

Table S1 Sample collection details. During the NT process, berries were collected at six time points (T0, T1, T2, T3, T4 and T5). During the FR process, berries were collected at four time points (T0, T1, T2, and T4). Under both conditions, T0 corresponds to fully-ripe berries, T1 to 22 days after harvest, T2 to 33 days after harvest, and T4 to 65 days after harvest. Furthermore, in terms of percentage weight loss, NT-T2 corresponds to FR-T1 (14%), NT-T3 to FR-T2 (18%), and NT-T5 to FR-T4 (30%).

	Sampling Time Points					
	T0 (Harvest)	T1	T2	T3	T4	T5
Sampling Data	September 12 th 2011	October 4 th 2011	October 14 th 2011	November 3 rd 2011	November 16 th 2011	January 10 th 2012
NT Weight loss (%)	0	10	14	18	22	30
NT Dehydration day	0	22	33	52	65	120
FR Weight loss (%)		14	18		30	
FR Dehydration day		22	33		65	

Table S2 Titratable acidity and pH values during postharvest dehydration. (n = 3 ± standard deviation).

Time point	Process	Titratable acidity (g/L of tartaric acid)	pH
T0	NT/FR	5.10 ± 0.11	3.18 ± 0.06
T1	NT	5.59 ± 0.11	3.51 ± 0.04
	FR	5.46 ± 0.26	3.43 ± 0.12
T2	NT	5.48 ± 0.17	3.46 ± 0.05
	FR	5.44 ± 0.26	3.44 ± 0.08
T3	NT	5.45 ± 0.15	3.44 ± 0.05
T4	NT	4.51 ± 0.14	3.49 ± 0.04
	FR	4.64 ± 0.31	3.59 ± 0.10
T5	NT	5.17 ± 0.16	3.75 ± 0.07

TABLE S3 Primer sets.

GENE	GENE ID	SEQUENCE 5'→3'
<i>VvTPS07</i>	VIT_18s0001g04280	Fw - TACCTTAGCCGCCCCTAATG Rev - AGCACTACCAAACCGAGAGA
<i>VvSTS27</i>	VIT_16S0100G00990	Fw - ATTCTGCAGGTGCCATTGCA Rev - ATACCAAGTGGGTCAAAAGCC
<i>Laccase</i>	VIT_18s0001g01280	Fw - TCACAGTGATTGGACCCGAA Rev - AATCAGAGGCATTGGGGTCA
<i>Pectinesterase family</i>	VIT_16s0022g00700	Fw - AGTGTCGCCAACTTTATAGCT Rev - ATCATCATAGACCAGACCTGA
<i>WRKY DNA-binding protein 72</i>	VIT_17s0000g05810	Fw - CTTACATCAATAATGGGTGCTA Rev - TGACTGATAGGTAGAAACAGC
<i>Alpha-dioxygenase</i>	VIT_14s0066g01670	Fw - GGATCGTCATTACCCAGAGA Rev - GATCAATGGGGAACACGAAG
<i>VvUBIQUITIN1</i>	VIT_16s0098g01190	Fw - TCTGAGGCTTCGTGGTGGTA Rev - AGGCGTGCATAACATTGCG

FIGURE S1 Principal component analysis of transcriptomic data from Corvina berries collected during postharvest dehydration in 2010.

