

Supplementary Material

SupplementaryFigure

TcMYB29a-promoter

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+ CATCTCACCA ATTTTCCCAT ACAGATGATG CTCAAAGTCA AGTCACGAGG AGGAGGATCC AATTCAAAAC
- GTAGAGTGGT TAAAAGGGTA TGTCTACTAC GAGTTTCAGT TCAGTGCTCC TCCTCCTAGG TTAAGTTTTG

+ CTCCTTTTAA CGGAATTTAC TTAAGTTCAG GCAATGTAAC AGTGAAAATG GTGCTTTTTG AGGATAAAGA
- GAGGAAAATT GCCTTAAATG AATTCAAGTC CGTTACATTG TCACTTTTAC CACGAAAAAC TCCTATTTCT

+ AAGAATGAAG GAATAGCTAC TAGGACCCAT ACTTTAGTCT GCATGCTATT ATTAAGATGT GGCTGTAAAA
- TTCTTACTTC CTTATCGATG ATCCTGGGTA TGAAATCAGA CGTACGATAA TAATTCTACA CCGACATTTT

+ GCCCACCTTT AAAGAGACAA TATTCAAACT AGGGCATAAA AAGCCTGGTA GAAAGCAGGA AATCTAATGA
- CGGGTGGAAT TTTCTCTGTT ATAAGTTTGA TCCCGTATTT TTCGGACCAT CTTTCGTCCT TTAGATTACT

+ TAATAAATTG ACAACAGTGA ATTCCTCAGC TGAAACGTTA TGAAGATAAA TATGACATAG GGAAAAGTAT
- ATTATTTAAC TGTTGTCACT TAAGGASTGC ACTTTGCAAT ACTTCTATTT ATACTGTATC CCTTTTCATA

+ GAGGGTGTTG AATACAAGGA TTAATTGATT CACTTACAAT TGACAGGTGC AGTAAAGTAA AGTAAAGATT
- CTCCACAAC TTATGTTTCT AATTAATAA GTGAATGTTA ACTGTCCACG TCATTTTCATT TCATTTCTAA

+ AAAGATAAGG TCCTTTGTAA GTATTTTTTT GAACCAATAC ATTTGGCGCT CTTCACTATA CATAAGATTG
- TTTCTATTCC AGGAAACATT CATAAAAAAA CTTGGTTATG TAAACCGCGA GAAGTGATAT GTATTCTAAC

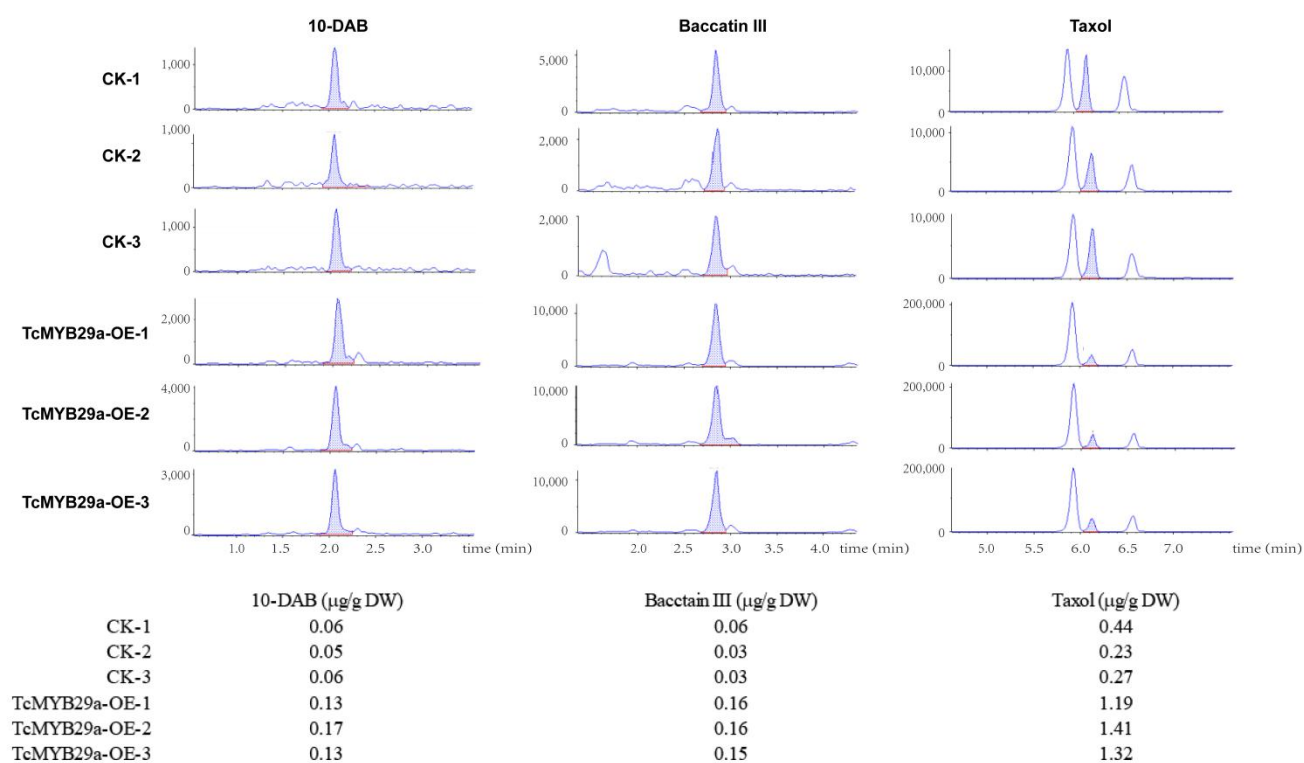
+ TACACTTATA CATGCATGTA CTTATATATA AAATCACTAA ATTTATGTTA ATATGAAGTC ACTAGATTTA
- ATGTGAATAT GTACGTACAT GAATATATAT TTTAGTGATT TAAATACAAT TATACTTCAG TGATCTAAAT

