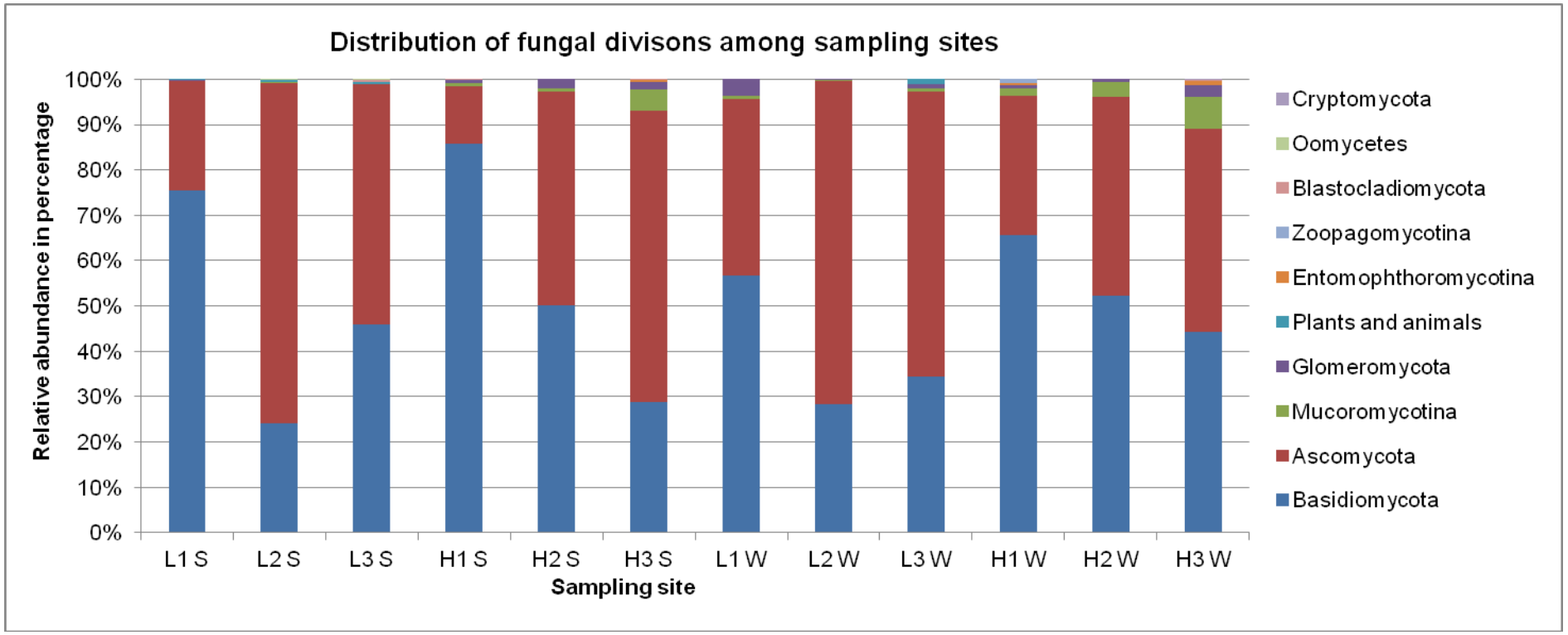
Supplementary figure 1: Distribution of fungal divisions among sampling sites (L = litter, H = humic horizon, S = summer, W = winter, 1 = site one, 2 = site two, 3 = site three)

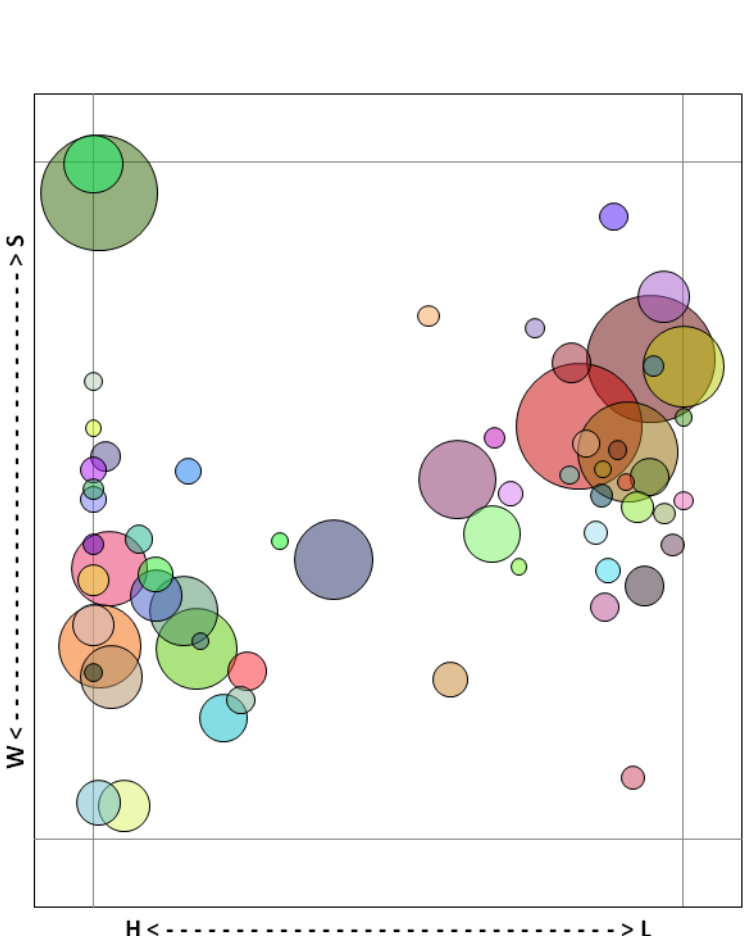


Notes to supplementary figures 2-13: Distribution of fungal sequences among horizons and seasons.

