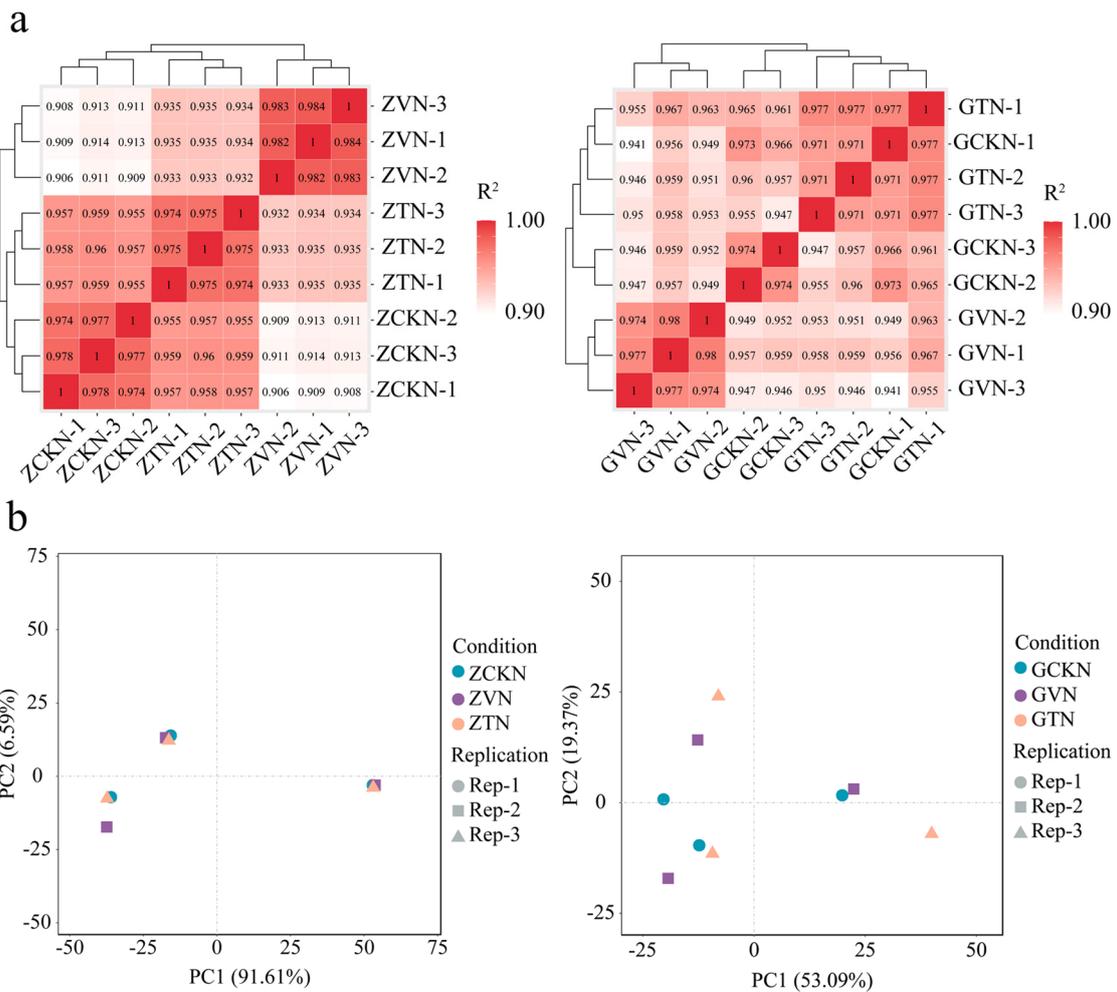


Table S1. Primers and Sequences for qRT-PCR

Gene ID/name	Forward primer (5'-3')	Reverse primer (5'-3')
<i>Zm00001d003015</i>	CCCGGGGAGATGAAGTGAAG	CAAACACGGGCAATGGTGTT
<i>Zm00001d017279</i>	CTCGAGTGCCTCAAGGAGTG	TCGAAGTTGGTTACAGGGCG
<i>Zm00001d052335</i>	GGCTCCAACAACGGACAGAT	ACATCAACGCGACGATCTCA
<i>Zm00001d032992</i>	GTCTACGTCGCCAAGACCAA	ACGTACCACAGCCGAATGTT
<i>GLYMA_01G137700</i>	CCCTATCCAAATGCCGTACCA	TCCATGTAGTGCTGAAGCTAGA
<i>GLYMA_19G212300</i>	GTCTTGGTACCCCTCGAAGC	GATCGATGTTGCAGCTGTGG
<i>GLYMA_19G006200</i>	ACAAACTGGTTGCTCGGACA	GACACGTGACTATACCTGCCA
<i>GLYMA_13G138300</i>	ACGAAACGGCAGTGTTC	GTGTCTAATATCACCCCAAGTG
		TTT
<i>Action1</i>	GATTCCTGGGATTGCCGAT	TCTGCTGCTGAAAAGTGCTGAG
<i>β-Actin</i>	GTATTGGACTCTGGTGATGG	AGCAGAGGTGGTGAACAT



