

Supplementary Table S1 The primers for RT-qPCR analysis of the walnut genes

Gene name	5'-primer	3'-primer
<i>18S RNA</i>	5'-GGTCAATCTTCTCGTTCCTT-3'	5'-TCGCATTTCGCTACGTTCTT-3'
<i>GAPDH</i>	5'-GATCAGCGATGCAATGGAGA-3'	5'-TGCGAACCAATTCCACTGTC-3'
<i>JrMYB44</i>	5'-AGAGACATAGATCGGGTC-3'	5'-ATGATCTGGTCCTCCTCT-3'
<i>JrGSTTaul</i>	5'-GTATGAGTACATAGAAG-3'	5'-TTAATCCAGAACCAGCT-3'
<i>JrGST2</i>	5'-ATGGCAGCCATCAGACTC-3'	5'-AGTGATTGCTCTTGATTG-3'
<i>JrGST3</i>	5'-ATGGTATTGGAAGATGG-3'	5'-AATTGCAGTAGATTAAAG-3'
<i>JrGST6</i>	5'-ATGAAAGCTGGTGAACAT-3'	5'-TCCATCCACACAGATATG-3'
<i>JrGST7</i>	5'-ATGGTAAGCCAGGAGGTG-3'	5'-ACTCAGCCATCACCTTAC-3'
<i>JrGST8</i>	5'-ATGTCCACGGCTGTGTCCA-3'	5'-GGTTCGTTCCATACAGTC-3'
<i>JrGST9</i>	5'-GAAGAGTGATATCAAGCT-3'	5'-ATGTATTGGACAATGATG-3'
<i>JrGST10</i>	5'-ATGGCATCCGGACTTGTG-3'	5'-TCTCCTTATACCAATCAG-3'
<i>JrGST11</i>	5'-ATGGCGAACAGCAGCAGT-3'	5'-AGAGACTCAGAGATGGAT-3'
<i>JrGST12</i>	5'-ATGGAACAATGAGGTCAG-3'	5'-TGTTGCATAATACCTTAC-3'
<i>JrGSTF8</i>	5'-GCTCATCTCCGTCAACAT-3'	5'-CCACTGTTCTATGGATGC-3'
<i>JrGSTT3</i>	5'-GCGATATGAGCGAACATG-3'	5'-TGGAGACGTCATCTTCC-3'
<i>JrGSTU8</i>	5'-ACAAGAGTCTACCCTT-3'	5'-ACAGCATTCTCATGCTG-3'
<i>JrGSTU19</i>	5'-GATCAGGTGATTCTGCTG-3'	5'-GAGGGATTACATACAGG-3'
<i>JrGSTU23</i>	5'-GTGAAGCTGATTGCCACT-3'	5'-GTCCTTCCATGTCTCCTC-3'
<i>JrAPX1</i>	5'-ATGGCTGCACCAGTAGTT-3'	5'-GTAGAGATCGGCATATGT-3'
<i>JrAPX2</i>	5'-TGCTCACAAGTGTGCAAT-3'	5'-CAGACGAAGTACACCAGC-3'
<i>JrAPX3</i>	5'-CGGTACCATGAAGCTAGG-3'	5'-ACAATATCCTGATCACAG-3'
<i>JrGPX1</i>	5'-CAGAACAGCACAGTCCAC-3'	5'-CTAAGATCTGTTTCATTG-3'
<i>JrGPX2</i>	5'-ATGGCTACCATGCCGTT-3'	5'-TCCATAGTCGATCTGGCG-3'
<i>JrCAT1</i>	5'-CATGATATTACTCACCTT-3'	5'-AGGCATGGATCACGTCTG-3'
<i>JrSOD1</i>	5'-ATGAGTACTGTGAAAGCT-3'	5'-TAGGAGATCCATGATGCT-3'
<i>JrSOD2</i>	5'-ACAGTAACGATGTCAAG-3'	5'-GATCACCAGCATGACGAT-3'
<i>JrSOD3</i>	5'-ATGCAAGCTGCACTGTCAG-3'	5'-CGTACATTGACAGTTGTG-3'
<i>JrSOD4</i>	5'-ATGGCTGTAGCATTCGCAT-3'	5'-TAGGTTCTCCACATAAGC-3'
<i>JrSOD5</i>	5'-CTAGGTCTAGGCCTTCGC-3'	5'-CAACCTAGGGAAGTGTG-3'
<i>JrSOD6</i>	5'-ACGAGCACTGCCATAGCT-3'	5'-GTACTCCGTCAGTAGCTC-3'
<i>JrPOD1</i>	5'-CATTCTGGCAATTGCAGC-3'	5'-TCATACAGCCTGCTTATG-3'
<i>JrPOD2</i>	5'-ATGGTAGCTCTTGCAAGAG-3'	5'-AGTACATATCTTGGTCTG-3'
<i>JrPOD6</i>	5'-TGTACTATTGGAGATGAT-3'	5'-CATCATCAATAACTTCAT-3'
<i>JrVHAc4</i>	5'-TGTATGGGAGCTGCTTAC-3'	5'-AGAGATGTGCGTAGCCAT-3'
<i>JrWRKY2</i>	5'-CTAGCCAAGCTACACCTG-3'	5'-TCTGCACAATGATTCTAG-3'
<i>JrWRKY7</i>	5'-AGCAGAGTCAGCAGCAAC-3'	5'-GTGCAGAAGCCGAAGGCT-3'
<i>JrWRKY6</i>	5'-GATGAGAACTCGTTGTCT-3'	5'-ATCTGGGAACCTTATTAG-3'
<i>JrWRKY31</i>	5'-AGACGATGTTGATGATTC-3'	5'-ACCAAGCATATCTCTCAG-3'
<i>JrWRKY53</i>	5'-GTACAACATCGTCATCAC-3'	5'-TTGAGATATCGTCAGTGC-3'
<i>JrWRKY70</i>	5'-GACCAGCTAATTGAAGGC-3'	5'-GGAGATACTCCTGCAACT-3'
<i>JrERF02</i>	5'-AGTGGAGCACGAGATCAT-3'	5'-GGATGTTCTGAATTGCAGC-3'
<i>JrERF03</i>	5'-ATGGTGAGCTTACGAAGG-3'	5'-AGATGAGCTCGAACCAGT-3'
<i>JrERF15</i>	5'-AGTCAAGCTCCAACTCGT-3'	5'-AGCTCCTCATTCGTACC-3'
<i>JrERF11</i>	5'-ATGTGGCTAGTCCAGCAT-3'	5'-ATTGCACGTCCTCAGCACT-3'

<i>JrERF16</i>	5'-TTCTGGAACCTCCGACAG-3'	5'-ATGACTAGGCCATGGAG-3'
<i>JrERF27</i>	5'-TCTGCTCTCACTCAGGTT-3'	5'-TGCATCCTCAGCTGTGT-3'
<i>JrERF47</i>	5'-CTTCGAGCGAAGATGAGT-3'	5'-GGTCTTCTACTGCTCGAT-3'
<i>JrPP2C03</i>	5'-TTGCCATGAACGTCTCCA-3'	5'-AACCAAGGCAGTAGAACCC-3'
<i>JrPP2C09</i>	5'-TGGATCTGCTGCTGCTAT-3'	5'-CAGCAGGTTCAAGTATGC-3'
<i>JrPP2C17</i>	5'-TCCACTCCAAGGACAGTT-3'	5'-ACGTATGCATCACCAAGC-3'
<i>JrPP2C28</i>	5'-GGCTATCAATGCAATGGC-3'	5'-TGACATGGTGCTCTGAAG-3'
<i>JrPP2C36</i>	5'-GAAGCGATAACCCCTAACC-3'	5'-TCTTCCTCCAGCACTTC-3'
<i>JrDREB1A</i>	5'-GAGAGTTCTCCCTTGTCT-3'	5'-TCCTGGACGTCTTGTTAG-3'
<i>JrDREB1D</i>	5'-AGACTCCGAGAGTAGTAGCT-3'	5'-GCCATATCCTGGACTTCTTG-3'
<i>JrDREB2C</i>	5'-GCATGTCTTCGGAGACAACT-3'	5'-ACGCTGTAGTAACCTACCAG-3'
<i>JrDREB2F</i>	5'-GAAGAGAACTAGACTCTGG-3'	5'-GACATGAACACTAGGTTGG-3'
<i>JrDREB2A</i>	5'-CGTAAGGTTCCAGCCAAGG-3'	5'-AGCCCTTGACAGCTTCATC-3'
<i>JrMYC1</i>	5'-TGAGACCTCACCAACGAT-3'	5'-ATGTCCAAGTCCTGATCG-3'
<i>JrMYC2</i>	5'-CCTGAATGGTGGATCTACTCC-3'	5'-ACCTGACCATCCAATGTTACT-3'
<i>JrDof1</i>	5'-ATGTCCACGCTGTGACTC-3'	5'-GATGCCGTTGACGATGAAG-3'
<i>JrDof2</i>	5'-AGTCACCAACAGATGTCC-3'	5'-GAGGCTGACCTCTTGTTT-3'
<i>JrDof3</i>	5'-ATGGCTGATCGAGCTCGC-3'	5'-CTATAGGGGGTTTCTGGT-3'
<i>JrDof4</i>	5'-TTCAATGGCTGATCGAGC-3'	5'-AGAGTTGGAACCCGATTG-3'
<i>JrDof6</i>	5'-ACTGAGGATCCTGGCATT-3'	5'-TAGACTCCACCTGCAGTT-3'
<i>JrWD40-1</i>	5'-ATCAAGACGGTTCTGACG-3'	5'-TGAGGAGGCTCTTAAGCT-3'
<i>JrWD40-3</i>	5'-ATCAACGGTGACCTTCAC-3'	5'-CTTCATCATCACCCGATG-3'
<i>JrWD40-15</i>	5'-TACAAGCTCCACTACGAG-3'	5'-TCTTACTGCCACCATTC-3'
<i>JrWD40-18</i>	5'-TGAGGAGCCTGATGATTC-3'	5'-TAAGTCCACCCAAGCATC-3'
<i>JrWD40-26</i>	5'-TTCTCTGGATGATGCAGC-3'	5'-ATGATCCTTCAGGACCTG-3'
<i>JrWD40-35</i>	5'-AAGTGGAGATGGTGACAG-3'	5'-TCAGAGTCCTCATCATCC-3'

Supplementary Table S2 The primers used for gene clone and construction of recombinant vectors.

