

Supporting Information

Title: Linking molecular wood-inhabiting fungal diversity and community dynamics to ecosystem functions and processes in Central European forests

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Assignment of decay classes and dendrochronological dating

Deadwood logs were assigned to four decay classes based on information on remaining mass (%) by k-means cluster analysis as described in Hoppe et al. (2014) and Kahl et al. (2012). This approach was performed to use the decay class as a categorical variable, which is independent from an observers guessing in the field. In addition we also assigned decay classes according to a “conventional” independent approach commonly used in Germany (compare Müller-Using & Bartsch 2009), during the initial sampling campaign. Both approaches significantly correlated ($\rho = 0.74$, $p = 0.0001$).

Decay rates were calculated based on a single exponential model (Harmon et al. 1986) using information on mass loss (density and volume loss) and time since death obtained by dendrochronological dating of the deadwood. Tree rings in heavily decayed dead wood were made visible by freezing the fresh piece of dead wood and then placing it in molten paraffin for 2-3 days (melting point 56-59°C, Merck, Darmstadt, Germany) (Krüger et al. 2014). The paraffin replaces the evaporating water and stabilizes the dead wood after cooling. Tree rings were made visible by planing the surface with a razor blade.

Detailed WIF dynamics and sharedness of cOTUs and families: *Fagus* vs. *Picea* logs

(A) Detailed WIF dynamics in *Fagus* and *Picea* logs

In *Fagus* deadwood (Fig. S5), the decay class 1 was highly dominated by *Xylariaceae* (total abundance 26%; mainly comprising *Annulohyphoxylon cohaerens* 17.4%, *Hypoxylon rubiginosum* 5.45%), followed by *Polyporaceae* (total abundance 14.6%; mainly *Trametes versicolor* 12.3%), *Physalacriaceae* (total abundance 10.4%; mainly *Armillaria cepistipes* 6.39%, *Armillaria gallica* 3.78%) and *Leotiaceae* (total abundance 8.18%; mainly *Neobulgaria pura* 7.43%). In decay class 2, *Polyporaceae* (mean abundance 17.8%; mainly *Fomes fomentarius* 13.3% and *Meruliaceae* (mean abundance 17%; mainly *Phlebia livida* 8.37% were dominant fungal families followed by *Xylariaceae* that dropped in their abundances to 10% (dominated by *Xylaria hypoxylon* 7.65%) when compared to decay class 1. With advancing decay (decay class 3), *Xylariaceae* further dropped to 5.15% (dominated by *Kretzschmaria deusta* 4.54%), whereas other families that dominated the deadwood decay class 2 remained dominant. In decay class 4, *Mycenaceae* (mean abundance 23%; dominated by *Mycena alnetorum* 16.1%) became the most dominant family followed by *Marasmiaceae* (mean abundance 15.5%; mainly *Megacollybia platyphylla* 7.99%) and *Polyporaceae* (mean abundance 10.1%; dominated by *Trametes versicolor* 10.1%). *Xylariaceae* (mean abundance 0.74%) almost disappeared from this most advanced decay class.

In *Picea* deadwood (Fig. S6), all decay classes were highly dominated by Agaricomycetes I.S. (mean abundance 26.4%, 42.7%, 29.6%, 17% in decay classes 1-4, respectively; almost fully corresponding to *Resinicium bicolor*). *Stereaceae* were frequently detected in decay class 1 (mean abundance 21.7%; dominated by *Amylostereum areolatum* 19.9%), however, they declined in abundance in decay class 2 and 3 (mean abundances

1.18% and 2.69%, respectively) and increased in their abundance in decay class 4 again (mean abundance 7.31%; dominated by *Amylostereum chailletii* 7.29%). *Physalacriaceae* were frequently detected in decay class 1 (mean abundance 14.2%; dominated by *Armillaria cepistipes* 6.85% and *Armillaria gallica* 6.11%) but were of low abundance in other decay classes. *Bondarzewiaceae* (represented by *Heterobasidion* sp.) were frequently detected in all decay classes (mean abundances 10.3 – 18.9%) except in decay class 2 (1.87%). *Mycenaceae* were frequently found in decay classes 1 and 2 (mean abundances 7.88% and 12.5% both dominated by *Mycena rubromarginata*), whereas in decay class 3 and 4 they were much less frequent (mean abundances 2.77% and 3.71%). *Fomitopsidaceae* were frequently detected from decay class 2, 3 and 4 (mean abundances 7.44%, 17.1% and 5.81% dominated by *Fomitopsis pinicola*). *Schizoporaceae* were only highly frequently detected in decay class 4 (mean abundance 11.9%; dominated by *Hyphodontia alutacea* 5.73%, and *Hyphodontia alutaria* 3.08%).

(B) Sharedness of cOTUs and families between *Fagus* and *Picea*

We examined the sharedness of WIF cOTUs and genera between the tree species (Fig. S4). At the level of species (Fig. S4A), this was only possible for species that received unequivocally the same epithet. Among the 160 where this was the case, 74 species (22 Ascomycota, 50 Basidiomycota, and 2 zygomycetes) were found on both *Picea* and *Fagus* logs. Some of them are not normally reported on this particular substrate, e.g. *Xylariaceae* species *Annulohypoxylon cohaerens*, *Hypoxylon fragiforme*, *Hypoxylon rubiginosum*, *Kretzschmaria deusta* and *Nemania serpens* are known from literature to exclusively occur on *Fagus* logs and few other deciduous tree species, but in our case could also be detected with marginal abundances on *Picea* logs. At the level of genus, to assume sharedness

identification to sp. of same genus minimally suffices, and with this, 35 genera are unique to *Fagus*, 34 to *Picea*, and 58 genera are shared (Fig. S4B).

Table S1. Sampling design: Distribution of deadwood logs according to tree species and the respective 9 forest plots which were assigned to three different forest management types.

		Management type		
		Natural beech forests (3 plots)	Age-class managed beech forests (3 plots)	Age-class managed spruce forests (3 plots)
Deadwood tree species	<i>Fagus sylvatica</i>	8	8	8
	<i>Picea abies</i>	8	6	10

Table S2. List of MID tags for deadwood logs (samples) and additional characterization of sampling design. For further details regarding remaining mass of the respective deadwood log, compare Fig. S1 in Hoppe et al. (2014).

