Probable xyloglucan endotransglucosylase/hydrolase protein 28 OS=Arabidopsis thaliana GN=XTH28 PE=2 SV=1//1.41362e-159
Medtr4g120760	sp|P17641|PRS1_SOLTU Pathogenesis-related protein STH-21 OS=Solanum tuberosum GN=STH-21 PE=2 SV=1//5.27338e-10
Medtr5g015590	sp|O81108|ACA2_ARATH Calcium-transporting ATPase 2, plasma membrane-type OS=Arabidopsis thaliana GN=ACA2 PE=1 SV=1//0

Down-regulated genes in MtCBF4 overexpressing lines

Gene ID	**Annotation**
Medtr4g080020	sp|Q9SIM9|ORE9_ARATH F-box protein ORE9 OS=Arabidopsis thaliana GN=ORE9 PE=1 SV=2//0

Medtr5g096530	sp|C0LGR3|Y4265_ARATH Probable LRR receptor-like serine/threonine-protein kinase At4g26540 OS=Arabidopsis thaliana GN=At4g26540 PE=1 SV=1//0
Medtr5g041700	sp|Q9C554|EXPA1_ARATH Expansin-A1 OS=Arabidopsis thaliana GN=EXPA1 PE=2 SV=1//1.46842e-06
Medtr8g087710	sp|P08995|NO26_SOYBN Nodulin-26 OS=Glycine max PE=1 SV=2//2.08445e-140
Medtr3g110420	sp|O80592|AAP8_ARATH Amino acid permease 8 OS=Arabidopsis thaliana GN=AAP8 PE=1 SV=1//1.4954e-91
Medtr3g073010	sp|Q920N2|BPL1_MOUSE Biotin--protein ligase OS=Mus musculus GN=Hlcs PE=1 SV=1//8.91162e-38
Medtr7g092580	-//-
Medtr5g033880	sp|Q9LDE3|FBK9_ARATH F-box/kelch-repeat protein At1g23390 OS=Arabidopsis thaliana GN=At1g23390 PE=2 SV=1//1.87865e-67
Medtr2g099790	-//-
Medtr5g072500	sp|Q2MHE4|HT1_ARATH Serine/threonine-protein kinase HT1 OS=Arabidopsis thaliana GN=HT1 PE=1 SV=1//4.73441e-10
Medtr5g026080	-//-
Medtr1g086380	sp|Q06GT0|PSBA_PIPCE Photosystem Q(B) protein OS=Piper cenocladum GN=psbA PE=3 SV=1//7.57385e-33
Medtr5g072455	-//-
Medtr6g057520	-//-
Medtr3g065690	-//-
Medtr3g079850	sp|O64774|Y1146_ARATH G-type lectin S-receptor-like serine/threonine-protein kinase At1g61460 OS=Arabidopsis thaliana GN=At1g61460 PE=2 SV=4//1.26825e-17
Medtr1g042940	-//-
Medtr4g050770	sp|P06585|PSBA_PEA Photosystem Q(B) protein OS=Pisum sativum GN=psbA

	PE=1 SV=3//2.39174e-70
Medtr6g078380	sp|Q7XKV4|BGL12_ORYSJ Beta-glucosidase 12 OS=Oryza sativa subsp. japonica GN=BGLU12 PE=2 SV=2//0
Medtr4g059900	-//-
Medtr1g080020	sp|Q9SPK4|PPCK1_ARATH Phosphoenolpyruvate carboxylase kinase 1 OS=Arabidopsis thaliana GN=PPCK1 PE=1 SV=1//1.91095e-110
Medtr7g071220	-//-
Medtr4g018675	-//-
Medtr3g062880	-//-
Medtr5g054900	sp|Q9SX27|PAN_ARATH Transcription factor PERIANTHIA OS=Arabidopsis thaliana GN=PAN PE=1 SV=1//1.2416e-100
Medtr5g062190	sp|A2RAR6|EXGA_ASPNC Probable glucan 1,3-beta-glucosidase A OS=Aspergillus niger (strain CBS 513.88 / FGSC A1513) GN=exgA PE=3 SV=1//1.79071e-19
Medtr7g077340	sp|Q8W4Y8|IBB_LENCU Bowman-Birk type proteinase inhibitor OS=Lens culinaris PE=1 SV=2//6.35597e-39
Medtr3g020920	-//-
Medtr2g035430	sp|O64759|CAAT5_ARATH Cationic amino acid transporter 5 OS=Arabidopsis thaliana GN=CAT5 PE=1 SV=1//2.48843e-107
Medtr3g021040	-//-
Medtr2g066235	-//-
Medtr3g085710	-//-
Medtr5g032030	sp|Q6SZ87|NAT11_ARATH Nucleobase-ascorbate transporter 11 OS=Arabidopsis thaliana GN=NAT11 PE=2 SV=1//2.78617e-08
Medtr7g102170	-//-
Medtr2g101410	sp|P87053|POF1_SCHPO F-box/WD repeat-containing protein pof1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=pof1 PE=1