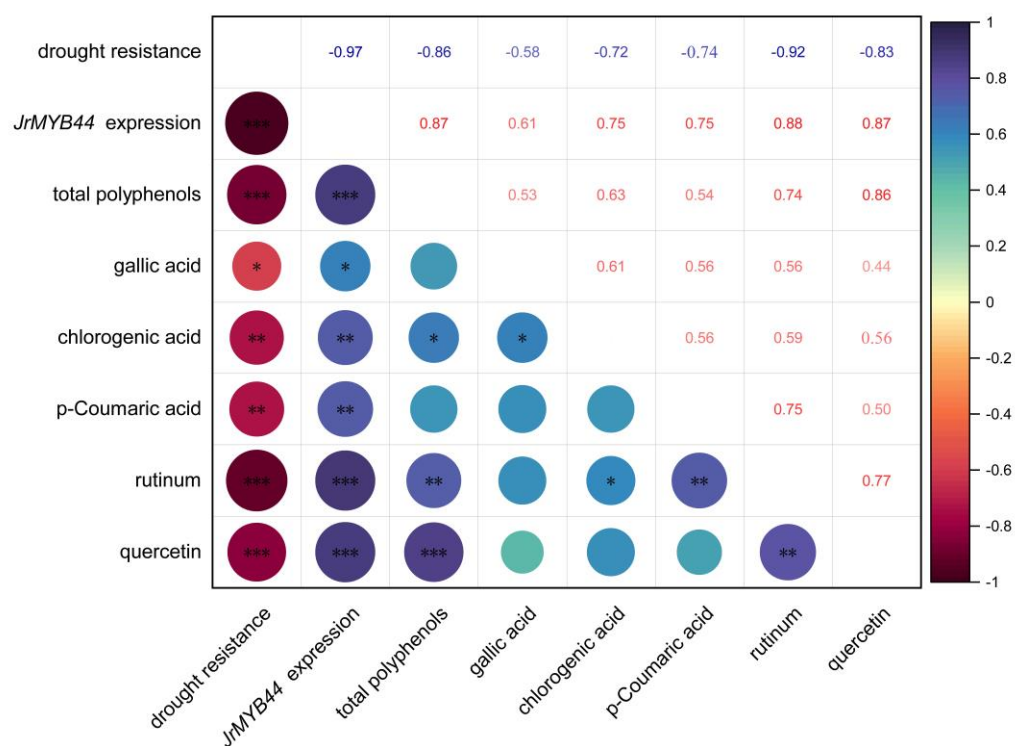
Gene/Construct	5'-primer (5'—3')	3'-primer (5'—3')
35S::JrMYB44	ATCGTCTAGAATGGAGGCGTCACAGAGAGAC	CGATGGTACCTCAAAGTTCAAGCCTGGCCAT
35S::JrWRKY7	ATCGGGATCCATGGCCGTGGAGTTCATGATG	CGATGGTACCTCAAGAGGATTCTAGGATCAG
35S::JrDREB2A	ATCGTCTAGAATGGCTGACGGGCAAAGAAG	CGATGGTACCTCATAAAAGCATTCCAAGT
35S::JrMYC2	ATCGGGATCCATGGACGAGATTATCTCTTCC	CGATGGTACCCTAACTCCGCATACTTTGCAG
JrDof1	TCGGGATCCATGCAAGACCCAGCAACATTC	CGATGGTACCCTACTGAGATCTTGAACCTGG
pHis2-Motif1	AATTCAACGGAACGGAACGGGAGCT	CCCGTTCGGTTCCGTTG
pHis2-Motif1M	AATTCGACCGGACCGGACCGAGCT	CGTCCGGTCCGGTCCG
pHis2-Motif1S	GGAATTCTGTGAACGGTAATCGATG	CTCTCAGAACCATCAAAGGAGCTCG
pHis2-Motif1SM1	GGAATTCTGTG GGACC TAATCGATG	
pHis2-Motif1SM2	GGAATTCTGTGTAATCGATGAAAAT	
pCAM-Motif1	GATCCAACGGAACGGAACGGCCCTTCCTCTATATAAGGAAGTTCAT TTCATTTGGAGAGAACACGGA	AGCTTCCGTGTTCTCTCCAAATGAAATGAACTTCCTTATATAGAGGAA GGGCCGTTCGGTTCCGTTG
pCAM-Motif1M	GATCCGGACCGGACCGGACCCCTTCCTCTATATAAGGAAGTTCATT TCATTTGGAGAGAACACGGA	AGCTTCCGTGTTCTCTCCAAATGAAATGAACTTCCTTATATAGAGGAA GGGGGTCCGGTCCGGTCCG
pCAM-Motif1S	GGATCCTGTGAACGGTAATCGATG	AAGCTTCCGTGTTCTCTCCAAATGAAATGAACTTCCTTATATAGAGGA AGGGCTCTCAGAACCATCAAAG
pCAM-Motif1SM1	GGATCCTGTG GGACC TAATCGATG	
pCAM-Motif1SM2	GGATCCTGTGTAATCGATGAAAAT	
pHis2-Motif2	AATTCCGGTTGCGGTTGCGGTTGGAGCT	CCAACCGCAACCGCAACCGG
pHis2-Motif2M	AATTCATTCCATTCTTCTATTCTGAGCT	CAGGAATAGGAATAGGAATG
pHis2-Motif2S	GGAATTTCGATCGGTTGACAGAGTTAC	CTCTCAGACTGGGGACTCGGAGCTCG
pHis2-Motif2SM1	GGAATTTCGAT ATTCTACAGAGTTAC	
pHis2-Motif2SM2	GGAATTTCGATACAGAGTTACTTCGTC	
pCAM-Motif2	GATCCCGGTTGCGGTTGCGGTTGCCCTTCCTCTATATAAGGAAGTTC ATTCATTTGGAGAGAACACGGA	AGCTTCCGTGTTCTCTCCAAATGAAATGAACTTCCTTATATAGAGGAA GGGCAACCGCAACCGCAACCGG
pCAM-Motif2M	GATCCATTCTATTCTATTCTCCCTTCCTCTATATAAGGAAGTTCA TTTCATTTGGAGAGAACACGGA	AGCTTCCGTGTTCTCTCCAAATGAAATGAACTTCCTTATATAGAGGAA GGGAGGAATAGGAATAGGAATG
pCAM-Motif2S	GGATCCGATCGGTTGACAGAGTTAC	AAGCTTCCGTGTTCTCTCCAAATGAAATGAACTTCCTTATATAGAGGA AGGGCTCTCAGACTGGGGACTCG
pCAM-Motif2SM1	GGATCCGATATTCTACAGAGTTAC	

pCAM-Motif2SM2	GGATCCGATACAGAGTTACTTCGTC	
pHis2	GCCTTCGTTTATCTTGCCTGCTC	CGATCGGTGCGGGCCTCTTC
pCAMBIA1301	TAGAGTCGACCTGCAGGCAT	ATCATCATCATAGACACACG
pROKII	TTTCATTTGGAGAGAACACG	TGCCAAATGTTTGAACGATC
pGAD	CTATTCGATGATGAAGATACCCACCAAACCC-3'	GTGAACTTGCGGGGTTTTTCAGTATCTACG-3'
pGAD-JrMYB44	TGGCCATTATGGCCCGGGATGGAGGCGTCACAGAGAG	GACATGTTTTTTCCCGGGTCAAAGTTCAAGCCTGGCCAT
AD-JrWRKY2	TGGCCATTATGGCCCGGGATGTCAAAGAAGGACCAGGAAT	GACATGTTTTTTCCCGGGCTATGTTATCTGCTCTTCTT
BD-JrWRKY7	CATGGAGGCCGAATTCATGGCCGTGGAGTTCATGATG	GCAGGTCGACGGATCCTCAAGAGGATTCTAGGATCAG
pSupre1300-JrMYB44	ATCGTCTAGAATGGAGGCGTCACAGAGAGAC	CGATGGTACCTCAAAGTTCAAGCCTGGCCAT
pGreenI-JrWRKY7	CGATGGTACCATGGCCGTGGAGTTCATGAT	ATCGGGATCCTCAAGAGGATTCTAGGATCAG
pGreenII-JrDREB2A	CGATGGTACCATGGCTGACGGGCAAAGAAG	ATCGGGATCCTCATAAAAGCATTTCCAAG
AD-JrMYB44	TGGCCATTATGGCCCGGGATGGAGGCGTCACAGAGAGAC'	GACATGTTTTTTCCCGGG TCAAAGTTCAAGCCTGGCCAT
BD-JrMYB44	CATGGAGGCCGAATTC ATGGAGGCGTCACAGAGAGAC	AAGGAAAAAAGCGGCCGCTCAAAGTTCAAGCCTGGCCAT
AD-JrMYC2	TGGCCATTATGGCCCGGGATGGACGAGATTATCTCTTCC	GACATGTTTTTTCCCGGGCTAACTCCGCATACTTTGCAG
BD-JrMYC2	CATGGAGGCCGAATTCATGGACGAGATTATCTCTTCC	GCAGGTCGACGGATCCCTAACTCCGCATACTTTGCAG
AD-JrDof1	CTAGTCTCTAGAGGATCCATGCAAGACCCAGCAACATT	AGGTCGACGGATCCCTACTGAGATCTTGAACCTGG
BD-JrDof1	GCAGGTCGACGGATCCATGCAAGACCCAGCAACATTC	AAGGAAAAAAGCGGCCGCTACTGAGATCTTGAACCTGG
pFGC-JrMYB44-Cis	ATCGTCTAGAGTCAGGCAAGTCGTGCCG	CGATGGATCCGGTGTCATCGCTCATCAT
pFGC-JrMYB44-Anti	ATCGGGTACCGGTGTCATCGCTCATCAT	CGATGAGCTCGTCAGGCAAGTCGTGCCG
NLuc-JrMYB44	CGATGGTACCATGGAGGCGTCACAGAGAGAC	ATCGTCTAGATCAAAGTTCAAGCCTGGCCAT
CLuc-JrMYC2	CGATGGTACCATGGACGAGATTATCTCTTCC	ATCGGGATCCCTAACTCCGCATACTTTGCAG
CLuc-JrDof1	CGATGGTACCATGCAAGACCCAGCAACATTC	ATCGGGATCCCTACTGAGATCTTGAACCTGG
JrMYB44-His	TAAGAAGGAGATATACAT ATGGAGGCGTCACAGAGAGACAT	GTGGTGGTGGTGGTGTCTCGAGTAAGTTCAAGCCTGGCCATGTAAC
GST-JrDof1	GATCTGGATCCGCGTGGATCCATGCAAGACCCAGCAACATT	GTCACGATGGTGCACCTCGACTACTGAGATCTTGAACCTGG

