

Table 1 Suppl. Gene names and accession numbers of proteins used for phylogenetic tree construction.

Gene names	Accession numbers
<i>AtMYB30</i>	AT3G28910
<i>AtMYB60</i>	AT1G08810
<i>AtMYB62</i>	AT1G68320
<i>AtMYB2</i>	AT2G47190
<i>AtMYB13</i>	AT1G06180
<i>AtMYB14</i>	AT2G31180
<i>AtMYB15</i>	AT3G23250
<i>AtMYB31</i>	AT1G74650
<i>AtMYB41</i>	AT4G28110
<i>AtMYB44</i>	AT5G67300
<i>AtMYB49</i>	AT5G54230
<i>AtMYB70</i>	AT2G23290
<i>AtMYB73</i>	AT4G37260
<i>AtMYB74</i>	AT4G05100
<i>AtMYB77</i>	AT3G50060
<i>AtMYB78</i>	AT5G49620
<i>AtMYB94</i>	AT3G47600
<i>AtMYB96</i>	AT5G62470
<i>AtMYB102</i>	AT4G21440
<i>AtMYB112</i>	AT1G48000
<i>AtMYB116</i>	AT1G25340
<i>NtMYB1</i>	NP_001312823
<i>NtMYB2</i>	XP_009629052
<i>DcMYB1</i>	XP_017224603
<i>GbMYB5</i>	AEF14025
<i>MdMYB121</i>	NP_001315719
<i>OsMYB2</i>	XP_015628446
<i>OsMYB4</i>	XP_015633465.1
<i>OsMYB91</i>	XP_015620377
<i>SbMYB15</i>	AKP07635.1
<i>TaMYB1</i>	ABC86569.1
<i>TaMYB19</i>	AEV91143.1
<i>TaMYB30</i>	AEV91153.1
<i>TaMYB32</i>	AEV91155.1
<i>TaPIMP1</i>	ABU93236.1
<i>ZmMYB001</i>	AC217264.3_FGT005
<i>ZmMYB003</i>	GRMZM2G037650_T01
<i>ZmMYB007</i>	GRMZM2G070849_T01
<i>ZmMYB012</i>	GRMZM2G106558_T02
<i>ZmMYB016</i>	GRMZM2G131937_T01
<i>ZmMYB017</i>	GRMZM2G143046_T01
<i>ZmMYB018</i>	GRMZM2G147346_T01
<i>ZmMYB020</i>	GRMZM2G308034_T01
<i>ZmMYB024</i>	AC165178.2_FGT004
<i>ZmMYB027</i>	GRMZM2G048295_T01
<i>ZmMYB030</i>	GRMZM2G087955_T01
<i>ZmMYB036</i>	GRMZM2G139284_T01
<i>ZmMYB037</i>	GRMZM2G166337_T01
<i>ZmMYB038</i>	GRMZM2G176327_T01
<i>ZmMYB049</i>	GRMZM2G139688_T01
<i>ZmMYB051</i>	GRMZM2G158700_T01
<i>ZmMYB053</i>	GRMZM2G160840_T01
<i>ZmMYB064</i>	GRMZM2G055158_T01
<i>ZmMYB066</i>	GRMZM2G108959_T01
<i>ZmMYB069</i>	GRMZM2G127857_T01
<i>ZmMYB070</i>	GRMZM2G131442_T01
<i>ZmMYB071</i>	GRMZM2G138427_T01
<i>ZmMYB072</i>	GRMZM2G162434_T01
<i>ZmMYB080</i>	GRMZM2G070523_T01

