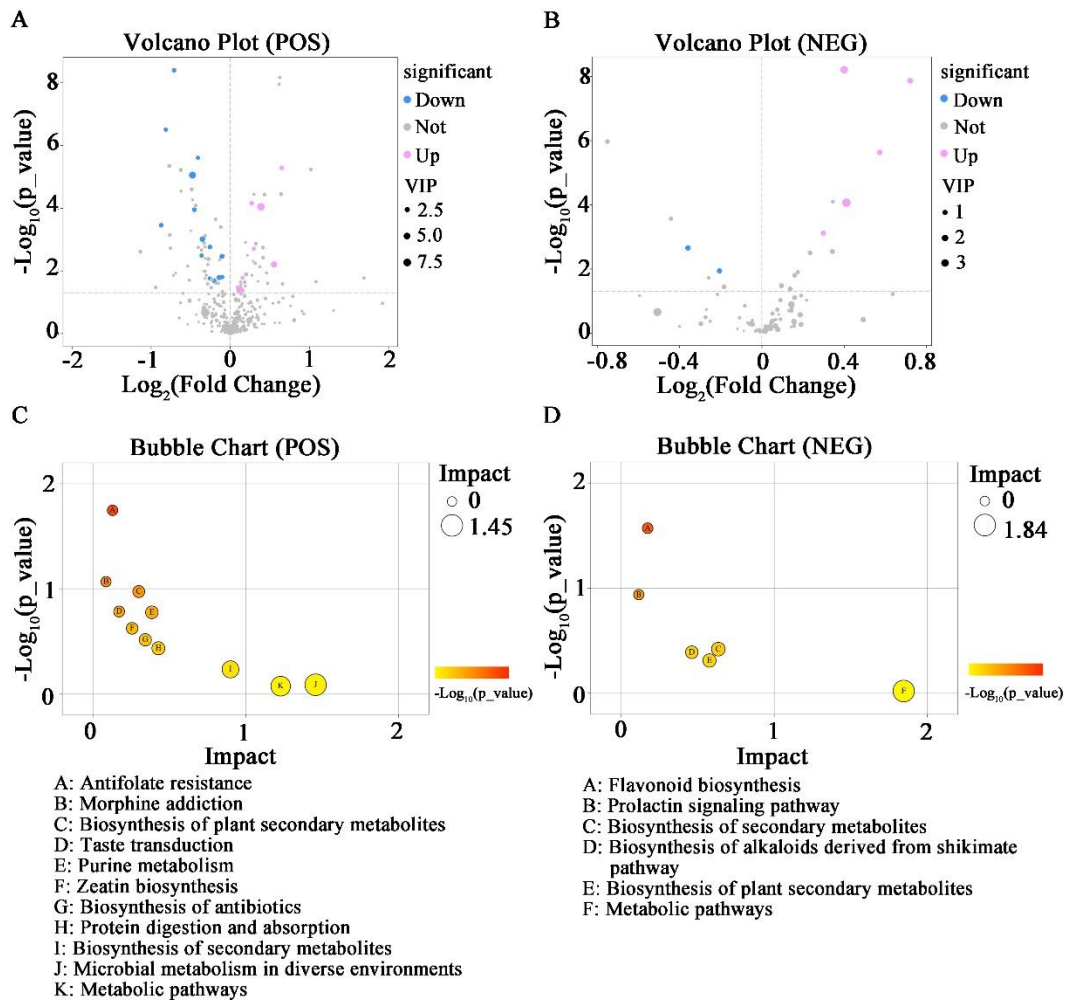
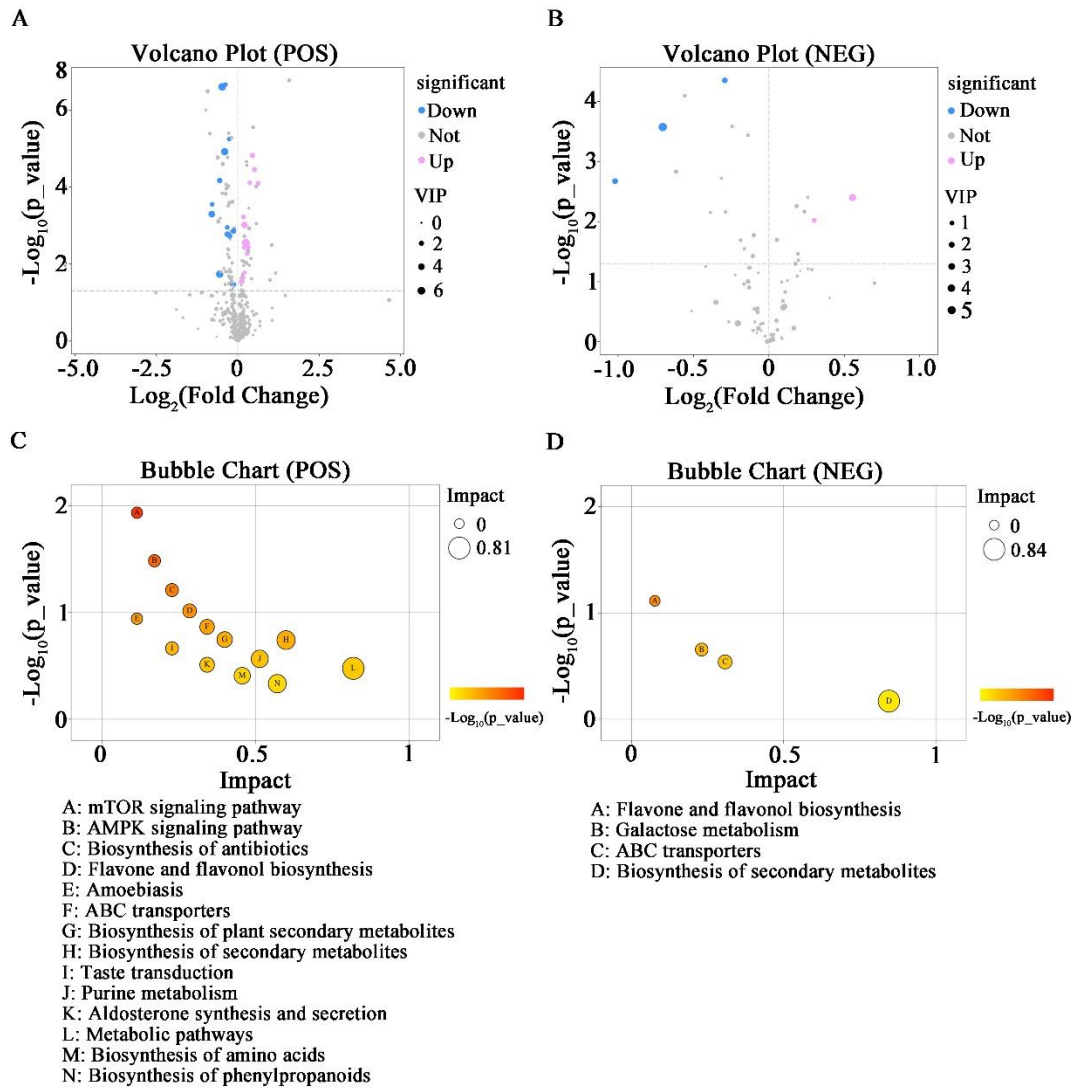