	SV=1//3.07527e-09
Medtr1g072095	-//-
AC233577_31	sp|P45458|MASY_SOYBN Malate synthase, glyoxysomal (Fragment) OS=Glycine max PE=2 SV=1//1.50806e-60
Medtr3g080010	sp|Q69KJ0|RTL3_ORYSJ Ribonuclease 3-like protein 3 OS=Oryza sativa subsp. japonica GN=Os06g0358800 PE=2 SV=1//6.03713e-07
Medtr4g072980	sp|P33080|AX10A_SOYBN Auxin-induced protein X10A OS=Glycine max PE=2 SV=1//3.28902e-10
Medtr3g082050	sp|Q6L8G0|ZIP5_ORYSJ Zinc transporter 5 OS=Oryza sativa subsp. japonica GN=ZIP5 PE=2 SV=1//3.29281e-33
Medtr6g088320	sp|Q9SVV2|XTH26_ARATH Probable xyloglucan endotransglucosylase/hydrolase protein 26 OS=Arabidopsis thaliana GN=XTH26 PE=2 SV=1//3.50498e-135
Medtr3g077030	-//-
Medtr7g008970	-//-
Medtr5g065960	-//-
Medtr4g026570	-//-
Medtr5g074740	sp|P22195|PER1_ARAHY Cationic peroxidase 1 OS=Arachis hypogaea GN=PNC1 PE=1 SV=2//4.58101e-12
Medtr6g088140	sp|P38605|CAS1_ARATH Cycloartenol synthase OS=Arabidopsis thaliana GN=CAS1 PE=1 SV=2//1.03539e-32
Medtr4g057430	sp|P93046|XTH31_ARATH Probable xyloglucan endotransglucosylase/hydrolase protein 31 OS=Arabidopsis thaliana GN=XTH31 PE=2 SV=2//6.36393e-10
Medtr7g099200	-//-
Medtr7g102155	-//-
Medtr1g083020	sp|Q43191|LOX15_SOLTU Probable linoleate 9S-lipoxygenase 5 OS=Solanum

	tuberosum GN=LOX1.5 PE=2 SV=1//0
Medtr2g028580	sp|Q9LT96|Y5977_ARATH Probable leucine-rich repeat receptor-like protein kinase At5g49770 OS=Arabidopsis thaliana GN=At5g49770 PE=2 SV=1//0
Medtr6g006240	-//-
Medtr8g069250	-//-
Medtr2g008470	sp|P53392|SUT2_STYHA High affinity sulfate transporter 2 OS=Stylosanthes hamata GN=ST2 PE=2 SV=1//0
Medtr4g057450	sp|Q9SJL9|XTH32_ARATH Probable xyloglucan endotransglucosylase/hydrolase protein 32 OS=Arabidopsis thaliana GN=XTH32 PE=2 SV=1//7.13429e-47
Medtr8g102040	-//-
Medtr7g046365	-//-
Medtr5g078110	-//-
Medtr5g091180	sp|Q84WU2|UBP13_ARATH Ubiquitin carboxyl-terminal hydrolase 13 OS=Arabidopsis thaliana GN=UBP13 PE=1 SV=1//1.72842e-38
Medtr1g080440	sp|Q9FRS6|PXL1_ARATH Leucine-rich repeat receptor-like protein kinase PXL1 OS=Arabidopsis thaliana GN=PXL1 PE=2 SV=1//6.54401e-44
Medtr3g076920	-//-
Medtr4g022470	sp|O48850|VA725_ARATH Vesicle-associated membrane protein 725 OS=Arabidopsis thaliana GN=VAMP725 PE=2 SV=2//3.45125e-14

Supplemental Table 2. Oligonucleotide probes used in EMSA assays and the artificial fragment sequence used in Yeast one-hybrid assay.