CWD ID	MID tag used in pyrosequencing	Tree species	Forest manag.	Plot ID	Gauss-Krüger coordinates		Coordinates		Altitude	Soil type
					RW	HW	Latitude	Longitude		
8270	ACGAGTGCCT	<i>F. sylvatica</i>	spruce age-class	AEW1	3524799	5371201	48.478064°N	9.334397°E	763 m	Cambisol
8271	ACGCTCGACA	<i>P. abies</i>	spruce age-class	AEW1	3524799	5371201	48.478064°N	9.334397°E	763 m	Cambisol
8273	AGACGCACTC	<i>P. abies</i>	spruce age-class	AEW1	3524799	5371201	48.478064°N	9.334397°E	763 m	Cambisol
8276	AGCACTGTAG	<i>P. abies</i>	spruce age-class	AEW1	3524799	5371201	48.478064°N	9.334397°E	763 m	Cambisol
8277	ATCAGACACG	<i>F. sylvatica</i>	spruce age-class	AEW1	3524799	5371201	48.478064°N	9.334397°E	763 m	Cambisol
8820	ATATCGCGAG	<i>P. abies</i>	spruce age-class	AEW2	3526110	5360300	48.37998°N	9.351452°E	749 m	Leptosol
8821	CGTGTCTCTA	<i>F. sylvatica</i>	spruce age-class	AEW2	3526110	5360300	48.37998°N	9.351452°E	749 m	Leptosol
8822	CTCGCGTGTC	<i>P. abies</i>	spruce age-class	AEW2	3526110	5360300	48.37998°N	9.351452°E	749 m	Leptosol
8823	TAGTATCAGC	<i>P. abies</i>	spruce age-class	AEW2	3526110	5360300	48.37998°N	9.351452°E	749 m	Leptosol
8824	TCTCTATGCG	<i>P. abies</i>	spruce age-class	AEW2	3526110	5360300	48.37998°N	9.351452°E	749 m	Leptosol
8825	TGATACGTCT	<i>P. abies</i>	spruce age-class	AEW2	3526110	5360300	48.37998°N	9.351452°E	749 m	Leptosol
8279	TACTGAGCTA	<i>P. abies</i>	spruce age-class	AEW3	3526400	5363890	48.412253°N	9.355592°E	715 m	Cambisol
8280	CATAGTAGTG	<i>F. sylvatica</i>	spruce age-class	AEW3	3526400	5363890	48.412253°N	9.355592°E	715 m	Cambisol
8281	CGAGAGATAC	<i>P. abies</i>	spruce age-class	AEW3	3526400	5363890	48.412253°N	9.355592°E	715 m	Cambisol

CWD ID	MID tag used in pyrosequencing	Tree species	Forest manag.	Plot ID	Gauss-Krüger coordinates		Coordinates		Altitude	Soil type
					RW	HW	Latitude	Longitude		
8282	ATACGACGTA	<i>F. sylvatica</i>	spruce age-class	AEW3	3526400	5363890	48.412253°N	9.355592°E	715 m	Cambisol
8283	TCACGTACTA	<i>F. sylvatica</i>	spruce age-class	AEW3	3526400	5363890	48.412253°N	9.355592°E	715 m	Cambisol
8807	CGTCTAGTAC	<i>F. sylvatica</i>	spruce age-class	AEW3	3526400	5363890	48.412253°N	9.355592°E	715 m	Cambisol
8809	TCTACGTAGC	<i>F. sylvatica</i>	spruce age-class	AEW3	3526400	5363890	48.412253°N	9.355592°E	715 m	Cambisol
8842	TGTACTACTC	<i>F. sylvatica</i>	beech age-class	AEW4	3518205	5362394	48.399088°N	9.244828°E	783 m	Cambisol
8845	ACGACTACAG	<i>F. sylvatica</i>	beech age-class	AEW4	3518205	5362394	48.399088°N	9.244828°E	783 m	Cambisol
8846	CGTAGACTAG	<i>F. sylvatica</i>	beech age-class	AEW4	3518205	5362394	48.399088°N	9.244828°E	783 m	Cambisol
8826	TACGAGTATG	<i>P. abies</i>	beech age-class	AEW5	3530770	5364730	48.419609°N	9.414683°E	809 m	Cambisol
8827	TACTCTCGTG	<i>F. sylvatica</i>	beech age-class	AEW5	3530770	5364730	48.419609°N	9.414683°E	809 m	Cambisol
8828	TAGAGACGAG	<i>F. sylvatica</i>	beech age-class	AEW5	3530770	5364730	48.419609°N	9.414683°E	809 m	Cambisol
8810	TCGTCGCTCG	<i>F. sylvatica</i>	beech age-class	AEW6	3533100	5361900	48.394042°N	9.445939°E	767 m	Cambisol
8811	ACATACGCGT	<i>P. abies</i>	beech age-class	AEW6	3533100	5361900	48.394042°N	9.445939°E	767 m	Cambisol
8812	ACGCGAGTAT	<i>P. abies</i>	beech age-class	AEW6	3533100	5361900	48.394042°N	9.445939°E	767 m	Cambisol
8813	ACTACTATGT	<i>P. abies</i>	beech age-class	AEW6	3533100	5361900	48.394042°N	9.445939°E	767 m	Cambisol
8815	ACTGTACAGT	<i>F. sylvatica</i>	beech age-class	AEW6	3533100	5361900	48.394042°N	9.445939°E	767 m	Cambisol
8817	AGACTATACT	<i>P. abies</i>	beech age-class	AEW6	3533100	5361900	48.394042°N	9.445939°E	767 m	Cambisol

CWD ID	MID tag used in pyrosequencing	Tree species	Forest manag.	Plot ID	Gauss-Krüger coordinates		Coordinates		Altitude	Soil type
					RW	HW	Latitude	Longitude		
8818	AGCGTCGTCT	<i>F. sylvatica</i>	beech age-class	AEW6	3533100	5361900	48.394042°N	9.445939°E	767 m	Cambisol
8819	AGTACGCTAT	<i>P. abies</i>	beech age-class	AEW6	3533100	5361900	48.394042°N	9.445939°E	767 m	Cambisol
8832	ATAGAGTACT	<i>F. sylvatica</i>	beech age-class	AEW7	3519430	5362080	48.396228°N	9.261357°E	773 m	Leptosol
8833	CACGCTACGT	<i>P. abies</i>	beech age-class	AEW7	3519430	5362080	48.396228°N	9.261357°E	773 m	Leptosol
8834	CAGTAGACGT	<i>P. abies</i>	beech age-class	AEW7	3519430	5362080	48.396228°N	9.261357°E	773 m	Leptosol
8835	CGACGTGACT	<i>F. sylvatica</i>	beech age-class	AEW7	3519430	5362080	48.396228°N	9.261357°E	773 m	Leptosol
8285	TACACACACT	<i>F. sylvatica</i>	beech natural forest	AEW8	3528400	5360600	48.38258°N	9.382386°E	779 m	Cambisol
8286	TACACGTGAT	<i>F. sylvatica</i>	beech natural forest	AEW8	3528400	5360600	48.38258°N	9.382386°E	779 m	Cambisol
8288	TACAGATCGT	<i>P. abies</i>	beech natural forest	AEW8	3528400	5360600	48.38258°N	9.382386°E	779 m	Cambisol
8289	TACGCTGTCT	<i>P. abies</i>	beech natural forest	AEW8	3528400	5360600	48.38258°N	9.382386°E	779 m	Cambisol
8290	TAGTG TAGAT	<i>P. abies</i>	beech natural forest	AEW8	3528400	5360600	48.38258°N	9.382386°E	779 m	Cambisol
8294	TCGATCACGT	<i>P. abies</i>	beech natural forest	AEW8	3528400	5360600	48.38258°N	9.382386°E	779 m	Cambisol
8295	TCGCACTAGT	<i>F. sylvatica</i>	beech natural forest	AEW8	3528400	5360600	48.38258°N	9.382386°E	779 m	Cambisol

