Aquaporin translation tunes plant water transport to external conditions in grapevine

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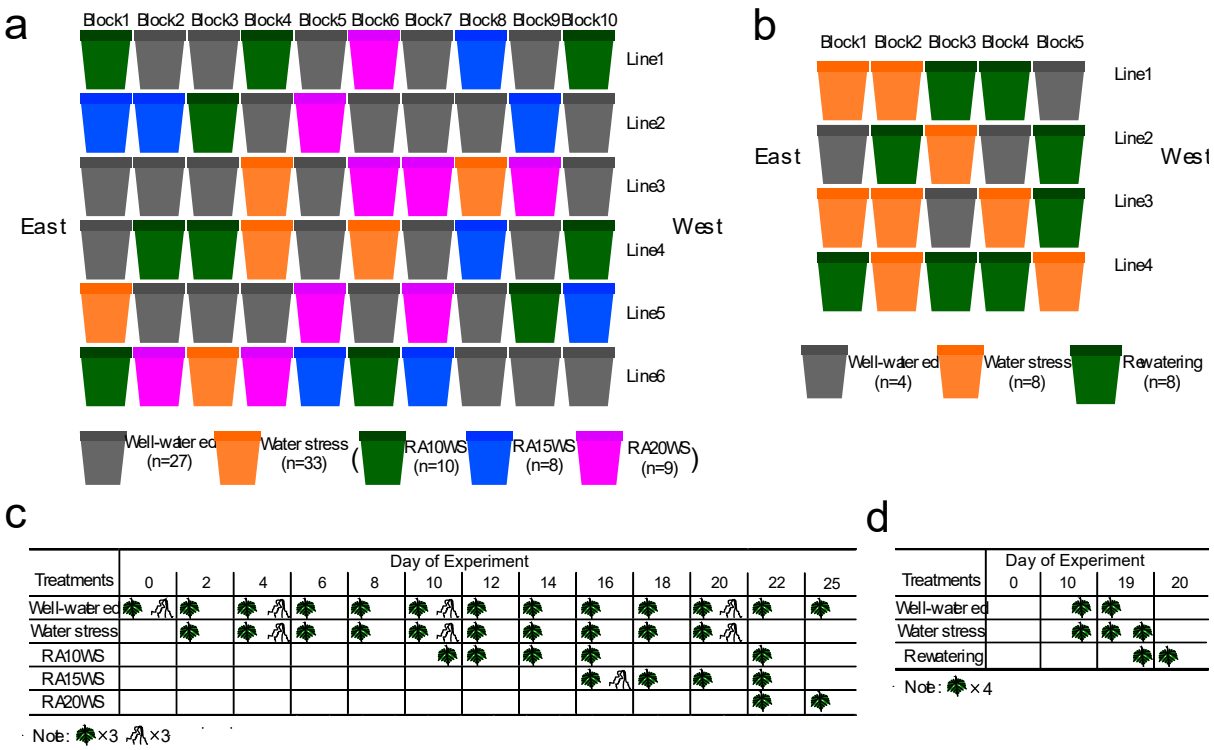


c

Treatments	Day of Experiment 0	2	4	6	8	10	12	14	16	18	20	22	25
Well-watered													
Water stress													
RA10WS													
RA15WS													
RA20WS													