<i>ZmMYB083</i>	GRMZM2G095904_T01
<i>ZmMYB085</i>	GRMZM2G145444_T01
<i>ZmMYB090</i>	GRMZM2G455869_T01
<i>ZmMYB092</i>	GRMZM2G048910_T01
<i>ZmMYB095</i>	GRMZM2G078820_T01
<i>ZmMYB107</i>	GRMZM2G031323_T01
<i>ZmMYB108</i>	GRMZM2G045748_T01
<i>ZmMYB109</i>	GRMZM2G050550_T01
<i>ZmMYB110</i>	GRMZM2G056407_T01
<i>ZmMYB111</i>	GRMZM2G104551_T01
<i>ZmMYB113</i>	GRMZM2G126566_T01
<i>ZmMYB115</i>	GRMZM2G169356_T01
<i>ZmMYB119</i>	GRMZM2G028054_T01
<i>ZmMYB120</i>	GRMZM2G047600_T01
<i>ZmMYB129</i>	GRMZM2G330475_T01
<i>ZmMYB138</i>	GRMZM2G098179_T01
<i>ZmMYB139</i>	GRMZM2G134279_T01
<i>ZmMYB142</i>	GRMZM5G803308_T01
<i>ZmMYB143</i>	AC197146.3_FGT002

Table 2 Suppl. List of gene names and accession numbers used for motif analysis

Gene names	Accession numbers
<i>AtMYB30</i>	AT3G28910
<i>AtMYB60</i>	AT1G08810
<i>AtMYB62</i>	AT1G68320
<i>AtMYB2</i>	AT2G47190
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<i>AtMYB14</i>	AT2G31180
<i>AtMYB15</i>	AT3G23250
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<i>AtMYB41</i>	AT4G28110
<i>AtMYB44</i>	AT5G67300
<i>AtMYB49</i>	AT5G54230
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<i>AtMYB73</i>	AT4G37260
<i>AtMYB74</i>	AT4G05100
<i>AtMYB77</i>	AT3G50060
<i>AtMYB78</i>	AT5G49620
<i>AtMYB94</i>	AT3G47600
<i>AtMYB96</i>	AT5G62470
<i>AtMYB102</i>	AT4G21440
<i>AtMYB112</i>	AT1G48000
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<i>NtMYB1</i>	NP_001312823
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<i>OsMYB4</i>	XP_015633465.1
<i>OsMYB91</i>	XP_015620377
<i>SbMYB15</i>	AKP07635.1
<i>TaMYB1</i>	ABC86569.1
<i>TaMYB19</i>	AEV91143.1
<i>TaMYB30</i>	AEV91153.1
<i>TaMYB32</i>	AEV91155.1
<i>TaPIMP1</i>	ABU93236.1
<i>ZmMYB027</i>	GRMZM2G048295_T01
<i>ZmMYB030</i>	GRMZM2G087955_T01
<i>ZmMYB036</i>	GRMZM2G139284_T01
<i>ZmMYB049</i>	GRMZM2G139688_T01
<i>ZmMYB053</i>	GRMZM2G160840_T01
<i>ZmMYB066</i>	GRMZM2G108959_T01
<i>ZmMYB070</i>	GRMZM2G131442_T01
<i>ZmMYB071</i>	GRMZM2G138427_T01
<i>ZmMYB085</i>	GRMZM2G145444_T01
<i>ZmMYB092</i>	GRMZM2G048910_T01
<i>ZmMYB095</i>	GRMZM2G078820_T01
<i>ZmMYB107</i>	GRMZM2G031323_T01
<i>ZmMYB108</i>	GRMZM2G045748_T01
<i>ZmMYB109</i>	GRMZM2G050550_T01
<i>ZmMYB111</i>	GRMZM2G104551_T01
<i>ZmMYB113</i>	GRMZM2G126566_T01
<i>ZmMYB115</i>	GRMZM2G169356_T01
<i>ZmMYB119</i>	GRMZM2G028054_T01
<i>ZmMYB139</i>	GRMZM2G134279_T01
<i>ZmMYB142</i>	GRMZM5G803308_T01
<i>ZmMYB143</i>	AC197146.3_FGT002

Table 3 Suppl. The names and numbers of *ZmMYB* genes responding to different treatments. Total 22 genes were induced by at least one kind of stress treatment. These are *ZmMYB*27, 30, 36, 49, 53, 66 70 71, 85, 92, 95, 107, 108, 109, 110, 111, 113, 115, 119, 139, 142 and 143. Expression of *ZmMYB* 30, 36 and 95 was upregulated in four stress treatment. *ZmMYB*53 responds only to cold; *ZmMYB*49 responds only to PEG; *ZmMYB* 71 and 107 respond only to ABA; *ZmMYB* 110 and 115 respond only to NaCl.