CWD ID	MID tag used in pyrosequencing	Tree species	Forest manag.	Plot ID	Gauss-Krüger coordinates		Coordinates		Altitude	Soil type
					RW	HW	Latitude	Longitude		
8296	TCTAGCGACT	<i>F. sylvatica</i>	beech natural forest	AEW9	3530840	5359140	48.369336 °N	9.41522 °E	753 m	Leptosol
8297	TCTATACTAT	<i>F. sylvatica</i>	beech natural forest	AEW9	3530840	5359140	48.369336 °N	9.41522 °E	753 m	Leptosol
8298	TGACGTATGT	<i>F. sylvatica</i>	beech natural forest	AEW9	3530840	5359140	48.369336 °N	9.41522 °E	753 m	Leptosol
8801	TGTGAGTAGT	<i>P. abies</i>	beech natural forest	AEW9	3530840	5359140	48.369336 °N	9.41522 °E	753 m	Leptosol
8804	ACAGTATATA	<i>P. abies</i>	beech natural forest	AEW9	3530840	5359140	48.369336 °N	9.41522 °E	753 m	Leptosol

Table S3. Decay rate, remaining mass and wood physico-chemical parameters of *Fagus* (FASY) and *Picea* (PIAB) deadwood logs in different decay classes (DC 1 through 4; including number of logs per decay class).

DC:	FASY_1 (8)	FASY_2 (6)	FASY_3 (7)	FASY_4 (3)	PIAB_1 (5)	PIAB_2 (5)	PIAB_3 (5)	PIAB_4 (9)
Decay rate k (y ⁻¹)	0.05 ± 0.01	0.05 ± 0	0.07 ± 0.01	0.09 ± 0.02	0.04 ± 0.01	0.04 ± 0.01	0.08 ± 0	0.08 ± 0.01
Remaining mass (%)	80.28 ± 2.82	58.16 ± 1.46	45.57 ± 1.4	30.75 ± 1.9	75.25 ± 2.01	58.26 ± 2.4	47.64 ± 1.5	31.19 ± 0.97
Density (g*cm ⁻³)	0.51 ± 0.02	0.37 ± 0.01	0.31 ± 0.01	0.2 ± 0.03	0.35 ± 0.01	0.27 ± 0.01	0.22 ± 0.01	0.15 ± 0.01
Rel. wood moisture (% dry mass)	49.83 ± 5.5	114.21 ± 14.66	138.22 ± 22.94	155.15 ± 9.14	48.72 ± 11.59	65.45 ± 13.38	95.27 ± 8.91	163.06 ± 24.62
C %	48.41 ± 0.16	47.92 ± 0.18	47.52 ± 0.37	47.51 ± 0.33	49.29 ± 0.31	49.92 ± 0.22	49.16 ± 0.35	51.39 ± 0.94
N %	0.13 ± 0.01	0.15 ± 0.01	0.18 ± 0.02	0.25 ± 0.02	0.08 ± 0.01	0.08 ± 0	0.08 ± 0	0.14 ± 0.02
C/N	365.22 ± 14.87	324.02 ± 22.45	282.87 ± 31.53	193.7 ± 15.62	629.69 ± 48.44	602.56 ± 19.24	591.22 ± 38.75	422.87 ± 52.44
C (g*cm ⁻³)	0.248 ± 0.01	0.175 ± 0.007	0.145 ± 0.005	0.093 ± 0.015	0.172 ± 0.005	0.134 ± 0.002	0.106 ± 0.008	0.079 ± 0.003
N (g*cm ⁻³)	0.0007 ± 0	0.0006 ± 0.0001	0.0005 ± 0	0.0005 ± 0.0001	0.0003 ± 0	0.0002 ± 0	0.0002 ± 0	0.0002 ± 0
Total Lignin (%)	26.09 ± 0.48	28.52 ± 0.73	31.21 ± 1.14	30.49 ± 2.18	29.5 ± 0.59	31.63 ± 1.06	33.63 ± 2.31	45.23 ± 3.78
pH	5.25 ± 0.1	4.84 ± 0.08	5.12 ± 0.14	4.99 ± 0.13	4.63 ± 0.1	4.33 ± 0.03	4.04 ± 0.16	4.26 ± 0.15

Table S4. Mean ligninolytic enzyme activities and macro/ micro nutrients of *Fagus* and *Picea* deadwood logs.

Parameters	<i>Fagus sylvatica</i>	<i>Picea abies</i>
Lac (mU/g)	51.5 ± 11.2	26.6 ± 10.3
MiP (mU/g)	15 ± 4.9	14.4 ± 5.8
MnP (mU/g)	18 ± 9	13.8 ± 6.1
Mn (µg/g)	12.2 ± 3	24.2 ± 3.2
Mg (mg/g)	0.2 ± 0	0.1 ± 0
Ca (mg/g)	0.4 ± 0	0.4 ± 0
K (mg/g)	0.6 ± 0.1	0.4 ± 0.1
Fe (µg/g)	3.8 ± 1.2	5.1 ± 1
Al (µg/g)	0.8 ± 0.2	1.5 ± 0.3
Cu (µg/g)	0.4 ± 0	0.4 ± 0
Zn (µg/g)	30.2 ± 3.3	45.2 ± 2.8
Ni (µg/g)	0.5 ± 0.3	0.1 ± 0

Table S5. Total observed OTU richness and estimated OTU richness (Chao1 and ACE) of *Fagus* and *Picea* deadwood logs in different decay classes (DC).

Deadwood species	Parameters	DC 1	DC 2	DC 3	DC 4	Total
<i>Fagus sylvatica</i>	OTU richness	44.8 ± 6.7	62 ± 10.2	68.9 ± 9	62.7 ± 14.8	58.3 ± 5.1
	Chao1	173.3 ± 24.3	163.1 ± 20.6	161.4 ± 22.1	182.6 ± 38.8	168.4 ± 12.6
	ACE	162 ± 22.2	171.1 ± 15.6	160.9 ± 20.7	176.2 ± 31.9	165.7 ± 11.1
	cOTU richness	36.25 ± 5.38	50.83 ± 8.96	60.57 ± 8	55.67 ± 9.92	49.42 ± 4.57
<i>Picea abies</i>	OTU richness	41.8 ± 5.4	69.6 ± 6.1	68 ± 5.5	74.8 ± 8.6	65.4 ± 4.6
	Chao1	125.4 ± 15.3	162.5 ± 19.4	162.1 ± 12.7	170.7 ± 19.6	157.7 ± 10
	ACE	139.1 ± 19.5	166.8 ± 16.2	173.4 ± 16.8	186 ± 22.5	169.6 ± 11.1
	cOTU richness	31.6 ± 8.24	55.2 ± 6.04	53.6 ± 5.17	66.89 ± 8.76	54.33 ± 4.71

Table S6. Summary of fungal sequences, OTU statistics and fungal phyla distribution from MOTHUR analysis.

