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Article

PgMYB2, a MeJA-Responsive Transcription Factor, Positively Regulates the Dammarenediol Synthase Gene Expression in *Panax ginseng*

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Supplementary Materials:

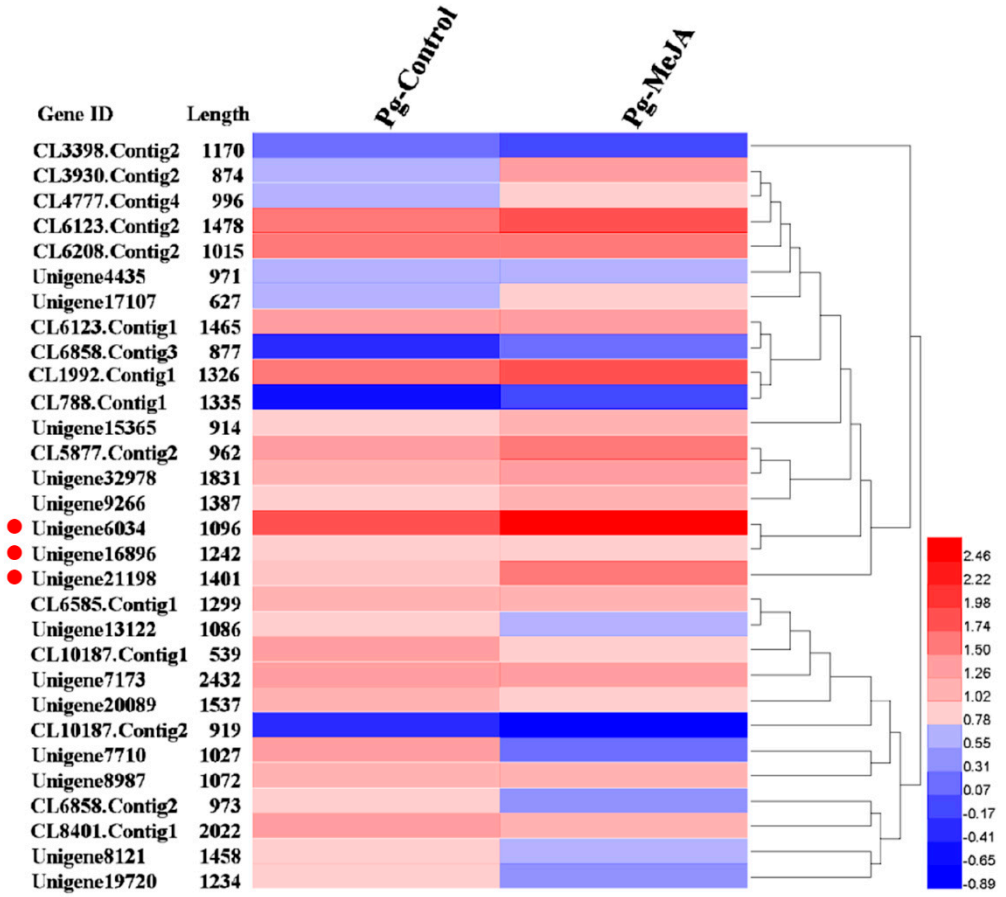

Figure S1. Heatmap of 30 *R2R3-MYB* unigenes. The levels of expression were determined based on comparison of the intensity of two colors (red and blue) from two samples (Pg-Con and Pg-MeJA). The gradation of color indicated different values which were measured using lg (FPKM). The values

were shown with the 'color-scale' at the right-bottom. The red circles represented three unigenes for subsequent screening. The heatmap was generated by HemI program (http://hemi.biocuckoo.org/index.php).

