

Supplementary materials

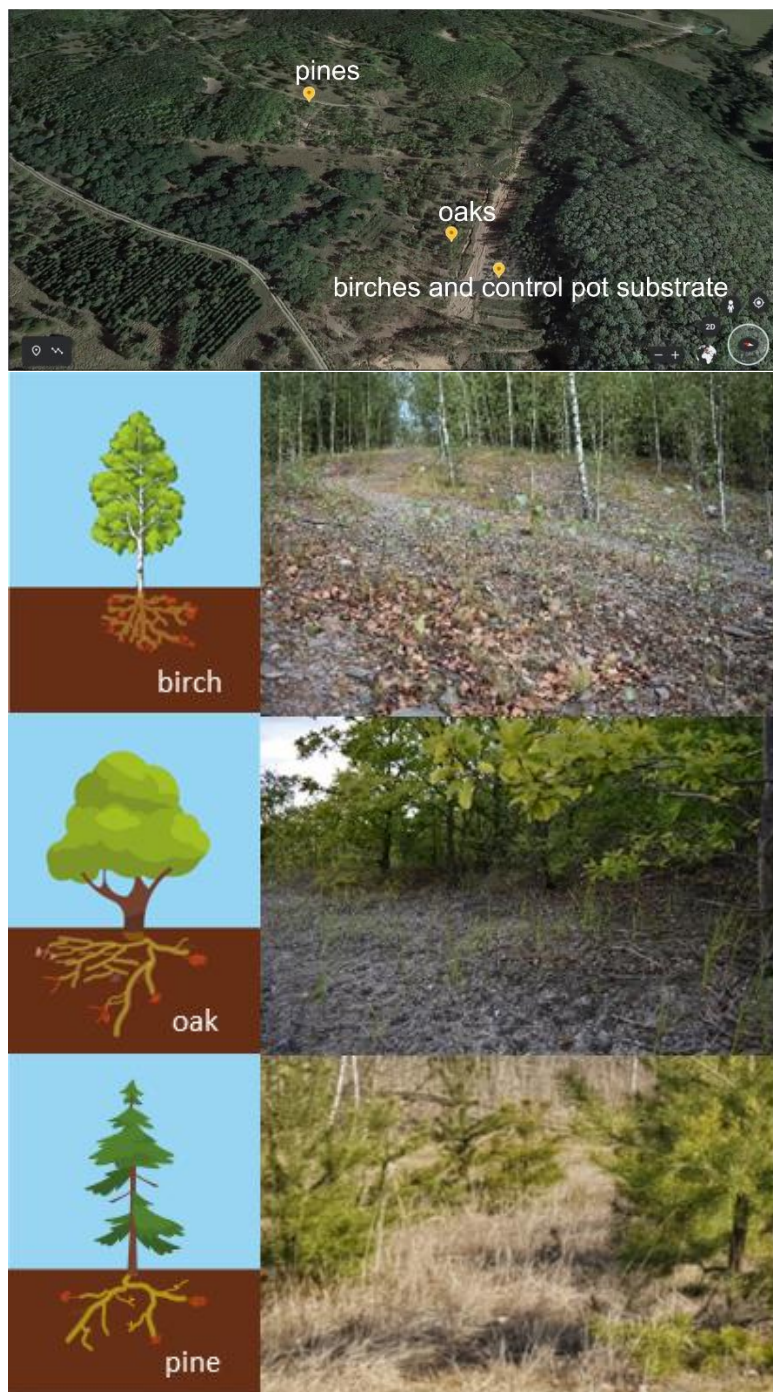


Figure S1. Sampling sites of birch, oak and pine stands at Kanigsberg near Ronneburg in the former uranium mining area, Germany, including a map from Google Earth, WEB version from 2017.

Table S1. Selected soil chemical parameters in the different variants of the experiment (Bogdanova et al. 2023)

Variant	pH	TC (%)	TN (%)	TP (mg/kg)
B_MR	4.44 ± 0.32	0.87 ± 0.24	0.11 ± 0.01	669 ± 173
B_BS	3.75 ± 0.30	1.07 ± 0.05	0.13 ± 0.01	603 ± 198
B_POT	6.03 ± 0.36	0.39 ± 0.05	0.07 ± 0.00	769 ± 285
O_MR	3.54 ± 0.10	3.45 ± 0.35	0.31 ± 0.05	786 ± 127
O_BS	3.56 ± 0.09	2.60 ± 0.85	0.27 ± 0.07	802 ± 193
O_POT	5.32 ± 0.42	0.36 ± 0.01	0.07 ± 0.00	843 ± 100
P_MR	5.20 ± 1.47	0.87 ± 0.13	0.09 ± 0.01	347 ± 61
P_BS	6.21 ± 0.53	1.11 ± 0.44	0.10 ± 0.03	369 ± 37
P_POT	5.52 ± 0.22	0.37 ± 0.01	0.07 ± 0.00	718 ± 178
SUB	3.47 ± 0.01	0.33 ± 0.01	0.07 ± 0.00	801 ± 121

B, birch; O, oak; P pine; MR, mycorrhizosphere of field plant; BS, bulk soil; SUB, control pot substrate;
TC, total carbon content; TN, total nitrogen content; TP total phosphorus content.

Table S2: Content of bioavailable metals (µg/g soil) in the different variants of the experiment (Bogdanova et al. 2023)

Variant	Al	Cd	Co	Cr	Cu	Fe	Mn	Mo	Ni	Pb	Sr	V	Zn	Cs	U
B_MR1	320.000	0.031	0.442	0.143	9.060	43.600	8.412	0.065	0.440	0.013	0.258	0.065	0.842	0.145	2.976
B_BS1	311.200	0.044	0.664	0.297	9.840	58.930	11.160	0.065	0.560	0.013	0.285	0.065	1.100	0.118	2.775
B_MR2	344.100	0.032	0.620	0.200	10.240	47.500	10.657	0.065	0.600	0.013	0.281	0.065	0.900	0.125	2.887
B_BS2	328.300	0.022	0.390	0.200	11.900	24.470	10.400	0.065	0.400	0.013	0.287	0.065	1.100	0.097	3.115
B_MR3	298.900	0.035	0.481	0.180	11.700	71.400	10.820	0.065	0.501	0.013	0.313	0.065	1.300	0.078	2.660
B_BS3	262.900	0.022	0.334	0.125	7.860	10.360	7.056	0.065	0.250	0.078	0.292	0.065	0.671	0.122	3.746
O_MR1	7.000	0.217	0.560	0.125	4.740	5.393	126.200	0.234	0.870	0.091	3.222	0.652	5.220	0.038	0.493
O_BS1	6.500	0.058	0.413	0.125	3.420	1.870	22.768	0.130	0.930	0.015	1.554	1.080	0.650	0.029	0.729
O_MR2	6.500	0.072	0.635	0.160	4.040	1.821	45.400	0.180	1.590	0.032	1.902	0.960	1.150	0.027	0.860
O_BS2	6.500	0.114	0.610	0.125	3.720	2.280	55.800	0.187	0.930	0.042	1.898	0.740	2.950	0.123	0.799
O_MR3	7.700	0.127	0.688	0.140	2.863	3.999	73.330	0.173	1.280	0.119	2.889	0.263	3.250	0.236	0.712
O_BS3	6.500	0.099	0.671	0.140	4.400	2.300	49.847	0.159	1.270	0.085	3.268	0.884	1.020	0.033	0.868
P_MR1	9.400	0.046	0.399	0.125	3.670	1.510	50.480	0.065	0.950	0.453	10.900	0.065	0.750	0.035	3.516
P_BS1	10.220	0.041	0.630	0.450	2.930	1.600	58.450	0.065	1.080	0.465	11.075	0.065	0.700	0.045	2.639
P_MR2	38.000	0.320	2.400	0.125	9.734	2.300	218.000	0.065	7.445	0.510	14.198	0.077	7.800	0.082	6.810
P_BS2	189.400	0.079	1.186	0.125	12.010	8.360	45.941	0.065	1.710	2.576	11.079	0.065	3.800	0.105	5.199
P_MR3	8.100	0.038	0.313	0.125	2.560	2.666	67.450	0.114	0.580	0.369	43.980	0.157	0.650	0.029	4.414
P_BS3	6.800	0.020	0.232	0.125	1.770	1.300	13.582	0.065	0.400	0.340	11.875	0.065	0.650	0.047	3.829
SUB	312.200	0.042	1.230	0.125	8.410	8.970	24.800	0.065	0.460	0.013	1.131	0.065	1.380	0.094	1.419

B, birch; O, oak; P pine; MR, mycorrhizosphere of field plant; BS, bulk soil; SUB, control pot substrate.