Treatments	Number of genes	Gene names
PEG6000	13	<i>ZmMYB</i> 27, 30, 36, 49, 66, 70, 92, 95, 108, 109, 111, 119, 142
NaCl	14	<i>ZmMYB</i> 27, 30, 36, 85, 92, 95, 108, 109, 110, 111, 113, 115, 142, 143
ABA	14	<i>ZmMYB</i> 27, 30, 36, 66, 70, 71, 85, 92, 95, 107, 109, 113, 139, 143
Cold	6	<i>ZmMYB</i> 30, 36, 53, 95, 139, 142
PEG+NaCl+ABA+cold	3	<i>ZmMYB</i> 30, 36, 95
PEG+NaCl+ABA	6	<i>ZmMYB</i> 27,30, 36, 92, 95 109
PEG+NaCl+cold	4	<i>ZmMYB</i> 30, 36, 95 142
PEG +ABA+cold	3	<i>ZmMYB</i> 30, 36, 95
NaCl+ABA+cold	3	<i>ZmMYB</i> 30, 36, 95
PEG+NaCl	9	<i>ZmMYB</i> 27, 30, 36, 92, 95, 108, 109 111 142
NaCl+ABA	9	<i>ZmMYB</i> 27, 30 36 85 92 95 109 113 143
ABA+cold	3	<i>ZmMYB</i> 30 36 95
PEG+cold	4	<i>ZmMYB</i> 30 36 95 142
NaCl+cold	4	<i>ZmMYB</i> 30 36 95 142
PEG+ABA	8	<i>ZmMYB</i> 27, 30, 36, 66, 70, 92, 95, 109

Table 4 Suppl. List of primers.