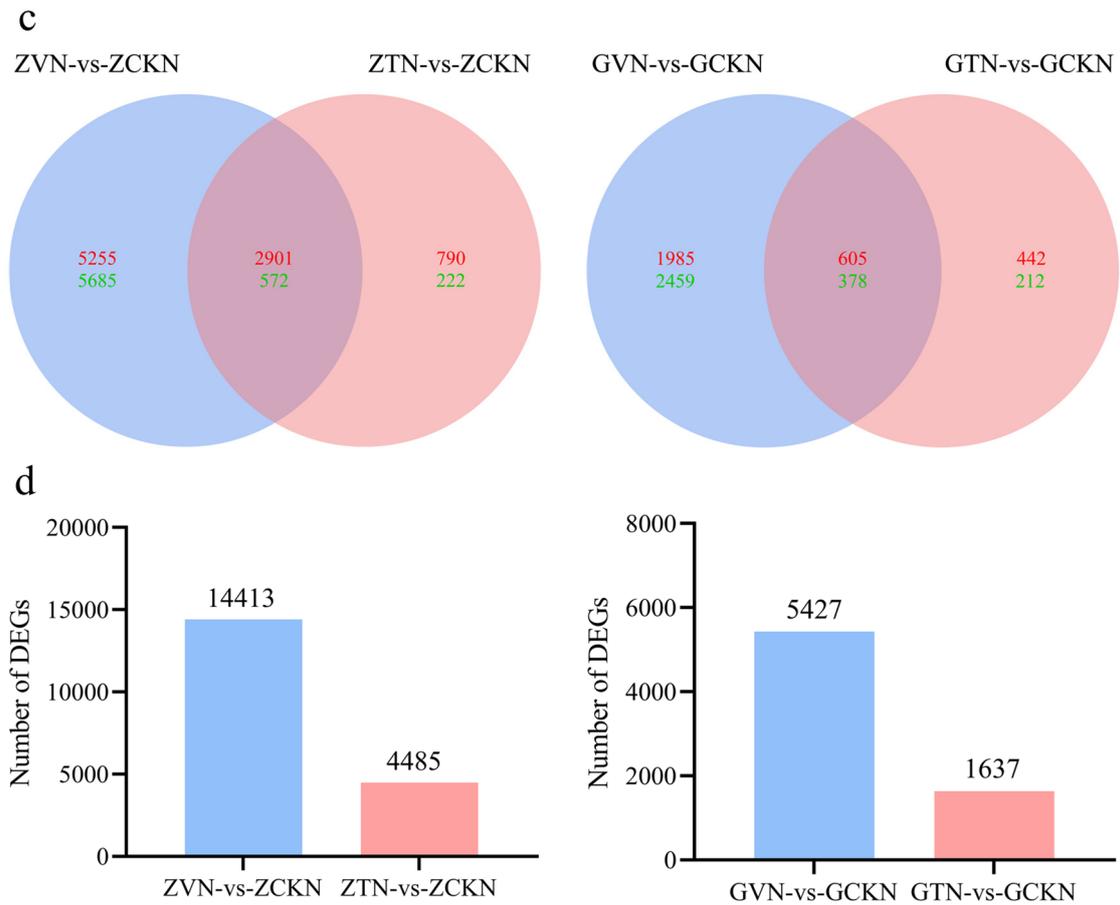


Figure S1. Gene expression patterns of volatile matter treatment groups of two species compared with the control group (a) correlation analysis between different treatment groups of two species (b) principal component analysis (PCA) (c) Wien diagram comparing up-regulated and down-regulated DEG numbers (d) changes in total DEG numbers