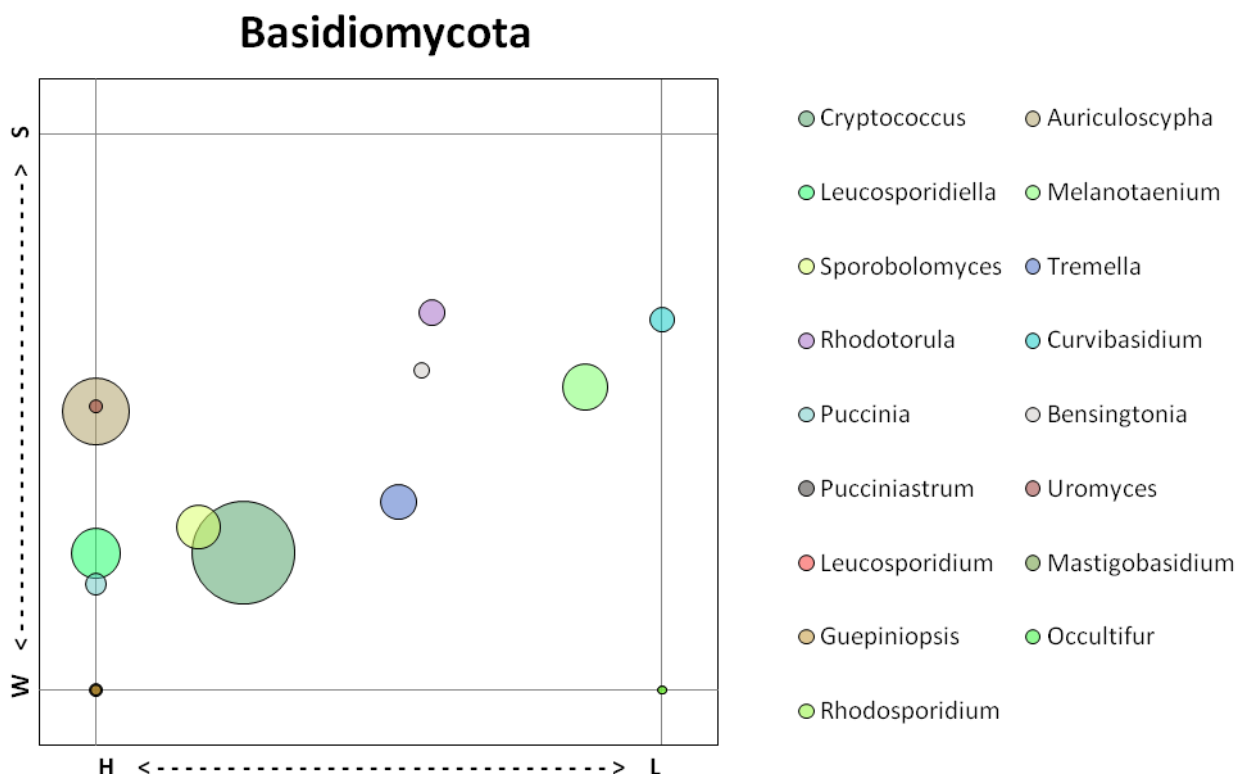
The S/W ratio indicates the relative abundance of certain taxon in the summer and is thus counted as the relative abundances in the LS + HS divided by the sum of LS + HS + LW + HW. The L/H indicates the preference of the taxon for the litter and soil and is calculated in the similar way. The position in the bottom left corner corresponds to exclusive occurrence in the soil in winter while that in the upper right corner indcates exclusive occurrence in the litter in summer.W = winter, S = summer, H = humus, L = litter

Supplement figure 2:2D graph of genera with relative abundance over 20.

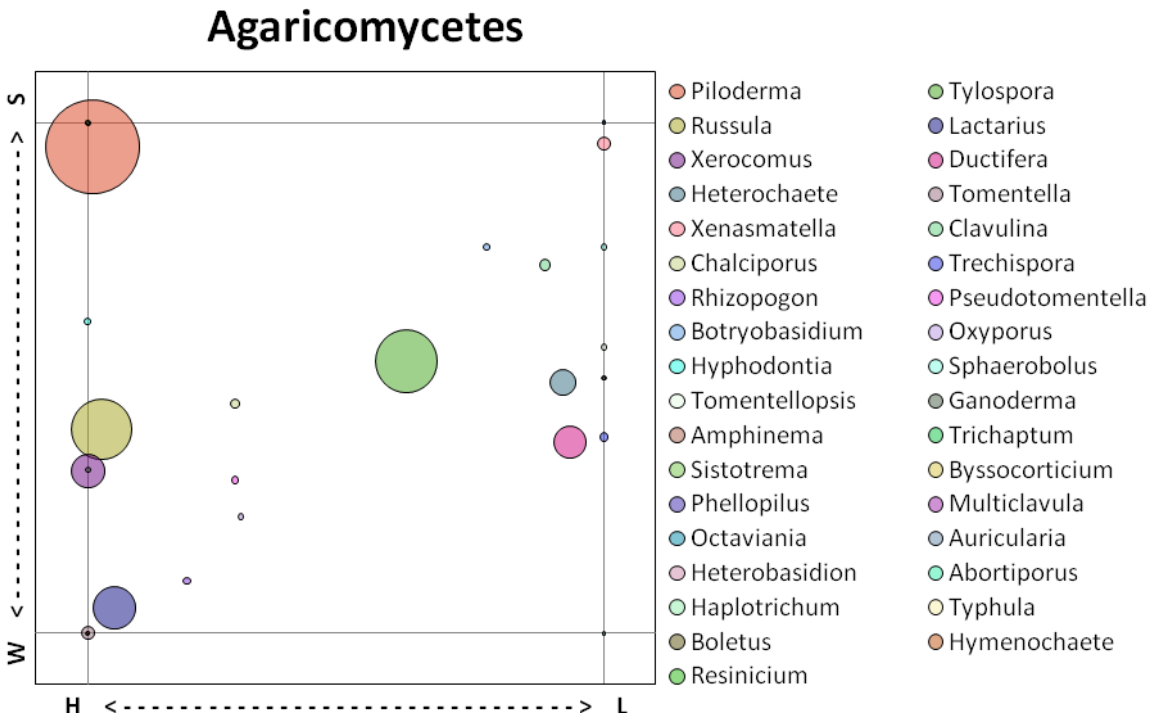
Most abundant genera of total fungal community


W <- - - -

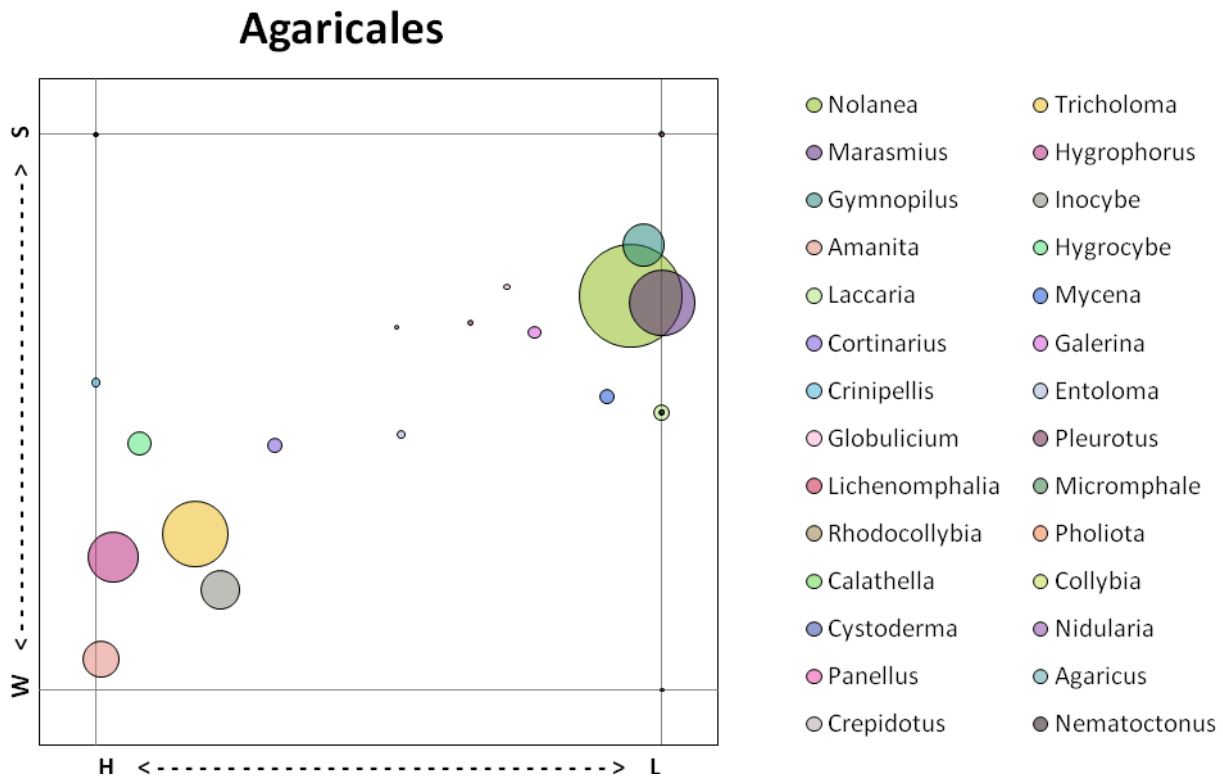
Supplement figure 3: 2D graph Basidiomycota