Primer name	Primer sequence
46 ZmMYBs Q-PCR primers	
ZmMYB001-F	AGTGGAGCTCCCTTCAAACC
ZmMYB001-R	AGCTCCTGCAGCATCTGTTC
ZmMYB003-F	CGTCTGCGGTGGACTAACTA
ZmMYB003-R	GCGATCTGGGACCATCTATT
ZmMYB007-F	GTCCATGCTCCAGATGCTC
ZmMYB007-R	ATCCAGAGGTAGCGCATCA
ZmMYB012-F	CACAGGAGAAGACGGCAGTA
ZmMYB012-R	TGCAGAAGCCTGGGTAGTAG
ZmMYB016-F	GCGTAATATCTGCGAGCAAC
ZmMYB016-R	CTCCAGCATTGAGAACGATG
ZmMYB017-F	ATCTTGATCAGTCGGTGGTG
ZmMYB017-R	TCCAAGGCCCAAAAGTTATC
ZmMYB018-F	CTCGACGACAGCTTCTGGT
ZmMYB018-R	CAGAACTCCATGTCCTCGTC
ZmMYB020-F	AGGAAGACCTCATCGTCACC
ZmMYB020-R	TCTTGCTCAGCTTCGTGTTT
ZmMYB024-F	GCAGACCGACATCCACAC
ZmMYB024-R	GGCAGAGGCTCCACCTTAG
ZmMYB027-F	GGTGACCGAGTCGTCCAT
ZmMYB027-R	CTGTCGTCGAACTGGAAGTC
ZmMYB030-F	CTCCTTGTCGTTGTCCCTCT
ZmMYB030-R	CTTGCTTGCTTGAGGTGT
ZmMYB036-F	GGTGTTTCGAGTACGAGACGA
ZmMYB036-R	ACAGGACGGTGGAAGTGG
ZmMYB037-F	TCGTCGCCTACATCAAGAAG
ZmMYB037-R	TCCGGCCTCAGGTAGTTAGT
ZmMYB038-F	CATGCTCCTCGTCAACTACG
ZmMYB038-R	TTAGTCTGGTCGTCTCTCG
ZmMYB049-F	ACAATCTGGCTGTGTGCTTC
ZmMYB049-R	GCTAGCATTGGCTTCATTCA
ZmMYB051-F	TTGACATGTTTCGACGAGAGC
ZmMYB051-R	TCCCAGATATCCTCCAGACC
ZmMYB053-F	CTCATCCTCGACCTCCACA
ZmMYB053-R	CGCGTCCTCCAGTAGTTCTT
ZmMYB064-F	TGGTCACCTTCCTCCTGTCT
ZmMYB064-R	GCCTCAGGTAGTTGGTCCAC
ZmMYB066-F	AGCGTGGAAGTTCCTCTCT
ZmMYB066-R	TCGTTGTCAGTCCTTTGAGG
ZmMYB069-F	TATTCCTCATCTCCCTGTTCC
ZmMYB069-R	ACGGATAGAGAAAGGCCAAA
ZmMYB070-F	TAGCTCCGATCTCCTTGGAT
ZmMYB070-R	AGCGCCGTCTCCATTAGTAG
ZmMYB071-F	TTACGAGCAGAAACGACGAG
ZmMYB071-R	TGAGGCATGGAACACTGAAT
ZmMYB072-F	CAAAGTCAAACACCCCTGTG
ZmMYB072-R	TGCCCAGTGTCAAATCTACC
ZmMYB080-F	CGGTGATTCTGAGAACTGGA
ZmMYB080-R	TGAACATTGAACGGGAAACA
ZmMYB083-F	TCATCCAAGTCCACCAAATG
ZmMYB083-R	CTTAGGCTCCAGTCGCTTCT
ZmMYB085-F	CTCACCTCGCTCTCCCTCT
ZmMYB085-R	GAAGGCGGGTGGAGTAGAC
ZmMYB092-F	CCAAGAAGACGACCACAGAA
ZmMYB092-R	AGAAAACATGGAGGCTACGG
ZmMYB095-F	CTCGTCTTCTCTCCGCTACC
ZmMYB095-R	TAGTCGACGACAACGAGTGG
ZmMYB107-F	TCGCCTACATCAAGAAGCAC
ZmMYB107-R	GATGTCCGGCCTCAGATAGT