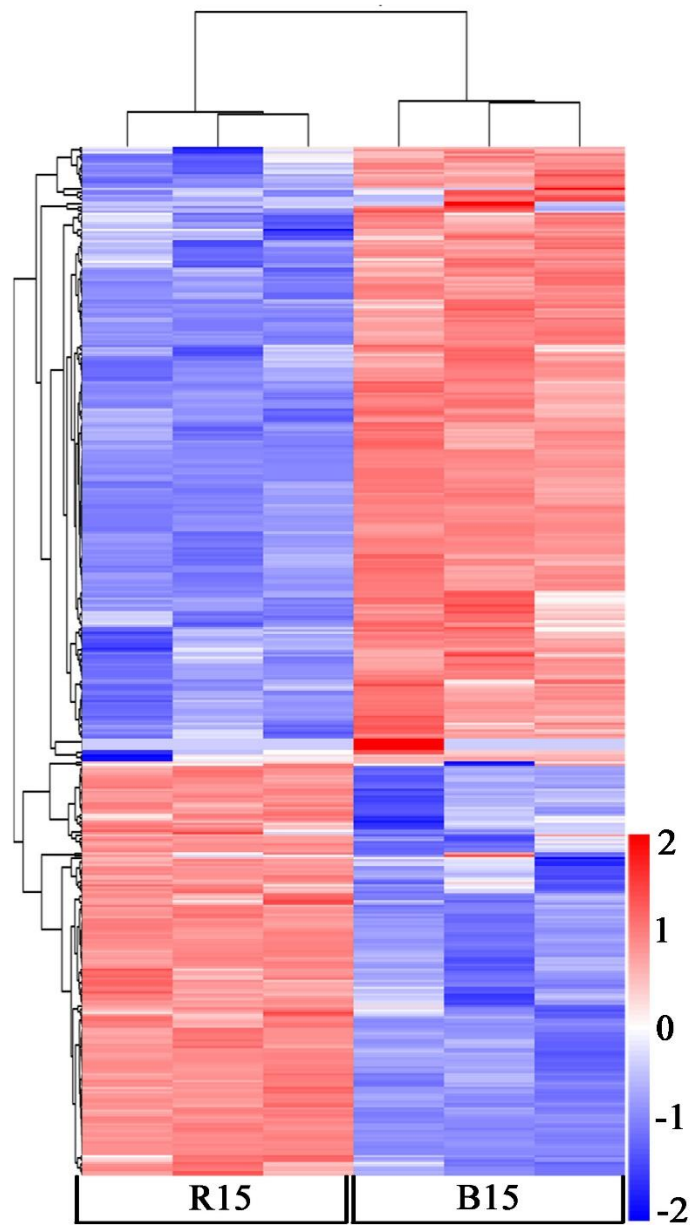
Supplementary Figure 1 Principal component analysis (PCA) and orthogonal projections to latent structures-discriminant analysis (OPLS-DA) of all samples.