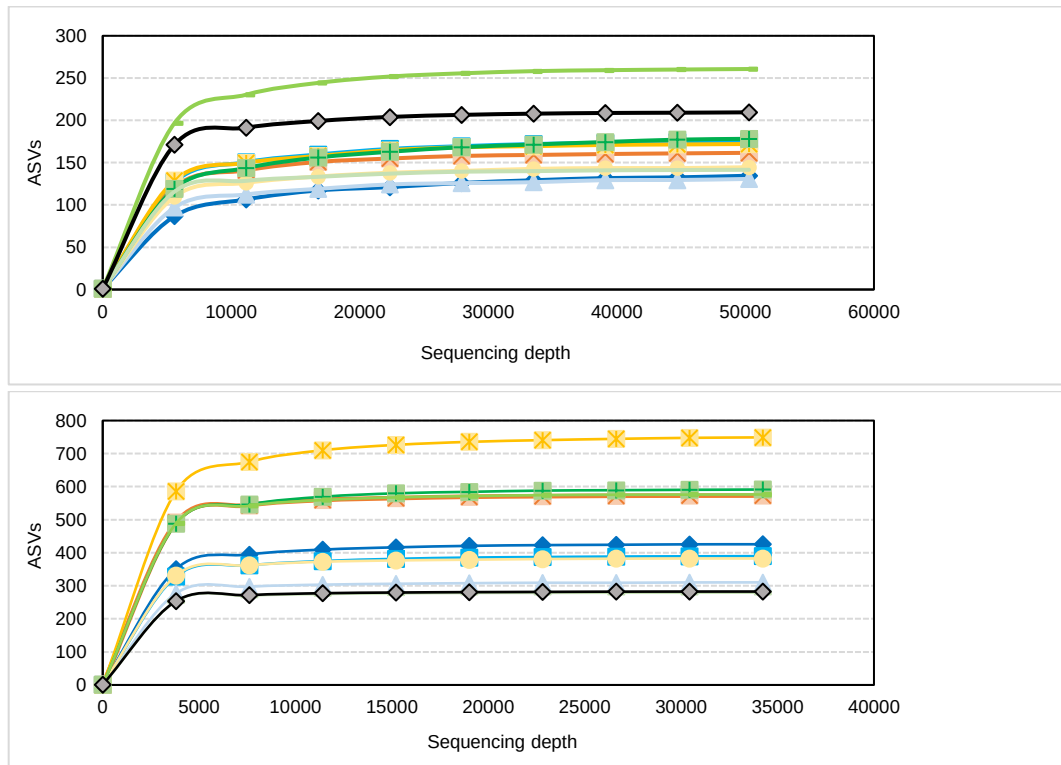


Figure S2. Rarefaction curves for fungal (upper) and bacterial sequences (down). ASV, amplicon sequence variant; B, birch (blue); O, oak (orange); P, pine (green); MR, mycorrhizosphere of field plant (dark color); BS, bulk soil (medium color); POT, mycorrhizosphere of pot plant (light color); SUB, control pot substrate (black).

Table S3. One-Way ANOVA, Kruskal-Wallis test, post hoc test output for significance of differences between variants of the experiment in diversity indices of bacterial communities.

Diversity Index	ANOVA						Kruskal-Wallis				Post Hoc comparisons						
	Cases	Sum of Squares	df	Mean Square	F	p	Factor	Statistic	df	p	Variant of comparisons		Mean Difference	SE	t	p tukey	p bonf
Richness	variant	2.521.500	1	2.521.500	0.746	0.436					B MR	B BS	-41.000	47.468	-0.864	0.436	0.436
	Residuals	13.519.333	4	3.379.833													
	variant	48.061.500	1	48.061.500	5.343	0.082					O MR	O BS	179.000	77.442	2.311	0.082	0.082
	Residuals	35.983.333	4	8.995.833													
	variant	337.500	1	337.500	0.010	0.927					P MR	P BS	-15.000	153.513	-0.098	0.927	0.927
	Residuals	141.397.333	4	35.349.333													
	variant	22.326.000	1	22.326.000	8.851	0.041					B MR	B POT	122.000	41.007	2.975	0.041*	0.041
	Residuals	10.089.333	4	2.522.333													
	variant	44.083.333	1	44.083.333	6.275	0.087					O MR	O POT	191.667	76.516	2.505	0.087	0.087
	Residuals	21.076.667	3	7.025.556													
	variant	150.416.667	1	150.416.667	4.270	0.108					P MR	P POT	316.667	153.239	2.066	0.108	0.108
	Residuals	140.893.333	4	35.223.333													
	variant	1.232.667	1	1.232.667	1.880	0.242					B POT	SUB	28.667	20.907	1.371	0.242	0.242
	Residuals	2.622.667	4	655.667													
	variant	12.241.200	1	12.241.200	4.164	0.134					O POT	SUB	101.000	49.497	2.041	0.134	0.134
	Residuals	8.820.000	3	2.940.000													
	variant	16.667	1	16.667	0.035	0.860					P POT	SUB	-3.333	17.714	-0.188	0.860	0.860
	Residuals	1.882.667	4	470.667													
	variant	47.051.556	2	23.525.778	0.875	0.464					B MR	O MR	-142.000	133.907	-1.060	0.570	0.989
	Residuals	161.380.000	6	26.896.667								P MR	-162.667	133.907	-1.215	0.488	0.810
											O MR	P MR	-20.667	133.907	-0.154	0.987	1.000
	variant	196.683.556	2	98.341.778	19.988	0.002					B BS	O BS	-362.000	57.271	-6.321	0.002*	0.002
	Residuals	29.520.000	6	4.920.000								P BS	-188.667	57.271	-3.294	0.038*	0.050
											O BS	P BS	173.333	57.271	3.027	0.053	0.070
Simpson dominance index	variant	9.923e -7	1	9.923e -7	0.384	0.569					B MR	B BS	8.133e -4	0.001	0.620	0.569	0.569
	Residuals	1.034e -5	4	2.585e -6													
							variant	1.190	1	0.275	O MR	O BS	0.005	0.004	1.154	0.313	0.313
							variant	0.429	1	0.513	P MR	P BS	-0.006	0.007	-0.899	0.419	0.419
	variant	6.787e -5	1	6.787e -5	17.007	0.015					B MR	B POT	-0.007	0.002	-4.124	0.015*	0.015
	Residuals	1.596e -5	4	3.991e -6													
	variant	6.694e -5	1	6.694e -5	8.910	0.058					O MR	O POT	-0.007	0.003	-2.985	0.058	0.058
	Residuals	2.254e -5	3	7.514e -6													
	variant	3.099e -6	1	3.099e -6	0.041	0.850					P MR	P POT	-0.001	0.007	-0.202	0.850	0.850
	Residuals	3.042e -4	4	7.605e -5													
	variant	1.012e -4	1	1.012e -4	32.639	0.005					B POT	SUB	-0.008	0.001	-5.713	0.005*	0.005
	Residuals	1.240e -5	4	3.100e -6													
	variant	2.543e -4	1	2.543e -4	34.126	0.010					O POT	SUB	-0.015	0.002	-5.842	0.010*	0.010
	Residuals	2.235e -5	3	7.451e -6													
	variant	2.445e -4	1	2.445e -4	47.712	0.002					P POT	SUB	-0.013	0.002	-6.907	0.002	0.002
	Residuals	2.050e -5	4	5.124e -6													
	variant	1.119e -4	2	5.596e -5	1.113	0.388					B MR	O MR	0.007	0.006	1.224	0.483	0.800
	Residuals	3.016e -4	6	5.026e -5								P MR	-7.360e -4	0.006	-0.127	0.991	1.000
											O MR	P MR	-0.008	0.006	-1.351	0.421	0.676