ZmMYB108-F	AACTTTACCGAGCAGGAGGA
ZmMYB108-R	TCCTCTTCGGCAAGTAGGAT
ZmMYB109-F	CGGAGTTCCTGTTGTTGATG
ZmMYB109-R	CATACCCATCATACGCTTGC
ZmMYB110-F	GATCGAGTCGTGGCTGTTT
ZmMYB110-R	GCTTGATCGATTGGACACAC
ZmMYB111-F	GGACGAGTTCAGCAGCATT
ZmMYB111-R	TGAGCTGTTGTTGTTGACCA
ZmMYB113-F	CGTTCCTTTACCGACGAGGAG
ZmMYB113-R	AAGAAGAGTCGTCGGGAGAA
ZmMYB115-F	CAAGTGGTAACACCGTCGTC
ZmMYB115-R	AGAGAAGACGTCGAGGCAGT
ZmMYB119-F	TGGCACACCTTATGGGACTA
ZmMYB119-R	GTGAGCATATTCGCTGAGGA
ZmMYB120-F	CGTGGAGGGATGCTCTACTT
ZmMYB120-R	AGAAGCTCCGACCAGCTCT
ZmMYB129-F	CGTCCTCCTCTTCCTCACAT
ZmMYB129-R	GGGATGAGATGAGCTGGATT
ZmMYB138-F	ACCAGGAGGACAGGCTCAT
ZmMYB138-R	AGTTCTTGACGTCGTTGTCG
ZmMYB139-F	GGCTACTCTTTGCTCGGTTT
ZmMYB139-R	CTACAAGCCGCTAGGGAATC
ZmMYB142-F	TATTCTCTCGAACCCTGTG
ZmMYB142-R	CTTTACACGGCTTTCAGCAA
ZmMYB143-F	GACCCCTTCGACCACAAGTC
ZmMYB143-R	CATCGTCGAACAACCAAGTTC
ZmMYB144-F	CGACACGTTCTGGTCGGAGAC
ZmMYB144-R	AACACTCCGAGCCAGTAGTCCAAG
ZmMYB145-F	CTTTGGGTTTGAGGATTTTCG
ZmMYB145-R	GGTTGGTGTGCATGTATGGT
ZmMYB154-F	CCGAGGAGACCATTCAATTT
ZmMYB154-R	GAGACAACATTTTGCGGTTTT
ZmMYB157-F	ATAAACCCCTCCTCCTCCTC
ZmMYB157-R	AAGAAAATGGGATGGACGAC
ZmActin-F (GRMZM2G126190)	GCATCCATGAGACCACCTACAAC
ZmActin-R	GATGGACCCTCCTATCCAGACAC

Q-PCR primers (14 stress related genes, 9 salt responsive genes and control genes)

P5CS1-F (AT2G39800)	TGGTGTCACTCTGGTGCGGTTG
P5CS-R	CACAAGCCTTCCCATCAAGTTCAG
ABI5-F (AT2G36270)	AATGGAGGAGGTGGTGGTGAG
ABI5-R	CTGCTGCTGCTTGTGTTGATTG
ABF3-F (AT4G34000)	TGTCTCACGGCTTTGGATTTGG
ABF3-R	GTTGGCTGCTGCTCACTCAC
RD29A-F (AT5G52310)	GTGACGACGAAGTTACCTATCTCC
RD29A-R	TCTCCGCCACATAATCTCTACCC
RD29B-F (AT5G52300)	CAGACAGAGGAGAGAGCAGAGAG
RD29B-R	CTTCAACCACCAGGAGCAAACG
RAB18-F (AT1G43890)	GTCTTACTGCTGAAGGTTCTGCTG
RAB18-R	ATCCAAGATGCTGCGGTTTAGG
RD20-F (AT2G33380)	TTAGCTCCGGTCACCAGTCA
RD20-R	CATGTATGGTTTTGGTAATGTTTCC
LEA14-F (AT1G01470)	GATTTCTTCTGATCGACAAAACCTA
LEA14-R	AGCAAACCCAACTTATTACATTACG
DREB2A-F (AT5G05410)	GACCTAAATGGCGACGATGT
DREB2A-R	TCGAGCTGAAACGGAGGTAT
RbohF-F (AT1G64060)	CTGCGGTTTCGCCATTC
RbohF-R	TGTTTCGTGCGCTCTG
RbohD-F (AT5G47910)	ATTACAAGCACCAAACCAG
RbohD-R	TGCCAAGCCATAACATCA
ATGolS2-F (AT1G56600)	GACGAGTCTCTTGATTACAAGAATGTT
ATGolS2-R	AAACTGCTGAAGTGTCTGTTGC
Actin2-F (AT3G18780)	GCCATCCAAGCTGTTCTCTC
Actin2-R	GCTCGTAGTCAACAGCAACAA
MYB2-F (AT2G47190)	GTTAGAAGAGGCAACATCACT

