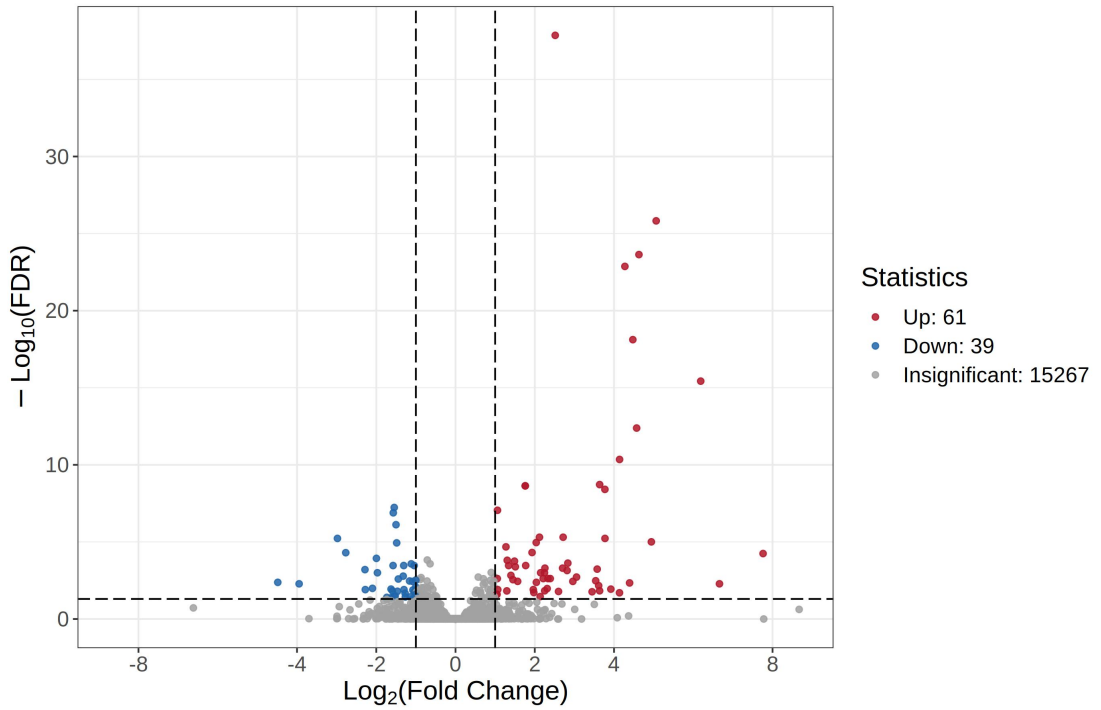
A



B

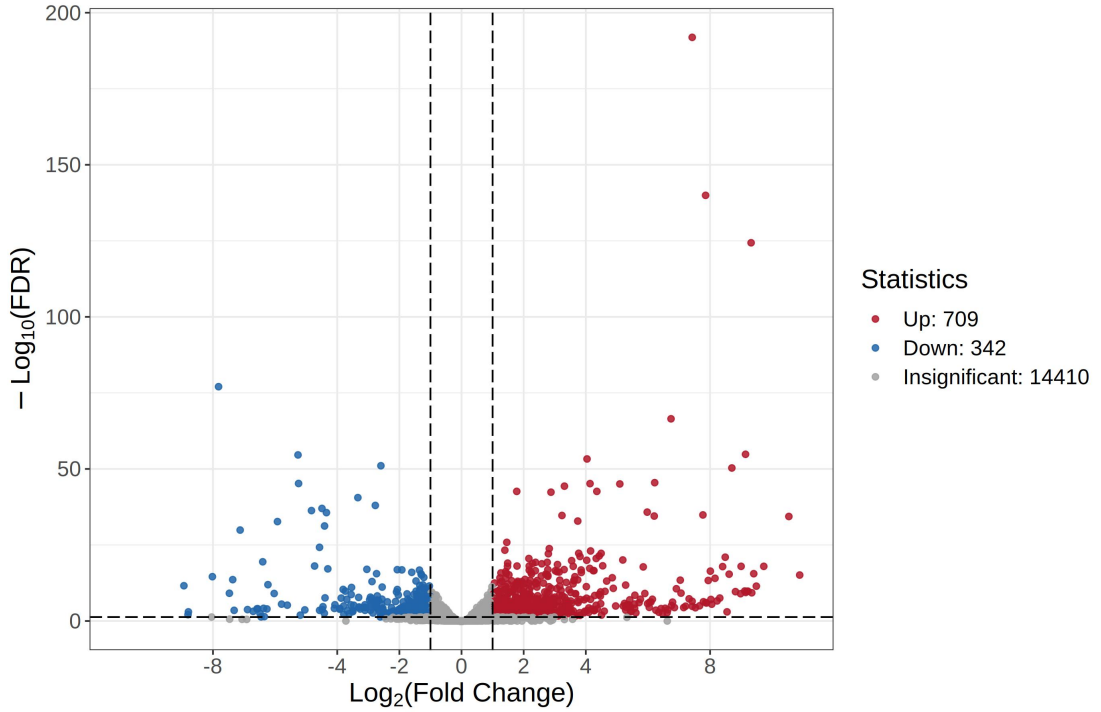
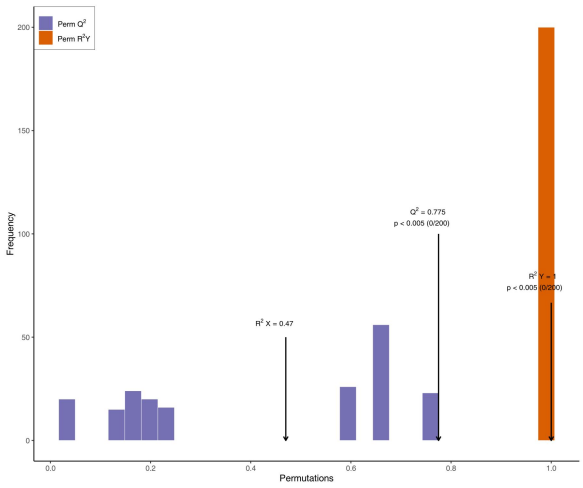


Figure S1. The volcano plot of DEGs in *G. elata*, where red represent upregulated genes, blue represent downregulated genes. (A) Stage2 vs Stage1. (B) Stage3 vs Stage2.