+ CATGAGATTG TTTGTGCAGG AATCTCGGAT GGTTTAAGAT TGGGGATAAA TTTGGATGTG GGCT ATG
- GTACTCTAAC AAACACGTCC TTAGAGCCTA CCAAATTCTA ACCCCTATTT AAACCTACAC CCGA TAC

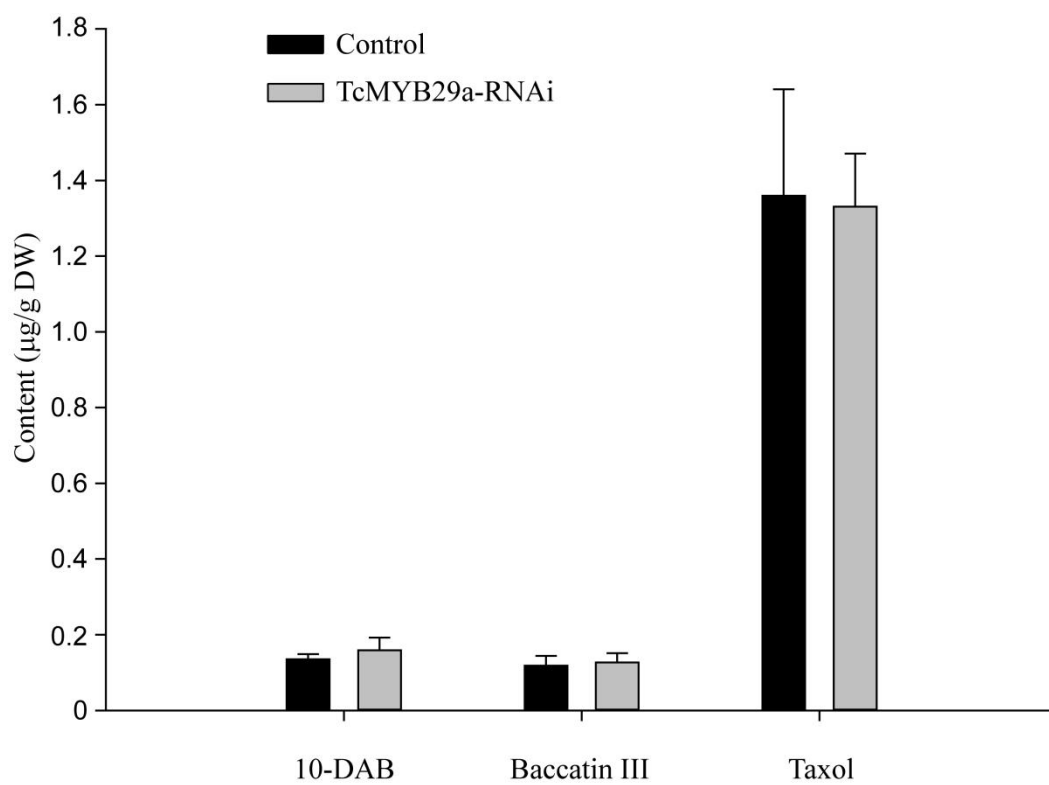
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 start codon of *TcMYB29a*

