



Legend: → Strand Helix — Coil

Figure S1 Predicted secondary structure of PpeDGYLA. Predictions were made using PSIPRED and GORIV.

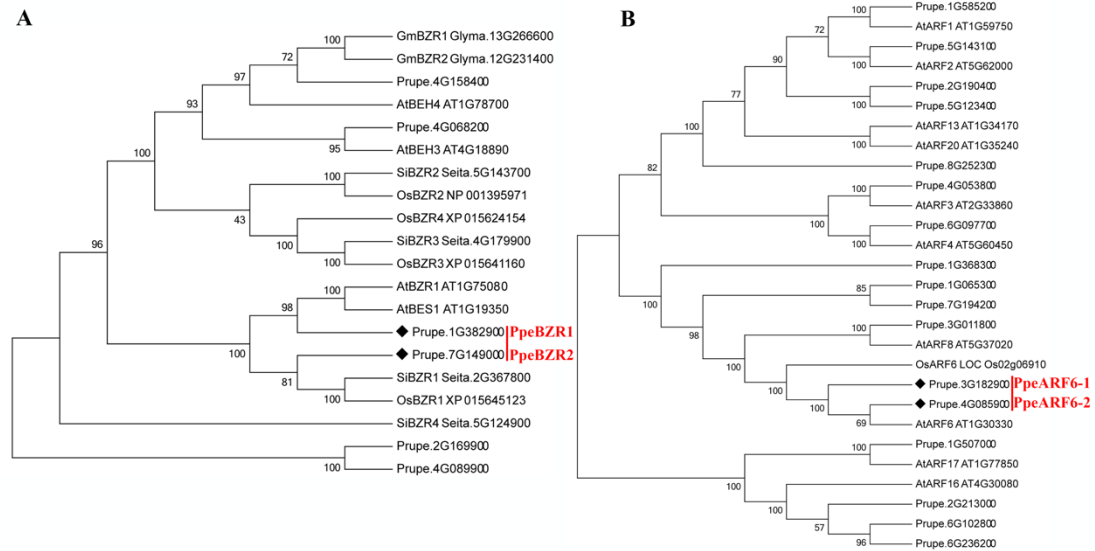


Figure S2 Phylogenetic tree of *BZR* (A) and *ARF* (B) transcription factor genes in the peach genome and the orthologous genes from other species, including *Glycine max*, *Arabidopsis thaliana*, *Oryza sativa* and *Setaria italica*. Accession numbers are listed after the gene name. The orthologous genes from peach of *BZR* and *ARF* analyzed in this study were in red.

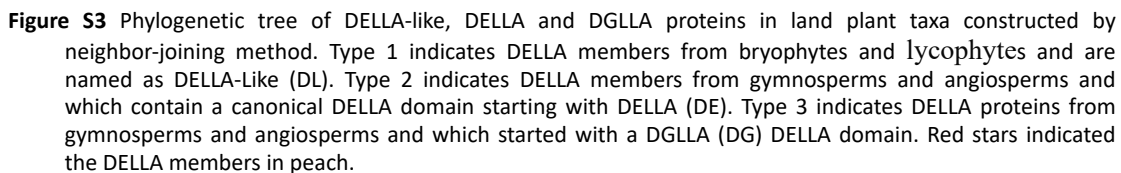


Figure S3 Phylogenetic tree of DELLA-like, DELLA and DGLLA proteins in land plant taxa constructed by neighbor-joining method. Type 1 indicates DELLA members from bryophytes and lycophytes and are named as DELLA-Like (DL). Type 2 indicates DELLA members from gymnosperms and angiosperms and which contain a canonical DELLA domain starting with DELLA (DE). Type 3 indicates DELLA proteins from gymnosperms and angiosperms and which started with a DGLLA (DG) DELLA domain. Red stars indicated the DELLA members in peach.