A



B

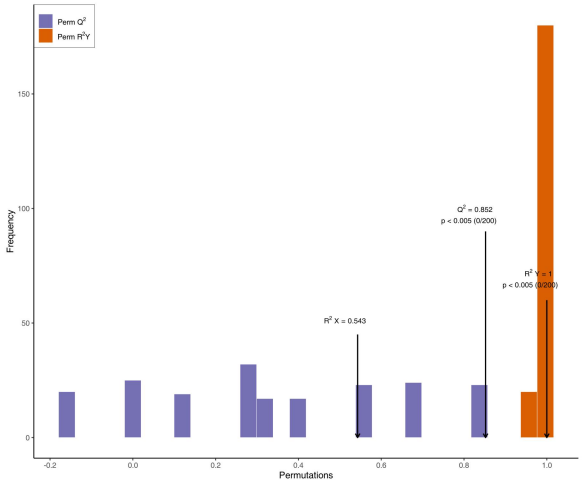
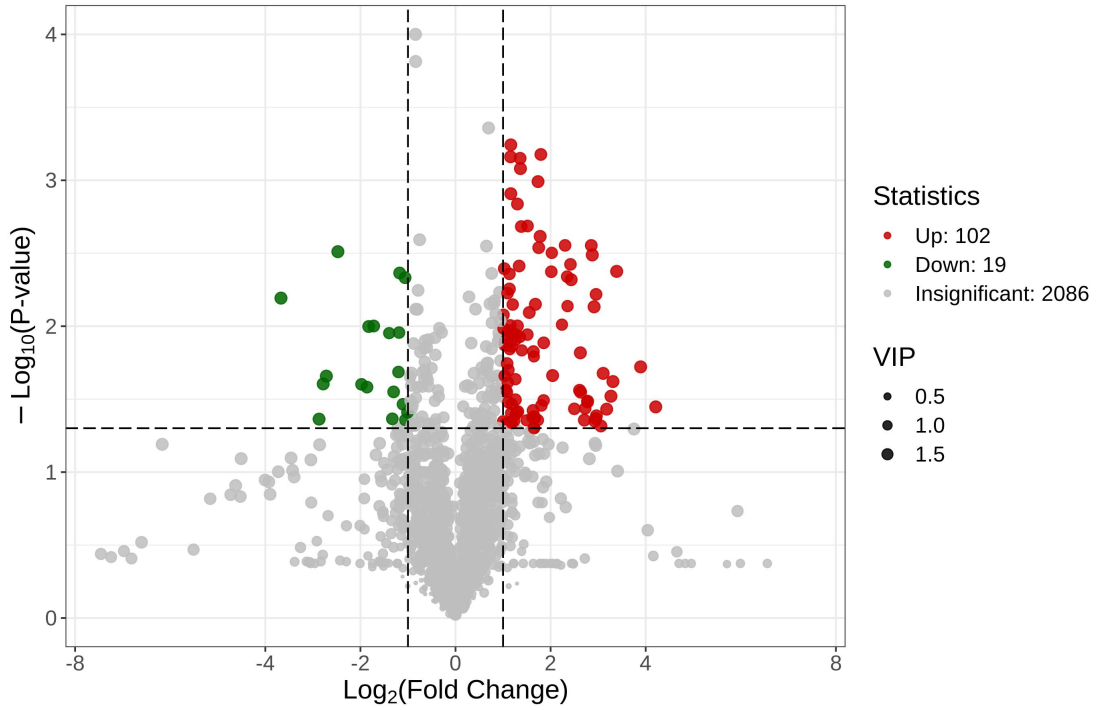


Figure S2. OPLS-DA. (A) Stage2 vs Stage1. (B) Stage3 vs Stage2.

A



B

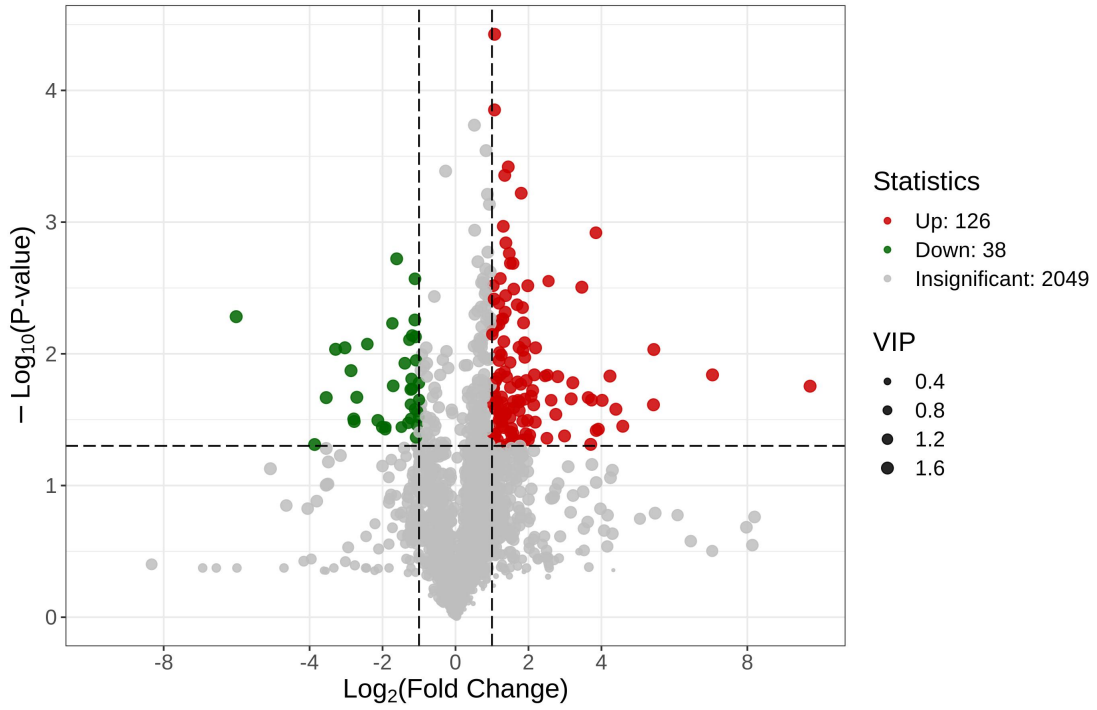


Figure S3. The volcano plot of SCMs in *G. elata*, where red represent upregulated metabolites, green represent downregulated metabolites. (A) Stage2 vs Stage1. (B) Stage3 vs Stage2.

