

Figure legends

Figure S1. Overview of analytical approaches for integration of metabolomes and transcriptomes of *Akebia trifoliata* fruit. The integrative approach was applied to study *A. trifoliata* fruit metabolite and transcript fluctuations during ripening and cracking. Data processing methods allowed for the identification of transcripts and metabolites as single and integrated datasets to find biomarkers within each dataset and trends between them for a global understanding of the cracking in *A. trifoliata* fruit.

Figure S2. The transcriptome analyses of *A. trifoliata* peels during ripening.

(a) The expression profiles of abundant genes. The red segments indicate a relatively high expression level of genes, while the blue segments indicate a relatively low expression level of genes.

(b-c) GO and KEGG annotation classification of genes

(d) Venn diagram of differentially expressed genes (DEGs)

(e) Four clusters of co-expressed DEGs and their kinetic patterns.

Figure S3. The heat map illustrates the expression patterns of differentially expressed genes (DEGs) within the photosynthesis pathway (a) and the photosynthesis-antenna proteins (b) pathway in *A. trifoliata* peels during ripening.

G: Green period, T: Transition period, P: Purple period, C: Cracking period. The red segments indicate a relatively high expression level of genes, while the blue segments indicate a relatively low expression level of genes.

Figure S4. The heat map illustrates the expression patterns of differentially expressed genes (DEGs) within the plant hormone signal transduction pathway in *A. trifoliata* peels during ripening.

G: Green period, T: Transition period, P: Purple period, C: Cracking period. The red segments indicate a relatively high expression level of genes, while the blue segments indicate a relatively low expression level of genes.

