Supplemental Figure S1. Multiple sequence alignments and phylogenetic analysis of MdMYB46 orthologs.

A. Multiple sequence alignments of AtMYB46 orthologs in Eucalyptus (Eucalyptus grandis; EgMYB2); Pine (Pinus taeda; PtMYB4), grapevine (Vitis vinifera; VvMYB46), alfalfa (Medicago truncatula; MtMYB46), soybean (Glycine max; GmMYB46), rice (Oryza sativa; OsMYB46), maize (Zea mays; ZmMYB46), sorghum (Sorghum bicolor; SbMYB46), barley (Hordeum vulgare; HvMYB46), brachypodium (Brachypodium distachyon; BdMYB46), birch (Betula platyphylla, BplMYB46) and apple (Malus × domestica Borkh, MdMYB46 ). R2, R3 functional regions were marked in the red box. B. Phylogenetic analysis of AtMYB46/83 orthologs. MYB58, MYB63 and their homologs (PtMYB1/8/21a, PnMYB28/192 and EgMYB1) are included as the outgroup. AtMYB46 and MdMYB46 were marked with red frame. Proteins in the blue half brackets represent the members in the same subfamily with MdMYB46.
Supplemental Figure S2. Transcriptional levels of *MdMYB46* in transgenic apple. A. Schematic shown the overexpressing and RNAi vector of *MdMYB46*. B. *MdMYB46* expression levels in non-transgenic GL-3 apple plants, *MdMYB46*-overexpressing apple plants (OE-MdMYB46) and *MdMYB46*-RNAi plants (RNAi-MdMYB46). The error bars indicate the standard deviation (SD) from three biological replicates. Asterisk indicates significant differences between the transgenic lines and GL-3 (*P* < 0.05, based on t-test).
Supplemental Figure S3. Phenotypes of *MdMYB46*-overexpressing Arabidopsis and apple. A. Phenotypic differences between *MdMYB46*-overexpressing Arabidopsis plants and non-transgenic wild type (WT). The curling blade was marked in the red box. B. Differences in petal structure between *MdMYB46*-overexpressing Arabidopsis and WT. C. Phenotype of *MdMYB46*-overexpressing apple plants and WT.
Supplemental Figure S4. Differences in transcriptional levels of lignin biosynthesis-related genes between *MdMYB46*-overexpressing Arabidopsis plants and wild type. A-E. The error bars indicate the standard deviation (SD) from three biological replicates. Different letters indicate significant differences (*P* < 0.05, based on Duncan’s multiple range test). WT represents the non-transgenic wild type while L1, L3 and L6 represent the transgenic lines.
Supplemental Figure S5. Changes in expression of genes related to cellulose biosynthesis in \textit{MdMYB46}-overexpressing Arabidopsis and apple. A. Transcriptional levels of cellulose biosynthesis-related genes in \textit{MdMYB46}-overexpressing apple plants and non-transgenic plants (GL-3). B-D. Transcriptional levels of cellulose biosynthesis-related genes in \textit{MdMYB46}-overexpressing Arabidopsis plants and the non-transgenic wild type (WT). The error bars indicate the standard deviation (SD) from three biological replicates. Different letters indicate significant differences ($P < 0.05$, based on Duncan’s multiple range test).
Supplemental Figure S6. Transcriptional levels of stress signaling genes under ABA, salt and drought stress and in *MdMYB46* transgenic apples. A. B. C. The expression levels of stress signaling genes in non-transgenic GL-3 apple plants under ABA, NaCl and mannitol treatment. The error bars indicate the standard deviation (SD) from three biological replicates. Different letters indicate significant differences (*P* < 0.05, based on Duncan’s multiple range test).
## Supplemental Table S1 Primers used in this study

