Supplemental data

Supplemental Results

Grouping of varieties based on specific classes of molecules

We characterized the three groups of varieties in more detail by building PCA models based on profiles of specific classes of molecules and by constructing an O2PLS-DA correlation plot. The PCA score scatter plots revealed the clear clustering of samples into three groups, as shown for the total metabolite content (Figure 2A), only for anthocyanins (Supplementary Figure S10A) and for flavonols and other flavonoids (Supplementary Figure S10B). In contrast, the analysis of hydroxybenzoic and hydroxycinnamic acids with hydroxytyrosol clearly separated Corvina from Sangiovese, and instead clustered with Merlot, Syrah and Cabernet Sauvignon (Supplementary Figure S10C). PCA plots of flavan-3-ols/proanthocyanins and stilbenes revealed sample scattering so that the six varieties could not be differentiated according to these molecules (data not shown). The correlation loading plot of O2PLS based on anthocyanins confirmed that class 1 (Merlot, Syrah and Cabernet Sauvignon) is characterized by malvidin, petunidin and delphinidin (acetyl) and (coumaroyl) 3-O-glucosides, class 3 (Oseleta) by cyanidin, peonidin and petunidin-3-O-glucoside, and Corvina and Sangiovese were negatively characterized by delphinidin-3-O-glucosides (Supplementary Figure S10D and Supplementary Dataset S13). In the case of flavonols and other flavonoids, class 1 was characterized by a high content of acylated flavanones in particular the acetylated dihydrosyringetin, Oseleta by tetrahydroxy-monomethoxyflavanone, and Corvina and (Taxifolin), Sangiovese bv dihydroquercetin kaempferol and quercetin-O-glucosides (Supplementary Figure S10E and Supplementary Dataset S13). Finally, the model for hydroxycinnamic and hydroxybenzoic acids revealed that Oseleta was characterized by a high content of hydroxycinnamic acids, Corvina by high levels of hydroxytyrosol, and that Merlot, Syrah, Cabernet Sauvignon and Sangiovese were characterized by an intermediate behavior between classes 2 and 3 (Supplementary Figure S10F and Supplementary Dataset S13).

More detailed metabolic characterization of intra-group varieties

Differences among the three varieties in group 1, and between the two in group 2, were characterized in more detail by building new PCA and O2PLS models (**Figure 2A**). Merlot, Syrah and Cabernet Sauvignon (group 1) were clearly separated by PCA (**Supplementary Figure S11A**) and the correlation loading plot of the resulting O2PLS model (R2X(cum): 0.735 and Q2(cum): 0.97) showed that Merlot was characterized by high stilbene and proanthocyanidin levels, Syrah

was distinguished by high levels of anthocyanin (coumaroyl)-3-O-glucosides, and Cabernet Sauvignon contained high levels of anthocyanin (acetyl)-3-O-glucosides (**Supplementary Figure S11B; Supplementary Dataset S14**). Corvina and Sangiovese (group 2) (**Figure 2A**) were distinguished by the high content of hydroxytyrosol and some flavonoids in Corvina and the high levels of some anthocyanin-3-O-glucosides in Sangiovese (**Supplementary Figure S11C and D**; **Supplementary Dataset S15**).

Supplemental Figures

Figure S1.



Figure S1. Overview of the postharvest dehydration process. **A** and **B**, Titratable acidity and pH trends. **C**, Initial berry weight of the six varieties. **D**, D-gluconic acid content at the T0 and Tend in the six genotypes.

Figure S2.



Figure S2. PCA score scatter plot of the model obtained for the metabolites detected by HPLC-ESI-MS in the six genotypes in all stages of postharvest. PCA score scatter plot is colored according to variety.





Figure S3. Accumulation trends of anthocyanins (**A**), flavonols and other flavonoids (**B**), hydroxycinnamic/hydroxybenzoic acids (**C**) and flavan-3-ols and proanthocyanindins (**D**) during the postharvest process in the six varieties. Values were determined by HPLC-MS analysis and indicated as sum of the peak areas (arbitrary units).





Figure S4. PCA score scatter plot of the model obtained for the volatile metabolites detected by GC-MS in all stages of Corvina berries. PCA score scatter plot is colored according to postharvest stage.

Figure S5.



Figure S5. Hierarchical clustering of volatile organic compounds modulation during postharvest in Corvina berries. The heat map describes the accumulation (red) or depletion (blue) of each detected metobolite. The 72 compounds were included in eight classes of molecules described by different colors. Data have been normalized for berry weight loss and row mean centered (TmeV 4.4).