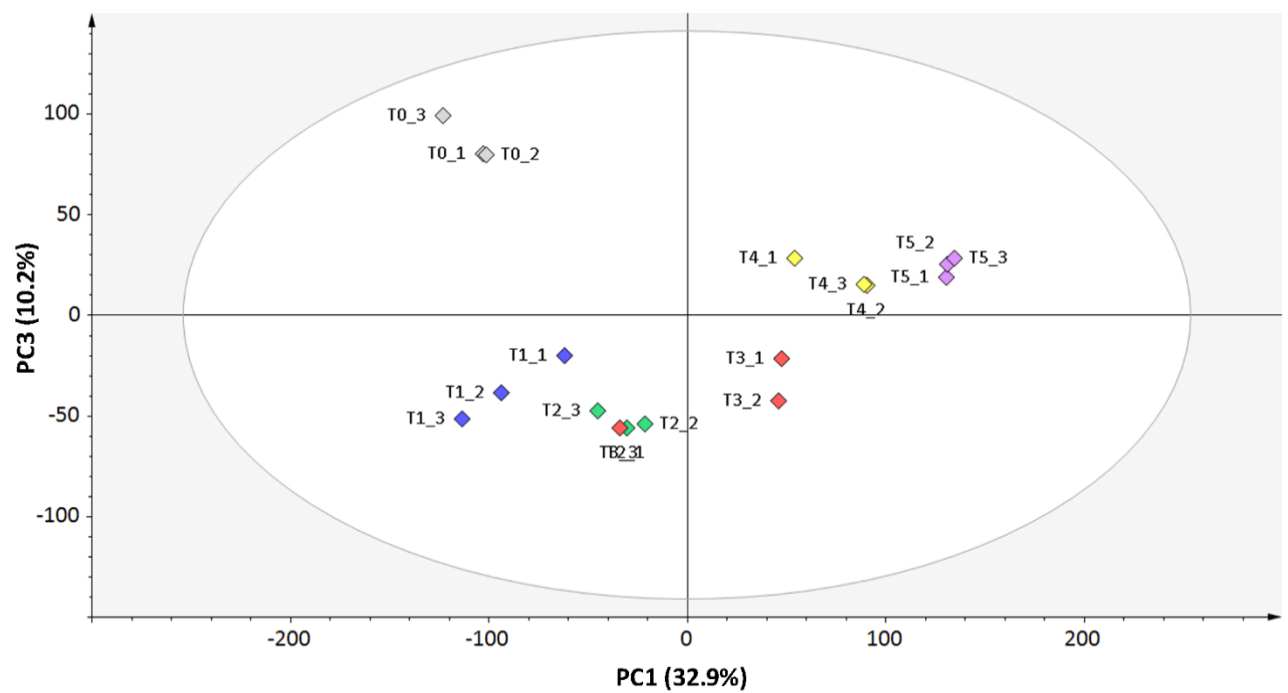


FIGURE S2 qRT-PCR verification of microarray data. Expression profiles obtained by microarray analysis (left) and qPCR (right) for (a) *VvSTS27* (b) *LAC* (c) *PME*, and (d) *VvTPS07* under NT and FR postharvest dehydration conditions. Microarray data are reported as the average of three biological replicates. Error bars represent standard deviations (n = 3).

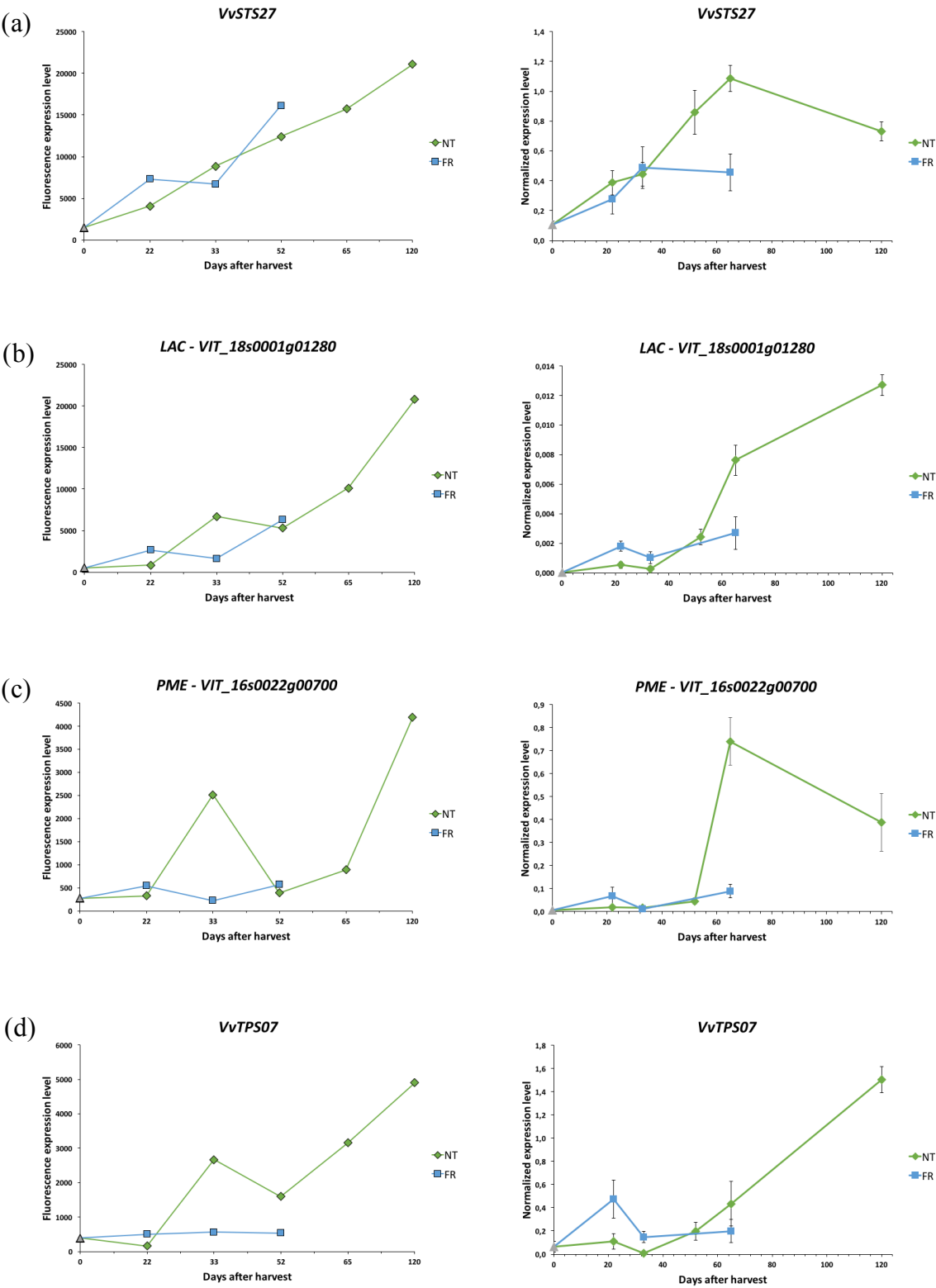


FIGURE S3 Overview of the NT and FR postharvest dehydration processes during the 2013 vintage. (a) Dehydration kinetics of Corvina and Sangiovese berries under NT and FR postharvest conditions, with sampling time points highlighted. For both varieties and under both conditions, T0 corresponds to fully-ripe berries, T1 to berries sampled at 18% weight loss and T2 to berries sampled at 30% weight loss. (b) Trends of relative humidity in the two dehydrating rooms used to reproduce NT and FR dehydration processes. (c) Trends of temperature in the two dehydrating rooms.

