

Fig S1. Non-metric multidimensional scaling (NMDS) analysis of fungal communities based on the Bray-Curtis dissimilarity index. Data used for this analysis contain OTUs > 10 sequences. Each point represents data from a single sample. nMDS of fungal communities from treated and untreated vines (A) of all regions (B), in 2014 and 2015 (C) in different types of tissue (D).

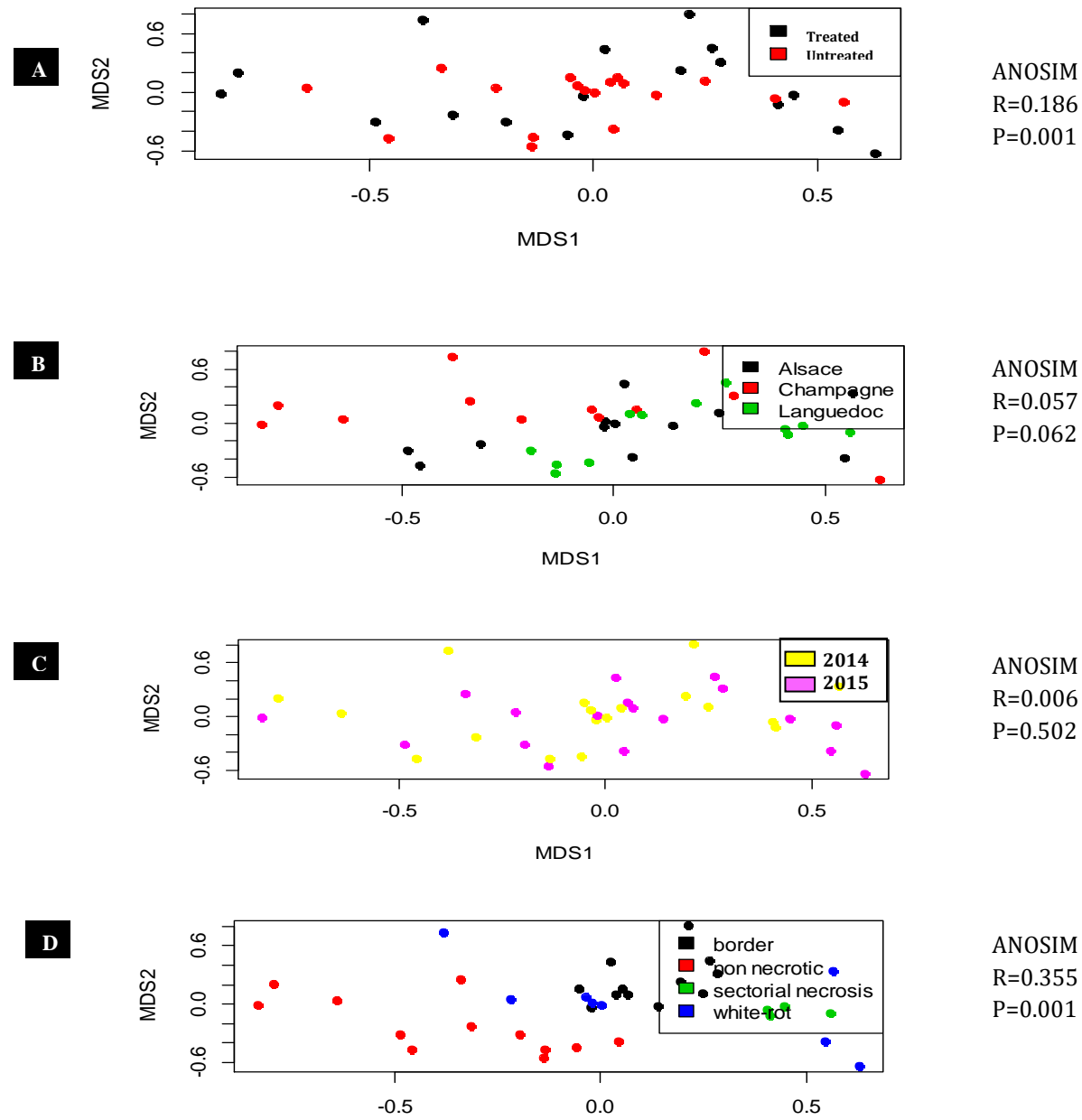


Figure S2. Non-metric multidimensional scaling (NMDS) analysis of fungal communities of untreated vines based on the Bray-Curtis dissimilarity index. Data used for this analysis contain all OTUs. Each point represents data from a single sample. Data used for this analysis contain all OTUs. nMDS of fungal communities from three regions (A) and from different types of tissues (B).

