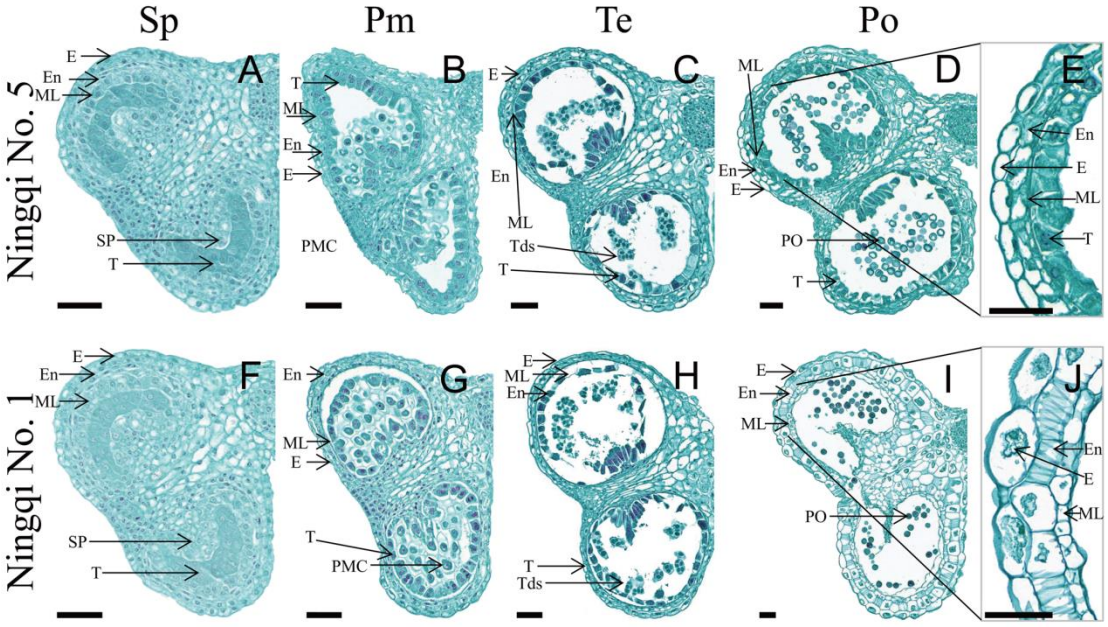

Figure S1. Paraffin sections of Ningqi No. 5 and Ningqi No. 1 pollen sacs at different development stages. A–E. pollen sac development of Ningqi No. 5; F–J. pollen sac development of Ningqi No. 1; (**A**,**F**), pollen sacs of Sp stage; (**B**,**G**), pollen sacs at Pm stage; (**C**,**H**), pollen sacs at Te stage; (**D**,**I**), pollen sacs at Po stage; (**E**,**J**), anther wall layers at Po stage. E, epidermis; EN, endothecium; ML, middle layer; T, tapetum; Tds, tetrad; PMC, pollen mother cell; SP, sporogenous cell; Po, pollen grain. Scale bar = 50 μm.

