

Title:

Comparative transcriptome analysis of the floral transition in *Rosa chinensis* ‘Old Blush’ and *R. odorata* var. *gigantea*

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Supplementary information

This file contains four supplementary figures and captions of four supplementary files.

Figure legends

Fig. S1. Morphological characteristics of shoot apical meristem (SAM) between different developmental stages in OB and GIG. Morphological changes of SAM were analyzed at a histological level: (A) the upper panel represents the floral transition process of OB, (B) the down panel shows the floral transition process and the secondary vegetative meristem of GIG. The morphology of SAM is narrow at the VM stage, and the SAM becomes broad and showed a pronounced conic which indicates the evidence of phase-change from the VM to TM stage. Then, the SAM sequentially differentiates sepal primordia, and turns into the FM stage. The secondary axillary buds of GIG maintain vegetative growth after flowering, which was identified at the SVM stage. Black bar: 50µm.

Fig. S2. Scatterplot of enriched GO in pairwise comparisons. The scatterplot of enriched GO terms ($p < 0.05$) in molecular function in the VM-OB vs. TM-OB comparison (A), in the VM-GIG vs. TM-GIG comparison (B), and in the SVM-GIG vs. TM-GIG comparison (C). Bubble color indicates the p-value of GO terms; bubble size indicates the frequency of GO terms in the underlying GOA database.

Fig. S3. Measurement of hormones, soluble sugar and starch contents in different developmental stages of OB and GIG, respectively. Values are means of three replicates \pm SE.

Fig. S4. MapMan analysis showing differences between pairwise comparisons. (A) MapMan metabolism overview maps showing the transcript levels of stage-specific DEGs in the VM-GIG vs. TM-GIG comparison. (B) MapMan metabolism overview maps showing the transcript levels of stage-specific DEGs in the SVM-GIG vs. TM-GIG comparison. (C) MapMan metabolism overview maps showing the transcript levels of DEGs in the VM-OB vs. TM-OB comparison. The color indicates \log_2 value of fold changes, green color represents down-regulated transcripts, and red color represents up-regulated transcripts.