MYB2-R	CACTAATCTCGGCATCCAA
RD22-F (AT5G25610)	CGATTTCGTCTTCCTCTGAT
RD22-R	TACTCCGCCTTTACCTACT
AtNHX1-F (AT5G27150)	AAGAGCAGCGTTCGTCTTTC
AtNHX1-R	TGAGACCAGACCACCAAATCAC
AtNHX2-F (AT3G05030)	TCAATCCACATTCCGTCCTC
AtNHX2-R	AAACCTCGAAGGCTGTTTGG
AtHKT1-F (AT4G10310)	ACAAAGCGTGACGAGTATGG
AtHKT1-R	TAGCACCGTCACTCCAAGAAG
AtCHX16-F (AT1G64170)	ACGGTTTGCCCTTTTGGAAC
AtCHX16-R	TGAAATCGCGGTCACAGAAC
AtMPK4-F (AT4G01370)	AAGCAGACGCATCACAGTTG
AtMPK4-R	TTGAACGGCCTCACACATAC
AtMPK6-F (AT2G43790)	TAAGTTCCCGACAGTGCATCC
AtMPK6-R	TGGGCCAATGCGTCTAAAAC
AtSOS1-F (AT2G01980)	AGAACACAGAGGTCTCATGAGC
AtSOS1-R	TGCCGAAAATGCTGAGTTGC
AtSOS2-F (AT5G35410)	TGACAGGCGACAGGATTTTG
AtSOS2-R	TGAGTTCGCTACAGCCTCAATG
AtSOS3-F (AT5G24270)	CGCCGGTCCATGAAAAAGTC
AtSOS3-R	TTCGGATTTCGTGAAGAAGCG
Ectopic expression vector construction	
ZmMYB030-F	GAAGGTACCATGGCGGCGTCGCCTTCCCCGTCC
ZmMYB030-R	AGGTCTAGACTAGTCGATCTCGGCCATGCCCATC