| Primer Name | Primer Sequence |
|-------------|----------------|
| **For transgenic vectors** | |
| MdMYB46-eGFP | F: GTCGACATGAGGAAGCCAGAACCCTCC  
R: GGATCCACTTTGGTAGTCAAGAAAAAG |
| MdMYB46 (Y2H) | F:GGATCTTGAGGAAGCCAGAACCCTCC  
R:GTCGACTCAACTTTGGTAGTCAAGAAAAAG |
| MdMYB46-N | F:GGATCTCAGGAAGCCAGAACCCTCC  
R:GTTCGACTCACTTTGGTAGTCAAGAAAAAG |
| (Y2H) | F:GGA TCCTGAGGAAGCCAGAACCCTCC  
R:GTCGACTCACTTTGGTAGTCAAGAAAAAG |
| MdMYB46-C | F:GGA TCCTGAGGAAGCCAGAACCCTCC  
R:GTCGACCTCACTTTGGTAGTCAAGAAAAAG |
| (Y2H) | F:GGA TCCTGAGGAAGCCAGAACCCTCC  
R:GTCGACCTCACTTTGGTAGTCAAGAAAAAG |
| MdMYB46- pRI | F: GTCGACATGGAACAAAAGTTGATTTCTGAA  
R: GGATCCATGAGGAAGCCAGAACCCTCC |
| MYC-MdMYB46- pRI | F: GTCGACATGGAAGCCAGAACCCTCC  
R: GGATCCACCTGAGGAAGCCAGAACCCTCC |
| RNAi-MdMYB46 | FF:TCTAGATCCCTCCCCATAGATGGTTTCA  
FR:AAGCTTAACCCTCAGGTACCATC |
| **For EMSA probes** | |
| pMdMYB58 | F: TGGTGCTTTTGAGATTATTAGGTGTATTTGGAGCCGCAAT  
R: ATTCGCGCTCACCACATACCTAATAAATCTCAAGCAACCA |
| pMdMYB63 | F: TTTGTGTTGGAGGTCAATTTGGTAGTTTCCACACCAA  
R: CTTCGTTGGAACCTAACCACATGGACCTCACAACAAA |
| pMdCAD | F: TAATATAGGAAGCATAATTTTTAATTAAT  
R: ATTTAGTAAAATTTTGCTTCCATAATTTA |
| pMdCOMT | F: ACACAAATAGTCAACCTAATTTGTTAGTGTATTTGTCA  
R: TGACAAATACTACCAATTGACCTCACAACAAA |
| pMdCCR | F: ACACCAACTAATAACACACCAACTAAAATCATCATTATT  
R: AAAAAATGATATTTTATGTTAGGTTTATTGAGGGTTT |
| pMdRD22 | F: ATCTTAATTAGGTGTGTGAGACATCTTTGCAATAAAA  
AAACCAACTCATATT |
R: AATATGAGTTGGTTTTTTATTGCAAGATGTCTCGACACA
CCTAATTAAGAT

pMdRD29A  
F: AAAAAATTGATTTACCTAACATTACTACTTAT
R: ATAATAGTAGTATGITAGTATGAAATATCAATTATTT

pMdAREB1A  
F: AATTCAACCTAACCTTTAATCCGTATTATATATGGATGAG
TTGGTGTGGATATTGG
R: CCAAAATCACCAACCCCAACTCACATCAAAATATATAGAATGATT
AAAGTTAGGTTGAATT