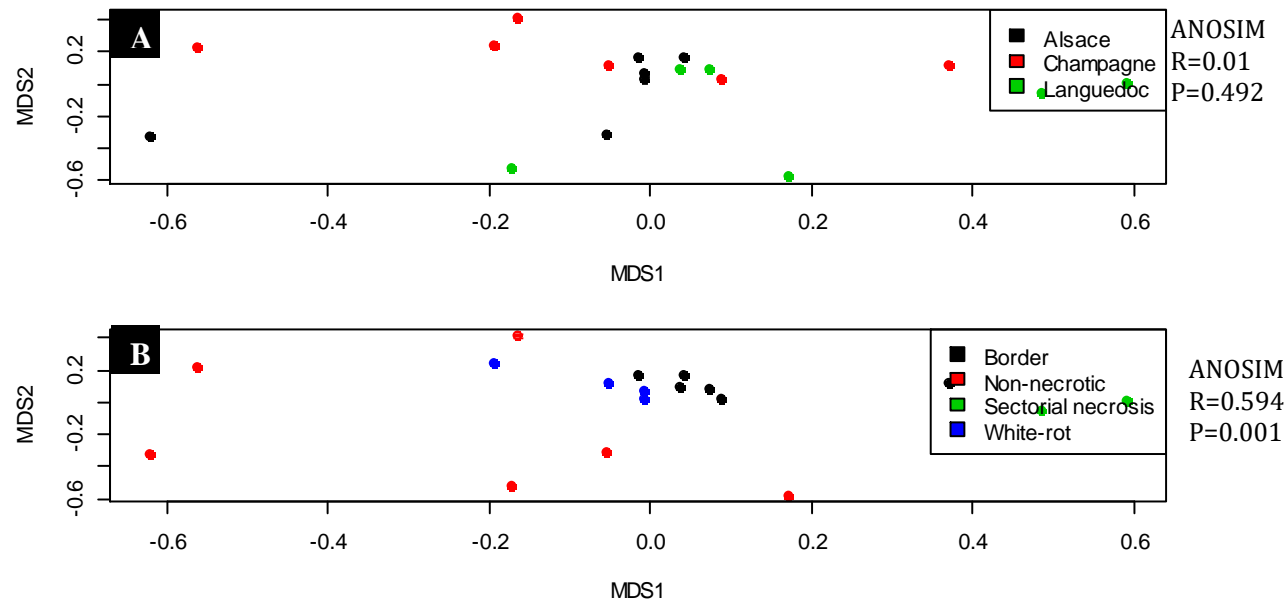


Figure S3. Non-metric multidimensional scaling (NMDS) analysis of bacterial communities of untreated vines based on the Bray-Curtis dissimilarity index. Data used for this analysis contain all OTUs. Each point represents data from a single sample. Data used for this analysis contain all OTUs. nMDS of fungal communities from three regions (A) and from different types of tissues (B).

