

Supplementary materials

Intra- and inter-annual changes in root endospheric microbial communities of *Vitis vinifera* are mainly deterministic

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Contents :

Contents:	
Supplementary Figures:	
Fig. S1 Graphs showing annual temperature and total precipitation per day in 2018 and 2019	page 2
Fig. S2 Rarefaction curves for (A) “all bacteria” samples and (B) “all fungi” samples.	page 3
Fig. S3 Redundancy analyses (RDA) plots of the microbial communities.	page 4
Fig. S4 Comparisons of Bray Curtis dissimilarity between intra- (J19&S19) and inter-annual (S18&S19) time points for two cultivars.	page 5
Fig. S5 Comparisons of Bray Curtis dissimilarity between intra- (J19&S19) and inter-annual (S18&S19) time-points for each combination of scion and rootstock.	page 6
Fig. S6 Partition of deterministic and stochastic processes of fungal community assembly (neutral community model (NCM)).	page 7
Fig. S7 Modified normalized stochasticity ratios (MST) estimated to measure the relative importance of deterministic processes of assembly for each combination of scion and rootstock.	page 8
Fig. S8 Root microbiota structure of different rootstock within each cultivar.	page 9
Fig. S9 Effects of rootstock, sampling time and their interaction on the microbial community composition based on variation partition analysis (VPA).	page 10
Supplementary Tables:	
Table S1 Information about the rootstock genotype and the cultivar of scion for the grapevine	page 11
Table S2 Abiotic characteristics for each sampling field.	page 12
Table S3 Details of the sequence clusters specific of a given sampling campaign.	page 13

Supplementary Figures

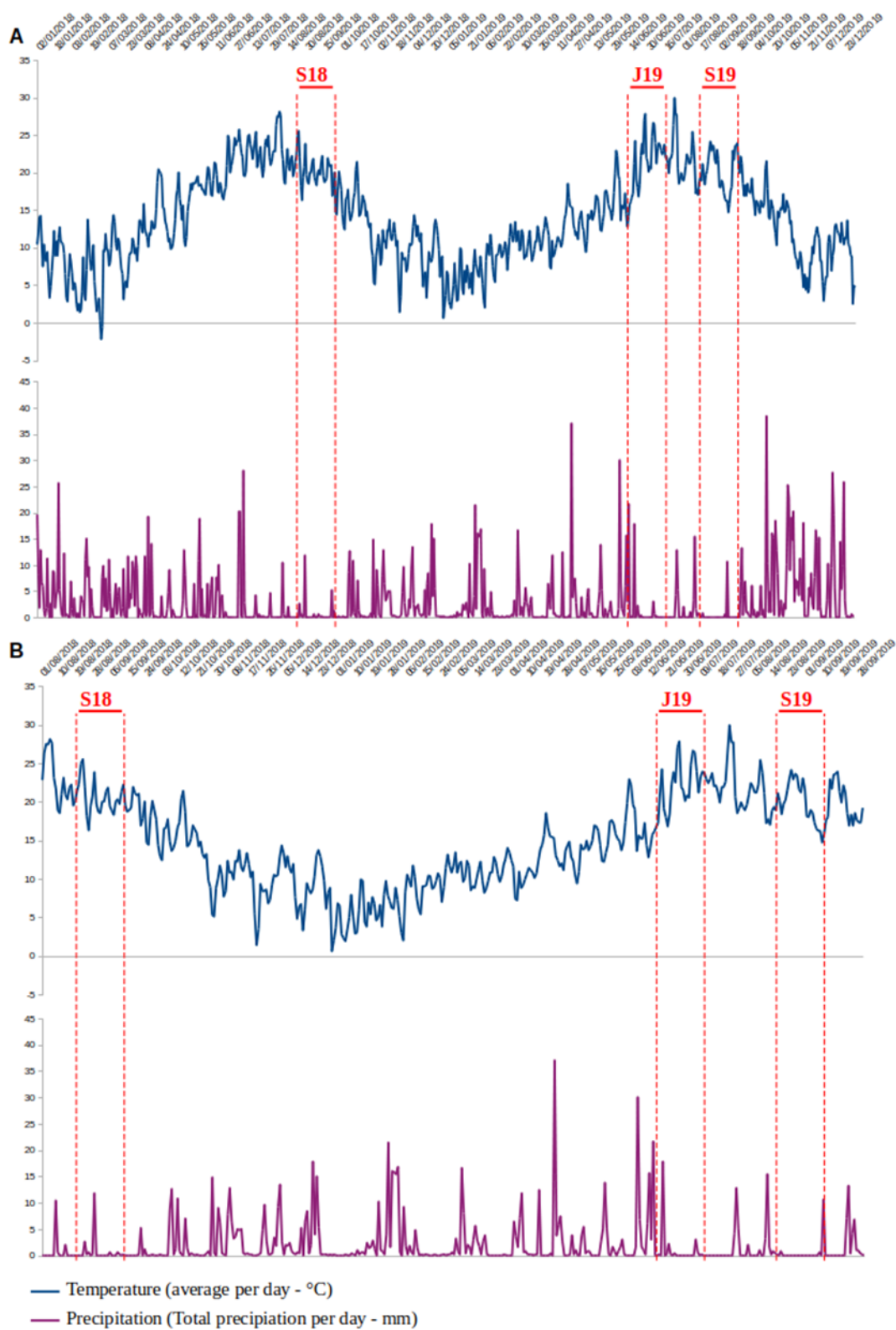


Fig. S1 Graphs showing annual temperature and total precipitation per day in 2018 and 2019.

Curves showing average temperatures per day (blue lines, °C) and total precipitation per day (purple lines, mm of rain) in the two years analyzed, 2018 and 2019 (A) and during the sampling period, i.e. from September 2018 to September 2019 (B). The panel B is a zoom-in of the two years' data shown in panel A. The red dashed lines indicate the three sampling periods of interest (S18, J19 and S19).