	variant	6.078e-5	2	3.039e-5	1.860	0.235					B BS	O BS	0.003	0.003	0.994	0.607	1.000
	Residuals	9.804e-5	6	1.634e-5								P BS	0.006	0.003	1.928	0.211	0.306
											O BS	P BS	0.003	0.003	0.934	0.641	1.000
Gini-Simpson index	variant	1.042e-6	1	1.042e-6	0.392	0.565					B MR	B BS	-8.333e-4	0.001	-0.626	0.565	0.565
	Residuals	1.063e-5	4	2.657e-6													
							variant	1.190	1	0.275	O MR	O BS	-0.005	0.004	-1.151	0.314	0.314
							variant	0.429	1	0.513	P MR	P BS	0.006	0.007	0.900	0.419	0.419
	variant	6.801e-5	1	6.801e-5	16.785	0.015					B MR	B POT	0.007	0.002	4.097	0.015*	0.015
	Residuals	1.621e-5	4	4.052e-6													
	variant	6.660e-5	1	6.660e-5	9.023	0.057					O MR	O POT	0.007	0.002	3.004	0.057	0.057
	Residuals	2.214e-5	3	7.382e-6													
	variant	3.082e-6	1	3.082e-6	0.040	0.850					P MR	P POT	0.001	0.007	0.201	0.850	0.850
	Residuals	3.044e-4	4	7.610e-5													
	variant	1.009e-4	1	1.009e-4	32.694	0.005					B POT	SUB	0.008	0.001	5.718	0.005*	0.005
	Residuals	1.234e-5	4	3.085e-6													
	variant	2.540e-4	1	2.540e-4	34.666	0.010					O POT	SUB	0.015	0.002	5.888	0.010*	0.010
	Residuals	2.199e-5	3	7.328e-6													
	variant	2.432e-4	1	2.432e-4	48.869	0.002					P POT	SUB	0.013	0.002	6.991	0.002*	0.002
	Residuals	1.991e-5	4	4.977e-6													
	variant	1.119e-4	2	5.594e-5	1.110	0.389					B MR	O MR	-0.007	0.006	-1.219	0.485	0.805
	Residuals	3.023e-4	6	5.038e-5								P MR	7.667e-4	0.006	0.132	0.990	1.000
											O MR	P MR	0.008	0.006	1.352	0.421	0.676
	variant	6.083e-5	2	3.041e-5	1.860	0.235					B BS	O BS	-0.003	0.003	-0.999	0.604	1.000
	Residuals	9.813e-5	6	1.635e-5								P BS	-0.006	0.003	-1.928	0.211	0.306
Shannon diversity index											O BS	P BS	-0.003	0.003	-0.929	0.644	1.000
	variant	0.013	1	0.013	0.587	0.486					B MR	B BS	-0.092	0.120	-0.766	0.486	0.486
	Residuals	0.086	4	0.021													
	variant	0.005	1	0.005	0.172	0.700					O MR	O BS	0.056	0.134	0.415	0.700	0.700
	Residuals	0.108	4	0.027													
	variant	0.044	1	0.044	0.206	0.673					P MR	P BS	0.170	0.375	0.454	0.673	0.673
	Residuals	0.844	4	0.211													
	variant	0.156	1	0.156	8.061	0.047					B MR	B POT	0.322	0.113	2.839	0.047*	0.047
	Residuals	0.077	4	0.019													
	variant	0.464	1	0.464	11.031	0.045					O MR	O POT	0.622	0.187	3.321	0.045*	0.045
	Residuals	0.126	3	0.042													
							variant	1.190	1	0.275	P MR	P POT	0.613	0.376	1.629	0.179	0.179
	variant	0.040	1	0.040	5.853	0.073					B POT	SUB	0.164	0.068	2.419	0.073	0.073
	Residuals	0.027	4	0.007													
	variant	0.235	1	0.235	6.840	0.079					O POT	SUB	0.442	0.169	2.615	0.079	0.079
	Residuals	0.103	3	0.034													
	variant	0.054	1	0.054	6.629	0.062					P POT	SUB	0.189	0.073	2.575	0.062	0.062
	Residuals	0.032	4	0.008													
	variant	0.503	2	0.252	1.644	0.270					B MR	O MR	-0.578	0.319	-1.810	0.245	0.361
	Residuals	0.918	6	0.153								P MR	-0.316	0.319	-0.989	0.610	1.000
											O MR	P MR	0.262	0.319	0.821	0.705	1.000
	variant	0.882	2	0.441	22.065	0.002					B BS	O BS	-0.726	0.115	-6.285	0.002*	0.002
	Residuals	0.120	6	0.020								P BS	-0.578	0.115	-5.006	0.006*	0.007
											O BS	P BS	0.148	0.115	1.279	0.456	0.744
	variant	1.261e-4	1	1.261e-4	2.254	0.208					B MR	B BS	-0.009	0.006	-1.501	0.208	0.208

Berger-Parker index	Residuals	2.239e -4	4	5.597e -5													
	variant	0.003	1	0.003	2.475	0.191					O MR	O BS	0.041	0.026	1.573	0.191	0.191
	Residuals	0.004	4	0.001													
							variant	1.190	1	0.275	P MR	P BS	-0.035	0.032	-1.089	0.337	0.337
	variant	5.022e -4	1	5.022e -4	7.596	0.051					B MR	B POT	-0.018	0.007	-2.756	0.051	0.051
	Residuals	2.644e -4	4	6.611e -5													
	variant	6.446e -4	1	6.446e -4	7.516	0.071					O MR	O POT	-0.023	0.008	-2.742	0.071	0.071
	Residuals	2.573e -4	3	8.576e -5													
	variant	7.457e -4	1	7.457e -4	0.483	0.525					P MR	P POT	0.022	0.032	0.695	0.525	0.525
	Residuals	0.006	4	0.002													
	variant	0.002	1	0.002	43.058	0.003					B POT	SUB	-0.041	0.006	-6.562	0.003*	0.003
	Residuals	2.310e -4	4	5.775e -5													
	variant	0.005	1	0.005	68.884	0.004					O POT	SUB	-0.061	0.007	-8.300	0.004*	0.004
	Residuals	1.969e -4	3	6.563e -5													
	variant	0.006	1	0.006	79.542	< .001					P POT	SUB	-0.066	0.007	-8.919	< .001*	< .001
	Residuals	3.246e -4	4	8.115e -5													
							variant	3.289	2	0.193	B MR	O MR	0.026	0.027	0.956	0.628	1.000
												P MR	-0.016	0.027	-0.588	0.831	1.000
											O MR	P MR	-0.041	0.027	-1.544	0.338	0.521
							variant	2.489	2	0.288	B BS	O BS	-0.025	0.021	-1.151	0.521	0.881
												P BS	0.010	0.021	0.479	0.883	1.000
											O BS	P BS	0.035	0.021	1.630	0.305	0.463

B birch, O oak, P pine; MR field plant mycorrhizosphere, BS bulk soil, POT pot plant mycorrhizosphere, SUB control pot substrate, grey cells: not determined, asterisks: significant p values (< 0.05).

Table S4. One-Way ANOVA, Kruskal-Wallis test, post hoc test output for significance of differences between variants of the experiment in diversity indices of fungal communities.

Diversity Index	ANOVA						Kruskal-Wallis				Post Hoc comparisons						
	Cases	Sum of Squares	df	Mean Square	F	p	Factor	Statistic	df	p	Variant of comparisons		Mean Difference	SE	t	p tukey	p bonf
Richness	variant	2.090.667	1	2.090.667	1.052	0.363					B MR	B BS	37.333	36.397	1.026	0.363	0.363
	Residuals	7.948.667	4	1.987.167													
	variant	160.167	1	160.167	0.074	0.799					O MR	O BS	10.333	38.058	0.272	0.799	0.799
	Residuals	8.690.667	4	2.172.667													
	variant	9.204.167	1	9.204.167	3.155	0.150					P MR	P BS	78.333	44.100	1.776	0.150	0.150
	Residuals	11.668.667	4	2.917.167													
	variant	48.167	1	48.167	0.038	0.856					B MR	B POT	5.667	29.242	0.194	0.856	0.856
	Residuals	5.130.667	4	1.282.667													
	variant	326.700	1	326.700	0.085	0.789					O MR	O POT	16.500	56.516	0.292	0.789	0.789
	Residuals	11.498.500	3	3.832.833													
	variant	2.480.667	1	2.480.667	6.831	0.059					P MR	P POT	40.667	15.560	2.614	0.059	0.059
	Residuals	1.452.667	4	363.167													
	variant	8.893.500	1	8.893.500	40.425	0.003					B POT	SUB	-77.000	12.111	-6.358	0.003*	0.003
	Residuals	880.000	4	220.000													
							variant	0.333	1	0.564	O POT	SUB	-64.500	57.088	-1.130	0.341	0.341
	variant	6.936.000	1	6.936.000	31.527	0.005					P POT	SUB	-68.000	12.111	-5.615	0.005*	0.005
	Residuals	880.000	4	220.000													
	variant	2.907.556	2	1.453.778	1.345	0.329					B MR	O MR	-23.333	26.844	-0.869	0.677	1.000

