



Fig. S1. Sampling locations and aerial view of the inactive resin industry, linked to Fig. 1. (A) Aerial view of the resin industry, marking the forest soil sampling site (circle in red) in an open area near *Pinus* trees and other vegetation in the vicinity of the industry, as well as the location of resinous soil sampling (red marker) within the resin processing pavilion. **(B)** Front entrance of the 50-year-old abandoned resin factory, showing structures that remain partially intact, including sections of the ceilings and walls. **(C)** Subsamples of forest soil collected from the sampling site, which were combined to create a composite soil sample for subsequent analysis.

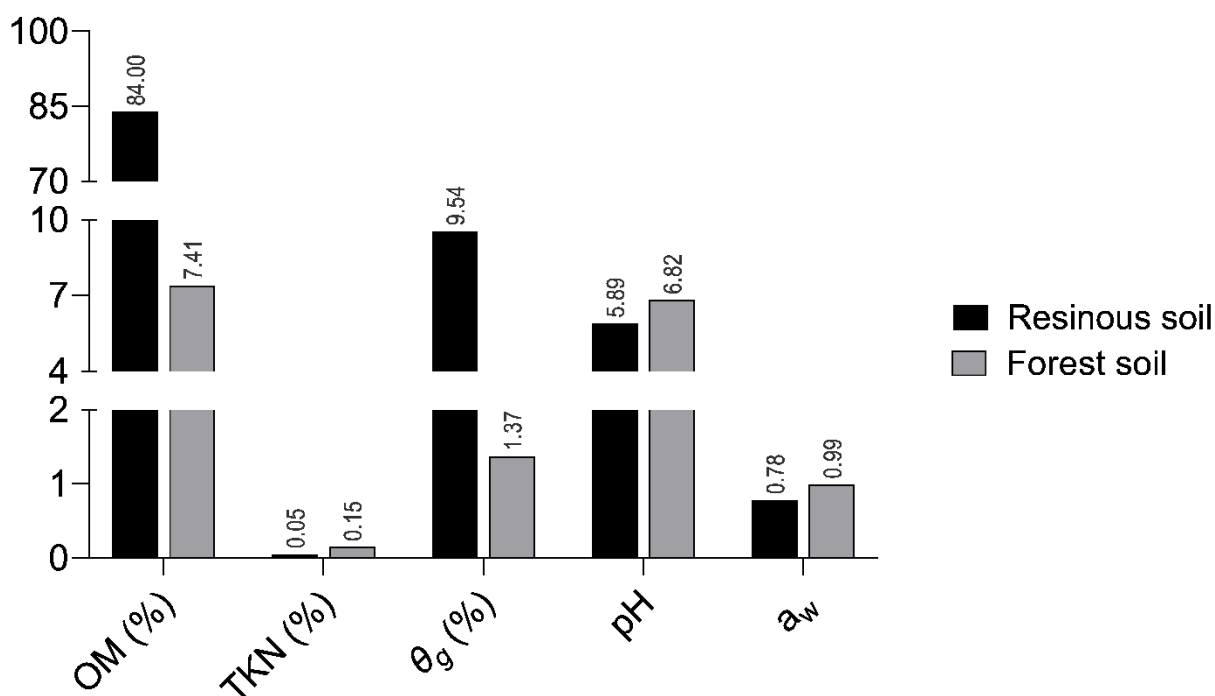


Fig. S2. Physicochemical properties of resinous soil (RS) and forest soil (FS). pH, gravimetric water content (θ_g), total Kjeldahl nitrogen (TKN), organic matter (OM), and water activity (a_w) were determined following ISO and EN standards (see Methods). RS was moderately acidic (pH 5.9), extremely rich in organic matter (84%), and nitrogen-poor (0.05%), reflecting the resin chemical imprint, whereas FS exhibited typical values for *Pinus* soils (7.4% OM, 0.15% TKN). RS retained considerably higher humidity (95.4 g·kg⁻¹) than FS (13.8 g·kg⁻¹), although its water activity was lower (0.78 vs. 0.90), indicating that much of the retained water is not freely available for microbial activity and thus may favour extremotolerant taxa. Graphs were produced in GraphPad Prism version 9.0.0 (GraphPad Software, LLC, 2020; San Diego, CA, USA). Software available at: <https://www.graphpad.com>.

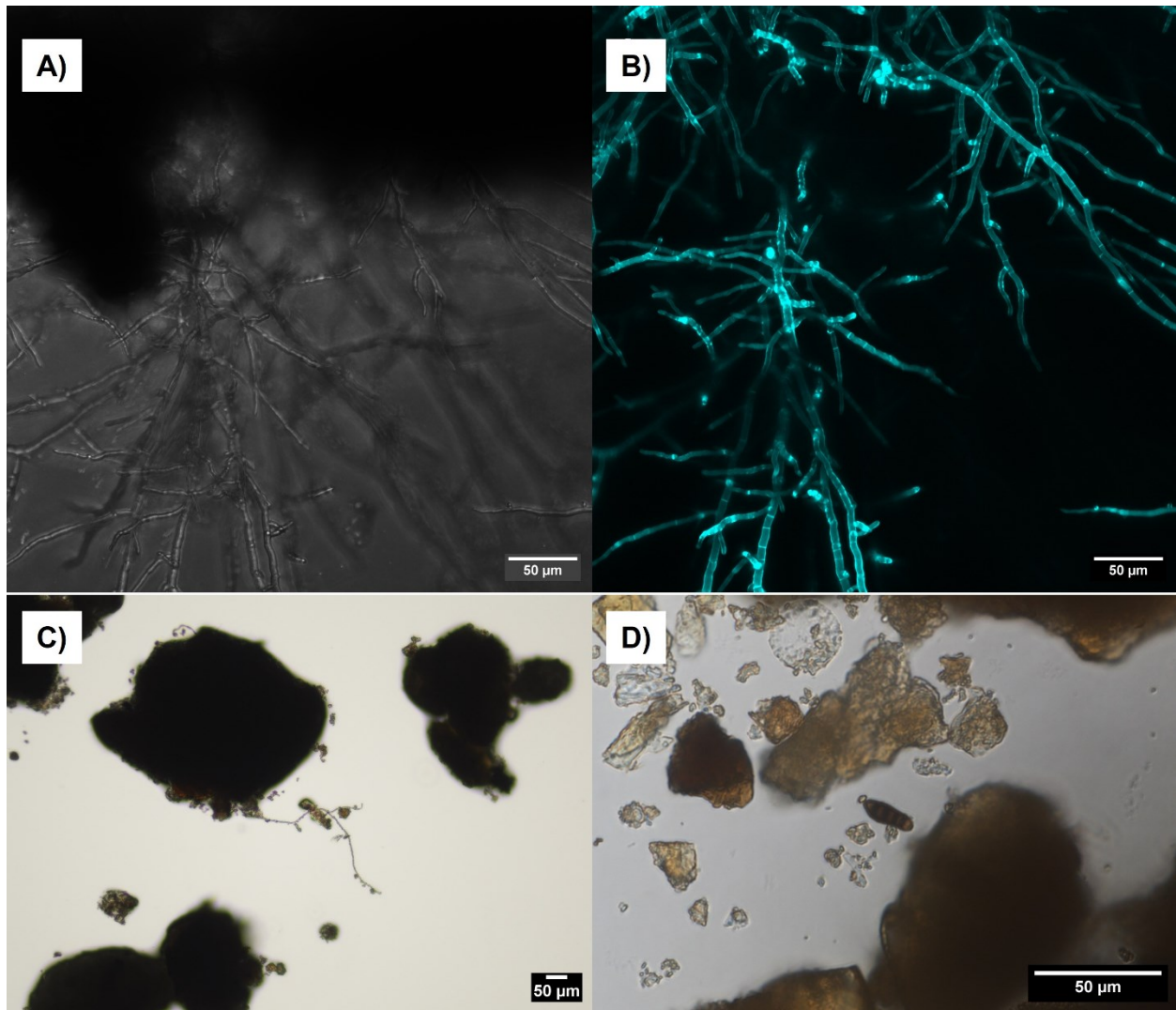


Fig. S3. Confocal and light microscopy imaging of fungal growth from resinous soil particles.

These analyses were performed to validate the SEM observations shown in Fig. 2 and to confirm that fungal material present in the resinous soil remained viable for growth. Resinous soil samples (~0.5 g) were incubated in 8-well IBIDI chamber slides containing semi-solid MEA for up to 48 h (30 °C, dark). Samples were either directly visualised by light microscopy or stained with calcofluor white for confocal analysis. **(A-B)** Confocal microscopy images show fungal hyphae emerging from resinous soil particles, **(A)** visible as dark spots and **(B)** hyphae stained with calcofluor white and displayed in cyan using a Look-Up Table (LUT) in Fiji. Confocal Z-series stacks (step size 200 nm) were acquired on a Zeiss LSM 880 point scanning confocal microscope with an Airyscan detector, using a 63× Plan-Apochromat 1.4 NA DIC oil immersion objective (Zeiss) and 405, 488, and 561 nm laser lines. Image acquisition and Airyscan processing were

performed with Zeiss Zen 2.3 (black edition). **(C–D)** Light microscopy confirmed the confocal observations, with **(C)** showing hyphal development around resinous soil particles after 24 h of incubation; **(D)** depicts the morphology of the resinous soil matrix under transmitted light, including a structure resembling a putative fungal spore. Light microscopy was performed with an inverted phase-contrast fluorescence microscope (Eclipse Ts2-FL, Nikon) equipped with a 5.9 MP CMOS camera (IZAZA). Scale bar: 50 μm .

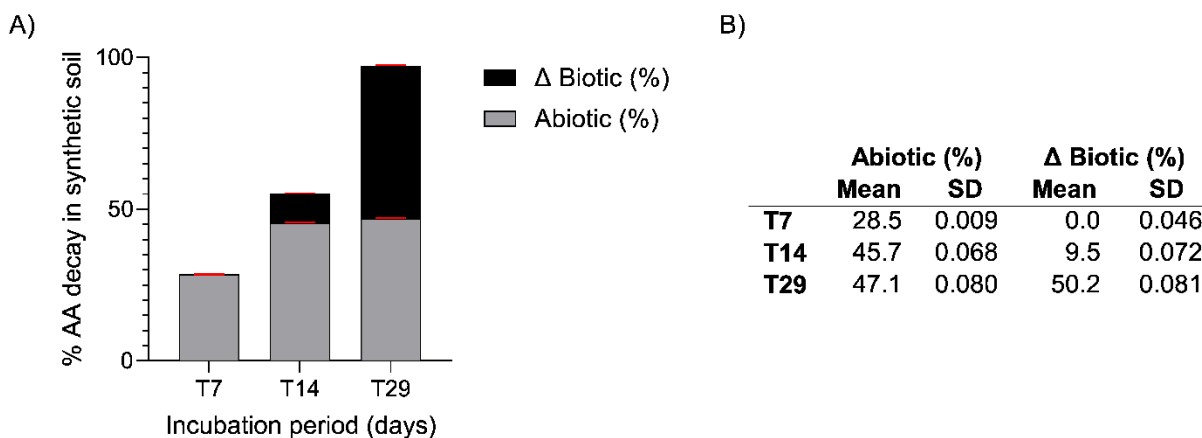


Fig. S4. Abiotic and biotic decay of abietic acid (AA) in synthetic soil. Results demonstrate that microbial activity was fundamental for the depletion of AA (abietic acid) under the tested laboratory conditions. **(A)** Stacked bar plot showing abiotic degradation (grey) and the effective biotic contribution (Δ , black) to AA decay at 7, 14 and 29 days of incubation. Bars represent mean values ($n = 3$); error bars (red) show standard deviations. **(B)** Table summarising mean $\pm$ SD values for abiotic degradation and Δ . AA degradation was assessed in synthetic soil (sand, kaolinite, bentonite, CaCO_3 and humic acid) spiked with AA ($0.12 \text{ mg} \cdot \text{g}^{-1}$) and inoculated with a peptone water extract of the resinous soil microbial community. Abiotic controls were incubated in parallel. Biotic degradation became evident after 14 days and exceeded 50% total AA loss by day 29, whereas no additional decay occurred in abiotic controls beyond day 14. Graphs were produced in GraphPad Prism version 9.0.0 (GraphPad Software, LLC, 2020; San Diego, CA, USA). Software available at: <https://www.graphpad.com>.