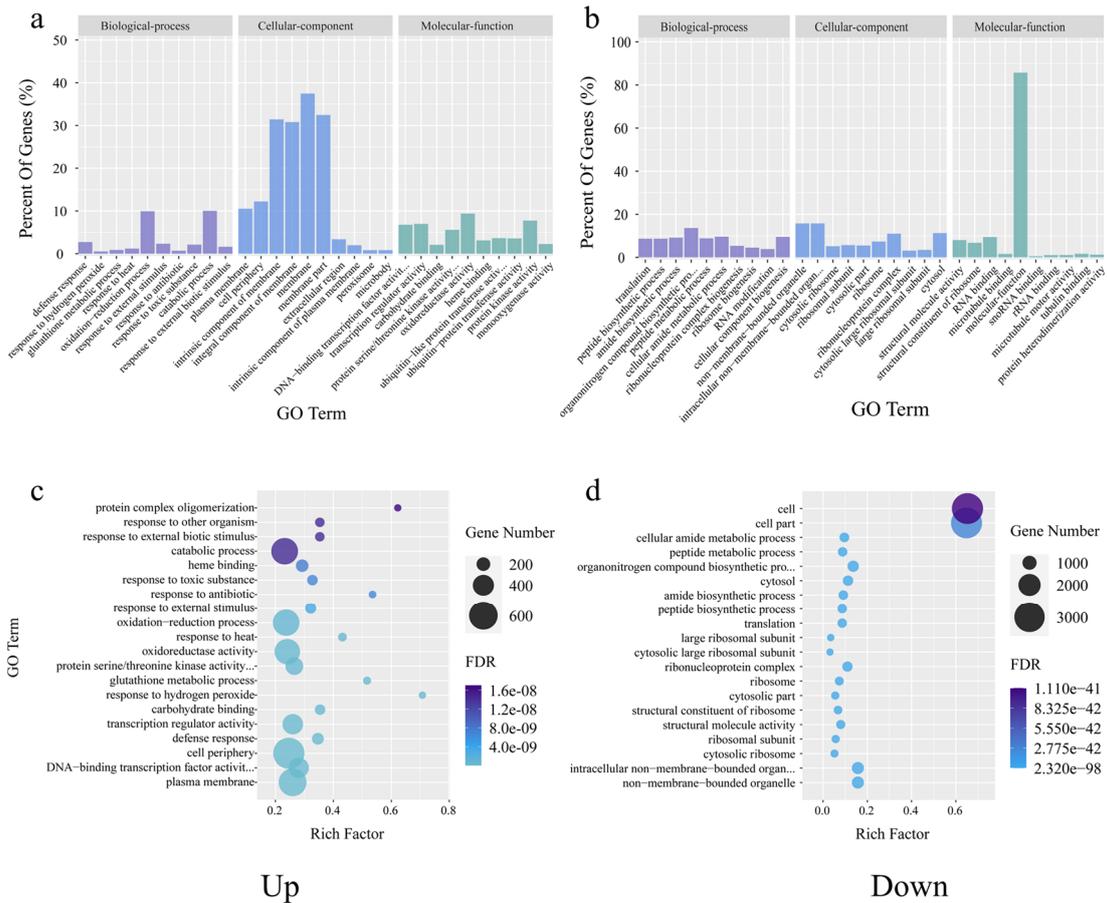


Figure S2. Histogram for GO classification (a, b) annotation of the DEGs in the treatments ZVN-vs-ZCKN. The bubbles diagram (c) showed top 20 pathway of significantly enrichment of the up-regulated and down-regulated DEGs on GO.

Note: (a, b) The X-axis indicated the name of pathway, and the Y-axis represents the percent of genes involved DEGs in each pathway. (c,d) the X-axis was the rich factor, the Y-axis represents the name of the pathway. The bubbles size represents the number of DEGs involved. The bubbles color indicates the enrichment degree of pathway.

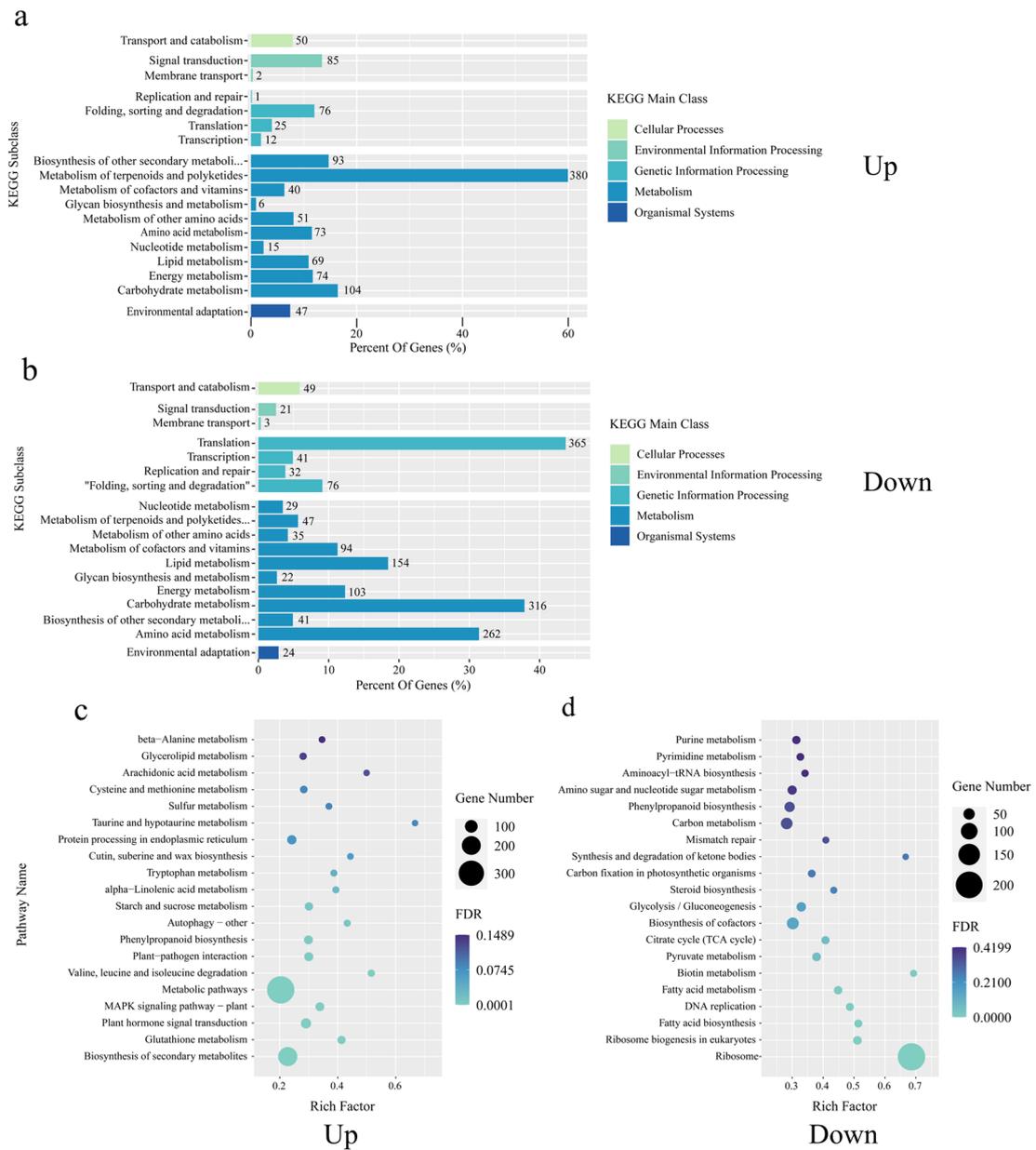


Figure S3. Histogram for KEGG pathway (a, b) annotation of the DEGs in the treatments ZVN-vs-ZCKN. The bubbles diagram (c, d) showed the top 20 pathways of significant enrichment of the up-regulated and down-regulated DEGs on KEGG.

Note: (a, b) The X-axis indicated the percent of genes involved DEGs in each pathway, and the Y-axis represents the name of the pathway. (c, d) the X-axis was the rich factor, the Y-axis represents the name of the pathway. The bubbles size represents the number of DEGs involved. The bubbles color indicates the enrichment degree of pathway.