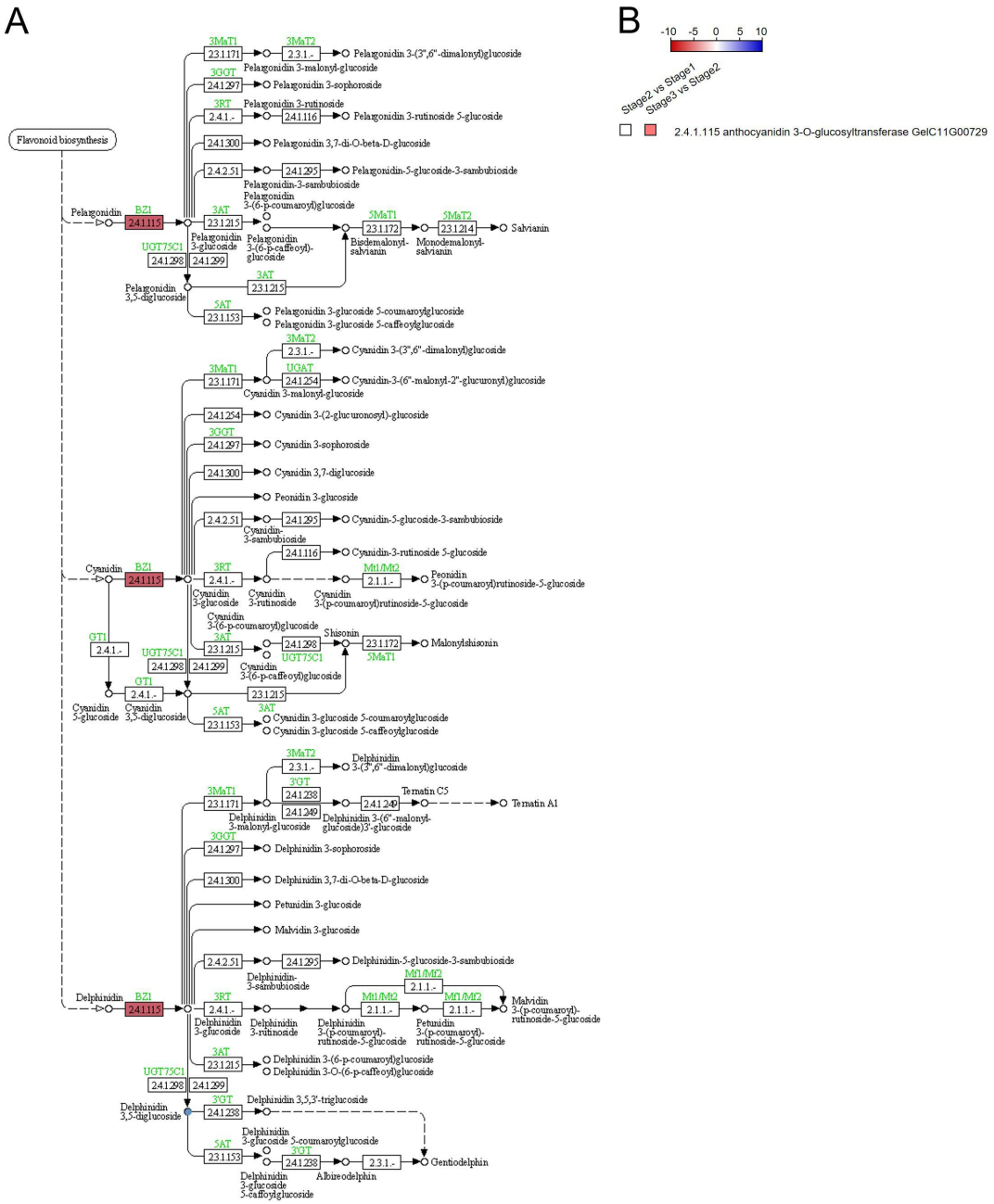


Figure S4. Integrative analysis of transcriptome and metabolome data for the Anthocyanin biosynthesis pathway (ko00942) in *G. elata*. (A) Mapping of enriched DEGs in Stage3 vs Stage2. Red and blue boxes represent genes with up-regulated and down-regulated expression, respectively. Red and blue dots represent metabolites with up-regulated and down-regulated accumulation, respectively. (B) Expression pattern of DEGs involved in Anthocyanin biosynthesis metabolism at diferent stages.

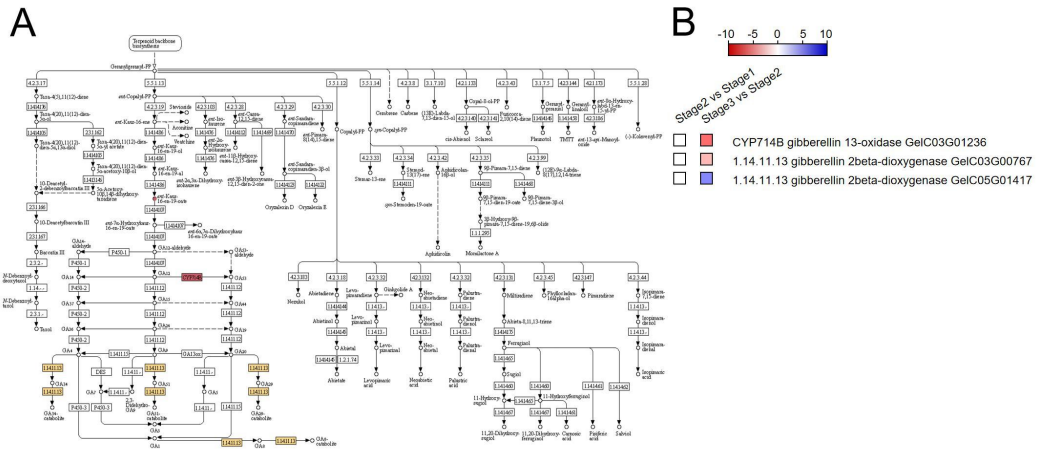


Figure S5. Integrative analysis of transcriptome and metabolome data for the Diterpenoid biosynthesis pathway (ko00904) in *G. elata*. (A) Mapping of enriched DEGs in Stage3 vs Stage2. Red and blue boxes represent genes with up-regulated and down-regulated expression, respectively. Red and blue dots represent metabolites with up-regulated and down-regulated accumulation, respectively. (B) Expression pattern of DEGs involved in Diterpenoid biosynthesis metabolism at diferent stages.