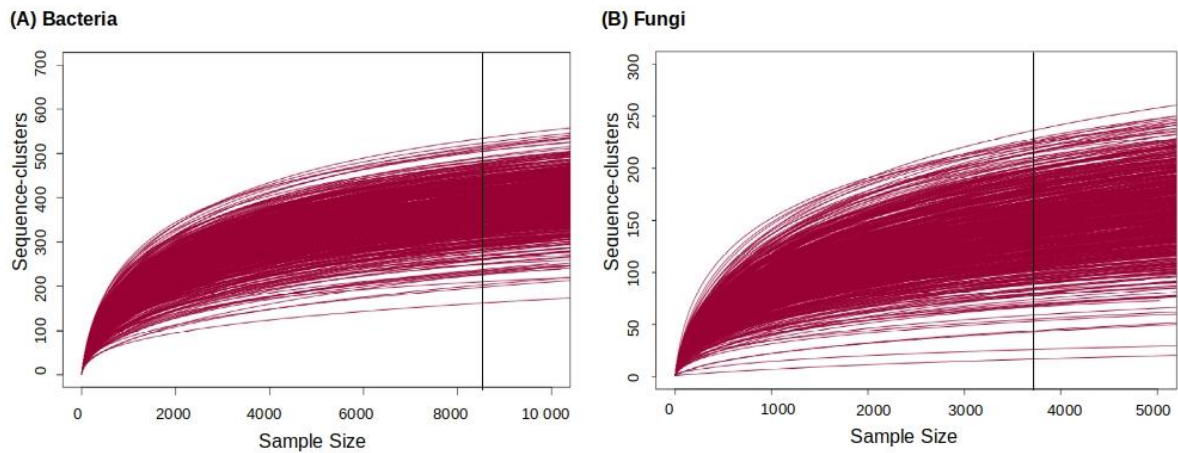
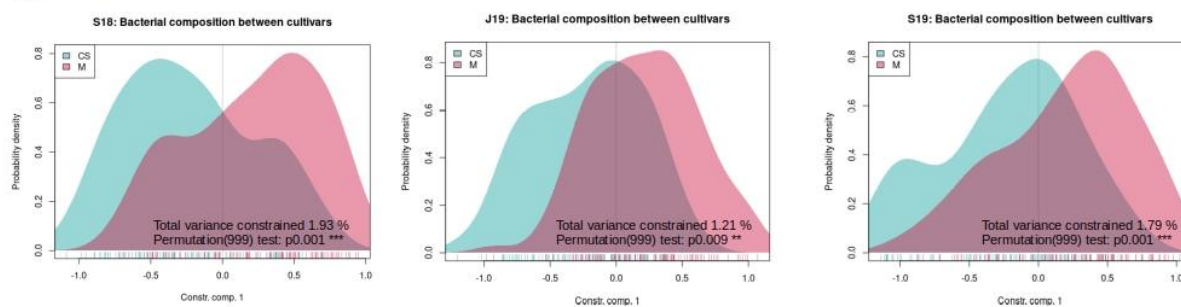


Fig. S2 Rarefaction curves for (A) “all bacteria” samples and (B) “all fungi” samples.

Curves show the total assigned sequence clusters detected relative to sample size in sequence number. The vertical lines correspond to the number of sequence clusters at which data were rarefied (8500 for bacteria, and 3700 for fungi).

RDA

(A) Bacteria



(B) Fungi

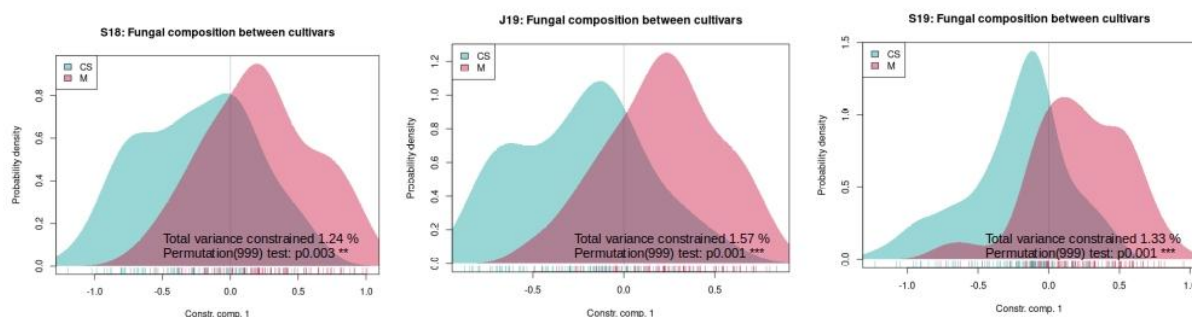


Fig. S3. Redundancy analyses (RDA) plots of the microbial communities.

Results of RDA analyses testing the significance of the effect of the cultivar (CS Cabernet Sauvignon and M Merlot) on the composition of the root bacterial (A) and fungal (B) communities on the three sampling dates. Results of the permutation tests testing the effect of the cultivar (***: $p < 0.001$) and the percentage of variance explained are included in the plots. Cabernet Sauvignon cultivars are shown in blue and Merlot in pink.