Table S1. Sequencing quality metrics and clustering outcomes for resinous and forest soil samples. Resinous soil datasets RS1 and RS2 (each with three biological replicates, RS.I–III), their merged dataset (RS), and forest soil samples (FS; two biological replicates, FS.I–II) are shown. Metrics before and after quality filtering with fastp include total reads (M, millions), base counts (Mbp, millions of base pairs), quality scores (Q20, Q30, %), GC content (GC, %), duplication rates (DR1, DR2, %), low-quality reads (LQR, %), adapter contamination (AC, %), and overlap failure rates (OF, %). Clustering results from SEED2.1 are also reported: most abundant sequence count (ASC), sequence length range (SLR, bp), and number of clusters (CL). Data are presented as total values, mean and standard deviations across replicates.

Sequencing results								Merge pair-end reads and quality filtering								Processing and analyses			
	Soil Sample	Reads (M)	Bases (Mbp)	Q20 (%)	Q30 (%)	GC (%)	DR1 (%)	Reads (M)	Bases (Mbp)	Q20 (%)	Q30 (%)	GC (%)	DR2 (%)	LQR (%)	AC (%)	OF (%)	ASC	SLR (bp)	CL
RS1	I	53.1	14.97	90.24	81.51	51.95	26.67	22.4	5.53	97.76	93.2	51.1	26.67	3.12	0.117	15.9	65 188	107 - 299	476
	II	45.1	12.18	91.42	83	52.07	32.8	19.5	6.02	98.12	93.45	51	32.8	3.35	0.115	16.3			
	III	55.2	14.97	90.51	82	51.89	32.93	23.9	6.83	98.22	93.51	51	32.93	3.42	0.087	16.75			
	Total	153.5	42.12					65.8	18.38										
	Mean ± SD	51.1±5.3						21.9±2.2											
RS2	I	67.6	10.12	89.99	80.42	51.95	33.62	28.3	4.26	97.77	92.91	51	33.62	2.95	0.117	16.25	53 779	117 - 299	341
	II	38.7	12.18	90.24	81.51	52.08	25	15.9	5.53	97.95	93.2	51.1	25	2.84	0.115	16.5			
	III	100.0	25.67	90.27	80.77	51.79	30.56	41.6	10.99	97.97	93.35	51	30.56	2.66	0.087	17.74			
	Total	206.3	47.97					85.7	20.78										
	Mean ± SD	68.8±30.7						28.6±12.9											
RS	RS																119 027	107 - 299	620
FS	I	120.1	36.16	86.54	76.61	58.94	4.72	34.4	10.18	98.22	93.51	57.4	4.72	3.88	0.294	41.17	-	-	-
	II	111.5	33.57	85.92	75.76	59.53	3.4	28.6	8.49	97.93	92.65	58	3.4	4.12	0.291	47.47	-	-	-
	Total	231.7	69.73					63.0	18.67								60 809	114 - 402	511
	Mean ± SD	115.8±6.1						31.5±4.1											

Table S2 (Supplementary file S1 - Excel file). Taxonomic classification of OTUs in the RS1 resinous soil dataset. OTUs were derived from ITS2 sequences and assigned using the UNITE+INSD fungal reference dataset (DOI: 10.15156/BIO/2959330). The table reports OTU IDs, type, sequence abundance (including replicates S3I–S3III), accession numbers, UNITE Species Hypotheses (SH), alignment statistics, and putative taxonomy (kingdom to species). Empty fields indicate OTUs that passed ITS2 extraction but lacked a UNITE match.

Table S3 (Supplementary file S2 - Excel file). Taxonomic classification of OTUs in the RS2 resinous soil dataset. OTUs were derived from ITS2 sequences and assigned using the UNITE+INSD fungal reference dataset (DOI: 10.15156/BIO/2959330). The table reports OTU IDs, type, sequence abundance (including replicates S3I–S3III), accession numbers, UNITE Species Hypotheses (SH), alignment statistics, and putative taxonomy (kingdom to species). Empty fields indicate OTUs that passed ITS2 extraction but lacked a UNITE match.

Table S4. Tests of normality and homogeneity of variance for alpha diversity metrics in resinous soil datasets RS1 and RS2. Shapiro–Wilk test p -values are shown for each dataset (RS1, RS2), and Levene’s test p -values are shown for variance across datasets. Metrics with $p>0.05$ in the Shapiro–Wilk test were considered normally distributed; metrics with $p>0.05$ in Levene’s test were considered to have equal variances.

Metric	Shapiro-Wilk (p -value)		Levene's Test (p -value)
	RS1	RS2	
Richness	0.4633	0.5542	0.8674
Shannon	0.9413	0.5145	0.4189
Simpson	0.7804	0.8777	0.5484
Inverse Simpson	0.7077	0.9695	0.7364
Chao1	0.1916	0.2823	0.7492
Evenness	0.7077	0.9695	0.7364

Table S5. Summary statistics for alpha diversity indices in resinous soil datasets RS1 and RS2. The table provides the numerical values underlying the boxplots in Fig. 3A, including minimum, first quartile (Q1), median, mean, third quartile (Q3), maximum, and interquartile range (IQR) for each metric. Reported indices include observed richness (R), Shannon diversity (H'), Simpson's diversity (1-D), Inverse Simpson (1/D), Chao1 and Evenness (E).

Dataset	Metric	Min	Q1	Median	Mean	Q3	Max	IQR
RS1	R	196.0	199.0	202.0	201.7	204.5	207.0	5.5
	H'	2.903	2.947	2.99	2.988	3.03	3.07	0.08336
	1-D	0.8886	0.8935	0.8985	0.897	0.9012	0.9038	0.00763
	1/D	8.974	9.991	10.524	10.473	11.061	11.766	0.71155
	Chao1	265.0	284.6	304.1	313.4	337.6	371.0	53.0
	E	65.55	66.49	67.42	67.52	68.5	69.57	2.0092
RS2	R	216.0	237.5	259.0	260.3	282.5	306.0	45.0
	S	3.163	3.165	3.168	3.187	3.199	3.231	0.0339
	1-D	0.9061	0.9084	0.9107	0.9106	0.9129	0.915	0.00444
	1/D	10.65	10.92	11.2	11.2	11.48	11.77	0.55702
	Chao1	286.0	351.2	416.5	375.8	420.6	424.8	69.375
	E	68.18	74.18	80.17	81.7	88.46	96.75	14.2849
RS	R	288.0	303.5	319.0	322.3	339.5	360.0	36.0
	S	3.03	3.066	3.102	3.1	3.135	3.167	0.0685
	1-D	0.8965	0.9013	0.9062	0.9043	0.9082	0.9102	0.0068
	1/D	9.663	10.161	10.659	10.485	10.897	11.134	0.7358
	Chao1	382.0	430.3	478.6	476.2	523.3	568.0	93.0
	E	95.05	97.89	100.73	103.94	108.39	116.04	10.49
FS	R	358.0	360.2	362.5	362.5	364.8	367.0	4.5
	S	2.996	3.034	3.072	3.072	3.11	3.148	0.0762
	1-D	0.8568	0.8664	0.8759	0.8759	0.8855	0.8951	0.0191
	1/D	6.984	7.621	8.257	8.257	8.894	9.53	1.273
	Chao1	533.0	533.1	533.2	533.2	533.3	533.4	0.182
	E	113.7	115.9	118.1	118.1	120.3	122.5	4.395

Table S6. Alpha diversity indices for resinous and forest soil datasets. The resinous soil datasets include the independent datasets RS1 and RS2, grouped by community fraction and replicate sample, and the full RS dataset resulting from their merge. Metrics are reported for the entire fungal community (all taxa), the abundant fraction, and the rare fraction, across biological replicates (RS.I–III for RS datasets and FS.I–II for forest dataset). Indices include observed richness (R), Shannon diversity (S), Simpson diversity (1–D), inverse Simpson (1/D), Chao1 and evenness.

Dataset	Sample	Observed Richness (R)	Shannon (S)	Simpson (1-D)	Inverse Simpson (1/D)	Chao1	Evenness (E)
RS1	all taxa	I	207	3.070204	0.9038176	10.396911	67.42224
		II	202	2.903482	0.8885646	8.973813	69.57164
		III	196	2.989936	0.8985295	9.855077	65.55325
	abundant taxa	I	207	3.070204	0.903818	10.396911	67.422239
		II	202	2.903482	0.888565	8.973813	69.571643
		III	196	2.989936	0.898529	9.855077	65.55325
	rare taxa	I	17	2.426089	0.868473	7.602986	7.007164
		II	17	2.353609	0.858567	7.070486	7.22295
		III	17	2.390892	0.866107	7.468652	7.110318
RS2	all taxa	I	259	3.23061	0.9150065	11.76561	80.17062
		II	216	3.16809	0.9061171	10.65157	68.17988
		III	306	3.162802	0.9106948	11.19756	96.74965
	abundant taxa	I	18	2.5113739	0.878627	8.2390639	7.1673916
		II	18	2.4414367	0.8671719	7.5285252	7.3727081
		III	18	2.4701992	0.8757442	8.0479148	7.2868619
	rare taxa	I	241	4.1130796	0.9708375	34.290637	58.593566
		II	198	4.1857329	0.9742765	38.874928	47.303543
		III	288	4.1462705	0.9719214	35.614349	69.460012
RS	all taxa	I	319	3,1668	0,9102	11,1343	100,7312
		II	288	3,0299	0,8965	9,6628	95,0519
		III	360	3,1024	0,9062	10,6594	116,0401
	abundant taxa	I	18	2,4902	0,8755	8,0328	7,2282

Dataset	Sample	Observed Richness (R)	Shannon (S)	Simpson (1-D)	Inverse Simpson (1/D)	Chao1	Evenness (E)
	II	18	2,4104	0,8638	7,3440	171	7,4678
	III	18	2,4540	0,8732	7,8889	171	7,3349
	I	301	4,0924	0,9692	32,4766	375,1	73,5507
	rare taxa II	270	4,2027	0,9741	38,5762	306,25	64,2443
	III	342	4,1329	0,9712	34,7564	450,1	82,7504
	all taxa S2I	367	2,9956	0,8568	6,9845	533	122,5147
	S2II	358	3,1480	0,8951	9,5304	533	113,7242
	abundant S2I	17	2,0828	0,7860	4,6720	153	8,1619
	taxa S2II	17	2,2876	0,8462	6,5003	153	7,4312
	rare taxa S2I	350	4,4418	0,9773	44,0950	436	78,7973
	S2II	341	4,5118	0,9771	43,6276	421	75,5804

A)

	RS1_I	RS1_II	RS1_III	RS2_I	RS2_II	RS2_III
RS1_I						
RS1_II	0.11451102					
RS1_III	0.11551313	0.13668081				
RS2_I	0.05480617	0.14021230	0.12238025			
RS2_II	0.10892527	0.08117903	0.14036418	0.09731712		
RS2_III	0.12346845	0.14940444	0.05320770	0.10373140	0.12934816	

B)

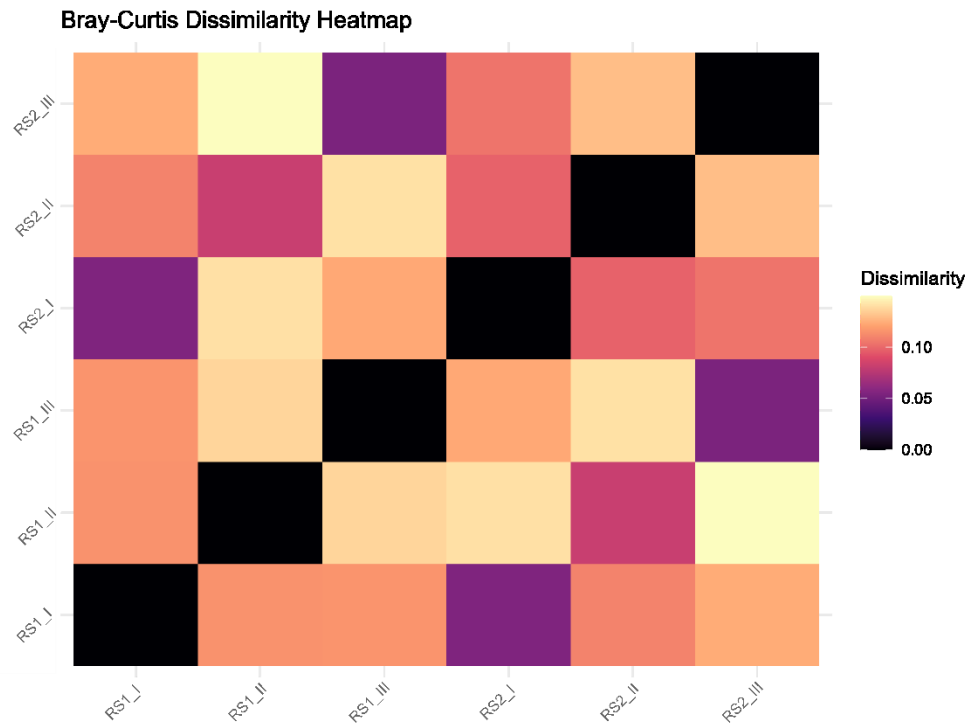


Fig. S5. Pairwise Bray–Curtis dissimilarities among fungal communities in resinous soil datasets RS1 and RS2. (A) Tabular representation of the Bray–Curtis dissimilarity matrix, showing pairwise compositional differences between replicates. Higher values indicate greater differences; diagonal values are zero, reflecting identical sample comparisons. (B) Heatmap visualisation of the same matrix, with shading intensity representing dissimilarity: darker shades correspond to higher similarity (lower dissimilarity values), while lighter shades indicate greater compositional differences.