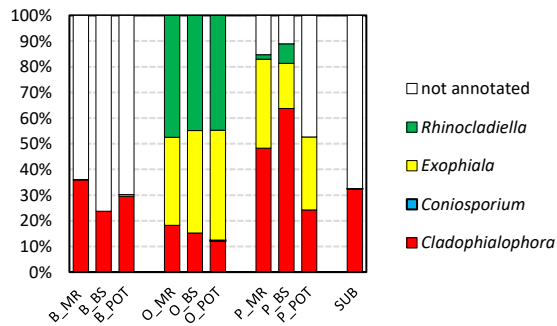
	Residuals	6.485.333	6	1.080.889								P MR	-44.000	26.844	-1.639	0.301	0.457	
												O MR	P MR	-20.667	26.844	-0.770	0.734	1.000
	variant	15.100.222	2	7.550.111	2.076	0.206						B BS	O BS	3.667	49.242	0.074	0.997	1.000
	Residuals	21.822.667	6	3.637.111									P BS	-85.000	49.242	-1.726	0.271	0.405
												O BS	P BS	-88.667	49.242	-1.801	0.248	0.366
Simpson dominance index	variant	3.481e -4	1	3.481e -4	0.080	0.791						B MR	B BS	-0.015	0.054	-0.283	0.791	0.791
	Residuals	0.017	4	0.004														
	variant	0.005	1	0.005	0.663	0.461						O MR	O BS	0.060	0.073	0.814	0.461	0.461
	Residuals	0.032	4	0.008														
	variant	0.009	1	0.009	1.970	0.233						P MR	P BS	-0.078	0.056	-1.403	0.233	0.233
	Residuals	0.019	4	0.005														
	variant	1.236e -5	1	1.236e -5	3.606e -4	0.986						B MR	B POT	0.003	0.151	0.019	0.986	0.986
	Residuals	0.137	4	0.034														
							variant	0.333	1	0.564		O MR	O POT	-0.164	0.159	-1.032	0.378	0.378
	variant	0.002	1	0.002	0.447	0.540						P MR	P POT	0.033	0.050	0.668	0.540	0.540
	Residuals	0.015	4	0.004														
							variant	3.857	1	0.050		B POT	SUB	0.203	0.147	1.382	0.239	0.239
							variant	3.000	1	0.083		O POT	SUB	0.270	0.155	1.739	0.180	0.180
	variant	0.014	1	0.014	30.670	0.005						P POT	SUB	0.096	0.017	5.538	0.005*	0.005
	Residuals	0.002	4	4.474e -4														
	variant	0.016	2	0.008	1.913	0.228						B MR	O MR	0.100	0.053	1.869	0.227	0.333
	Residuals	0.026	6	0.004									P MR	0.077	0.053	1.434	0.383	0.605
												O MR	P MR	-0.023	0.053	-0.435	0.903	1.000
variant	0.033	2	0.017	2.338	0.177						B BS	O BS	0.025	0.069	0.359	0.932	1.000	
Residuals	0.043	6	0.007									P BS	0.140	0.069	2.027	0.187	0.267	
											O BS	P BS	0.115	0.069	1.667	0.291	0.440	
Gini-Simpson index	variant	3.481e -4	1	3.481e -4	0.080	0.791						B MR	B BS	0.015	0.054	0.283	0.791	0.791
	Residuals	0.017	4	0.004														
	variant	0.005	1	0.005	0.662	0.461						O MR	O BS	-0.060	0.073	-0.814	0.461	0.461
	Residuals	0.032	4	0.008														
	variant	0.009	1	0.009	1.971	0.233						P MR	P BS	0.078	0.056	1.404	0.233	0.233
	Residuals	0.019	4	0.005														
	variant	1.233e -5	1	1.233e -5	3.598e -4	0.986						B MR	B POT	-0.003	0.151	-0.019	0.986	0.986
	Residuals	0.137	4	0.034														
							variant	0.333	1	0.564		O MR	O POT	0.164	0.159	1.032	0.378	0.378
	variant	0.002	1	0.002	0.447	0.540						P MR	P POT	-0.033	0.050	-0.669	0.540	0.540
	Residuals	0.015	4	0.004														
							variant	3.857	1	0.050		B POT	SUB	-0.203	0.147	-1.382	0.239	0.239
							variant	3.000	1	0.083		O POT	SUB	-0.270	0.155	-1.739	0.180	0.180
	variant	0.014	1	0.014	30.665	0.005						P POT	SUB	-0.096	0.017	-5.538	0.005*	0.005
	Residuals	0.002	4	4.474e -4														
	variant	0.016	2	0.008	1.913	0.228						B MR	O MR	-0.100	0.053	-1.869	0.227	0.332
	Residuals	0.026	6	0.004									P MR	-0.077	0.053	-1.434	0.383	0.605
												O MR	P MR	0.023	0.053	0.435	0.903	1.000
variant	0.033	2	0.017	2.338	0.178						B BS	O BS	-0.025	0.069	-0.359	0.932	1.000	
Residuals	0.043	6	0.007									P BS	-0.140	0.069	-2.026	0.187	0.267	
											O BS	P BS	-0.115	0.069	-1.667	0.292	0.440	
	variant	0.162	1	0.162	0.971	0.380						B MR	B BS	0.329	0.334	0.985	0.380	0.380

Shannon diversity index	Residuals	0.669	4	0.167													
	variant	0.019	1	0.019	0.125	0.741					O MR	O BS	-0.114	0.321	-0.354	0.741	0.741
	Residuals	0.619	4	0.155													
	variant	0.922	1	0.922	3.879	0.120					P MR	P BS	0.784	0.398	1.970	0.120	0.120
	Residuals	0.951	4	0.238													
	variant	0.398	1	0.398	0.782	0.427					B MR	B POT	-0.515	0.583	-0.884	0.427	0.427
	Residuals	2.038	4	0.510													
	variant	0.124	1	0.124	0.187	0.694					O MR	O POT	0.322	0.743	0.433	0.694	0.694
	Residuals	1.988	3	0.663													
	variant	0.073	1	0.073	1.101	0.353					P MR	P POT	-0.221	0.210	-1.049	0.353	0.353
	Residuals	0.265	4	0.066													
	variant	2.940	1	2.940	7.521	0.052					B POT	SUB	-1.400	0.511	-2.742	0.052	0.052
	Residuals	1.564	4	0.391													
							variant	3.000	1	0.083	O POT	SUB	-1.568	0.690	-2.272	0.108	0.108
	variant	1.628	1	1.628	177.835	< .001					P POT	SUB	-1.042	0.078	-13.34	< .001*	< .001
	Residuals	0.037	4	0.009													
	variant	0.874	2	0.437	2.623	0.152					B MR	O MR	-0.669	0.333	-2.006	0.191	0.275
	Residuals	1.000	6	0.167								P MR	-0.653	0.333	-1.959	0.203	0.293
											O MR	P MR	0.016	0.333	0.047	0.999	1.000
	variant	2.057	2	1.028	4.979	0.053					B BS	O BS	-0.226	0.371	-0.609	0.821	1.000
	Residuals	1.239	6	0.207								P BS	-1.108	0.371	-2.986	0.055	0.073
Berger-Parker index											O BS	P BS	-0.882	0.371	-2.377	0.119	0.165
	variant	0.002	1	0.002	0.212	0.669					B MR	B BS	0.032	0.070	0.460	0.669	0.669
	Residuals	0.030	4	0.007													
	variant	0.012	1	0.012	0.795	0.423					O MR	O BS	0.090	0.101	0.891	0.423	0.423
	Residuals	0.061	4	0.015													
	variant	0.021	1	0.021	1.122	0.349					P MR	P BS	-0.118	0.111	-1.059	0.349	0.349
	Residuals	0.074	4	0.018													
	variant	7.639e-4	1	7.639e-4	0.013	0.914					B MR	B POT	0.023	0.195	0.116	0.914	0.914
	Residuals	0.228	4	0.057													
							variant	0.333	1	0.564	O MR	O POT	-0.185	0.180	-1.028	0.380	0.380
	variant	0.004	1	0.004	0.283	0.623					P MR	P POT	0.054	0.101	0.532	0.623	0.623
	Residuals	0.061	4	0.015													
							variant	0.429	1	0.513	B POT	SUB	0.245	0.188	1.300	0.263	0.263
							variant	3.000	1	0.083	O POT	SUB	0.365	0.174	2.100	0.127	0.127
	variant	0.037	1	0.037	11.694	0.027					P POT	SUB	0.158	0.046	3.420	0.027*	0.027
	Residuals	0.013	4	0.003													
	variant	0.012	2	0.006	0.496	0.632					B MR	O MR	0.088	0.089	0.983	0.613	1.000
	Residuals	0.072	6	0.012								P MR	0.056	0.089	0.630	0.810	1.000
											O MR	P MR	-0.032	0.089	-0.353	0.934	1.000
	variant	0.075	2	0.037	2.401	0.171					B BS	O BS	0.030	0.102	0.297	0.953	1.000
	Residuals	0.093	6	0.016								P BS	0.206	0.102	2.029	0.186	0.266
											O BS	P BS	0.176	0.102	1.732	0.269	0.402

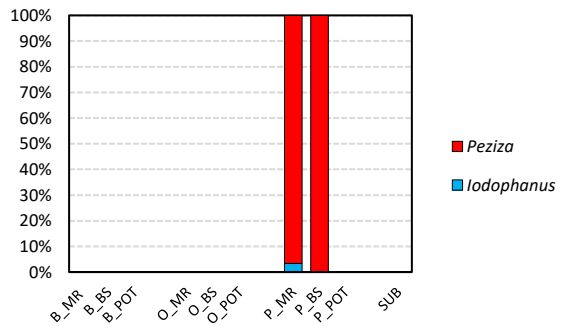
B birch, O oak, P pine; MR field plant mycorrhizosphere, BS bulk soil, POT pot plant mycorrhizosphere, SUB control pot substrate, grey cells: not determined, asterisks: significant p values (< 0.05).