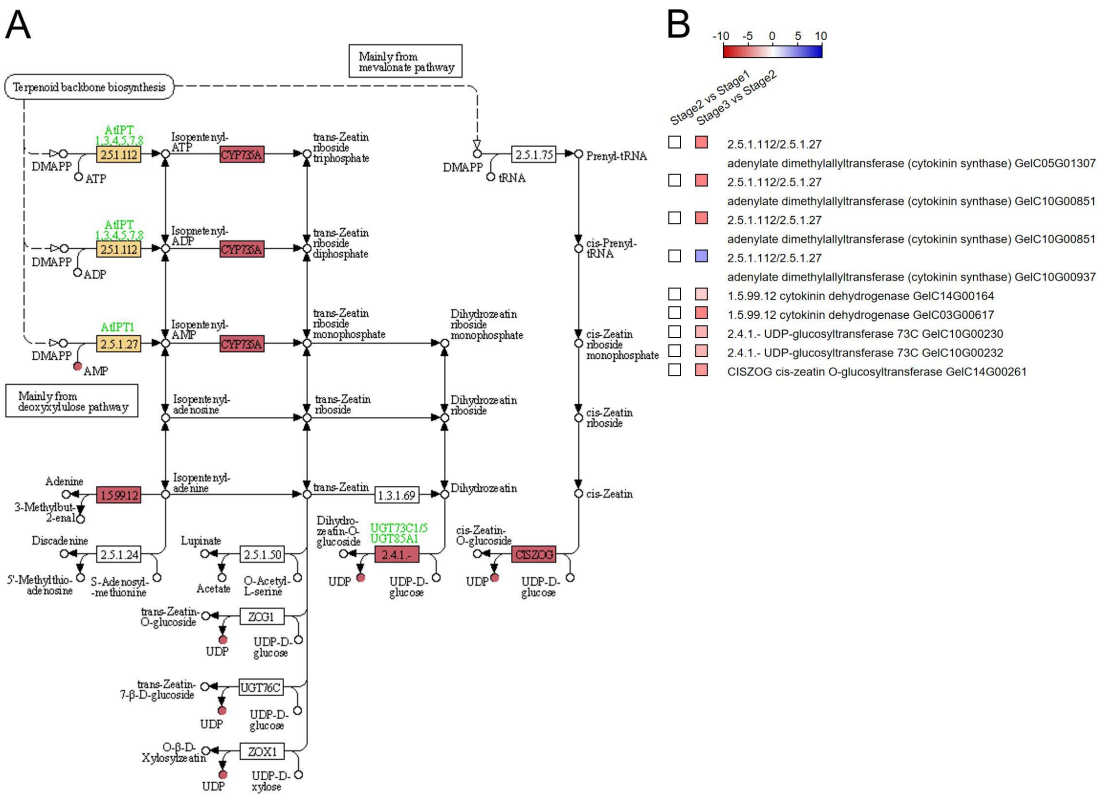


Figure S6. Integrative analysis of transcriptome and metabolome data for the Zeatin biosynthesis pathway (ko00908) in *G. elata*. (A) Mapping of enriched DEGs in Stage3 vs Stage2. Red and blue boxes represent genes with up-regulated and down-regulated expression, respectively. Red and blue dots represent metabolites with up-regulated and down-regulated accumulation, respectively. (B) Expression pattern of DEGs involved in Zeatin biosynthesis at diferent stages.

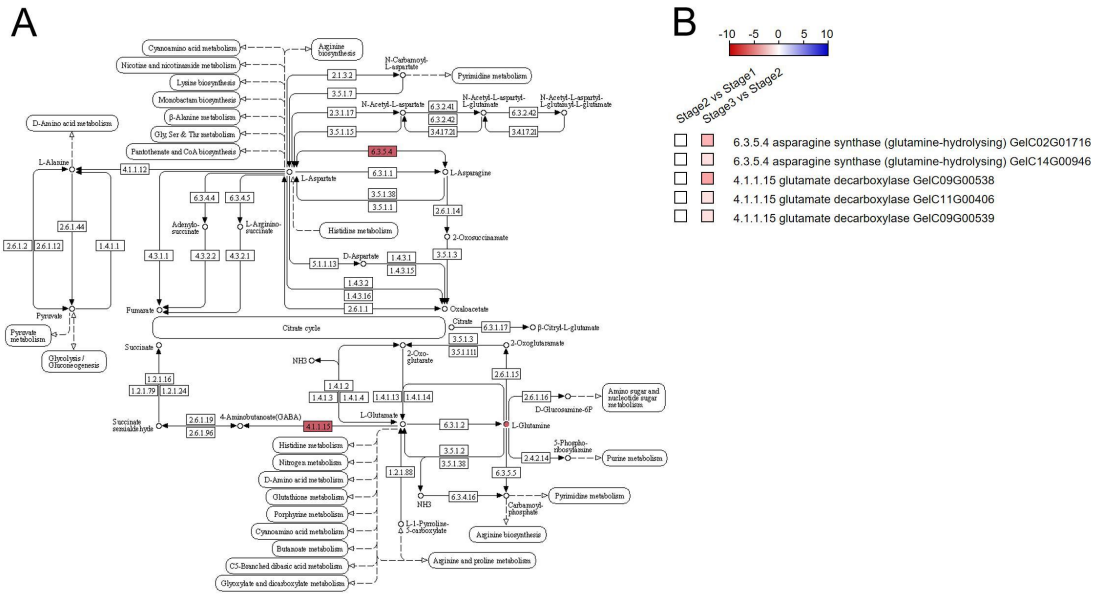


Figure S7. Integrative analysis of transcriptome and metabolome data for the Alanine, aspartate and glutamate metabolism pathway (ko00250) in *G. elata*. (A) Mapping of enriched DEGs in Stage3 vs Stage2. Red and blue boxes represent genes with up-regulated and down-regulated expression, respectively. Red and blue dots represent metabolites with up-regulated and down-regulated accumulation, respectively. (B) Expression pattern of DEGs involved in Alanine, aspartate and glutamate metabolism at diferent stages.