Table S7. Shared and unique fungal genera between resinous soil datasets RS1 and RS2.

Relative abundance values are shown at the dataset level, calculated from three biological replicates, each with two technical subsamples (RS1 and RS2). The relative abundance values represent the proportion of each genus within a dataset and are expressed in scientific notation. Taxonomic assignments are provided at the genus level. Genera uniquely detected in one dataset is highlighted in grey.

Putative Taxonomic classification (genus level)	Relative abundance	
	RS1	RS2
<i>Agaricostilbales gen incertae sedis</i>	5.58E-05	6.14E-05
<i>Akanthomyces</i>	1.86E-05	1.53E-05
<i>Alternaria</i>	1.86E-05	4.60E-05
<i>Amorphotheca</i>	0.002622085	0.003896542
<i>Arcticomycetes</i>	1.86E-05	0
<i>Ascomycota gen incertae sedis</i>	1.67E-04	1.69E-04
<i>Aspergillus</i>	0.007717484	0.008728868
<i>Aureobasidium</i>	5.58E-05	7.67E-05
<i>Basidiomycota gen incertae sedis</i>	0.022259828	0.021354279
<i>Beauveria</i>	1.86E-05	0
<i>Beskidomyces</i>	1.86E-05	3.07E-05
<i>Biscogniauxia</i>	1.86E-05	6.14E-05
<i>Blastobotrys</i>	5.02E-04	6.90E-04
<i>Buckleyzyma</i>	3.16E-04	5.06E-04
<i>Candida</i>	0.04332949	0.047280091
<i>Capnobotryella</i>	0	3.07E-05
<i>Capnodiales gen incertae sedis</i>	1.49E-04	3.84E-04
<i>Capronia</i>	5.02E-04	7.36E-04
<i>Chaenotheca</i>	1.86E-05	0
<i>Chaenothecopsis</i>	1.49E-04	2.30E-04
<i>Chaetothyriales gen incertae sedis</i>	0.001320341	0.001319302
<i>Chionosphaera</i>	2.42E-04	1.23E-04

Putative Taxonomic classification (genus level)	Relative abundance	
	RS1	RS2
<i>Chionosphaeraceae gen incertae sedis</i>	0	3.07E-05
<i>Ciliolarina</i>	0.001896827	0.001825545
<i>Cladosporium</i>	0.001097185	0.001687479
<i>Claussenomyces</i>	8.00E-04	0.001840886
<i>Colacogloea</i>	0.046546658	0.045945448
<i>Coniosporium</i>	1.86E-05	3.07E-05
<i>Coniothyrium</i>	0	1.53E-05
<i>Constantinomyces</i>	0	4.60E-05
<i>Coprinellus</i>	1.86E-05	0
<i>Coprinopsis</i>	0	1.53E-05
<i>Cryptosporiopsis</i>	0	1.53E-05
<i>Cuniculitrema</i>	0	1.53E-05
<i>Cyberlindnera</i>	0	1.53E-05
<i>Cyphellophora</i>	0	1.53E-05
<i>Cyphobasidiales gen incertae sedis</i>	5.58E-05	1.23E-04
<i>Cystobasidiomycetes gen incertae sedis</i>	1.86E-05	6.14E-05
<i>Cystobasidium</i>	2.60E-04	2.15E-04
<i>Cytospora</i>	0	3.07E-05
<i>Dactylella</i>	1.12E-04	1.23E-04
<i>Debaryomyces</i>	0.034328858	0.037968275
<i>Devriesia</i>	1.86E-05	3.07E-05
<i>Dothideomycetes gen incertae sedis</i>	0.006992227	0.010078851
<i>Elixia</i>	2.60E-04	5.68E-04
<i>Eocronartium</i>	3.91E-04	6.75E-04
<i>Epicoccum</i>	1.30E-04	3.84E-04
<i>Erythrobasidiales gen incertae sedis</i>	0.001078588	0.001104532
<i>Eurotiomycetes gen incertae sedis</i>	0.269461078	0.255100789
<i>Exobasidiaceae gen incertae sedis</i>	0.001803846	0.0021477
<i>Exobasidium</i>	8.18E-04	0.001165895

Putative Taxonomic classification (genus level)	Relative abundance	
	RS1	RS2
<i>Exophiala</i>	0.023189646	0.025358206
<i>Extremaceae gen incertae sedis</i>	1.86E-05	1.53E-05
<i>Filobasidium</i>	3.72E-05	1.23E-04
<i>Fulgidea</i>	1.86E-05	1.07E-04
<i>Fungi gen incertae sedis</i>	0.060103396	0.051698217
<i>Gloniopsis</i>	1.86E-05	0
<i>Guomyces</i>	0.040502845	0.035989323
<i>Gymnoascus</i>	8.74E-04	0.00150339
<i>Hamamotoa</i>	1.86E-05	7.67E-05
<i>Helicoma</i>	0	1.23E-04
<i>Helotiales gen incertae sedis</i>	0	7.67E-05
<i>Herpotrichiellaceae gen incertae sedis</i>	9.30E-05	1.53E-04
<i>Histoplasma</i>	0	1.53E-05
<i>Hohenbuehelia</i>	5.76E-04	6.14E-04
<i>Hyaloscypha</i>	1.86E-05	0
<i>Hyaloscyphaceae gen incertae sedis</i>	0.001190166	0.001549412
<i>Hyphodontia</i>	0	1.53E-05
<i>Hypocreales gen incertae sedis</i>	3.72E-05	1.84E-04
<i>Infundichalara</i>	0.020065459	0.02331789
<i>Kondoa</i>	0	1.53E-05
<i>Kurtzmanomyces</i>	2.98E-04	3.99E-04
<i>Lecanoromycetes gen incertae sedis</i>	8.93E-04	0.001672138
<i>Leptosillia</i>	0	1.53E-05
<i>Leptospora</i>	0	1.53E-05
<i>Leucosporidium</i>	0	1.53E-05
<i>Lophium</i>	0.007661695	0.008406713
<i>Meira</i>	1.30E-04	2.45E-04
<i>Meyerozyma</i>	5.58E-05	1.53E-05
<i>Microbotryomycetes gen incertae sedis</i>	0	3.07E-05

Putative Taxonomic classification (genus level)	Relative abundance	
	RS1	RS2
<i>Mortierellales gen incertae sedis</i>	7.44E-05	1.53E-04
<i>Mucor</i>	0	1.53E-05
<i>Myriangiales gen incertae sedis</i>	0.00310559	0.003528365
<i>Mytilinidion</i>	0.006266969	0.008958979
<i>Naematelia</i>	0.002082791	0.002669285
<i>Naohidea</i>	0	1.53E-05
<i>Neocatenulostroma</i>	3.72E-05	7.67E-05
<i>Neodevriesia</i>	2.79E-04	8.74E-04
<i>Neodevriesiaceae gen incertae sedis</i>	0.002919627	0.004418127
<i>Neophaeomoniella</i>	0	1.53E-05
<i>Neophysalospora</i>	1.86E-05	0
<i>Ochrocladosporium</i>	9.30E-05	2.15E-04
<i>Ochroconis</i>	6.69E-04	6.75E-04
<i>Oidiodendron</i>	0.002473314	0.004111312
<i>Oliveonia</i>	1.86E-05	1.53E-05
<i>Paecilomyces</i>	1.86E-05	0
<i>Paraphoma</i>	0.001766653	0.002101678
<i>Paratritirachium</i>	1.86E-05	0
<i>Penicillium</i>	0.05285082	0.058095297
<i>Peniophora</i>	1.86E-05	0
<i>Petriellopsis</i>	0	1.53E-05
<i>Petrophila</i>	0	1.53E-05
<i>Pezizomycotina gen incertae sedis</i>	1.86E-05	0
<i>Phaeomoniella</i>	0.001190166	0.001902249
<i>Phallus</i>	1.86E-05	0
<i>Phialocephala</i>	0.005932235	0.008406713
<i>Pleurotus</i>	0	1.53E-05
<i>Pragmopora</i>	0.00993045	0.01305495
<i>Pringsheimia</i>	1.86E-05	0

Putative Taxonomic classification (genus level)	Relative abundance	
	RS1	RS2
<i>Pseudallescheria</i>	0	1.53E-05
<i>Pseudeurotium</i>	7.44E-05	7.67E-05
<i>Pseudomicrostroma</i>	0	1.53E-05
<i>Pseudoophiobolus</i>	0	1.53E-05
<i>Pseudopithomyces</i>	1.86E-05	0
<i>Pyronema</i>	3.72E-05	3.07E-05
<i>Rhinoclatidiella</i>	0.001320341	0.001580094
<i>Rhizopus</i>	1.86E-05	1.53E-05
<i>Rhodosporidiobolus</i>	1.86E-05	1.53E-05
<i>Rhodotorula</i>	0.016773906	0.017764551
<i>Robertozyma</i>	1.86E-04	2.45E-04
<i>Saccharomyces</i>	0	1.53E-05
<i>Saccharomycetales gen incertae sedis</i>	5.58E-05	1.84E-04
<i>Sagenomella</i>	2.05E-04	2.30E-04
<i>Sarea</i>	0.00896344	0.013791305
<i>Saxophila</i>	3.72E-05	0
<i>Scedosporium</i>	0.00503961	0.005952198
<i>Scolecobasidium</i>	1.12E-04	4.60E-05
<i>Scolecoclachnum</i>	0	1.53E-05
<i>Scutellinia</i>	1.86E-05	0
<i>Septonema</i>	8.37E-04	0.001165895
<i>Solicoccozyma</i>	1.30E-04	7.67E-05
<i>Sorocybe</i>	0.078272027	0.064292946
<i>Spizellomycetaceae gen incertae sedis</i>	1.86E-05	4.60E-05
<i>Sporidiobolaceae gen incertae sedis</i>	0	1.53E-05
<i>Sporobolomyces</i>	0.130546361	0.116635474
<i>Stemphylium</i>	0	1.53E-05
<i>Sugiyamaella</i>	7.44E-05	1.53E-05
<i>Sydowia</i>	0	3.07E-05

Putative Taxonomic classification (genus level)	Relative abundance	
	RS1	RS2
<i>Symbiotaphrina</i>	0.029140477	0.033105268
<i>Syncephalastrum</i>	0	1.53E-05
<i>Syzygospora</i>	7.44E-05	4.60E-05
<i>Talaromyces</i>	0	1.53E-05
<i>Trametes</i>	0	1.53E-05
<i>Tremellales gen incertae sedis</i>	7.44E-05	9.20E-05
<i>Trichoderma</i>	1.86E-05	4.60E-05
<i>Trichosporon</i>	1.12E-04	1.53E-05
<i>Tympanidaceae gen incertae sedis</i>	1.86E-05	1.53E-05
<i>Vishniacozyma</i>	0	1.53E-05
<i>Xenochalara</i>	1.86E-05	1.53E-05
<i>Xenopolyscytalum</i>	1.86E-05	3.07E-05
<i>Xylodon</i>	0	1.53E-05
<i>Yamadazyma</i>	2.99E-03	3.31E-03
<i>Yunzhangia</i>	6.55E-03	5.81E-03
<i>Zalaria</i>	1.30E-04	2.91E-04

Table S8 (Supplementary file S3 - Excel file). Taxonomic classification of OTUs in the RS combined resinous soil dataset. OTUs were derived from ITS2 sequences and assigned using the UNITE+INSD fungal reference dataset (DOI: 10.15156/BIO/2959330). The table reports OTU IDs, type, sequence abundance (including replicates S3I–S3III), accession numbers, UNITE Species Hypotheses (SH), alignment statistics, and putative taxonomy (kingdom to species). Empty fields indicate OTUs that passed ITS2 extraction but lacked a UNITE match.