Parameter	<i>Fagus</i>	<i>Picea</i>
Total sequences	39,640	42,163
Average sequences per sample	1,651.63	1,756.79
Total OTUs in all samples	506	504
Average OTUs per sample	58.29	65.41
Number of OTUs per phylum:		
Ascomycota	265	217
Basidiomycota	201	242
zygomycetes	6	7
Entomophthoromycota	0	1
Glomeromycota	0	1
Chytridiomycota	1	1
Unknown fungal OTUs	33	35

Table S7. Relationships between fungal richness, abundances of fungal families and cOTUs and activities of ligninolytic enzymes revealed by non-parametric Kendall-tau correlation analysis. Significant correlation ($P < 0.05$) are displayed in **bold**. Marginal significant correlations ($P < 0.1$) are displayed in *italics*.

Parameter	Enzyme activities in <i>Fagus</i> (mU/g)			Enzyme activities in <i>Picea</i> (mU/g)		
	Laccase	MiP	MnP	Laccase	MiP	MnP
Fungal OTU richness (observed)	-0.09	-0.23	-0.04	-0.34	-0.14	-0.24
Fungal cOTU richness	-0.12	-0.25	-0.10	-0.16	-0.16	-0.26
Fungal OTU richness (Chao1)	0.01	-0.13	0.07	-0.26	-0.04	-0.15
Fungal OTU richness (ACE)	0.02	-0.22	0.09	-0.24	-0.07	-0.18
Family abundances						
Agaricomycetes I.S.	0.27	0.00	0.11	0.22	0.01	0.06
<i>Bondarzewiaceae</i>	NA	NA	NA	0.23	0.37	0.45
<i>Chaetosphaeriaceae</i>	-0.16	-0.30	-0.25	-0.12	-0.07	-0.08
<i>Coniochaetaceae</i>	-0.18	-0.06	-0.20	-0.34	-0.23	-0.27
<i>Dacrymycetaceae</i>	0.02	-0.13	-0.32	-0.43	-0.38	-0.44
<i>Diatrypaceae</i>	-0.18	-0.01	0.07	NA	NA	NA
<i>Fomitopsidaceae</i>	-0.21	-0.18	0.07	-0.24	-0.21	-0.24
<i>Helotiaceae</i>	-0.06	-0.01	-0.11	-0.09	-0.02	-0.14
<i>Helotialaceae</i>	NA	NA	NA	-0.27	-0.14	-0.25
<i>Herpotrichiellaceae</i>	-0.11	0.07	-0.15	-0.29	-0.17	-0.36
<i>Hyaloscyphaceae</i>	-0.12	-0.37	-0.19	-0.01	-0.02	-0.02
<i>Leotiaceae</i>	0.02	0.23	-0.08	NA	NA	NA
<i>Marasmiaceae</i>	0.05	0.04	0.22	-0.05	-0.02	-0.12
<i>Meruliaceae</i>	0.23	0.06	0.23	-0.23	-0.10	-0.17
mitosporic Helotiales	-0.04	-0.42	-0.09	0.09	0.04	0.12
<i>Mycenaceae</i>	0.19	0.10	-0.20	-0.30	-0.14	-0.33
<i>Peniophoraceae</i>	0.10	0.22	0.04	NA	NA	NA
<i>Physalacriaceae</i>	0.11	0.01	0.07	0.22	0.06	0.18
<i>Polyporaceae</i>	0.09	-0.08	0.23	-0.07	-0.12	-0.14
<i>Schizoporaceae</i>	0.30	0.01	0.10	-0.22	0	-0.06
<i>Stereaceae</i>	NA	NA	NA	0.08	0	0.03
<i>Strophariaceae</i>	-0.21	0.24	0.25	-0.15	-0.11	0.14
<i>Trechisporaceae</i>	NA	NA	NA	0.02	0.22	0.19
<i>Xylariaceae</i>	-0.02	0.32	0.17	-0.08	0.01	-0.11
cOTU abundances						
<i>Amylostereum areolatum</i>	NA	NA	NA	-0.11	-0.20	-0.16
<i>Amylostereum chailletii</i>	NA	NA	NA	0.16	0.13	0.09
<i>Annulohypoxylon cohaerens</i>	-0.07	0.37	-0.19	NA	NA	NA
<i>Armillaria cepistipes</i>	0.02	-0.04	-0.02	0.14	0.00	0.14
<i>Armillaria gallica</i>	-0.20	-0.22	-0.03	0.32	0.17	0.30
<i>Ascocoryne cylichnium</i>	0.14	-0.30	-0.12	-0.11	-0.02	-0.09
<i>Ascocoryne sarcoides</i>	-0.12	0.08	-0.18	NA	NA	NA
<i>Bjerkandera adusta</i>	0.10	0.30	0.19	NA	NA	NA
<i>Botryobasidium botryosum</i>	NA	NA	NA	-0.03	0.10	0.01
<i>Calocera cornea</i>	-0.01	-0.22	-0.22	NA	NA	NA
<i>Ceriporiopsis gilvescens</i>	0.13	-0.01	0.18	NA	NA	NA
<i>Dacrymyces stillatus</i>	NA	NA	NA	-0.30	-0.30	-0.35
<i>Eutypa spinosa</i>	-0.16	-0.03	0.18	NA	NA	NA
<i>Fomes fomentarius</i>	0.12	0.12	0.26	NA	NA	NA
<i>Fomitopsis pinicola</i>	-0.21	-0.18	0.07	-0.19	-0.22	-0.20
<i>Heterobasidion sp.</i>	NA	NA	NA	0.23	0.37	0.45
<i>Hyphodontia alutacea</i>	NA	NA	NA	-0.25	-0.11	-0.19
<i>Hyphodontia alutaria</i>	NA	NA	NA	0.05	0.23	0.16
<i>Hypoxylon fragiforme</i>	-0.09	0.32	-0.06	NA	NA	NA
<i>Hypoxylon rubiginosum</i>	0.33	0.42	0.19	NA	NA	NA

Parameter	Enzyme activities in <i>Fagus</i> (mU/g)			Enzyme activities in <i>Picea</i> (mU/g)		
	Laccase	MiP	MnP	Laccase	MiP	MnP
<i>Marasmius alliaceus</i>	0.09	0.22	0.31	NA	NA	NA
<i>Megacollybia platyphylla</i>	-0.05	-0.23	0.09	NA	NA	NA
<i>Mycena alnetorum</i>	0.43	0.12	0.13	-0.05	0.08	-0.06
<i>Mycena purpureofusca</i>	-0.08	-0.24	-0.42	NA	NA	NA
<i>Mycena rubromarginata</i>	NA	NA	NA	-0.41	-0.25	-0.41
<i>Neobulgaria pura</i>	0.08	0.35	0.02	NA	NA	NA
<i>Oudemansiella mucida</i>	0.14	0.21	0.20	NA	NA	NA
<i>Peniophora incarnata</i>	0.10	0.22	0.04	NA	NA	NA
<i>Peniophorella praetermissa</i>	0.26	-0.03	0.01	0.03	-0.05	-0.10
<i>Phialocephala dimorphospora</i>	-0.12	-0.37	-0.18	NA	NA	NA
<i>Phlebia livida</i>	0.05	0.06	0.20	-0.12	0.05	-0.19
<i>Resinicium bicolor</i>	0.21	0.09	0.02	0.29	0.10	0.12
<i>Scopolooides hydroides</i>	0.02	-0.29	-0.18	NA	NA	NA
<i>Sistotrema brinkmanii</i>	0.01	0.13	0.09	-0.09	-0.13	-0.11
<i>Trametes versicolor</i>	0.00	-0.15	0.09	NA	NA	NA
<i>Xylaria hypoxylon</i>	-0.13	0.16	0.00	NA	NA	NA

Table S8. Relationships between fungal richness, abundances of fungal families and cOTUs and wood decomposition rates as revealed by non-parametric Kendall-tau correlation analysis. Significant correlation ($P < 0.05$) are displayed in **bold**. Marginal significant correlations ($P < 0.1$) are displayed in *italics*.