Name	**Sequences (5'-3')**
MtCAS15-F	TTATTCACGTAAAAAATTGCCCACGTACCGACATACTGCGTACATTTTTTTCTTGGTAT
MtCAS15-R	ATACCAAGAAAAAAATGTACGCAGTATGTCGGTACGTGGGCAATTTTTTACGTGAATAA
MtCAS15 mu-F	TTATTCACGTAAAAAATTGCCCACGaaaaaaaaaACTGCGTACATTTTTTTCTTGGTAT
MtCAS15 mu-R	ATACCAAGAAAAAAATGTACGCAGTtttttttttCGTGGGCAATTTTTTACGTGAATAA
MtCBF4P1-F	GAAAATACCCCTGCGCTAGTTAACTAACGTAGGTATAAAATTAACATGAC
MtCBF4P1-R	GTCATGTTAATTTTATACCTACGTTAGTTAACTAGCGCAGGGGTATTTTC
MtCBF4P1-mF	GAAAATACCCCTGCGCTAGTggggggggGTAGGTATAAAATTAACATGAC
MtCBF4P1-mR	GTCATGTTAATTTTATACCTACCCCCCCCCACTAGCGCAGGGGTATTTTC
MtCBF4P2-F	AAAGTACCAAGTACTTACTAACCACACTGTTTTTCAACTAGTAGAATTATAACAAACTTTCCTTCTACTATTCTT
MtCBF4P2-R	AAGAATAGTAGAAGGAAAGTTTGTTATAATTCTACTAGTTGAAAAACAGTGTGGTTAGTAAGTACTTGGTACTTT
MtCBF4P2-mF	AAAGTACCAAGTACTTAGGGGGGGCACTGTTTTTCAACTAGTAGAATTAGGGGGGGCTTTCCTTCTACTATTCTT
MtCBF4P2-mR	AAGAATAGTAGAAGGAAAGCCCCCCCTAATTCTACTAGTTGAAAAACAGTGCCCCCCCTAAGTACTTGGTACTTT
MtCBF4P3-F	CATCACAACACAACCAAGCTCATATTAAATCTTAAAAAATTAAAAGCACGGTTATTAACAAACTACCGTGTTTTG
MtCBF4P3-R	CAAAACACGGTAGTTTGTTAATAACCGTGCTTTTAATTTTTTAAGATTTAATATGAGCTTGGTTGTGTTGTGATG
MtCBF4P4-F	AACTTTGTTTGGATACACGTTGAAATGAAACTAACATGCACTGTTCGGGTGGTATTGACAAAAAAACAAT
MtCBF4P4-R	ATTGTTTTTTTGTCAATACCACCCGAACAGTGCATGTTAGTTTCATTTCAACGTGTATCC

	AAACAAAGTT
MtCBF4P5-F	TGTCCCACATTCAATTCCTTAACCATAGTACATACCGTGG
MtCBF4P5-R	CCACGGTATGTACTATGGTTAAGGAATTGAATGTGGGACA
MtCBF4P6-F	GTTTAACCTAGCTATCGAATTAAAGAACCTCAAGTCATACAATTCGCAAACTTCAGTCT
MtCBF4P6-R	AGACTGAAGTTTGCGAATTGTATGACTTGAGGTTCTTTAATTCGATAGCTAGGTTAAAC
Y1HMYB-F	agcttTAGTTAACTAACGTAGGTTAGTTAACTAACGTAGGTTAGTTAACTAACGTAGGTc
Y1HMYB-R	tcgagACCTACGTTAGTTAACTAACCTACGTTAGTTAACTAACCTACGTTAGTTAACTAa

Underlined bases indicate the DRE or MYB *cis*-elements.

Supplemental Table 3. List of yeast two-hybrid assay clones identified with MtMYB3 protein as bait.