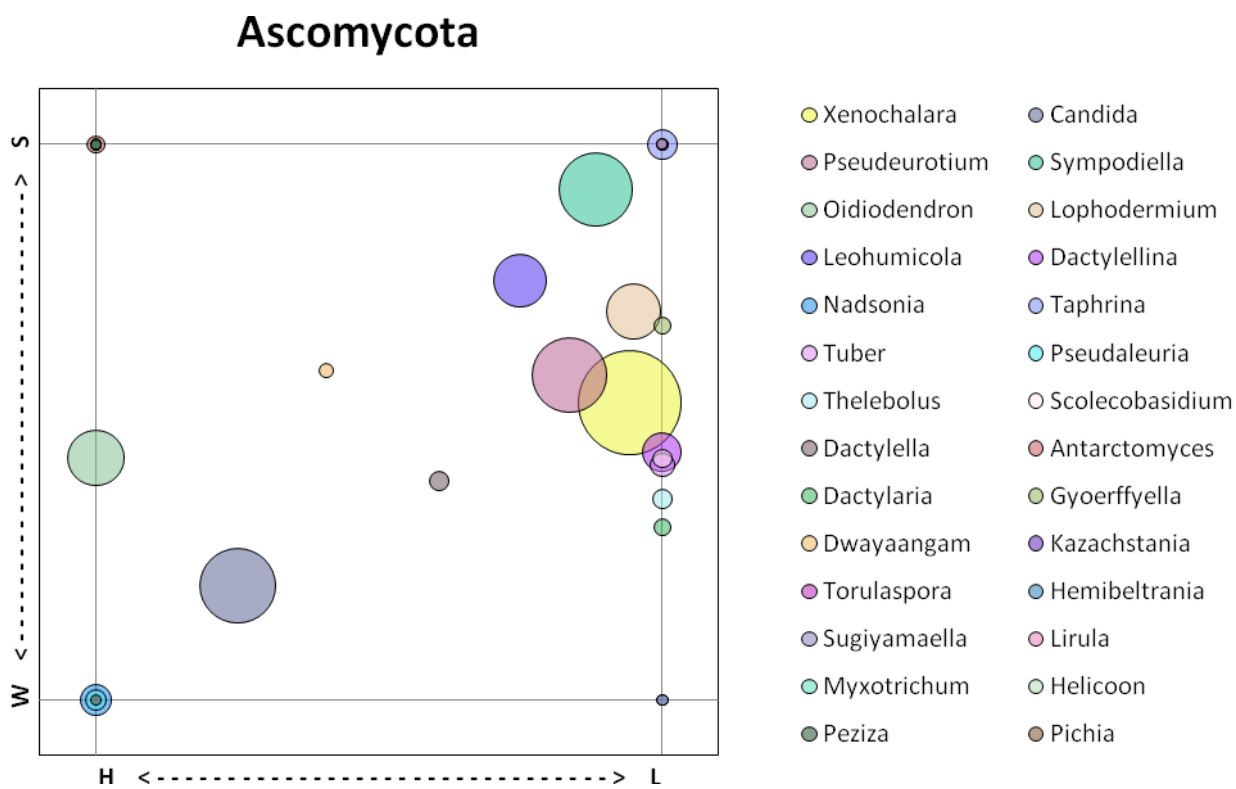
Supplement figure 4: 2D graph Agaricomycetes



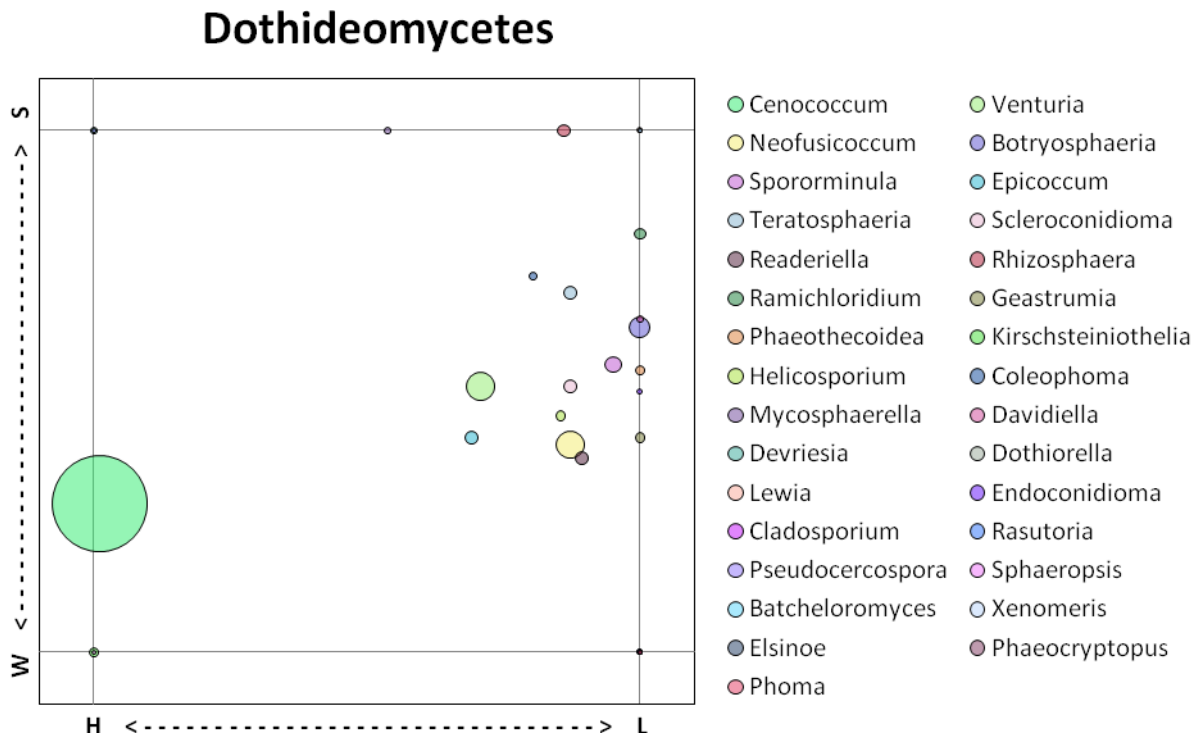
Supplement figure 5: 2D graph Agaricales