Parameter	<i>Fagus</i>		<i>Picea</i>	
	τ	<i>P</i>	τ	<i>P</i>
Fungal OTU richness (observed)	0.06	0.672	0.17	0.258
Fungal cOTU richness	0.07	0.636	0.20	0.20
Fungal OTU richness (Chao1)	0.01	0.921	0.13	0.382
Fungal OTU richness (ACE)	0.02	0.882	0.13	0.382
Family abundances				
Agaricomycetes I.S.	-0.12	0.421	-0.29	0.058
<i>Bondarzewiaceae</i>	NA	NA	0.08	0.596
<i>Chaetosphaeriaceae</i>	0.23	0.123	-0.19	0.181
<i>Coniochaetaceae</i>	0.10	0.501	-0.07	0.655
<i>Dacrymycetaceae</i>	0.26	0.070	-0.12	0.357
<i>Diatrypaceae</i>	0.10	0.495	NA	NA
<i>Fomitopsidaceae</i>	0.10	0.480	-0.23	0.185
<i>Helotiaceae</i>	0.08	0.588	0.13	0.312
<i>Helotiales</i>	NA	NA	0.21	0.224
<i>Herpotrichiellaceae</i>	-0.11	0.471	-0.06	0.793
<i>Hyaloscyphaceae</i>	0.17	0.233	-0.14	0.432
<i>Leotiaceae</i>	-0.27	0.065	NA	NA
<i>Marasmiaceae</i>	-0.01	0.955	-0.13	0.474
<i>Meruliaceae</i>	-0.12	0.394	0.09	0.705
mitosporic Helotiales	0.26	0.079	0.13	0.434
<i>Mycenaceae</i>	0.15	0.305	0.15	0.450
<i>Peniophoraceae</i>	-0.22	0.131	NA	NA
<i>Physalacriaceae</i>	-0.06	0.688	0.10	0.577
<i>Polyporaceae</i>	0.16	0.280	0.25	0.161
<i>Schizoporaceae</i>	0.23	0.110	0.43	0.005
<i>Stereaceae</i>	NA	NA	-0.08	0.668
<i>Strophariaceae</i>	-0.22	0.125	0.21	0.204
<i>Trechisporaceae</i>	NA	NA	0.24	0.150
<i>Xylariaceae</i>	-0.44	0.003	-0.07	0.605
cOTU abundances				
<i>Amylostereum areolatum</i>	NA	NA	-0.18	0.252
<i>Amylostereum chailletii</i>	NA	NA	-0.03	0.846
<i>Annulohypoxylon cohaerens</i>	-0.12	0.428	NA	NA
<i>Armillaria cepistipes</i>	-0.09	0.524	0.02	0.879
<i>Armillaria gallica</i>	0.00	1.000	0.29	0.059
<i>Ascocoryne cylichnium</i>	0.19	0.193	-0.03	0.868
<i>Ascocoryne sarcoides</i>	0.06	0.678	NA	NA
<i>Bjerkandera adusta</i>	-0.07	0.629	NA	NA
<i>Botryobasidium botryosum</i>	NA	NA	0.43	0.005
<i>Calocera cornea</i>	0.25	0.091	NA	NA
<i>Ceriporiopsis gilvescens</i>	0.01	0.919	NA	NA
<i>Dacrymyces stillatus</i>	NA	NA	-0.14	0.351
<i>Eutypa spinosa</i>	0.05	0.729	NA	NA
<i>Fomes fomentarius</i>	-0.01	0.929	NA	NA
<i>Fomitopsis pinicola</i>	0.10	0.480	-0.15	0.321
<i>Heterobasidion sp.</i>	NA	NA	0.08	0.617
<i>Hyphodontia alutacea</i>	NA	NA	0.32	0.036
<i>Hyphodontia alutaria</i>	NA	NA	0.32	0.036
<i>Hypoxylon fragiforme</i>	-0.25	0.083	NA	NA
<i>Hypoxylon rubiginosum</i>	-0.23	0.122	NA	NA

Parameter	<i>Fagus</i>		<i>Picea</i>	
	τ	<i>P</i>	τ	<i>P</i>
<i>Marasmius alliaceus</i>	-0.07	0.626	NA	NA
<i>Megacollybia platyphylla</i>	0.18	0.210	NA	NA
<i>Mycena alnetorum</i>	0.04	0.790	0.45	0.003
<i>Mycena purpureofusca</i>	0.31	0.034	NA	NA
<i>Mycena rubromarginata</i>	NA	NA	0.01	0.973
<i>Neobulgaria pura</i>	-0.29	0.049	NA	NA
<i>Oudemansiella mucida</i>	0.07	0.629	NA	NA
<i>Peniophora incarnata</i>	-0.22	0.131	NA	NA
<i>Peniophorella praetermissa</i>	0.14	0.353	-0.21	0.177
<i>Phialocephala dimorphospora</i>	0.41	0.005	NA	NA
<i>Phlebia livida</i>	-0.13	0.374	NA	NA
<i>Resinicium bicolor</i>	-0.15	0.319	-0.19	0.219
<i>Scopoloides hydroides</i>	0.12	0.431	NA	NA
<i>Sistotrema brinkmanii</i>	-0.11	0.449	-0.15	0.315
<i>Trametes versicolor</i>	0.32	0.031	NA	NA
<i>Xylaria hypoxylon</i>	-0.31	0.033	NA	NA

Table S9. Fungal cOTUs and their potential roles in deadwood decomposition. FASY= *Fagus sylvatica*, PIAB = *Picea abies*.