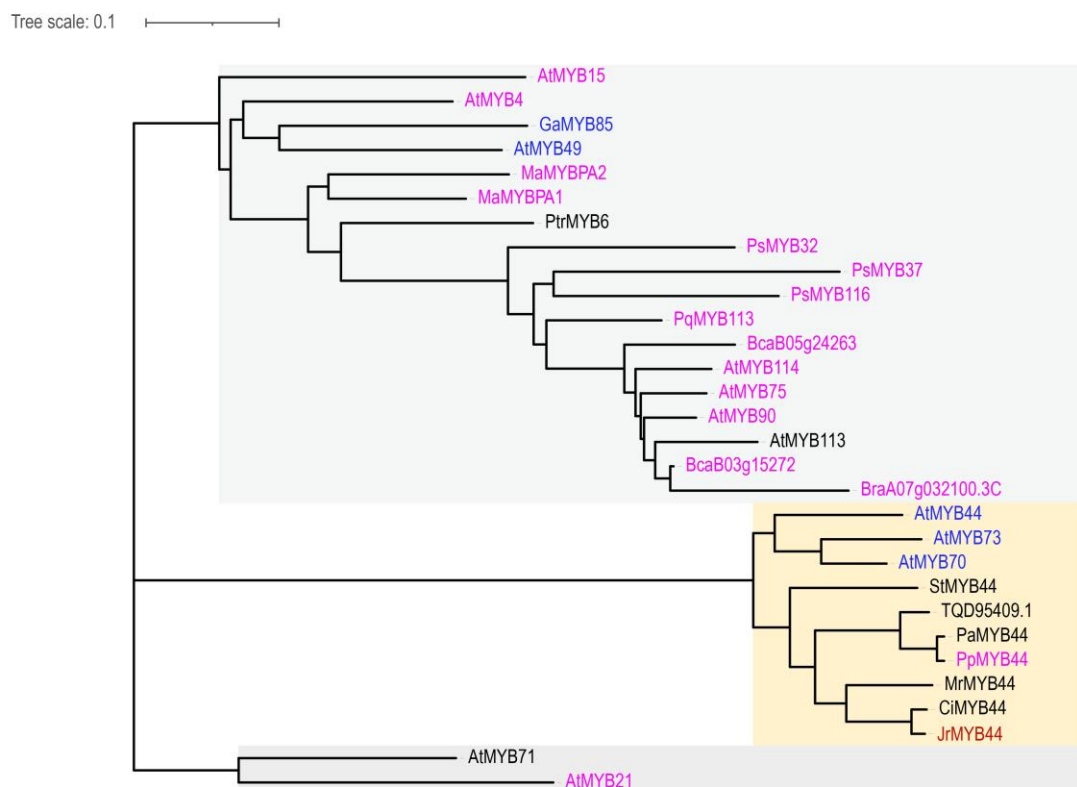
Supplementary Table S3 Primers for RT-qPCR of the *Arabidopsis thaliana*.

Gene name	Accession No.	5'-primer	3'-primer
<i>AtSnRK2.2</i>	AT3G50500.2	5'-CGCCTTCCCATTTGGCTAT-3'	5'-AGGTGCCGGACTTCCATCT-3'
<i>AtSnRK2.3</i>	AT5G66880.1	5'-ATGCACGACAGTGATCGA-3'	5'-TGATAGCCAGATGAGTCG-3'
<i>AtSnRK2.6</i>	AT4G33950.1	5'-GGTATGAACTCGTCAAGG-3'	5'-GTTCTCCTCCAGATGCAT-3'
<i>AtPYL1</i>	AT5G46790.1	5'-GTTGCTCATCTCTCCTAGC-3'	5'-TCTCCGATCATCGTCCAAC-3'
<i>AtPYL2</i>	AT2G26040.1	5'-TCATAACCCAACGCATCC-3'	5'-TCGTCATCGACGAACCTCA-3'
<i>AtPYL3</i>	AT1G73000.1	5'-CAGAGTTAACGGTAACGG-3'	5'-GAACTCGTTGACCGATGT-3'
<i>AtPYL4</i>	AT2G38310.1	5'-ATGATGATCGCGTCGTTTC-3'	5'-GGAGGCTACCAACGTTATC-3'
<i>AtPYL5</i>	AT5G05440.1	5'-GGTCCGATCAAGAGAGTGT-3'	5'-TACGGCACTGTCTGATGAAG-3'
<i>AtABF1</i>	AT1G49720.2	5'-TGATGAGCTTCAGAGCAC-3'	5'-CAGACTTCATCGACAGTC-3'
<i>AtABF2</i>	AT1G45249.3	5'-TCGATATACTCGTTGACG-3'	5'-TCTGACTAAGCGTTTCGAG-3'
<i>AtABF3</i>	AT4G34000.1	5'-GTCTATGAACATGGATGA-3'	5'-AGTGAACCTTGTCTCTGC-3'
<i>AtABF4</i>	AT3G19290.3	5'-ATGGACTGCTGAGGAAGC-3'	5'-GAGGCACATTTCGACTCAC-3'
<i>AtDREB1A</i>	NM_118680.1	5'-TCGTGAGACTCGTCACC-3'	5'-GATTCGGAGTCTCCAAGC-3'
<i>AtDREB1B</i>	AB013816.1	5'-TCGTGAGACTCGTCACC-3'	5'-AAGTTGAGACATGCTGAT-3'
<i>AtDREB1C</i>	NM_118679.1	5'-GCTGAGATGGCAGCTCGT-3'	5'-ATGAGCATCCGTCGTCAT-3'
<i>AtDREB2A</i>	NM_120623.2	5'-TACTACTGTGGCTGAGAG-3'	5'-CTGCTACCTCGATTAGG-3'
<i>AtDREB2B</i>	NM_111939.2	5'-AGAGTACAACGAGATTGT-3'	5'-ACCGTACATAGCGGTAGC-3'
<i>AtDREB2C</i>	NM_129594.2	5'-TGGAGAGAGTACAATGAG-3'	5'-GCTTCATATGAACCTGGAG-3'
<i>AtDREB2G</i>	NM_121850.1	5'-ACTCTATGGACACGAGGC-3'	5'-CACTTGAAGACGAACATC-3'
<i>AtSOD1</i>	AT1G08830.1	5'-ATGGCGAAAGGAGTTGCAG-3'	5'-TGTCGATTAGCATCCTCAG-3'
<i>AtSOD2</i>	AT2G28190.1	5'-ATGGCTGCCACCAACAC-3'	5'-CTGAGTCATCTTGGGTC-3'
<i>AtSOD3</i>	AT1G12520.1	5'-GTCAGTGGCAACGACTTCAG-3'	5'-GCTGAGGCATGGCTCGATC-3'
<i>AtP5CS1</i>	AT2G39800.1	5'-ACGTATCGTCGTTAAGGT-3'	5'-TGAGGCTTCTGAAGATCC-3'
<i>AtP5CS2</i>	AT3G55610.1	5'-AGGTGGAAGATTGGCTCT-3'	5'-GTAAGCCATGAGACTGCTC-3'
<i>AtGSTT1</i>	AT5G41210.1	5'-CAGATCGAATGTCACAG-3'	5'-TGATCAGCAACACTTGG-3'
<i>AtGSTT2</i>	AT5G41240.1	5'-GTTGATGGCAGACTTAAGC-3'	5'-TTCTCAGCTTCAGCAGCT-3'
<i>AtGSTT3</i>	AT5G41220.1	5'-GTGTATGCGGATCGAATG-3'	5'-CTACACTTGGGTATGCTG-3'
<i>AtGSTU1</i>	AT2G29490.1	5'-GCGTGCCATACGAATACT-3'	5'-GGATCTGGTCATCGATG-3'
<i>AtGSTU2</i>	AT2G29480.1	5'-AGTCGTAGAGTCGAGATG-3'	5'-TAGGGATCGTGAGGTAG-3'
<i>AtGSTU3</i>	AT2G29470.1	5'-TTCAGTCGTAGAGTCGAG-3'	5'-CATATGGACTTTGCGGTAG-3'
<i>AtGSTU4</i>	AT2G29460.1	5'-GTGCCTTACGAGTACTTG-3'	5'-TGGTCCAACCTGTTTCATC-3'
<i>AtGSTU5</i>	AT2G29450.1	5'-CATACCGTACGAGTACGT-3'	5'-AATCTGTTTCATCGACGAG-3'
<i>AtGSTU6</i>	AT2G29440.1	5'-GGTGTAACGTACGAATAC-3'	5'-AAGACTCGAGCCTTGGAT-3'
<i>AtGSTU7</i>	AT2G29420.1	5'-ATGAGTTCTGAGCAAG-3'	5'-AGACCAGAATCGAGCCAT-3'
<i>AtGSTU8</i>	AT3G09270.1	5'-GAGTAGAGATGGTCCT-3'	5'-GCACGTTCTAAGGATC-3'
<i>AtGSTU9</i>	AT5G62480.1	5'-ACTCCATGGATCATTCGC-3'	5'-AAGGACTCAGAGATGGGT-3'
<i>AtGSTU10</i>	AT1G74590.1	5'-ACATGGGACGTGGATAAG-3'	5'-TGTCCACGTCTCATCGAT-3'
<i>AtGSTU11</i>	AT1G69930.1	5'-AGCTACTAGGAGCATGGC-3'	5'-GAGCCAAGTCTCATCAAC-3'
<i>AtGSTU12</i>	AT1G69920.1	5'-CGAATACTACTGTGAAGC-3'	5'-GACGTATTGGACGATGTTG-3'
<i>AtGSTU13</i>	AT1G27130.1	5'-CTGTCAAGTACGAGTAC-3'	5'-GTCATCGATGTACTGAG-3'
<i>AtGSTU14</i>	AT1G27140.1	5'-ACCTGATGATGATCTTGGG-3'	5'-GAAGCACTTGTCGTCGAT-3'
<i>AtGSTU15</i>	AT1G59670.1	5'-CGGATCTAAGAGTGAGCT-3'	5'-CGGTAACCACTTGTTCATC-3'
<i>AtGSTU16</i>	AT1G59700.1	5'-AGGAGTATGGTACAGTCC-3'	5'-GTTCCACGTCTCATCAATG-3'
<i>AtGSTU17</i>	AT1G10370.1	5'-GAAGCTGATCGGTGCATG-3'	5'-TGGACTCACTCACCGGTTT-3'