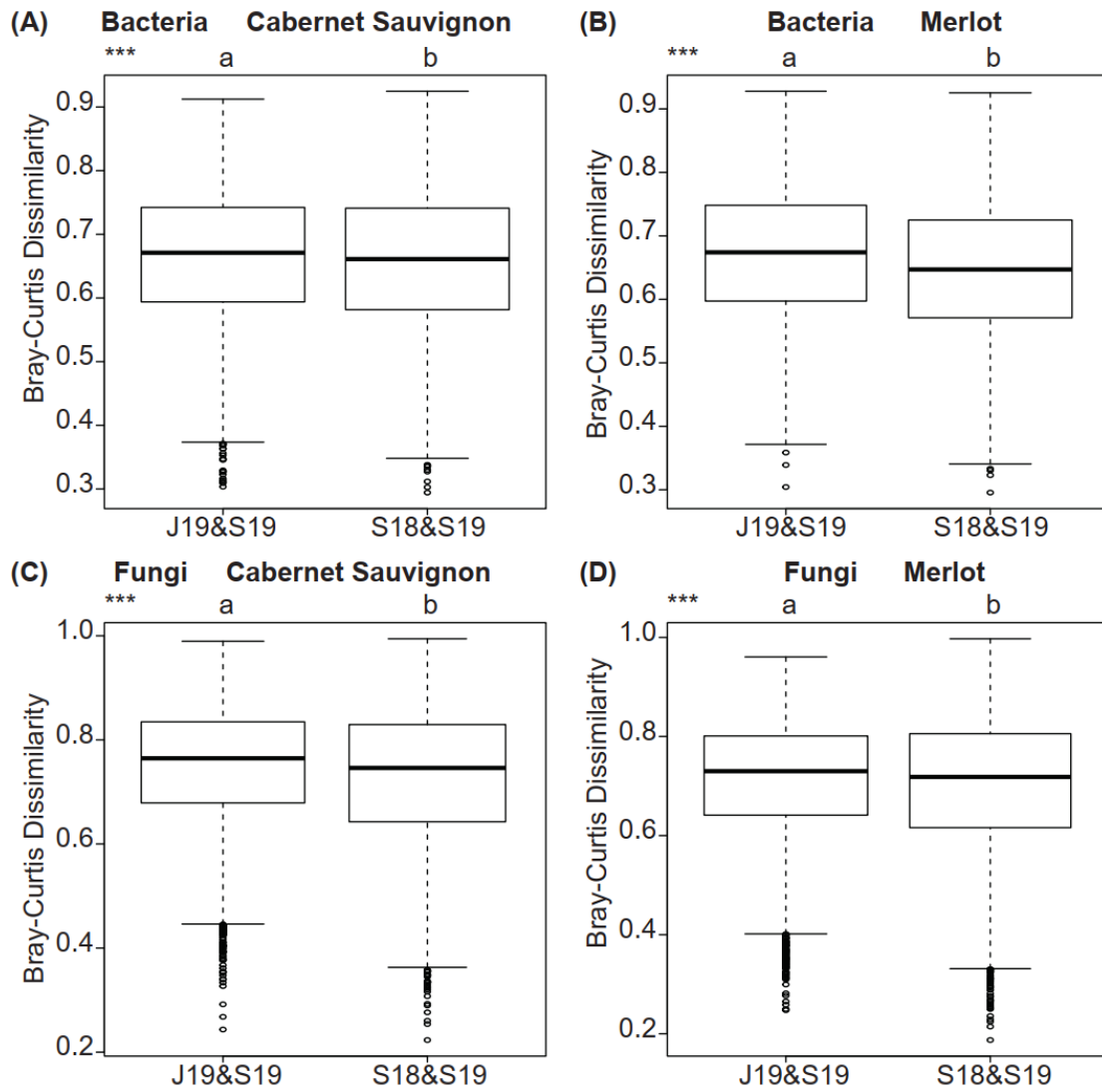


Fig. S4 Comparisons of Bray Curtis dissimilarity between intra- (J19&S19) and inter-annual (S18&S19) time points for two cultivars.

Statistical comparison was tested using Wilcoxon's rank sum tests.

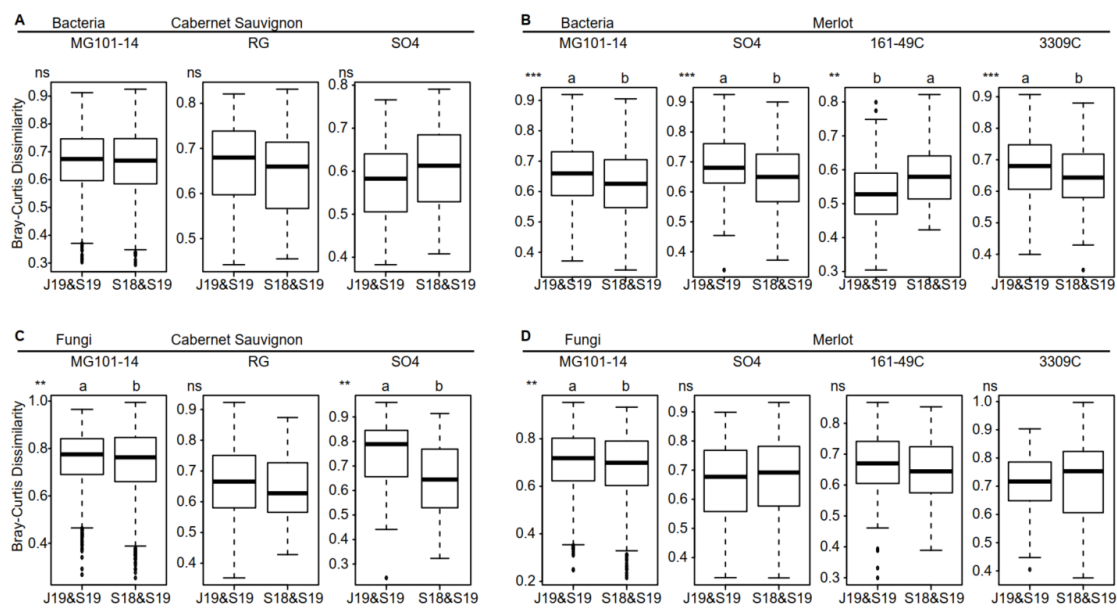


Fig. S5 Comparisons of Bray Curtis dissimilarity between intra- (J19&S19) and inter-annual (S18&S19) time-points for each combination of scion and rootstock. Statistical comparison was tested using Wilcoxon's rank sum tests.