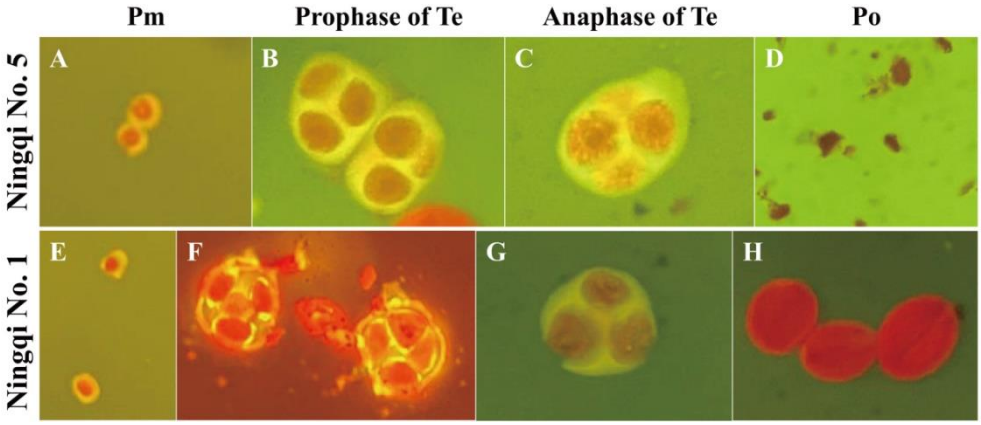

Figure S2. Callose development in Ningqi No.5 and Ningqi No.1 at different development stages: red is nuclear material, yellow is callose. (**A**,**E**), There was no significant change in callose in Pm stage in Ningqi No.1 and Ningqi No.5; **B**, There are clearly visible tetrads in the pollen sac cavity and thin callose outside the tetrads at prophase of Te stage in Ningqi No.5; **C**, Callose is not degraded at anaphase of Te stage in Ningqi No.5; **D**, At the Po stage, no microspore was found in Ningqi No.5; **F**, There are clearly visible tetrads in the pollen sac, and the callose wall around the tetrads is thick at prophase of Te stage in Ningqi No.1; **G**, Callose began degradation and becomes thin at anaphase of Te stage in Ningqi No.1; **H**, At the Po stage, round and deeply colored microspores can be seen in Ningqi No.1.

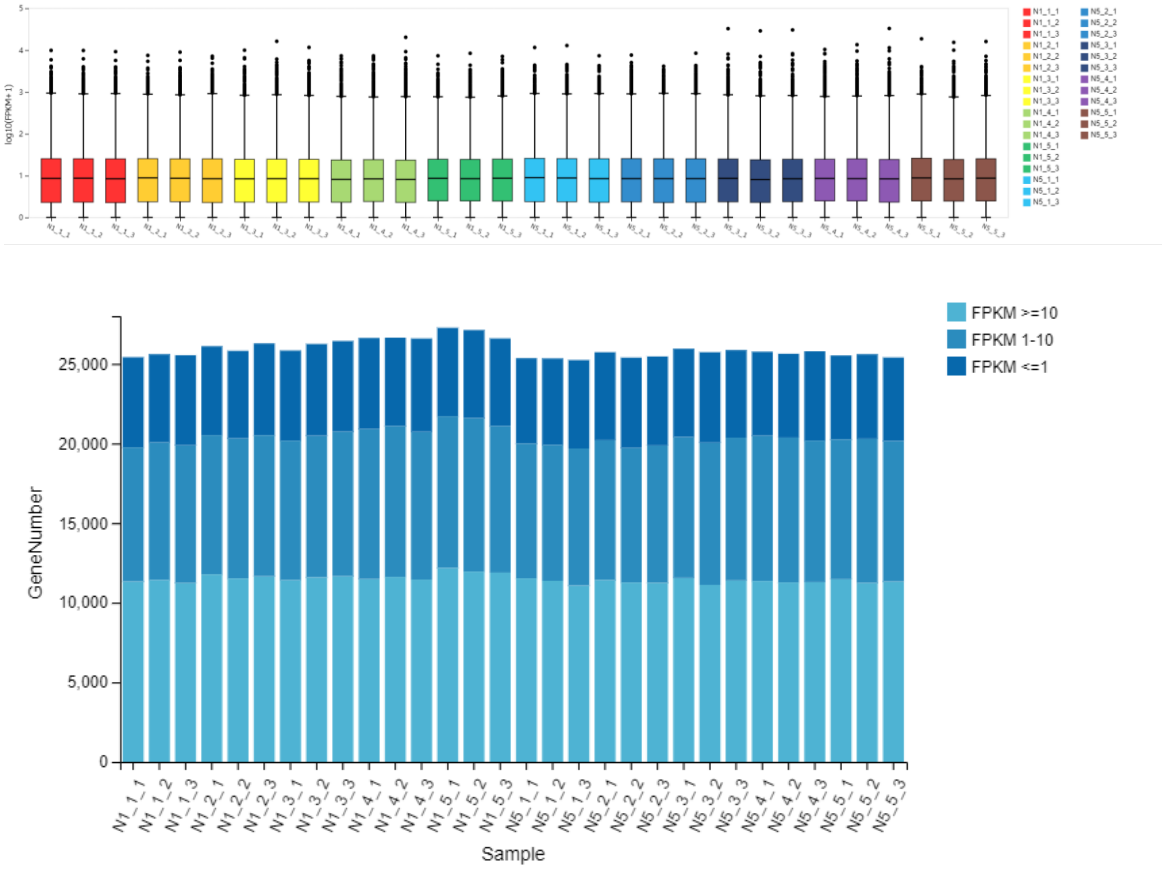

Figure S3. Gene expression levels and number of expression genes. (**A**) Box-plot of all gene expression levels base on FPKM, y-axis is log10 (FPKM+1), x-axis represent different samples; (**B**) Bar-plot of number of expressed genes in each sample, y-axis is gene number, x-axis represent different samples, the diminishing gray shows different expressed levels based on FPKM.

