

Supplementary information

1 Original Research Article

2 Transcriptome Profiles Reveal the Crucial Roles of Hormone and

3 Sugar in the Bud Dormancy of *Prunus mume*

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17 **Supplementary Table legends**

18 **Supplementary Table S1:** The total information of the 5831 DEGs at four dormancy
19 stages.

20 **Supplementary Table S2:** Gene ontology enrichment analysis of all 5831 DEGs.
21 Gene sets that were significant at p-value < 0.05 are presented in table.

22 **Supplementary Table S3:** Signaling pathway enrichment analysis of all 5831 DEGs.

23 **Supplementary Table S4:** MapMan Bins of “Metabolism_overview” and
24 “Regulation_overview” between two successive stages.

25 **Supplementary Table S5:** Detail information of hormone-regulated DEGs.

26 **Supplementary Table S6:** Detail information of sugar-regulated DEGs.

27 **Supplementary Table S7:** Detail information of dormancy candidate genes.

28 **Supplementary Table S8:** Primers information used in qPCR analysis

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30 **Supplementary Figure legends**

31 **Supplementary Figure S1:** PCA analysis of the 12 transcriptome data of *P. mume*.
32 Samplings were under four different conditions: EDI, EDII, EDIII and NF.

33 **Supplementary Figure S2:** Venn diagram of 5831 DEGs between two stages.
34 Analysis was under four different conditions: EDI, EDII, EDIII and NF.

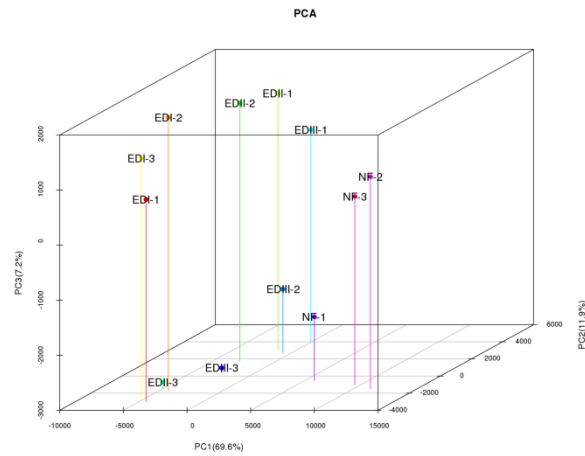
35 **Supplementary Figure S3:** Gene ontology categories of DEGs of *P.mume*. Analysis
36 was under four different conditions: EDI, EDII, EDIII and NF. **(a)** EDI vs. EDII; **(b)** EDII
37 vs. EDIII; **(c)** EDIII vs. NF. Up-regulated genes are illustrated in red and
38 down-regulated genes are in green.

39 **Supplementary Figure S4:** KEGG pathway categories of DEGs of *P.mume*. Analysis
40 was under four different conditions: EDI, EDII, EDIII and NF. **(a)** EDI vs. EDII; **(b)** EDII
41 vs. EDIII; **(c)** EDIII vs. NF.

42 **Supplementary Figure S5:** A global view of metabolism and regulation changes for
43 three successive stage comparisons with MapMan analysis. **(a)**
44 “Metabolism_overview” of EDI vs. EDII; **(b)** “Metabolism_overview” of EDII vs.
45 EDIII; **(c)** “Metabolism_overview” of EDIII vs. NF; **(d)** “Regulation_overview” of EDI
46 vs. EDII; **(e)** “Regulation_overview” of EDII vs. EDIII; **(f)** “Regulation_overview” of
47 EDIII vs. NF. Up-regulated genes are illustrated in red and down-regulated genes are
48 in green.

49 **Supplementary Figure S6:** Expression detection of selected transcripts by RNA-Seq
50 and qRT-PCR. Analysis was under four different conditions: EDI, EDII, EDIII and NF.

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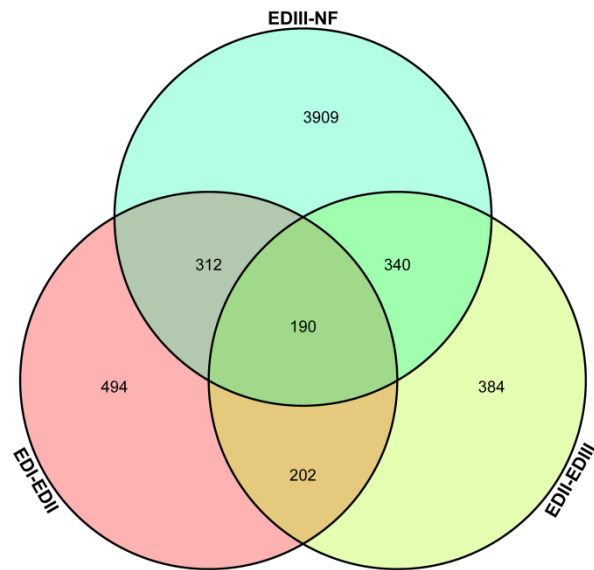


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53 **Figure S1** PCA analysis of the 12 transcriptome data of *P. mume*. Samplings were
 54 under four different conditions: EDI, EDII, EDIII and NF.