Accession	Annotation
EF468488	*Medicago truncatula* MYB transcription factor MYB61
XM_003592927	*Medicago truncatula* 2Fe-2S ferredoxin superfamily protein
XM_003594014	*Medicago truncatula* methionine sulfoxide reductase B
XM_003597038	*Medicago truncatula* cytochrome b6-F complex iron-sulfur subunit
XM_003592050	*Medicago truncatula* ABA/WDS induced protein
XM_003624441	*Medicago truncatula* basic helix loop helix protein BHLH23
XM_013594115	*Medicago truncatula* pyrroline-5-carboxylate reductase
XM_003612616	*Medicago truncatula* phosphoribulokinase
XM_003601109	*Medicago truncatula* pyruvate dehydrogenase E1 beta subunit
XM_003606315	*Medicago truncatula* zinc finger, C3HC4 type (RING finger) protein
XM_013601005	*Medicago truncatula* synaptotagmin
XM_003618130	*Medicago truncatula* polyribonucleotide nucleotidyltransferase
XM_003625029	*Medicago truncatula* N-acetyltransferase

Supplemental Table 4. Primers used in this study.

Primer Name	**Primer Sequences (5’-3’)**
For cloning and genotyping	
subcellular localization	
pE3025-*MtMYB5*-F	CTCGAGGATGGATACTAATTACAAAAC
pE3025-*MtMYB5*-R	GGTACCCACTCCAAATATCCTTGTCAT
pE3025-*MtMYB61*-F	CTCGAGGATGAGAGGTATGGATATTAA
pE3025-*MtMYB61*-R	GGTACCCCGCA AGTAAATTGTATTTTAT
Overexpression vector	
pMDC32-*MtCBF4*-F	GGTACCATGTTTACTATGAATCAATTTTCG
pMDC32-*MtCBF4*-R	CGATCGTAATTTATCATCATCATCTTTGTAATCGATGTCGTGGTCCTTATAGTCACCATCATGATCTTTGTAATCAAATGAGTAACTCCACAATGAAACT
pMDC32-*MtMYB3*-F	GGTACCATGGATACTAATTACAAA
pMDC32-*MtMYB3*-R	ACTAGTTCATTTATCATCATCATCTTTGTAATCGATGTCGTGGTCCTTATAGTCACCATCATGATCTTTGTAATCTAAATCATCAGCCAATTGTT
pMDC32-*MtMYB61*-F	GGTACCATGAGAGGTATGGATATTAAGGT
pMDC32-*MtMYB61*-R	CGATCGTCATTTATCATCATCATCTTTGTAATCGATGTCGTGGTCCTTATAGTCACCATCATGATCTTTGTAATCCGCAAGTAAATTGTATTTTATTTCA
Yeast-two-hybrid	
pGBKT7-*MtMYB61*-F	CATATGAGAGGTATGGATATTAAGGTTC
pGBKT7-*MtMYB61*-R	GTCGACTCACGCAAGTAAATTGTATTTTAT
pGADT7-*MtMYB3*-F	GAATTCATGGATACTAATTACAAAAC
pGADT7-*MtMYB3*-R	CTCGAGTCATAAATCATCAGCCAATT
pGADT7-*MtMYB3*N-F	CATATGGATACTAATTACAAAAC
pGADT7-*MtMYB3*N-R	CTCGAGTCACACCACTCTTGTTCTCCA
pGADT7-*MtMYB3*C-F	GAATTCATGGTGAAGCAAGCTAGGCAA

