**Supplementary Materials**

Fig. S1. Venn diagrams showing the changes of DEGs expression in all comparison groups.

Table S1. Result of the *de novo* transcriptome assembly.

Table S2. Up- and down-regulation DEGs in comparison groups T/CK.

Table S3. Up- and down-regulation DEGs in comparison groups R/T.

Table S4. Up- and down-regulation DEGs in comparison groups R/CK.

Table S5. The 29 DEGs up-regulated in T/CK and down-regulated in R/T.

Table S6. The 44 DEGs down-regulated in T/CK and up-regulated in R/T.

Table S7. Enriched significantly GO terms in T/CK (P-adjust<0.05).

Table S8. Top 20 GO terms enriched in R/T.

Table S9. Top 20 GO terms enriched in R/CK.

Table S10. Statistical enrichment analysis for KEGG pathways in T/CK.

Table S11. Statistical enrichment analysis for KEGG pathways in R/T.

Table S12. Statistical enrichment analysis for KEGG pathways in R/CK.

Table S13. The differentially expressed transcription factors (TFs) between different treatment.

Table S14. The differentially expressed transporter proteins (TPs) between different treatment.

Table S15. The differentially expressed unigenes associated with ROS scavenging between different treatment.

Table S16. The differentially expressed unigenes associated with Proline metabolism pathway.

Table S17. qRT-PCR primers used in this study.