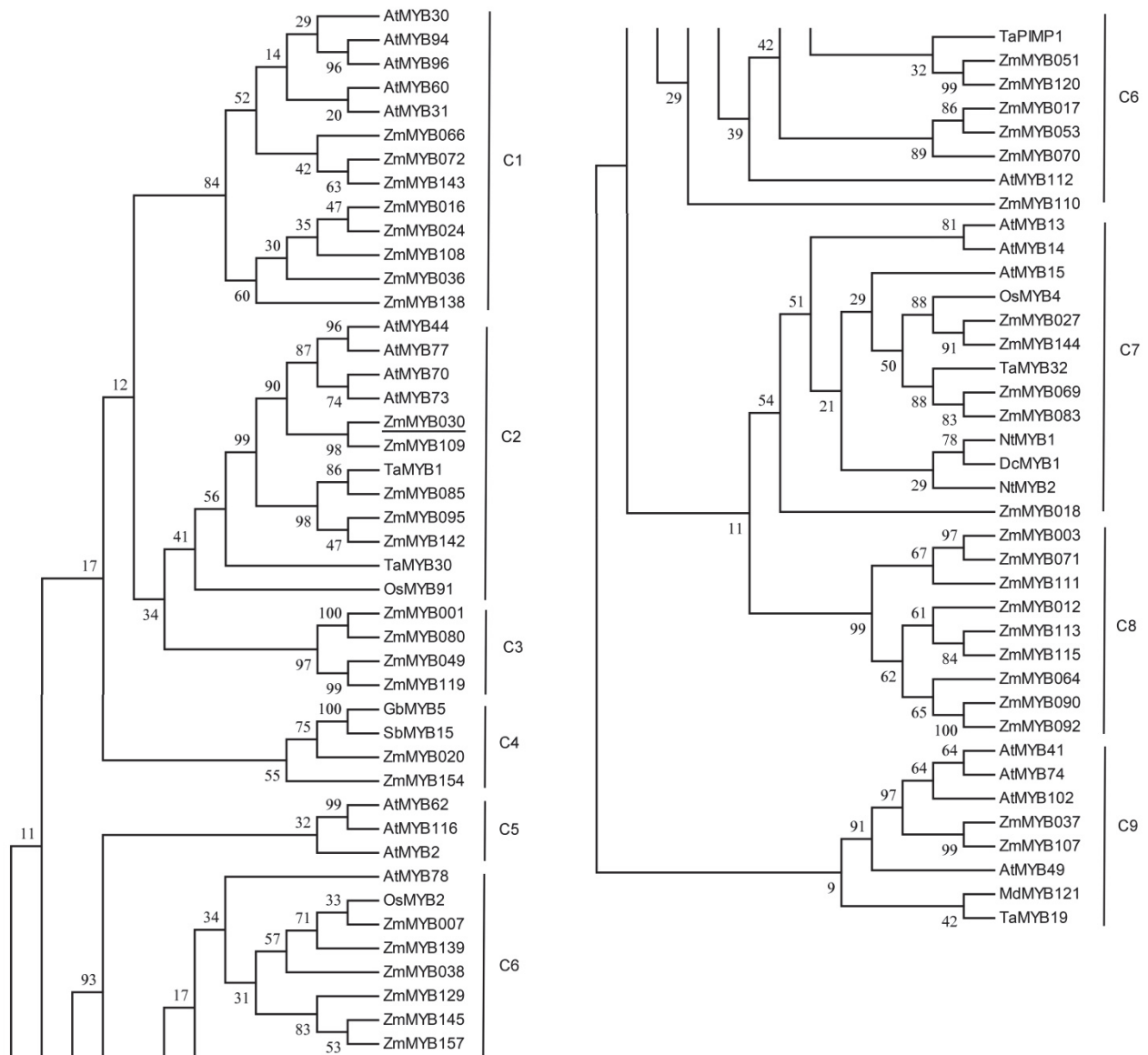


Fig. 1 Suppl. Phylogenetic relationship of 46 maize R2R3-MYB proteins and its orthologs from other species. The complete amino acid sequences of the 46 maize MYB proteins, 21 *Arabidopsis* MYB proteins, 5 wheat MYB proteins, 2 tobacco MYB proteins, 3 rice MYB proteins and other 4 R2R3-MYB proteins were aligned by *ClustalW*, and the neighbor-joining tree was constructed using *MEGA 6* with 1000 bootstrap replicates. The evolutionary distances were computed using the p-distance method. There are total 9 clades in the phylogenetic tree labeled C1 to C9. ZmMYB30 was underlined because that functional analysis was carried out on this gene in this paper. The gene name and accession number of 81 proteins were listed in Table 1 Suppl.