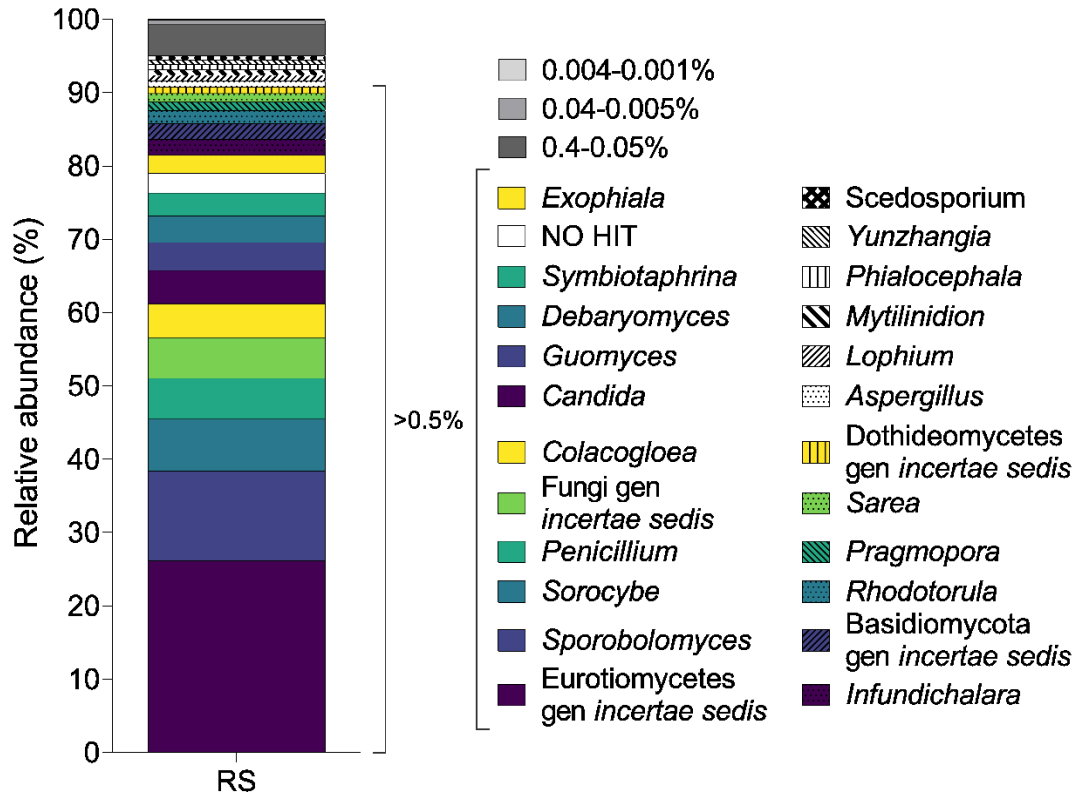


Fig. S6. Taxonomic composition and dominance structure of the resinous soil (RS) mycobiome at the genus level. Relative abundance of the most abundant fungal genera detected in the RS mycobiome, based on classified OTUs. Bars represent mean relative abundance across RS replicates, with genera ordered by decreasing abundance. The community is dominated by Ascomycota and Basidiomycota taxa, while minor phyla (e.g. Mortierellomycota, Chytridiomycota, and Mucoromycota) occur at negligible abundances. A substantial proportion of reads could not be confidently classified beyond higher taxonomic ranks, including taxa assigned to *incertae sedis* and unclassified (“no hit”) categories, highlighting pronounced taxonomic uncertainty. A small number of dominant genera, together with unclassified and *incertae sedis* taxa, account for the majority of total abundance, whereas a long tail of low-abundance genera each contributes $\leq 1\%$, illustrating the highly uneven structure of the RS fungal community. These results support Fig. 4 in the main text.

Table S9. Summary of fungal genera detected in resin-rich (RS) soil based on ITS amplicon data. All genera are listed, with a dashed line indicating the 0.5% relative abundance (RA) threshold for reference. Ecological tags for resinicolous (R), hydrocarbon-associated/degrading (HAD), and conifer-associated (CA) genera are provided. For each genus, the table also reports number of OTUs (#OTU), total RA (%), and UNITE SH scope (single vs. multiple SHs, with representative codes). Dominant OTUs are shown with best-hit species, SH code, accession, % identity, and % coverage. Species-level matches below ~98.5% ID and/or 98% coverage should be interpreted at the genus level. Gen. *incertae sedis* denotes unresolved genus placement; “No HIT” indicates OTUs without a confident match. The full OTU dataset is provided in Table S8.

Genus	Ecology tag	#OTU	RA (%)	UNITE SH scope	Dominant					
					OTU	Best-hit species	SH	Accession	%ID	%Cov
<i>Eurotiomycetes gen. incertae sedis</i>		32	26.153	M: SH0912803.10FU, SH0912804.10FU, SH0960493.10FU	OTU001	<i>Eurotiomycetes sp</i>	SH0912804.10FU	MT872624	89.3	100
<i>Sporobolomyces</i>	HAD	8	12.287	M: SH0844758.10FU, SH0911881.10FU	OTU002	<i>Sporobolomyces salmonicolor</i>	SH0844758.10FU	PP115452	100	100
<i>Sorocybe</i>	R	21	7.061	S: SH0828639.10FU	OTU003	<i>Sorocybe resinae</i>	SH0828639.10FU	EU030275	98.1	98.2
<i>Penicillium</i>	HAD	43	5.563	M: SH0767731.10FU, SH0939704.10FU, H0939673.10FU, SH0939727.10FU, H0940202.10FU, SH0940189.10FU, H0940637.10FU, SH0903477.10FU	OTU007	<i>Penicillium corylophilum</i>	SH0767731.10FU	OR069551	100	100
<i>Fungi gen. incertae sedis</i>		24	5.542	M: SH1043354.10FU, SH1015287.10FU, H1027636.10FU, SH0905231.10FU, H1015351.10FU, SH0801445.10FU, H0972129.10FU, SH0976523.10FU, SH0750559.10FU	OTU004	<i>Fungi sp</i>	SH1043354.10FU	MN071391	100	100
<i>Colacogloea</i>	CA	12	4.622	M: SH0733979.10FU, SH0734002.10FU, H0880564.10FU, SH0880564.10FU, H0733965.10FU, SH0880566.10FU, H0733979.10FU, SH0733981.10FU, H0733981.10FU, SH0880564.10FU	OTU005	<i>Colacogloea philyla</i>	SH0733979.10FU	MW710094	100	100
<i>Candida</i>	HAD	5	4.546	S: SH0892767.10FU	OTU006	<i>Candida keroseneae</i>	SH0892767.10FU	FJ235127	100	100
<i>Guomyces</i>		11	3.804	S: SH0926074.10FU	OTU008	<i>Guomyces nicotianae</i>	SH0926074.10FU	MH188916	99.6	100
<i>Debaryomyces</i>	HAD	3	3.632	S: SH0887078.10FU	OTU009	<i>Debaryomyces hansenii</i>	SH0887078.10FU	OR905858	100	100
<i>Symbiotaphrina</i>	CA	9	3.13	S: SH0950131.10FU	OTU010	<i>Symbiotaphrina microtheca</i>	SH0950131.10FU	MT813950	98.1	98.1
No HIT		48	2.675							
<i>Exophiala</i>	HAD	27	2.441	M: SH0974819.10FU, SH0904668.10FU, H0986908.10FU, SH0944003.10FU, H0904555.10FU, SH0904651.10FU, H0976639.10FU, SH0974823.10FU, H0904731.10FU, SH0976373.10FU, H0986904.10FU	OTU015	<i>Exophiala dermatitidis</i>	SH0974819.10FU	OR387067	99.5	100

Genus	Ecology tag	#OTU	RA (%)	UNITE SH scope	Dominant					
					OTU	Best-hit species	SH	Accession	%ID	%Cov
<i>Infundichalara</i>	CA	14	2.18	S: SH1012176.10FU	OTU011	<i>Infundichalara sp</i>	SH1012176.10FU	UDB03608770	100	100
<i>Basidiomycota gen. incertae sedis</i>		83	2.176	M: SH0926075.10FU, SH0964646.10FU	OTU013	<i>Basidiomycota sp</i>	SH0926075.10FU	GU062229	100	98.4
<i>Rhodotorula</i>	HAD	5	1.732	M: SH0733984.10FU, SH0946271.10FU, H0877593.10FU, SH0840832.10FU	OTU016	<i>Rhodotorula sp</i>	SH0733984.10FU	KT265804	99.6	99.1
<i>Pragmopora</i>	CA	4	1.169	M: SH0931161.10FU, SH0945270.10FU, SH0966706.10FU	OTU018	<i>Pragmopora sp</i>	SH0966706.10FU	OQ383503	100	100
<i>Sarea</i>	R	9	1.163	M: SH0737869.10FU, SH0738016.10FU, SH0965184.10FU	OTU021	<i>Sarea sp</i>	SH0737869.10FU	MT809296	100	100
<i>Dothideomycetes gen. incertae sedis</i>		4	0.868	M: SH0868844.10FU, SH0868848.10FU, SH1020519.10FU	OTU023	<i>Dothideomycetes sp</i>	SH0868844.10FU	EF434047	95.7	100
<i>Aspergillus</i>	HAD	11	0.828	M: SH0940075.10FU, SH0878054.10FU, H0888269.10FU, SH0939958.10FU	OTU027	<i>Aspergillus fumigatus</i>	SH0940075.10FU	OR752067	100	100
<i>Lophium</i>	R	5	0.806	M: SH0924980.10FU, SH0924986.10FU	OTU019	<i>Lophium mytilinum</i>	SH0924980.10FU	OM337540	99.3	98.7
<i>Mytilinidion</i>	R	3	0.773	S: SH0849718.10FU	OTU020	<i>Mytilinidion resinicola</i>	SH0849718.10FU	OM337573	98.2	100
<i>Phialocephala</i>	CA	5	0.728	S: SH0905449.10FU	OTU022	<i>Phialocephala fluminis</i>	SH0905449.10FU	MK782435	100	100
<i>Yunzhangia</i>		1	0.614	S: SH0862656.10FU	OTU024	<i>Yunzhangia sp</i>	SH0862656.10FU	OM980413	86.3	57
<i>Scedosporium</i>	HAD	1	0.554	S: SH0970687.10FU	OTU025	<i>Scedosporium sp</i>	SH0970687.10FU	OP856539	91.3	91.1
<i>Neodevriesiaceae gen. incertae sedis</i>		1	0.375	S: SH0950063.10FU	OTU028	<i>Neodevriesiaceae sp</i>	SH0950063.10FU	UDB02025080	96.2	92.9
<i>Oidiodendron</i>	HAD	4	0.339	S: SH0946103.10FU	OTU029	<i>Oidiodendron griseum</i>	SH0946103.10FU	LC639279	100	100
<i>Myriangiales gen. incertae sedis</i>		3	0.334	S: SH0915560.10FU	OTU030	<i>Myriangiales sp</i>	SH0915560.10FU	LC272919	97.5	100
<i>Amorphotheca</i>	HAD	3	0.334	S: SH0946018.10FU	OTU031	<i>Amorphotheca resinae</i>	SH0946018.10FU	LC646545	100	100
<i>Yamadazyma</i>	HAD	1	0.318	S: SH0892770.10FU	OTU032	<i>Yamadazyma tumulicola</i>	SH0892770.10FU	KY105956	100	100
<i>Naematelia</i>		3	0.24	S: SH0743871.10FU	OTU038	<i>Naematelia encephala</i>	SH0743871.10FU	MZ314474	100	100
<i>Exobasidiaceae gen. incertae sedis</i>		2	0.198	M: SH0934667.10FU, SH0934675.10FU	OTU044	<i>Exobasidiaceae sp</i>	SH0934675.10FU	KC785575	100	100
<i>Paraphoma</i>	HAD	2	0.197	M: SH0821637.10FU, SH0821638.10FU	OTU040	<i>Paraphoma fimeti</i>	SH0821638.10FU	MH864711	100	100
<i>Ciliolarina</i>		11	0.193	M: SH1012176.10FU, SH1012259.10FU	OTU043	<i>Ciliolarina sp</i>	SH1012176.10FU	UDB07674985	98.6	100
<i>Phaeomoniella</i>		4	0.158	M: SH0801449.10FU, SH0801460.10FU	OTU045	<i>Phaeomoniella sp</i>	SH0801460.10FU	OR091314	100	100
<i>Rhinocladiella</i>	HAD	2	0.147	S: SH0885672.10FU	OTU046	<i>Rhinocladiella atrovirens</i>	SH0885672.10FU	MH864788	100	100