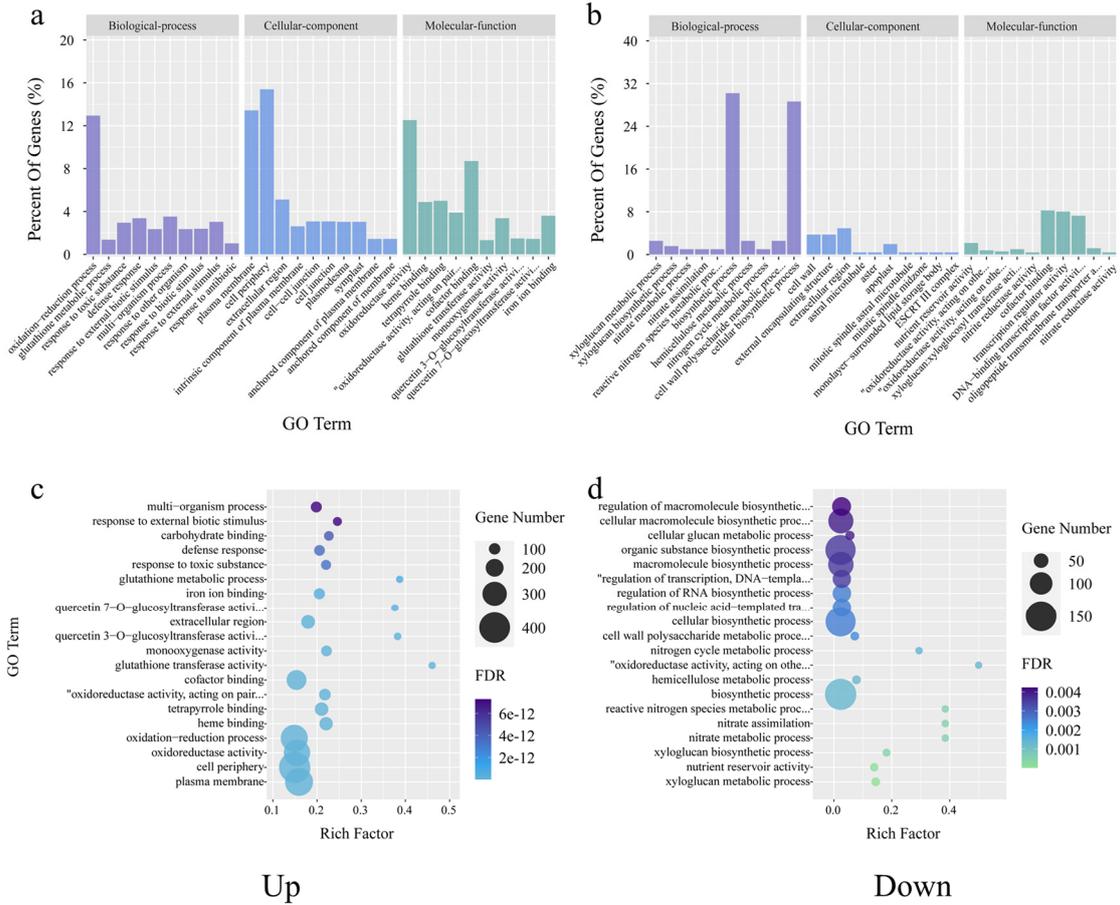


Figure S4. Histogram for GO classification (a, b) annotation of the DEGs in the treatments ZTN VS ZCKN. The bubbles diagram (c, d) showed top 20 pathway of significantly enrichment of the up-regulated and down-regulated DEGs on GO.

Note: (a, b) The X-axis indicated the name of pathway, and the Y-axis represents the percent of genes involved DEGs in each pathway. (c,d) the X-axis was the rich factor, the Y-axis represents the name of the pathway. The bubbles size represents the number of DEGs involved. The bubbles color indicates the enrichment degree of pathway.