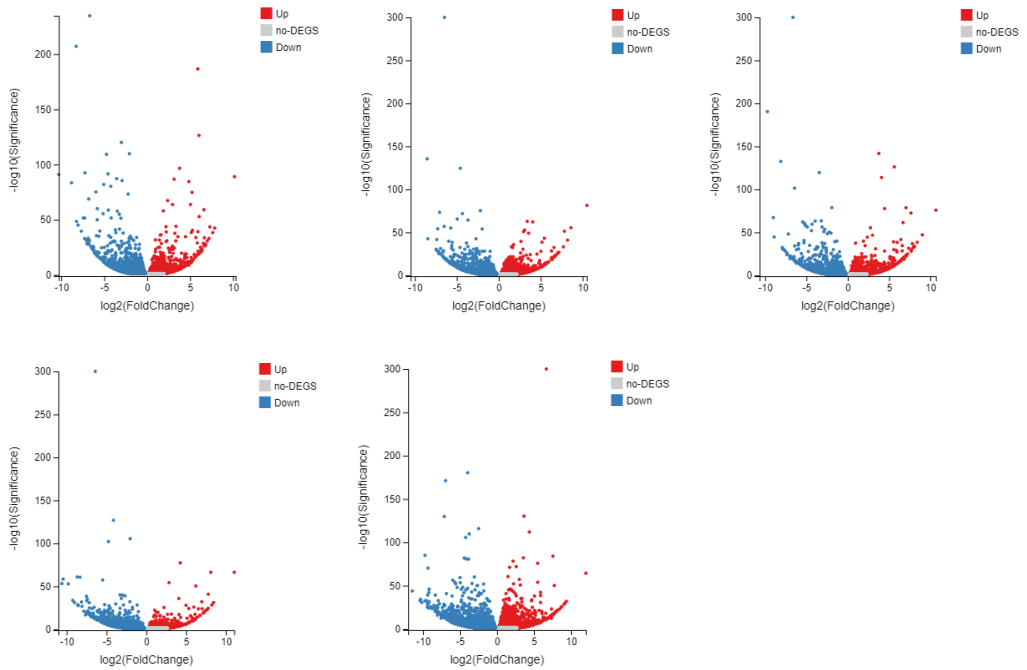

Figure S4. Volcano plots of all time points' DEGs. (**A**) Ar. (**B**) Sp. (**C**) Pm. (**D**) Te. (**E**) Po. (F) 4:00. X-axis is log2 (fold change), Y-axis is -log10 (Significance), blue point means fold change of differential expression higher than 1 and Significance lower than 0.05.

