Using comprehensive omics analysis throughout grape berry development to unveil a regulatory network for aroma accumulation

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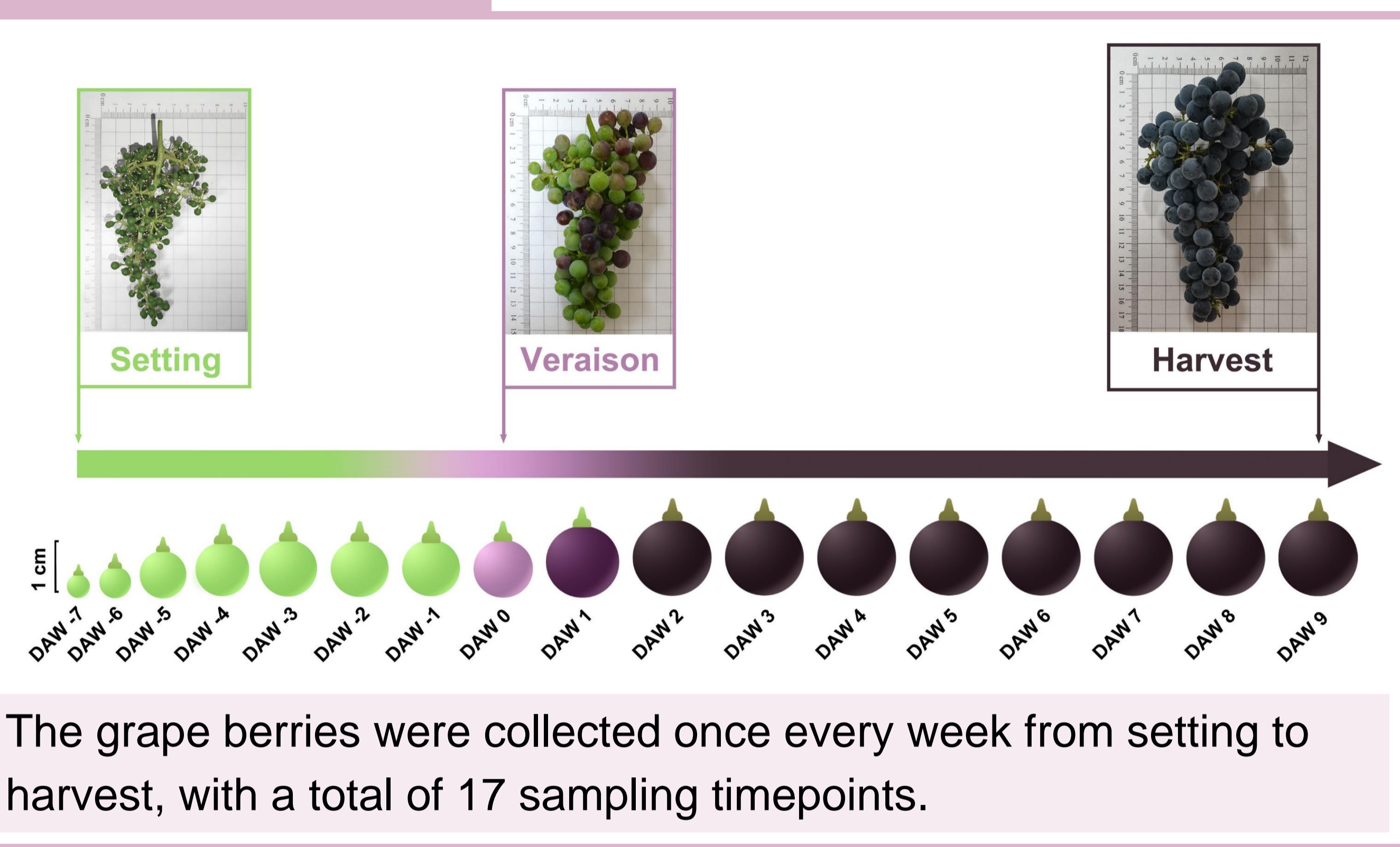[2]Key