<i>AtGSTU18</i>	AT1G10360.1	5'-TGAAGCTGATCGGCTCAT-3'	5'-AGTTCCAAGCCTCGTCGAT-3'
<i>AtGSTU19</i>	AT1G78380.1	5'-ATGAGGACAAGGATCGCA-3'	5'-AGAACCTAGCTTGAGCTC-3'
<i>AtGSTU20</i>	AT1G78370.1	5'-AGTATGTTCTGGGATGAGG-3'	5'-GACGTACTGGACAACGTT-3'
<i>AtAPX1</i>	AT1G07890.1	5'-CCGTGAGCGAAGATTACAAG-3'	5'-GAGCAATGTGGATACCACTG-3'
<i>AtAPX2</i>	AT3G09640.1	5'-GCTGTTTCTAGAGATGCAAG-3'	5'-GGAACAGCTCCTTGATAG-3'
<i>AtWRKY71</i>	AT1G29860.1	5'-CTCACTAGAGAAGGTCTTC-3'	5'-TCACCAACACCATGTAGGT-3'
<i>AtWRKY63</i>	AT1G66600.1	5'-ACATCGATCACAAGGCTG-3'	5'-TTTGAGGCACAAGACCTG-3'
<i>AtWRKY57</i>	AT1G69310.1	5'-ATCTGAGCAACGACGACT-3'	5'-GAACTTGAGGTAGCTGAG-3'
<i>AtWRKY1</i>	AT2G04880.1	5'-CATACCAGTGGCTGTAAC-3'	5'-CAGTTGTATCCGTCTTCC-3'
<i>AtWRKY25</i>	AT2G30250.1	5'-ACTATCCAGAGAGAACCG-3'	5'-GGTTGAGATTGTAGCTGC-3'
<i>AtPP2C3</i>	AT2G29380.1	5'-AAGTAGTGACCGACGCATGT-3'	5'-TGGACTGGATACGTCGACAT-3'
<i>AtPP2CF1</i>	AT3G05640.1	5'-GCTAGATCCTTCTCGATC-3'	5'-GATGGCACAGTCCTGATT-3'
<i>AtDOF1</i>	AT1G51700.1	5'-CAGTCGATGATGATGACG-3'	5'-ACTAGACGGAGAAGAACC-3'
<i>AtDOF2.1</i>	AT2G28510.1	5'-GTCCAAGATGTGAATCTCC-3'	5'-GGTTCTGAAGTGGATCAGT-3'
<i>AtDOF2.4</i>	AT2G37590.1	5'-TGGAGGTCATGTTCTTCG-3'	5'-TGAGTGAGGCTGTAGTTG-3'
<i>AtDOF2</i>	AT3G21270.1	5'-TGATGGCGAAGCAACAAC-3'	5'-TGGTTGCGTTCTTACGAG-3'
<i>AtWD401</i>	AT1G24130.1	5'-TCCTCAACGTCATCATCG-3'	5'-TTGGCAACTACGTTACGG-3'
<i>AtWD402</i>	AT1G24530.1	5'-TCATCTTCCTCACTCAGC-3'	5'-CTTACTTCGTGTCCAGAC-3'
<i>AtWD403</i>	AT1G29320.2	5'-AAGTGACTGAAGCTCGTG-3'	5'-TCTGAGACTCACATCTCC-3'
<i>Actin2</i>	AT3G18780	5'-TGCAGGAGATGATGCTCC-3'	5'-ATACGAAGCTCATTGTAG-3'
<i>GAPDH</i>	AT1G13440	5'-TCTCGATCTCAATTTTCGCAAAA-3'	5'-CGAAACCGTTGATTCCGATT-3'
<i>AtMYB44</i>	AT5G67300.1	5'-CATGGAGTCCTGAAGAAG-3'	5'-AGAAGACGAGCAATCGTC-3'
<i>AtMYB70</i>	AT2G23290.1	5'-AAGGACCATGGAGTCCT-3'	5'-AGTGCGACCATTGAGAAG-3'
<i>AtMYB73</i>	AT4G37260.1	5'-ATGATCTGTTGCAGAGGC-3'	5'-GGTTCGTCCATTGAGAAG-3'



Supplementary Fig. S1 Correlation analysis of drought resistance, *JrMYB44* expression and polyphenols. *, **, and *** indicates significant correlation at $P < 0.05$, $P < 0.01$ and $P < 0.001$ level, accordingly.



Supplementary Fig. S2 Phylogenetic tree analysis of JrMYB44 protein and its homologs from other species based on sequence alignments of the encoded proteins using neighbor-joining method in MEGA7. Jr, *Juglans regia*; At, *Arabidopsis thaliana*; Ga, *Gossypium arboreum*; Ma, *Musa acuminata*; Ptr, *Populus trichocarpa*; Ps, *Pisum sativum*; Pq, *Paeonia qiui*; BraA07g032100.3C is a MYB of *Brassica rapa*, BcaB05g24263 and BcaB03g15272 are MYBs of *B. carinata*; St, *Senna tora*; TQD95409.1 is a MYB of *Malus baccata*; Pa, *Prunus avium*; Pp, *P. persica*; Mr, *Morella rubra*; Ci, *Carya illinoensis*. Purple and blue indicated genes related to polyphenol synthesis and stress response, respectively. Red marked walnut JrMYB44.

(A) AtMYB44

Sequence ID: Query_4498859 Length: 305 Number of Matches: 1

Range 1: 3 to 277 [Graphics](#)[Next Match](#) [Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps
234 bits(596)	2e-80	Compositional matrix adjust.	139/305(48%)	190/293(64%)	38/293(12%)
Query 9	DRVKGWSPPEDEMLRLKLVQSGQARSWSVSKAIGRSGKSLRWCNQLSPEVHRPFT	68			
Sb jct 3	DR-KGPWSPPEDE LR-LV G R-W+VSK+I GRSGKSLRWCNQLSP+VHRPF+ DRKGPWSPPEDEQLRLVVKYGFPRNVTVSKSIPGRSGKSLRWCNQLSPQVHRPFS	62			
Query 69	LEEDQIIIVKHAHYGNKWTIARLLNGRTDNAIKHNWSTLKRYSMSDDTTATTTEET	128			
Sb jct 63	EED+ I +AHA++GNKWATIARLLNGRTDNA+KNHNWSTLKRK D +E+ AEEDETIARAHAFGNKWATIARLLNGRTDNAVKNHNWSTLKRKCGY-DHRYDGSSED-	120			
Query 129	LSRPHKK--SAGPPPLVTSSRHYSAGSPSGSDVSDSS-LPAISTSHVIRPGARSCAIP	185			
Sb jct 121	RP K+ SAG PP+VT + S GSP+GSDVSDSS +P + + +P R A+ -HRPVKRSVAGSPPVVT--GLVMSPGSPGTSDVSDSTIPILPSVELFKPVPRGAVVL	177			
Query 186	PSHRDESPPHNQKEDNRDNKIEPSTLLSLSLPGTE-----SYEFSVRDGPFPREY	238			
Sb jct 178	P PI + + +P T LSLSLPG + S+E ++ + R + PL-----PI-----ETSSSSDDPPTLSLSLPGADVSEENSHESHTNNTTSSR-H	224			
Query 239	RKSNPSVVDN-----KYSTKTFP--PDLVSMQDMIRTEVRSYMARLE 281				
Sb jct 225	+N+ S +P + + K+FP + ++V+Q+MI+ EVRSYM ++ NHNVTVSMPFSGGFRGAIEEMGKSPGNGGEFMAVVOEMIAEVRSYMTEMQ 277				