Ascomycota

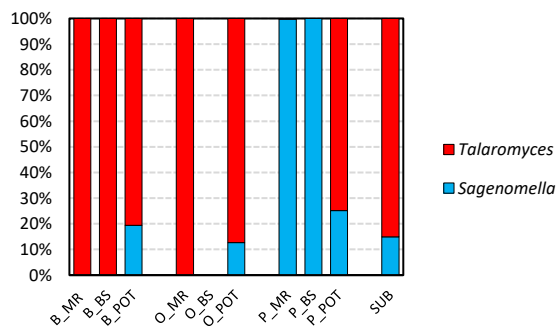
Herpotrichiellaceae



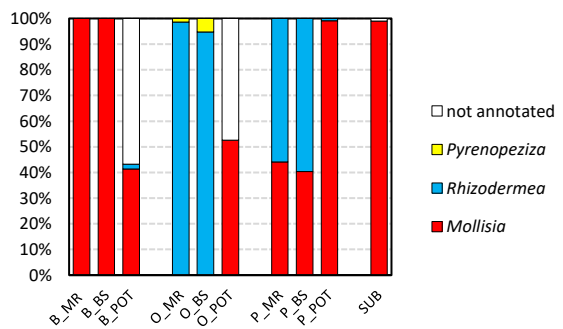
Pezizaceae



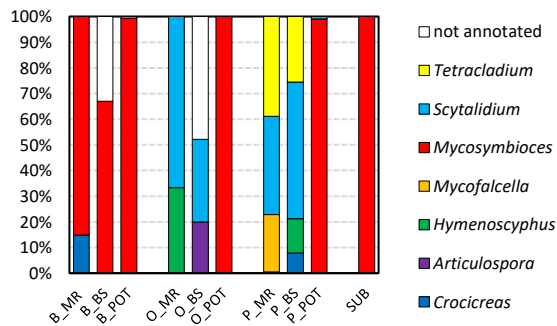
Trichocomaceae



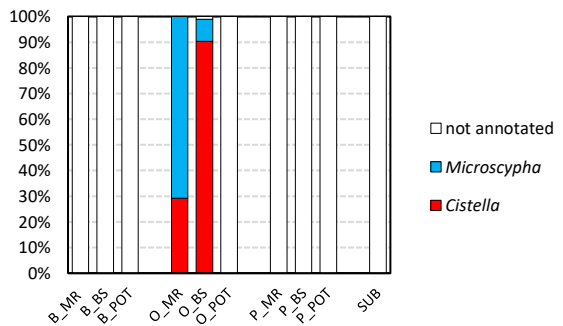
Dermateaceae



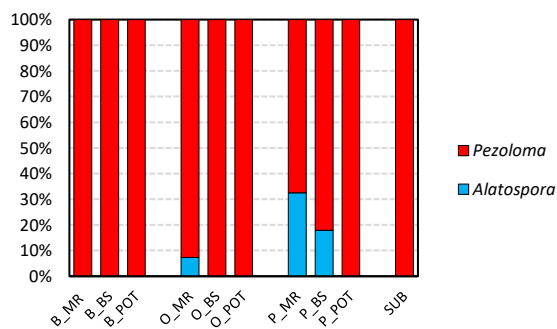
Helotiaceae



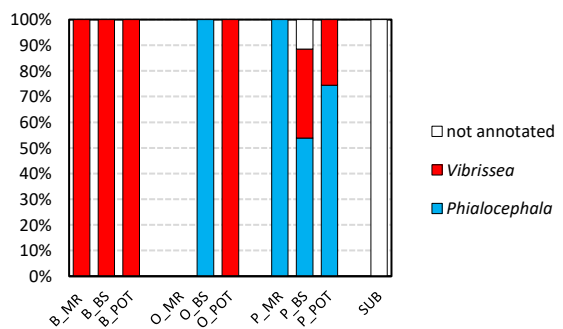
Hyaloscyphaceae



Leotiaceae



Vibrisseaceae



Basidiomycota

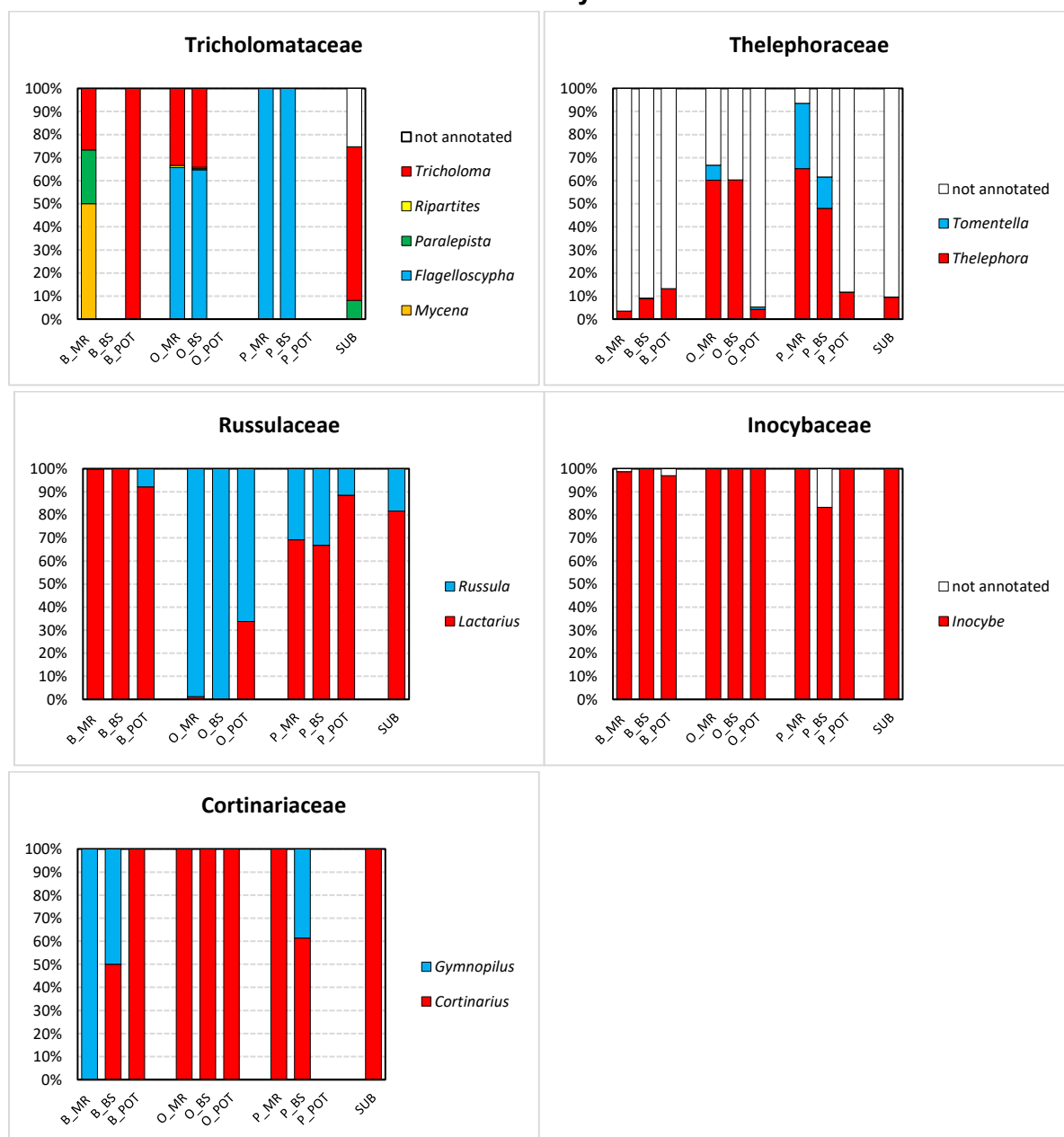


Figure S3. Characterization of the most representative fungal families at genus level. B, birch; O, oak; P, pine; MR, mycorrhizosphere of field plants; BS, bulk soil; POT, mycorrhizosphere of pot plants; SUB; control pot substrate. Some genera were the only members of their families and are therefore not shown with a diagram. So, for *Mortierellaceae*, 100 % *Mortierella* was present in each variant. *Serendipita* (100 % of *Serendipitaceae*) was present in the variants O_MR, O_BS and all pine variants, but absent from other variants. *Hebeloma* (the only *Hymenogastraceae* member) was observed in O_BS and O_POT as well as for all pine variants and absent from other variants. *Laccaria* (the only *Hydrangiaceae*) was present in all variants aside from O_MR and O_BS. *Tylospora* (*Atheliaceae*) was present only in P_MR and P_BS. *Penicillium* (*Aspergillaceae*), *Trichoderma* (*Hypocreaceae*) and *Pisolithus* (*Pisolithaceae*) were the only members of their families and present in all variants.

Table S5. Indices of similarity between fungal communities determined for trees within variants of the experiment.