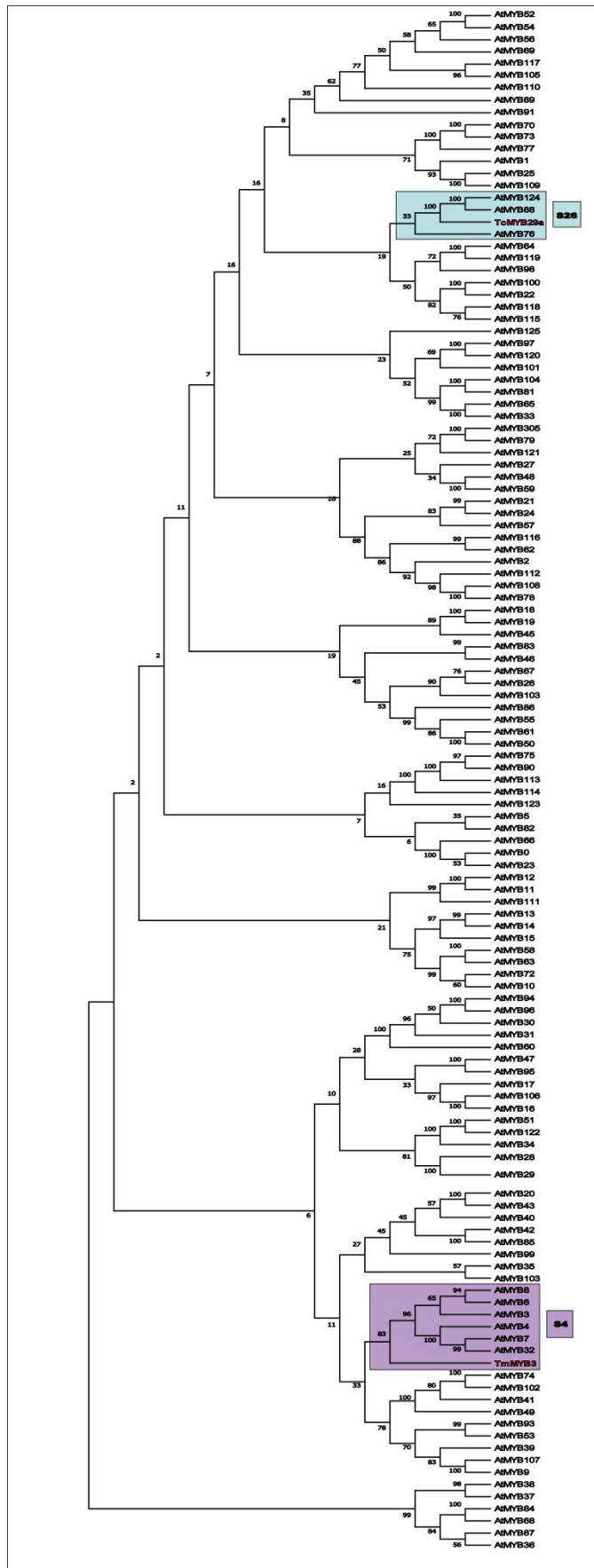
Supplementary Figure S1 Predicated AERB site in the promoter region of *TcMYB29a*. The red box indicated the predicted cis-acting element involved in the abscisic acid responsiveness. PlantCARE (<http://bioinformatics.psb.ugent.be/webtools/plantcare/html/>) was used to identify the cis-acting elements of promoter of *TcMYB29a*.



Supplementary Figure S2 LC-MS quantified the contents of taxanes in control and TcMYB29a-OE cells.