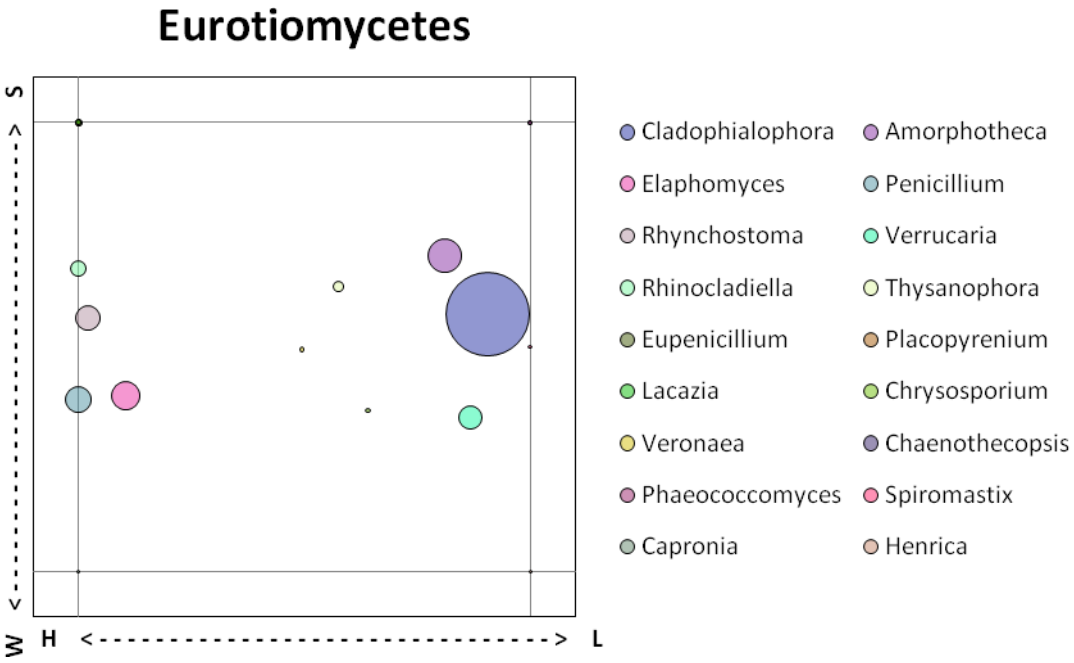
Supplement figure 6: 2D graph Ascomycota



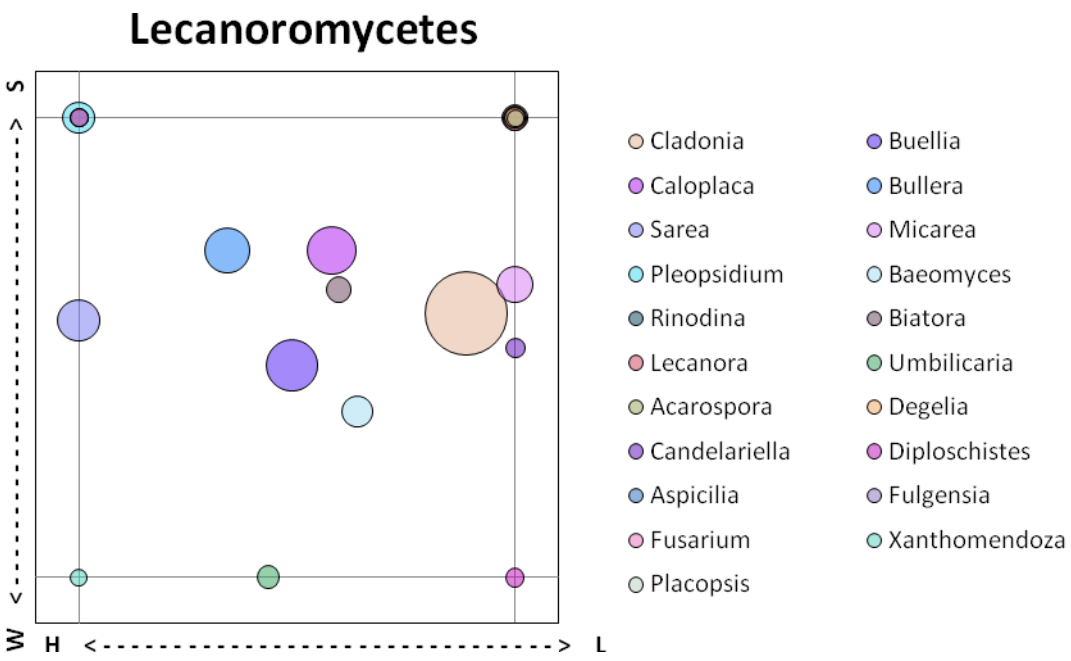
Supplement figure 7: 2D graph Dothideomycetes



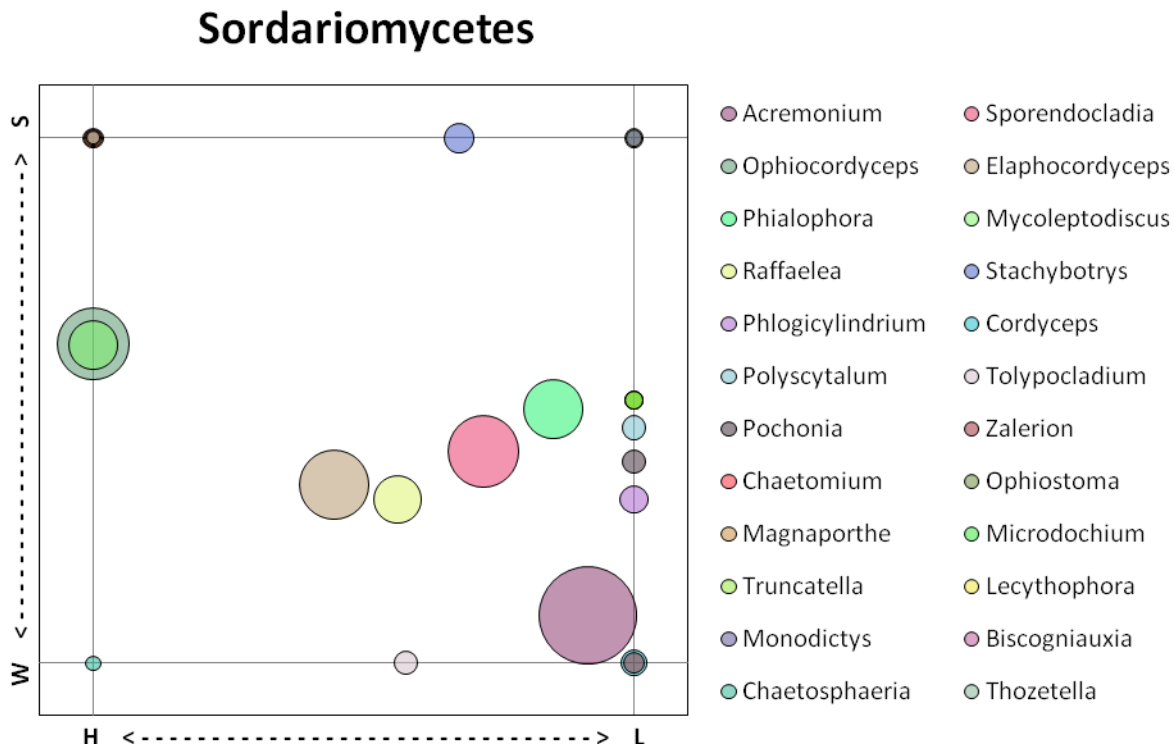
Supplement figure 8: 2D graph Eurotiomycetes