Sample	Fungal cOTUs (Abundance in %)	Potential roles in deadwood decomposition	Published ecological role	Reference
8280 (FASY)	<i>Fomes fomentarius</i> (75.22)	laccase producer	important producer of lignocellulose-degrading enzymes endo-1,4- β - glucanase, 1,4- β -glucosidase, cellobiohydrolase, endo-1,4- β - xylanase, 1,4- β -xylosidase, MNP, and laccase	Větrovský et al. (2013)
8282 (FASY)	<i>Annulohypoxylon cohaerens</i> (46.18)	MiP producer	<i>Annulohypoxylon spp.</i> are excellent producers of hydrolytic enzymes	Robl et al. (2013)
8283 (FASY)	<i>Mycena alnetorum</i> (48.22)	laccase producer	laccase and peroxidase producer	Eduardo et al. (1997)
8298 (FASY)	<i>Trametes versicolor</i> (30.43)	important decomposer (causing high mass loss)	important decomposer (causing high mass and lignin loss)	Valmaseda et al. (1990)
8810 (FASY)	<i>Armillaria gallica</i> (18.92)	MnP producer	<i>Armillaria spp.</i> caused high mass and lignin loss	Valmaseda et al. (1990)
8818 (FASY)	<i>Kuehneromyces mutabilis</i> (36.62)	laccase producer	laccase producer	Cho et al. (1999)
8820 (PIAB)	<i>Resinicium bicolor</i> (66.50)	MiP and MnP producer	white-rot fungus able to produce ligninolytic enzymes, especially laccase	Shah et al. (2014)
8823 (PIAB)	<i>Amylostereum chailletii</i> (65.61)	important decomposer (causing high mass loss)	saprotrophic decay fungus occurring on fallen conifer logs	Vasiliauskas et al. (1998)
8825 (PIAB)	<i>Resinicium bicolor</i> (62.97)	laccase producer	white-rot fungus able to produce ligninolytic enzymes, especially laccase	Shah et al. (2014)
8828 (FASY)	<i>Trametes versicolor</i> (87.51)	important decomposer (causing high mass loss)	important decomposer (causing high mass and lignin loss)	Valmaseda (1990)
8832 (FASY)	<i>Phlebia livida</i> (43.49)	laccase producer	<i>Phlebia spp.</i> known as laccase producers	Arora & Rampal (2002)

Figure S1. Number of sequence reads and number of detected OTUs (rarefaction curves calculated as individual rarefaction in PAST) of all samples used in the study. Four decay classes of (a) *Fagus* (FASY) and (b) *Picea* (PIAB) differentiated by line colors.

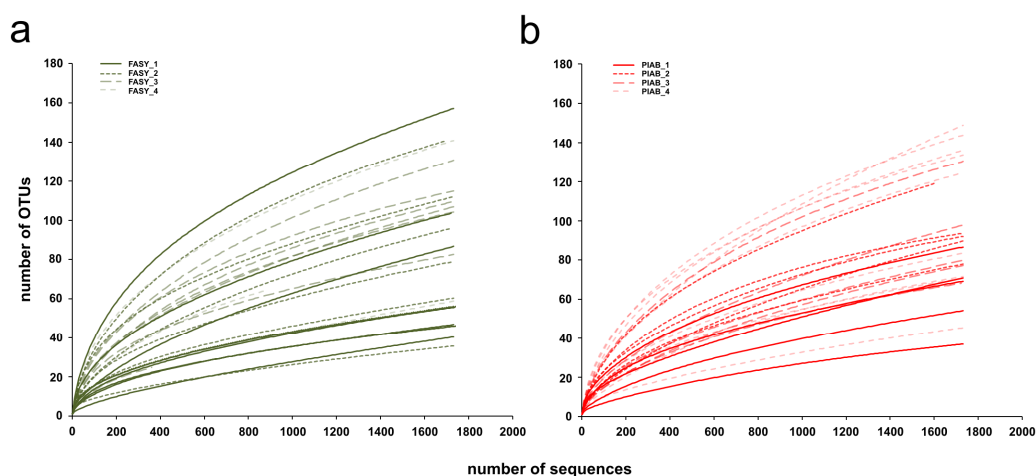


Figure S2. Relationships between fungal OTUs richness and decay classes (as determined by density (a) and remaining mass (b)), green = *Fagus sylvatica*, red = *Picea abies*.

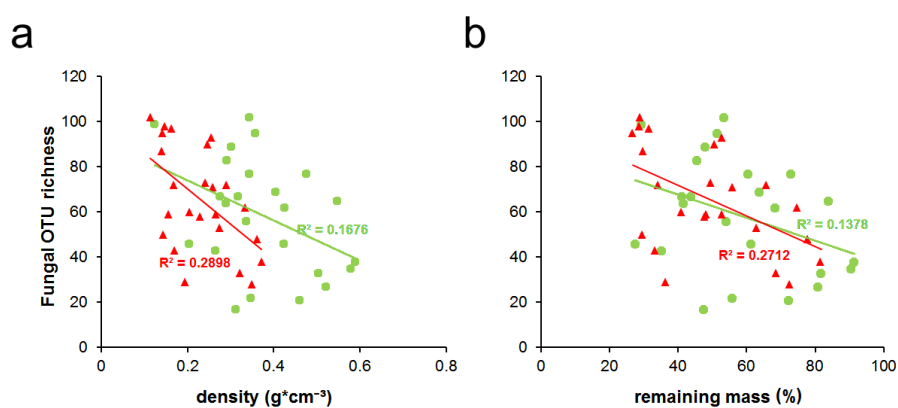


Figure S3. Heatmap displaying cOTU abundances and presences per sample. This figure is a companion to Fig. 2 of the main text and contains only the cOTUs that appear labeled in that figure. The rows are sorted by the number of sequences on the family level, which also only includes the cOTUs appearing in this table.