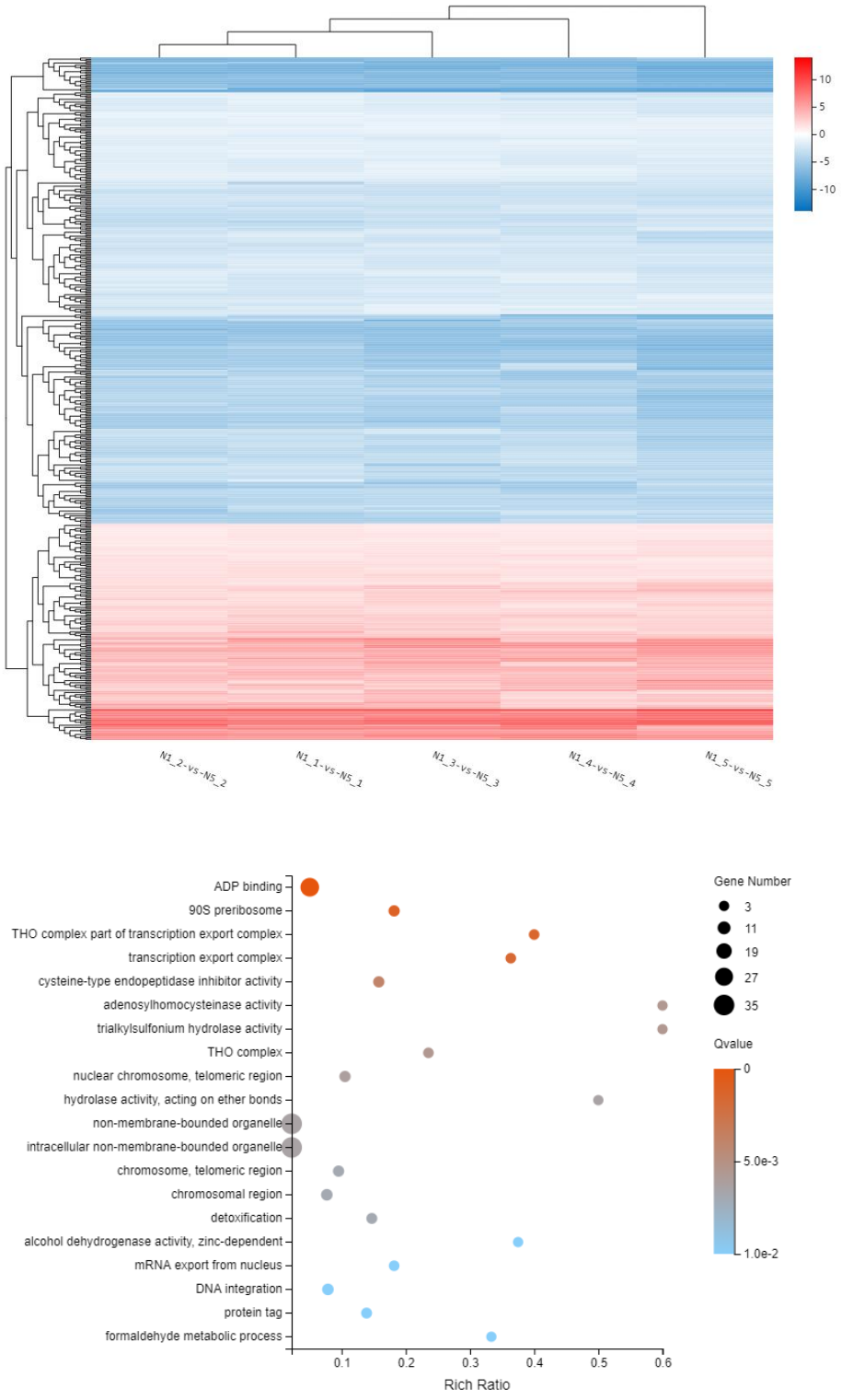

Figure S5. DEGs of all control groups. (**A**) heatmap of 489 DEGs in anther; each row corresponds to a gene, each column corresponds to control group, the color of every cell indicates the expression level based on z-score normalization. (**B**) significant GO enrichment of 489 DEGs; X-axis is rich ratio and different GO terms is in Y-axis.