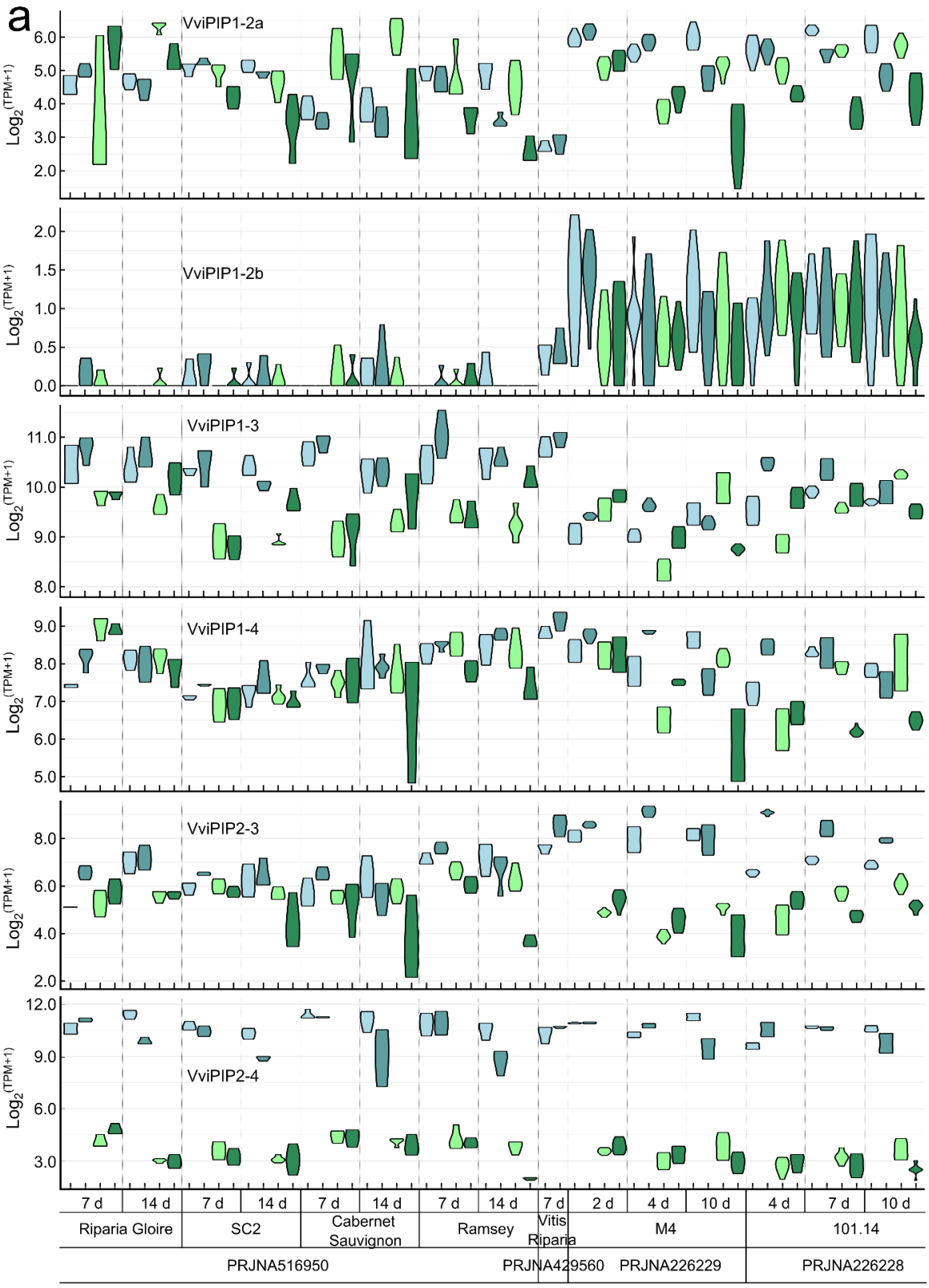
Note: ×3 ×3

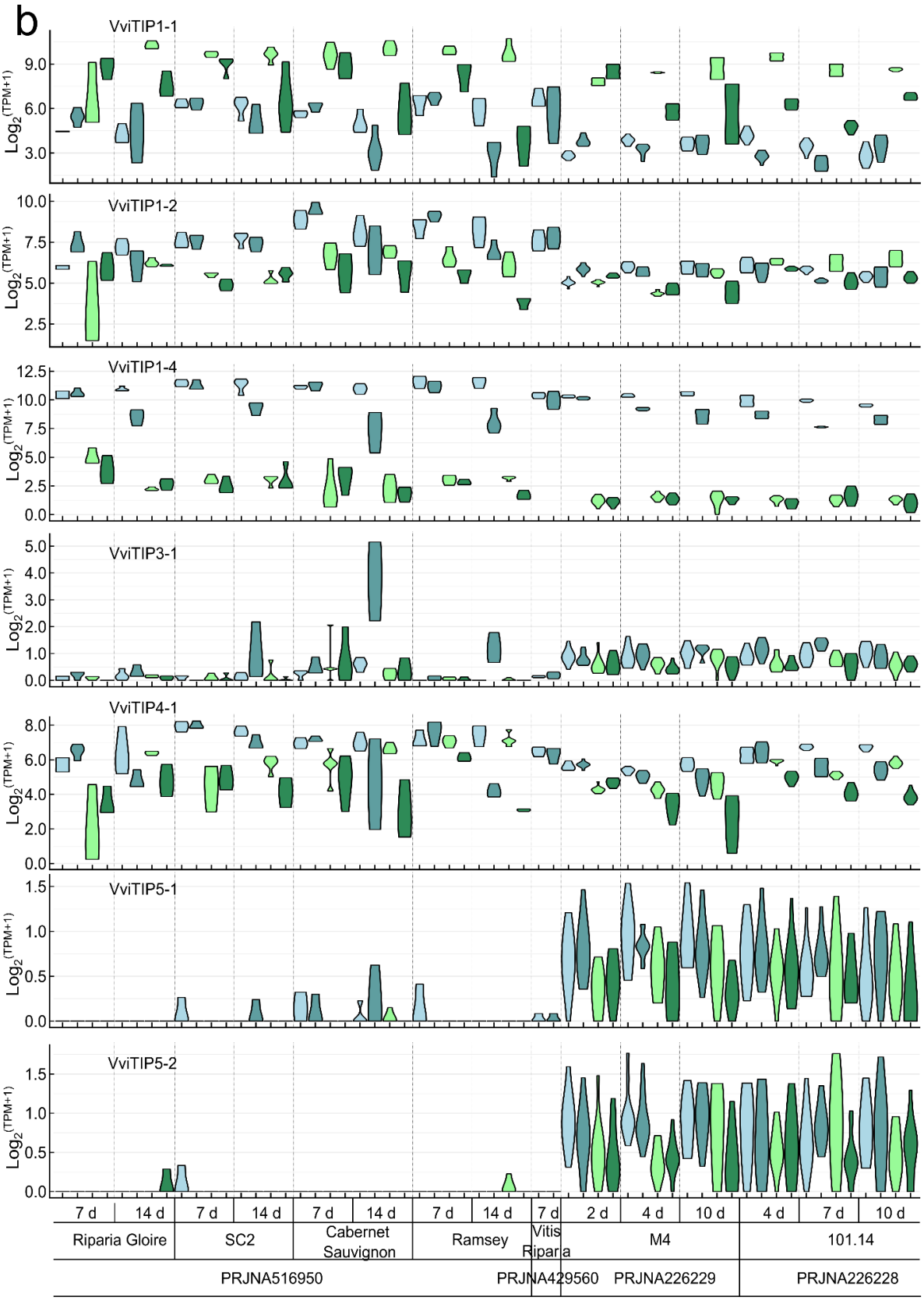
d

Treatments	Day of Experiment 0	10	19	20
Well-watered				
Water stress				
Rewatering				