pMdDREB2A  
F: AAAGCGCAAAAAACCAAAACCAGCAGAAAAAG
R: CTTTTTCTGCTGGTTTGGTGTTCCTCGCTTT

For reporter genes

pMdMYB58  
F: CTGCAGATGGTGTTGGCAAACTTTACA
R: GGATCCCATATGAAATCAGTTGGAAGAGGAAGGAAGA

pMdMYB63  
F: CTGCAGTTAATCCTAACTATAGAGTGTTGCT
R: GGATCCCTAGTAGGAGATGGGAAACGTC

pMdCAD  
F: CTGCAGGTGTAATAATGGGCAAGAAGATTA
R: GGATCCGACACATTTTAGTTATGAGAATTA

pMdCOMT  
F: CTGCAGGAGGTGTGGCTGCTGATCATG
R: GGATCCCTGAGAGCAAGGAAGGCAAGTAAT

pMdCCR  
F: CTGCAGAAACCTATTGAGATTGCATTAC
R: GGATCCCTGAGAGCAGAGCAGACAGAG

pMdRD22-P4  
F: CTGCAGATTGAATAACCAAAATCAAAGAAGAGAAGA
R: GGATCCCTGTTTTTGTTGTCACGTA

pMdRD29A-P1  
F: CTGCAGTGGCAGGAGCCTACGATTCCTCC
R: GGATCCCTGACGTGCACATGGTCACGTA

pMdAREB1A-P2  
F: CTGCAGGATCTATCGAGGATGACTCTT
R: GGATCCATCATTTATGTTTCAATGAA

pMdDREB2A-P1  
F: CTGCAGCAAAATCGGCAAATCCTCCGAAT
R: GGATCCCAACTCAACCAACACCTCAGAA

pMdRD22m  
F: TAATTAAGTGTGTCGAGACATCTTGGCAATA
AAAGGCAAACCTCA
R: TAGGTGTGCTTTTATTGCAAGGATTTGTCACGTA
CTGCACACACTTATA

pMdRD29Am  
F: CTAATAATTTGATTTGCTAACCATTACTACTATTAT
R: ATATAAATGTGATGAGGCAAAATCAAATTTTAG
| Gene          | Primer 1 Sequence | Primer 2 Sequence |
|--------------|-------------------|-------------------|
| pMdAREB1Am   | F: CAGCCTAACTTTAAATCCGTTTATTTATTGGATTGAGT | R: ATCACTAAACCTCAATCCAAATAAAACCGGATTTAAAAGTGTCG |
| pMdDREB2Am   | F: GCAAAGCGCAAAGCCAACCGCAGAAAAAGGC | R: GCCCTTTTTCTGCTGTTTTGCTTTTGCGCTTTTC |
| For ChIP-PCR  |                   |                   |
| pMdMYB58     | F: AGTCTCGCTATATGGTATATG | R: GGTACTCTAAAACAAATTATAAG |
| pMdMYB63     | F: AAGAGTGCTGGTTTTTGCA | R: TCATGATTTTTAAAGCGATCGTT |
| pMdCAD       | F: CCCAATTCCGGTGATGAAAT | R: GCAGAAACCGAATGATGTC |
| pMdCOMT      | F: AGTACATTTTTACTAAAGGG | R: ACAGATGCTGAGTCTATAGTAT |
| pMdCCR       | F: AGTCATTTTACACCATGATC | R: ATGTGACAGGAGTAACCATGAC |
| pMdRD22-P1   | F: ATGTGTCTTTTAACTAA | R: TGTAGGAGCAAGGAGAGAC |
| pMdRD22-P2   | F: GTTAACAGATTTATCTAG | R: GGACTGGTCACTGGTTTGTAC |
| pMdRD22-P3   | F: CAATGACCAGTCCAAGCTATA | R: GATGTGTATTTTAGGCATTCA |
| pMdRD22-P4   | F: ACTAAAATCCAAGCACCATGT | R: CACCGGAAATGAAAGGACAGAC |
| pMdRD29A-P1  | F: GATGTAGTGTGGTATAAAT | R: CTAGGGTTTACAAACATTGGACA |
| pMdRD29A-P2  | F: TCCTCTATCCTACCTACTCT | R: TCTGTCGCTTCTGGAGCGAGCA |
| pMdAREB1A-P1 | F: GCTGCAGAAGCCCTTTGATT | R: AGTCAATTCCTGATACATATCA |
| pMdAREB1A-P2 | F: GAATAAGGTCTATGTCTATTTT | R: TGGACAAATAACATGCATGAG |
| pMdAREB1A-P3 | F: CGTTGTCCGGCTCAAGCCTTTC | R: TCCACGTTTTCTTGAATGGAG |
| Gene          | Primer 1 | Primer 2 |
|--------------|----------|----------|
| pMdDREB2A-P1 | F: TATCGGAAATATCTAGAGGA | R: ATTCGAGAAAAGTCGAAAGCT |