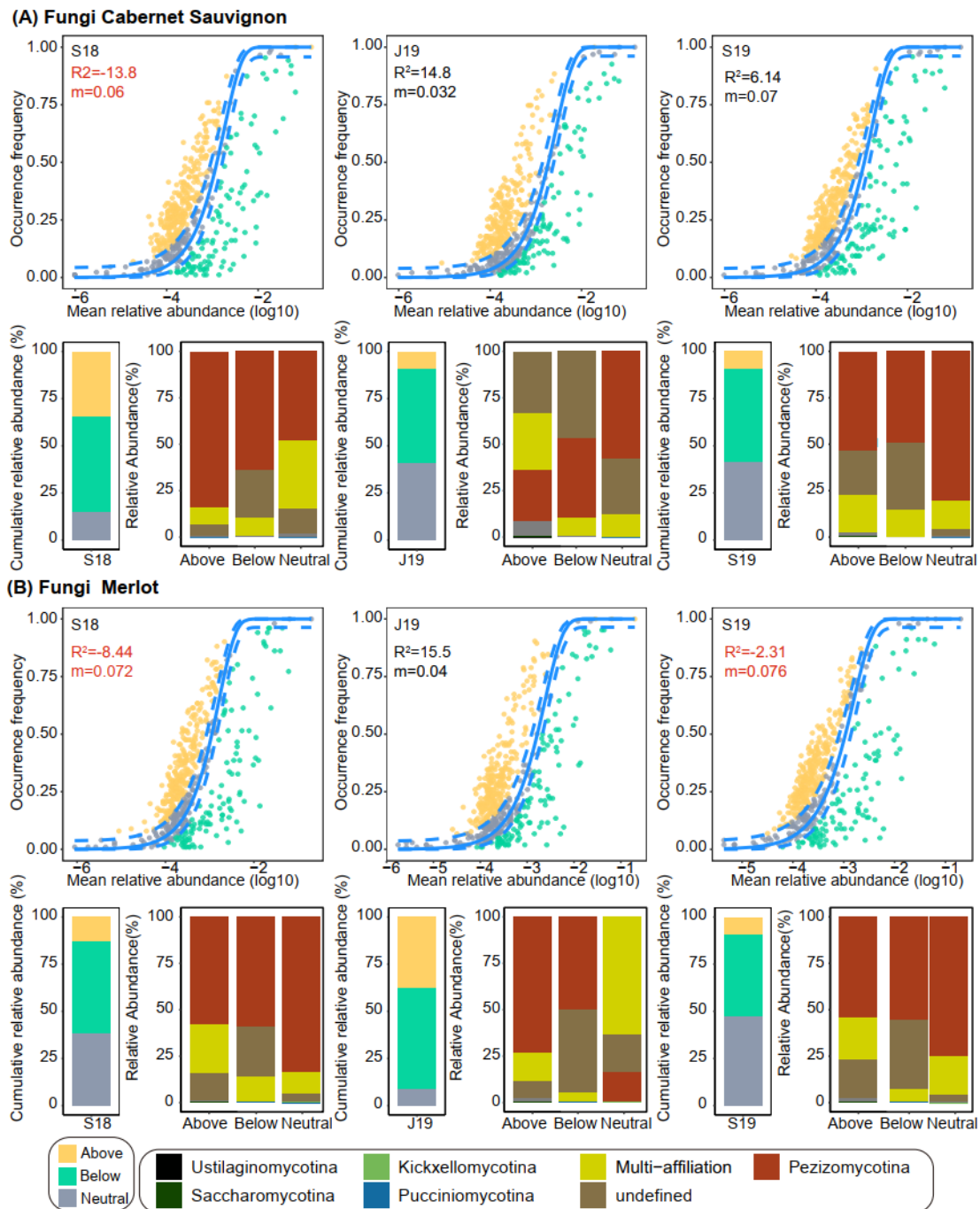


Fig. S6 Partition of deterministic and stochastic processes of fungal community assembly (neutral community model (NCM)).

(A) S18/J19/S19-Cabernet-Sauvignon and (B) S18/J19/S19-Merlot, served as the community source to create neutral models. The first graphs for each time point showed the occurrence frequencies predicted through the NCM. The sequence-clusters occurring more frequently than expected were dotted in yellow while the ones occurring less frequently were colored in green. The solid blue line indicates the best fit of the model and the dashed ones indicate 95% confidence intervals. The dashed lines indicate the envelope of neutrally. “m” (estimate rate) and R^2 ($0 < R^2 \leq 1$, adequacy of the model fitting) are indicated on the graphs. The single bar charts indicated cumulative sequence-clusters occurrence frequencies of Above, Neutral and Below partitions; the combined bar charts represent ranked cumulative relative abundance of taxonomic groups (Phylum and Sub-phylum) of the three sequence-cluster partitions

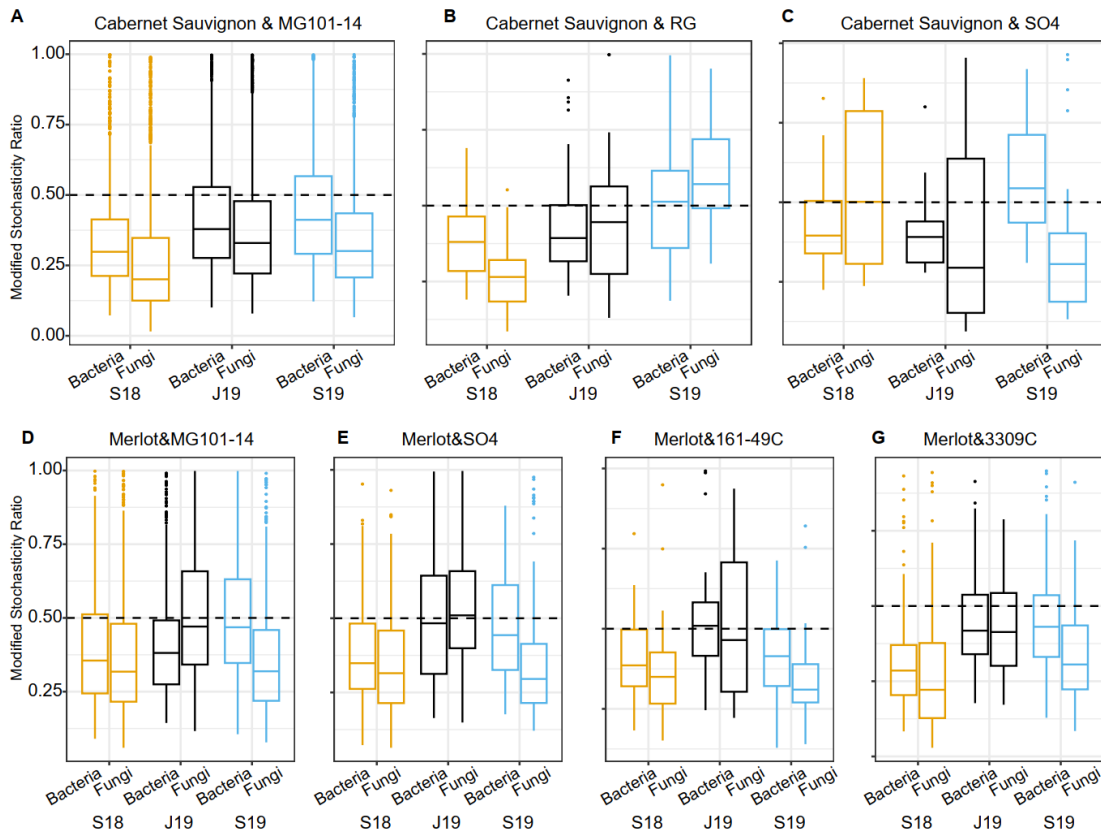


Fig. S7 Modified normalized stochasticity ratios (MST) estimates to measure the relative importance of deterministic processes of assembly for each combination of scion and rootstock.

Bar plots showed the bacterial and fungal MST values under different treatments. S18-yellow; J19-black; S19-blue: September 2019.