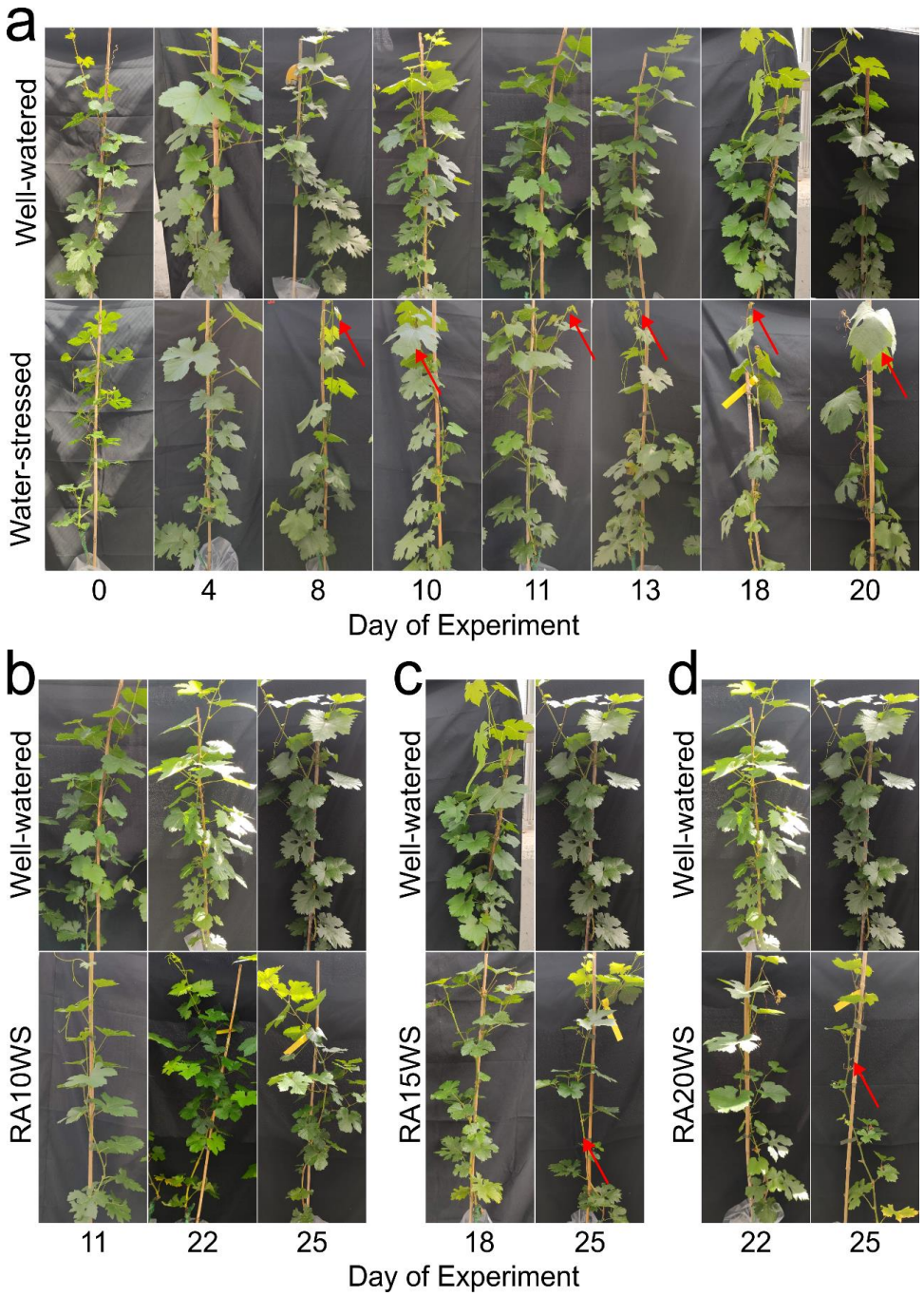
Note: ×4

Supplementary Fig. 1. Experimental settings of the two water deficit stress experiments. (a) Randomization of plants on the bench for the first water deficit stress experiment. Different treatments are colored according to the legend; among them, RA10WS, RA15WS, and RA20WS represent rewatering after 10, 15, and 20 days of water stress. **(b)** Randomization of plants for the second water deficit stress experiment. RA19WS represents rewatering after 19 days of water stress. **(c)** Leaf and root sampling time-points of the first experiment. Three biological replicates were collected. **(d)** Leaf sampling design of the second experiment for gene expression analysis by polysome profiling. Four biological replicates were collected.