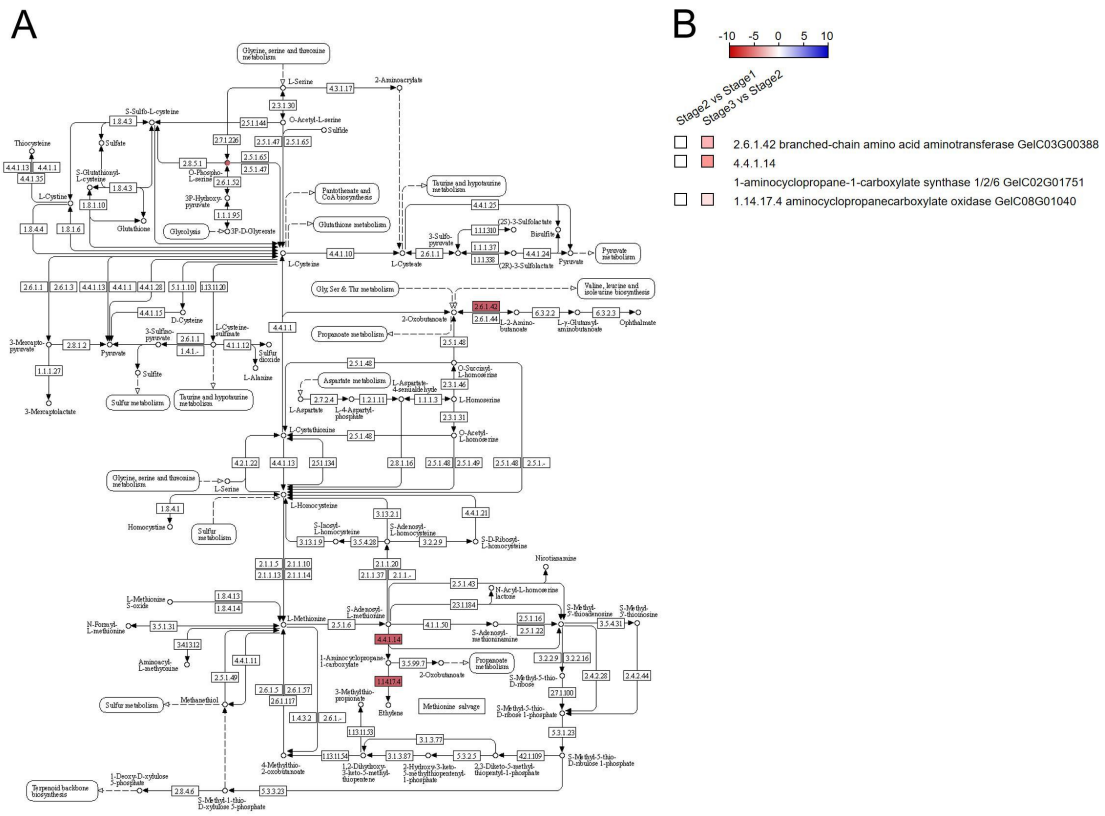


Figure S8. Integrative analysis of transcriptome and metabolome data for the Cysteine and methionine metabolism pathway (ko00270) in *G. elata*. (A) Mapping of enriched DEGs in Stage3 vs Stage2. Red and blue boxes represent genes with up-regulated and down-regulated expression, respectively. Red and blue dots represent metabolites with up-regulated and down-regulated accumulation, respectively. (B) Expression pattern of DEGs involved in Cysteine and methionine metabolism at diferent stages.

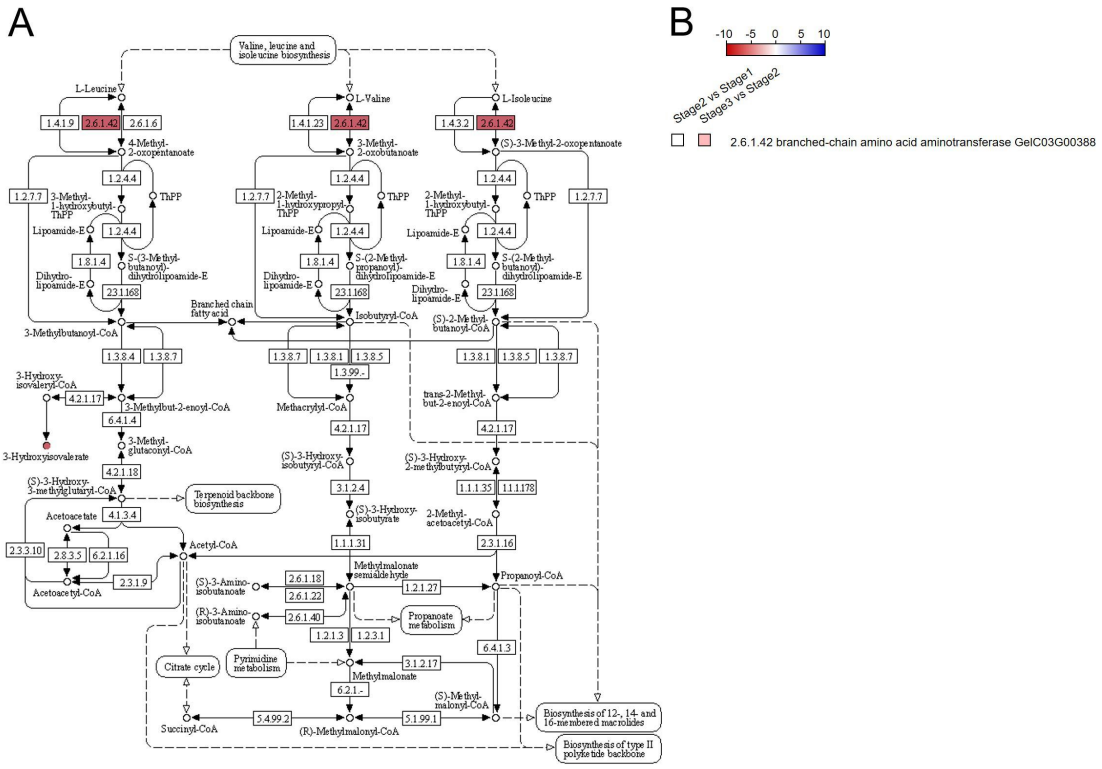


Figure S9. Integrative analysis of transcriptome and metabolome data for the Valine, leucine and isoleucine degradation pathway (ko00280) in *G. elata*. (A) Mapping of enriched DEGs in Stage3 vs Stage2. Red and blue boxes represent genes with up-regulated and down-regulated expression, respectively. Red and blue dots represent metabolites with up-regulated and down-regulated accumulation, respectively. (B) Expression pattern of DEGs involved in Valine, leucine and isoleucine degradation at diferent stages.