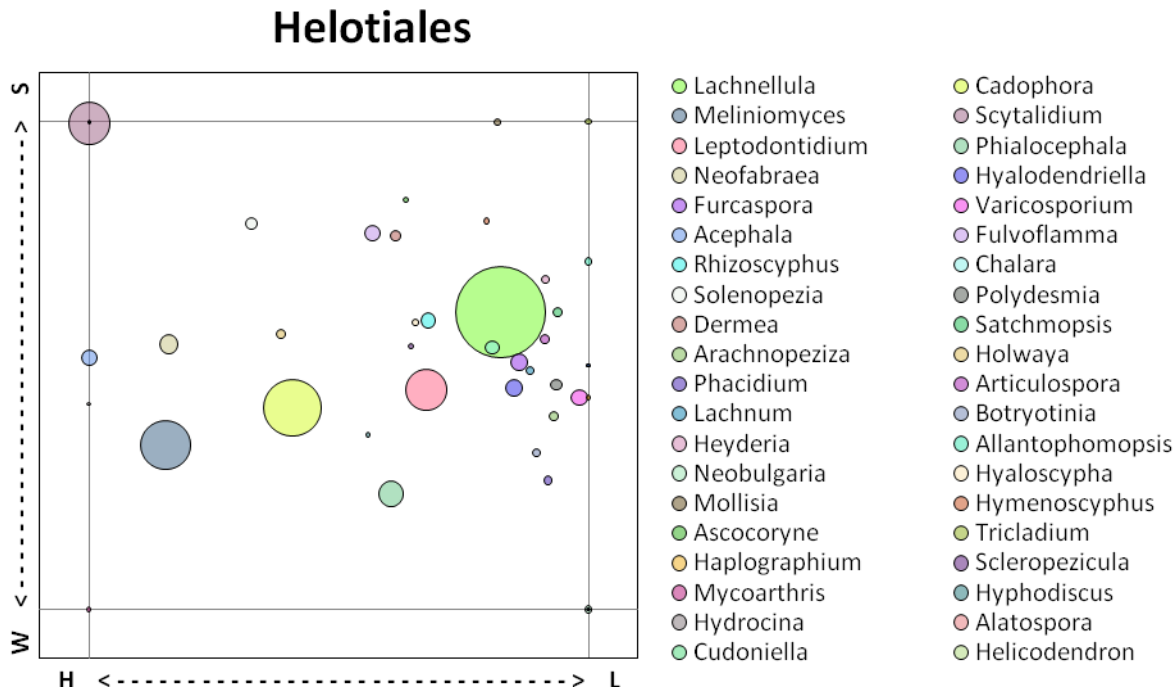
Supplement figure 9: 2D graph Lecanoromycetes



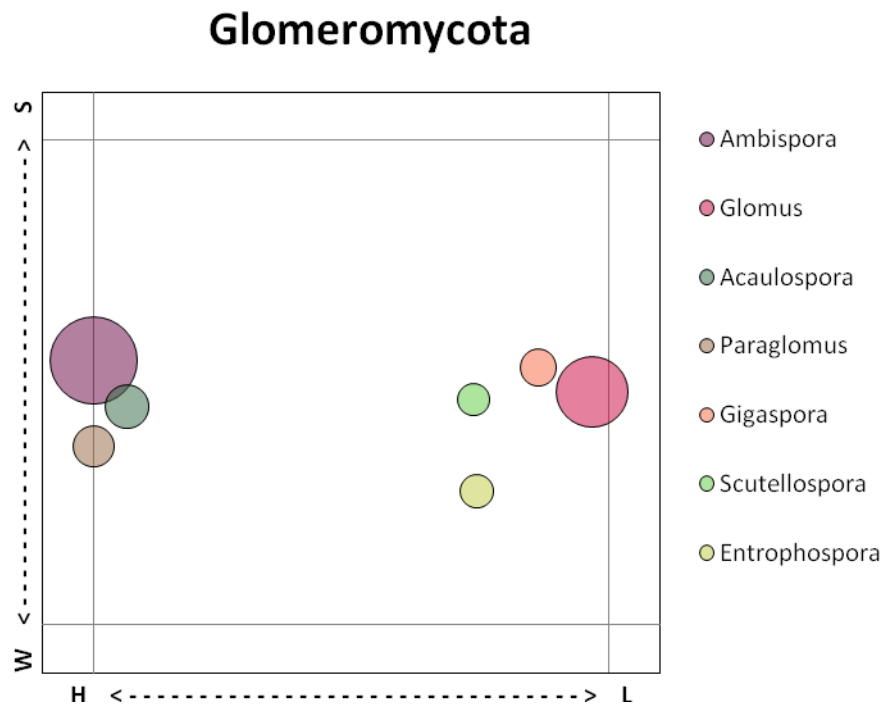
Supplement figure 10: 2D graph Sordariomycetes



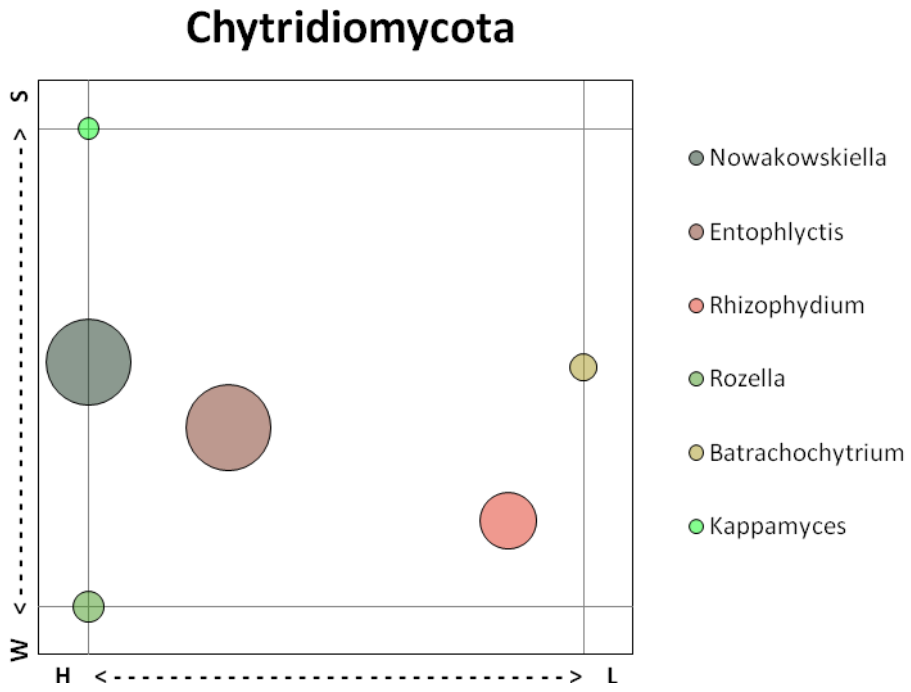
Supplement figure 11: 2D graph Helotiales



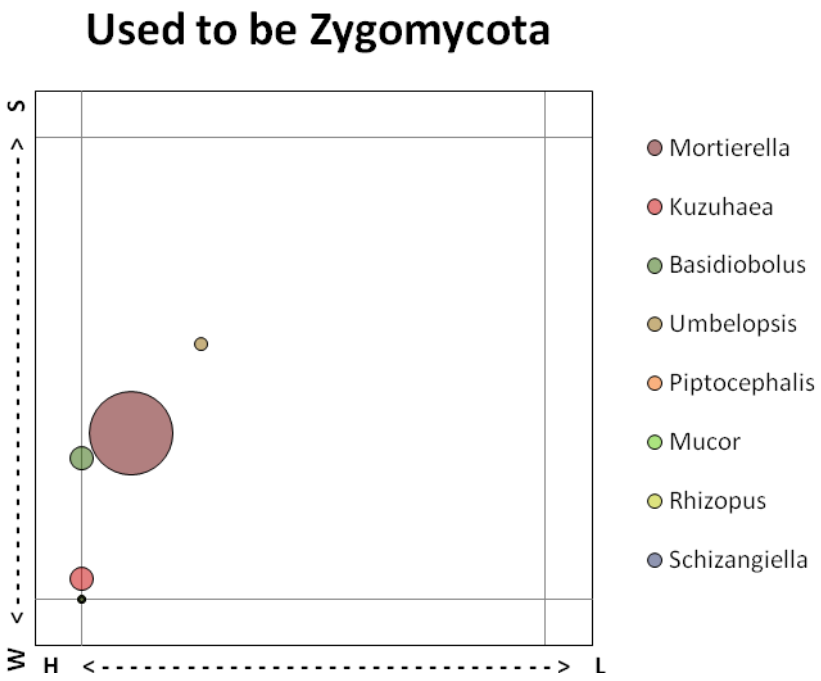
Supplement figure 12: 2D graph Glomeromycota