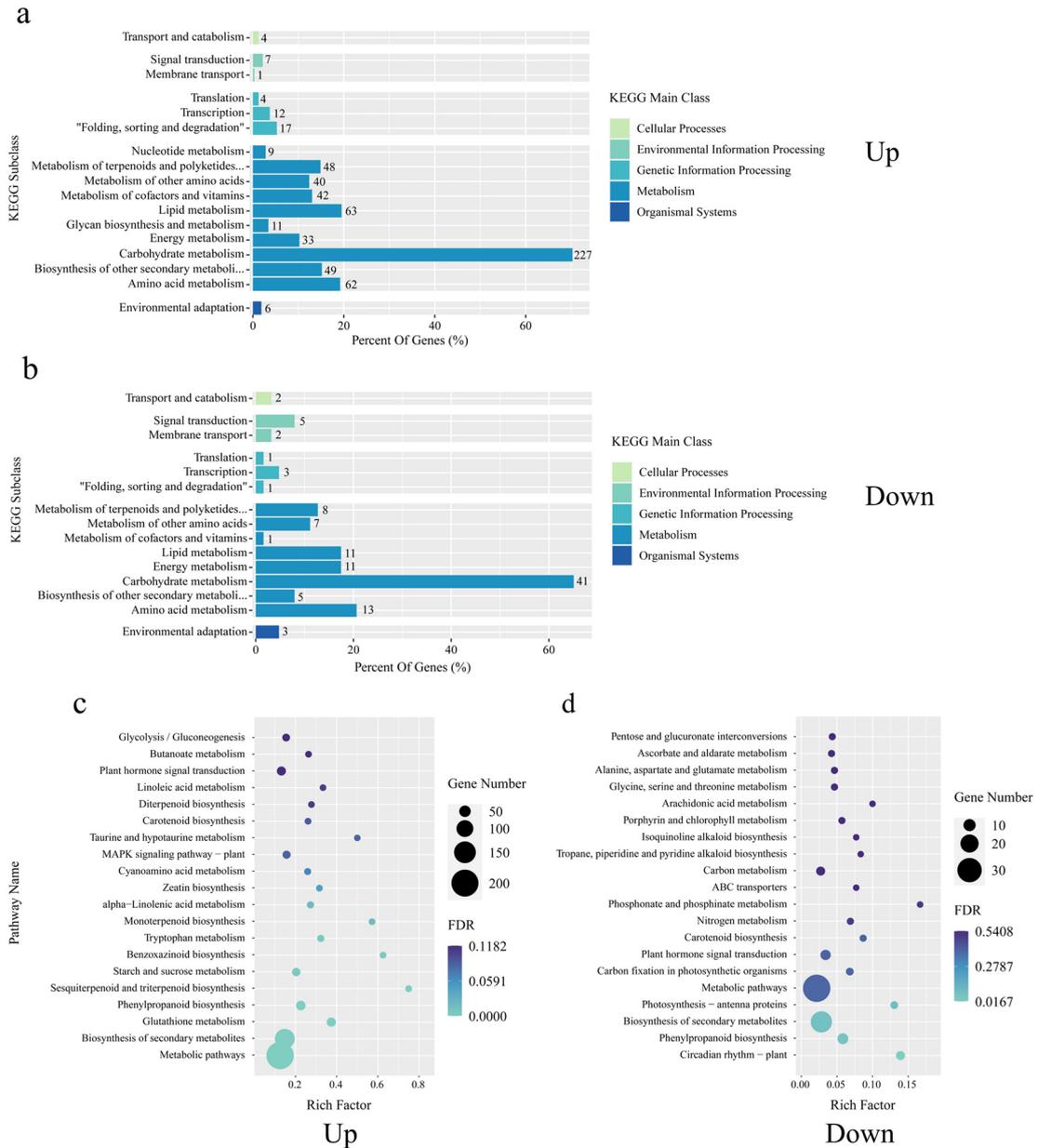


Figure S5. Histogram for KEGG pathway (a, b) annotation of the DEGs in the treatments ZTN VS ZCKN. The bubbles diagram (c, d) showed the top 20 pathways of significant enrichment of the up-regulated and down-regulated DEGs on KEGG.

Note: (a, b) The X-axis indicated the percent of genes involved DEGs in each pathway, and the Y-axis represents the name of the pathway. (c, d) the X-axis was the rich factor, the Y-axis represents the name of the pathway. The bubbles size represents the number of DEGs involved. The bubbles color indicates the enrichment degree of pathway.

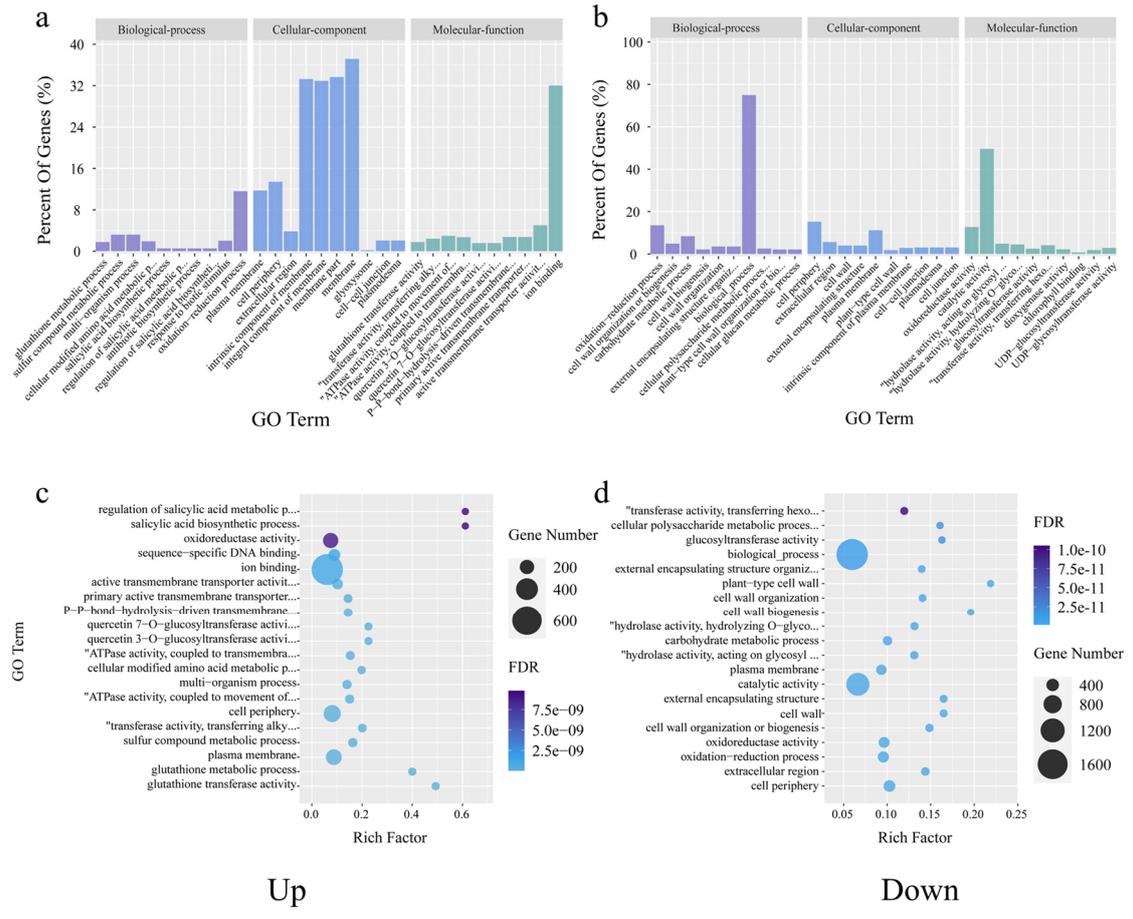


Figure S6. Histogram for GO classification (a, b) annotation of the DEGs in the treatments GVN VS GCKN. The bubbles diagram (c, d) showed top 20 pathway of significantly enrichment of the up-regulated and down-regulated DEGs on GO.