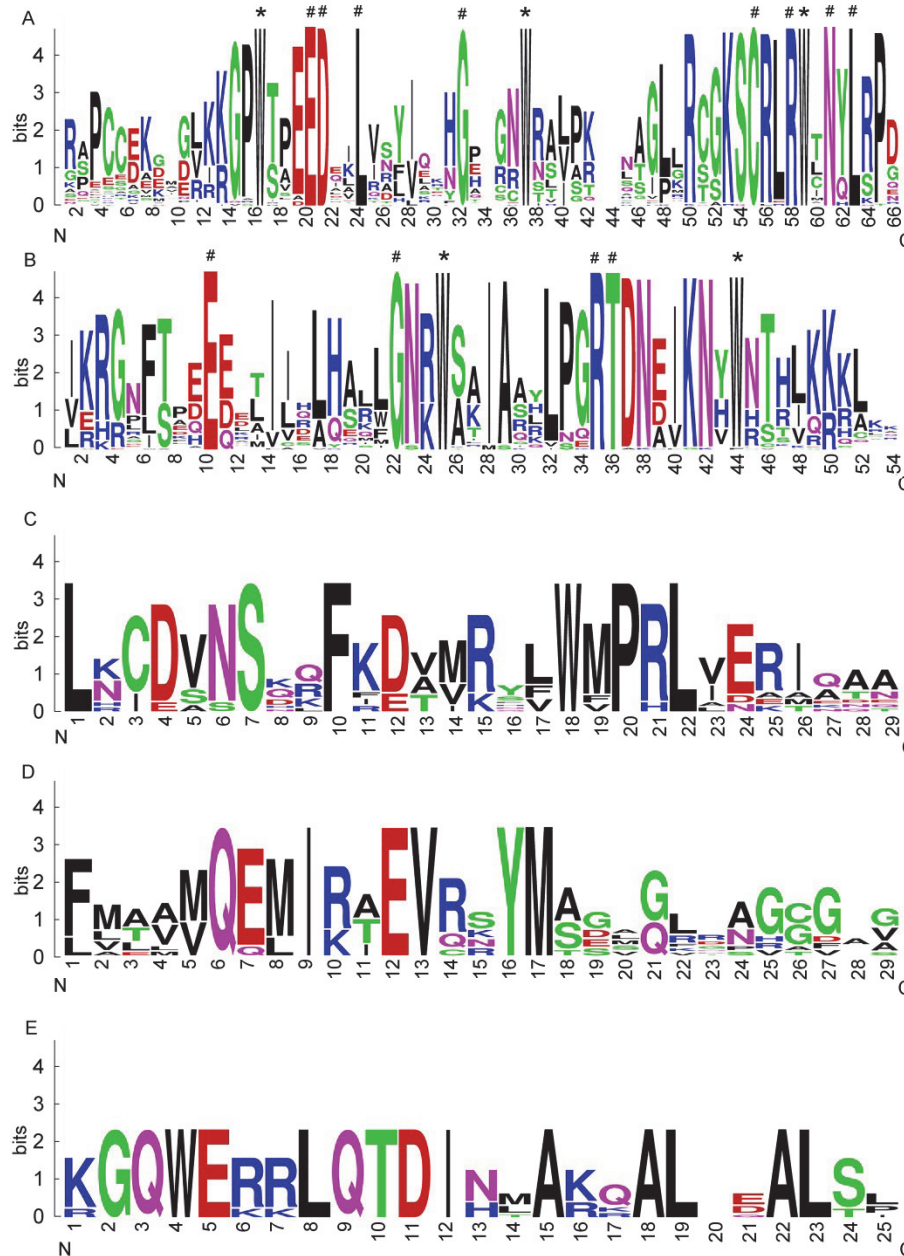


Fig. 2 Suppl. Sequence conservation analysis of the R2 and R3 repeat and C-terminus motifs in the 57 stress-responsive R2R3-MYB proteins from maize and other species. The sequence logos of the R2 (A) and R3 (B) MYB repeats were based on full-length alignments of all the 57 R2R3-MYB domains (the gene name and accession number of 57 proteins are listed in Table 2 Suppl.). The *asterisks* indicate the conserved tryptophan residues (W) in the MYB domain and the # indicates the position of the conserved amino acid that is identical among all the 57 R2R3-MYB proteins. Sequence logos for the three conserved C-terminus motifs (C-E) of R2R3-MYB proteins (C - motif 1 for 10 MYB proteins including OsMYB2, ZmMYB139, AtMYB78, AtMYB112, ZmMYB070, TaPIMP1, AtMYB2, ZmMYB053, AtMYB62, and AtMYB116; D - motif 2 for 10 MYB proteins including AtMYB70, AtMYB44, ZmMYB085, TaMYB1, ZmMYB142, AtMYB77, AtMYB73, ZmMYB095 ZmMYB030, and ZmMYB109 and E - motif 3 for 6 MYB proteins including AtMYB96, AtMYB94, ZmMYB108, AtMYB31, ZmMYB036 and AtMYB30). The overall height of each stack indicates the conservation of the sequence at that position, whereas the height of letters within each stack represents the relative frequency of the corresponding amino acid.