cOTU = species	family ^a	<i>Fagus sylvatica</i>		<i>Picea abies</i>		total		sum on family level*	
		n seqs	n samples	n seqs	n samples	n seqs	n samples	n seqs	n samples
<i>Resinicium bicolor</i>	Agaricomycetes I.S. (B)	319	11	10646	20	10965	31	10965	31
<i>Mycena alnetorum</i>	Mycenaceae (B)	1667	4	136	6	1803	10	5982	42
<i>Mycena rubromarginata</i>		0	0	1625	12	1625	12		
<i>Mycena purpureofusca</i>		1114	6	0	0	1114	6		
<i>Mycena galericulata</i>		635	4	11	2	646	6		
<i>Mycena arcangeliana</i>		0	0	535	5	535	5		
<i>Mycena crocata</i>		258	2	1	1	259	3		
<i>Annulohypoxylon cohaerens</i>	Xylariaceae (A)	2487	8	3	2	2490	10	5253	42
<i>Hypoxylon rubiginosum</i>		897	10	2	2	899	12		
<i>Xylaria hypoxylon</i>		837	3	0	0	837	3		
<i>Kretzschmaria deusta</i>		563	5	4	2	567	7		
<i>Hypoxylon fragiforme</i>		458	9	2	1	460	10		
<i>Armillaria cepistipes</i>	Physalaciaceae (B)	1858	13	999	8	2857	21	5243	45
<i>Armillaria gallica</i>		792	12	765	6	1557	18		
<i>Oudemansiella mucida</i>		829	6	0	0	829	6		
<i>Heterobasidium</i> sp.	Bondarzewiaceae (B)	6	2	4606	11	4612	13	4612	13
<i>Trametes versicolor</i>	Polyporaceae (B)	2513	7	1	1	2514	8	4409	17
<i>Fomes fomentarius</i>		1712	4	6	2	1718	6		
<i>Datronia mollis</i>		177	3	0	0	177	3		
<i>Phlebia livida</i>	Meruliaceae (B)	1588	4	4	3	1592	7	4405	33
<i>Ceriporiopsis gilvescens</i>		831	3	4	1	835	4		
<i>Scopuloides hydnoides</i>		629	9	0	0	629	9		
<i>Phlebia radiata</i>		523	2	0	0	523	2		
<i>Bjerkandera adusta</i>		413	6	1	1	414	7		
<i>Phanerochaete sordida</i>		412	4	0	0	412	4		
<i>Amylostereum areolatum</i>	Stereaceae (B)	4	2	2018	8	2022	10	3352	16
<i>Amylostereum chailletii</i>		1	1	1329	5	1330	6		
<i>Fomitopsis pinicola</i>	Fomitopsidaceae (B)	267	6	2326	8	2593	14	3300	21
<i>Antradia sinuosa</i>		1	1	402	3	403	4		
<i>Ischnoderma benzoinum</i>		0	0	304	3	304	3		
<i>Marasmius alliaceus</i>	Marasmiaceae (B)	1520	7	5	4	1525	11	2678	21
<i>Megacollybia platyphylla</i>		1150	7	3	3	1153	10		
<i>Hyphodontia alutacea</i>	Schizoporaceae (B)	5	2	880	3	885	5	2043	23
<i>Hyphodontia alutaria</i>		1	1	493	11	494	12		
<i>Hyphodontia subalutacea</i>		472	2	1	1	473	3		
<i>Hyphodontia nespori</i>		0	0	191	3	191	3		
<i>Eutypa spinosa</i>	Diatrypaceae (A)	1239	9	0	0	1239	9	1239	9
<i>Neobulgaria pura</i>	Leotiaceae (A)	1108	5	0	0	1108	5	1108	5
<i>Dacrymyces stillatus</i>	Dacrymycetaceae (B)	10	4	808	16	818	20	1069	36
<i>Calocera cornea</i>		161	13	90	3	251	16		
<i>Ascocoryne sarcoides</i>	Helotiaceae (A)	622	13	27	5	649	18	1010	42
<i>Ascocoryne cylichnium</i>		313	13	48	11	361	24		
<i>Kuehneromyces mutabilis</i>	Strophariaceae (B)	662	2	0	0	662	2	983	8
<i>Hyphaloma capnoides</i>		3	1	318	5	321	6		
<i>Peniophorella praetermissa</i>	Agaricomycetes I.S. (B)	100	6	831	11	931	17	931	17
<i>Peniophora incarnata</i>	Peniophoraceae (B)	894	4	0	0	894	4	894	4
<i>Phialocephala dimorphospora</i>	mitosporic Helotiales (A)	424	14	18	5	442	19	442	19
<i>Inonotus radiata</i>	Hymenochaetaceae (B)	437	2	2	2	439	4	439	4
<i>Sistotrema brinkmanii</i>	Hydnaceae (B)	144	10	158	11	302	21	302	21
<i>Zignoella pulviscula</i>	Chaetosphaeriaceae (A)	3	3	273	2	276	5	276	5
<i>Sistotremastrum niveocreum</i>	Trechisporaceae (B)	16	2	245	4	261	6	261	6
<i>Botrybasidium botryosum</i>	Botrybasidiaceae (B)	67	3	109	8	176	11	176	11
<i>Phialocephala fusca</i>	Ophiostomataceae (A)	2	1	162	2	164	3	164	3

(A) = Ascomycota

(B) = Basidiomycota

^afor Agaricomycetes I.S. the actual family level is not known
heatmap from white to dark within each column

Figure S4. Comparison of sharedness and species (= cOTU) distribution. Green colors indicate *Fagus*, red colors *Picea*. (a) Table of 74 species that are shared between *Fagus* and *Picea* made as MS Excel in-cell dot chart. The left and right columns are filled by a heatmap corresponding to overall cOTU size in number of sequences while the bars are relative to cOTU size within the tree species. Up to 150 sequences this dot chart is size-correct. (b) Area-correct Venn diagram for sharedness of genera (Pan-Omics Research, Pacific Northwest National Laboratory).

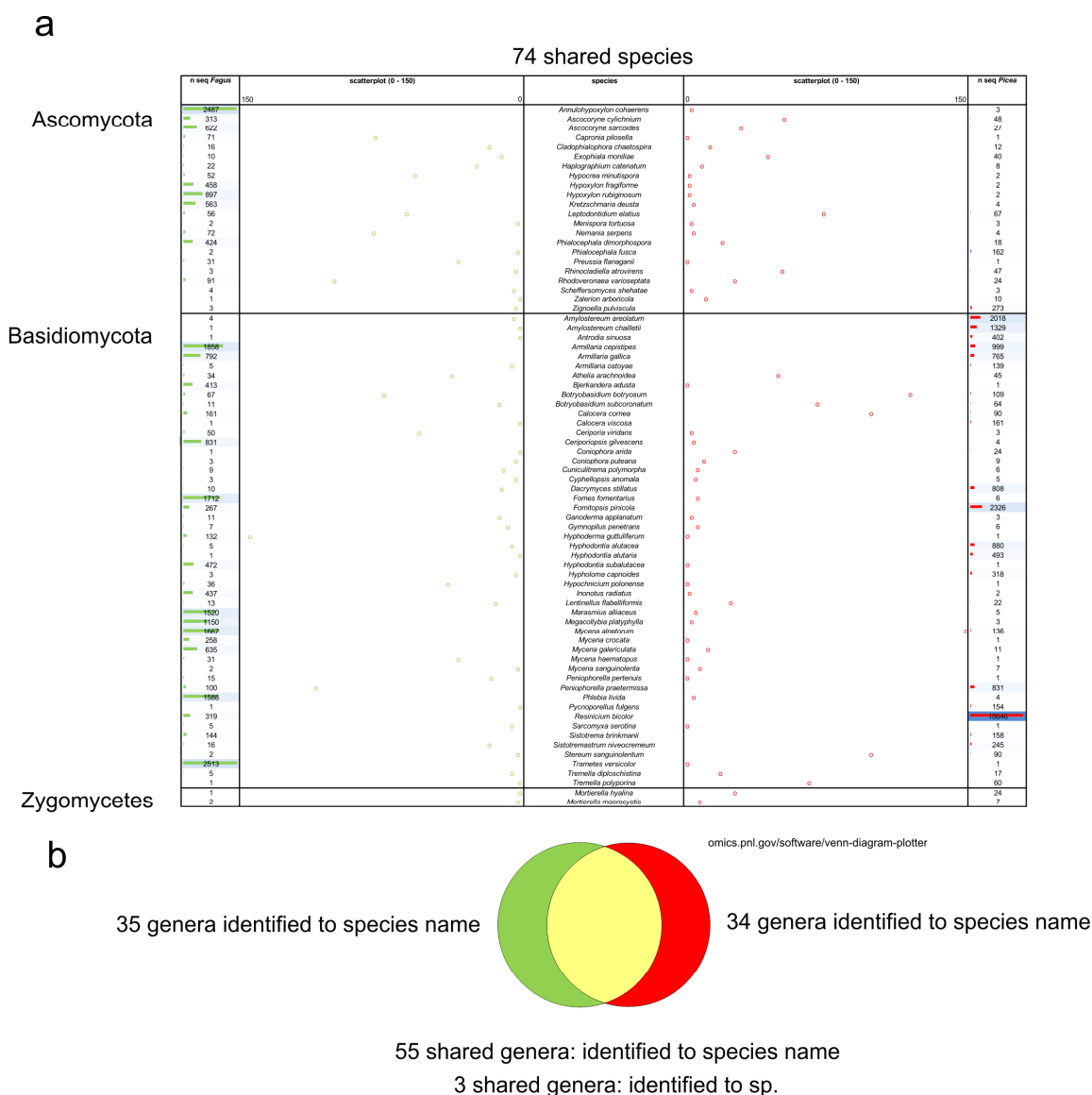


Figure S5. Heatmap (green-white) of mean abundances of highly detected fungal families and cOTUs in different decay classes (DC, labeled FASY_1 through FASY_4) in *Fagus sylvatica* deadwood logs.