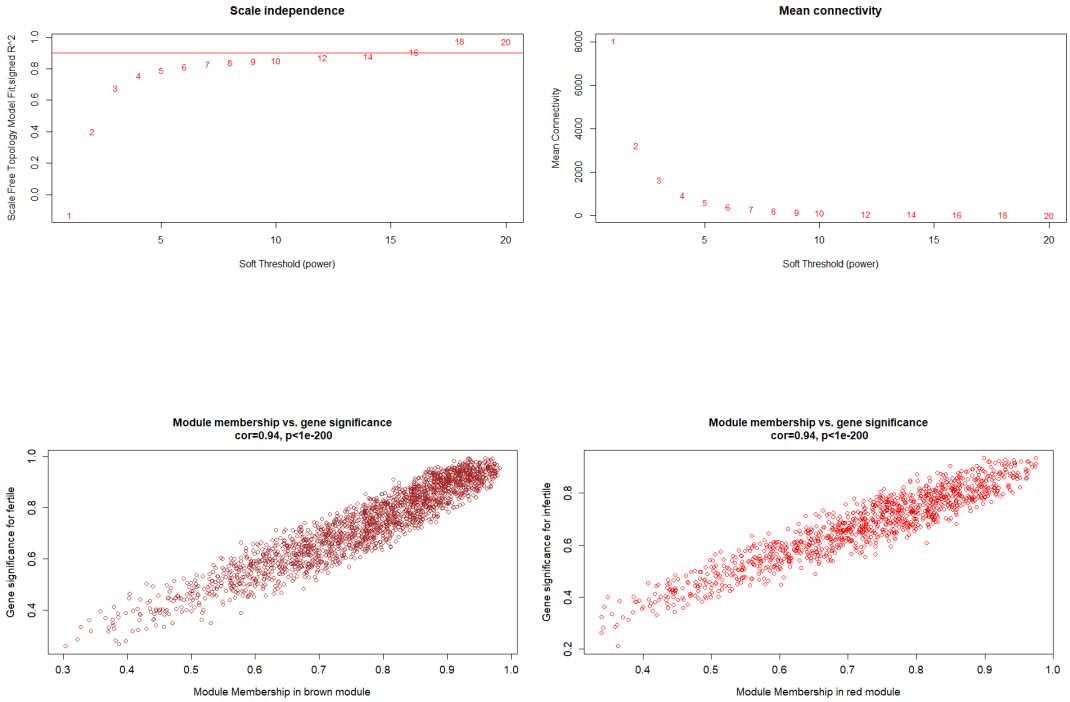

Figure S6. (**A**) The network topology for various soft thresholding powers. The left panel shows the scale-free fit index (y-axis) as a function of the soft-thresholding power(x-axis). The right panel displays the mean connectivity (degree, y-axis) as a function of the soft-thresholding power(x-axis); (**B**) The relationship between genes in module and the representative traits of the module. The left panel shows gene significance for fertile.The right panel displays gene significance for infertile.