Figure S6.



Figure S6. PCA score scatter plot of the model obtained for the transcripts detected by microarray analysis at harvest in each variety (explained variance = 69.2%). PCA score scatter plot is colored according to variety.

Figure S7.

Corvina	Sangiovese	Merlot	Syrah	Oseleta	Cabernet Sauvignon	
T1/T0 T2/T0 T3/T0 T4/T0 T5/T0	T1/T0 T2/T0 T3/T0 T4/T0 T5/T0	T1/T0 T2/T0 T3/T0 T4/T0	T1/T0 T2/T0 T3/T0	T1/T0 T2/T0 T3/T0	T1/T0 T2/T0 T3/T0	
						VIT_09s0002g04720 Coatomer protein complex, subunit beta 2 VIT_18s0075g00590 Laccase
						VIT_03s0063g02650 Hydrolase, alpha/beta fold
						VIT_08s0040g02430 Unknown protein
						VIT_0650009g03670 F-box family protein 👷
						VIT_07s0005g01360 Zinc finger (C3HC4-type ring finger)
						VIT_05s0029g00080 SERK family receptor-like protein kinase
						VII_1850001g07870 Unknown protein VII_06s0004g00130 Pyruvate kinase
						VIT_01s0026g00980 Glycosyl transferase family 8 protein 🛠
						VIT_07s0005g01430 PROLIFERA protein
						VIT_00s2648g00010 FAD-dependent pyridine nucleotide-disulphide oxidoreductase
						VIT_09s0054g00910 Chaperone BCS1 mitochondrial
						VIT_17s0000g04370 Wall-associated kinase
						VIT_00s2376g00010 NADH dehydrogenase putative
						VIT_02s0154g00350 L-lactate dehydrogenase A
						VIT_1850001900 KKF3 (receptor-like kinase in in howers 3) VIT_05s0020g02170 Sugar transporter ERD6-like 16
						VIT_02s0025g03300 Potassium channel tetramerisation domain-containing protein
						VIT_13s0019g00540 Ethylene-responsive protein
						VIT_01s0146g00150 BCL-2-associated athanogene 5
						VIT_13s0320g00030 Unknown protein *
						VII_085003800130 Ammonium transporter 2 VIT_10s0003g00470 Trans-resveratrol di-0-methyltransferase - VvROMT
						VIT_14s0068g01250 Mitochondrial phosphate transporter
						VIT_18s0001g14690 Protein kinase
						VIT_01s0011g03430 Fw2.2 OKFX VIT_18s0001g00340 Diphenol oxidase
						VIT_03s0063g01820 AOS (allene oxide synthase)
						VIT_17s0000g03560 myb domain protein 62 VIT_07c0031g01090 Accorbate oxidate
						VIT_00s0225g00050 MATE efflux family protein
						VIT_04s0008g05700 ACT domain-containing protein
						VIT_18s0001g00840 Syringolide-induced protein 14-1-1 VIT_16s0098e01260 Intramitochondrial sorting protein MSP1 protein
						VIT_06s0004g02590 Carbonic anhydrase
						VIT_01s0150g00440 Respiratory burst oxidase protein D (RBOHD)
						VIT_0550062g00790 NSL1 (necrotic spotted lesions 1) VIT_18s0001g15130 WD40 repeat protein
						VIT_16s0100g00770 Stilbene synthase (VvSTS9)
and the second						VIT_06s0004g01020 Dirigent protein *
						VIT_16s0100g0090 Stilbene synthase (VVS1527) 👷
						VIT_16s0039g01070 Glutathione S-transferase 25 GSTU7
						VIT_19s0015g01750 WD-40 repeat VIT_17s0000a04020 ATP-dependent Clopprotease adaptor protein CloS containing protein
						VIT_14s0081g00010 IAA16
						VIT_14s0060g00900 Unknown protein
						VII_050038804450 Basic Leucine Zipper Transcription Factor (VVbZIP07) VIT_05s0020g01820 Integral membrane family protein UPE0497
						VIT_13s0064g01260 DNA-damage-repair/toleration protein (DRT100) *
						VIT_14s0030g01950 Transferase
						VIT_01s0026g00730 Unknown protein
						VIT_01s0026g00940 ARR3 typeA 🙁
						VII_1050001g03400 Cytochrome D5 DIF-F (VVCytoB5) VIT_18s0089g00180 1-4-beta-mannan endohvdrolase
						VIT_07s0031g00420 SHN1 (SHINE 1) *
						VIT_02s0025g01450 Unknown protein *
						VIT_13s0074g00700 ABC Transporter (VvPDR27 - VvABCG57)
						VIT_02s0033g00380 myb VVMYBA1 similar
						VII_UISUUZ6gUZ6ZU Expansin (VVEXPA1) * VII 12s0028g03610 Cellulase
						VIT_04s0008g06000 ERF/AP2 Gene Family (VvERF045) *
						VIT_14s0171g00180 Leucine-rich repeat transmembrane protein kinase *
						VII_1050042g01500 Unknown protein VIT_13s0074g00390 CYP77A2 *
						VIT_04s0008g02250 Beta-ketoacyl-CoA synthase \star
						VIT_02s0033g00390 VvMybA2 *
						VIT_18s0075g00250 Unknown protein 🗴
						VIT_00s0207g00010 Anthranilate N-benzoyltransferase protein 1
						VII_UUS1682gUUU1U Copper amine oxidase 🛠
						VIT_06s0009g00690 NIMA-related kinase NEK6
						VIT_17s0000g01930 Potassium transporter 2
						VII_1350067g03890 Beta-ketoaryl-CoA synthase
						VIT_07s0141g00290 IAA16
						VIT_16s0039g01670 Cinnamoyl-CoA reductase
						vii_ussuu//guu/su basic helix-loop-helix (bHLH) family VIT_14s0006g02990_3-ketoacyl-Co4_synthase
						VIT_02s0025g01380 Endo-1-4-beta-glucanase
						VIT_06s0004g02680 Lysine decarboxylase *
						VII_04S0025g01330 Polygalacturonase GH28
						VIT_18s0001g02790 Unknown protein
						VIT_14s0083g01110 Brassinosteroid-6-oxidase
						AUTTSO145B00100 Ouklown biofein