Laboratory of Viticulture and Enology, Ministry of Agriculture and Rural Affairs, Beijing 100083, China
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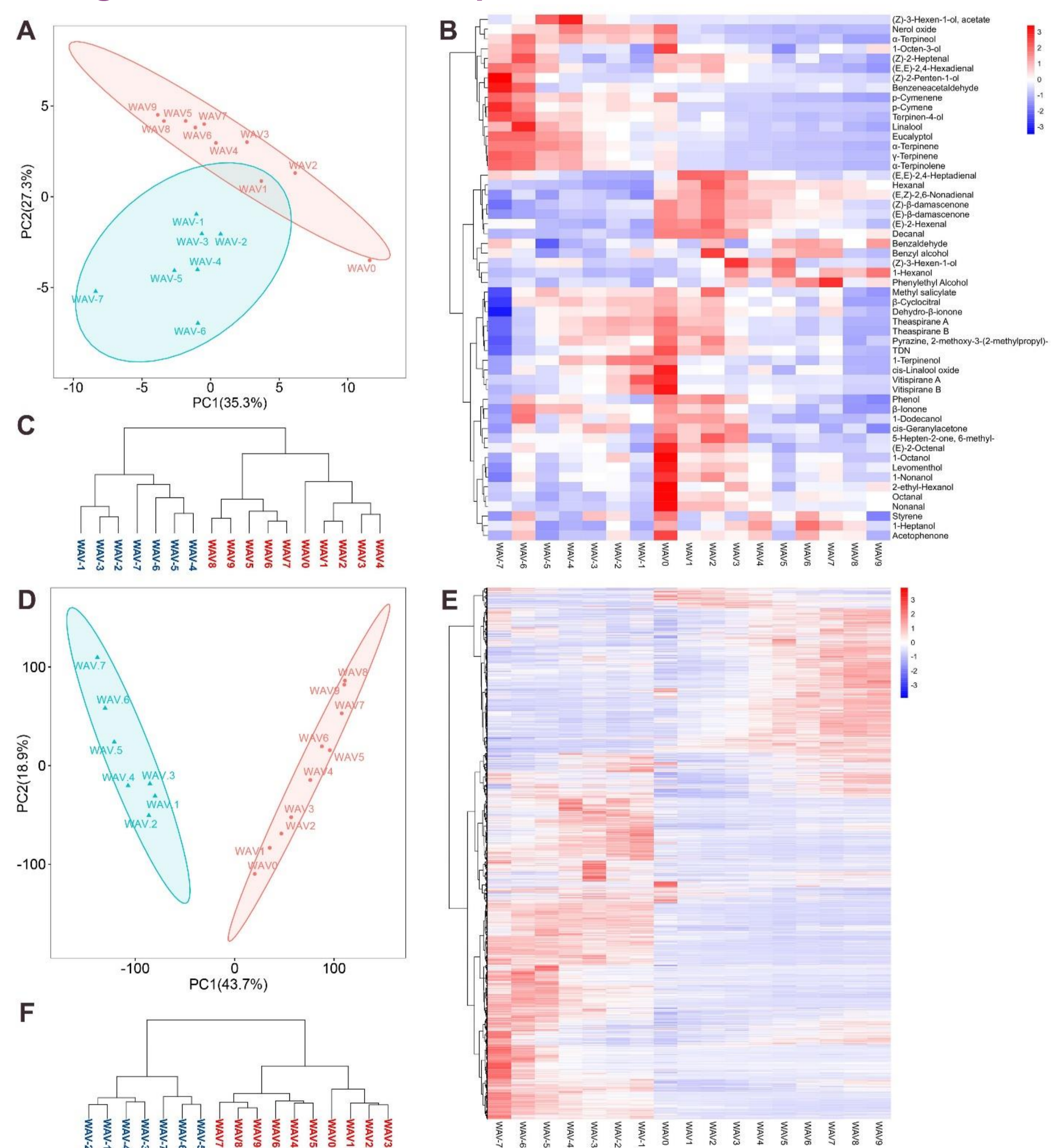
Introduction