Supplementary Figure S3 LC-MS quantified the contents of taxanes in control and TcMYB29a-RNAi cells.



Supplementary Figure S4 Schematic representation of the relationships between TcMYB29a, TmMYB3 and the different R2R3-MYB subgroups from *Arabidopsis*. The tree was inferred using the neighbor-joining method and 1000 bootstraps with putative full length MYB amino acid sequences with Clustal W software. The subgroups were designated as previously reported (Hu *et al.*, 2020)

Supplementary Table S1 Primers used in this study.

Gene Name	Sequence	Application
TcMYB29a	F: ATGAGCTATGAAGAGATGAATTCT R: TTATAGCCTGTTGGATAGTGAGAG	Construction for 35s:GFP-TcMYB29a
R-1	F1: TGTAGGAGAATGGATGTCGTGAAGATT R1: CCTTAATACGTGTAATTTGATGTCTCTCTTCC	CHIP-qPCR
R-2	F2: GCCTCAAGAATATGTGCATCACCCCC R2: GGTGGGGAAATTGTTGGGAAGGATCG	CHIP-qPCR
R-3	F1: ACAATTCTTCTCACCCCCTGCCAT R1: GGTAGCGCTAAAGGTGGGGGAA	CHIP-qPCR
R-4	F2: GTATCCATTGCATTACCCACGTGC R2: CCAAGGTCATTTCAAACGTTAGATTCCAT	CHIP-qPCR
R-5	F1:TCCTTTAGTGACACCTTGCAACC R1:TCCAAATGCCCAATGACCTCCTGT	CHIP-qPCR
R-6	F2:TCCCTTAGGGCTTTTTCCAGGGAC R2:ACTGCCGAAAACTAATTCACAGT	CHIP-qPCR
R-7	F3:GTGTCCAATCGTCCGTAATGAGCA R3:TGTAGTGAACATGGGGCGGTGA	CHIP-qPCR
R-8	F1:TGCTTTTGCGCAAGTGTGGCA R1:AACCTTGCGGGCCTGATCCT	CHIP-qPCR
R-9	F2:GCCCCGTGCATCACAGTGGTTGT R2:AGCTAGCCGGTGCCAACTCCTT	CHIP-qPCR
CDS-1	qF: ACAAATTCGGCGGCTGCGTG qR: AACGAGGCTGTCTTGCCCCAA	CHIP-qPCR

CDS-2	qF: AGATGTCGTGGCCCGCTCAA qR: AGCGCACCAGGGCCGAAAAA	CHIP-qPCR
CDS-3	qF: TGCCTGCCTTCGCCCAAAACA qR: AGCCGCCCAGCAAAAGGGTA	CHIP-qPCR
CDS-4	qF: TCGATGCGGCCACCTCCAAT qR:TCGCTAGCCAGGCCAATGCT	CHIP-qPCR
pY1-ABAi	Y1F: agcacatgcctcgaggtcgacAGTGGAGAATCATAGACAACTACCTCTAA Y1R: gaaaagcttgaattcgagctcAGGTCGAGGAACCTGGATATAAGC	Y1H
pY2-ABAi	Y2F: agcacatgcctcgaggtcgacGTCTCAATGTATCCATTGCATTACCC	Y1H
	Y2R: gaaaagcttgaattcgagctcTTTGAAGAAAACCAAAACAAAGA	
pB1-ABAi	B1F: gcacatgcctcgaggtcgacCCGTTACCGTTACCGTTAgagctcgaattcaagcttttc	Y1H
	B1R: gaaaagcttgaattcgagctcTAACGGTAACGGTAACGGgtcgacctcgaggcatgtgc	
pmB1-ABAi	mB1F: gcacatgcctcgaggtcgacCCGAATCCGAATCCGAATgagctcgaattcaagcttttc	Y1H
	mB1R: gaaaagcttgaattcgagctcATTCGGATTTCGGATTTCGGgtcgacctcgaggcatgtgc	
pY3-ABAi	Y3F: gaaaagcttgaattcgagctcTTGTCCGAAAATATTGTGTTCTTTG	Y1H
	Y3R: agcacatgcctcgaggtcgacCTCTAATTGTTTCAGAACAGAGCGG	
AD-TcMYB29a	F: gccatggaggccagtgaattcATGAGCTATGAAGAGATGAATTCTATTTT R: acgattcatctgcagctcgagTTATAGCCTGTTGGATAGTGAGAGCC	Y1H
B1 Probe	F: tacaatccccgagtactccccctCCGTTAagttaagcatcctctcttccccca R: tgggggaagaggaggtatcctaactTAACGGaggggggagtactcgggggattgta	EMSA
Mutant Probe	F: tacaatccccgagtactccccctCCATagttaagcatcctctcttccccca R: tgggggaagaggaggtatcctaactATGGaggggggagtactcgggggattgta	EMSA