AtMYB73

Sequence ID: Query_4498861 Length: 320 Number of Matches: 1

Range 1: 5 to 277 [Graphics](#)[Next Match](#) [Previous Match](#)

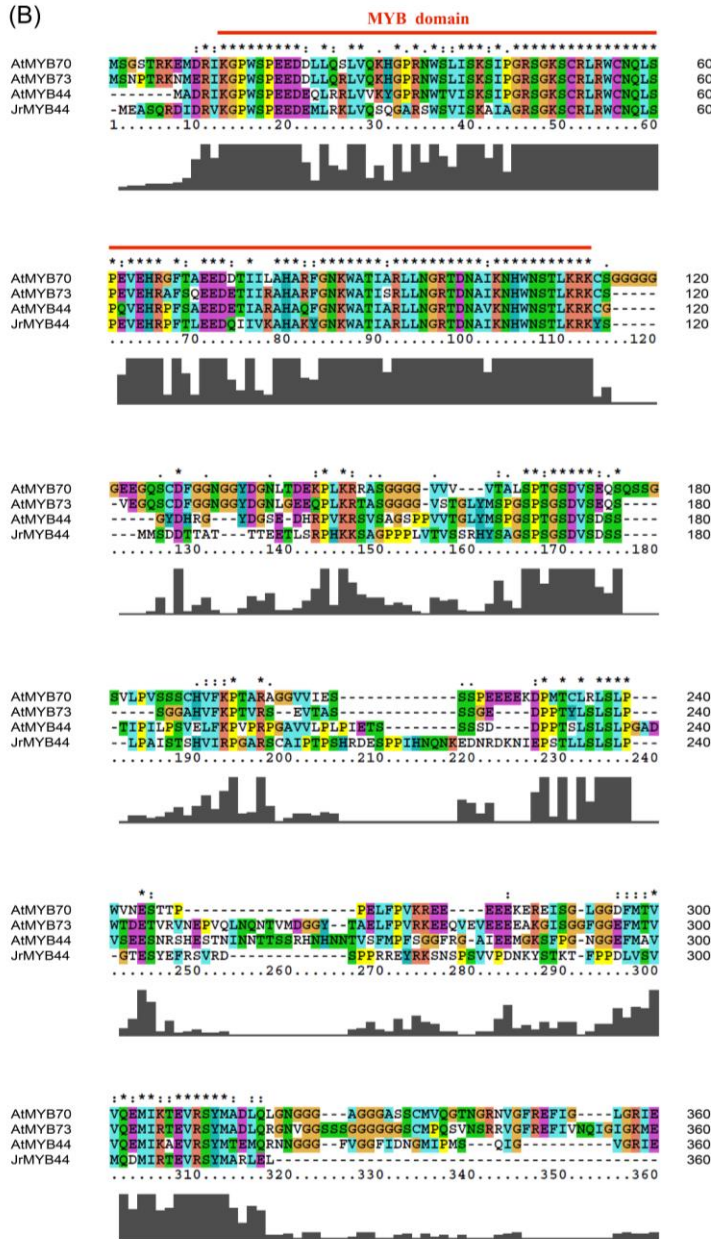
Score	Expect	Method	Identities	Positives	Gaps
233 bits(593)	1e-79	Compositional matrix adjust.	139/305(46%)	185/305(60%)	59/305(19%)
Query 4	SQRIDRVKGPWSPPEDEMLRLKLVQSGQARSWSVSKAIGRSGKSLRWCNQLSPEVE	63			
Sb jct 5	+++++R+KGPWSPPEED+L+LVQ G R+WS+ISK+I GRSGKSLRWCNQLSPEVE TRKNMERIKGPWSPPEEDLLQLVQKHGPRNWSLISKIPGRSGKSLRWCNQLSPEVE	64			
Query 64	HRPFTLEEDQIIIVKHAHYGNKWTIARLLNGRTDNAIKHNWSTLKRYSMS--DDT	120			
Sb jct 65	HR F+ EED+ I+AH++GNKWATI+RLNGRTDNAIKHNWSTLKRK S+ D HRAFQEEDETIARAHAFGNKWATISRLNGRTDNAIKHNWSTLKRKCSVEGQSCDFG	124			
Query 121	TATTEETLS--RPHKKSAGPPPLVTSSRHYSAGSPSGSDVSDSS-LPAISTSHVIRPGA	178			
Sb jct 125	+ L +P K+A V+ + + S GSPSGSDV+ S +HV +P GNGGYDNLGEEQPLRTASGGGGVS-TGLVMSPGSPGSDVSEQSGG--AHVFKPTV	180			
Query 179	RSCAIPTPSHRDESPPHNQKEDNRDNKIEPSTLLSLSLPOTESYEFVRDGPFPREY	238			
Sb jct 181	RS T S E PP T LSLSLP T+ +VR + P + RSEY--TASSSGEDFP-----TYLSLSLPWTD--ETVRVNEPQLN	217			
Query 239	RKSNPSVVDNKNYSTKTFP-----PDLVSMQDMIRTEVRSY 276				
Sb jct 218	+ + V D Y+ + PP + ++V+Q+MI+ TEVRSY QNT-----VMDGGYTAEFLFPVRKEEQVEVEEAKGISGGGFGFMTVQEMIRTEVRSY	272			
Query 277	MARLE 281				
Sb jct 273	MA L+ MADLQ 277				

AtMYB70

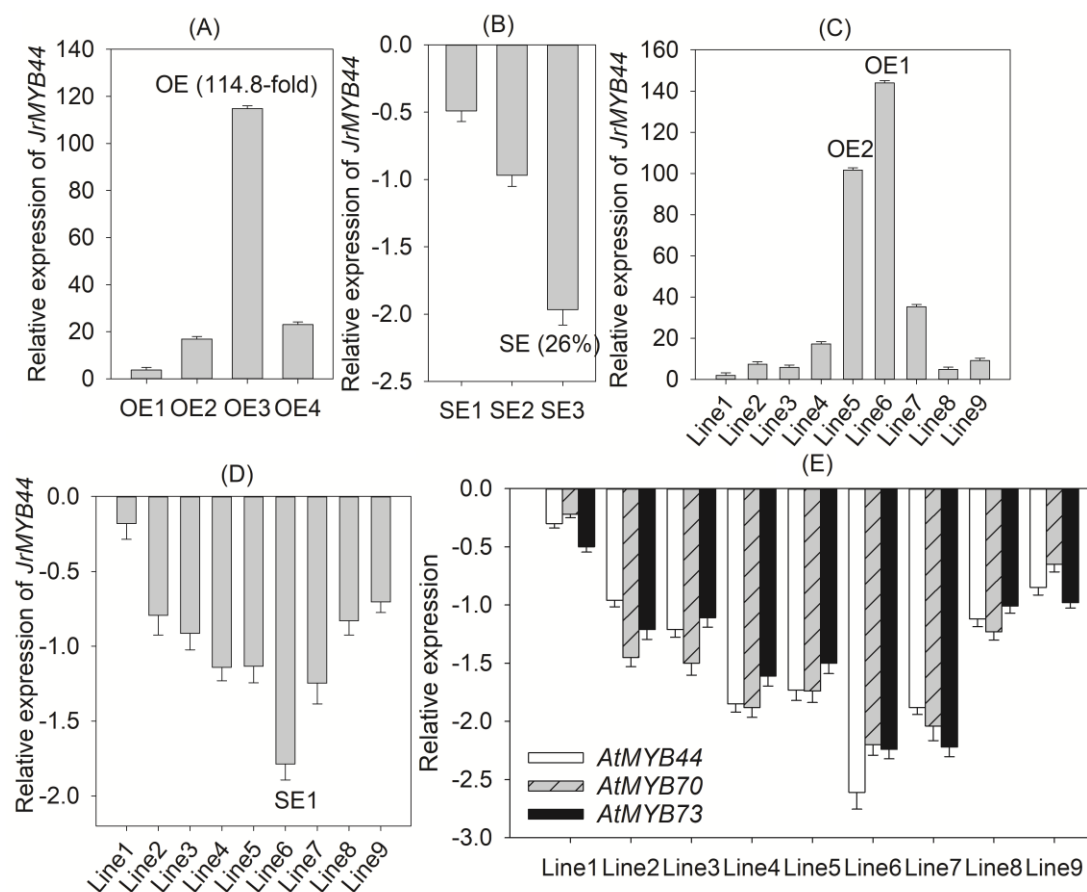
Sequence ID: Query_4498860 Length: 309 Number of Matches: 1

Range 1: 4 to 274 [Graphics](#)[Next Match](#) [Previous Match](#)