Pleasant aromas are an important part of a high quality wine which can greatly increase its economic value. The aromas in grape berry contribute to the varietal property in wine, which are the most recognizable. Therefore, it is crucial to understand the accumulation pattern and regulatory mechanism of aroma compounds in grapes. However, we know very limited about regulatory network involving aroma accumulation. In this study, we integrated the volatile metabolome and transcriptome of *Vitis vinifera* L. cv. Cabernet Sauvignon grapes throughout the whole development to generate a global map of grape berry aroma metabolic pathways and to propose their potential regulatory networks.

Materials

The grape berries were collected once every week from setting to harvest, with a total of 17 sampling timepoints.

Results

① Dynamics of the volatile metabolome and transcriptome throughout the whole development


Both PCA and Treeclustering classified the grape berries into pre- and post-veraison categories based on metabolome and transcriptome data, suggesting that the aroma metabolism was greatly altered during the period.

② Five clusters of coordanated patterns of metabolome and transcriptome
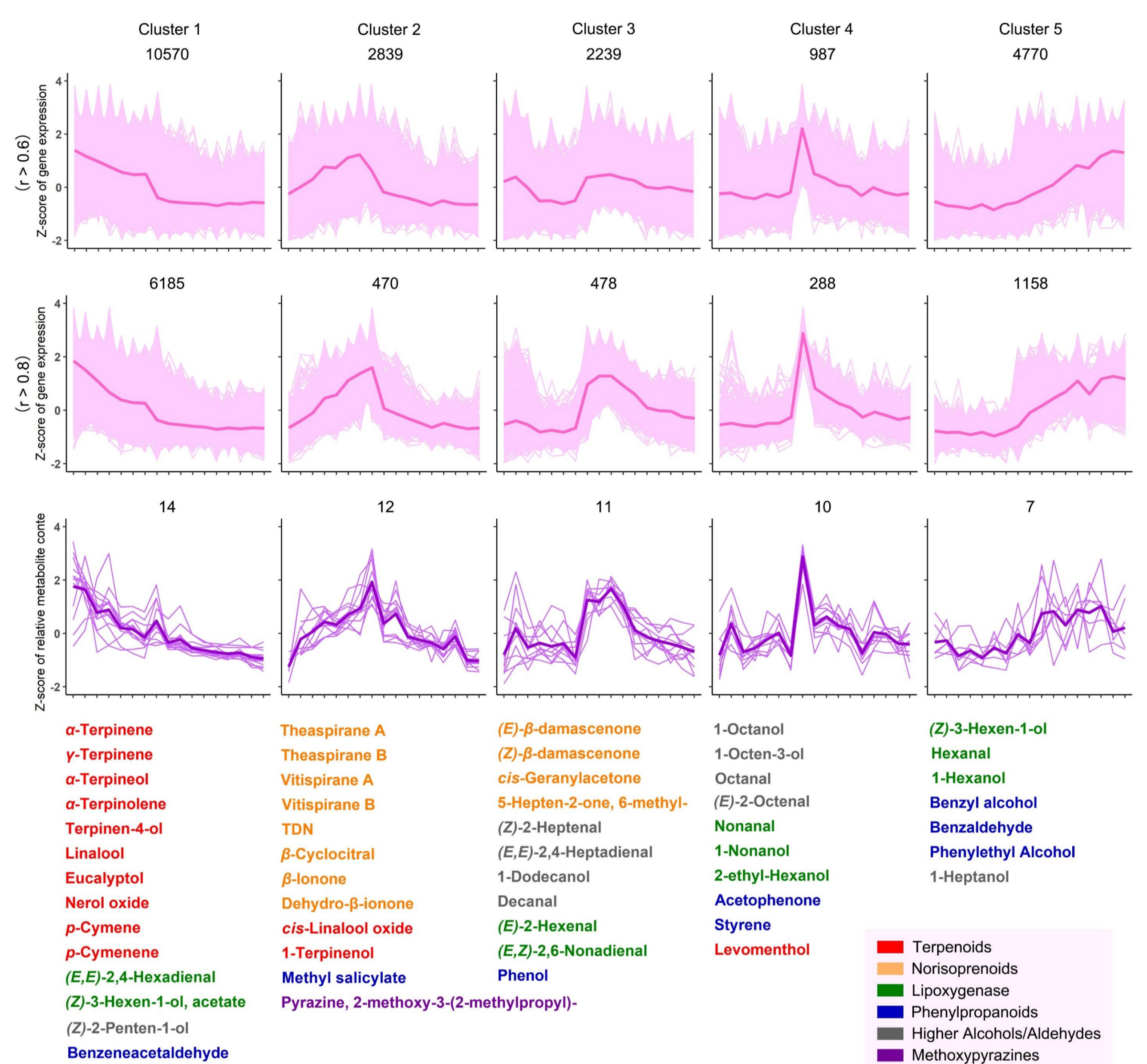
we divided all 54 annotated metabolites into 5 clusters based on their accumulation patterns using the k-means clustering algorithm. A rigorous multiple test correction ($r \geq 0.8$ & $r \geq 0.6$) was used to filter the genes that significantly correlated with each metabolite. A total of 16,320 genes were found to be associated with at least one metabolite.