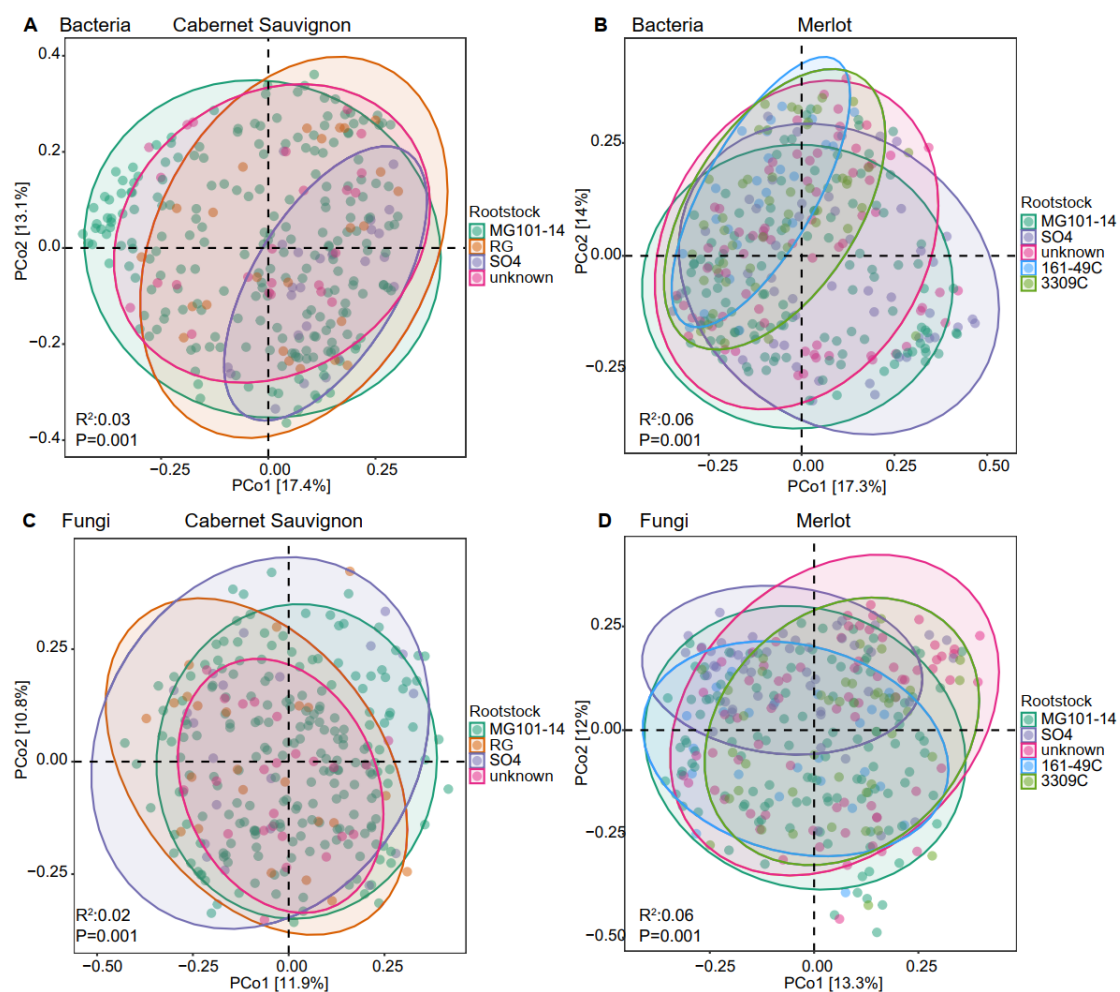


Fig. S8 Root microbiota structure of different rootstock within each cultivar.

(A, B) PCoA analysis showed the bacterial structure of different rootstocks within each cultivar. (C, D) PCoA analysis showed the fungal structure of different rootstocks within each cultivar. Ellipses in each figure represent the 95% confidence interval. Statistics indicated with R^2 and P values obtained from a PERMANOVA with the adonis2 function in R using the rootstock type as factor.

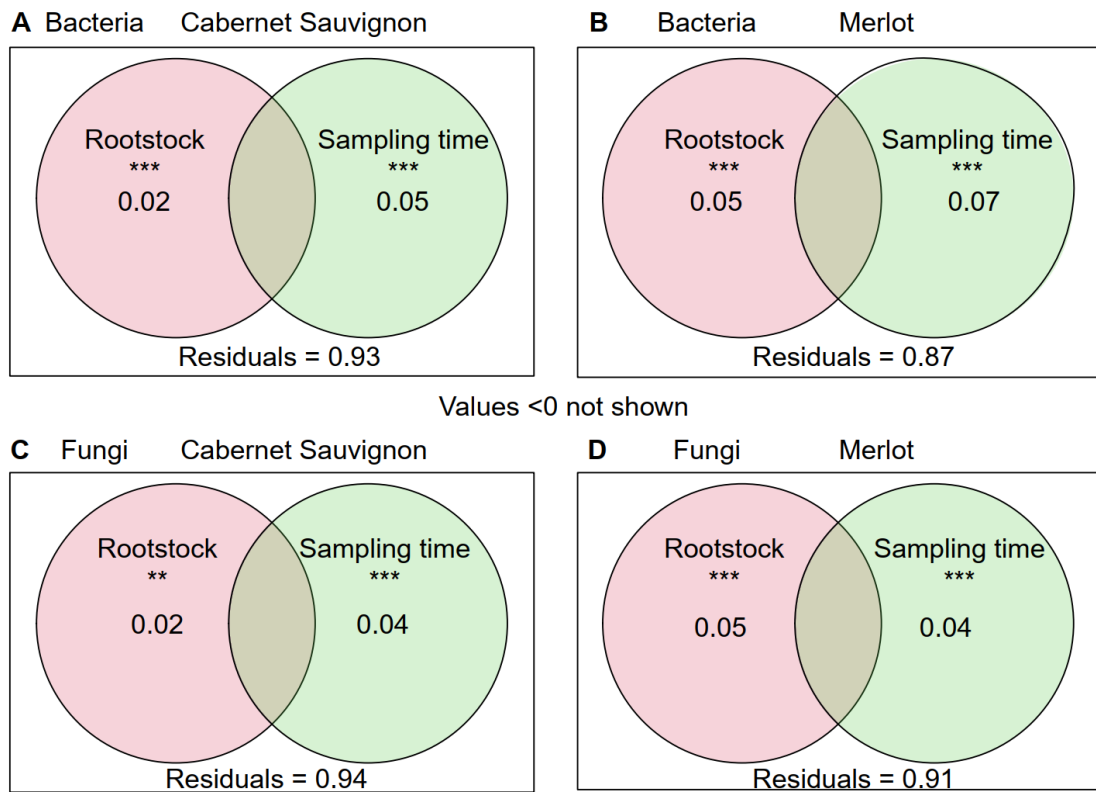


Fig. S9 Effects of rootstock, sampling time and their interaction on the microbial community composition based on variation partition analysis (VPA).

Supplementary Tables

Table S1 Information about the rootstock genotype and the cultivar of scion for the grapevine.

