SUPPLEMENTARY DATA
Destanque, A., Picot, A., Pensec, F., Pawtowski, A., Rolland, N., Treguer-Fernandez, S., … Coton, M. (2024).
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https://doi.org/10.20870/oeno-one.2024.58.3.8105

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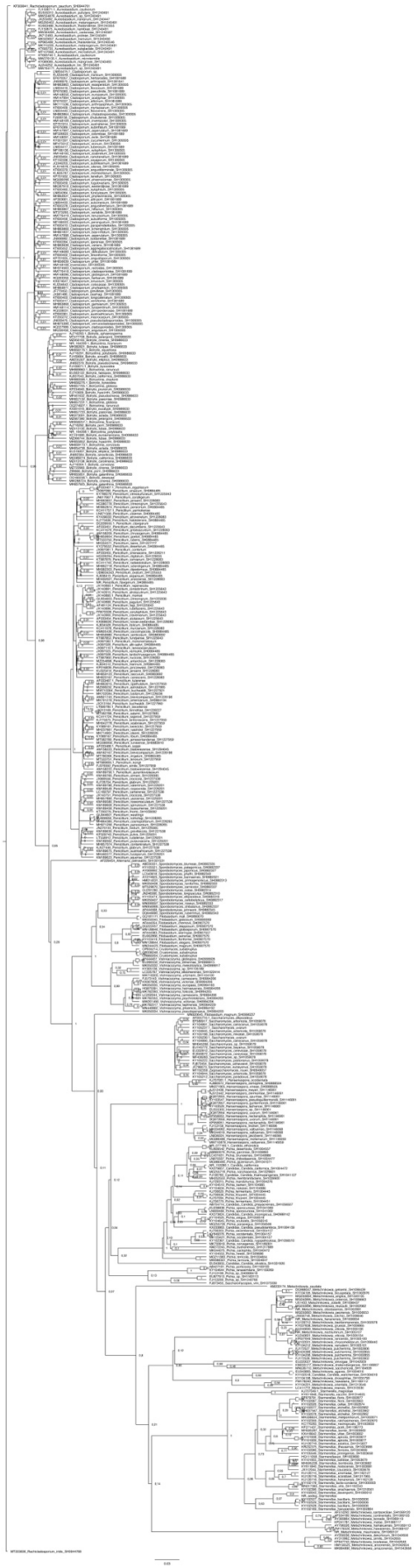


Figure S1: Phylogenetic tree of 13 identified fungal genera constructed with 473 reference sequences.