Note: (a, b) The X-axis indicated the name of pathway, and the Y-axis represents the percent of genes involved DEGs in each pathway. (c,d) the X-axis was the rich factor, the Y-axis represents the name of the pathway. The bubbles size represents the number of DEGs involved. The bubbles color indicates the enrichment degree of pathway.

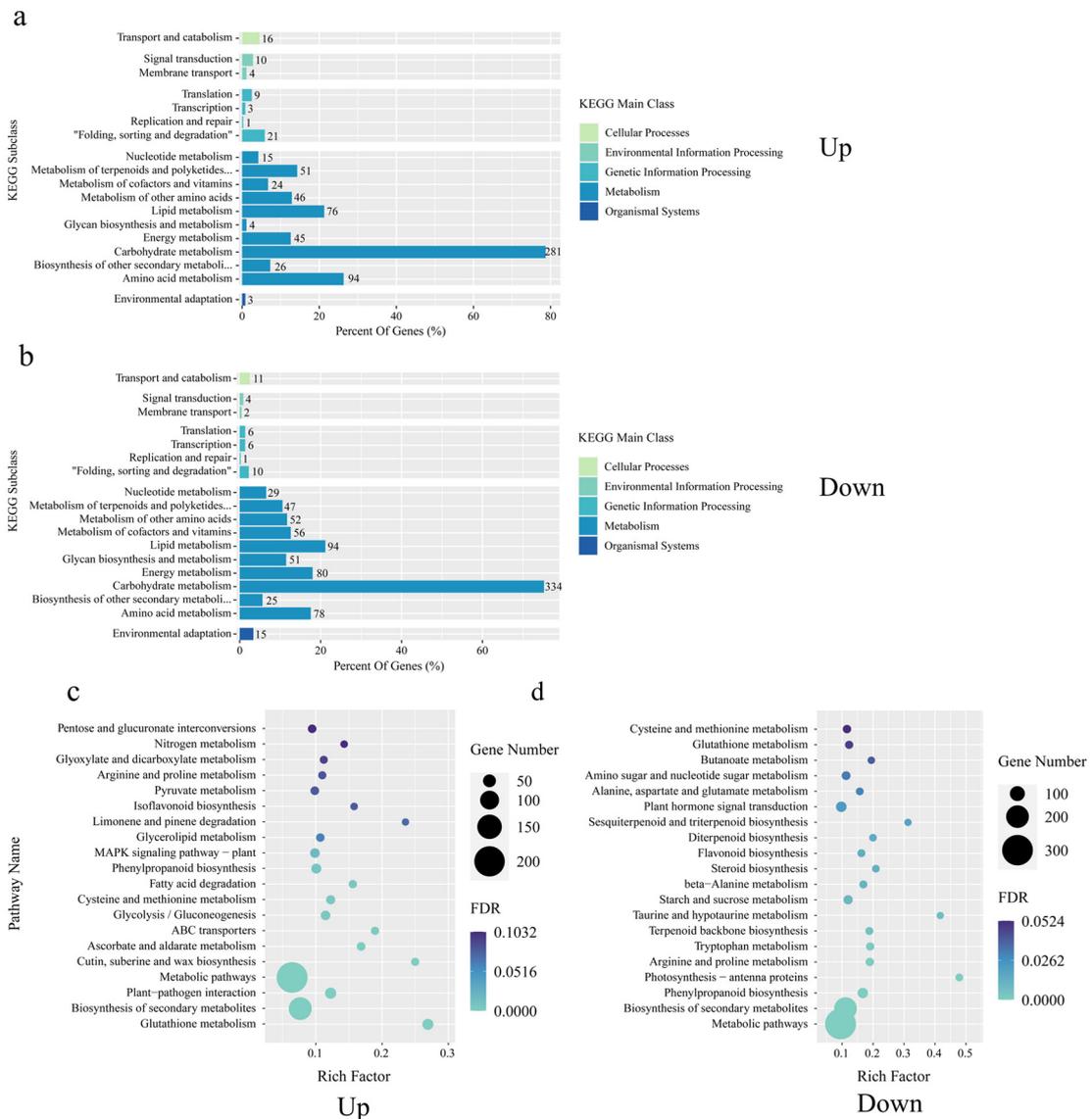


Figure S7. Histogram for KEGG pathway (a, b) annotation of the DEGs in the treatments GVN VS GCKN. The bubbles diagram (c, d) showed the top 20 pathways of significant enrichment of the up-regulated and down-regulated DEGs on KEGG.

Note: (a, b) The X-axis indicated the percent of genes involved DEGs in each pathway, and the Y-axis represents the name of the pathway. (c, d) the X-axis was the rich factor, the Y-axis represents the name of the pathway. The bubbles size represents the number of DEGs involved. The bubbles color indicates the enrichment degree of pathway.