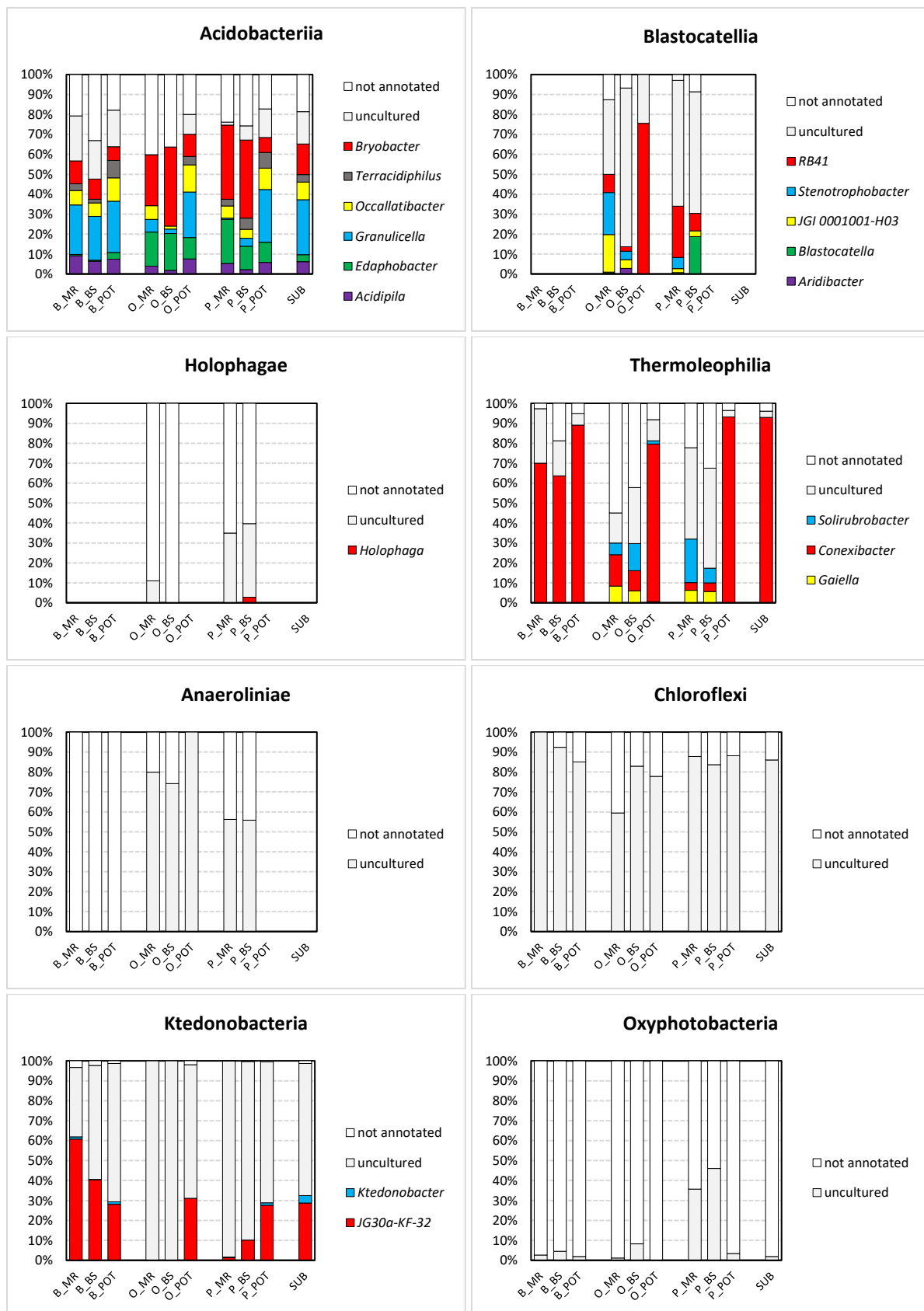
Index	Estimate	s.e.	95%Lower	95%Upper
B MR				
Sorensen	0.202	0.013	0.177	0.227
Jaccard	0.078	0.006	0.066	0.090
Bray-Curtis	0.437	0.001	0.435	0.439
O MR				
Sorensen	0.199	0.007	0.187	0.212
Jaccard	0.077	0.003	0.071	0.082
Bray-Curtis	0.062	0.000	0.061	0.062
P MR				
Sorensen	0.145	0.009	0.128	0.162
Jaccard	0.054	0.004	0.047	0.061
Bray-Curtis	0.083	0.002	0.078	0.087
B BS				
Sorensen	0.267	0.007	0.253	0.281
Jaccard	0.108	0.004	0.101	0.115
Bray-Curtis	0.509	0.001	0.507	0.512
O BS				
Sorensen	0.180	0.011	0.159	0.201
Jaccard	0.068	0.005	0.059	0.077
Bray-Curtis	0.104	0.001	0.103	0.106
P BS				
Sorensen	0.149	0.005	0.140	0.158
Jaccard	0.055	0.002	0.052	0.059
Bray-Curtis	0.173	0.001	0.171	0.145
B POT				
Sorensen	0.199	0.007	0.186	0.213
Jaccard	0.077	0.003	0.071	0.083
Bray-Curtis	0.062	0.000	0.061	0.062
O POT				
Sorensen	0.124	0.002	0.120	0.128
Jaccard	0.066	0.001	0.064	0.068
Bray-Curtis	0.012	0.008	0.000	0.027
P POT				
Sorensen	0.225	0.005	0.216	0.235
Jaccard	0.088	0.002	0.084	0.093
Bray-Curtis	0.306	0.001	0.304	0.308
SUB				
Sorensen	0.214	0.006	0.204	0.225
Jaccard	0.083	0.003	0.079	0.088
Bray-Curtis	0.118	0.001	0.116	0.119

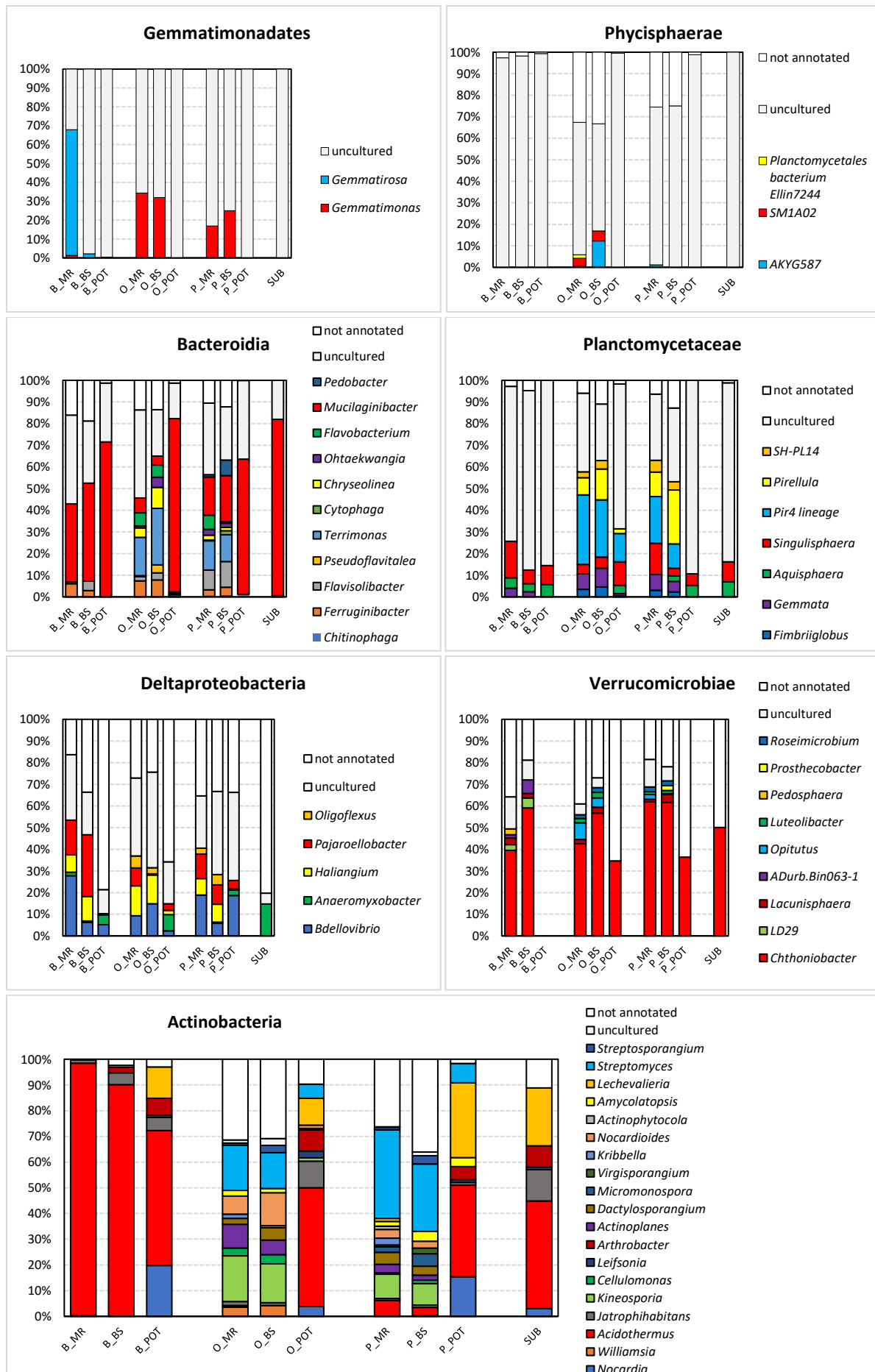
B birch, O oak, P pine; MR field plant mycorrhizosphere, BS bulk soil, POT pot plant mycorrhizosphere, SUB control pot substrate.

Table S6. Highest abundant fungal families in different variants of the experiment.

Index	B_MR	B_BS	B_POT	O_MR	O_BS	O_POT	P_MR	P_BS	P_POT	SUB
<i>Mortierellaceae</i>	1	0	0	2	1	1	1	4	1	1
<i>Thelephoraceae</i>	24	6	44	4	3	37	11	15	31	1
<i>Serendipitaceae</i>	0	0	0	2	3	0	1	3	0	0
<i>Russulaceae</i>	7	15	0	47	53	0	7	11	0	0
<i>Pisolithaceae</i>	0	0	12	0	0	1	0	0	1	4
<i>Atheliaceae</i>	0	0	0	0	0	0	4	1	0	0
<i>Tricholomataceae</i>	0	0	0	3	3	0	0	0	0	0
<i>Inocybaceae</i>	34	42	5	0	0	5	29	18	19	1
<i>Hymenogastraceae</i>	0	0	0	0	0	0	4	0	0	0
<i>Hydnangiaceae</i>	0	0	6	0	0	0	0	0	0	0
<i>Cortinariaceae</i>	0	0	0	0	0	0	5	0	0	0
<i>Hypocreaceae</i>	0	0	2	1	2	1	5	1	3	2
<i>Pezizaceae</i>	0	0	0	0	0	0	2	1	0	0
<i>Vibrisseaceae</i>	0	0	0	0	0	2	1	1	2	1
<i>Leotiaceae</i>	19	8	13	7	2	12	6	4	14	23
<i>Hyaloscyphaceae</i>	8	12	4	0	1	10	0	0	8	9
<i>Helotiaceae</i>	0	2	0	0	2	0	0	0	0	1
<i>Dermateaceae</i>	0	0	3	0	0	2	1	1	3	7
<i>Trichocomaceae</i>	0	1	0	0	0	0	3	3	0	1
<i>Aspergillaceae</i>	0	0	1	1	0	0	1	1	1	3
<i>Herpotrichiellaceae</i>	1	3	2	22	13	15	6	4	4	10
less than 1%	1	2	3	3	5	1	3	10	3	8
unidentified	5	8	6	6	10	10	9	22	10	27

Five highest abundant families labeled in 100-80-60-40-20% black shadows; B, birch; O, oak; P, pine; MR, mycorrhizosphere of field plant; BS, bulk soil; POT, mycorrhizosphere of pot plant; SUB, control pot substrate.