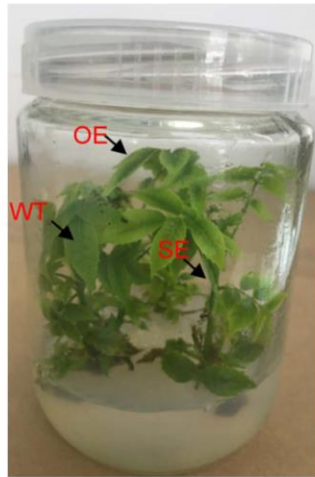
Score	Expect	Method	Identities	Positives	Gaps
219 bits(557)	2e-74	Compositional matrix adjust.	132/304(43%)	171/304(56%)	57/304(18%)
Query 3	ASQRIDRVKGPWSPPEDEMLRLKLVQSGQARSWSVSKAIGRSGKSLRWCNQLSPEV	62			
Sb jct 4	+++++R+KGPWSPPEED+L+LVQ G R+WS+ISK+I GRSGKSLRWCNQLSPEV STRKEMDRKGPWSPPEEDLLQLVQKHGPRNWSLISKIPGRSGKSLRWCNQLSPEV	63			
Query 63	EHRPFTLEEDQIIIVKHAHYGNKWTIARLLNGRTDNAIKHNWSTLKRYSMSDDTTA	122			
Sb jct 64	EHR FT EED I+ AHA++GNKWATIARLLNGRTDNAIKHNWSTLKRK S EHRGFTAEEDDTIILAHAFGNKWATIARLLNGRTDNAIKHNWSTLKRKCSGGGGGEE	123			
Query 123	TTITE-----TLRPHKKSAGPPPLVTSSRHYSAGSPSGSDVSDSS-----L	165			
Sb jct 124	+ + T +P K+ A +A SP+GSDV+ S L GQSCDFGNGGYDNLDEKPLKRAS--GGGGVVVTALSPGSDVSEQSGSGSVL	179			
Query 166	PAISTSHVIRPGARSCAIPTPSHRDESPPHNQKEDNRDNKIEPSTLLSLSLPGTESYE	226			
Sb jct 180	P S+ HV +P AR+ + S E + + +P T L LSLP PVSSSCHVFKPTARAGGVIESSPEE-----EEKDPMTCRLSLPFWN--	223			
Query 226	FRSVRDSPPPREYRKSNSPSVVP-----DNKYSTKTFPDLVSMQDMIRTEVRSYMA	278			
Sb jct 224	+ + P + P + + D ++V+Q+MI+ TEVRSYMA -----ESTTPPELFPVKEEKEERIEISGLGDFMTVQEMIKTEVRSYMA	270			
Query 279	RLEL 282				
Sb jct 271	L+L DLQL 274				

(B)

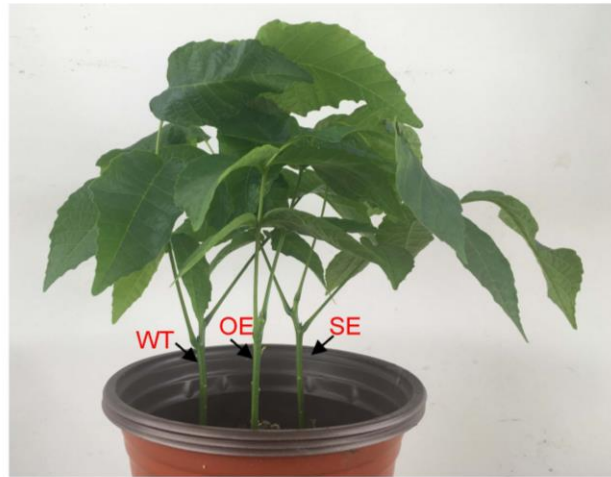
Supplementary Fig. S3 Amino acid sequence alignment and conserved domain of JrMYB44 and AtMYBs. A, Amino acid sequence alignment using blastp of NCBI. JrMYB44 was the Query, while AtMYB44, AtMYB73 and AtMYB70 were Sb jct. B, Conserved domain analysis using Clustal X.



Supplementary Fig. S4 The relative expression of *JrMYB44* in transformed lines. A-B, four overexpressed and three suppressed walnut lines transformed by *JrMYB44*. C-D, nine overexpressed and nine suppressed *A. thaliana* lines transformed by *JrMYB44*. E, The relative expression of *AtMYBs* in *JrMYB44* suppression *Arabidopsis* lines.

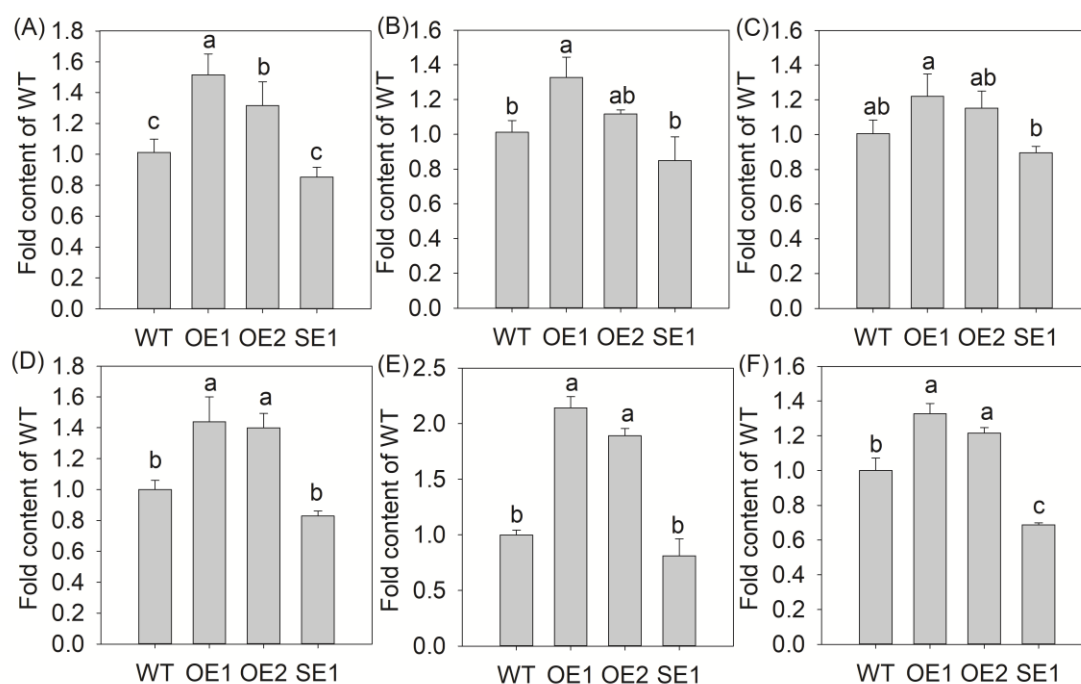


(A) Tissue culture seedlings (TCS)

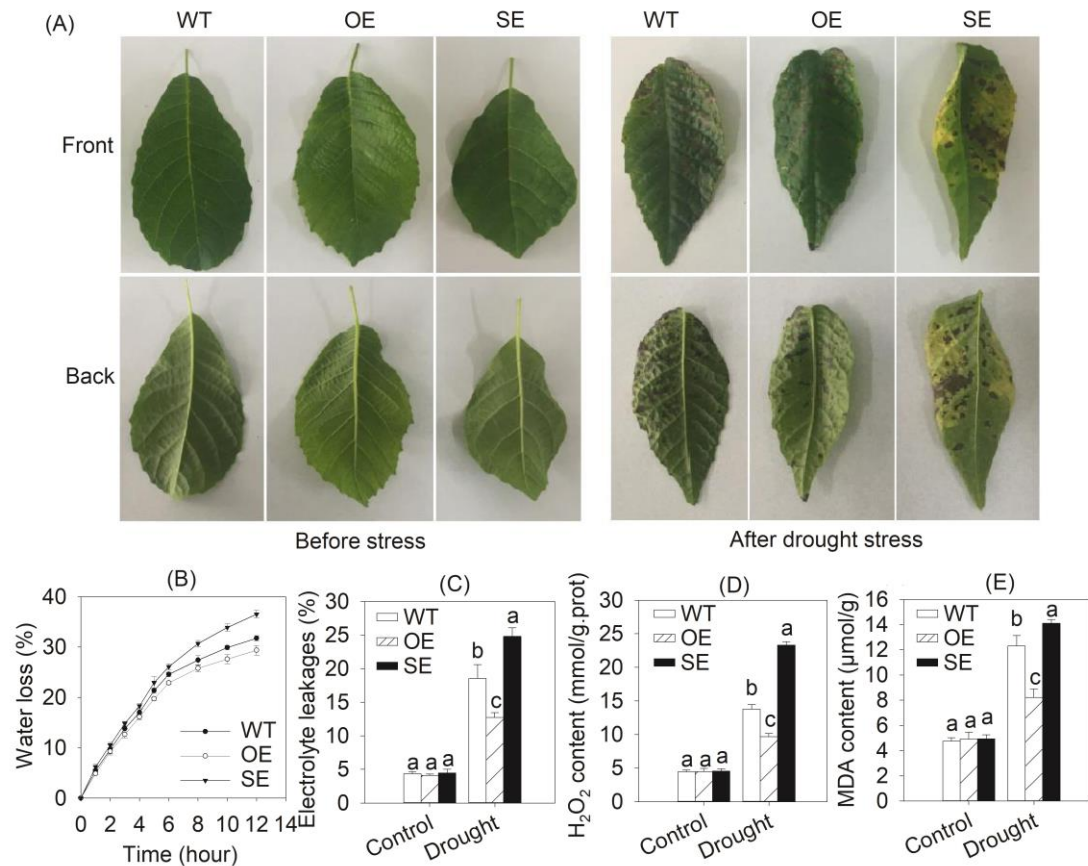


(B) Potted seedlings (PS)