Genus	Ecology tag	#OTU	RA (%)	UNITE SH scope	Dominant					
					OTU	Best-hit species	SH	Accession	%ID	%Cov
<i>Cladosporium</i>	HAD	2	0.144	S: SH0962330.10FU	OTU047	<i>Cladosporium cladosporioides</i>	SH0962330.10FU	PP1511174	100	100
<i>Hyaloscyphaceae</i> <i>gen. incertae sedis</i>		1	0.139	S: SH1012135.10FU	OTU048	<i>Hyaloscyphaceae sp</i>	SH1012135.10FU	OU953798	100	100
<i>Claussenomyces</i>		3	0.137	S: SH0966817.10FU M: SH0828390.10FU,	OTU049	<i>Claussenomyces sp</i>	SH0966817.10FU	UDB03126426	92.3	100
<i>Chaetothyriales gen. incertae sedis</i>		9	0.133	SH0870926.10FU, SH0944887.10FU, SH0961637.10FU, SH0961639.10FU, SH0974827.10FU, SH0986077.10FU, SH1001257.10FU	OTU056	<i>Chaetothyriales sp</i>	SH0986077.10FU	KX822546	86.8	78.7
<i>Lecanoromycetes gen. incertae sedis</i>		3	0.132	M: SH0960444.10FU, SH0960482.10FU	OTU050	<i>Lecanoromycetes sp</i>	SH0960444.10FU	LC015666	93.6	100
<i>Gymnoascus</i>		3	0.122	S: SH0875505.10FU	OTU052	<i>Gymnoascus halophilus</i>	SH0875505.10FU	MZ133732	92.5	100
<i>Septonema</i>		1	0.115	S: SH1015806.10FU	OTU054	<i>Septonema sp</i>	SH1015806.10FU	LS998796	95	100
<i>Erythrobasidiales gen. incertae sedis</i>		2	0.109	S: SH0949870.10FU	OTU057	<i>Erythrobasidiales sp</i>	SH0949870.10FU	UDB05377383	100	100
<i>Exobasidium</i>		3	0.099	S: SH0934681.10FU	OTU060	<i>Exobasidium sp</i>	SH0934681.10FU	AM901832	98.2	100
<i>Neodevriesia</i>		7	0.068	M: SH0763609.10FU, SH0763657.10FU, SH0763677.10FU, SH0763728.10FU, SH0851402.10FU	OTU066	<i>Neodevriesia fraseriae</i>	SH0763677.10FU	OX346372	98.6	100
<i>Ochroconis</i>		3	0.068	M: SH0735104.10FU, SH0735889.10FU	OTU062	<i>Ochroconis sp</i>	SH0735889.10FU	MZ573462	100	100
<i>Blastobotrys</i>		5	0.06	M: SH0843807.10FU, SH0958738.10FU	OTU070	<i>Blastobotrys arbuscula</i>	SH0843807.10FU	OU989284	100	100
<i>Hohenbuehelia</i>		1	0.06	S: SH0815720.10FU	OTU065	<i>Hohenbuehelia grisea</i>	SH0815720.10FU	OR898185	98.5	100
<i>Capronia</i>		4	0.058	M: SH0974820.10FU, SH0974837.10FU, SH0976701.10FU, SH0976908.10FU	OTU071	<i>Capronia sp</i>	SH0974820.10FU	OR091312	95.3	100
<i>Eocronartium</i>		2	0.055	S: SH0867021.10FU	OTU069	<i>Eocronartium sp</i>	SH0867021.10FU	UDB05349834	83.5	88.4
<i>Elixia</i>		2	0.043	M: SH0737941.10FU, SH0737973.10FU	OTU075	<i>Elixia flexella</i>	SH0737941.10FU	KF360373	97.1	89.1
<i>Buckleyzyma</i>		2	0.04	S: SH0947752.10FU	OTU074	<i>Buckleyzyma sp</i>	SH0947752.10FU	UDB01571240	99.5	100
<i>Kurtzmanomyces</i>		3	0.035	M: SH0841248.10FU, SH0841251.10FU	OTU078	<i>Kurtzmanomyces sp</i>	SH0841251.10FU	OR623240	100	100
<i>Capnodiales gen. incertae sedis</i>		3	0.028	M: SH0763640.10FU, SH0843083.10FU, SH0959039.10FU	OTU084	<i>Capnodiales sp</i>	SH0959039.10FU	KU580076	100	100
<i>Epicoccum</i>		2	0.027	S: SH0862152.10FU	OTU083	<i>Epicoccum nigrum</i>	SH0862152.10FU	OR762723	100	100
<i>Cystobasidium</i>		4	0.024	M: SH0964621.10FU, SH0964631.10FU, SH0964652.10FU, SH0964714.10FU	OTU116	<i>Cystobasidium calyptogenae</i>	SH0964714.10FU	OQ690209	96.5	100
<i>Robertozyma</i>		1	0.023	S: SH0964633.10FU	OTU088	<i>Robertozyma ningxiaensis</i>	SH0964633.10FU	MK050392	90.8	91.1
Dominant										

Genus	Ecology tag	#OTU	RA (%)	UNITE SH scope	OTU	Best-hit species	SH	Accession	%ID	%Cov
<i>Sagenomella</i>	R	1	0.022	S: SH0973416.10FU	OTU093	<i>Sagenomella griseoviridis</i>	SH0973416.10FU	GQ169320	100	100
<i>Zalaria</i>		1	0.022	S: SH0915545.10FU	OTU092	<i>Zalaria alba</i>	SH0915545.10FU	MW710662	100	100
<i>Meira</i>		2	0.019	M: SH0847946.10FU, SH0885763.10FU	OTU100	<i>Meira sp</i>	SH0885763.10FU	UDB019754	100	100
<i>Chaenothecopsis</i>		2	0.019	M: SH0838720.10FU, SH0843146.10FU	OTU096	<i>Chaenothecopsis sp</i>	SH0843146.10FU	OQ717810	94.2	88.7
<i>Ascomycota gen. incertae sedis</i>		3	0.018	M: SH0763728.10FU, SH0868842.10FU, SH0905238.10FU	OTU102	<i>Ascomycota sp</i>	SH0763728.10FU	MK212381	100	100
<i>Chionosphaera</i>		2	0.018	S: SH0899106.10FU	OTU099	<i>Chionosphaera cuniculicola</i>	SH0899106.10FU	OQ694453	86.4	97.7
<i>Ochrocladosporium</i>		1	0.016	S: SH0960075.10FU	OTU103	<i>Ochrocladosporium elatum</i>	SH0960075.10FU	OW985768	100	100
<i>Herpotrichiellaceae gen. incertae sedis</i>		1	0.013	S: SH0974827.10FU	OTU109	<i>Herpotrichiellaceae sp</i>	SH0974827.10FU	MG707511	99.5	100
<i>Saccharomycetales gen. incertae sedis</i>		3	0.013	S: SH0850121.10FU	OTU122	<i>Saccharomycetales sp</i>	SH0850121.10FU	MK782305	96.8	100
<i>Dactylella</i>		1	0.012	S: SH0965749.10FU	OTU110	<i>Dactylella tenuis</i>	SH0965749.10FU	DQ494360	99.4	100
<i>Hypocreales gen. incertae sedis</i>	HAD	1	0.012	S: SH0838052.10FU	OTU111	<i>Hypocreales sp</i>	SH0838052.10FU	KF780603	100	100
<i>Mortierellales gen. incertae sedis</i>		1	0.012	S: SH0846888.10FU	OTU113	<i>Mortierellales sp</i>	SH0846888.10FU	HQ611336	100	100
<i>Solicoccozyma</i>		1	0.01	S: SH0953911.10FU	OTU117	<i>Solicoccozyma sp</i>	SH0953911.10FU	OP941495	96.9	99.6
<i>Cyphobasidiales gen. incertae sedis</i>		1	0.009	S: SH0964639.10FU	OTU120	<i>Cyphobasidiales sp</i>	SH0964639.10FU	MK491201	99	100
<i>Filobasidium</i>		1	0.008	S: SH0958692.10FU	OTU125	<i>Filobasidium sp</i>	SH0958692.10FU	OP470251	90.8	100
<i>Pseudeurotium</i>		2	0.008	M: SH0881750.10FU, SH0950387.10FU	OTU139	<i>Pseudeurotium sp</i>	SH0950387.10FU	UDB0681378	100	100
<i>Scolecobasidium</i>		1	0.008	S: SH0985059.10FU	OTU126	<i>Scolecobasidium globale</i>	SH0985059.10FU	MZ503735	100	100
<i>Tremellales gen. incertae sedis</i>		1	0.008	S: SH0881288.10FU	OTU124	<i>Tremellales sp</i>	SH0881288.10FU	KF274277	100	100
<i>Cystobasidiomycetes gen. incertae sedis</i>		2	0.007	M: SH0845488.10FU, SH0950025.10FU	OTU143	<i>Cystobasidiomycetes sp</i>	SH0950025.10FU	MN654822	82.8	74.8
<i>Fulgidea</i>		1	0.007	S: SH0737922.10FU	OTU135	<i>Fulgidea sierrae</i>	SH0737922.10FU	KF360402	96.5	92.2
<i>Helicoma</i>		1	0.007	S: SH0924978.10FU	OTU132	<i>Helicoma isiola</i>	SH0924978.10FU	AB597207	99.4	100
<i>Aureobasidium</i>		3	0.007	M: SH0925964.10FU, SH1024970.10FU	OTU146	<i>Aureobasidium pullulans</i>	SH0925964.10FU	OR769498	100	100
<i>Agaricostilbales gen. incertae sedis</i>		2	0.006	M: SH0958718.10FU, SH0992159.10FU	OTU148	<i>Agaricostilbales sp</i>	SH0992159.10FU	UDB0952315	89.7	76.4
<i>Neocatenulostroma</i>		2	0.006	S: SH0843027.10FU	OTU145	<i>Neocatenulostroma sp</i>	SH0843027.10FU	UDB02020736	98.6	100
<i>Trichosporon</i>		1	0.006	S: SH0856167.10FU	OTU137	<i>Trichosporon sp</i>	SH0856167.10FU	OR378530	100	100

Genus	Ecology tag	#OTU	RA (%)	UNITE SH scope	Dominant					
					OTU	Best-hit species	SH	Accession	%ID	%Cov
<i>Hamamotoa</i>		1	0.005	S: SH0946266.10FU	OTU151	<i>Hamamotoa singularis</i>	SH0946266.10FU	KJ706356	100	100
<i>Syzygospora</i>		1	0.005	S: SH0847499.10FU	OTU147	<i>Syzygospora alba</i>	SH0847499.10FU	JN053509	95.7	96.3
<i>Biscogniauxia</i>		1	0.004	S: SH0995683.10FU	OTU158	<i>Biscogniauxia mediterranea</i>	SH0995683.10FU	OR913034	100	100
<i>Helotiales gen. incertae sedis</i>		1	0.004	S: SH0925502.10FU	OTU154	<i>Helotiales sp</i>	SH0925502.10FU	MK782308	99.3	100
<i>Sugiyamaella</i>		1	0.004	S: SH0948279.10FU	OTU157	<i>Sugiyamaella sp</i>	SH0948279.10FU	UDB07650033	92.4	92.9
<i>Beskidomyces</i>		2	0.003	S: SH0897344.10FU	OTU210	<i>Beskidomyces laricis</i>	SH0897344.10FU	OQ600167	99.3	100
<i>Coniosporium</i>		1	0.003	S: SH0905534.10FU	OTU182	<i>Coniosporium sp</i>	SH0905534.10FU	UDB04121108	92	100
<i>Constantinomyces</i>		3	0.003	M: SH0938058.10FU, SH0938147.10FU	OTU441	<i>Constantinomyces sp</i>	SH0938147.10FU	KX148023	99.3	100
<i>Extremaceae gen. incertae sedis</i>		1	0.003	S: SH0983459.10FU	OTU184	<i>Extremaceae sp</i>	SH0983459.10FU	AJ972856	97.9	100
<i>Meyerozyma</i>		1	0.003	S: SH0887053.10FU	OTU163	<i>Meyerozyma guilliermondii</i>	SH0887053.10FU	OR761551	98.4	100
<i>Pyronema</i>		1	0.003	S: SH0974277.10FU	OTU169	<i>Pyronema sp</i>	SH0974277.10FU	OR778324	100	100
<i>Spizellomycetaceae gen. incertae sedis</i>		2	0.003	M: SH0745575.10FU, SH0745609.10FU	OTU179	<i>Spizellomycetaceae sp</i>	SH0745575.10FU	UDB07378601	94.4	100
<i>Xenopolyscytalum</i>		2	0.003	S: SH1012135.10FU	OTU215	<i>Xenopolyscytalum sp</i>	SH1012135.10FU	UDB07499237	97.9	97.9
<i>Alternaria</i>	HAD	2	0.003	M: SH0856386.10FU, SH0856613.10FU	OTU185	<i>Alternaria sp</i>	SH0856386.10FU	UDB0995635	100	100
<i>Devriesia</i>	HAD	3	0.003	M: SH0950072.10FU, SH1015336.10FU	OTU465	<i>Devriesia sp</i>	SH0950072.10FU	UDB05114722	99.3	100
<i>Trichoderma</i>	HAD	1	0.003	S: SH1025978.10FU	OTU175	<i>Trichoderma euskadiense</i>	SH1025978.10FU	OR885094	100	100
<i>Akanthomyces</i>		1	0.002	S: SH0740357.10FU	OTU202	<i>Akanthomyces lecanii</i>	SH0740357.10FU	OR415647	100	100
<i>Capnobotryella</i>		1	0.002	S: SH0763614.10FU	OTU193	<i>Capnobotryella sp</i>	SH0763614.10FU	AJ972850	95.2	96.1
<i>Chionosphaeraceae gen. incertae sedis</i>		1	0.002	S: SH0958714.10FU	OTU199	<i>Chionosphaeraceae sp</i>	SH0958714.10FU	UDB01886795	82.8	76.2
<i>Cytospora</i>		1	0.002	S: SH0754434.10FU	OTU224	<i>Cytospora sp</i>	SH0754434.10FU	UDB05026986	96.1	99.4
<i>Microbotryomycetes gen. incertae sedis</i>		1	0.002	S: SH0927678.10FU	OTU231	<i>Microbotryomycetes sp</i>	SH0927678.10FU	UDB04173865	95.1	100
<i>Oliveonia</i>		1	0.002	S: SH0971208.10FU	OTU195	<i>Oliveonia sp</i>	SH0971208.10FU	UDB02410273	99	100
<i>Rhizopus</i>		1	0.002	S: SH0980336.10FU	OTU213	<i>Rhizopus sp</i>	SH0980336.10FU	UDB06512388	98.9	100
<i>Rhodosporidiobolus</i>		1	0.002	S: SH0877606.10FU	OTU230	<i>Rhodosporidiobolus poonsookiae</i>	SH0877606.10FU	OK050801	89.2	96.7
<i>Saxophila</i>		2	0.002	S: SH1015359.10FU	OTU401	<i>Saxophila tyrrhenica</i>	SH1015359.10FU	KP791764	94.3	98.6