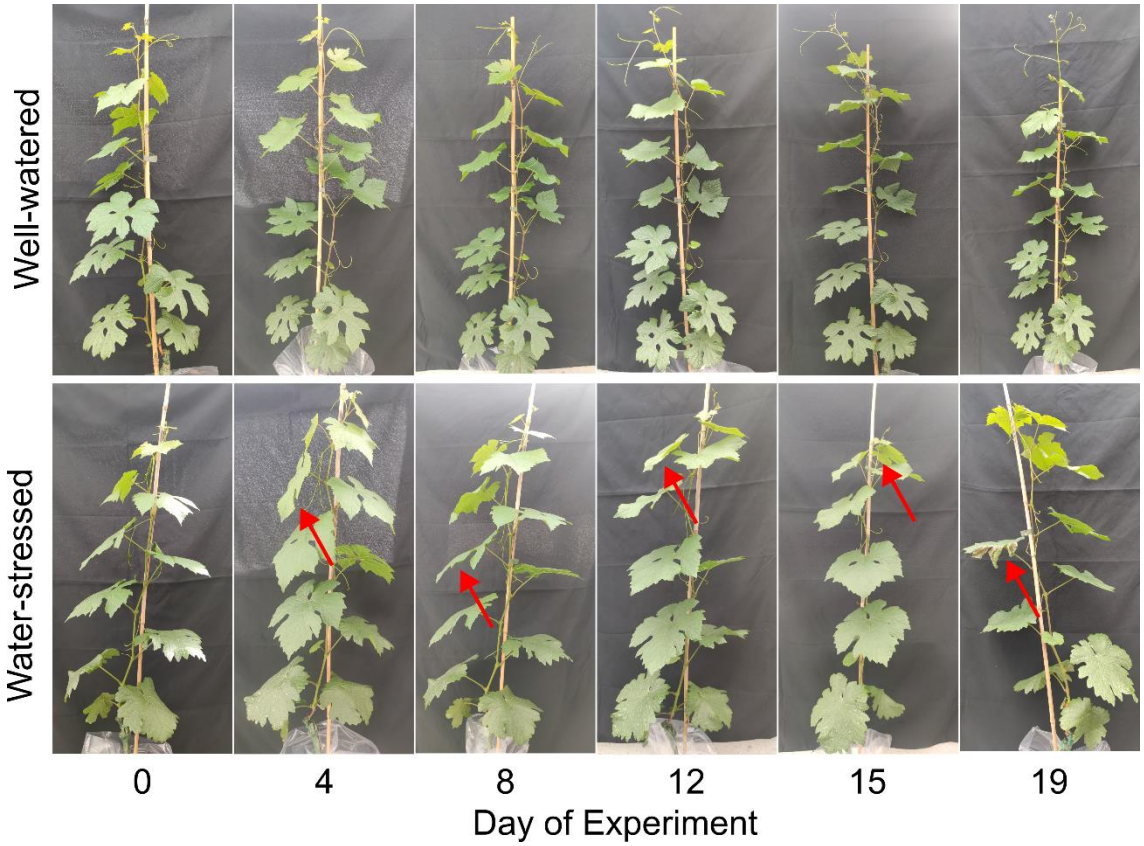

a
VviPIP1-2a
VviPIP1-2b
VviPIP1-3
VviPIP1-4
VviPIP2-3
VviPIP2-4
Log2(TPM+1)
7 d
14 d
2 d
4 d
10 d
Riparia Gloire
SC2
Cabernet Sauvignon
Ramsey
Vitis Riparia
M4
101.14
PRJNA516950
PRJNA429560
PRJNA226229
PRJNA226228


b
VviTIP1-1
VviTIP1-2
VviTIP1-4
VviTIP3-1
VviTIP4-1
VviTIP5-1
VviTIP5-2
Log2(TPM+1)
7 d
14 d
2 d
4 d
10 d
Riparia Gloire
SC2
Cabernet Sauvignon
Ramsey
Vitis Riparia
M4
101.14
PRJNA516950
PRJNA429560
PRJNA226229
PRJNA226228