For qRT-PCR

| Gene          | Primer 1 | Primer 2 |
|--------------|----------|----------|
| MdMYB46(DL)  | F: CATCCTCACCTGCAATAAAAAA | R: GGTAGTCAAGAAAGGAAATG |
| MdMYB58(DL)  | F: TGGCTTACCTTTACTGGAAAGT | R: TGAATGGGAGGAAATTGGTGT |
| MdMYB63(DL)  | F: GTTACTTGCAAAAGTGAGCTT | R: AAGAAAGCCACGTTGAAAGT |
| MdC4H(DL)    | F: ACATGAACCTCCAGGATGCCA | R: GAGATACTGAAGTCGTTCCC |
| MdC3H(DL)    | F: CTACTTCATTTTGAGACGAG | R: CGGAGTAGGCACGACTTGAC |
| MdCAD(DL)    | F: ATGCAAGAAGCTGCTGACTCA | R: GAAGCTCCCTCTGATTTGTCTT |
| MdF5H(DL)    | F: AGCCCTCTAGGTTCCTGAAAG | R: GTCAAGCTCAGTGGTCCAT |
| MdHCT(DL)    | F: TGCTTTGGTGCGTATGGA TGA | R: CCAAGTCGGAATCATGGATGA |
| Md4CL(DL)    | F: CCCTGATACGGGTGCTCGCT | R: CGGTCGACGATGAGAGACTCG |
| MdCOMT(DL)   | F: GGTGAAGGTTGGGTTGTGAT | R: GATTCGAGCCAGGACAGGTGAA |
| MdCCR        | F: TCACATTCTGGCTGATTGAGAC | R: CTTCTGGTTTTGGAACCTTGAT |
| MdCESA4      | F: TGTTACTTTGTTCAGTTCCTT | R: ATCCCAATATACACCCGAGTT |
| MdCESA8      | F: GGCCCTGCTCTTCTCCCTGTT | R: CTCACTGTGATGTTCCAGAGA |
| MdRD22(DL)   | F: TGATGGGGTGAATGTTAAAG | R: GAACCCAGACACATGTCA |
| MdRD29A(DL)  | F: CTGAAGAAGGTAAGAGGAGGA | R: CCTTCAAAATATCTCCTTG |
| MdRD29B(DL)  | F: CCAAATTACCATCCTCACC | R: CCTTGGACCTTCTGCTC |


| Gene Name       | Forward Primer       | Reverse Primer       |
|-----------------|----------------------|----------------------|
| MdAREB1A(DL)    | CAGAGAATCAGCTGCCAGGT | TCTCCATGTCCTGATTCCTTC |
| MdAREB1B(DL)    | TTAGAACTAGAGGCAGAAGT | CTGTCAATGTTCGTGTAAG |
| MdDREB2A(DL)    | AAGAAAAGGGAGGGAGTAAT | ATAGTTGTAACCTCCATCTC |
| MdDREB2B(DL)    | CTCTAATTCTGTCATCTA  | AACATGTAATTCCCTCTGATA |
| MdActin         | TGGTGAAAGGCTGGATTTG  | CTGTGAGCAGAACTGGGTG |
| At4CL           | ATGATGTGGAAGCAATTCGTGT | GGTTGGGTCAAACAGTTGTAT |
| AtCCOAOMT       | GAAAATTTGGAGGAGTATTTG | CCACTGTTGGACAAAACCTAGAG |
| AtCESA4         | GGGTCATTGTCTCATCTTT  | TGCGGTTCCTCTCATTTAAC |
| AtCESA7         | TAGACAGAAACAGAAACACC | CACTCTCGACAAAGTACA |
| AtCESA8         | CCTTTTGGGTGATTCCTTC  | CGTATCTTCTCTTAGCAA |
| AtMYB46         | ACCACCTTACGAGTTGAACA | TGTTGGAATGACCTTTGAG |
| AtMYB58         | GGTTCATAGATGGTTGACATCA | GGTTGAAATGACTTTCTAGG |
| AtMYB63         | TCAAGAGCAACACAGAAGAA | TCTCTCTACCTCTCCATCAT |
| At18S           | ACACGGGAGGTAGTGACAA  | CCTCCAATGGATCTCGTTA |
### Supplemental Table S2 Sequence of cis-elements in this study