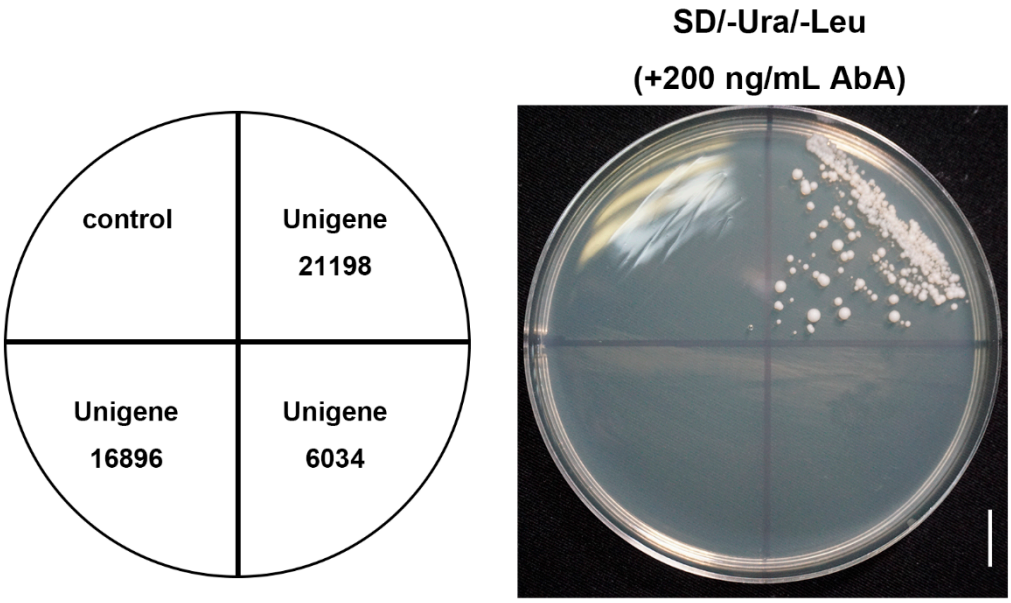

Figure S2. The screening assay of 3 unigenes in Y1H Gold. The pABAi-*DDSpro* were used as the bait and the pGADT7-Rec used as the control. Only the yeast cells with pGADT7-Unigene 21198 (*PgMYB2)* could grow on the SD/-Ura/-Leu selective medium added with 200 ng/mL AbA. Scale bar = 1 cm.

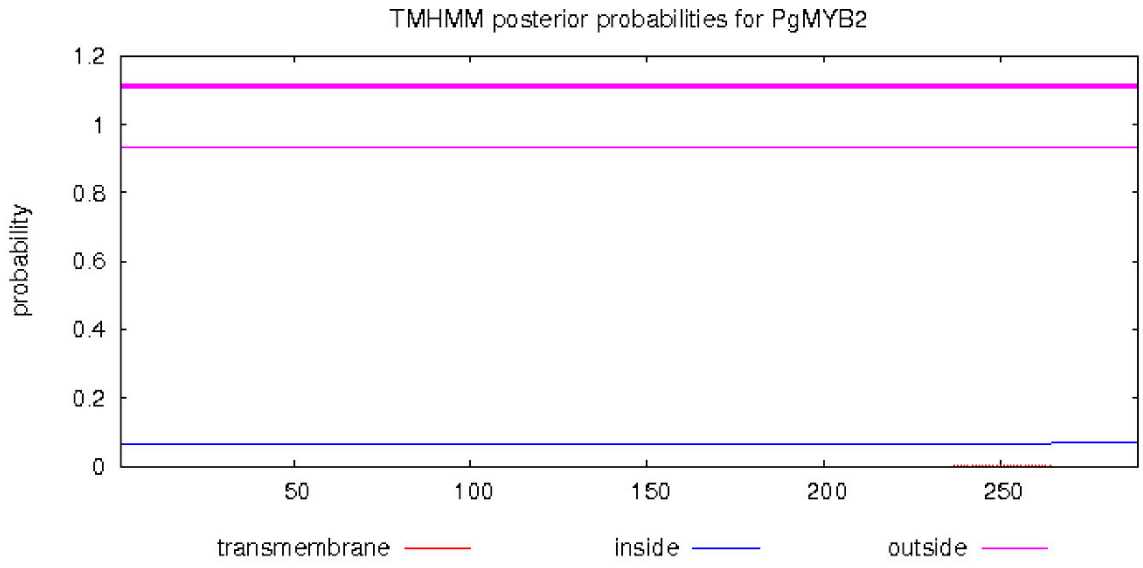

Figure S3. The transmembrane domain of PgMYB2. Predicted by TMHMM Server v. 2.0 (http://www.cbs.dtu.dk/services/TMHMM/).

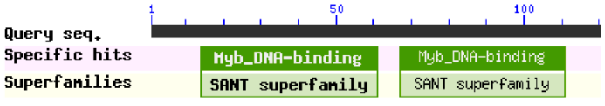

Figure S4. The MYB DNA binding sites of PgMYB2. Predicted by the NCBI conserved domains finder (https://www.ncbi.nlm.nih.gov/Structure/cdd/wrpsb.cgi).