Field	Scion Cultivar	Rootstock genotype	Rootstock
P103	Cabernet-Sauvignon	MG101-14	Vitis riparia x Vitis rupestris
P108	Cabernet-Sauvignon	MG101-14	Vitis riparia x Vitis rupestris
P112a	Cabernet-Sauvignon	MG101-14	Vitis riparia x Vitis rupestris
P19	Cabernet-Sauvignon	MG101-14	Vitis riparia x Vitis rupestris
P31	Cabernet-Sauvignon	SO4	Vitis berlandieri x Vitis riparia (Euryale Rességuier)
P44	Cabernet-Sauvignon	MG101-14	Vitis riparia x Vitis rupestris
P51	Cabernet-Sauvignon	MG101-14	Vitis riparia x Vitis rupestris
P56	Cabernet-Sauvignon	MG101-14	Vitis riparia x Vitis rupestris
P57	Cabernet-Sauvignon	RG	Selection of Vitis riparia Michaux
P68	Cabernet-Sauvignon	unknown	unknown
P84b	Cabernet-Sauvignon	MG101-14	Vitis riparia x Vitis rupestris
P58a	Cabernet-Sauvignon	MG101-14	Vitis riparia x Vitis rupestris
P106	Merlot	MG101-14	Vitis riparia x Vitis rupestris
P35	Merlot	161-49C	Vitis riparia x Vitis berlandieri crossbreeding
P38	Merlot	MG101-14	Vitis riparia x Vitis rupestris
P42	Merlot	unknown	unknown
P47	Merlot	MG101-14	Vitis riparia x Vitis rupestris
P52a	Merlot	unknown	unknown
P62	Merlot	unknown	unknown
P63	Merlot	SO4	Vitis berlandieri x Vitis riparia (Euryale Rességuier)
P64b	Merlot	3309C	Vitis riparia (tomenteux) & Vitis rupestris cv. Martin
P64c	Merlot	SO4	Vitis berlandieri x Vitis riparia (Euryale Rességuier)
P69	Merlot	3309C	Vitis riparia (tomenteux) & Vitis rupestris cv. Martin
P84a	Merlot	MG101-14	Vitis riparia x Vitis rupestris
P59b	Merlot	MG101-14	Vitis riparia x Vitis rupestris

Table S2 Abiotic characteristics for each sampling field.

Values of abiotic factors are detailed for each field. One-way anova was used for testing the cultivar effect on each abiotic characteristic. OM: organic matter

Field	% OM	C/N ratio	pH	P2O5 (g/kg)	Cultivar
P103	1.85	11.69	7.73	0.075	Cabernet-Sauvignon
P108	2.22	12.18	6.3	0.066	Cabernet-Sauvignon
P112a	2.11	6.32	7.97	0.097	Cabernet-Sauvignon
P19	1.52	8.66	6.75	0.251	Cabernet-Sauvignon
P31	3.9	14.1	6.3	0.231	Cabernet-Sauvignon
P44	1.4	12.7	6.7	0.155	Cabernet-Sauvignon
P51	1.46	10.48	7.91	0.258	Cabernet-Sauvignon
P56	1.32	9.25	7.33	0.111	Cabernet-Sauvignon
P57	1.21	8.48	7.43	0.144	Cabernet-Sauvignon
P68	1.25	8.97	6.04	0.235	Cabernet-Sauvignon
P84b	1.73	12.27	7.84	0.173	Cabernet-Sauvignon
P58a	3.69	11.85	7.15	0.091	Cabernet-Sauvignon
P106	1.34	10.82	6.63	0.098	Merlot
P35	1.77	10.61	6.73	0.218	Merlot
P38	2.7	10.6	7.3	0.244	Merlot
P42	1.86	11.38	7.84	0.354	Merlot
P47	0.67	12.17	7.87	0.133	Merlot
P52a	1.5	12	7.6	0.156	Merlot
P62	1.24	9.49	7.19	0.126	Merlot
P63	1.29	7.21	8.1	0.106	Merlot
P64b	0.43	4.46	6.52	0.047	Merlot
P64c	0.97	9.25	6.27	0.048	Merlot
P69	1.29	11.03	7.01	0.127	Merlot
P84a	1.35	12.46	7.4	0.212	Merlot
P59b	1.6	9.12	6.63	0.104	Merlot
P value	0.0632	0.557	0.877	0.864	NA

Table S3. Details of the sequence clusters specific of a given sampling campaign.

The tables show unique sequence clusters on a given sampling date (S18: September 2018; J19: June 2019 and S19: September 2019) and between two sampling dates (S18/J19; S18/S19 and J19/S19). The taxonomic affiliations shown in the table are limited to the genus level. Colored names of “Cluster” indicate that the cluster is specific to one sampling date and shared between the two cultivars (Cabernet Sauvignon and Merlot) (red: bacteria specific to S18; blue: bacteria specific to J19; green: bacteria specific to S19; orange: fungi specific to S18).

Bacteria	Specific sequence clusters
Carbernet Sauvignon	
S18	Cluster_63 Proteobacteria, Gammaproteobacteria, Burkholderiales, Comamonadaceae, Ideonella
	Cluster_77 Proteobacteria, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae, Novosphingobium
	Cluster_208 Dependuntiae, Babeliae, Babeliales, Vermiphilaceae, unknown genus
	Cluster_295 Proteobacteria, Alphaproteobacteria Rhizobiales , Rhizobiaceae, Mesorhizobium
	Cluster_310 Proteobacteria, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae, Sphingopyxis
	Cluster_333 Bacteroidota, Bacteroidia, Chitinophagales, Chitinophagaceae, Ferruginibacter
	Cluster_351 Proteobacteria, Alphaproteobacteria, Caulobacterales, Hyphomonadaceae, Hirschia
	Cluster_373 Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiales Incertae Sedis, Phreatobacter
	Cluster_446 Proteobacteria, Alphaproteobacteria, Caulobacterales, Caulobacteraceae, Brevundimonas
	Cluster_469 Bacteroidota, Bacteroidia, Sphingobacteriales, Sphingobacteriaceae, Pedobacter
	Cluster_631 Bacteroidota, Bacteroidia, Flavobacteriales, Flavobacteriaceae, Flavobacterium
	Cluster_712 Proteobacteria, Gammaproteobacteria, Burkholderiales, Comamonadaceae, Methylibium
J19	Cluster_422 Bacteroidota, Bacteroidia, Flavobacteriales, Flavobacteriaceae, Flavobacterium
	Cluster_693 Bacteroidota, Bacteroidia, Sphingobacteriales, Sphingobacteriaceae, Pedobacter
	Cluster_729 Bacteroidota, Bacteroidia, Flavobacteriales, Flavobacteriaceae, Flavobacterium
	Cluster_919 Proteobacteria, Gammaproteobacteria, Burkholderiales, Comamonadaceae, Multi-affiliation
S19	none
S18/J19	Cluster_148 Bacteroidota, Bacteroidia, Flavobacteriales, Flavobacteriaceae, Flavobacterium
	Cluster_247 Proteobacteria, Alphaproteobacteria, Caulobacterales, Caulobacteraceae, Caulobacter
	Cluster_301 Bacteroidota, Bacteroidia, Flavobacteriales, Flavobacteriaceae,