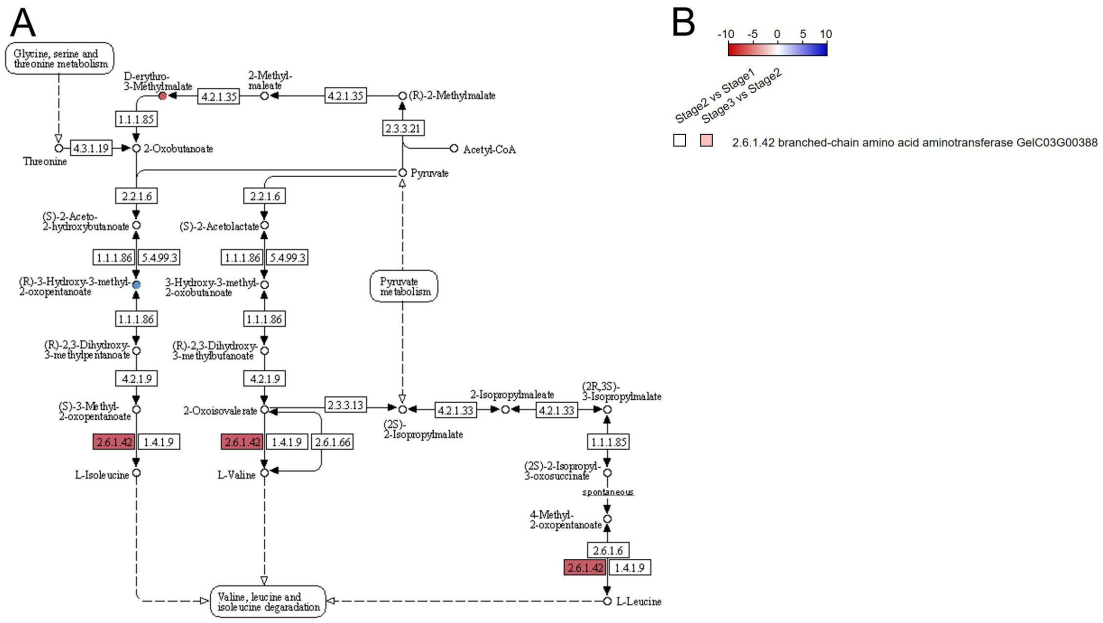


Figure S10. Integrative analysis of transcriptome and metabolome data for the Valine, leucine and isoleucine biosynthesis pathway (ko00290) in *G. elata*. (A) Mapping of enriched DEGs in Stage3 vs Stage2. Red and blue boxes represent genes with up-regulated and down-regulated expression, respectively. Red and blue dots represent metabolites with up-regulated and down-regulated accumulation, respectively. (B) Expression pattern of DEGs involved in Valine, leucine and isoleucine biosynthesis at diferent stages.

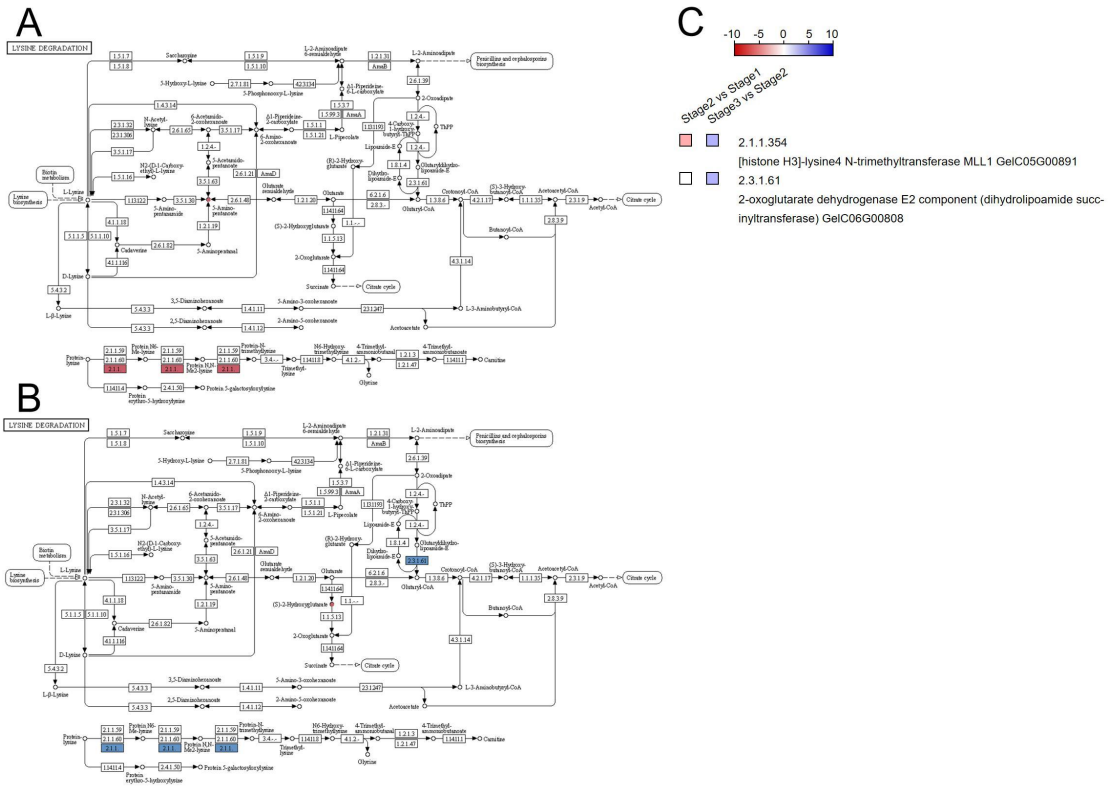


Figure S11. Integrative analysis of transcriptome and metabolome data for the Lysine degradation pathway (ko00310) in *G. elata*. (A) Mapping of enriched DEGs in Stage2 vs Stage1. Red and blue boxes represent genes with up-regulated and down-regulated expression, respectively. Red and blue dots represent metabolites with up-regulated and down-regulated accumulation, respectively. (B) Mapping of enriched DEGs in Stage3 vs Stage2. (C) Expression pattern of DEGs involved in Lysine degradation at diferent stages.