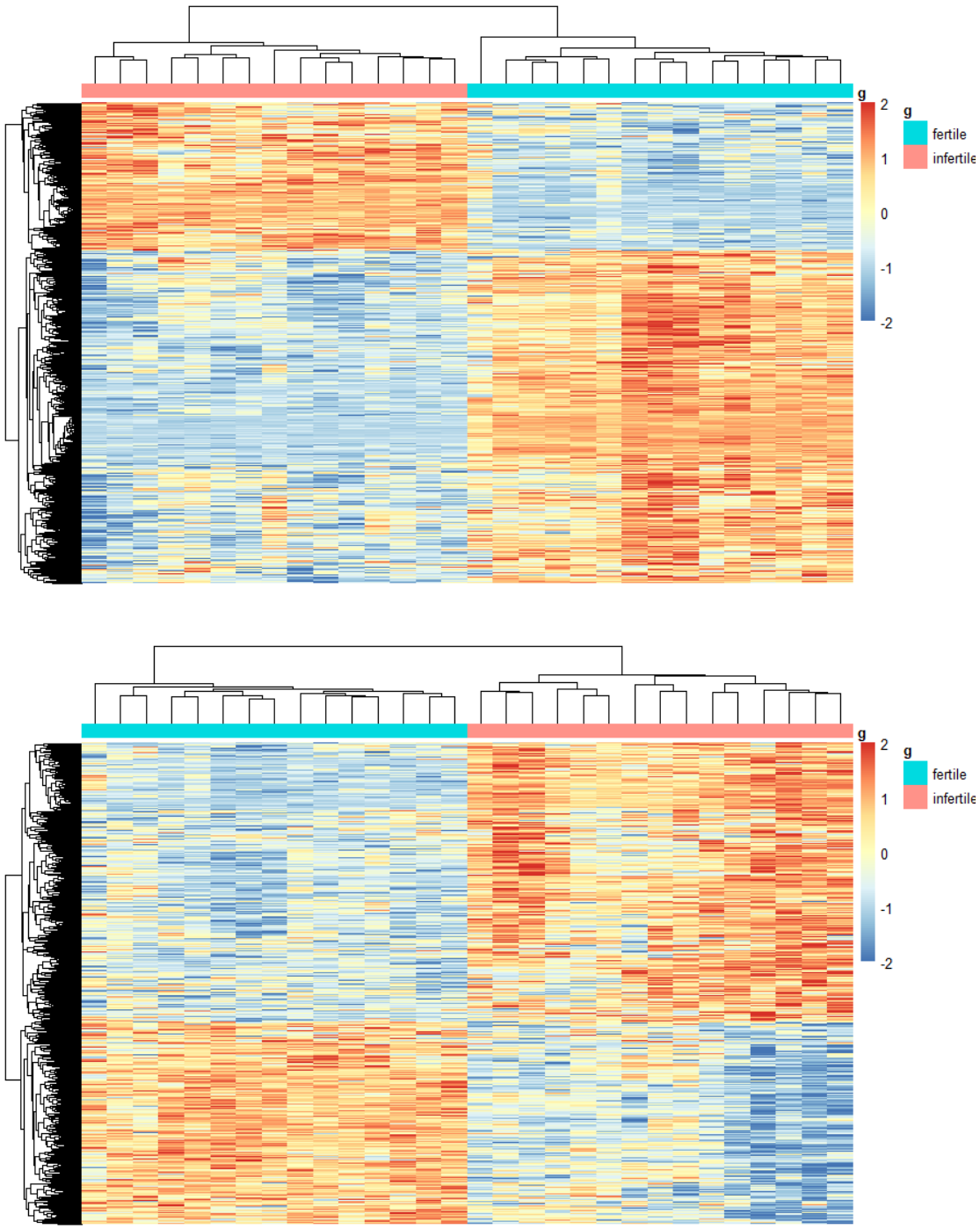

Figure S7. The expression of genes in the MEbrown and MEred modules in different samples. (**A**) MEbrown; (**B**) MEred.