③ Construction of transcriptional regulatory networks
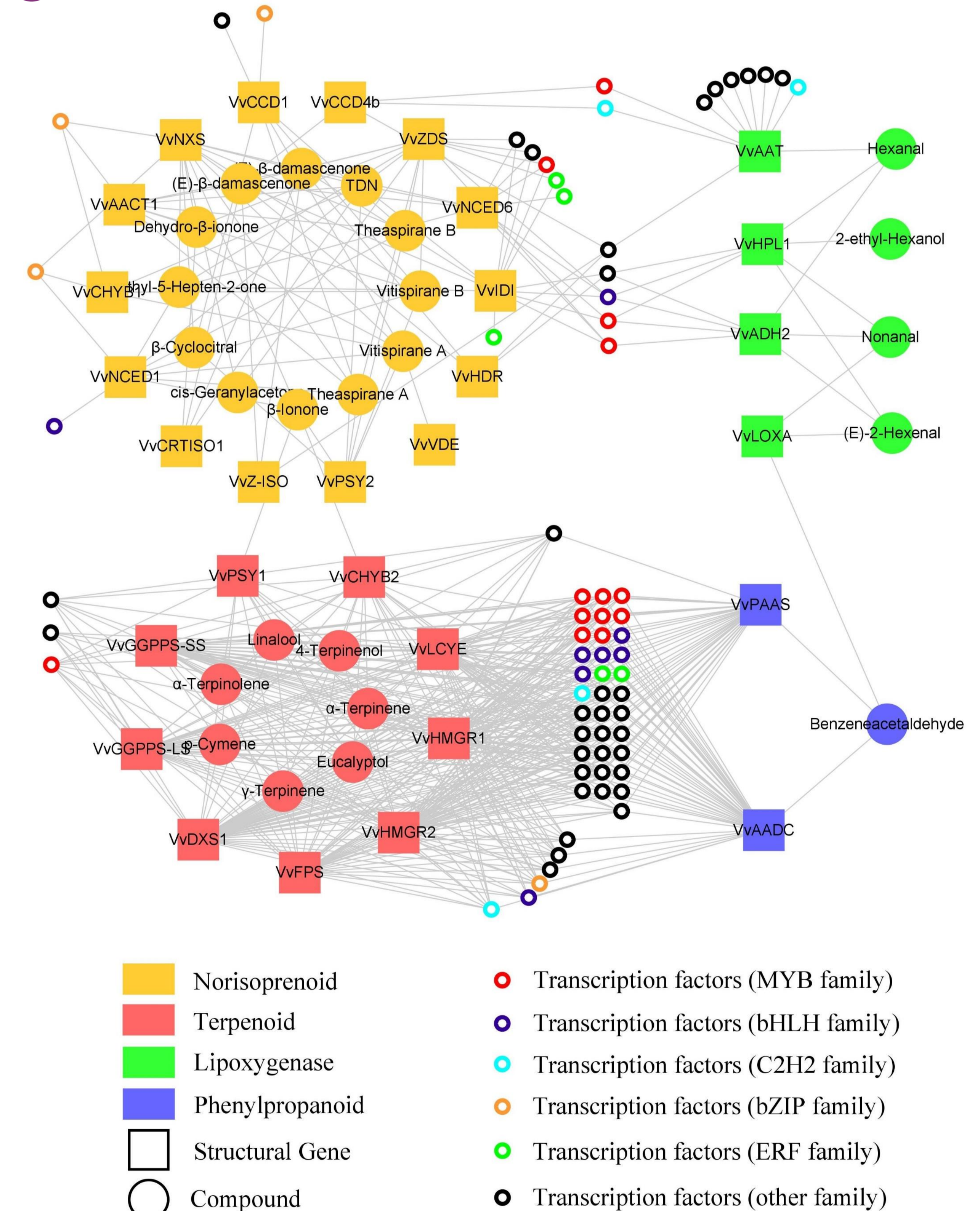
We extracted 69 transcription factors that were co-expressed ($r \geq 0.8$) with structural genes of four important aroma biosynthetic pathways in grapes and mapped the correlation network. These transcription factors were predicted to be associated with the regulation of one or two aroma metabolic pathways, which will be further verified.

Conclusion

- VviMYB5b was reported to upregulate terpene content, and it was found to be highly correlated with terpene and other arome biosynthetic gene expression in our network, which is suggested that the present networks were effective to identify potential regulatory factors.
- Some new potential transcription factors from the neworks were found primarily.

Acknowledgement