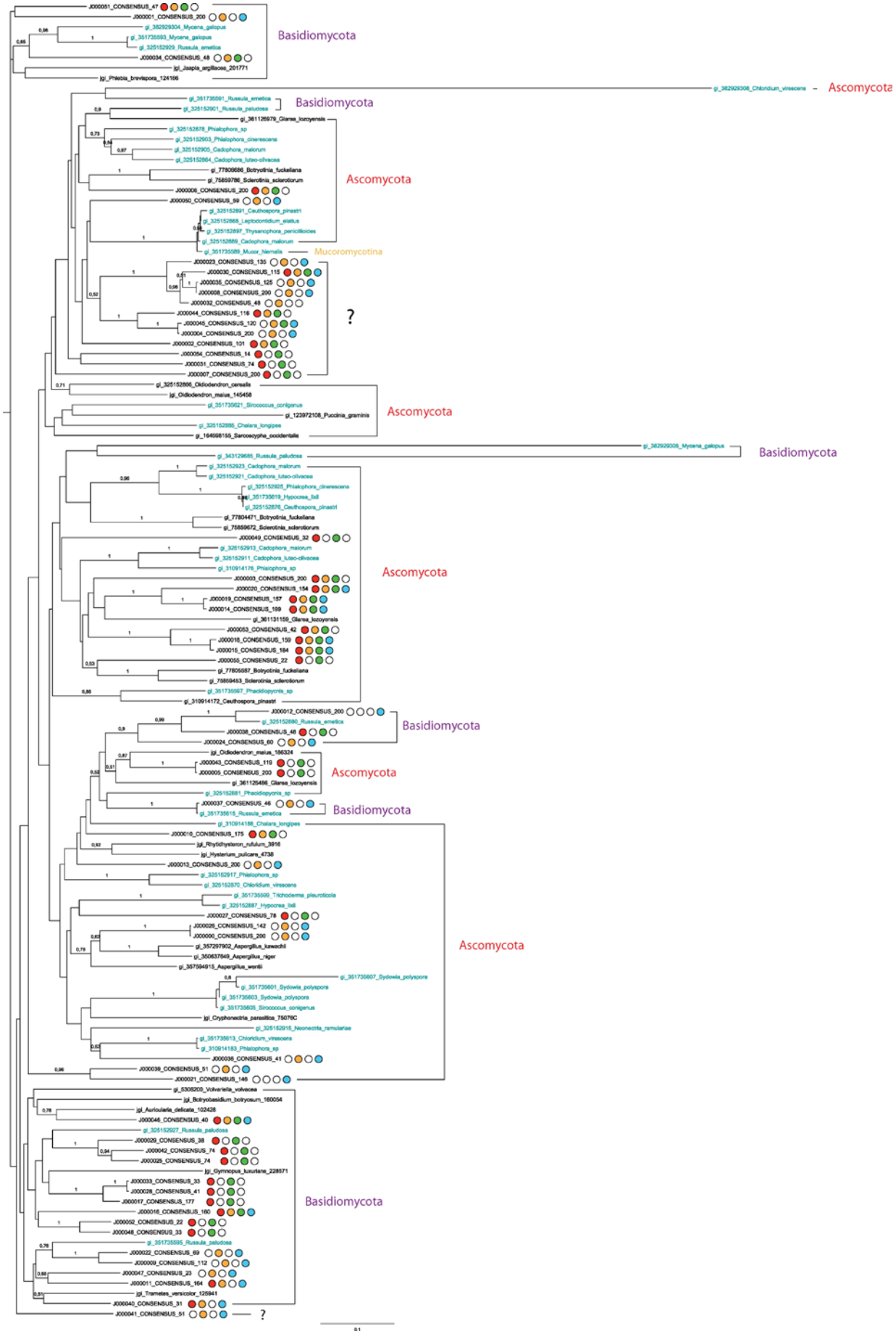
Supplement figure 13: 2D graph Chytridiomycota



Supplement figure 14: 2D graph of genera that used to be in phylum Zygomycota

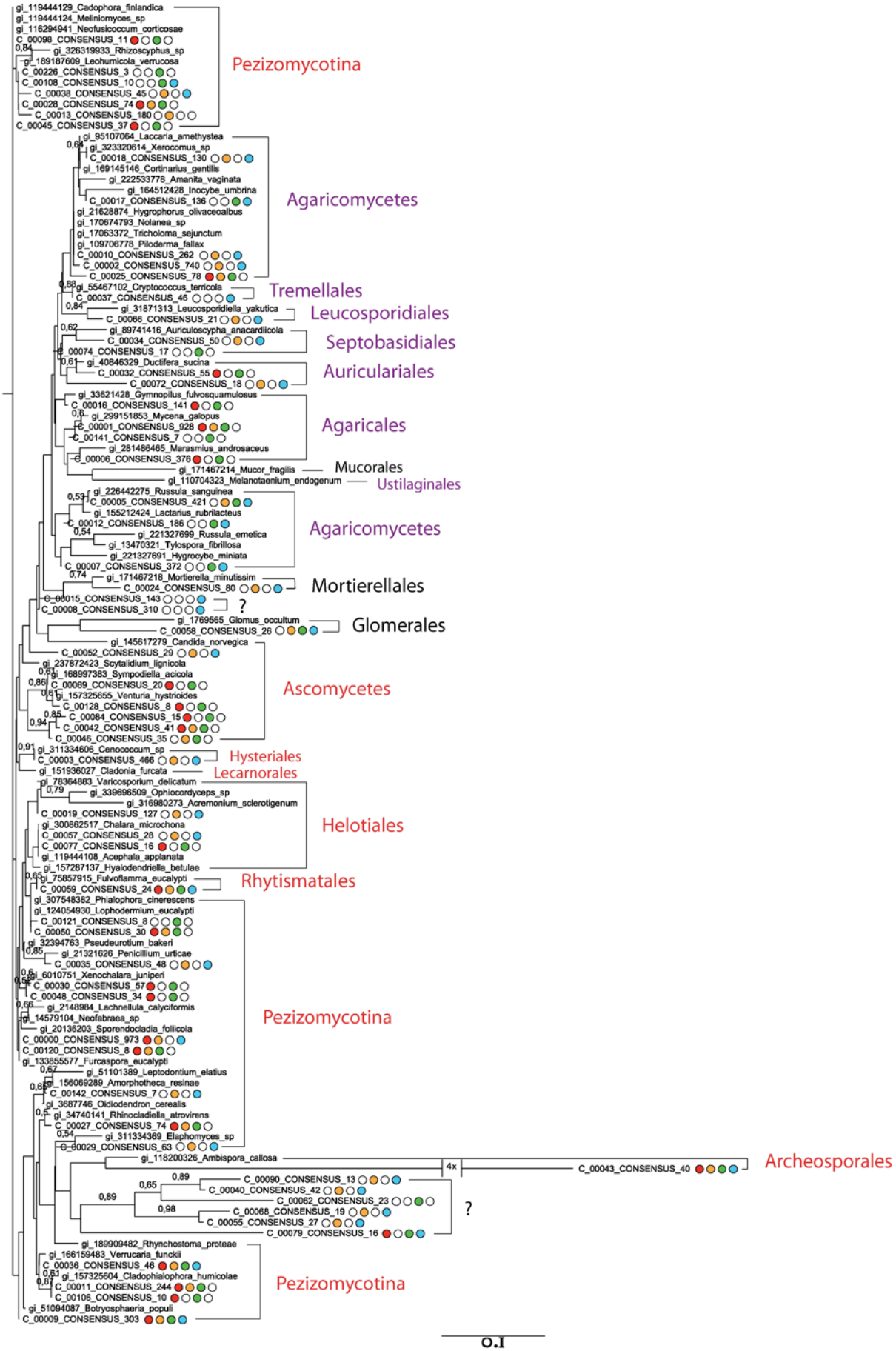


Supplementary figure 15: BioNJ phylogenetic tree based on *cbhI* sequences of 56 most abundnat OTUs. Sequences in green are cloned *cbhI* of fungi isolated by growing method from the *P.abies* needles or gained from fungal collection according to Štrusová *et al.* (2012). Sequences are marked according horizon and the season they were found in. Red circle represents LS, orange HS, green LW and blue HW in all phylogenetical trees.