Figure S7. Heat map of commonly differentially modulated genes in the six genotypes during the postharvest process. Asterisk indicates genes also associated to the final and initial stages of the process identified by PCA.

Figure S8.



Figure S8. Gene expression of the most up-regulated (1^{st} percentile) and down-regulated (99^{th} percentile) Corvina transcripts we identified during the ripening and postharvest process in Corvina pulp (**A**) and skin (**B**), as reported in the expression atlas (Fasoli et al., 2012).





Figure S9. Ratio of the average expression level in the three postharvest stages analyzed by Fasoli et al., (2012) in pulp and skin of most downregulated genes. Positive fold changes are shown in pink and negative fold changes are shown in green.

Figure S10.



Figure S10. PCA score scatter plots of the models obtained for anthocyanins (A), flavonols and other flavonoids (B), and hydroxycinnamic, hydroxybenzoic acids and hydroxytyrosol (C), detected by HPLC-ESI-MS at harvest in the six varieties. O2PLS-DA correlation loading plots of the threeclass models for the anthocyanins (D), flavonols and other flavonoids (E), and hydroxycinnamic, hydroxybenzoic acids and hydroxytyrosol (F), according to the unsupervised PCAs. Groups of metabolites are shown in different colors. Abbreviations: ac = anthocyanins; ac-ac = acylated anthocyanins; ac-c = coumaroyl anthocyanins; f = other flavonoids; fl = flavonols; hb = hydroxybenzoic acids; hc = hydroxycinnamic acids; ht = hydroxytyrosol.





Figure S11. A, PCA score scatter plot of the model obtained for the metabolites detected by HPLC-ESI-MS at harvest for Merlot, Cabernet Sauvignon and Syrah, **B**, O2PLS-DA correlation loading plot of the three-class model according to the unsupervised PCA in **A. C**, PCA score column plot of the model obtained for the metabolites detected by HPLC-ESI-MS at harvest for Corvina and Sangiovese at harvest, **D**, O2PLS-DA correlation loading plot of the two-class model according to the unsupervised PCA in **C.** Groups of metabolites are shown in different colors. Abbreviations: CA= Cabernet Sauvignon; ME= Merlot; SY= Syrah; aa = amino acids; ac = anthocyanin; ac-ac = acylated anthocyanins; ac-c = coumaroyl anthocyanins; f = other flavonoids; fl = flavonols; hb = hydroxybenzoic acids; hc = hydroxycinnamic acids; ht = hydroxytyrosol; oa = organic acid; p = procyanidins; s = sugars; st = stilbenes.