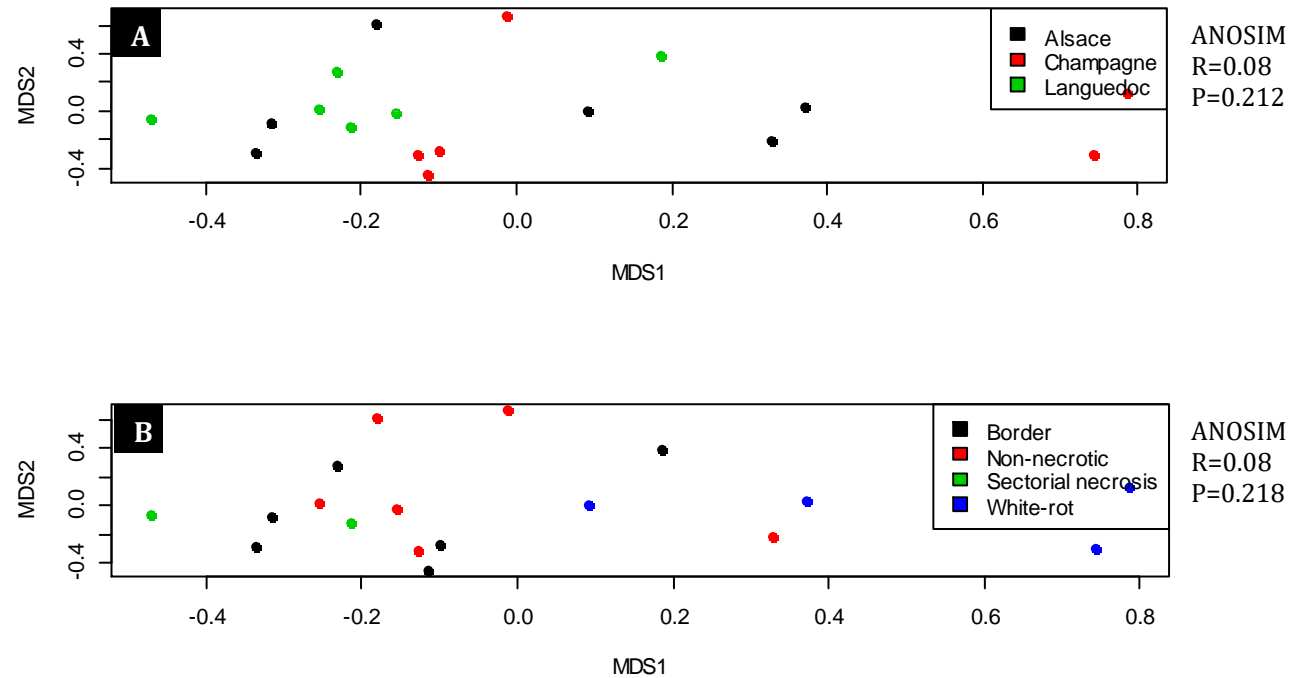


Table S1. Number of fungal and bacterial OTUs and reads per sample.

Region	Woody tissues	Year	OTUs number Bacteria	Number of reads
Alsace	non necrotic	2014	905	269102
Alsace	non necrotic	2015	1274	26607
Champagne	non necrotic	2014	1051	169588
Champagne	non necrotic	2015	1341	56452
Languedoc	non necrotic	2014	1531	67069
Languedoc	non necrotic	2015	1184	101447
Champagne	border	2014	787	66647
Champagne	border	2015	2090	119157
Alsace	border	2014	634	43405
Alsace	border	2015	1266	109393
Languedoc	border	2014	-	-
Languedoc	border	2015	1100	53123
Alsace	white-rot	2014	258	45720
Alsace	white-rot	2015	653	150876
Champagne	white-rot	2014	405	79056
Champagne	white-rot	2015	591	120819
Languedoc	sectorial necrosis	2014	1273	176102
Languedoc	sectorial necrosis	2015	1513	134858

“-“ : PCR did not work

Region	Woody tissues	Year	OTUs number Fungi	Number of reads
Alsace	non necrotic	2014	439	306871
Alsace	non necrotic	2015	389	77800
Champagne	non necrotic	2014	316	44178
Champagne	non necrotic	2015	370	88752
Languedoc	non necrotic	2014	387	53890
Languedoc	non necrotic	2015	348	53129
Champagne	border	2014	295	91815
Champagne	border	2015	249	53893
Alsace	border	2014	242	94211
Alsace	border	2015	319	89336
Languedoc	border	2014	300	96616
Languedoc	border	2015	335	103790
Alsace	white-rot	2014	230	35990
Alsace	white-rot	2015	256	72382
Champagne	white-rot	2014	178	16144
Champagne	white-rot	2015	239	57372
Languedoc	sectorial necrosis	2014	273	71638
Languedoc	sectorial necrosis	2015	263	48993

Table S2. Fungal strains isolated from grapevine woody tissues in 2015

	Region	Tissue	Arsenite
<i>Phaeomoniella chlamydospora</i>	Alsace	Black punctuation	treated
<i>Fomitiporia mediterranea</i>	Champagne	Border	untreated
<i>Eutypa lata</i>	Alsace	Sectorial necrosis	treated
<i>Trichoderma</i> sp.	Champagne	Black punctuation	treated
<i>Penicillium</i> sp. Strain 1	Champagne	Border	treated
<i>Penicillium</i> sp. Strain 2	Languedoc	Non-necrotic	treated

Table S3. Simpson and Shannon indexes of non-necrotic, border and white-rot tissues of Alsace, Champagne and Languedoc in 2014 and 2015.