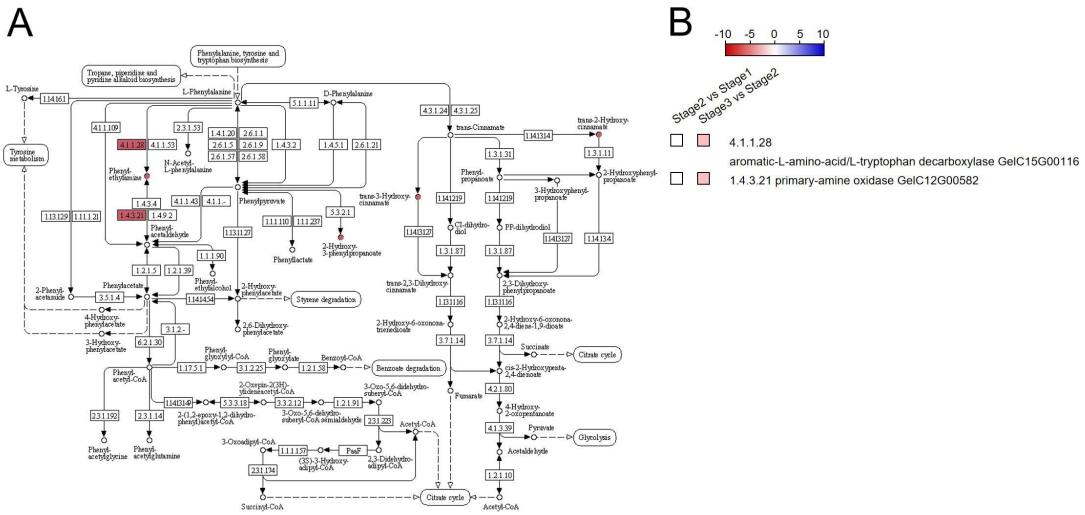


Figure S12. Integrative analysis of transcriptome and metabolome data for the Phenylalanine metabolism pathway (ko00360) in *G. elata*. (A) Mapping of enriched DEGs in Stage3 vs Stage2. Red and blue boxes represent genes with up-regulated and down-regulated expression, respectively. Red and blue dots represent metabolites with up-regulated and down-regulated accumulation, respectively. (B) Expression pattern of DEGs involved in Phenylalanine metabolism at diferent stages.

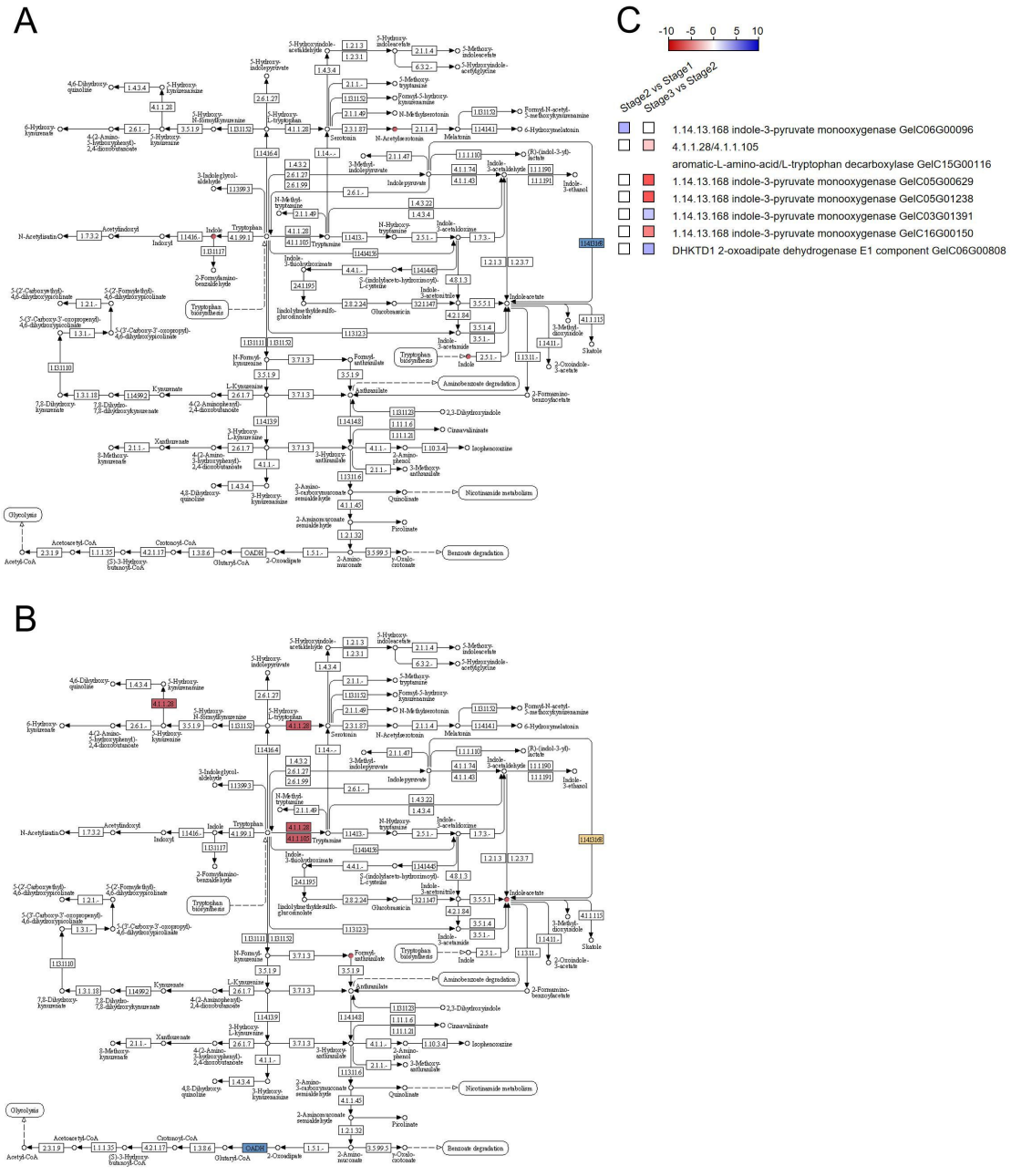


Figure S13. Integrative analysis of transcriptome and metabolome data for the Tryptophan metabolism pathway (ko00380) in *G. elata*. (A) Mapping of enriched DEGs in Stage2 vs Stage1. Red and blue boxes represent genes with up-regulated and down-regulated expression, respectively. Red and blue dots represent metabolites with up-regulated and down-regulated accumulation, respectively. (B) Mapping of enriched DEGs in Stage3 vs Stage2. (C) Expression pattern of DEGs involved in Tryptophan metabolism at diferent stages.