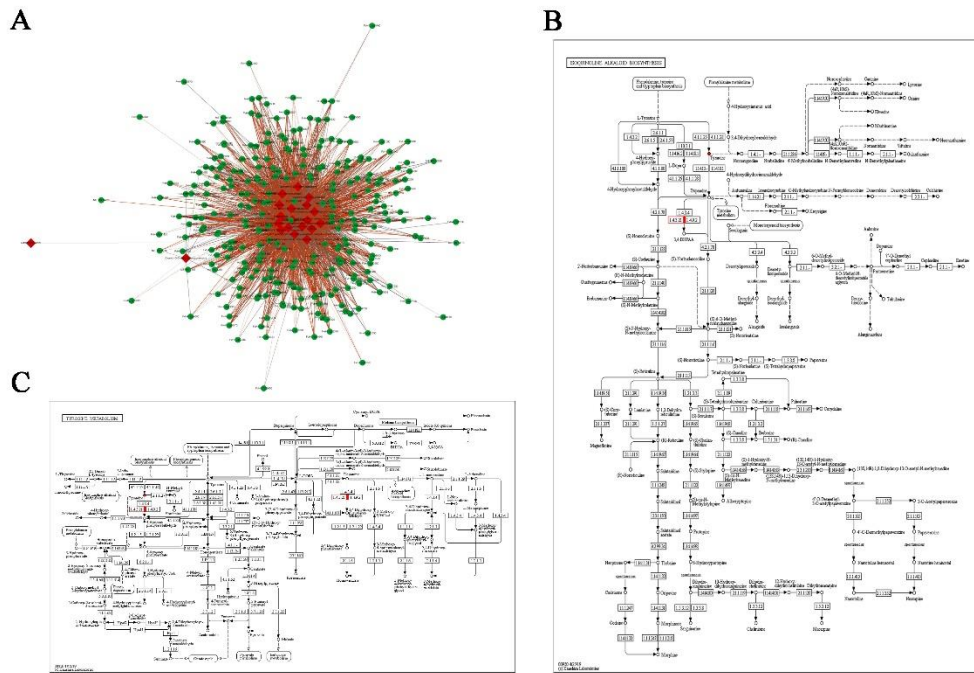
Supplementary Figure 2 Statistical and KEGG-enrichment analyses of different metabolites in strawberry receiving white- and red-light treatments. (A) Statistical analyses of differentially expressed metabolites in positive detection mode. **(B)** Statistical analyses of differentially expressed metabolites in negative detection mode. **(C)** KEGG enrichment analyses of the differentially expressed metabolites (POS). **(D)** KEGG enrichment analyses of the differentially expressed metabolites (NEG).