Genus	Ecology tag	#OTU	RA (%)	UNITE SH scope	Dominant					
					OTU	Best-hit species	SH	Accession	%ID	%Cov
<i>Sydowia</i>		1	0.002	S: SH0972258.10FU	OTU222	<i>Sydowia polyspora</i>	SH0972258.10FU	OR069631	100	100
<i>Tympanidaceae gen. incertae sedis</i>		1	0.002	S: SH0946025.10FU	OTU216	<i>Tympanidaceae sp</i>	SH0946025.10FU	UDB06914778	94.4	97.9
<i>Xenochalara</i>		1	0.002	S: SH1012233.10FU	OTU204	<i>Xenochalara sp</i>	SH1012233.10FU	UDB07491230	99.3	100
<i>Arcticomyces</i>		1	0.001	S: SH0934675.10FU	OTU568	<i>Arcticomyces warmingii</i>	SH0934675.10FU	MT223780	97.1	100
<i>Beauveria</i>		1	0.001	S: SH0740100.10FU	OTU515	<i>Beauveria pseudobassiana</i>	SH0740100.10FU	OR827162	97.5	100
<i>Chaenotheca</i>		1	0.001	S: SH1009772.10FU	OTU323	<i>Chaenotheca xyloxena</i>	SH1009772.10FU	AF298138	98.7	100
<i>Coniothyrium</i>		1	0.001	S: SH0960075.10FU	OTU509	<i>Coniothyrium telephii</i>	SH0960075.10FU	PP033949	100	100
<i>Coprinellus</i>		1	0.001	S: SH1003957.10FU	OTU429	<i>Coprinellus radians</i>	SH1003957.10FU	OQ346259	99.5	100
<i>Coprinopsis</i>		1	0.001	S: SH0858492.10FU	OTU565	<i>Coprinopsis pseudonivea</i>	SH0858492.10FU	MW822599	99.5	100
<i>Cryptosporiopsis</i>		1	0.001	S: SH0966602.10FU	OTU467	<i>Cryptosporiopsis sp</i>	SH0966602.10FU	UDB04470396	99.3	100
<i>Cuniculitrema</i>		1	0.001	S: SH0912325.10FU	OTU544	<i>Cuniculitrema sp</i>	SH0912325.10FU	UDB04472691	99.4	100
<i>Cyberlindnera</i>		1	0.001	S: SH0958759.10FU	OTU305	<i>Cyberlindnera mississippiensis</i>	SH0958759.10FU	OW988561	100	100
<i>Gloniopsis</i>		1	0.001	S: SH0912800.10FU	OTU386	<i>Gloniopsis subrugosa</i>	SH0912800.10FU	MH535871	100	100
<i>Histoplasma</i>		1	0.001	S: SH0882528.10FU	OTU537	<i>Histoplasma capsulatum</i>	SH0882528.10FU	FJ897698	98.8	98.2
<i>Hyaloscypha</i>		1	0.001	S: SH0966890.10FU	OTU389	<i>Hyaloscypha sp</i>	SH0966890.10FU	UDB03470178	99.3	100
<i>Hyphodontia</i>		1	0.001	S: SH1004753.10FU	OTU548	<i>Hyphodontia subalutacea</i>	SH1004753.10FU	UDB07673531	100	100
<i>Kondoa</i>		1	0.001	S: SH0880181.10FU	OTU449	<i>Kondoa phyllada</i>	SH0880181.10FU	KY103886	91	100
<i>Leptosillia</i>		1	0.001	S: SH0762921.10FU	OTU322	<i>Leptosillia pistaciae</i>	SH0762921.10FU	OQ696196	96.8	100
<i>Leptospora</i>		1	0.001	S: SH0965249.10FU	OTU278	<i>Leptospora sp</i>	SH0965249.10FU	UDB03038609	99.4	100
<i>Leucosporidium</i>		1	0.001	S: SH1022674.10FU	OTU512	<i>Leucosporidium scottii</i>	SH1022674.10FU	OR687493	100	100
<i>Mucor</i>		1	0.001	S: SH0747765.10FU	OTU549	<i>Mucor pseudolusitanicus</i>	SH0747765.10FU	OR885026	98.9	100
<i>Naohidea</i>		1	0.001	S: SH0844762.10FU	OTU252	<i>Naohidea sebacea</i>	SH0844762.10FU	OK039352	85.8	98.6
<i>Neophaeomoniella</i>		1	0.001	S: SH0801479.10FU	OTU379	<i>Neophaeomoniella zymoides</i>	SH0801479.10FU	OP437840	100	100
<i>Neophysalospora</i>		1	0.001	S: SH0871746.10FU	OTU298	<i>Neophysalospora eucalypti</i>	SH0871746.10FU	OP315771	99.5	100
<i>Paecilomyces</i>		1	0.001	S: SH0752344.10FU	OTU287	<i>Paecilomyces divaricatus</i>	SH0752344.10FU	OM280146	98.8	100
<i>Paratritirachium</i>		1	0.001	S: SH0907362.10FU	OTU274	<i>Paratritirachium sp</i>	SH0907362.10FU	KX766170	97.2	100

Genus	Ecology tag	#OTU	RA (%)	UNITE SH scope	Dominant					
					OTU	Best-hit species	SH	Accession	%ID	%Cov
<i>Peniophora</i>		1	0.001	S: SH0734755.10FU	OTU545	<i>Peniophora sp</i>	SH0734755.10FU	OP023249	99	100
<i>Petriellopsis</i>		1	0.001	S: SH0970640.10FU	OTU553	<i>Petriellopsis sp</i>	SH0970640.10FU	UDB04294304	81.4	96.3
<i>Petrophila</i>		1	0.001	S: SH0842946.10FU	OTU338	<i>Petrophila incerta</i>	SH0842946.10FU	AY559372	99.3	100
<i>Pezizomycotina gen. incertae sedis</i>		1	0.001	S: SH0846887.10FU	OTU477	<i>Pezizomycotina sp</i>	SH0846887.10FU	UDB04349073	99.2	87.1
<i>Phallus</i>		1	0.001	S: SH0734441.10FU	OTU562	<i>Phallus impudicus</i>	SH0734441.10FU	OR708694	100	100
<i>Pleurotus</i>		1	0.001	S: SH0822656.10FU	OTU280	<i>Pleurotus ostreatus</i>	SH0822656.10FU	OR613450	100	100
<i>Pringsheimia</i>		1	0.001	S: SH0740742.10FU	OTU490	<i>Pringsheimia sp</i>	SH0740742.10FU	UDB05247480	90	100
<i>Pseudallescheria</i>		1	0.001	S: SH0970643.10FU	OTU359	<i>Pseudallescheria ellipsoidea</i>	SH0970643.10FU	KJ607253	87.1	93.7
<i>Pseudomicrostroma</i>		1	0.001	S: SH0969905.10FU	OTU406	<i>Pseudomicrostroma glucosiphilum</i>	SH0969905.10FU	OM337566	99.6	100
<i>Pseudoophiobolus</i>		1	0.001	S: SH0740652.10FU	OTU504	<i>Pseudoophiobolus mathieui</i>	SH0740652.10FU	MG520949	99.3	100
<i>Pseudopithomyces</i>		1	0.001	S: SH0991327.10FU	OTU337	<i>Pseudopithomyces chartarum</i>	SH0991327.10FU	OR569668	99.3	100
<i>Saccharomyces</i>		1	0.001	S: SH0760250.10FU	OTU410	<i>Saccharomyces cerevisiae</i>	SH0760250.10FU	OP046435	99.6	100
<i>Scolecoclachnum</i>		1	0.001	S: SH0908381.10FU	OTU478	<i>Scolecoclachnum nigricans</i>	SH0908381.10FU	MK584975	95	94.6
<i>Scutellinia</i>		1	0.001	S: SH1027467.10FU	OTU365	<i>Scutellinia sp</i>	SH1027467.10FU	MK019050	100	100
<i>Sporidiobolaceae gen. incertae sedis</i>		1	0.001	S: SH0993541.10FU	OTU433	<i>Sporidiobolaceae sp</i>	SH0993541.10FU	UDB07546702	94.5	100
<i>Stemphylium</i>		1	0.001	S: SH0856291.10FU	OTU291	<i>Stemphylium globuliferum</i>	SH0856291.10FU	OQ832651	99.4	100
<i>Syncephalastrum</i>		1	0.001	S: SH1006583.10FU	OTU430	<i>Syncephalastrum racemosum</i>	SH1006583.10FU	OQ734577	99	100
<i>Trametes</i>		1	0.001	S: SH0762231.10FU	OTU257	<i>Trametes versicolor</i>	SH0762231.10FU	OQ102311	98.4	100
<i>Vishniacozyma</i>		1	0.001	S: SH0937368.10FU	OTU404	<i>Vishniacozyma sp</i>	SH0937368.10FU	OP470296	100	100
<i>Xylodon</i>		1	0.001	S: SH0965020.10FU	OTU400	<i>Xylodon sp</i>	SH0965020.10FU	UDB07537072	99.5	100
<i>Cyphellophora</i>	HAD	1	0.001	S: SH0870090.10FU	OTU304	<i>Cyphellophora sp</i>	SH0870090.10FU	KU582303	99.4	100
<i>Talaromyces</i>	HAD	1	0.001	S: SH0901488.10FU	OTU542	<i>Talaromyces rademirici</i>	SH0901488.10FU	MH861711	97	99.4

Table S10 (Supplementary file S4 - Excel file). Taxonomic classification of OTUs in the pooled resinous soil (RS) and forest soil (FS) dataset. OTUs were derived from ITS2 sequences from all samples clustered jointly at 97% similarity and assigned using the UNITE+INSD fungal reference dataset (DOI: 10.15156/BIO/2959330). The table reports OTU IDs, type, sequence abundance (including replicate counts for RS1–RS3 and FS1–FS2), accession numbers, UNITE Species Hypotheses (SH), alignment statistics, and putative taxonomy (kingdom to species). Empty fields indicate OTUs that passed ITS2 extraction but lacked a confident UNITE match.

Table S11. Summary of statistical comparisons for alpha diversity metrics between resinous soil (RS) and forest soil (FS). Median and interquartile range (IQR) values are reported for observed richness (R), Shannon diversity (H'), Simpson's diversity ($1-D$) and Inverse Simpson index ($1/D$), calculated per sample using the *vegan* package in R from relative abundance data (no rarefaction). Differences between soil types were assessed using Wilcoxon rank-sum test and effect sizes were estimated using Cliff's Delta. No significant differences were detected (all $p > 0.05$), though large effect sizes were detected for richness and evenness metrics.