See complementary file

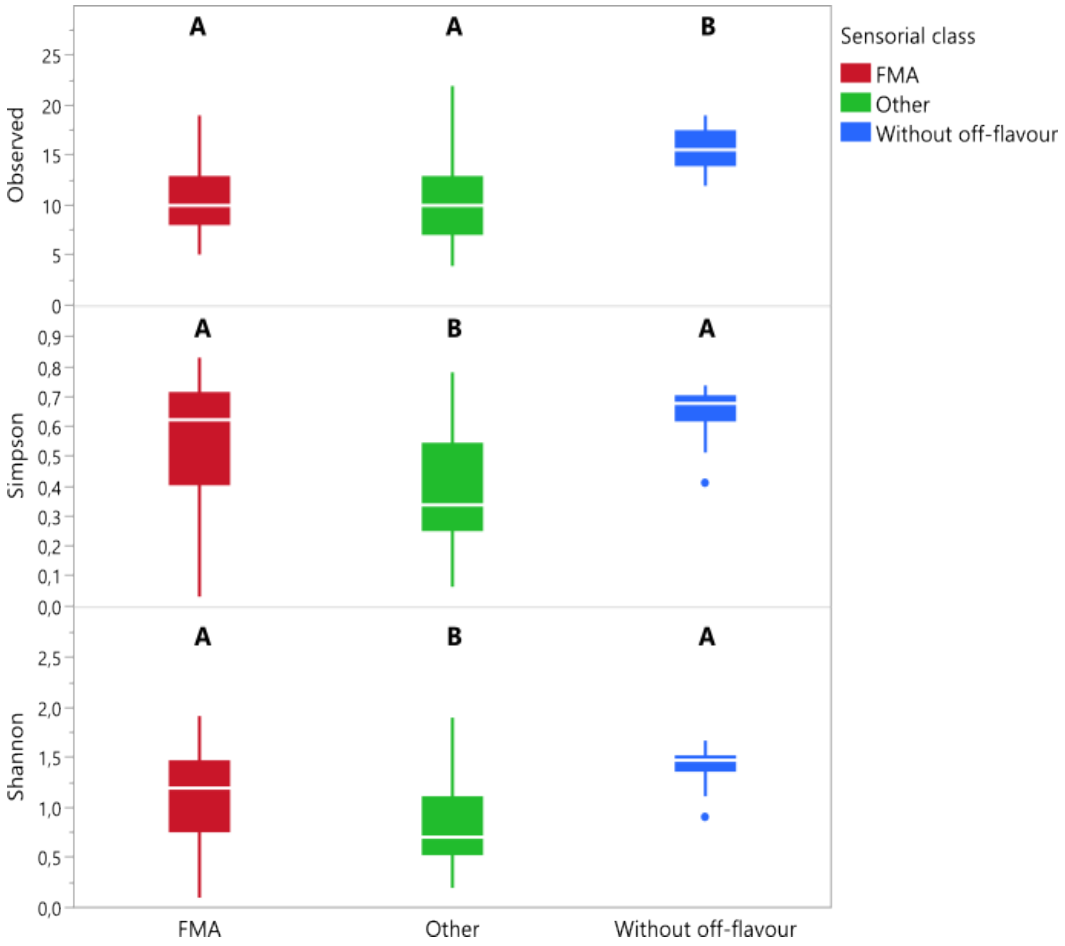
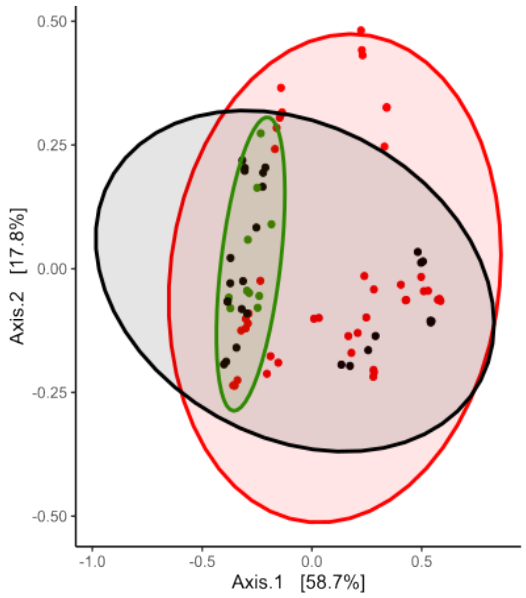


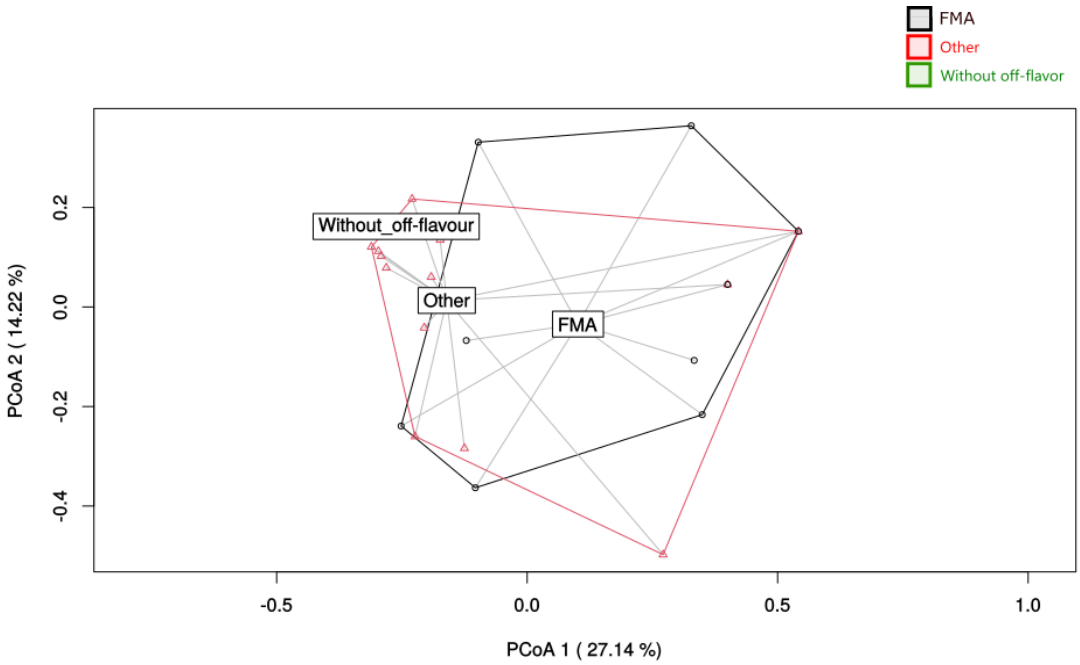
Figure S2: Boxplot of alpha diversity index Observed, Shannon and Simpson of the sensorial class at must stage and based on metagenetic ASV table merged at genus level and rarefy at 14,563 reads. Letters represent differences between sensorial classes (performed with either Wilcoxon for Observed or Tukey HSD for Simpson and Shannon).