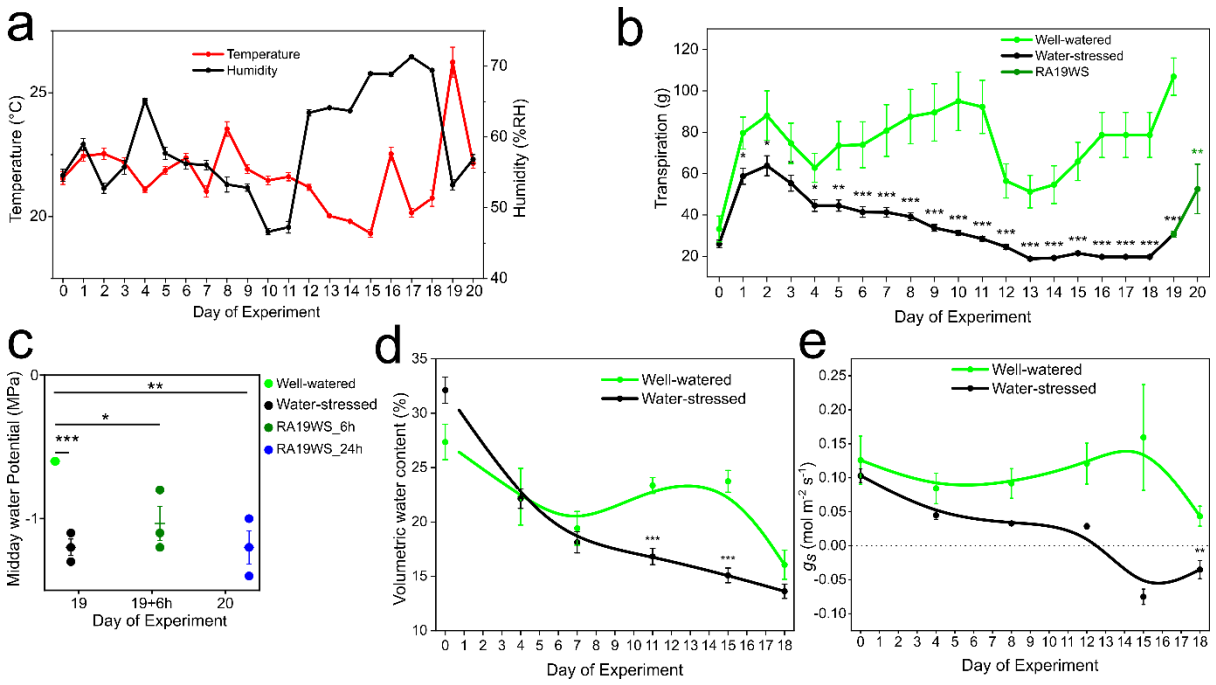
Supplementary Fig. 2. Overview of *Vitis* aquaporin gene expression in roots and leaves of different rootstock genotypes and 'Cabernet Sauvignon' cv. upon water stress treatments. Visualization of data taken from four publicly available transcriptomic datasets (PRJNA226228, PRJNA226229, PRJNA516950, PRJNA429560) for PIPs (**a**) and TIPs (**b**) genes. Violin plots represent the distribution of expression values expressed as log2 (TPM+1) of the replicates for each condition. On the x-axis the different projects, genotypes and experimental settings are reported. Samples tissue, either root or leaf, and condition are indicated by the blue or green color as in the legend.



Supplementary Fig. 3. Water stress significantly altered grapevine growth under varying irrigation regimes during the August 2023 water stress experiment. (**a**) Comparative images of grapevines under well-watered and water-stressed conditions. (**b**), (**c**), (**d**) Comparative images of well-watered grapevines and those subjected to rewatering following water stress, designated as RA10WS, RA15WS, and RA20WS, corresponding to plants rewatered after 10, 15, and 20 days of water deficit, respectively. These denote mild, moderate, and severe water stress levels, respectively. All images were captured at midday, with red arrows highlighting wilted leaves and shoots.



Supplementary Fig. 4. Water stress significantly altered grapevine growth under varying irrigation regimes during the March 2024 water stress experiment. The top panels are well-watered plants, and the bottom panels are water-stressed plants. Images were taken at midday. The water-stressed plants show symptoms such as scorched and wilted leaves as indicated by red arrows.



Supplementary Fig. 5. Second water deficit experiment (March 2024). (**a**) Mean air temperature and humidity in the greenhouse throughout the experiment. The data represent mean ± SEM (n=288). (**b**) Daily whole plant transpiration throughout the experiment. (**c**) Midday water potential in the leaves. Data are mean ± SEM (n=3). (**d**) Volumetric water content in the soil. A spline curve was used to connect data points. The data represent mean ± SEM (n=4 biological replicates in the well-watered group, n=16 biological replicates in the water-stressed group). (**e**) Stomatal conductance (g_s) of the top leaves. The data in (**b**), (**d**), and (**e**) represent mean ± SEM (n=4 in the well-watered group, n=16 in the water-stressed group, and n=3 biological replicates in the RA19WS group). A spline curve was used to connect data points in (**d**) and (**e**). A two-sided and unpaired Student's t-test was used to test the statistical significance in (**b**), (**c**), (**d**), and (**e**); * represents $p < 0.05$, ** represents $p < 0.01$, and *** represents $p < 0.001$.