



Figure S1. Hierarchical clustering tree of the correlation between significantly enriched biological processes of genes associated with *VviSOC1a*, based on *Vitis* OneGenE [1]. Point sizes represent the significance level based on p-values. Gene Ontology (GO) enrichment was performed using the ShinyGO database [2]. Yellow boxes highlight important pathways related to the predicted function of *VviSOC1a* in flower development.

References

1. Pilati S, Malacarne G, Navarro-Payá D, Tomè G, Riscica L, et al. 2021. *Vitis* OneGenE: a causality-based approach to generate gene networks in *Vitis vinifera* sheds light on the laccase and dirigent gene families. *Biomolecules* 11:1744.
2. Ge SX, Jung D, Yao R, 2020. ShinyGO: a graphical gene-set enrichment tool for animals and plants. *Bioinformatics* 36:2628-2629.
3. Fasoli M, Dal Santo S, Zenoni S, Tornielli GB, Farina L, et al. 2012. The grapevine expression atlas reveals a deep transcriptome shift driving the entire plant into a maturation program. *The Plant Cell* 24:3489-3505.