



Figure S3. Heatmap of VviSOC1a and associated flowering-related gene (Vitis OneGenE) expression profiles over 54 different grapevine (cultivar ‘Corvina’) tissue types and developmental stages according to the grapevine expression atlas [3] and visualised on the Vitviz website. The hierarchical clustering tree segregates for two major clusters, including reproductive and vegetative tissue. The colour scale bar is based on log₂-based values and ranges from red (highest) to blue (lowest). Genes include VviSOC1b (VIT_16s0022g02400), VviSOC1c (VIT_02s0025g04650), VviFUL1 (VIT_17s0000g04990), VviSVP2 (VIT_18s0001g07460), VviSVP3 (VIT_15s0107g00120), VviSVP4 (VIT_03s0017g00360), VviSVP5 (VIT_03s0167g00070), VviSVP6 (VIT_03s0167g00100), VviSVP7 (VIT_03s0017g00390), VviSEP1 (VIT_14s0083g01050), VviSEP3 (VIT_01s0010g03900), VviAP3b (VIT_04s0023g02820), VviAG1 (VIT_12s0142g00360) and VviAG2 (VIT_10s0003g02070). AG, AGAMOUS; AP, APETALA; FUL, FRUITFULL; SEP, SEPALLATA; SOC1, SUPPRESSOR OF OVEREXPRESSION OF CONSTANS1; SVP, SHORT VEGETATIVE PHASE.

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.