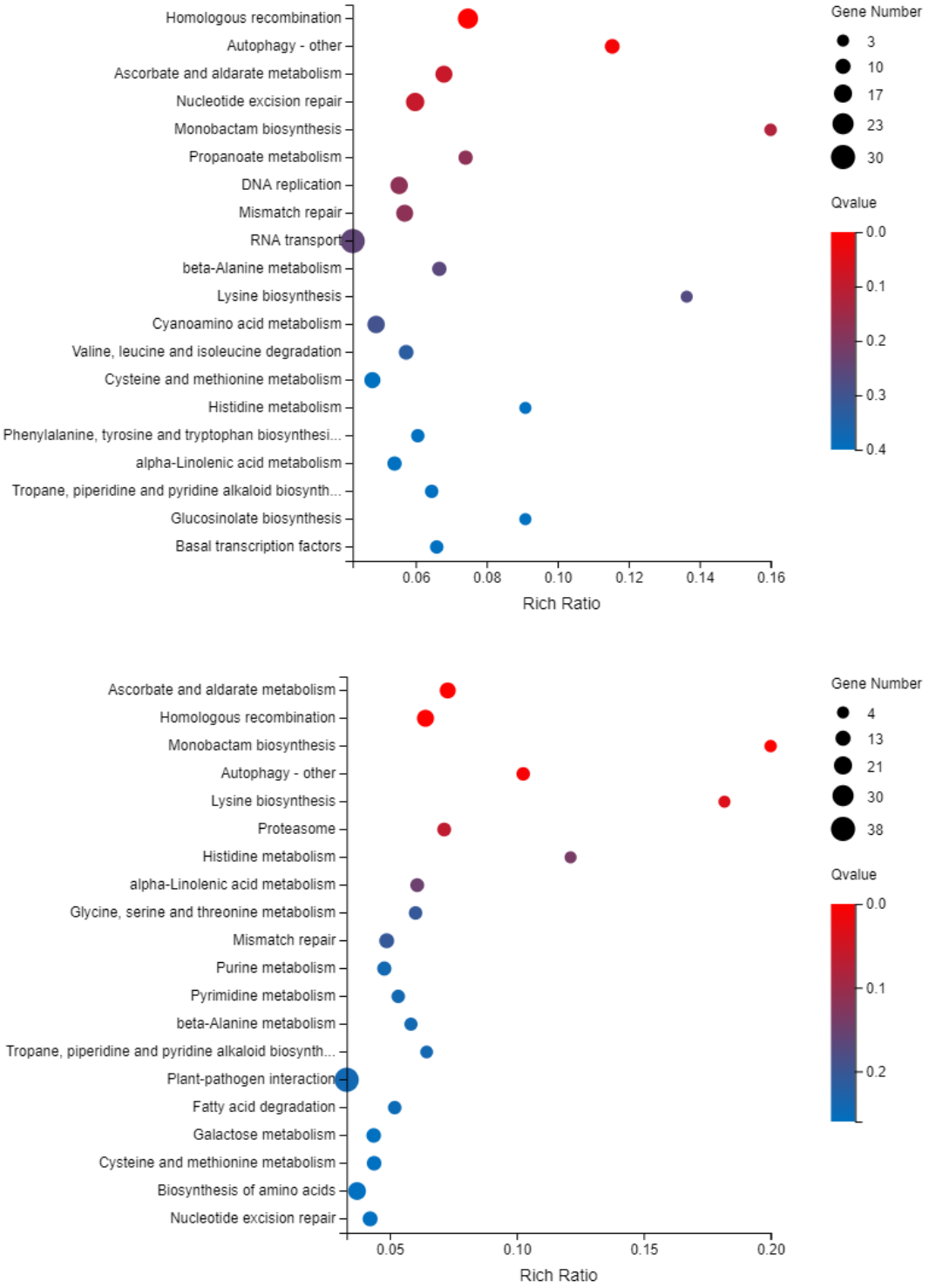

Figure S8. KEGG enrichment bubble map of genes in MEbrown and MEred Modules. (**A**) MEbrown; (**B**) MEred.

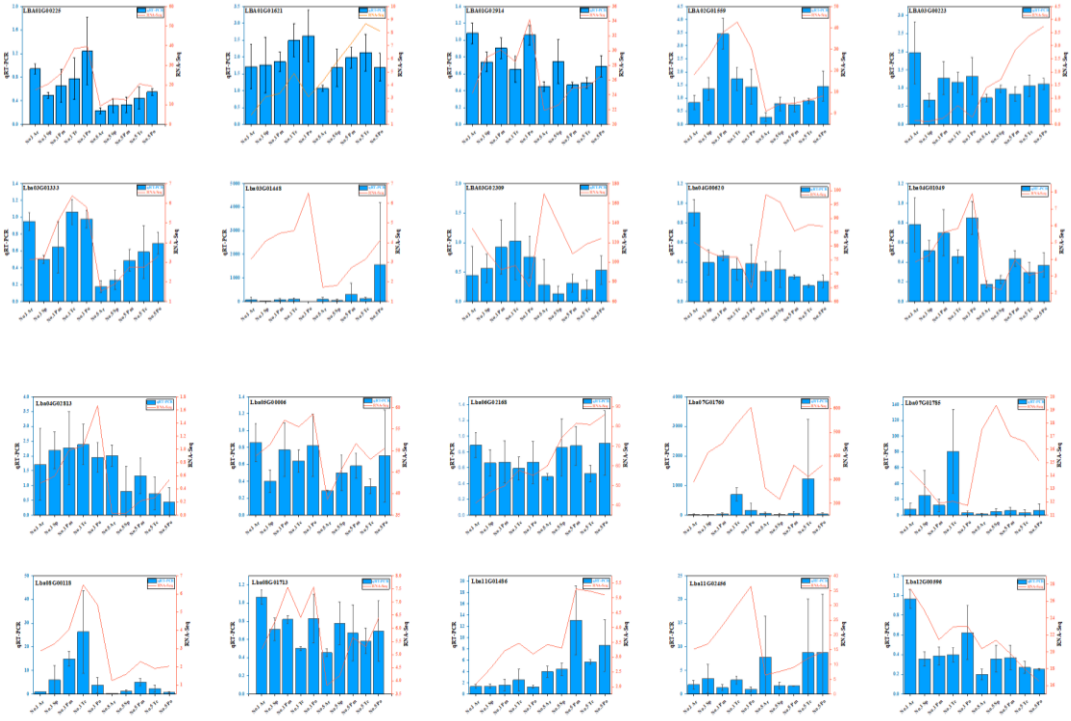

Figure S9. Verification of qRT-PCR expression of some genes.