Simpson (2014)	Alsace	Non-necrotic	Border	White rot
Treated	Fungi	0.42	0.11	0.62
	Bacteria	0.86	0.87	0.64
Untreated	Fungi	0.89	0.55	0.19
	Bacteria	0.70	0.98	0.95

Simpson (2014)	Champagne	Non-necrotic	Border	White rot
Treated	Fungi	0.79	0.68	0.43
	Bacteria	0.45	0.99	0.62
Untreated	Fungi	0.53	0.37	0.32
	Bacteria	0.09	0.98	0.84

Simpson (2014)	Languedoc	Non-necrotic	Border	Sectorial necrosis
Treated	Fungi	0.91	0.76	0.76
	Bacteria	0.98	-	0.87
Untreated	Fungi	0.91	0.45	0.67
	Bacteria	0.92	0.80	0.97

Simpson (2015)	Alsace	Non-necrotic	Border	White rot
Treated	Fungi	0.85	0.65	0.78
	Bacteria	0.99	0.84	0.59
Untreated	Fungi	0.69	0.60	0.24
	Bacteria	0.79	0.96	0.79

Simpson (2015)	Champagne	Non-necrotic	Border	White rot
Treated	Fungi	0.81	0.77	0.56
	Bacteria	0.98	0.98	0.76
Untreated	Fungi	0.74	0.36	0.13
	Bacteria	0.99	0.99	0.77

Simpson (2015)	Languedoc	Non-necrotic	Border	Sectorial necrosis
Treated	Fungi	0.84	0.64	0.79
	Bacteria	0.35	0.94	0.96
Untreated	Fungi	0.89	0.41	0.85
	Bacteria	0.98	0.69	0.99

Shannon (2014)	Alsace	Non-necrotic	Border	White rot
Treated	Fungi	1.04	0.43	1.53
	Bacteria	2.51	3.4	1.39
Untreated	Fungi	2.89	1.24	0.57
	Bacteria	1.73	4.98	4.40

Shannon (2014)	Champagne	Non-necrotic	Border	White rot
Treated	Fungi	2.64	1.43	1.17
	Bacteria	1.59	4.87	1.34
Untreated	Fungi	1.26	0.90	0.99
	Bacteria	0.37	5.24	2.37

Shannon (2014)	Languedoc	Non-necrotic	Border	Sectorial necrosis
Treated	Fungi	3.06	1.70	1.80
	Bacteria	5.40	-	3.27
Untreated	Fungi	3.19	1.01	1.60
	Bacteria	4.28	2.63	4.77

Shannon (2015)	Alsace	Non-necrotic	Border	White rot
Treated	Fungi	2.60	1.52	1.79
	Bacteria	5.94	3.39	1.59
Untreated	Fungi	2.14	1.57	0.66
	Bacteria	2.13	4.45	2.33

Shannon (2015)	Champagne	Non-necrotic	Border	White rot
Treated	Fungi	2.16	1.83	1.51
	Bacteria	5.50	5.51	1.97
Untreated	Fungi	2.38	0.92	0.44
	Bacteria	6.25	5.86	2.15

Shannon (2015)	Languedoc	Non-necrotic	Border	Sectorial necrosis
Treated	Fungi	2.73	1.36	2.03
	Bacteria	1.60	4.52	4.48
Untreated	Fungi	3.17	0.94	2.21
	Bacteria	5.36	1.93	5.51

Table S4. Statistical results of the Kruskal-Wallis tests for the 20 most abundant fungal species. In yellow, the statistics showed significant differences.

Kruskal_Wallis test (non parametrique)	<i>Alternaria spp.</i>	<i>Aspergillus spp.</i>	<i>Aureobasidium pullulans</i>	<i>Unknown Agaricales genus</i>	<i>Cladosporium spp.</i>	<i>Diplodia seriata</i>	<i>Eutypa lata</i>	<i>Fomitiporia mediterranea</i>	<i>Hypocrea lixii</i>	<i>Ionotus hispidus</i>	<i>Lepiota brunneoincarnata</i>	<i>Mucor circinelloides.</i>	<i>Mycena maurella</i>	<i>Penicillium spp.</i>	<i>Phaeoacremonium viticola</i>	<i>Phaeoacremonium chlamydosporum</i>	<i>Phaeoacremonium fraxinopennysylvanicum</i>	<i>Sebacina vermifera</i>	<i>Seimatosporium vitis</i>	<i>Trichoderma atroviride</i>
Tissues	0.03 (Non-necrotic tissue differ from the other)	0,472	0.05 (Non-necrotic tissue differ from the other)	0,3491	0,043	0.018 (sectorial necrosis differ from other)	0,594	0,9182	0,238	0,453	0,453	0,75	0,88	0,632	0,147	0.006 (border from the other tissue)	0,499	0,616	0,1122	0,702
Region	0,205	0,125	0,737	0,07	0,519	0,09	0,082	0,894	0,28	0,441	0,86	0,663	0,894	0,352	0.004 (Languedoc from the other region)	0,325	0,472	0,6	0.035	0,47
Treated/Untreated	0,75	0,07	0,964	0,757	0,825	0,269	0,08	<0.001	0,401	0,026	0,03	0,543	0,02	0,475	0,691	0,894	0,724	0,5658	0,02	0,233