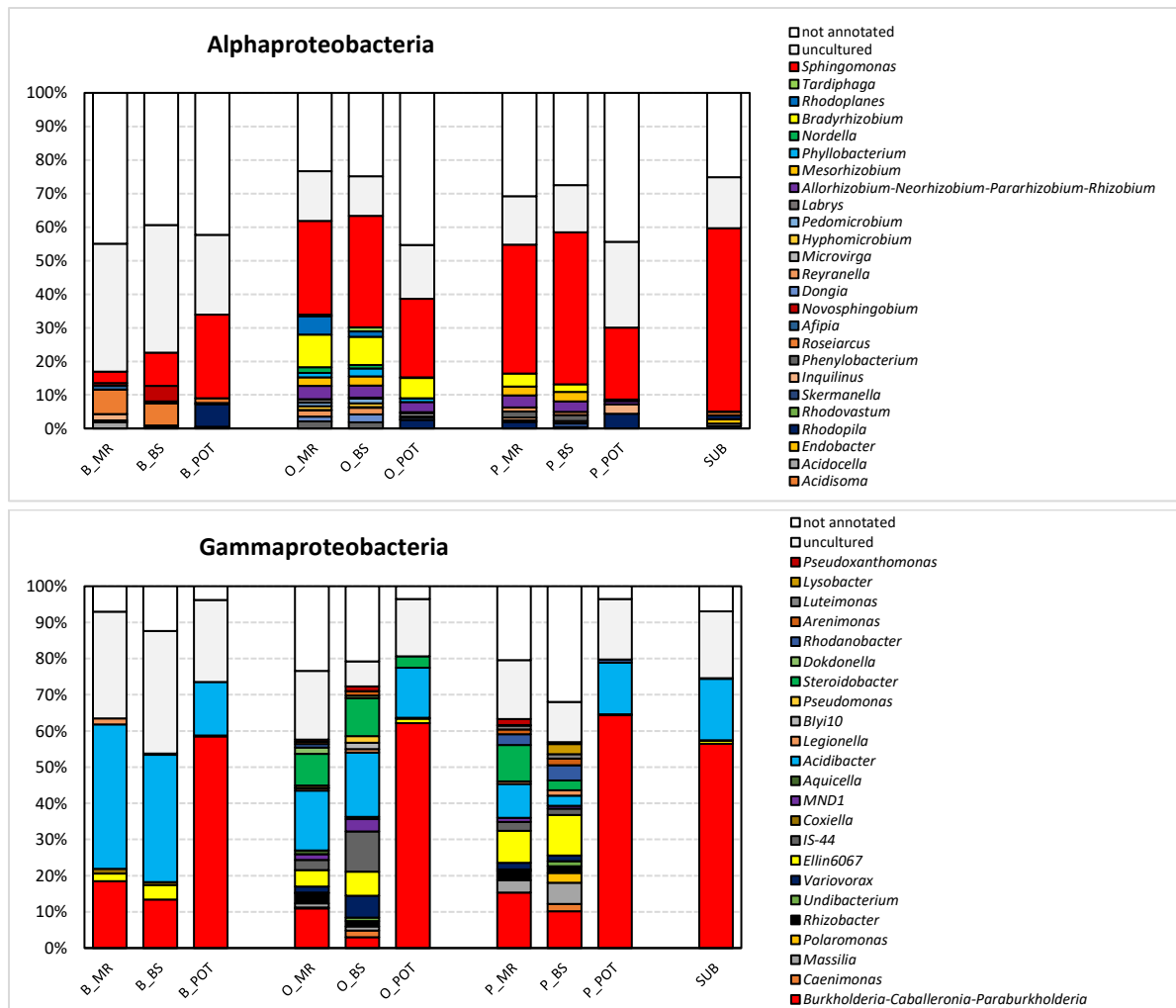


Figure S4. Characterization of the most representative bacterial classes at genus level. B, birch; O, oak; P, pine; MR, mycorrhizosphere of field plants; BS, bulk soil; POT, mycorrhizosphere of pot plants; SUB, control pot substrate; y-axis represents relative abundance of bacterial genera within a considered bacterial class.

Table S7. Highest abundant bacterial classes in different variants of the experiment.

Index	B_MR	B_BS	B_POT	O_MR	O_BS	O_POT	P_MR	P_BS	P_POT	SUB
Verrucomicrobiae	4	2	0	10	8	0	6	4	0	0
Gammaproteobacteria	6	5	4	10	10	5	10	10	7	2
Deltaproteobacteria	1	2	0	2	3	0	2	2	1	0
Alphaproteobacteria	20	13	16	28	26	21	25	28	17	15
Planctomycetacia	4	5	1	4	4	2	3	2	1	1
Phycisphaerae	9	7	12	4	3	10	4	3	14	7
Gemmatimonadetes	0	2	0	2	1	0	1	2	0	0
Oxyphotobacteria	3	1	5	1	1	4	1	2	3	3
Ktedonobacteria	11	16	20	0	0	19	5	4	20	26
Chloroflexia	0	1	0	0	0	1	1	1	0	1
Anaerolineae	0	0	0	1	1	0	2	2	0	0
Bacteroidia	8	10	3	13	12	4	12	16	6	1
Thermoleophilia	0	1	2	2	2	2	1	1	1	6
Actinobacteria	4	3	5	4	3	7	8	5	5	5
Acidimicrobia	0	0	1	0	0	1	1	0	1	3
Holophagae	0	0	0	0	0	0	2	2	0	0
Blastocatellia (Gr. 4)	0	0	0	4	9	0	2	2	0	0
Acidobacteriia	20	20	17	4	2	13	5	4	16	11
less than 1%	2	1	0	1	1	0	1	1	0	0
unidentified	6	10	13	8	13	11	10	9	8	18

Five highest abundant families labeled in 100-80-60-40-20% black shadows; B, birch; O, oak; P, pine; MR, mycorrhizosphere of field plant; BS, bulk soil; POT, mycorrhizosphere of pot plant; SUB, control pot substrate.

Table S8. Indices of similarity between bacterial communities determined for trees within variants of the experiment.

Index	Estimate	s.e.	95%Lower	95%Upper
B MR				
Sorensen	0.572	0.002	0.569	0.575
Jaccard	0.308	0.001	0.305	0.311
Bray-Curtis	0.508	0.001	0.505	0.511
O MR				
Sorensen	0.317	0.002	0.314	0.321
Jaccard	0.134	0.001	0.132	0.136
Bray-Curtis	0.265	0.001	0.262	0.268
P MR				
Sorensen	0.222	0.002	0.218	0.226
Jaccard	0.087	0.001	0.085	0.089
Bray-Curtis	0.144	0.001	0.142	0.146
B BS				
Sorensen	0.541	0.002	0.537	0.546
Jaccard	0.282	0.002	0.2785	0.286
Bray-Curtis	0.520	0.002	0.518	0.523
O BS				
Sorensen	0.413	0.001	0.411	0.415
Jaccard	0.190	0.001	0.189	0.191
Bray-Curtis	0.351	0.001	0.348	0.353
P BS				
Sorensen	0.242	0.001	0.240	0.244
Jaccard	0.096	0.001	0.095	0.097
Bray-Curtis	0.199	0.001	0.197	0.202
B POT				
Sorensen	0.756	0.002	0.753	0.760
Jaccard	0.509	0.003	0.504	0.514
Bray-Curtis	0.784	0.001	0.781	0.786
O POT				
Sorensen	0.535	0.001	0.533	0.538
Jaccard	0.365	0.001	0.363	0.368
Bray-Curtis	0.614	0.002	0.609	0.619
P POT				
Sorensen	0.673	0.002	0.669	0.678
Jaccard	0.407	0.002	0.403	0.412
Bray-Curtis	0.708	0.002	0.704	0.712
SUB				
Sorensen	0.729	0.003	0.723	0.735
Jaccard	0.473	0.004	0.465	0.480
Bray-Curtis	0.814	0.002	0.811	0.817

B birch, O oak, P pine; MR field plant mycorrhizosphere, BS bulk soil, POT pot plant mycorrhizosphere, SUB control pot substrate.

Table S9. R-statistic of pairwise ANOSIM of field sampling sites based on the relative abundance of the most representative fungal taxa.