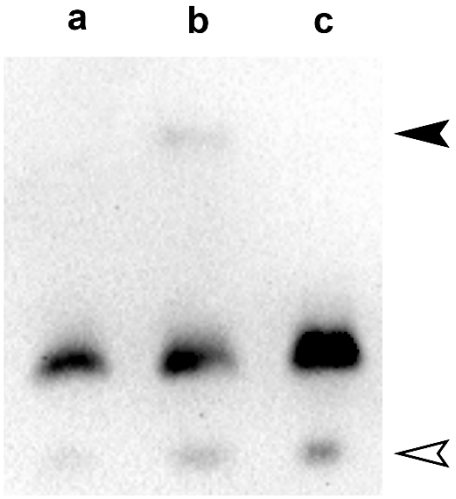

Figure S5. Binding assay of PgMYB2 to *MBS* site. Contents of reaction: (**a**) Free probe; (**b**) labeled probe (containing *MBSII* site) + PgMYB2: TF protein; (**c**) labeled probe (containing *MBS* site) + PgMYB2: TF protein. The protein-probe complexes were indicated with a solid arrow and the free probes were indicated with a hollow arrow.

Table S1. Specific primers used in the study.

Primer Name	Primer sequence (5′ to 3′)
PgMYB2-F	CCACTCTCAACGCATTCTC
PgMYB2-R	TAGGGGTAGGCACATTCTG
PgDDS-F	ATGTGGAAGCAGAAGGTT
PgDDS-R	AATTTTGAGCTGCTGGTG
β-actin-F	TGCCCCAGAAGAGCACCCTGT
β-actin-R	AGCATACAGGGAAAGATCGGCTTGA
1302-PgMYB2-F	AGAACACGGGGGACTCTTGACCAAGAAGAAATTGACGACGATG
1302-PgMYB2-R	GTGAAAAGTTCTTCTCCTTTACTATTCCTTTTCCCAACAGTCC
qPCR-*PgMYB2*-F	CGGATTATTGAGATGCGG
qPCR-*PgMYB2*-R	TGATGTGGGTGTTCCAGTAGTTC
qPCR-*PgDDS*-F	TGAGATTAGATGAAAACGAAC
qPCR-*PgDDS*-R	GGCAATGATAAGGGGAGGTGT
pABAi-*DDSpro*-F	AATTCGAGCTCGGTACCCGGGCTTGTAGTTTTGTGATTTTCC
pABAi-*DDSpro*-R	ATACAGAGCACATGCCTCGAGACTTGTTGGTATGTGGTGTAA
pGADT7-*PgMYB2*-F	CATATGGCCATGGAGGCCAGTATGATGGGACGTTCACCTTGC
pGADT7-*PgMYB2*-R	ATCTGCAGCTCGAGCTCGATGTCTATTCCTTTTCCCAACAGTCC
pCold/TF-*PgMYB2*-F	ATGGAGCTCGGTACCCTCGAGATGGGACGTTCACCTTGC
pCold/TF-*PgMYB2*-R	AGACTGCAGGTCGACAAGCTTATGTTTTCCCAACAGATGA
EMSA-*MBSI*-F	ACACGTCTAACACGTCAATTCTTTT
EMSA-*MBSI*-R	AAAAGAATTGACGTGTTAGACGTGT
EMSA-*MBSII*-F	GACTGGCATTGATTTAAAAGGCGGT
EMSA-*MBSII*-R	ACCGCCTTTTAAATCAATGCCAGTC
EMSA-mutant-*MBSII*-F	GACTGGCttccgggcacctGGCGGT
EMSA-mutant-*MBSII*-R	ACCGCCaggtgcccggaaGCCAGTC
pGreenII 0800-*DDSpro*-F	GACTAGTTTCTTCCAATACTTGTAG
pGreenII 0800-*DDSpro*-R	CATGCCATGGCATTCTTAAGTCTACTAC
pEGAD-*MYC-PgMYB2*-F	CCGGAATTCATGGGACGTTCACCTTGC
pEGAD-*MYC-PgMYB2*-R	CGCGGATCCACAATATCTGTAAAACCCA

pGreenII 0800-*DDSpro-xMBSII*-F	AAATCTGTCTCTGCTGACAAAAATTCCTAGACC
pGreenII 0800-*DDSpro-xMBSII*-R	GTCAGCAGAGACAGATTTTTGTTAAAGTTAAATAAAGAAAACTTGAACTA

MBS, MBSII and its mutation sites are underlined in the table. These primers were designed by Premier 5, Oligo 7 and SnapGene software.