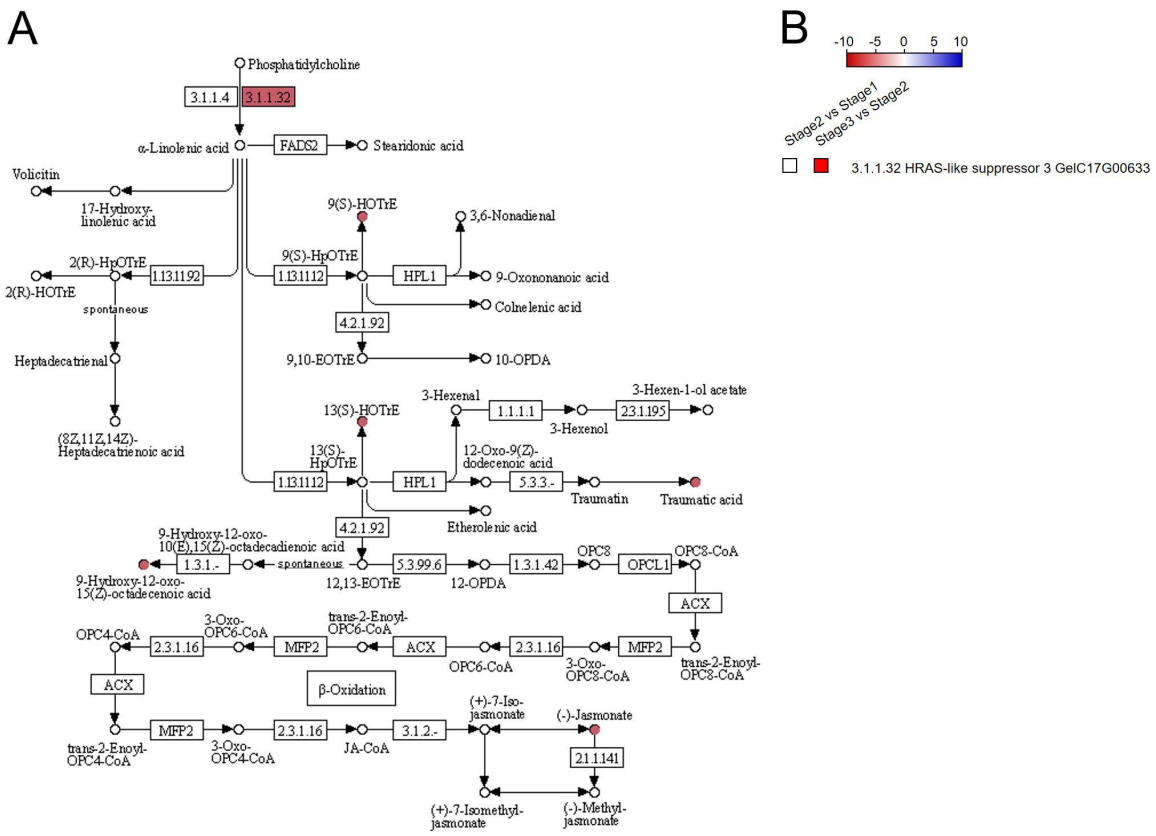


Figure S14. Integrative analysis of transcriptome and metabolome data for the alpha-Linolenic acid metabolism pathway (ko00592) in *G. elata*. (A) Mapping of enriched DEGs in Stage3 vs Stage2. Red and blue boxes represent genes with up-regulated and down-regulated expression, respectively. Red and blue dots represent metabolites with up-regulated and down-regulated accumulation, respectively. (B) Expression pattern of DEGs involved in alpha-Linolenic acid metabolism at diferent stages.

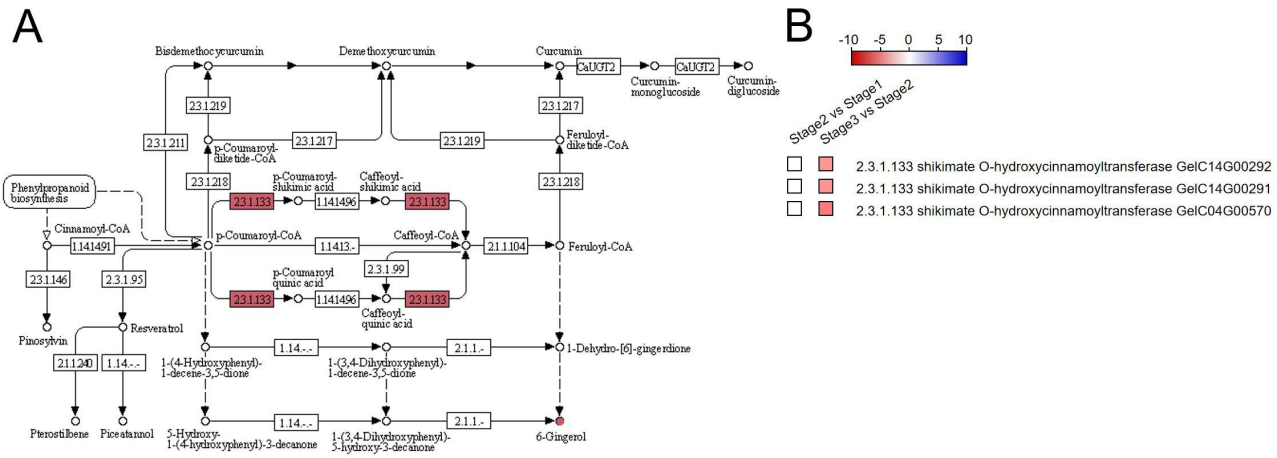


Figure S15. Integrative analysis of transcriptome and metabolome data for the stilbenoid, diarylheptanoid and gingerol biosynthesis pathway (ko00945) in *G. elata*. (A) Mapping of enriched DEGs in Stage3 vs Stage2. Red and blue boxes represent genes with up-regulated and down-regulated expression, respectively. Red and blue dots represent metabolites with up-regulated and down-regulated accumulation, respectively. (B) Expression pattern of DEGs involved in stilbenoid, diarylheptanoid and gingerol biosynthesis at diferent stages.