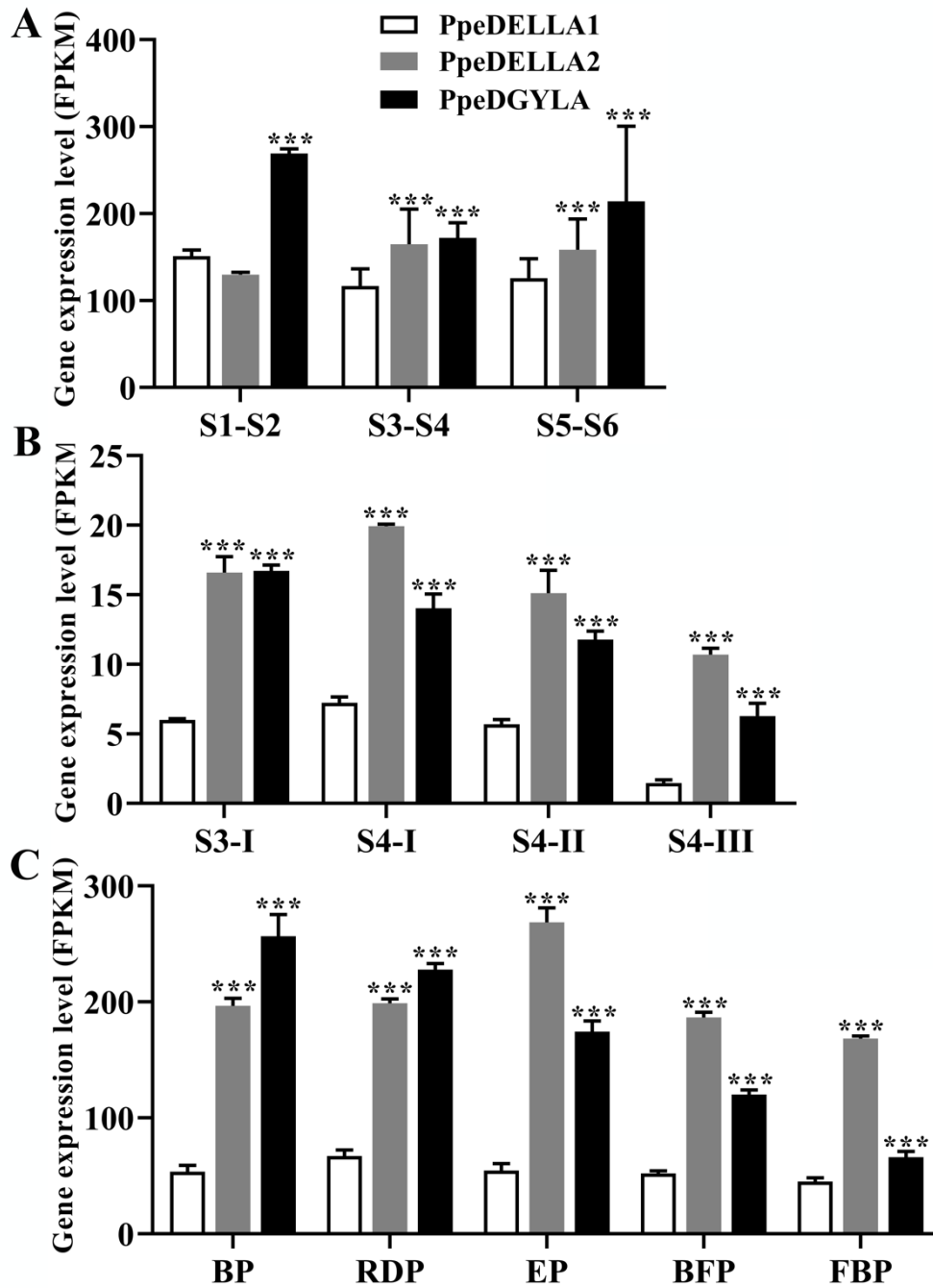


Figure S4 The transcript levels of the three peach *DELLA* genes based on RNA-seq transcriptome data. (A) In stem internodes, where internodes are numbered S1-S6 from top to bottom of stems, S1-S2, S3-S4 and S5-S6 represent combined samples of the internodes S1 and S2, S3 and S4, and S5 and S6. (B) In fruit, where S3-I, S4-I, S4-II, and S4-III represent 118, 120, 122 and 124 d after full bloom, respectively. (C) In flower, where BP: bud period; RDP: red dot period; EP: equivalent in size between petal and sepal period; BFP: budding flower period; FBP: full bloom period. *** indicate significant difference at $P < 0.001$