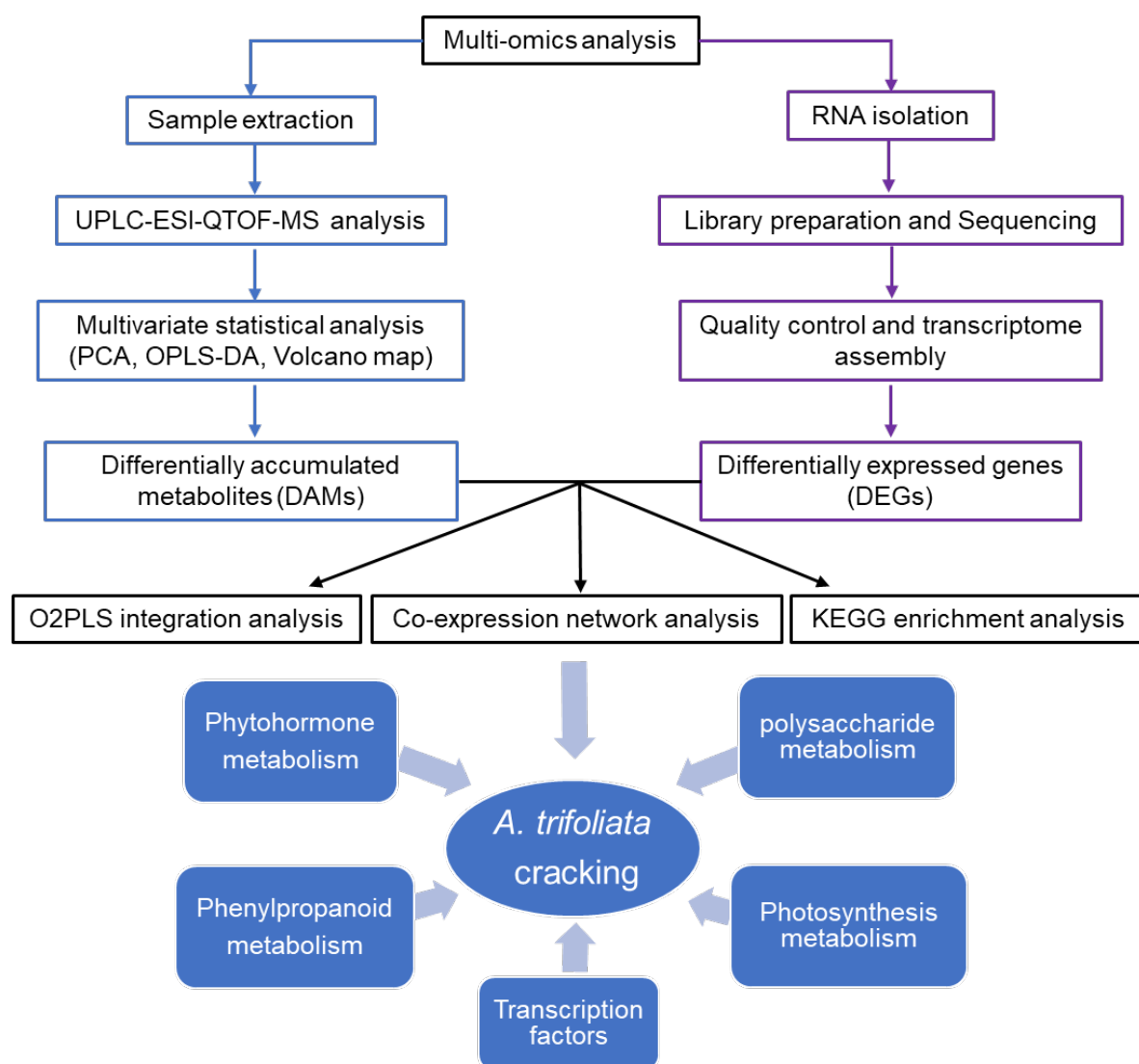


Figure S1

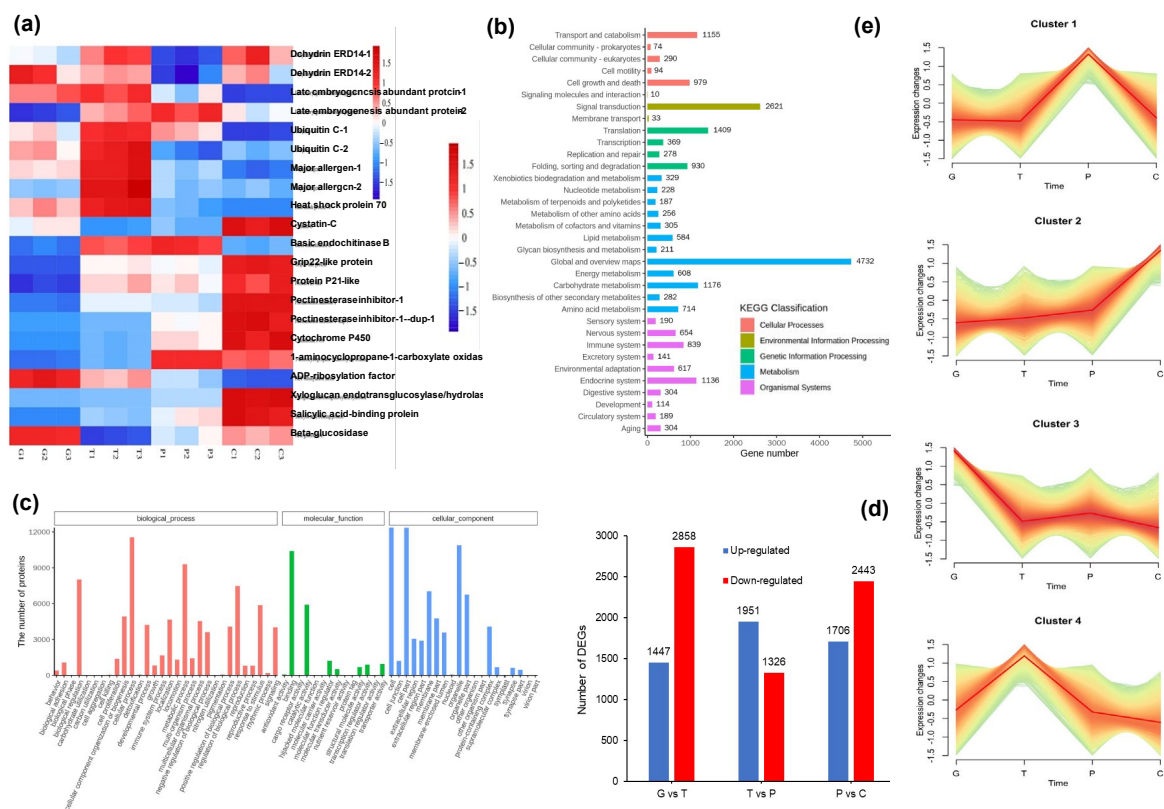