A



	R^2	p-value
Adonis test	0.108	0.002
Pairwize Adonis: OF - NOF	0.132	0.001
Pairwize Adonis: OF - FMA	0.047	0.027
Pairwize Adonis: NOF - FMA	0.084	0.041

B



	R^2	p-value
Adonis test	0.103	0.319

Figure S3: Principal Coordinate Analysis Plots (PCoA) based on fungal abundances at must stage determined with metagenetic data at the genus level (Bray-Curtis distances calculated at genus level with Hellinger data normalization) **A)** and with cultural data at the species level (Bray-Curtis distances calculated at species level with $\log_{10}$ data normalization) **B)**. For each approach, Adonis tests were performed between the 3 sensorial analysis classes.

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Table S1: (A) PCR conditions used for fungal identification of the fungal isolates obtained by the culture-dependent approach. According to the considered isolate, the D1/D2 region from the 26s DNA, actin, ITS, and b-tubulin genes were targeted using the NL1/NL4, Act512F/Act783R, ITS4/ITS5 and Bt2a/Bt2b primers, respectively. (B) PCR conditions used for the culture-independent (metagenetic) approach with the ITS3-F and ITS4-KYO1-R primers and FLD_ill adapter.

A

Mix Components	ITS 4/5	Bt2a/Bt2b	NL1/ NL4	ACT-512F/783R
Buffer	1 x	1 x	1 x	1 x
MgCl2	2 mM	1.5 mM	1.5 mM	2 mM
Primer Fwd (10µM)	0.2 µM	0.2 µM	0.2 µM	0.5 µM
Primer Rv (10µM)	0.2 µM	0.2 µM	0.2 µM	0.5 µM
dNTP	0.2 mM	0.2 mM	0.2 mM	0.2 mM
Go Taq	0.025 U/µL	0.025 U/µL	0.0125 U/µL	0.05 U/µL
Amplification cycles	Denaturing 1 cycles - 5 min - 95°C Annealing 29 cycles - 1 min - 95°C 29 cycles - 1min - 55°C 29 cycles - 1 min - 72°C Extension 1 cycles - 10 min - 72°C		Denaturing 1 cycles - 2 min - 95°C Annealing 36 cycles - 1 min - 95°C 36 cycles - 90 sec - 52°C 36 cycles - 2 min - 72°C Extension 1 cycles - 10 min - 72°C	Denaturing 1 cycles - 8 min - 95°C Annealing 29 cycles - 15 sec - 95°C 29 cycles - 20 sec - 58°C 29 cycles - 1 min - 72°C Extension 1 cycles - 5 min - 72°C

B

Mix Components	PCR indexation	PCR amplification
Qiagen 10X Buffer with15mM MgCl2		1 x
Roche 10X Buffer without MgCl2	1 x	
Roche MgCl2 25mM	1.8 mM	
Roche_DMSO	5%	5%
ITS3-F-FwR1		0.6 µM
ITS4-KYO1-RvR2		0.6 µM
dNTP mix 10 mM_NEB	0.2 mM	0.2 mM
Qiagen HotStarTaq 5U-ul		0.02 U/µL
Roche FastStart High Fi 5U-ul	0.05 U/µL	
Amplification cycles	Denaturing 1 cycles - 10 min - 95°C Annealing 15 cycles - 15 sec - 95°C 15 cycles - 30 sec - 60°C 15 cycles - 1 min - 72°C Extension 1 cycles - 3 min - 72°C	Denaturing 1 cycles - 15 min - 96°C Annealing 33 cycles - 30 sec - 96°C 33 cycles - 30 sec - 52°C 33 cycles - 1 min - 72°C Extension 1 cycles - 10 min - 72°C