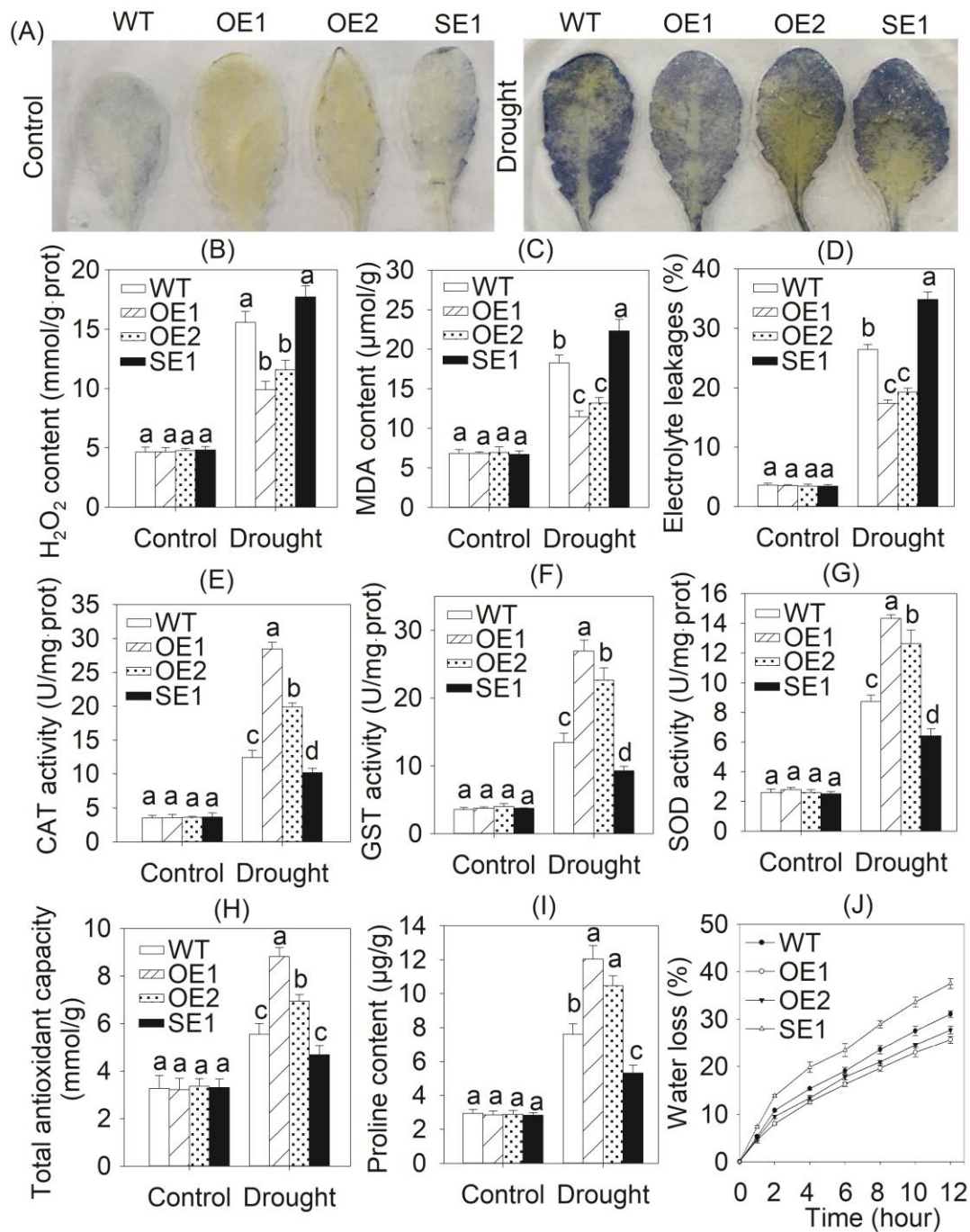
Supplementary Fig. S5 Phenotype of walnut WT, OE and SE. A, tissue culture seedlings (TCS). B, potted seedlings (PS).



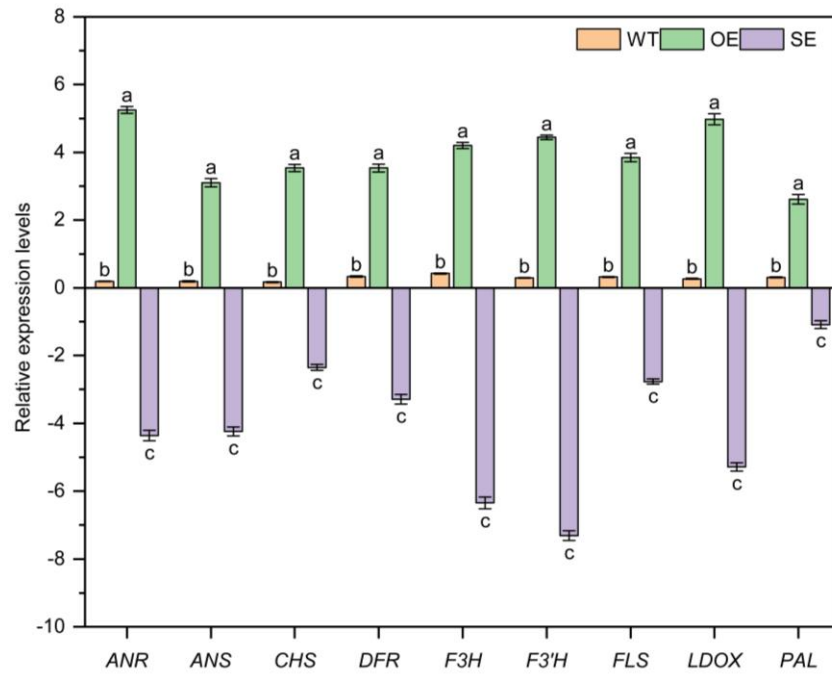
Supplementary Fig. S6 Total polyphenol content and components in *JrMYB44* transgenic *A. thaliana*. Aerial parts of WT, OE1, OE2, SE1 during bolting stage were collected for index determination. Error bars represent the SD (n=3). Lowercase indicates significant differences among WT, OE1, OE2, SE1 ($P < 0.05$). A, total polyphenol. B, catechin. C, chlorogenic acid. D, syringate. E, p-Coumaric acid. F, quercetin.



Supplementary Fig. S7 Drought stress tolerance analysis of *JrMYB44* by homologous transient overexpression in *J. regia*. WT, OE and SE tissue culture seedlings of the same age were transferred to pot conditions for four months, and treated with no watering for 12 d as drought stress. The significant differences among WT, OE, SE were marked with lowercase ($P < 0.05$). A, Leaf phenotype. B-E, water loss, electrolyte leakages (EL) rate, H₂O₂ content and MDA content, accordingly.



Supplementary Fig. S8 Drought stress tolerance analysis of *JrMYB44* by heterologous overexpression in *A. thaliana*. The significant differences among WT, OE, SE were marked with lowercase ($P < 0.05$). A, NBT staining. B-J, H_2O_2 content, MDA content, electrolyte leakages (EL) rate, CAT activity, GST activity, SOD activity, total antioxidant capacity, proline content and water loss according to A, accordingly.



Supplementary Fig. S9 Expression of genes related to the anthocyanin synthesis pathway in walnut WT, OE and SE lines. The relative expression level was related to the expression of internal reference genes from three repeats.

(A)

>*JrWRKY7* Promoter 1038 bp

GTGCGTATGATATATCTTTGTCAAAGGAAATCAAATCCAGTTTAGTCAAGCATAGGAAGGG
ACCTCAATTTGTGGGTGGGCACAATAAAATAAGTTTAGTACAAAATAGCATTGACTATTCTA
CGACTAGTCTATATTTAAATTTAAAAAAATAATATTACAATTTAGATTATGCAAGTAAGTA
TGAGAGATTACATGTAAAAAATTAATTTTTTAATAATAAATTCTATTATTTTTTAAAAAGAATA
AGTAGAGTTTGTACGTCATAAACTGTATCTAGCAGTACTCTTAATCTACATTTAATTTAATC
TGATTGGTTAAAACTAGCGATAATTACAGAAAATGTGTAACAAATACAATCAAGTTAATTGA
GAATTAGGCATAGGTTTGTGATATTGCAGAGAAAAACAGACCATACATGTAACGAATCAAA
TATGTGGTAGAAAAGGAAATGAACATAGGGAGATTTGAAAGTACCGGAAAAACAACAACA
AACAATAAGACATCCTTATTATTAACAACCTCCAATCAAAGTACTGTTTCAAAGCCCAGCAT
TACGAAGTCAACTCTACCGTGCTGGCAGGCAACAACAAATTAACCCACTTTCTCTCTCCA
ACACAGATCGAATGGTTAATTGCCAATGGTTTGACCTGATGTACGCCAATCTCAATTACACA
ACGTTCTGTAAGACTACATTAACCTTAACAGGCCCCACATCGATCAGATGAGGTCAATGTC
GTGACTAATAAAAAAAGGTTAAAAAATAGGAAATAAAATTAATAATTTGTGAACG
GTAATCGATGAAAATTGTCATGTAGTTGGGGCCTGATTCGCACCTACGGTTTGACGGGG
GCCGCTAGCGTGACAGGTCGGTCACGCTGTGGGCCAGTAGGGGACTGAGGAGGGCTAA
AAATTTAATGGGCACCTCTTTGACCAGAGACCCACCTTTTCGTTTTATTAGCTCTCCTCGTT
CCTTTTTACCTTTTCTCTTTCTGTTCTCTGTCTTTGATGGTTCTGAGAG

AMYBOX1	355 (+) TAACARA	S000020
MYBGAHV	355 (+) TAACAAA	S000181
MYBCOREATCYCB1	806 (+) AACGG	S000502

The underlined part was used in Y1H and GUS activity assay (Motif1S)

(B)