TcT5OHpro	SP1: AGATGGCCGAGATGTTGAAGACGAGC SP2: ATCTGCACCAGCTTCTCCTCGTTGGA SP3: CGGTAGCGGAGGTCAAACATGGTAGT	Genome walking
TcTSpro	SP1: TGGCTGTGCCCTGTTTTCCAAACCGA SP2: TCCGTCTCCGAGCGCATTGAACAT SP3: ACATTGTGGTGCCACAGATCGCCA	Genome walking
TcBAPT	SP1: TTCTGAGCCGCCCAGCAAAAAGGGTAA SP2:TGGGAGGCCTCATATTCAACCGGAGT SP3: TTCGACAATCTCCCAACTTCTCCCGC	Genome walking
TcDBTNBT	SP1:AACAGAGCACCTTCCCCCGTGCAA SP2:GTGCATTTAGCGCACGCACAACAA SP3: TTGGTAAAGGGCACACCCACGTT	Genome walking
TcTS	qF: ACAAATTCGGCGGCTGCGTG qR: AACGAGGCTGTCTCTGCCCCAA	qPCR
TcT5OH	qF: AGATGTCGTGGCCCGCTCAA qR: AGCGCACCAGGGCCGAAAAA	qPCR
TcT7OH	qF: ACTGTTGCACGTGTCGTGGTCC qR: TAGTGCGACACGCAGAACGC	qPCR
TcT10OH	qF: CGGGCCTGCGGGAACAAAT qR: ACCGAGCAAGTGCAGTGCGT	qPCR
TcBAPT	qF: TGCCTGCCTTCGCCCAAAACA qR: AGCCGCCCAGCAAAAGGGTA	qPCR
TcDBTNBT	qF: TCGATGCGGCCACCTCCAAT qR:TCGCTAGCCAGGCCAATGCT	qPCR
TcPAM	qF: TCGATGCGGCCACCTCCAAT qR: TCGCTAGCCAGGCCAATGCT	qPCR qPCR

TcT2OH	qF: AGCTGTTGAGCCGAACGGTGTC qR: CGGCCCCAAAAACCCTGCAACT	qPCR
TcGAPDH	qF: CGGAGACAGTCGATCAAGC qR: CCCATCCTCAACCCAATAA	qPCR
TcMYB29a	qF: GCTCAAAGGCGCAATGCAGA qR: ACAGTTTGGGCAAGGAAGGCA	qPCR
35S:TcMYB29a	F: accagtctctctcaagcttATGAGCTATGAAGAGATGAATTCTATTTT R: gctcctgcagctcgaggatccTTATAGCCTGTTGGATAGTGAGAGCC	LUC
pT5OH-LUC	F: ttctgcagcccgggggatcctAGTGGAGAATCATAGACAACTACCTCTAA R: TgtttttggcgtcttccatggTTTGAAGAAAACCAAAACAAAGA	LUC
pmT5OH-LUC	F: ttctgcagcccgggggatcctAGTGGAGAATCATAGACAACTACCTCTAA FP-R: tgggggaagaggagatccttaactATGAggggggagtactcgggggattgta FP-F: tacaatcccccgagtactccccctCCATagttaagcctcctcttccccca R: TgtttttggcgtcttccatggTTTGAAGAAAACCAAAACAAAGA	LUC

Reference

Hu, X., Zhang, L., Wilson, I., Shao, F., and Qiu, D.. (2020). The R2R3-MYB transcription factor family in *Taxus chinensis*: identification, characterization, expression profiling and posttranscriptional regulation analysis. *Peer J.* 8, e8473. doi:10.7717/peerj.8473.