Supplementary figure 16: BioNJ phylogenetic tree based on protein *CbhI* sequences. Sequences in green are clonned cbhI of fungi isolated by growing method from the *P.abies* needles or gained from fungal collection based on Štrusová (2012). Sequences are marked based on horizon and the season they were found in.

Supplementary figure 17: BioNJ phylogenetic tree based on ITS sequences of most abundant genera (over 1%). Sequences are marked based on horizon and the season they were found in. The branch of cluster 43 was shortened 4x of the length of phylogenetic distance standard at the bottom.



Supplementary table 1: Overview of statistical analyses of fungal genera with relative abundances over 20. LS, HS, LW, HW represents sums of relative abundance in each horizon and season. Canoco, Anova and Stamp are three statistics used to test significance of environmental influences on species. In the last column are percentages of PlutoF taxonomic hit, which can be the range if there were more than 1 OTUs merged into the genera or by single number when genus is based on data from 1 OTU.

Order	Genus	Ecology	Relative abundance in %	LS	HS	LW	HW	Canoco	Anova	Stamp	PlutoF % of hit
Helotiales	*Acephala*	DSE	0.29	0.00	17.82	0.00	16.64	H		H	57-100
Glomerellales	*Acremonium*	SAP	0.31	2.05	1.34	31.87	1.84				38
Agaricales	*Amanita*	ECM	1.22	0.00	6.84	1.33	138.52	H, W		H, W	90-100
Archaeosporales	*Ambispora*	ABM	0.42	0.00	27.70	0.00	23.02	H		H	26-28
Chaetothyriales	*Amorphotheca*	SAP	0.96	59.41	19.86	33.77	1.97	L, S	horizon	L, S	88-95
Septobasidiales	*Auriculoscypha*	PAR	0.38	0.00	23.09	0.00	22.93	H	horizon and season	H	72
Botryosphaeriales	*Botryosphaeria*	PAR	0.18	11.82	0.00	10.35	0.00	L	horizon	L	42-90
Helotiales	*Cadophora*	PAR	3.86	77.62	83.45	110.71	190.95			H, W	85-95
Saccharomycetales	*Candida*	SAP	0.48	1.42	6.15	12.87	36.77		season		32-35
Dothideomycetes	*Cenococcum*	ECM	4.21	0.00	140.29	5.31	359.38	H, W	season and horizon	H, W	95-100
Lecanorales	*Cladonia*	LICH	0.20	10.16	2.74	11.50	0.00	L			30-100
Chaetothyriales	*Cladophialophora*	SAP	6.16	345.11	61.66	324.53	8.48	L, S	season and horizon	L	85-95
Agaricales	*Cortinarius*	ECM	0.18	1.03	8.28	5.63	6.16				46-100
Filobasidiales	*Cryptococcus*	SAP	0.91	8.06	17.11	20.44	63.89	H, W		H, W	80-99
Auriculariales	*Ductifera*	SAP	0.96	36.61	4.86	71.01	2.70	L		L	95-97
Eurotiales	*Elaphomyces*	ECM	0.73	5.47	28.67	3.67	49.28			H	85-99
Helotiales	*Fulvoflamma*	SAP	0.27	11.97	13.21	6.54	0.86				70-90
Helotiales	*Furcaspora*	SAP	0.32	14.36	5.40	19.18	0.00		field		47
Glomerales	*Glomus*	ABM	0.27	0.00	0.00	31.77	1.05				26-38
Agaricales	*Gymnopilus*	SAP	1.60	147.40	6.25	38.18	0.00	L		L, S	90-99
Auriculariales	*Heterochaete*	SAP	0.62	30.77	5.85	38.03	0.00		field	L	98-99
Helotiales	*Hyalodendriella*	SAP	0.33	9.37	1.17	22.55	4.60	L	horizon	L	86-97
Agaricales	*Hygrocybe*	SAP	0.49	2.44	23.47	2.07	30.49	H	horizon	H	85-97
Agaricales	*Hygrophorus*	ECM	2.36	2.05	64.85	6.37	209.50	H		H	95-100

Helotiales	*Chalara*	SAP	0.22	6.69	3.24	14.68	1.84	L			83-95
Agaricales	*Inocybe*	ECM	1.41	0.00	0.00	37.14	131.69				95-99
Agaricales	*Laccaria*	ECM	0.22	0.00	0.00	26.53	0.00				61-100
Russulales	*Lactarius*	ECM	1.69	0.00	0.00	10.61	191.82				97-100
Helotiales	*Lachnellula*	SAP/PAR	9.81	514.77	202.75	454.95	4.41	L, S	field	L, S	90-100
Leotiomycetes	*Leohumicola*	SAP	0.23	14.41	5.75	5.91	1.05				84-95
Helotiales	*Leptodontidium*	DSE/ECM/Orch	2.02	72.86	14.93	91.21	63.97	L	field	L	88-97
Leucosporidiales	*Leucosporidiella*	SAP	0.21	0.00	6.10	0.00	18.65	H	horizon and season	H	78-89
Leotiomycetes	*Lophodermium*	SAP/PAR	0.25	19.10	0.67	9.37	0.86				83-95
Agaricales	*Marasmius*	SAP	4.02	316.20	0.00	165.65	0.00	L	horizon and season	L	95-100
Urocystales	*Melanotaenium*	PAR	0.18	9.47	0.00	9.33	2.95	L	horizon		29
Helotiales	*Meliniomyces*	DSE	2.88	17.68	93.77	35.37	198.96	H	season and horizon	H	90-100
Mortierellales	*Mortierella*	SAP	1.63	3.42	62.71	17.42	111.91	H, W		H	90-97
Agaricales	*Mycena*	SAP	0.19	6.82	1.34	13.59	0.86				48-98
Helotiales	*Neofabraea*	PAR	0.39	3.86	21.31	3.74	18.48			H	82-92
Botryosphaeriales	*Neofusicoccum*	PAR	0.35	11.18	5.31	25.03	0.00	L	season	L	45-54
Agaricales	*Nolanea*	SAP	10.01	686.47	64.43	448.78	1.72	L	field	L	95-100
Leotiomycetes	*Oidiodendron*	ErM	0.26	0.00	13.51	0.00	17.44	H	season and horizon	H	50-96
Hypocreales	*Ophiocordyceps*	PAR	0.17	0.00	12.23	0.00	7.91	H			34-88
Eurotiales	*Penicillium*	SAP	0.59	0.00	27.27	0.00	43.90	H	horizon and season	H	83-100
Helotiales	*Phialocephala*	DSE	0.75	9.03	3.01	45.14	32.29			L	88-98
Atheliales	*Piloderma*	ECM	8.32	0.00	952.09	10.11	36.23	H	horizon and season	H, S	88-95
Pseudeurotiaceae	*Pseudeurotium*	SAP	0.46	19.39	8.10	26.96	1.05	L		L	71-95
Chaetothyriales	*Rhinocladiella*	SAP	0.21	0.00	17.28	0.00	8.29	H		H	46-51
Helotiales	*Rhizoscyphus*	ErM	0.25	12.06	6.07	8.72	3.75				46-95
Eurotiomycetes	*Rhynchostoma*	SAP	0.52	0.00	35.24	1.26	25.78	H	horizon and season	H, S	85
Russulales	*Russula*	ECM	3.43	1.03	161.14	10.18	239.04	H	horizon and season	H	97-100
Leotiomycetes	*Scytalidium*	SAP	2.07	0.00	247.97	0.00	0.86				90-100
Microascales	*Sporendocladia*	SAP	0.17	0.00	1.84	14.63	3.81				44-91
mitosporic Ascomycota	*Sympodiella*	SAP	0.45	43.55	6.43	4.54	0.00	L, S	season	L, S	54-93
Agaricales	*Tricholoma*	ECM	4.05	27.29	99.81	57.42	300.90			H	90-95
Atheliales	*Tylospora*	ECM	3.72	117.31	119.63	158.31	51.43		field		90-100

