

Selection of reference genes for miRNA qRT-PCR under abiotic stress in grapevine

Meng Luo^{1,2}, Zhen Gao^{1,2}, Hui Li^{1,2}, Qin Li^{1,2}, Caixi Zhang^{1,2}, Wenping Xu^{1,2},
Shiren Song^{1,2}, Chao Ma^{1,2*}, Shiping Wang^{1,2,3*}

¹Department of Plant Science, School of Agriculture and Biology, Shanghai Jiao Tong University, Shanghai, China

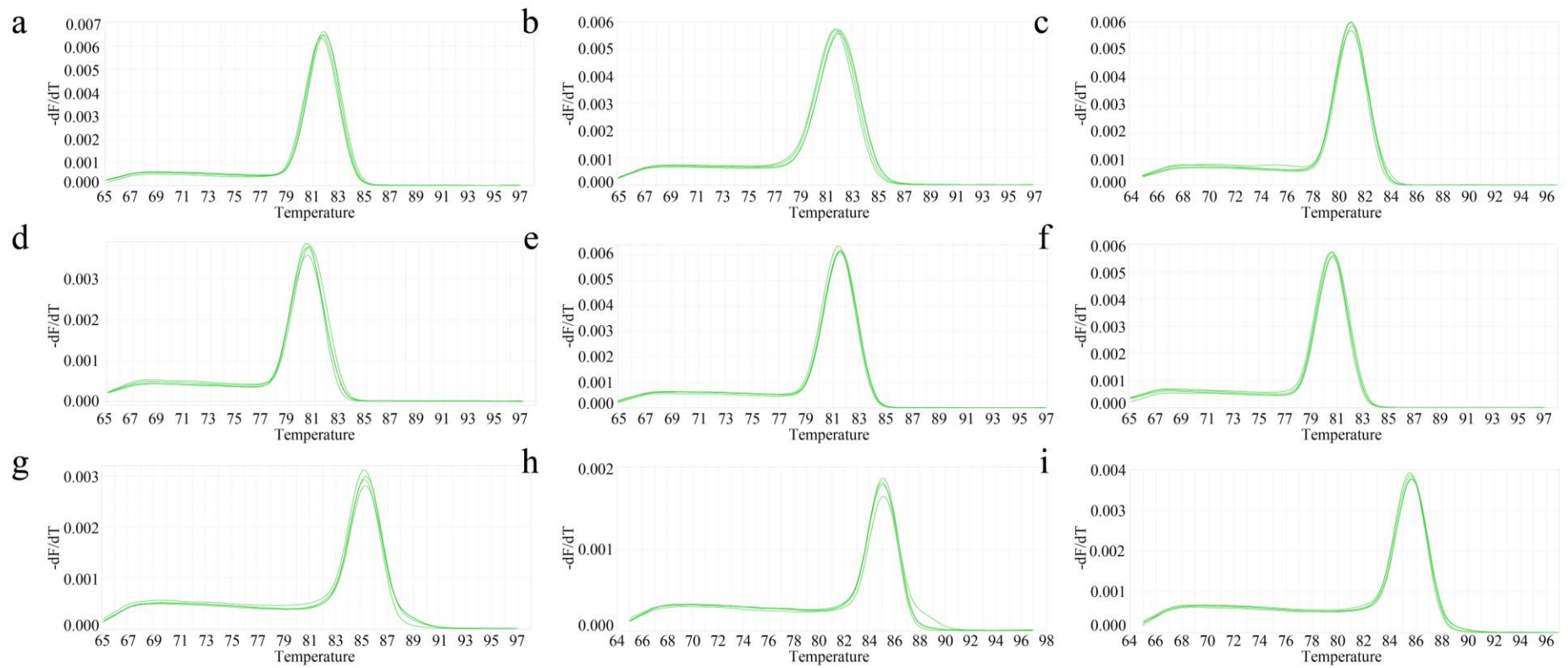
²Center for Viticulture and Enology, School of Agriculture and Biology, Shanghai Jiao Tong University, Shanghai 200240, China.