<i>Fagus sylvatica</i>	FASY_1	FASY_2	FASY_3	FASY_4
Family				
<i>Xylariaceae</i>	26 ±10.2	10 ±6.7	5.15 ±3.4	0.74 ±0.6
<i>Polyporaceae</i>	14.6 ±11.1	17.8 ±11.2	11.4 ±10.5	10.1 ±8.3
<i>Physalacriaceae</i>	10.4 ±4.6	9.81 ±4.4	8.24 ±4.9	1.43 ±1.2
<i>Leotiaceae</i>	8.18 ±6.4	0.75 ±0.7	0.01	0.02
<i>Meruliaceae</i>	7.6 ±3.7	17 ±8.5	12 ±6.6	8.07 ±5
<i>Marasmiaceae</i>	0.29 ±0.2	8.4 ±5.7	11.1 ±6.3	15.5 ±12.6
<i>Mycenaceae</i>	4.95 ±3.5	5.95 ±4	9.92 ±7.8	23 ±11.5
cOTU				
<i>Annulohypoxylon cohaerens</i>	17.4 ±9	0.11 ±0.1	0	0
<i>Trametes versicolor</i>	12.3 ±10.1	4.44 ±4	0.03	10.1 ±8.3
<i>Neobulgaria pura</i>	7.43 ±6.3	0.5 ±0.5	0	0
<i>Armillaria cepistipes</i>	6.39 ±3.1	7.68 ±4.2	1.18 ±0.8	1.24 ±1
<i>Peniophora incarnata</i>	6.16 ±5.5	0.11 ±0.1	0	0
<i>Hypoxylon rubiginosum</i>	5.45 ±3.4	1.25 ±0.7	0	0
<i>Mycena alnetorum</i>	4.72 ±3.5	1.29 ±1.2	0	16.1 ±13.1
<i>Armillaria gallica</i>	3.78 ±2.2	0.9 ±0.5	1.43 ±1	0.19 ±0.2
<i>Fomes fomentarius</i>	0	13.3 ±11.3	11.3 ±10.5	0
<i>Phlebia livida</i>	0	8.37 ±6.1	4.04 ±3.7	4.93 ±4
<i>Marasmius alliaceus</i>	0.29 ±0.2	7.87 ±5.8	3.61 ±2.2	7.47 ±6.1
<i>Xylaria hypoxylon</i>	0.08 ±0.1	7.65 ±7	0	0
<i>Eutypa spinosa</i>	0.31 ±0.2	4.45 ±3.1	6.22 ±5.4	0
<i>Inonotus radiata</i>	0.04	4.18 ±3.8	0	0
<i>Scopoloides hydroides</i>	0.32 ±0.3	4 ±3.4	0.26 ±0.2	3.09 ±1.3
<i>Mycena purpureofusca</i>	0.1 ±0.1	1.86 ±1.7	4.61 ±3.1	6.83 ±5.6
<i>Megacollybia platyphylla</i>	0	0.48 ±0.4	7.47 ±6.3	7.99 ±6.5
<i>Ceriporiopsis gilvescens</i>	0	0.6 ±0.5	6.26 ±5	0
<i>Oudemansiella mucida</i>	0.01	1.22 ±0.6	5.64 ±5.2	0
<i>Mycena galericulata</i>	0.02	0.02	5.15 ±4.8	0
<i>Kretzschmaria deusta</i>	0	0.19 ±0.2	4.54 ±2.9	0.74 ±0.6
<i>Hyphodontia subalutacea</i>	0	0	0	8.91 ±7.2
<i>Bjerkandera adusta</i>	0.66 ±0.5	3.19 ±2.6	0.01	0

Figure S6. Heatmap (red-white) of mean abundances of highly detected fungal families and cOTUs in different decay classes (DC, labeled PIAB_1 through PIAB_4) in *Picea abies* deadwood logs.

<i>Picea abies</i>	PIAB_1	PIAB_2	PIAB_3	PIAB_4
Family				
<i>Agaricomycetes</i> l.S.	26.4 ± 13.6	42.7 ± 3.2	29.6 ± 15.7	17 ± 8.6
<i>Stereaceae</i>	21.7 ± 10.3	1.18 ± 0.9	2.69 ± 2.4	7.31 ± 6.9
<i>Physalacriaceae</i>	14.2 ± 10.3	0	5.94 ± 3.3	0.79 ± 0.6
<i>Bondarzewiaceae</i>	12.3 ± 11	1.87 ± 1.6	18.9 ± 12.2	10.3 ± 9.7
<i>Mycenaceae</i>	7.88 ± 4.6	12.5 ± 6.7	2.77 ± 1.1	3.71 ± 2.1
<i>Fomitopsidaceae</i>	0.29 ± 0.2	7.44 ± 6.4	17.1 ± 10	5.81 ± 2.7
cOTU				
<i>Resinicium bicolor</i>	26.1 ± 13.7	36.6 ± 2.3	27.6 ± 15	16.5 ± 8.6
<i>Amylostereum areolatum</i>	19.9 ± 10	0.03	2.67 ± 2.4	0.02
<i>Heterobasidion</i> sp.	12.3 ± 11	1.87 ± 1.6	18.9 ± 12.2	10.3 ± 9.7
<i>Armillaria cepistipes</i>	6.85 ± 5	0	3.5 ± 3	0.58 ± 0.5
<i>Armillaria gallica</i>	6.11 ± 5.5	0	2.43 ± 2.1	0.03
<i>Mycena rubromarginata</i>	5.18 ± 2.9	8.66 ± 6.8	0.1 ± 0.1	2.48 ± 2
<i>Dacrymyces stillatus</i>	2.95 ± 2.5	4.31 ± 1.5	1.1 ± 0.5	0.55 ± 0.3
<i>Mycena arcangeliana</i>	2.2 ± 1.9	2.67 ± 2.4	0.74 ± 0.7	0.27 ± 0.3
<i>Amylostereum chailletii</i>	1.8 ± 1	0.12 ± 0.1	0.02	7.29 ± 6.9
<i>Peniophorella praetermissa</i>	0.3 ± 0.2	6.12 ± 4.9	2.02 ± 1.3	0.52 ± 0.5
<i>Fomitopsis pinicola</i>	0.02	7.23 ± 6.5	12.5 ± 6.9	3.71 ± 2.3
<i>Antrodia sinuosa</i>	0	0	4.49 ± 4	0.03
<i>Hyphodontia alutacea</i>	0	0	0	5.73 ± 3.6
<i>Hyphodontia alutaria</i>	0	0.01	0.09	3.08 ± 1.2

Figure S7. Some examples: *Fagus sylvatica* logs showing pseudosclerotial plates (PSPs) due to the colonization by *Xylariaceae*.



Supplemental References

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