Figure S1

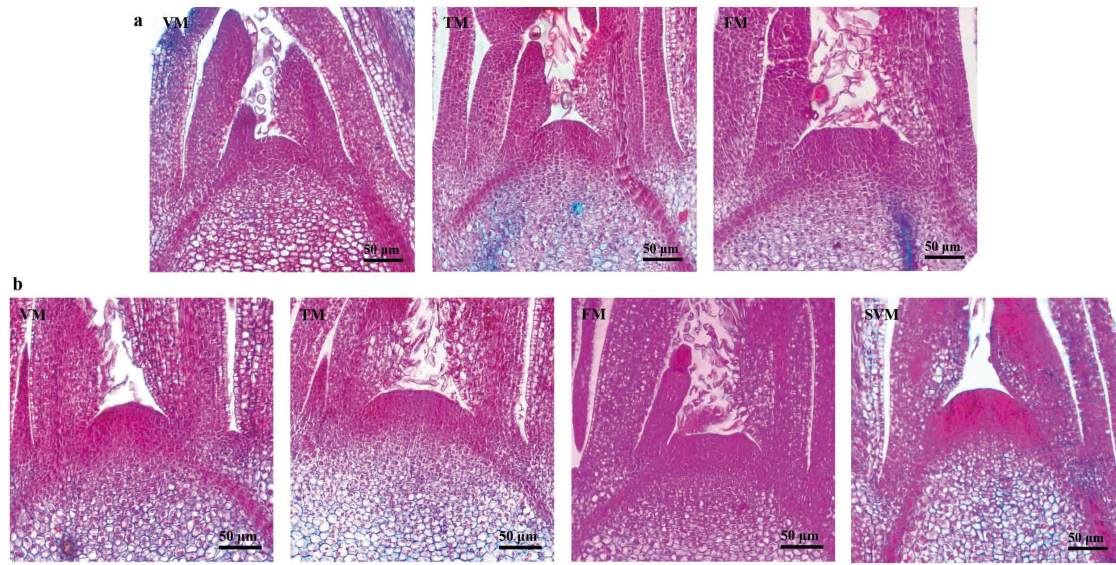


Figure S2

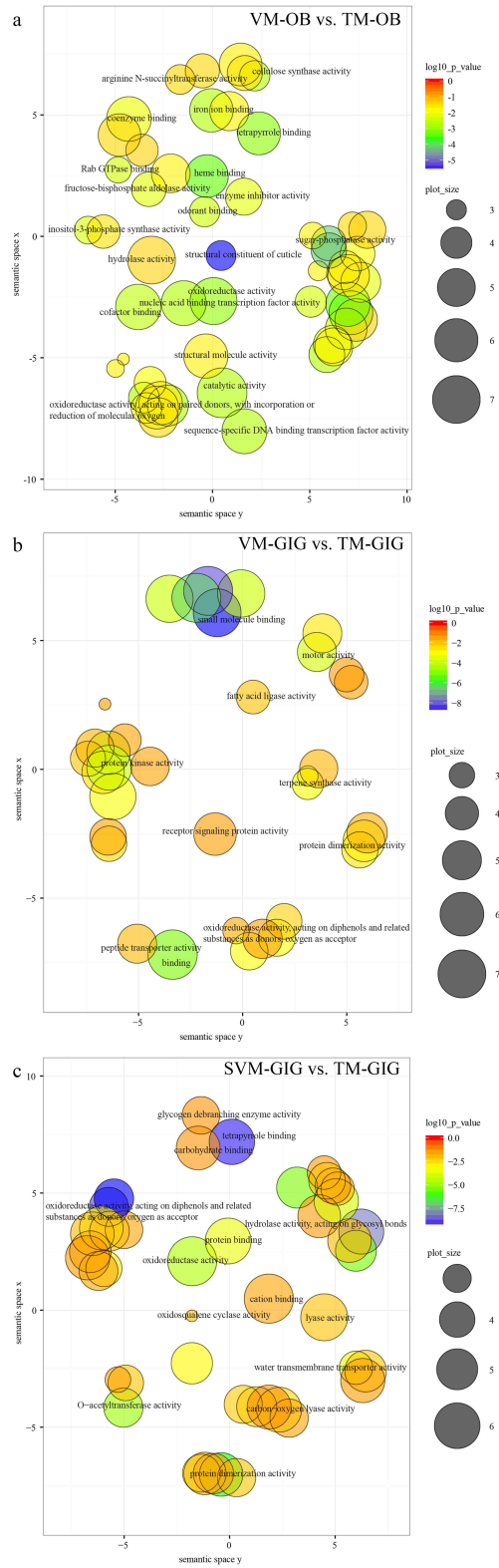
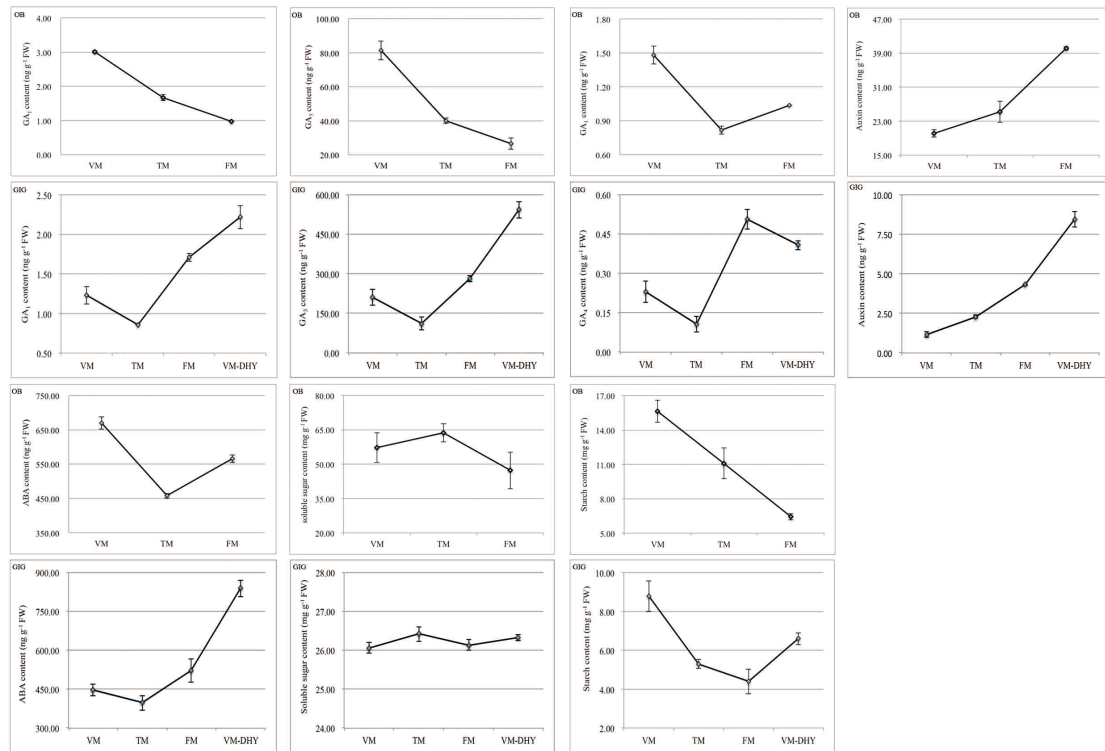


Figure S3



Supplementary Table S1. The identification of DEGs in each comparison of OB and GIG, respectively.

Supplementary Table S2. The relevant GO terms of DEGs in each comparison, including VM-GIG vs. TM-DH, SVM-GIG vs. TM-GIG, and VM-OB vs. TM-OB respectively.

Supplementary Table S3. The annotation of DEGs between pairwise comparisons by using the Mercator software.

Supplementary Table S4. Primers used to assay gene expression by RT-qPCR.