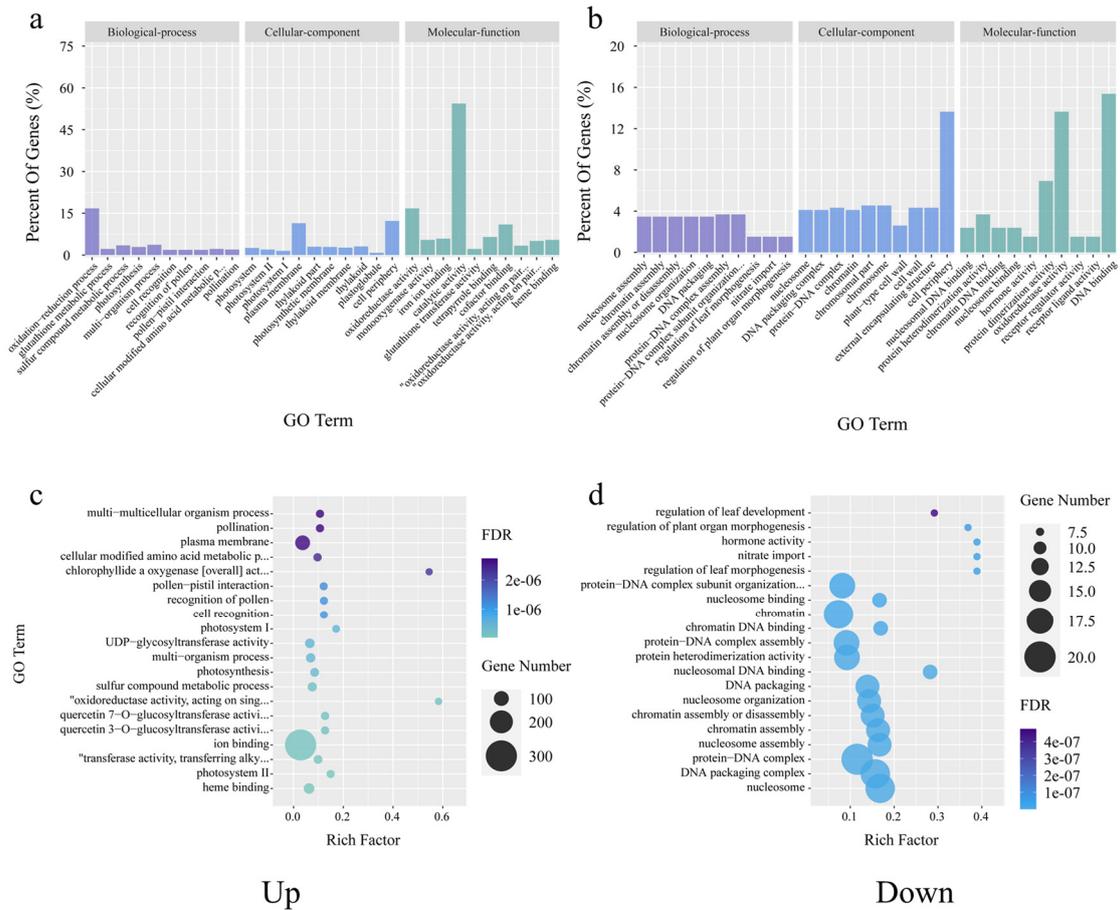


Figure S8. Histogram for GO classification (a, b) annotation of the DEGs in the treatments GTN VS GCKN. The bubbles diagram (c, d) showed top 20 pathway of significantly enrichment of the up-regulated and down-regulated DEGs on GO.

Note: (a, b) The X-axis indicated the name of pathway, and the Y-axis represents the percent of genes involved DEGs in each pathway. (c,d) the X-axis was the rich factor, the Y-axis represents the name of the pathway. The bubbles size represents the number of DEGs involved. The bubbles color indicates the enrichment degree of pathway.