pGADT7-*MtMYB3*C-R	CTCGAGTCATAAATCATCAGCCAATT
Pull-down	
pGEX-4T-1-*MtMYB3*GST-F	GAATTCATGGATACTAATTACAAAACCAATA
pGEX-4T-1-*MtMYB3*GST-R	CTCGAGTCATAAATCATCAGCCAATTGTTGC
pET30a-*MtMYB61*His-F	CATATGAGAGGTATGGATATTAAGGTTC
pET30a-*MtMYB61*His-R	CTCGAGCGCAAGTAAATTGTATTTTATTTCA
Bimolecular Fluorescence Complementation	
pSY735-*MtMYB61*-F	TGCGTCGACCATGAGAGGTATGGATATTAAG
pSY735-*MtMYB61*-R	CTGACTAGTTCACGCAAGTAAATTGTATTTTATTTC
pSY736-*MtMYB3*-F	TGCGTCGACCATGGATACTAATTACAAAAC
pSY736-*MtMYB3*-R	CTGACTAGTTCATAAATCATCAGCCAATTG
Transient expression assays in *Nicotiana benthamiana* leaves	
pCAMBIA1381-ProMtCBF4LUC-F	GGATCCTGAATTGAATTTCAAGCACATGTGA
pCAMBIA1381-ProMtCBF4LUC-R	GTCGACGTTCCAAAAAAAAAAAAAAAAGAATAGTAG
Transactivation analyses in yeast	
pBD GAL4-*MtMYB3*-F	GAATTCATGGATACTAATTACAAAAC
pBD GAL4-*MtMYB3*-R	GTCGACTCATAAATCATCAGCCAATT
pBD GAL4-*MtMYB61*-F	CCCGGGGGATGAGAGGTATGGATATTAA
pBD GAL4-*MtMYB61*-R	GTCGACTCACGCAAGTAAATTGTATTTTAT
For Real-time PCR	
Gene expression	
MtCBF1-realtimeF	TTATTGGATGTGGATGATTTTG
MtCBF1-realtimeR	AAATTTCATTGGCTGGAAGG
MtCBF2-realtimeF	GACACGGCTATTTCCACCTC
MtCBF2-realtimeR	TTCCACAGTGATACCTCTTCATC
MtCBF3-realtimeF	AACCTGCAACTACTCAAGCAAA

MtCBF3-realtimeR	AGCGCCATATTACTCCACATC
MtCBF4-realtimeF	CGGAAGCAAGGGATATTCAA
MtCBF4-realtimeR	CAAATTCCACGTCAGCAACA
MtMYB3-realtimeF	CAATTACCGGGAAGAACCGACA
MtMYB3-realtimeR	GCAGTTGCACCAGAAGATTGGA
MtMYB61-realtimeF	TCCCCGACACGAATAATCCA
MtMYB61-realtimeR	ACAAGCACCGCTCTTCTCCT
MtCAS15-realtimeF	GAGAACACCACGGTGAGTACAA
MtCAS15-realtimeR	CATGTTCATGACCCTCTCCA
MtLTI65-realtimeF	CAATGCGAATAGTTCAGGAAAA
MtLTI65-realtimeR	GTGTCCTTCCTTCATCCACAC
MtLTI6A-realtimeF	ATTCTTGCCATCATCCTTCC
MtLTI6A-realtimeR	AATGACGCCCCTGACAAAC
MtLTI6B-realtimeF	GGGCACAGCTACCTTCGTT
MtLTI6B-realtimeR	AAAGGGTGAGCACCAAACAG
MtCOR413-realtimeF	GCTGGGGAGGTTCTTTCTTT
MtCOR413-realtimeR	CAACCAATCAGGGAAATGCT
MtYGI3-realtimeF	ATTCCCAAGTTCGGGTTTTT
MtYGI3-realtimeR	CCAAGTGCCCTTTTAGGTTTC
MtYY46-realtimeF	CAAGACCCAGACGACGAAA
MtYY46-realtimeR	ACCTTGCAAAACAGCCAAAC
MtActin-realtimeF	CCCACTGGATGTCTGTAGGTT
MtActin-realtimeR	AGAATTAAGTAGCAGCGCAAA
ChIP-qPCR	
MtCAS15-ChIP-qPCRF1	CACCTTAATTTTGTCCAAGAGG
MtCAS15-ChIP-qPCRR1	GGGGAACGAGTGAAGAACAA
MtCAS15-ChIP-qPCRF2	CACCTGCTCTCTAATTTATTCACG

MtCAS15-ChIP-qPCRR2	TCCAGATCTACAATTGCTCTCAA
MtCAS15-ChIP-qPCRF3	GGCTCCAAATGTGCCAAG
MtCAS15-ChIP-qPCRR3	CATGAAGGCTCGTGATGGT
MtCBF4-ChIP-qPCRF1	CTCACGGGATACGAACATTG
MtCBF4-ChIP-qPCRR1	TTTTAGATTGGCCGCTTTCA
MtCBF4-ChIP-qPCRF2	TTCGCAAACTTCAGTCTTTTCTCTT
MtCBF4-ChIP-qPCRR2	GTCATGTTAATTTTATACCTACGTTAG
MtCBF4-ChIP-qPCRF3	TTATGGGACCGAGGGAGTAG
MtCBF4-ChIP-qPCRR3	TTTTGCCTCCCATTTAGACA

Underlined bases indicate restriction enzyme sites.