³Institute of Agro-food Science and Technology, Key Laboratory of Agro-products Processing Technology of Shandong, Shandong Academy of Agricultural Sciences, Jinan 250100, People's Republic of China

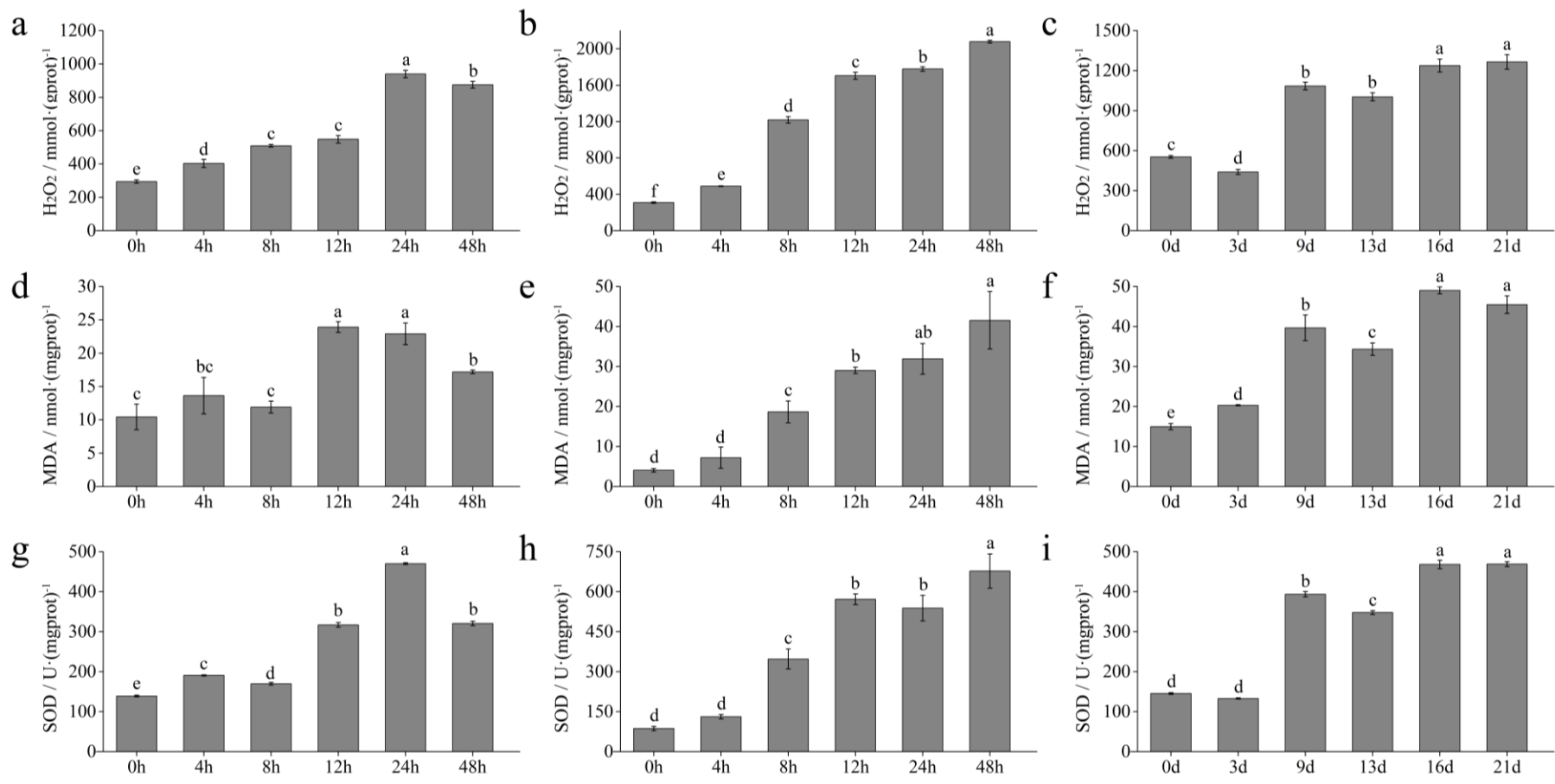
* **Corresponding author:** Department of Plant Science, School of Agriculture and Biology, Shanghai Jiao Tong University, Shanghai, China.

Tel& Fax: +0086-21-34205961

E-mail address: chaoma2015@sjtu.edu.cn, fruit@sjtu.edu.cn



Supplementary Figure S1. The melting peaks of candidate reference genes. Plots a-i represent the melting peaks of 5.8S rRNA, U6 snRNA, ACT, UBQ, GAPDH, EF1, miR160e, miR164a, and miR168, respectively.



Supplementary Figure S2. The physiological response of grapevine leaves for different stresses. Plots a-c represent the H_2O_2 content at six sampling time points under salinity, cold and drought stress, respectively; Plots d-f represent the MDA content at six sampling time points under salinity, cold and drought stress, respectively; Plots g-i represent the SOD activity at six sampling time points under salinity, cold and drought stress, respectively.