	Flavobacterium
	Cluster_437 Proteobacteria, Gammaproteobacteria, Legionellales, Legionellaceae, Legionella
	Cluster_508 Proteobacteria, Alphaproteobacteria, Caulobacterales, Caulobacteraceae, Phenylobacterium
	Cluster_812 Proteobacteria, Alphaproteobacteria, Caulobacterales, Caulobacteraceae, Brevundimonas
S18/S19	Cluster_261 Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Aminobacter
	Cluster_342 Proteobacteria, Gammaproteobacteria, Enterobacterales, Enterobacteriaceae, Escherichia-Shigella
	Cluster_375 Proteobacteria, Alphaproteobacteria, Caulobacterales, Caulobacteraceae, Brevundimonas
	Cluster_414 Proteobacteria, Gammaproteobacteria, Enterobacterales, Pectobacteriaceae, Pectobacterium
	Cluster_486 Actinobacteriota, Actinobacteria, Streptomycetales, Streptomycetaceae, Streptomyces
	Cluster_533 Proteobacteria, Gammaproteobacteria, Enterobacterales, Enterobacteriaceae, Escherichia-Shigella
	Cluster_574 Actinobacteriota, Actinobacteria, Streptomycetales, Streptomycetaceae, Streptomyces
	Cluster_590 Actinobacteriota, Actinobacteria, Streptomycetales, Streptomycetaceae, Streptomyces
	Cluster_608 Bacteroidota, Bacteroidia, Sphingobacteriales, Sphingobacteriaceae, Sphingobacterium
	Cluster_627 Proteobacteria, Alphaproteobacteria, Rickettsiales, SM2D12, unknown genus
	Cluster_673 Proteobacteria, Gammaproteobacteria, Enterobacterales, Enterobacteriaceae, Kosakonia
	Cluster_677 Proteobacteria, Gammaproteobacteria, Enterobacterales, Enterobacteriaceae, Kosakonia
	Cluster_682 Bacteroidota, Bacteroidia, Chitinophagales, Chitinophagaceae, Pseudoflavitalea
	Cluster_727 Actinobacteriota, Actinobacteria, Streptomycetales, Streptomycetaceae, Streptomyces
J19/S19	Cluster_335 Bacteroidota, Bacteroidia, Chitinophagales, Chitinophagaceae, Niastella
	Cluster_636 Bdellovibrionota, Bdellovibrionia, Bdellovibrionales, Bdellovibrionaceae, Bdellovibrio
Bacteria	
Merlot	
S18	Cluster_63 Proteobacteria, Gammaproteobacteria, Burkholderiales, Comamonadaceae, Ideonella
	Cluster_119 Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium
	Cluster_208 Dependientiae, Babeliae, Babeliales, Vermiphilaceae, unknown genus
	Cluster_261 Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Aminobacter
	Cluster_301 Bacteroidota, Bacteroidia, Flavobacteriales, Flavobacteriaceae,

	Flavobacterium
	Cluster_351 Proteobacteria, Alphaproteobacteria, Caulobacterales, Hyphomonadaceae, Hirschia
	Cluster_446 Proteobacteria, Alphaproteobacteria, Caulobacterales, Caulobacteraceae, Brevundimonas
	Cluster_469 Bacteroidota, Bacteroidia, Sphingobacteriales, Sphingobacteriaceae, Pedobacter
	Cluster_605 Proteobacteria, Alphaproteobacteria, Caulobacterales, Caulobacteraceae, Asticcacaulis
	Cluster_627 Proteobacteria, Alphaproteobacteria, Rickettsiales, SM2D12, unknown genus
	Cluster_631 Bacteroidota, Bacteroidia, Flavobacteriales, Flavobacteriaceae, Flavobacterium
	Cluster_673 Proteobacteria, Gammaproteobacteria, Enterobacterales, Enterobacteriaceae, Kosakonia
J19	Cluster_399 Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Rhodobacter
	Cluster_919 Proteobacteria, Gammaproteobacteria, Burkholderiales, Comamonadaceae, Multi-affiliation
S19	none
S18/J19	Cluster_36 Proteobacteria, Gammaproteobacteria, Burkholderiales, Comamonadaceae, Acidovorax
	Cluster_333 Bacteroidota, Bacteroidia, Chitinophagales, Chitinophagaceae, Ferruginibacter
	Cluster_383 Proteobacteria, Gammaproteobacteria, Enterobacterales, Erwiniaceae, Erwinia
	Cluster_437 Proteobacteria, Gammaproteobacteria, Legionellales, Legionellaceae, Legionella
	Cluster_508 Proteobacteria, Alphaproteobacteria, Caulobacterales, Caulobacteraceae, Phenylobacterium
	Cluster_582 Proteobacteria, Gammaproteobacteria, Burkholderiales, Comamonadaceae, unknown genus
	Cluster_711 Bacteroidota, Bacteroidia, Flavobacteriales, Flavobacteriaceae, Flavobacterium
	Cluster_729 Bacteroidota, Bacteroidia, Flavobacteriales, Flavobacteriaceae, Flavobacterium
	Cluster_812 Proteobacteria, Alphaproteobacteria, Caulobacterales, Caulobacteraceae, Brevundimonas
	Cluster_948 Proteobacteria, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae, Sphingobium
S18/S19	Cluster_77 Proteobacteria, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae, Novosphingobium
	Cluster_85 Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium
	Cluster_148 Bacteroidota, Bacteroidia, Flavobacteriales, Flavobacteriaceae, Flavobacterium
	Cluster_295 Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Mesorhizobium