Figure S2

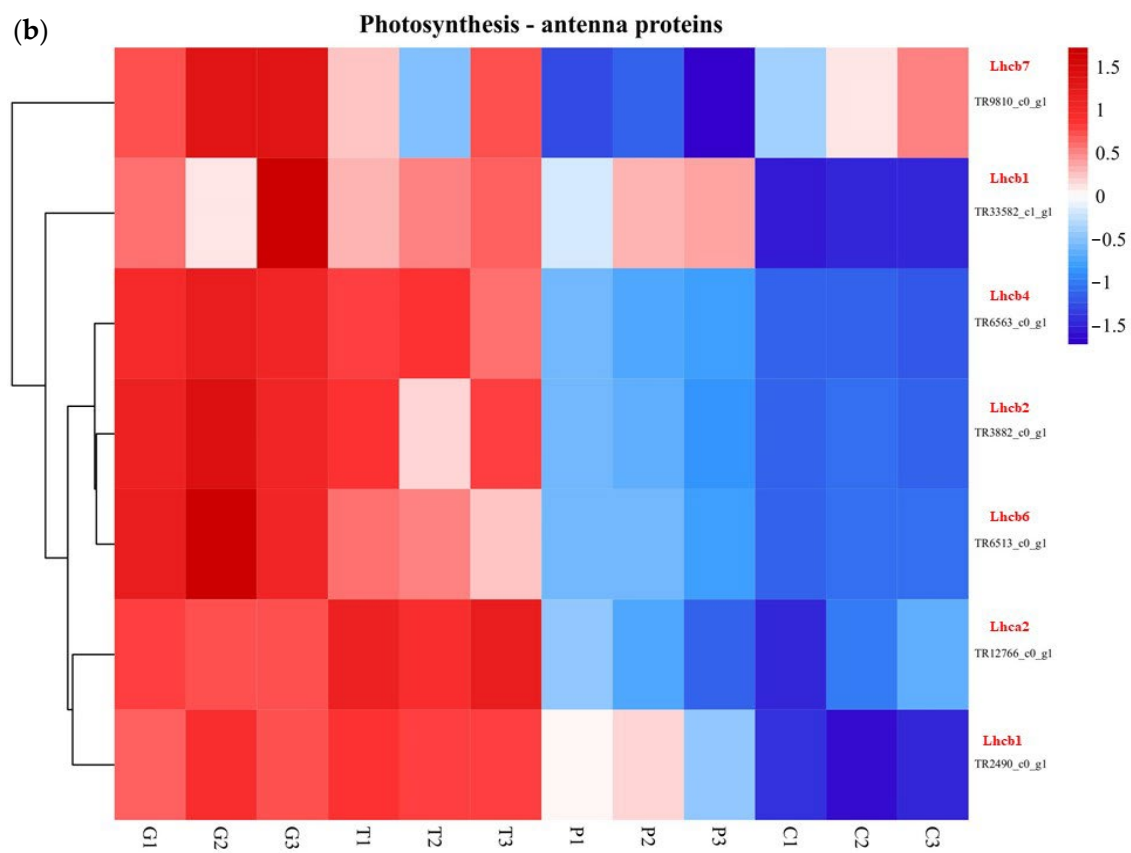
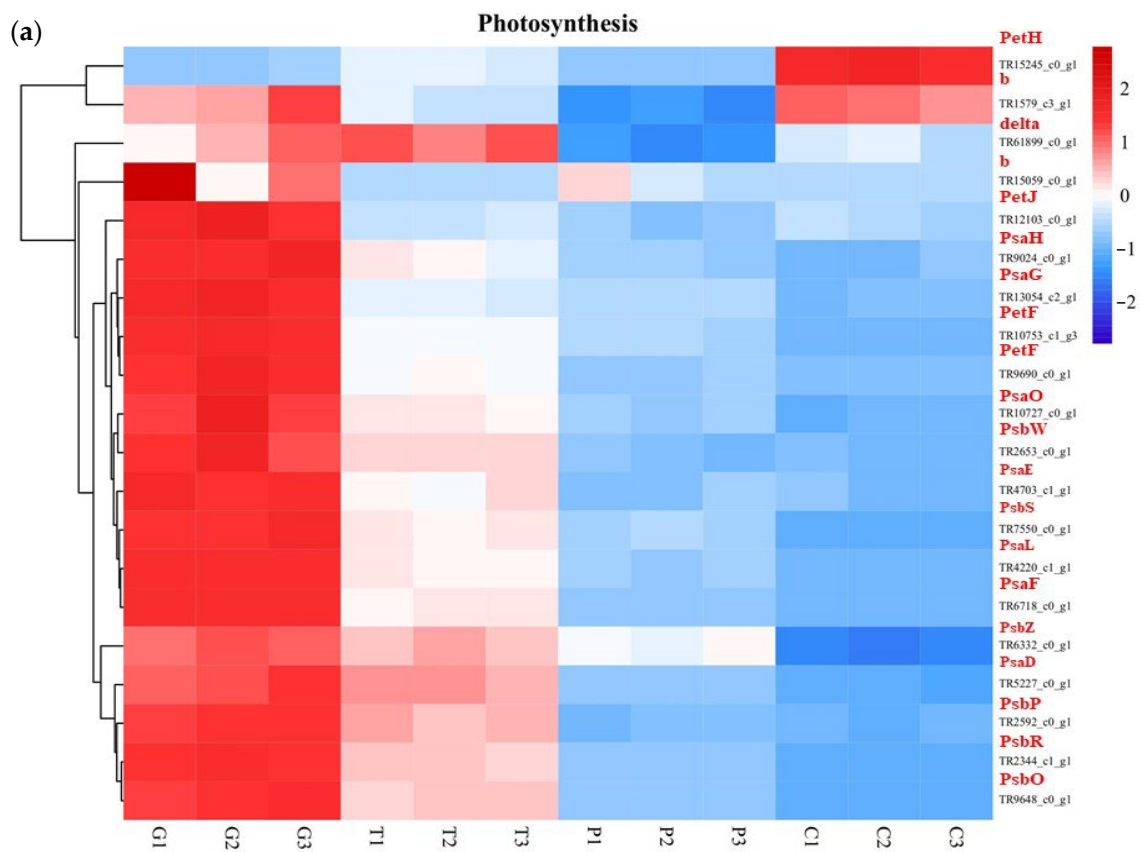


Figure S3