Metric	RS Median (IQR)	FS Median (IQR)	Wilcoxon p	Cliff's Delta	Effect Size
R	281 (29)	352 (5)	0.15	1.00	Large
H'	3.03 (0.07)	3.02 (0.09)	1.00	0.00	Negligible
1-D	0.90 (0.01)	0.87 (0.02)	0.39	-0.67	Large
1/D	10.19 (0.81)	7.84 (1.39)	0.39	-0.67	Large

Table S12. Diversity partitioning and between-community dissimilarity of resinous soil (RS) and forest soil (FS) mycobiomes. Metrics were calculated from the pooled OTU table (shared feature space). Gamma diversity (γ) reflects the total number of unique OTUs per environment; mean alpha diversity ($\bar{\alpha}$) is the average richness per sample; and Whittaker's beta ($\beta_w = \gamma / \bar{\alpha}$) reflects turnover among samples within each environment. For RS $\times$ FS, γ and $\bar{\alpha}$ were computed across all samples pooled from both environments to summarize overall turnover between environments. Bray–Curtis dissimilarity (DBC), computed from relative abundances, is reported as a single value (shown in the RS $\times$ FS row). Given limited replicates (RS n=3, FS n=2), results are descriptive and no formal hypothesis testing was performed. Higher β_w and DBC values indicate greater differentiation in community composition.

	Gamma Diversity (γ)	Mean Alpha Diversity (α)	Whittaker's Beta (β_w)	Bray-Curtis Dissimilarity (DBC)
RS	558	286.3	1.95	
FS	496	352.0	1.41	
RS x FS	1001	312.6	3.20	0.968

Table S13. Secondary BLASTn-based classification of OTUs unassigned by UNITE. OTUs lacking a UNITE match at e-value 1e–5 were queried against the NCBI nt database (e-value 0.05). The table lists best BLASTn hits for OTUs detected in resinous soil (RS) and forest soil (FS) samples including accession number, putative classification, geographic origin, host and/ or isolation source, e-value, coverage (%) and sequence similarity (%) and total raw counts per environment. The majority of OTUs lacked definitive fungal classification and suggesting undescribed lineages. These results provide further insight into the uncharacterized diversity of the resinous soil mycobiota and underscore the limitations of current reference databases.

OTU	Total Raw Counts <i>per</i> environment		Accession Number	Putative classification	Geo Location	BLASTn NCBI			
	RS	FS				Host/ Isolation source	E-value	Coverage [%]	Similarity [%]
OTU0020 ⁽¹⁾	2124	1	KP897691.1	uncultured fungus	Lithuania	Picea abies/ needles	0.010	20.21	90.24
OTU0094 ⁽¹⁾	21	84							
OTU0107	74	0							
OTU0141	47	0	PQ419044.1	<i>Aciculopsora</i> sp.	Norway	deciduous tree wood	2.25e-09	71.71	77.27
OTU0163	31	0	KP897691.1	uncultured fungus	Lithuania	Picea abies/ needles	7.11e-63	73.53	93.75
OTU0180	25	0							
OTU0185	23	0							
OTU0194	21	0	KP897691.1	uncultured fungus	Lithuania	Picea abies/ needles	1.66e-63	86.07	93.06
OTU0203	17	0	KM493723.1	uncultured fungus	Sweden	Norway-spruce stump	6.97e-87	100	98.94
OTU0217	14	0							
OTU0227	13	0							
OTU0253	10	0							

Total Raw Counts <i>per</i> environment			BLASTn NCBI						
OTU	RS	FS	Accession Number	Putative classification	Geo Location	Host/ Isolation source	E-value	Coverage [%]	Similarity [%]
OTU0256	9	0	KP897691.1	uncultured fungus	Lithuania	Picea abies/ needles	3.66e-60	73.84	92.61
OTU0318	0	5	KM493206.1	uncultured fungus	Sweden	Norway- spruce decaying log	8.23e-15	84.67	78.30
OTU0345	0	4							
OTU0374	4	0	MN904040.1	uncultured fungus	Lithuania	<i>Pinus sylvestris</i>	3.23e-09	81.19	73.21
OTU0397 ⁽²⁾	3	0	CP174167.1	<i>Metamycoplasma sualvi</i>	United Kingdom	<i>Sus scrofa domesticus</i>	0.047	23.29	79.31
OTU0488	2	0							
OTU0566	0	1							
OTU0569	0	1							
OTU0645	1	0	PQ419044.1	<i>Aciculopsora sp.</i>	Norway	deciduous tree wood	1.92e-35	76.51	92.11
OTU0722	1	0	MN904040.1	uncultured fungus	Lithuania	<i>Pinus sylvestris</i>	5.93e-31	100	78.89
OTU0724	1	0	OW734376.1	uncultured Ascomycota	China		8.49e-52	100	96.21
OTU0742	1	0							
OTU0743	1	0	KP897691.1	uncultured fungus	Lithuania	Picea abies/ needles	0.010	20.21	90.24
OTU0941 ⁽²⁾	1	0	OZ247818.1	<i>Caenorhabditis sp. BRC20456</i>			0.004	27.54	80.00
OTU0952	1	0							

Total Raw Counts <i>per</i> environment			BLASTn NCBI						
OTU	RS	FS	Accession Number	Putative classification	Geo Location	Host/ Isolation source	E-value	Coverage [%]	Similarity [%]
OTU0968	1	0	PQ419044.1	<i>Aciculopsora sp.</i>	Norway	deciduous tree wood	1.15e-06	72.19	75.46
OTU1066	1	0	OW734376.1	uncultured Ascomycota	China		1.49e-48	100	95.46
OTU1067	1	0							
OTU1074	1	0							

(1) marks OTUs shared between RS and FS, e.g. OTU20 enriched in RS and OTU94 enriched in FS; (2) marks OTUs aligning to non-fungal sequences.

Table S14 (Supplementary file S5 - Excel file). Full FungalTraits annotation table for OTUs detected in resinous soil (RS) and forest soil (FS). The table provides complete functional trait assignments for all OTUs based on the FungalTraits database, including lifestyle categories, growth form, decay traits, endophytic capacity, pathogenicity, biotrophic capacities, host associations, fruiting body and hymenium types, ectomycorrhizal traits, and photobiont attributes. Community-level trait coverage and RS/FS-specific annotations are also reported. This dataset represents the full output of the FungalTraits classification used in downstream analyses.

Table S15. Proportion of community abundance annotated for functional traits in resinous soil (RS) and forest soil (FS) mycobiomes. Values represent the percentage of total community relative abundance assigned to each trait category based on FungalTraits database annotations. Reported traits include primary and secondary lifestyle attributes, growth form, decay substrate and type, endophytic capacity, plant pathogenicity, aquatic and animal biotrophic capacities, host specificity, fruiting body and hymenium types, ectomycorrhizal exploration/lineage groups, and photobiont traits. Lower coverage values indicate traits with limited representation or incomplete database annotation.

	Trait	RS coverage (%)	FS coverage (%)
Relevant traits	Lifestyle (primary & secondary)	56,9	83,2
	Growth form	56.9	83.2
	Decay substrate	53.5	76.8
	Decay type	7.4	59.1
	Endophytic capacity	17.4	70.2
Secondary traits	Plant pathogen	4.5	15.2
	Aquatic	55.6	81.4
	Animal biotrophic capacity	23,4	63,0
	Specific hosts	2,4	1,6
	Fruiting body	33,4	22,0
	Hymenium type	33,1	22,0
	Ectomycorrhiza (exploration and lineage)	0,0	4,4
	Photobiont (primary & secondary)	0,06	0,03

Table S16. Major functional traits versus dominant genera in resinous (RS) and forest (FS) soils. The traits shown represent the most ecologically relevant categories for this study. For each trait level, relative abundances in RS and FS (%) and the percentage-point difference ($\Delta\text{pp} = \text{RS} - \text{FS}$) are reported. Traits are included regardless of Δpp , whereas genera are listed only when the trait difference exceeds 1.0 percentage point and the genus reaches $\geq 0.5\%$ relative abundance in the corresponding soil. Empty cells indicate genera below this abundance threshold. Relative abundances are aggregated at the genus level and reported to three decimal places. Bray–Curtis dissimilarity values are provided at the trait level.

Trait Category	Putative fungal trait and genera	RS (%)	FS (%)	Δpp (RS-FS)	log2FC (RS/FS)	BC
Lifestyle	mycoparasite	14.740	0.031	14.708	8.881	50.876
	<i>Sporobolomyces</i>	12.287				
	<i>Colacogloea</i>	2.311				
	unspecified saprotroph	9.199	30.078	-20.878	-1.709	
	nectar/tap saprotroph	8.562	0.073	8.489	6.870	
	<i>Candida</i>	2.273				
	<i>Debaryomyces</i>	1.816				
	litter saprotroph	5.974	2.095	3.879	1.512	
	<i>Infundichalara</i>	2.183				
	<i>Symbiotaphrina</i>	1.565				
	<i>Exophiala</i>	1.221				
	<i>Lophium</i>	0.806				
	<i>Cladosporium</i>		1.456			
	foliar endophyte	4.066	28.239	-24.173	-2.796	
	<i>Penicillium</i>	2.780	27.121			
	<i>Rhodotorula</i>	0.866				
	<i>Aspergillus</i>	0.414				
	<i>Acremonium</i>		0.719			

Trait Category	Putative fungal trait and genera	RS (%)	FS (%)	Δ pp (RS-FS)	log2FC (RS/FS)	BC
Lifestyle	resin saprotroph	3.531	0	3.531	21.752	
	<i>Sorocybe</i>	7.061				
	wood saprotroph	2.539	0.563	1.976	2.172	
	<i>Pragmopora</i>	1.169				
	<i>Mytilinidion</i>	0.773				
	fungal decomposer	2.446	0.072	2.374	5.095	
	<i>Colacogloea</i>	2.311				
	animal parasite	1.617	0.494	1.123	1.710	
	<i>Exophiala</i>	1.221				
	animal endosymbiont	1.567	0	1.567	20.579	
	<i>Symbiotaphrina</i>	1.565				
	soil saprotroph	1.338	8.977	-7.638	-2.746	
	<i>Phialocephala</i>		3.069			
	<i>Pseudogymnoascus</i>		2.166			
	<i>Pseudeurotium</i>		0.982			
	<i>Oidiodendron</i>		0.740			
	<i>Phallus</i>		0.587			
	plant pathogen	0.605	1.847	-1.242	-1.611	
	<i>Cladosporium</i>		1.456			
	root endophyte	0.532	3.809	-3.277	-2.840	
	<i>Phialocephala</i>		3.069			
	<i>Oidiodendron</i>		0.740			
	lichenized	0.060	0.033	0.028	0.879	
	epiphyte	0.043	0.061	-0.018	-0.492	
	nematophagous	0.030	0	0.030	14.884	
	root endophyte dark septate	0.029	0.045	-0.016	-0.621	

Trait Category	Putative fungal trait and genera	RS (%)	FS (%)	Δpp (RS-FS)	log2FC (RS/FS)	BC
Lifestyle	animal decomposer	0.004	0.204	-0.200	-5.601	
	dung saprotroph	0.004	1.031	-1.028	-8.091	
	<i>Pseudeurotium</i>		0.982			
	rock-inhabiting	0.003	0.021	-0.018	-2.669	
	sooty mold	0.003	0.001	0.003	2.029	
	unspecified symbiotroph	0	0.467	-0.467	-18.834	
	ectomycorrhizal	0	4.339	-4.339	-22.049	
	<i>Ruhlandiella</i>		2.535			
	<i>Rhizopogon</i>		1.128			
	<i>Laccaria</i>		0.572			
	root-associated	0	0.350	-0.350	-18.415	
	pollen saprotroph	0	0.180	-0.180	-17.459	
	animal-associated	0	0.059	-0.059	-15.854	
	arbuscular mycorrhizal	0	0.069	-0.069	-16.076	
	lichen parasite	0	0.002	-0.002	-10.685	
	ericoid mycorrhizal	0	0.075	-0.075	-16.192	
	algal parasite	0	0.017	-0.017	-14.076	
Growth form	dimorphic yeast	14.855	0.671	14.184	4.468	53.014
	<i>Sorocybe</i>	7.061				
	<i>Colacogloea</i>	4.622				
	<i>Exophiala</i>	2.442	0.169			
	filamentous mycelium	16.116	82.160	-66.044	-2.350	
	<i>Penicillium</i>	5.561	54.242			
	<i>Infundichalara</i>	2.183				
	<i>Pragmopora</i>	1.169				
	<i>Sarea</i>	1.162				