| Cis-element | Sequence |
|-------------|----------|
| M46RE       | (A/G)(G/T)(A/T)GGT(A/G) |
| SMRE        | ACC(A/T)A(A/C)(T/C) |
| SNBE        | (T/A)NN(C/T)(T/C/G)TNNNNNNNA(A/C)GN(A/C/T)(A/T) |
| ABRE        | ACGTGGC, ACGTGTC |
| DRE/TRE     | G/ACCGAC, GGCCGACAT |
| MYBCORE     | CAGTTA, CTGTTG |
| MYBR        | TGGTTAG |
### Supplemental Table S3 Accession number of each gene in this study

| Gene                  | Accession number       |
|-----------------------|------------------------|
| *MdMYB46*             | MD03G1176000           |
| *MdMYB83A*            | MD07G1010500           |
| *MdMYB83B*            | MD02G1312700           |
| *MdSND1*              | MD06G1121400           |
| *MdMYB58*             | MD05G1224100           |
| *MdMYB63*             | MD10G1205400           |
| *MdCAD*               | MD05G1089800           |
| *MdCCR*               | MD17G1222400           |
| *MdC3H*               | MD08G1242900           |
| *MdC4H*               | MD11G1052900           |
| *MdCOMT*              | MD05G1083900           |
| *MdF5H*               | MD02G1136000           |
| *Md4CL*               | MD13G1257800           |
| *MdHCT*               | MD17G1225100           |
| *MdAREB1A:*           | MD15G1081800           |
| *MdAREB1B*            | MD05G1082000           |
| *MdDREB2A*            | MD01G1158600           |
| *MdDREB2B*            | MD04G1165400           |
| *MdRD22*              | MD15G1098800           |
| *MdRD29A*             | MD01G1201000           |
| *MdRD29B*             | MD07G1268800           |
| *MdCESA4*             | MD00G1061100           |
| *MdCESA8*             | MD10G1276500           |
| *At4CL*               | AT1G51680              |
| *AtCCoAOMT*           | AT4G34050              |
| *AtCESA4*             | AT5G44030              |
| *AtCESA7*             | AT5G17420              |
| *AtCESA8*             | AT4G18780              |
| *AtMYB58*             | AT1G16490              |
| *AtMYB63*             | AT1G79180              |
### Supplemental Table S4 Partial study on genes related to stress response in apple

| Gene       | Accession number | References                      | Gene name in references |
|------------|------------------|---------------------------------|--------------------------|
| *MdAREB1A* | MD15G1081800     | Ma et al., 2017                 | *AREB3.2*                |
| *MdAREB1B* | MD05G1082000     | Ma et al., 2017; Shao et al., 2019 | *AREB2*                |
| *MdDREB2A* | MD01G1158600     | Zhao et al., 2012               | MDP0000147009            |
| *MdDREB2B* | MD04G1165400     | Zhao et al., 2012               | MDP0000153866            |
| *MdRD22*   | MD15G1098800     | Shao et al., 2019               | *MdRD22*                |
| *MdRD29A*  | MD01G1201000     | An et al., 2018                 | *MdRD29A*               |
| *MdRD29B*  | MD07G1268800     | Shao et al., 2019               | *MdRD29B*               |