Table S1 The primers of PpPIFs for qRT-PCR and vector construction

Name	Primer Sequences (5'-3')
PpeDELLA1-qF	TGTGGAGCAGGAGGCAAAC
PpeDELLA1-qR	TGACTCGGACCGGACGAT
PpeDELLA2-qF	GCAAACCACAACGGTCCAGT

PpeDELLA2-qR	GCTCTGACATCGCCTTATCCT
PpeDGYLA-qF	TTAGGGCTCTGCATTTGGGTT
PpeDGYLA-qR	GGTTGGCTGTGGTTGCTTCA
PpeDELLA1(pSAK277-Flag)-F	TCCAAAGAATTCCCCGGTACCATGAAGAGAGATCACCGCG
PpeDELLA1(pSAK277-Flag)-R	ATGATCTTTGTAATCCTCGAGCCGGGTTGACTCAGTCGAA
PpeDGYLA(pSAK277-Flag)-F	TCCAAAGAATTCCCCGGTACCATGGGGCCCTACGGTTCAA
PpeDGYLA(pSAK277-Flag)-R	ATGATCTTTGTAATCCTCGAGGACATGATTGGCATTATTA
PpePIF8(GAL4AD)-F	CAGATTACGCTCATATGATGAACCAGTGTGTTCCCAGC
PpePIF8(GAL4AD)-R	ACGATTCATCTGCAGCTCGAGGCTCTTAGAACTAGATGC
PpeDELLA1(GAL4AD)-F	CAGATTACGCTCATATGATGAAGAGAGATCACCGCGG
PpeDELLA1(GAL4AD)-R	CACCCGGGTGGAATTCTCACCGGGTTGACTCAGTCG
PpeDGYLA(GAL4AD)-F	GTACCAGATTACGCTCATATGATGGGGCCCTACGGTTCA
PpeDGYLA(GAL4AD)-R	ACGATTCATCTGCAGCTCGAGTTAGACATGATTGGCATTATTATT
PpeGID1c(GAL4BD)-F	TCAGAGGAGGACCTGCATATGATGGCTGGGACCAACGAAGT
PpeGID1c(GAL4BD)-R	TTATGCGGCCGCTGCAGACCGCACGCGATGAAAGTC
PpeDGYLA(GAL4BD)-F	TCAGAGGAGGACCTGCATATGATGGGGCCCTACGGTTCA
PpeDGYLA(GAL4BD)-R	TCGACGGATCCCCGGGAATTCTTAGACATGATTGGCATTATTATT
PpeBZR1(GAL4AD)-F	GGATCCCCGGGAATTCGAGAGGGAAAAGAGAGGGAAGAT
PpeBZR1(GAL4AD)-R	ATGCCACCCGGGTGGAATTCCTTAACCTTCGAGGCTTACCACTT
PpeBZR2(GAL4AD)-F	GCCATGGAGGCCAGTGAATTCGCTCAAAGGGTAAGCAGGTGG
PpeBZR2(GAL4AD)-R	ATGCCACCCGGGTGGAATTCCTGCCCTCCTGGTTATACACATT
PpeARF6-1(GAL4AD)-F	CAGATTACGCTCATATGATGAGACTTTCGTCTTCATC
PpeARF6-1(GAL4AD)-R	CATCTGCAGCTCGAGTTAGTAGTCCAGTGAGCC
PpeARF6-2(GAL4AD)-F	CAGATTACGCTCATATGAGGCTCTCATCTGCTGGTTTTAG
PpeARF6-2(GAL4AD)-R	TCATCTGCAGCTCGAGGGGTTGGAGGAGATGCAAATAT

Table S2 Physical and chemical properties of the PpeDGYLA

Characteristics	Predictive values
Number of amino acids	537
Molecular weight	59.16 KDa
Theoretical pI	5.58
The instability index (II)	43.68
Aliphatic index	90.86

Grand average of hydropathicity (GRAVY)	-0.138
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Alpha helix	46.00 %
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Extended strand	12.48 %
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Random coil	41.53 %
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