Trait Category	Putative fungal trait and genera	RS (%)	FS (%)	Δ pp (RS-FS)	log2FC (RS/FS)	BC
Growth form	<i>Aspergillus</i>	0.828	0.684			
	<i>Lophium</i>	0.806				
	<i>Mytilinidion</i>	0.773				
	<i>Phialocephala</i>	0.728	6.137			
	<i>Scedosporium</i>	0.555				
	<i>Cladosporium</i>		2.912			
	<i>Ruhlandiella</i>		2.535			
	<i>Pseudogymnoascus</i>		2.166			
	<i>Pseudeurotium</i>		1.964			
	<i>Oidiodendron</i>		1.480			
	<i>Sagenomella</i>		1.466			
	<i>Acremonium</i>		1.438			
	<i>Rhizopogon</i>		1.128			
	<i>Aspergillus</i>		0.684			
	<i>Phallus</i>		0.587			
	<i>Laccaria</i>		0.572			
	thallus photosynthetic	0.060	0.033	0.028	0.877	
	yeast	25.862	0.229	25.634	6.821	
	<i>Sporobolomyces</i>	12.287				
	<i>Candida</i>	4.546				
	<i>Debaryomyces</i>	3.632				
	<i>Symbiotaphrina</i>	3.130				
	<i>Rhodotorula</i>	1.732				
Decay type	zoosporic-rhizomycelial (chytrid-like)	0	0.138	-0.138	-10.433	
	mold	6.415	57.017	-50.602	-3.152	25.873
	<i>Penicillium</i>	5.561	54.242			
	<i>Aspergillus</i>	0.828	0.684			

Trait Category	Putative fungal trait and genera	RS (%)	FS (%)	Δpp (RS-FS)	log2FC (RS/FS)	BC
Decay type	<i>Sagenomella</i>	0.022	1.466			
	soft rot	0.899	1.632	-0.733	-0.860	
	<i>Mytilinidion</i>	0.773				
	<i>Acremonium</i>		1.438			
	white rot	0.064	0.059	0.005	0.108	
	brown rot	0	0.020	-0.020	-7.632	
	chitinolytic	0	0.178	-0.178	-10.796	
	keratinolytic	0	0.207	-0.207	-11.018	
	other	0.001	0	0.001	3.233	
	fungal material	17.184	0.053	17.131	8.348	55.081
Decay substrate	<i>Sporobolomyces</i>	12.287				
	<i>Colacogloea</i>	4.622				
	sugar-rich substrates	8.562	0.077	8.485	6.789	
	<i>Candida</i>	4.546				
	<i>Debaryomyces</i>	3.632				
	resins	7.061	0	7.061	16.108	
	<i>Sorocybe</i>	7.061				
	soil	6.383	58.963	-52.579	-3.207	
	<i>Penicillium</i>	5.561	54.242			
	<i>Pseudogymnoascus</i>		2.166			
	<i>Oidiodendron</i>		1.480			
	<i>Phallus</i>		0.587			
	leaf/fruit/seed	6.326	0.559	5.767	3.499	
	<i>Symbiotaphrina</i>	3.130				
	<i>Infundichalara</i>	2.183				
	<i>Lophium</i>	0.806				

Trait Category	Putative fungal trait and genera	RS (%)	FS (%)	Δ pp (RS-FS)	log2FC (RS/FS)	BC
Decay substrate	wood	2.598	0.571	2.027	2.186	
	<i>Pragmopora</i>	1.169				
	<i>Mytilinidion</i>	0.773				
	leaf/fruit/seed.animal material	2.520	0.229	2.291	3.461	
	<i>Exophiala</i>	2.442				
	leaf/fruit/seed.soil.dung.animal material	0.828	2.150	-1.322	-1.377	
	<i>Acremonium</i>		1.438			
	<i>Aspergillus</i>	0.828	0.684			
	roots.soil	0.728	7.633	-6.904	-3.389	
	<i>Phialocephala</i>	0.728	6.137			
	soil.animal material	0.704	0.452	0.252	0.638	
	hydrocarbon-rich substrates (fuel)	0.332	0	0.332	11.697	
	wood.leaf/fruit/seed.soil.dung.animal material	0.144	2.912	-2.768	-4.340	
	<i>Cladosporium</i>	0.144	2.912			
	wood.animal material	0.060	0	0.060	9.243	
	wood.leaf/fruit/seed.soil.animal material	0.012	0.003	0.008	1.807	
	animal material	0.008	0.296	-0.288	-5.123	
	soil.dung	0.008	1.974	-1.966	-8.009	
	<i>Pseudeurotium</i>		1.964			
	wood.leaf/fruit/seed	0.008	0.242	-0.234	-4.981	
	leaf/fruit/seed.soil	0.007	0.010	-0.003	-0.548	
	leaf/fruit/seed.roots.animal material.sugar-rich substrates	0.007	0.002	0.005	1.967	
	leaf/fruit/seed.soil.fungal material	0.003	0.007	-0.003	-0.949	
	leaf/fruit/seed.sugar-rich substrates	0.003	0.008	-0.005	-1.266	

Trait Category	Putative fungal trait and genera	RS (%)	FS (%)	Δ pp (RS-FS)	log2FC (RS/FS)	BC
Decay substrate	animal material.sugar-rich substrates	0.001	0	0.001	3.233	
	leaf/fruit/seed.soil.animal material	0.001	0.021	-0.021	-4.514	
	leaf/fruit/seed.wood	0.001	0	0.001	3.233	
	wood.leaf/fruit/seed.soil	0.001	0	0.001	3.233	
	animal material.dung	0	0.002	-0.002	-4.125	
	animal material.fungal material	0	0.087	-0.087	-9.770	
	dung	0	0.021	-0.021	-7.747	
	fungal material.algal material	0	0.003	-0.003	-5.083	
	leaf/fruit/seed.dung	0	0.005	-0.005	-5.654	
	leaf/fruit/seed.roots.soil.animal material	0	0.003	-0.003	-5.083	
	pollen	0	0.257	-0.257	-11.326	
	soil.roots	0	0.150	-0.150	-10.549	
	wood.fungal material	0	0.003	-0.003	-5.083	
	wood.leaf/fruit/seed.roots.animal material	0	0.003	-0.003	-5.083	
	wood.leaf/fruit/seed.roots.soil	0	0.002	-0.002	-4.125	
	wood.leaf/fruit/seed.soil.dung	0	0.109	-0.109	-10.086	
	wood.roots	0	0.002	-0.002	-4.125	
Endophytic capacity	foliar endophyte	8.329	59.532	-51.203	-2.837	31.083
	<i>Penicillium</i>	5.561	54.242			
	<i>Rhodotorula</i>	1.732				
	<i>Aspergillus</i>	0.828				
	<i>Cladosporium</i>		2.912			
	<i>Acremonium</i>		1.438			
	no endophytic capacity	5.376	0.691	4.685	2.960	
	<i>Colacogloea</i>	4.622	0.000			

Trait Category	Putative fungal trait and genera	RS (%)	FS (%)	Δp (RS-FS)	$\log_2 FC$ (RS/FS)	BC
Endophytic capacity	root endophyte dark septate	3.377	6.873	-3.496	-1.025	
	<i>Exophiala</i>	2.442				
	<i>Phialocephala</i>	0.728	6.137			
	root endophyte	0.335	1.619	-1.283	-2.271	
	<i>Oidiodendron</i>		1.480			
	root-associated	0	1.499	-1.499	-13.871	

Table S17 (Supplementary file S6 - Excel file). DESeq2 differential abundance analyses comparing resinous soil (RS) and forest soil (FS) mycobiomes. The file includes three RS replicate combinations (C1: RS.I+RS.II; C2: RS.I+RS.III; C3: RS.II+RS.III) tested against the two FS replicates. Sheets provide (i) full DESeq2 results, (ii) OTUs significantly enriched in RS, and (iii) OTUs significantly enriched in FS. These results support Fig. 7 in the main text.

Table S18 (Supplementary file S7 – Excel file). Metadata and Shannon diversity values for European GMSc sites used for comparison with resinous soil (RS) and forest soil (FS) samples. This table lists all European sampling sites retrieved from the Global Soil Mycobiome consortium (GMSc) and used as a reference dataset in comparisons with RS and FS mycobiomes. Metadata include geographic coordinates, country and regional descriptors, biome and biome type, as well as Shannon diversity values. This dataset supplies the full environmental and geographic context supporting comparative diversity and biogeographic analyses, namely Fig. 7a of the main text.

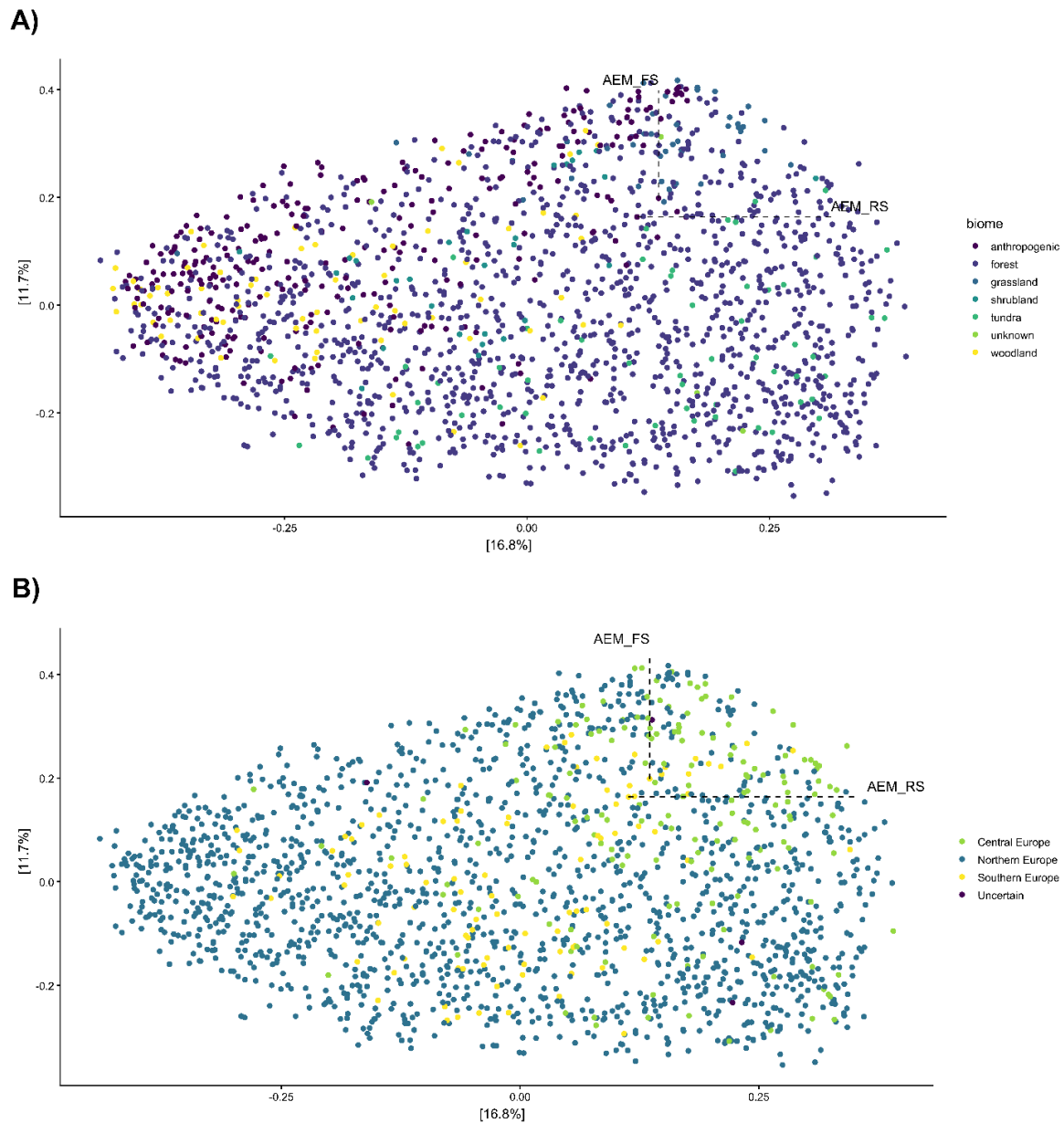


Fig. S7. Principal Coordinates Analysis (PCoA) of fungal community composition based on Bray–Curtis dissimilarity, including resinous soil (RS), forest soil (FS), and European reference soils from the Global Soil Mycobiome consortium (GSMc). The first two axes explain 16.8% (PCoA1) and 11.7% (PCoA2) of the total variance. **(A)** PCoA ordination with samples coloured according to biome classification (anthropogenic, forest, grassland, shrubland, tundra, woodland, or unknown). **(B)** The same ordination with samples coloured according to European biogeographic region (Northern, Central, and Southern Europe; uncertain classification shown separately). RS and FS samples cluster closely together and plot near the periphery of the Southern European soil cloud, indicating partial compositional similarity to Southern European fungal communities, with no strong association to a single biome or regional cluster.