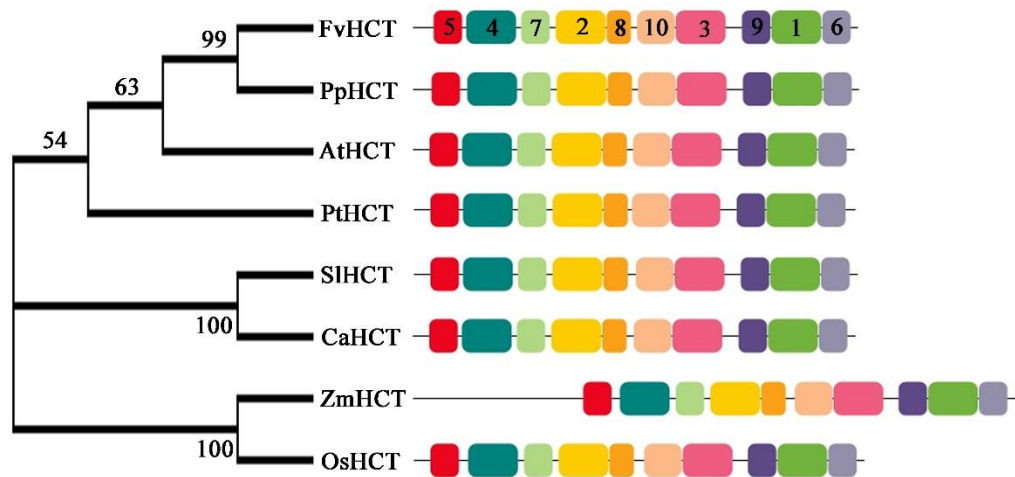
Supplementary Figure 3 Statistical and KEGG-enrichment analyses of different metabolites in strawberry receiving white- and blue-light treatments. (A) Statistical analyses of differentially expressed metabolites in positive detection mode. **(B)** Statistical analyses of differentially expressed metabolites in negative detection mode. **(C)** KEGG enrichment analyses of the differentially expressed metabolites (POS). **(D)** KEGG enrichment analyses of the differentially expressed metabolites (NEG).



Supplementary Figure 4 Hierarchical cluster-based heat map of differentially expressed genes (DEGs) receiving blue and red light treatment.



Supplementary Figure 5 The network_plot of DEMs (Positive detection mode) and DEGs. The grey line indicates negative correlation, red line indicates positive correlation; ellipse represents DEGs and square represents DEMs. (B) A detailed diagram of isoquinoline alkaloid biosynthesis. (C) A detailed diagram of tyrosine metabolism. Enzymes and metabolites with enhanced expression during the blue-light treatment are shown in red.



Supplementary Figure 6 Evolutionary analysis of HCT proteins in strawberry.

Phylogenetic and motif analyses of HCT proteins. The phylogenetic tree was constructed using the full-length HCT protein sequences. The protein motifs are denoted by different colored rectangles. To distinguish the different motifs, the 10 motifs are indicated by the numbers 1–10.