Table S5. Statistical results of the Kruskal-Wallis tests for the 20 most abundant bacterial genera. In yellow, the statistics showed significant differences.

Kruskal-Wallis test	<i>Ammibacterium</i> sp.	<i>Badyrhibacterium</i> sp.	<i>Brevundimonas</i> sp.	<i>Buttiauxella</i> sp.	<i>Cellulomonas</i> sp.	<i>Chryseobacterium</i> sp.	<i>Cloacibacterium</i> sp.	<i>Curto-bacterium</i> sp.	<i>Enterobacter</i> sp.	<i>Erwinia</i> sp.	<i>Methylobacterium</i> sp.	<i>Microbacterium</i> sp.	<i>Nocardia</i> sp.	<i>Pantoea</i> sp.	<i>Pseudomonas</i> sp.	<i>Raoultella</i> sp.	<i>Rhizobium</i> sp.	<i>Sodalis</i> sp.	<i>Sphingomonas</i> sp.	<i>Yersinia</i> sp.
Tissues	0.14	0.045	0.057	0.57	0.075	0.93	0.811	0.035	0.216	0.01	0.75	0.452	0.53	0.018	0.021	0.119	0.169	0.093	0.042	0.038
Region	0.125	0.1022	0.2351	0.486	0.573	0.9623	0.7545	0.064	0.732	0.3976	0.562	0.3874	0.149	0.103	0.703	0.593	0.83	0.5521	0.302	0.24
Treated/ Untreated	0.163	0.501	0.63	0.634	0.148	0.809	0.923	0.336	0.531	0.847	0.652	0.847	0.441	0.847	0.923	0.289	0.93	0.136	0.847	0.386

Table S6. ITS1 sequences of the 20 most abundant fungal OTUs identified in grapevine trunk.

In blue 18S, in purple 5.8S

#OTU-1 *Alternaria* spp. from to the *A. alternata* clade

AAGTCGTAACAAGGTCTCCGTAGGTGAACCTGCGGAGGGATCATTACACAAATATGAAGGCGGGCTGGAACCTCTCGGGGTACAGCCTTGC
TGAATTATTCACCCTTGTCTTTTTCGCTACTTCTTGTTCCTTGGTGGGTTCGCCCACCACTAGGACAAACATAAACCTTTTGTAATTGCAATCAG
CGTCAGTAACAAATTAATAATTACAACCTTTCAACAACGGATCTCTTGGTTCTGGCATCGATGAAGAACGCAGC

#OTU-2 *Aspergillus* spp. from to the *A. penicillioide*s clade

AAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGTTTGGGCGCCCCTTCTCGGGGTGTCCGTCCTCCCATCCGT
GTCTCTTTGTACCTGTTGCTTCGGCGGGGCCCGCCCTCCGTGGCCGCCGGGGGGCCTCCCTGGCCcccGGGCCCCTGCCCGCCGGAGACCTCAA
CCATGAACACTGTCTGAAGGTTGCAGTCTGAGTACCGATAGTAAAAATCGTTAAACCTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGA
AGAACGCAGC

#OTU-3 *Aurebasidium pullulans*

AAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTAAAGAGTAAGGGTGCTCAGCGCCCGACCTCCAACCTTTGTTGTTAAA
ACTACCTTGTTGCTTTGGCGGGACCGCTCGGTCTCGAGCCGCTGGGGATTTCGTCCCAGGCGAGCGCCCGCCAGAGTTAAACCAAACCTCTTGTT
ATTTAACCGGTCGTCTGAGTTAAATTTTGAATAAATCAAAACCTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGC

#OTU-4 Unknown *Agaricales* genus

AAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTATTGAATGTATTTGCAAGTTGGTTGTAGCTGGCTTCTCGGAGTATTGT
GCTCGCCACTTGCTCTACTACTTTTCCACCTGTGAACCTTTGTAGATCACGAATGAACTCTCGCCTGAAAATGGCGGTTTGAGGGACTTGTCC
CTTGATAGTTTCGTGGTCTATGTTTATATCTACCCTATGTTTGTCTTTGAATGTCTTTTAAATGGTCTTTGACCTTTAAATACTATACAACCTTTTAG
CAACGGATCTCTTGGCTCTCGCATC

#OTU-5 *Cladosporium* spp.