	Cluster_375 Proteobacteria, Alphaproteobacteria, Caulobacterales, Caulobacteraceae, Brevundimonas
	Cluster_414 Proteobacteria, Gammaproteobacteria, Enterobacterales, Pectobacteriaceae, Pectobacterium
	Cluster_574 Actinobacteriota, Actinobacteria, Streptomycetales, Streptomyetaceae, Streptomyces
	Cluster_583 Actinobacteriota, Actinobacteria, Streptomycetales, Streptomyetaceae, Streptomyces
	Cluster_608 Bacteroidota, Bacteroidia, Sphingobacteriales, Sphingobacteriaceae, Sphingobacterium
	Cluster_677 Proteobacteria, Gammaproteobacteria, Enterobacterales, Enterobacteriaceae, Kosakonia
J19/S19	Cluster_497 Bacteroidota, Bacteroidia, Flavobacteriales, Flavobacteriaceae, Flavobacterium
	Cluster_581 Bacteroidota, Bacteroidia, Sphingobacteriales, Sphingobacteriaceae, Pedobacter
Fungi	
Carbnet Sauvignon	Specific sequence clusters
S18	Cluster_196 Basidiomycota, undefined, Tremellomycetes, Tremellales, undefined, Cryptococcus
	Cluster_199 Ascomycota, Pezizomycotina, Sordariomycetes, Xylariales, Amphisphaeriaceae, Pestalotiopsis
	Cluster_201 Basidiomycota, undefined, Agaricomycetes, Agaricales, Physalacriaceae, Armillaria
	Cluster_233 Chytridiomycota, undefined, Multi-affiliation, Multi-affiliation, Multi-affiliation, Multi-affiliation
	Cluster_278 Basidiomycota, undefined, Agaricomycetes, Agaricales, Physalacriaceae, Armillaria
	Cluster_302 Basidiomycota, undefined, Agaricomycetes, Gomphales, Gomphaceae, Multi-affiliation
	Cluster_350 Ascomycota, Pezizomycotina, Sordariomycetes, Hypocreales, undefined, Fusarium
J19	Cluster_157 Ascomycota, Pezizomycotina, Pezizomycetes, Pezizales, Pyronemataceae, Tarzetta
	Cluster_253 Ascomycota, Pezizomycotina, Sordariomycetes, Diaporthales, Multi-affiliation, Multi-affiliation
	Cluster_317 Zygomycota, Mucoromycotina, undefined, Endogonales, Endogonaceae, Endogone
	Cluster_393 Basidiomycota, Ustilaginomycotina, Exobasidiomycetes, Exobasidiales, Exobasidiaceae, Exobasidium
S19	Cluster_152 Basidiomycota, undefined, Agaricomycetes, Agaricales, Physalacriaceae, Physalacria
	Cluster_231 Ascomycota, undefined, undefined, undefined, undefined, undefined
	Cluster_301 Basidiomycota, undefined, Agaricomycetes, Thelephorales, Thelephoraceae, Tomentella
	Cluster_371 Basidiomycota, undefined, Agaricomycetes, Agaricales, Multi-affiliation,

	Multi-affiliation
S18/J19	Cluster_433 Basidiomycota, undefined, Multi-affiliation
S18/S19	Cluster_241 Basidiomycota, undefined, Agaricomycetes, Agaricales, Bolbitiaceae, Agrocybe
	Cluster_268 Ascomycota, Pezizomycotina, Pezizomycetes, Pezizales, Sarcoscyphaceae, Komposocypha
	Cluster_358 Ascomycota, Pezizomycotina, Sordariomycetes, undefined, Apiosporaceae, Arthrimum
	Cluster_360 Basidiomycota, undefined, Agaricomycetes, Agaricales, Tricholomataceae, Multi-affiliation
	Cluster_406 Ascomycota, Pezizomycotina, Eurotiomycetes, Eurotiales, Trichocomaceae, Multi-affiliation
	Cluster_521 Ascomycota, Pezizomycotina, Multi-affiliation, Multi-affiliation, Multi-affiliation, Multi-affiliation
J19/S19	Cluster_194 Ascomycota, undefined, undefined, undefined, undefined, Ochroconis
	Cluster_251 Ascomycota, undefined, undefined, undefined, undefined, Anguillospora
	Cluster_368 Glomeromycota, undefined, Glomeromycetes, Diversisporales, Acaulosporaceae, Acaulospora
Fungi	
Merlot	
S18	Cluster_278 Basidiomycota, undefined, Agaricomycetes, Agaricales, Physalacriaceae, Armillaria
	Cluster_331 Ascomycota, Pezizomycotina, Sordariomycetes, Microascales, undefined, Ceratocystis
	Cluster_358 Ascomycota, Pezizomycotina, Sordariomycetes, undefined, Apiosporaceae, Arthrimum
	Cluster_388 Ascomycota, Pezizomycotina, Sordariomycetes, Multi-affiliation, Multi-affiliation
	Cluster_399 Basidiomycota, undefined, Agaricomycetes, Agaricales, Physalacriaceae, Armillaria
J19	Cluster_231 Ascomycota, undefined, undefined, undefined, undefined, undefined
	Cluster_250 Basidiomycota, undefined, Agaricomycetes, Atheliales, Atheliaceae, Cristinia
	Cluster_287 Chytridiomycota, undefined, undefined, undefined, undefined, undefined
	Cluster_368 Glomeromycota, undefined, Glomeromycetes, Diversisporales, Acaulosporaceae, Acaulospora
S19	none
S18/J19	Cluster_89 Ascomycota, Pezizomycotina, Dothideomycetes, Capnodiales, Davidiellaceae, Cladosporium
	Cluster_201 Basidiomycota, undefined, Agaricomycetes, Agaricales, Physalacriaceae, Armillaria
	Cluster_253 Ascomycota, Pezizomycotina, Sordariomycetes, Diaporthales, Multi-affiliation, Multi-affiliation
	Cluster_317 Zygomycota, Mucoromycotina, undefined, Endogonales, Endogonaceae, Endogone
	Cluster_407 Ascomycota, Pezizomycotina, Sordariomycetes, Hypocreales, undefined, Fusarium
S18/S19	Cluster_21 Ascomycota, Pezizomycotina, Sordariomycetes, Microascales, undefined,

	Ceratocystis
	Cluster_152 Basidiomycota, undefined, Agaricomycetes, Agaricales, Physalacriaceae, Physalacria
	Cluster_189 Ascomycota, Pezizomycotina, Laboulbeniomycetes, Pyxidiophorales, Pyxidiophoraceae, Pyxidiophora
	Cluster_223 Basidiomycota, Pucciniomycotina, Agaricostilbomycetes, undefined, undefined, Sporobolomyces
	Cluster_242 Ascomycota, Pezizomycotina, Pezizomycetes, Pezizales, Pyronemataceae, Multi-affiliation
	Cluster_342 Ascomycota, Pezizomycotina, Sordariomycetes, Coniochaetales, Coniochaetaceae, Multi-affiliation
J19/S19	Cluster_190 Glomeromycota, undefined, Glomeromycetes, Glomerales, Glomeraceae, undefined
	Cluster_211 Glomeromycota, undefined, Glomeromycetes, Glomerales, Glomeraceae, undefined
	Cluster_449 Ascomycota, Pezizomycotina, Sordariomycetes, Hypocreales, undefined, Fusarium