Helotiales	*Varicosporium*	SAP	0.31	11.08	0.67	25.63	0.00	L	season	L	94
Venturiales	*Venturia*	PAR	0.36	11.81	6.154	18.52	6.382	L		L	74-98
Verrucariales	*Verrucaria*	LICH	0.50	2.833	2.97	49.31	4.986	L, W	season	L, W	35-87
mitosporic Ascomycota	*Xenochalara*	SAP/ENDO/ORCH	0.89	34.87	4.36	65.66	1.72	L		L, W	95-99
Boletales	*Xerocomus*	ECM	1.03	0.00	39.31	0.00	84.75	H	horizon and season	H, W	99-100

Supplementary table 2: Overview of statistical analyses of most abundant 56 *cbhI* OTUs. LS, HS, LW, HW represents sums of relative abundance in each horizon and season. Canoco and Anova are two statistics used to test significance of environmental influences on species. Column Phylum shows taxonomic identifications of *cbhI* OTU based on BioNJ tree Supplementary figure 15.

Cluster	**Phylum**	**Relativ abundance in %**	**LS**	**HS**	**LW**	**HW**	**Anova**	**Canoco**
0	*Ascomycota*	14.28	0.00	933.64	46.01	734.03	horizon	
1	*Basidiomycota*	7.54	0.00	505.05	0.00	399.77	horizon	H
2	*Ascomycota*	7.78	410.58	134.01	372.02	17.23	horizon	L, S
3	*Ascomycota*	7.88	387.55	163.74	394.06	0.00	horizon	L, S
4	*?*	4.74	13.44	168.71	55.65	331.43		H, W
5	*Ascomycota*	4.36	252.65	14.62	256.24	0.00	horizon	L, S
6	*Ascomycota*	4.16	263.27	58.35	174.96	2.27	horizon	L, S
7	*Ascomycota*	3.18	238.55	9.68	132.94	0.00	horizon	L, S
8	*Ascomycota*	2.31	0.00	58.07	0.00	218.77	horizon	H, W
9	*Basidiomycota*	1.42	0.00	40.17	5.19	124.69	horizon	H, W
10	*Ascomycota*	1.72	141.23	0.76	64.10	0.00	horizon	L, S
11	*Basidiomycota*	1.41	60.53	5.02	102.04	1.13	horizon	L
12	*Basidiomycota*	0.94	0.00	0.00	0.00	113.25		
13	*Ascomycota*	0.81	0.00	57.21	0.00	40.49	horizon	H
14	*Ascomycota*	1.16	5.38	46.13	37.14	50.33	horizon	H
15	*Ascomycota*	0.89	9.12	34.56	16.12	46.43		H
16	*Basidiomycota*	0.81	12.56	37.22	35.43	11.63	field	
17	*Basidiomycota*	1.20	113.21	2.43	28.86	0.00	horizon	

18	*Ascomycota*	0.75	5.38	25.66	27.11	31.30		H
19	*Ascomycota*	0.54	8.06	27.93	10.38	18.51		H
20	*Ascomycota*	0.75	2.69	8.17	46.80	32.93		
21	*Ascomycota*	0.48	0.00	0.00	0.00	57.76		
22	*Basidiomycota*	0.67	0.00	16.12	10.03	53.72	horizon	H, W
23	*Ascomycota*	0.54	0.00	19.40	3.70	42.16	horizon	H
24	*Basidiomycota*	0.60	2.69	17.91	27.70	23.54		H
25	*Basidiomycota*	0.48	48.21	0.76	8.45	0.00		L
26	*Ascomycota*	0.35	0.00	31.43	0.94	9.97	horizon	H
27	*Ascomycota*	0.45	27.09	4.11	22.60	0.00		L
28	*Basidiomycota*	0.55	41.31	0.91	24.18	0.00	horizon	L
29	*Basidiomycota*	0.47	35.39	2.58	18.44	0.00		L
30	*Ascomycota*	0.35	10.75	9.29	13.02	9.45		
31	*Ascomycota*	0.54	25.64	2.21	36.47	0.00	horizon	L
32	*Ascomycota*	0.21	0.00	23.64	0.00	1.66		
33	*Basidiomycota*	0.29	15.25	1.53	17.89	0.00		L
34	*Basidiomycota*	0.34	0.00	3.64	36.97	0.00	field	
35	*Ascomycota*	0.27	0.00	9.14	0.00	22.79	horizon	H, W
36	*Ascomycota*	0.23	0.00	12.99	0.00	14.57	horizon	H
37	*Basidiomycota*	0.18	0.00	20.39	0.00	1.13		
38	*Basidiomycota*	0.35	17.13	0.91	23.56	0.00	horizon	L
39	*Ascomycota*	0.22	0.00	11.53	0.00	15.03	horizon	H
40	*Basidiomycota*	0.25	5.38	6.07	16.99	1.13		
41	*?*	0.22	0.00	24.71	0.00	2.27	field	
42	*Basidiomycota*	0.24	20.66	2.73	5.66	0.00		
43	*Ascomycota*	0.27	10.54	0.91	21.24	0.00	horizon	L
44	*Ascomycota*	0.21	12.81	0.91	11.28	0.00	field	L
45	*?*	0.20	2.69	8.57	7.55	5.58		
46	*Basidiomycota*	0.35	18.82	2.83	18.61	1.66		
47	*Basidiomycota*	0.24	0.00	5.57	10.98	12.32		
48	*Basidiomycota*	0.26	13.44	9.55	8.54	0.00		
49	*Ascomycota*	0.16	9.42	0.00	10.34	0.00		

50	*Ascomycota*	0.13	0.00	10.91	0.00	4.98		H
51	*Basidiomycota*	0.18	8.06	5.72	6.53	1.66		
52	*Basidiomycota*	0.23	13.44	3.05	10.98	0.00		
53	*Ascomycota*	0.18	8.06	5.96	7.12	0.00	field	
54	*Ascomycota*	0.23	10.02	2.60	14.67	0.00	horizon	L
55	*Ascomycota*	0.14	2.69	0.00	13.65	0.00	horizon	L, W