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## *Supplementary material*

### **Whole-metagenome-sequencing-based community profiles of *Vitis vinifera* L. cv. Corvina berries withered in two environmental conditions**

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### **1 Supplementary Figures and Tables**

#### **1.1 Supplementary Figures**

**Figure S1.** Overview of the scaffold size obtained through the assembly process and their bp content.

**Figure S2.** Phylogenetic tree based on >400 proteins optimized from among 3737 genomes. It includes the 15 genome bins obtained in this study, highlighting that the population bins belong to the families Clostridiaceae, Enterobacteriaceae, Enterococcaceae, Microbacteriaceae, Paenibacillaceae, Pseudomonadaceae.

#### **1.2 Supplementary Tables**

**Table S1.** Annotation of genes identified in the metagenomic assembly and assignment of the scaffolds to the microbial genomes. The protein-encoding genes identified with Prodigal were annotated using different procedures (see Methods for details). In columns (A-AA) are reported: (A) scaffold; (B) gene ID as “scaffold\_gene number”; (C) genome bins assignment (names and description of the genome bins are reported in Table 3); (D) COG ID; (E) COG ID “short code”; (F)

32 e-value of BLAST results for COG; (G) gene name, (H) gene function; (I) KEGG ID; (J) link to the  
33 KEGG function; (K) EggNOG gi code; (L) EggNOG ID; (M) EggNOG gene function; (N) e-value  
34 of eggNOG blast result; (O) gi code of blast search against NCBI microbial genomes; (P) NCBI  
35 gene ID; (Q) gene function description; (R) most similar species; (S) e-value for BLAST search  
36 against NCBI microbial genomes, (T) Pfam ID; (U) e-value for BLAST search against Pfam; (V)  
37 Pfam domain; (W-AA) Pfam domain description. “NA” = not assigned.

38 **Table S2.** Relative abundance of prokaryotic associated with grape surfaces of the TW and AW  
39 process obtained through the MetaPhlAn analyses.

40 **Table S3.** Coverage of the population bins of the TW and AW samples and their ratio.

41

42 **Table S4.** Percentage of proteins assigned to the COG classes for each genome bin. Percentage is  
43 calculated considering the total number of genes on each near-complete genome.