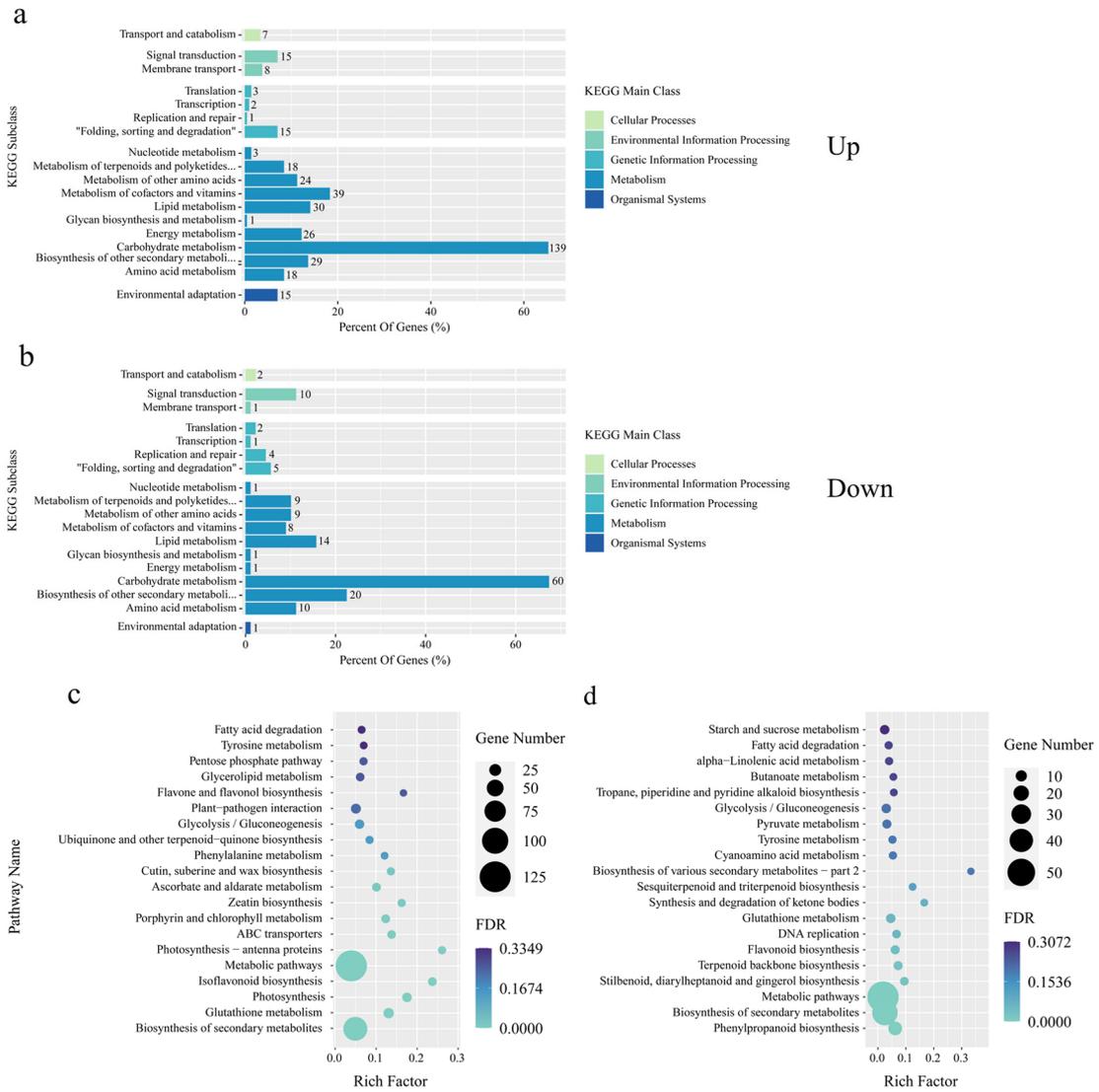


Figure S9. Histogram for KEGG pathway (a, b) annotation of the DEGs in the treatments GTN VS GCKN. The bubbles diagram (c, d) showed the top 20 pathways of significant enrichment of the up-regulated and down-regulated DEGs on KEGG.

Note: (a, b) The X-axis indicated the percent of genes involved DEGs in each pathway, and the Y-axis represents the name of the pathway. (c, d) the X-axis was the rich factor, the Y-axis represents the name of the pathway. The bubbles size represents the number of DEGs involved. The bubbles color indicates the enrichment degree of pathway.

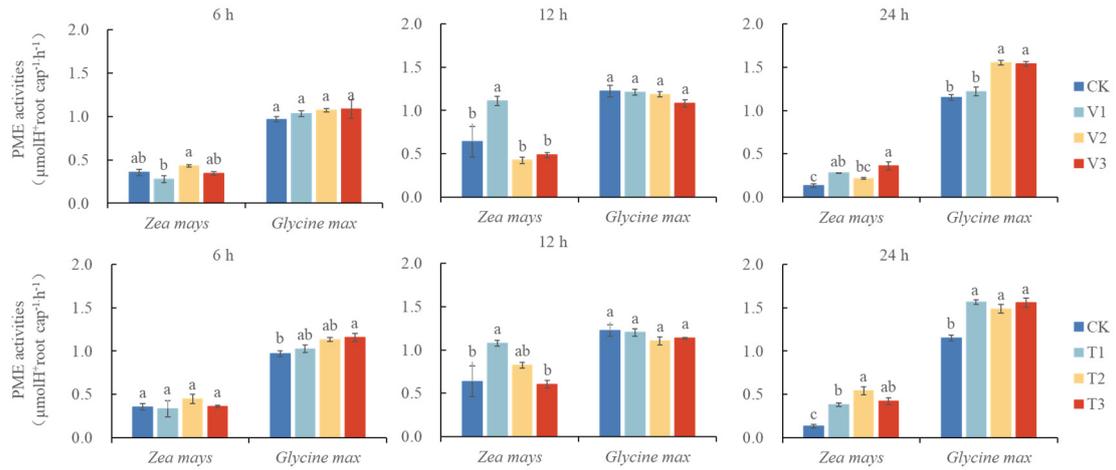


Figure S10. Pectin methylase(PME) activity

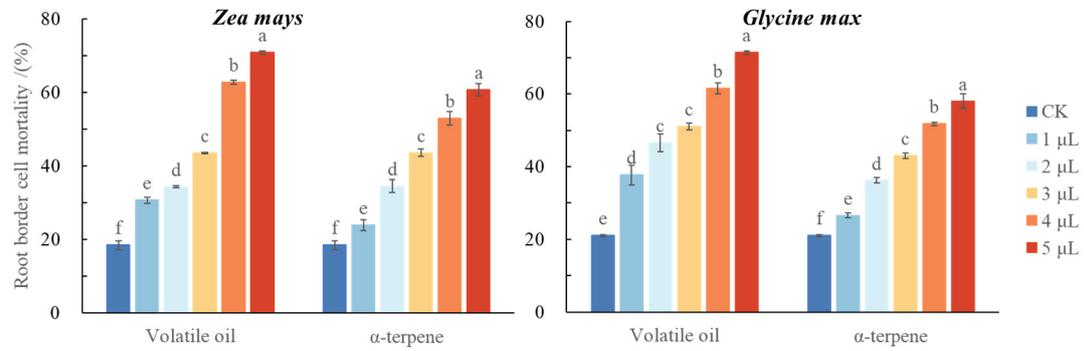


Figure S11. Changes in the activity of receptor root border cells under the action of volatiles from *C. ambrosioides*