AAGTCGTAACAAGGTCTCCGTAGGTGAACCTGCGGAGGGATCATTACAAGTGACCCCGGTCTAACCACCGGGATGTTTATAACCTTTGTTGT
CCGACTCTGTTGCCTCCGGGGCGACCCTGCCTTCGGGCGGGGGCTCCGGGTGGACACTTCAAACCTCTTGCCTAACCTTTGCAGTCTGAGTAAAC
TTAATTAATAAATTAACCTTTTAACAACGGATCTCTTGGTTCTGGCATCGATGAAGAACGCAGC

#OTU-6 *Diplodia seriata*

AAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTTCTCGGGCTTCGGCTCGAATCTCCCACCCTTTGTGAACATA
CCTCTGTTGCTTTGGCGGCTCTTTGCCGCGAGGAGGCCCTCGCGGGCCCCCGCGCGCTTTCTGCCAGAGGACCTTCAAACCTCCAGTCAGTAA
ACGTCGACGTCTGATAAACAAGTTAATAAACTAAAACTTTCAACAACGGATCTCTTGGTTCTGGCATCGATGAAGAACGCAGC

#OTU-7 *Eutypa lata*

AAGTCGTAACAAGGTTCTCCGTTGGTGAACCAGCGGAGGGATCATTACAGAGTTACCTAACTCCAAACCCATGTGAACTTACCTATGTTGCCTC
GGCGGGGAAGCCTACCCGGTACCTACCCTGTAGCTACCCGGGAGCGAGCTACCCTGTAGCCCGCTGCAGGCCTACCCGCCGGTGGACACTTA
AACTCTTGTTTTTTTAGTGATTATCTGAGTGTTTATACTTAATAAGTTAAAACTTTCAACAACGGATCTCTTGGTTCTGGCATCGATGAAGAAC
GCAGC

#OTU-8 *Fomitiporia mediterranea*

AAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTACGAGTTGGAACGTGGAGGTTGATGCTGGTGCA^{Tatata}GTGTACATGT
GCTCGCCTTCACACTCTTCATCCACTCAACCCCTGTGCACTTTATCAGAGTTAGTAATAGTATTGTGGTGGCAGCCGTTTGTTATTTCATTGTTAG
AAGCGGGGTAACCTCTTTCTAGCAGTAGTAATAATAACAATCTTGGTTCTACTACTATTACTGTGAACACTTTGACTTTTACTTATACAAACACT
TTGCTTGTTCTTGTGAATGTGAATGCTCCTTGTGAGCGAAATACAAATATACAACTTTCAACAACGGATCTCTTGGCTCTCGCATCGATGAAG
AACGCAGC

#OTU-9 *Hypocrea lixii* (*syn Trichoderma lixii*)

AAGTCGTAACAAGGTTCTCCGTTGGTGAACCAGCGGAGGGATCATTACCGAGTTTACAACCTCCCAAACCCAATGTGAACGTTACCAAACCTGTTG
CCTCGGCGGGATCTCTGCCCCGGGTGCGTCGCAGCCCCGGACCAAGGCGCCCGGAGGACCAACCTAAAACTCTTATTGTATACC^{ccc}TCGC
GGGTTTTTTTATAATCTGAGCCTTCTCGGCGCCTCTCGTAGGCGTTTCGAAAATGAATCAAACTTTCAACAACGGATCTCTTGGTTCTGGCAT
CGATGAAGAACGCAGC

#OTU-10 *Ionotus hispidus*

AAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTATCGAGTTTTGAAGCCGGAGGCCTGTGCTGGTGCGGAAACGCACATG
TGCACGGCTTTTCGTGCTCAAATCCATTTCAAACCCCTGTGCACTTTTGAACCGGTTGAAGTTAGTAGTGAGTAACACTTTTCGACTTGCGACCTA
GTACTGCGAGTAATACTAGTAGGAGGGTCTTTTGAAGGCCCTTTCGAACGTTTGAAAGCGGGAAAACGTTAAGAGAAGAGAGGGTGAAGGCGAG
CGCTTTGACTAGTTTGTATTACAAACCCTTTTATTGTTATGTGAATGTAATGCTCCTTGTGGGCGATAATTTGTACAACCTTTCAACAACGGATCT
CTAGGCTCTCGCATCGATGAAGAACGCAGC