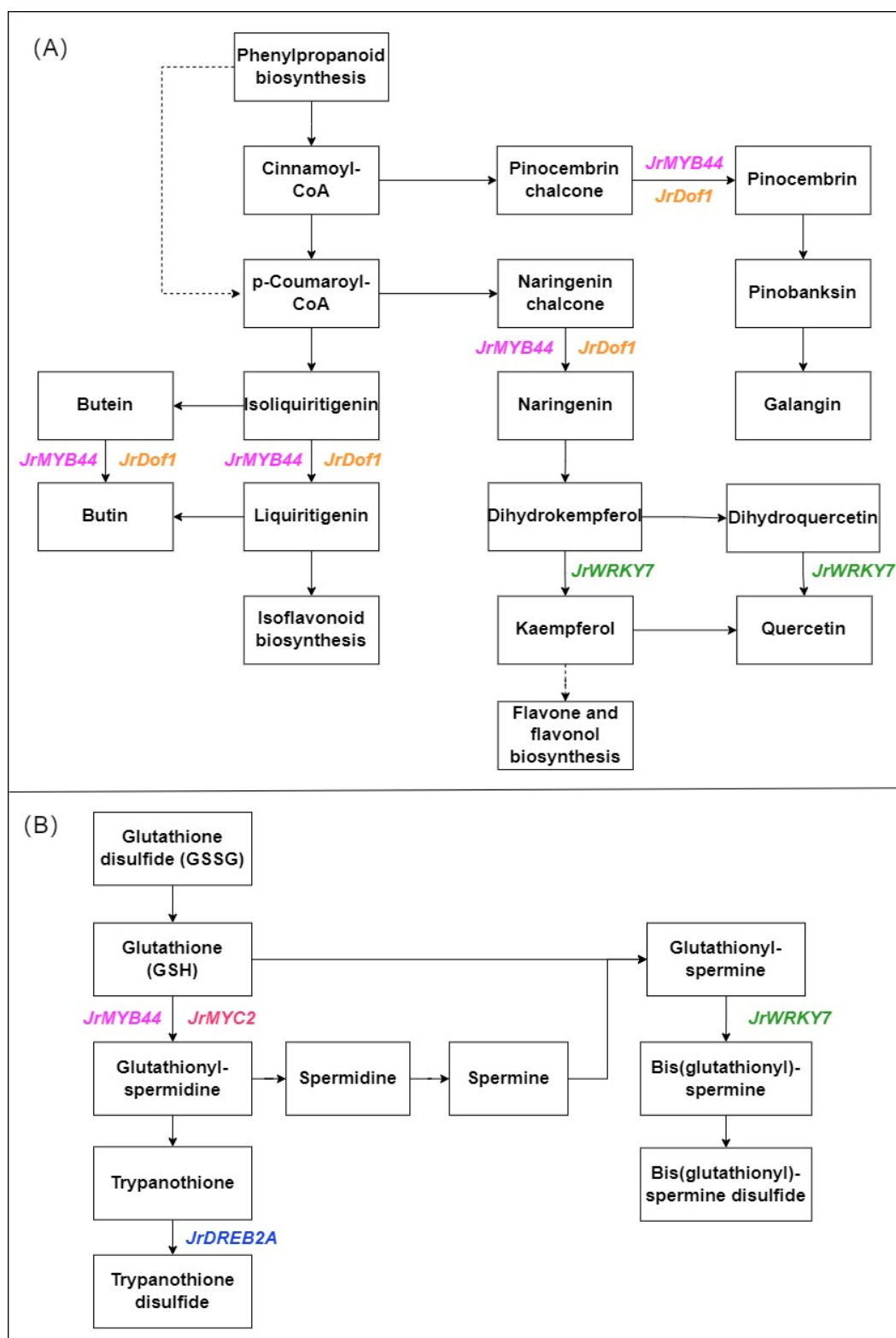
>*JrDREB2A* Promoter 506 bp

AAACCACTTTACACACACGCGTCATGTCCACCTTAAATGGAAATGAAACCAAGAATTAAA
CTTACCTTATACAGAAGAGAGCTTTGGATGCCGAGATAAATAGCCACAAGCCACGTGTCTC
AAATCTATCCGAGGATATGACACGGCAAGATAAATACGATAGCCACGTGATCGCATTACATA
AATATAGCCTTTATAGATAGATATGCATTGCGGAAACATCGCAGCAACAGAGAGAGTGCC
TGATGGCATGTTGTTATTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTATATATAT
ATATATATATATCGATATCCTTTGTTGATCGGTTGACAGAGTTACTTCGTCTCCAAGGCAAA
GGTCGCAATACCAGCGTTATCAAGACAAACAGAGCAAGCACTGCAAAACGCTACAACAAA
GAAACAAATATCATATATAGAGCTTAGAACTCGAGCTTCAACCGAGGCTTTTTGAACGAGT
CCCCAGTCTGAGAG

MYB1AT	1 (+) WAACCA	S000408
MYB1AT	47(+) WAACCA	S000408
MYBST1	135 (+) GGATA	S000180
MYBCORE	339 (+) CNGTTR	S000176

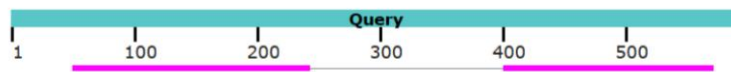
The underlined part was used in Y1H and GUS activity assay (Motif2S)

Supplementary Fig. S11 Promoter segments of *JrWRKY7* and *JrDREB2A*. The core sequences of *MYB* recognition related *cis*-elements were marked in green or yellow. Segments used in GUS activity assay were underlined. A, *JrWRKY7* promoter. B, *JrDREB2A* promoter.



Supplementary Fig. S12 The KEGG pathway based on the transcriptomes of *JrMYB44* overexpression line and WT. A, the flavonoid biosynthesis pathway covering *JrMYB44*, *JrDof1* and *JrWRKY7*. B, the isoflavonoid biosynthesis pathway covering *JrMYB44* and *JrMYC2*, *JrWRKY7*, *JrDREB2A*.

(A) **Distribution of the top 2 Blast Hits on 1 subject sequences**



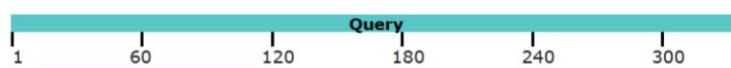
Range 1: 300 to 469 [Graphics](#)

Score	Expect	Method	Identities	Positives	Gaps
169 bits(427)	3e-50	Compositional matrix adjust.	84/179(47%)	121/179(67%)	17/179(9%)
Query 400	RRKGRKPANGREEPLNHVEAERQRREKLNQRFYSLRAVVPNVSKMDKASLLGDAISYINE				459
	+KRGRK GR+ P+NHVEAERQRREKLN RFY+LR+VVPNVSKMDKASLL DA+ YINE				
Sbjct 300	KKRGRKATTGRDSPVNHVEAERQRREKLNHRFYALRSVVPNVSKMDKASLLADAVVYINE				359
Query 460	LKSKLQQAESDKEEIQKKLDGMSKEGN-----NGKGCGRAKERKSSNQDSTASSIE				511
	LK+K+ +++++ KL+ +E N + + S + S+ TA++I				
Sbjct 360	LKAKI-----DDLEVKLEAQPREANMSNLSGMYDSRSITSTVDHTRLSSSSFTAAAIY				412
Query 512	MEIDVKIIGWDMIRVQCCKDHPGARFMEALKELDLEVNHASLSVVNDLMIQQATVKM				570
	+E VKI+G + +IR+QC ++P AR M+AL++L+ ++ HAS+S + LM+Q VK+				
Sbjct 413	VE--VKIVGSEALIRIQCPDVNYPHARLMDALRDLEFQIRHASISSIKGLMVQDVVVKV				469

Range 2: 24 to 214 [Graphics](#)

Score	Expect	Method	Identities	Positives	Gaps
142 bits(358)	6e-41	Compositional matrix adjust.	79/200(40%)	117/200(58%)	16/200(8%)
Query 51	TLQQRQLALIESAGENWTYAIFWQISHDFDSSSTGDNVTILGWGDGYKGEEDKEKKKNNT				110
	T+QQRLLQ +I+S E W Y+IFWQ S D + V+L WGDG+++G D K +N				
Sbjct 24	TIQQRLLQFIISRPEWIIYSIFWQTSKD-----SNGQVLSWGDGHFRGSRDFVSKVSND				78
Query 111	NTAEQEH-----RKRVRIR-ELNSLISGGIGVSDSNDEEVTDTEWFFLVSMTQSFVNGV				163
	+Q R RV + L SL + + V + D +VTD+EWFF+ VS+T+SF				
Sbjct 79	KGDQPRYGFGLDRTRVSKGVLQSLFAEDLDVDGVTLDGQVTDSEWFYAVSVTRSFVAVRD				138
Query 164	GLPGESFLNSRVIWLSGSGALTGSGCERAGQGQIYGLKTMVCIATQNGVVELGSSEVISQ				223
	G+ G ++ IWL+G L C+RA + +++G++T++C+AT GVVELGSSE I +				
Sbjct 139	GVLAGRAYSCGEYIWLADLELQFYECDRAREARLHGIQTLCVATSRGVVELGSSESIRE				198
Query 224	SSDLMHKVNLFNFNNGGNG 243				
	L+ +V +LF G GN				
Sbjct 199	DWGLVQQVKSLEF-----GAGN 214				

(B) **Distribution of the top 1 Blast Hits on 1 subject sequences**



Range 1: 12 to 111 [Graphics](#)

Score	Expect	Method	Identities	Positives	Gaps
107 bits(268)	8e-32	Compositional matrix adjust.	51/101(50%)	64/101(63%)	1/101(0%)
Query 14	KGAWTAEEDKKLISYIHEHGEGGWRDIPQKAGLKRCGKSCRLRWANYLKPDIKRGFSYE				73
	KG W+ EED+ L + G W I KA R GKSCRLRW N L P+++ F+ E				
Sbjct 12	KGPWSPEEDEMRLKLVQSQGARSWSVI-SKATAGRSGKSCRLRWCNQLSPEVEHRPFTLE				70
Query 74	EEQIIIMLHASRGNKWSVIARHLPKRTDNEIKNYWNTHLKK 114				
	E+QII+ HA GNKW+ IAR L RTDN IKN+WN+ LK+				
Sbjct 71	EDQIIIVKAHAKYGNKWATIARLLNGRTDNAIKNHWNSTLKR 111				

Supplementary Fig. S13 Amino acid sequence alignment using blastp of NCBI. A, JrMYC2 (Sbjct) and AtMYC3 (Query). B, JrMYB44 (Sbjct) and AtMYB29 (Query).