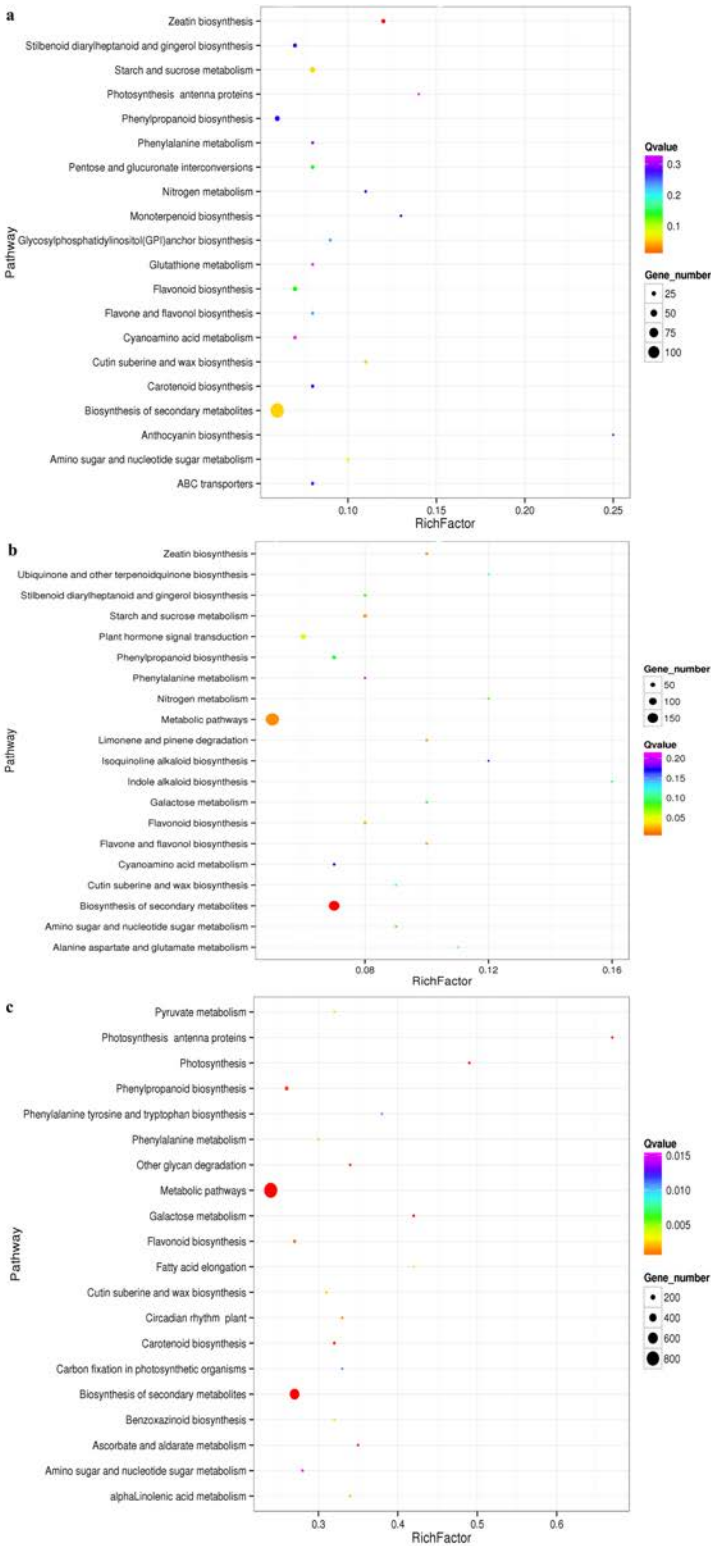
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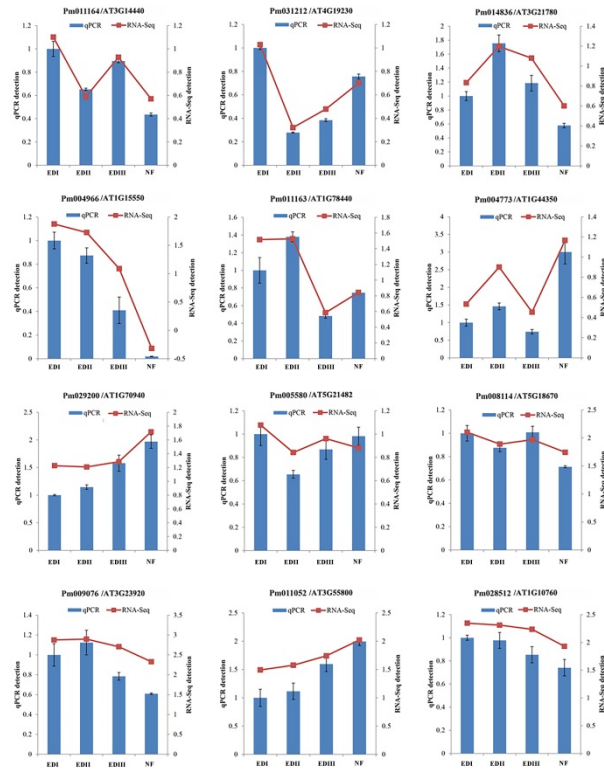


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58 **Figure S2** Venn diagram of 5831 DEGs between two stages. Analysis was under four
59 different conditions: EDI, EDII, EDIII and NF.



67 **Supplementary Figure S4:** KEGG pathway categories of DEGs of *P.mume*. Analysis
68 was under four different conditions: EDI, EDII, EDIII and NF. (a) EDI vs. EDII; (b) EDII
69 vs. EDIII; (c) EDIII vs. NF.



Supplementary Figure S6: Expression detection of selected transcripts by RNA-Seq and qRT-PCR. Analysis was under four different conditions: EDI, EDII, EDIII and NF.