#OTU-11 *Lepiota brunneoincarnata*

AAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTATTGAATAAACTTGGTGGGTTGTTGCTGGCTTCTTGGAGCATGTGCAC
GCTCATCGACTTTATCCATCCACCTGTGCACCTTCTGTAGTCTTTGAAATGAAAGCGGCTGAGCCTCGATGGGCATTTTGGCCTATCGGATGTG
AGGAATGCTTTTGTGAAGGCATGGCTCTCCTCAAAGGCCTGTGATCGTTTCTTGGACTATGTTttCCATATAACCACATAGCATGTTGTAGAATGT
ATCGGTGGGCCTCTGTGCCTATAGAACTCAATACAACCTTTCAGCAACGGATCTCTTGGCTCTCGCATCGATGAAGAACGCAGC

#OTU-12 *Mucor circinelloides*

AAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTAAATAATCAATAATTTTGGCTTGTCCATTATTATCTATTTACTGTGAAC
TGTATTATTACTTGACGCTTGAGGGATGCTCCACTGCTATAAGGATAGGCGGTGGGGATGTAAACCGAGTCATAGTCAAGCTTAGGCTTGGA
TCCTATTATTATTTACCAAAAGAATTTCAGAATTAATATTGTAACATAGACCTAAAAAATCTATAAAACAACCTTTTAACAACGGATCTCTTGGTT
CTCGCATCGATGAAGAACGCAGC

#OTU-13 *Mycena maurella*

AAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTACTGAATAACTGGAGTGTTGTAGCTGGCTTTTTCGGAGCATGTGCACGC
ATTTCAAATTCATCTTTACCACCTGTGCACTTTTGTAGACTGTGATAACTCTCAATGGTTTTTCCGTTGGATTGAAGGACTTGCGTCTAGCTGTC
TTTCGATTTACAGTCTATGTCTCATCTACTATAAAAAGTCTAGAATGTAACCTTGTGGGTCTTTTGACCTATAAAACTTATACAACTTTCAACA
ACGGATCTCTTGGCTCTCGCATCGATGAAGAACGCAGC

#OTU-14 *Penicillium* spp. from to the *P. glabrum* clade

AAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTACTGAGTGAGGGCCCTCTGGGTCCAACCTCCCACCCGTGTTTATTGTA
CCTTGTTGCTTCGGTGCGCCCGCCTACGGCCGCCGGGGGGCTTCTGCCCCCGGTCCGCGCGCACCGGAGACACTATTGAACTCTGTCTGAA
GATTGCAGTCTGAGCATAAACTAAATAAGTTAAAACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGC

#OTU-15 *Phaeocremonium viticola*

AAGTCGTAACAAGGTTCTCCGTTGGTGAACCAGCGGAGGGATCATTACAGAGTTTCATACTCCAAACCCTTTGTGAACATACCTGTTTCCGTTG
CTTCGGCAGGTCGGGGGTACCCCCCGCCGCCGGGGCCCCCTCGCGGGGTGCGCCGGCGGGCCTGCCGGAGGGGCACAAGACTCTGTAT
TTCAAAACTACCTCTCTGAGTTATCTTTACAAATAAGTAAAACCTTTCAACAACGGATCTCTTGGTTCTGGCATCGATGAAGAACGCAGC

#OTU-16 *Phaeomoniella chlamydospora*

AGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTATCGAGTCAGGGTCCTCTGGGCCCCGATCTCCAACCCTTTGTTTATCATA
CCTTTGTTGCTTTGGCAGACCCGTCCTTCGGGACCGTCGGGGGCGTTTCAGTCGCCTCTGGCCAGCGTCTGCCAGTAGCCCAACCAAAATTCTTT
GTTACATGTGACGTCTGAACGGTTCCATCAAAATCAAACCAA AACTTTCAACAACGGATCTCTTGGTTCTGGCATCGATGAAGAACGCAGC

#OTU-17 *Phaeoacremonium fraxinopennsylvanicum*

AAGTCGTAACAAGGTCTCCGTTGGTGAACCAGCGGAGGGATCATTACCGAGTCTCGTACTCCAAACCCTTTGTGAACATACCTGTTTCGTTGC
TTCGGCAGGCCCCGGGGGTCACCTCCCCGGCCCCGCCGCCGGCACCCCCCTCGCCGGGGCGCATGGCGGGCCTGCCGGAGGGGCACAGACTCTGTAT
TCAAAAACGTACCTCTCTGAGTTATCTTTACAAACAAGTAAA AACTTTCAACAACGGATCTCTTGGTTCTGGCATCGATGAAGAACGCAGC

#OTU-18 *Sebacina* spp.

AAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTAAATGAAC TTCAAGTCGGTCGTCTGTGCTGGTGGCAACACATGTGCACG
TCGGCTGCAAATCCACACACCTGTGCACCTTTGACTTTGGGATCCGCTGGTTGGCTTGTCCGACTTGCAGCTGGTTGACTTGTGTGTCGACCTG
GGTCTCAGGGTATTTTTACACATACTGAATGTAAACGGAATGTCACTGTGCATAATGCGCATAATAAC AACTTTCAACAACGGATCTCTTGGCTC
TCGCAT

#OTU-19 *Seimatosporium vitis*

AAGTCGTAACAAGGTCTCCGTTGGTGAACCAGCGGAGGGATCATTACAGAGTTATCTAACTCCCAAACCCATGTGAACTTACCATTGTTGCCT
CGGCAGAACCTACCCGGTACCTACCCTGTAACGACCTACCCTGTAGCGAGTTACCCGGGAACGGCCTACCCTGTAGCGCGCTGCCGGTGGACT
TCTAAACTCTTGTTATTTATTGTAATCTGAGCGTCTTATTTTAATAAGTCAA AACTTTCAACAACGGATCTCTTGGTTCTGGCATCGATGAAGA
ACGCAGC

#OTU-20 *Trichoderma atroviride*

AAGTCGTAACAAGGTCTCCGTTGGTGAACCAGCGGAGGGATCATTACCGAGTTTACAAC TCCCAAACCCAATGTGAACCATAACCAAACCTGTTG
CCTCGGCGGGGTACGCCCCGGGTGCGTCGCAGCCCCGGAACCAGGCGCCCGCCGGAGGGACCAACCAAACCTTTTTCTGTAGTCCCCTCGCG
GACGTTATTTCTTACAGCTCTGAGCAAAAATTCAAATGAATCAA AACTTTCAACAACGGATCTCTTGGTTCTGGCATCGATGAAGAACGCAG
C

Table S7. NCBI best BLASTN hits of the ITS1 sequences from the 20 most abundant fungal OTUs identified in grapevine trunk.

OTU	Best Hit NCBI	ID NCBI	Query coverage	E value	Identity %
1	<i>Alternaria</i> spp. from to the <i>A. alternata</i> clade	MT556702.1	100	1,00E-131	100
2	<i>Aspergillus</i> spp. from to the <i>A. penicillioides</i> clade	KF800460.1	100	3,00E-148	100
3	<i>Aurebasidium pullulans</i>	MT573468.1	100	7,00E-140	100
4	Unknown <i>Agaricales</i> genus	LC205406.1	100	6,00E-131	99
5	<i>Cladosporium</i> spp.	MT852065.1	100	1,00E-126	100
6	<i>Diplodia seriata</i>	MT587389.1	100	4,00E-137	100
7	<i>Eutypa lata</i>	MN433694.1	100	7,00E-145	100
8	<i>Fomitiporia mediterranea</i>	AY780427.1	100	0	100
9	<i>Hypocrea lixii</i>	KY554996.1	100	4,00E-152	100
10	<i>Ionotus hispidus</i>	FR686562.1	96	0,00E+00	99
11	<i>Lepiota brunneoincarnata</i>	KT002153.1	100	0	99
12	<i>Mucor circinelloides</i>	MG554336.1	100	3,00E-154	99
13	<i>Mycena maurella</i>	JF908413.1	100	8,00E-160	99
14	<i>Penicillium</i> spp. from to the <i>P. glabrum</i> clade	MT441616.1	100	5,00E-136	100
15	<i>Phaeocremonium viticola</i>	MN209190.1	98	4,00E-137	100
16	<i>Phaeomoniella chlamydospora</i>	KP887017.1	100	2,00E-141	100
17	<i>Phaeoacremonium fraxinopennsylvanicum</i>	MH862855.1	99	2,00E-139	100
18	<i>Sebacina</i> spp.	EU910901.1	95	1,00E-127	96
19	<i>Seimatosporium vitis</i>	NR_156595.1	98	2,00E-144	100
20	<i>Trichoderma atroviride</i>	AF456917.1	100	4,00E-144	100