	Field Birches sampling sites	Field Oaks sampling sites	Field Pines sampling sites
Field Birches sampling sites			
Field Oaks sampling sites	1.00*		
Field Pines sampling sites	0.45*	0.79*	

Asterisks represent significant differences ($p < 0.05$).

Table S10. PERMANOVA p-values of pairwise comparisons between field sampling sites based on the relative abundance of the most representative fungal taxa.

	Field Birches sampling sites	Field Oaks sampling sites	Field Pines sampling sites
Field Birches sampling sites			
Field Oaks sampling sites	0.01*		
Field Pines sampling sites	0.02*	0.01*	

Asterisks represent significant differences ($p < 0.05$).

Table S11. SIMPER analysis demonstrating the contribution (%) of the most abundant fungal families to Bray-Curtis dissimilarity between field sampling sites.

	Field Birches sampling sites	Field Oaks sampling sites	Field Pines sampling sites
Field Birches sampling sites			
Field Oaks sampling sites	Russulaceae (27.5%) Inocybaceae (26.4%) Herpotrichiellaceae (10.6%)		
Field Pines sampling sites	Inocybaceae (19.9%) Thelephoraceae (13.1%) Russulaceae (12.7%)	Russulaceae (31.8%) Inocybaceae (17.7%) Herpotrichiellaceae (9.9%)	

Only fungal families with a contribution higher than 10% are included in the table.

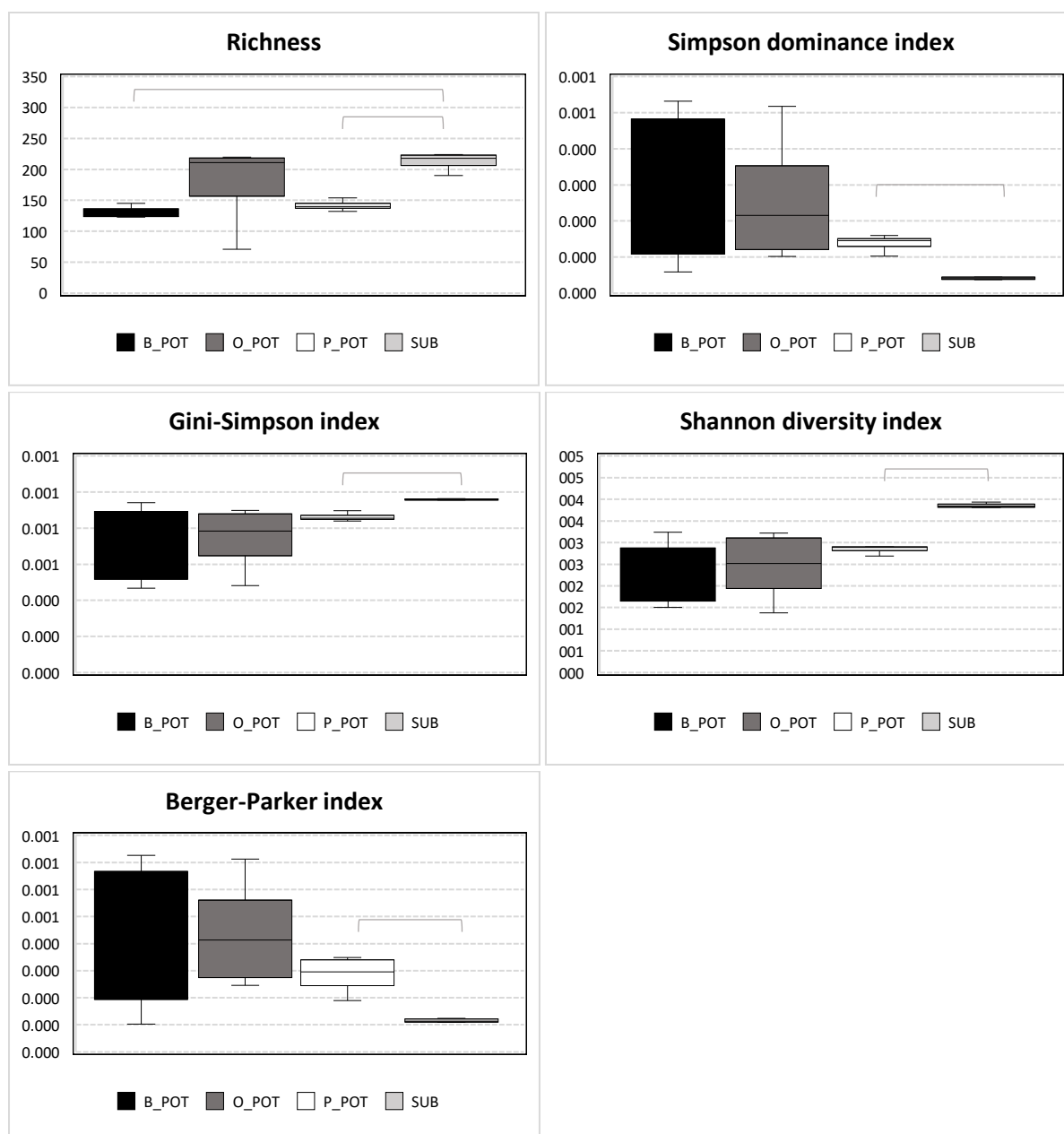


Figure S5. Pairwise comparisons of fungal community diversity indices based on ASVs between pot plant mycorrhizosphere and control pot substrate. B, birch; O, oak; P, pine; POT, mycorrhizosphere of pot plant; SUB, control pot substrate. Brackets indicate significant differences ($p < 0.05$).

Table S12. ANOVA test output of pairwise comparisons between field plant mycorrhizosphere, corresponding pot plant mycorrhizosphere and control pot substrate based on the relative abundance of the most representative fungal taxa.

Mean rank within groups	41.47
Mean rank between groups	101.5
R	0.6319
P	0.0001

Table S13. R-statistics of pairwise ANOSIM between field plant mycorrhizosphere, corresponding pot plant mycorrhizosphere and control pot substrate based on the relative abundance of the most representative fungal taxa.

	B_MR	B_POT	O_MR	O_POT	P_MR	P_POT	SUB
B_POT	0.63						
O_POT			0.75				
P_POT					0.30		
SUB	1	1	1	0.5	0.59		

B birch, O oak, P pine; MR field plant mycorrhizosphere, BS bulk soil, POT pot plant mycorrhizosphere, SUB control pot substrate. Asterisks represent significant values ($p < 0.05$).

Table S14. PERMANOVA test output of pairwise comparisons between field plant mycorrhizosphere, corresponding pot plant mycorrhizosphere and control pot substrate based on the relative abundance of the most representative fungal taxa.

Total sum of squares	4.236
Within-group sum of squares	1.385
F	4.46
P	0.0001

Table S15. PERMANOVA p-values of pairwise comparisons field plant mycorrhizosphere, pot plant mycorrhizosphere and control pot substrate based on the relative abundance of the most representative fungal taxa.

	B_MR	B_POT	O_MR	O_POT	P_MR	P_POT	SUB
B_POT	0.10						
O_POT			0.11				
P_POT					0.20		
SUB	0.10	0.10	0.10	0.10	0.10		

B birch, O oak, P pine; MR field plant mycorrhizosphere, BS bulk soil, POT pot plant mycorrhizosphere, SUB control pot substrate. Asterisks represent significant values ($p < 0.05$).

Table S16. R-statistics of pairwise ANOSIM of field sampling sites based on the relative abundance of the most representative bacterial taxa.

	Field Birches sampling site	Field Oaks sampling site	Field Pines sampling site
Field Birches sampling site			
Field Oaks sampling site	0.99*		
Field Pines sampling site	0.76*	0.23	

Asterisks represent significant differences ($p < 0.05$).

Table S17. PERMANOVA p-values of pairwise comparisons between field sampling sites based on the relative abundance of the most representative bacterial taxa.

	Field Birches sampling site	Field Oaks sampling site	Field Pines sampling site
Field Birches sampling site			
Field Oaks sampling site	0.01*		
Field Pines sampling site	0.01*	0.22	

Asterisks represent significant differences ($p < 0.05$).

Table S18. SIMPER analysis demonstrates the contribution (%) of the most abundant bacterial classes to Bray-Curtis dissimilarity between field sampling sites.

	Field Birches sampling site	Field Oaks sampling site	Field Pines sampling site
Field birches sampling site			
Field Oaks sampling site	Acidobacteriia (21.85%) Ktedonobacteria (17.15%) Alphaproteobacteria (13.89%)		
Field Pines sampling site	Acidobacteriia (22.04%) Alphaproteobacteria (14.87%) Ktedonobacteria (14.46%)	Alphaproteobacteria (12.2%) Verrucomicrobiae (11.27%) Blastocatellia (11.25%)	

Only bacterial classes with a contribution higher than 10% are included in the table.

Table S19. ANOSIM test output of pairwise comparisons between field plant mycorrhizosphere, pot plant mycorrhizosphere and control pot substrate based on the relative abundance of the most representative bacterial taxa.

Mean rank within groups	34.68
Mean rank between groups	102.3
R	0.7113
P	0.0001

Table S20. R-statistics of pairwise ANOSIM between field plant mycorrhizosphere, corresponding pot plant mycorrhizosphere and control pot substrate based on the relative abundance of the most representative bacterial taxa.

	B_MR	B_POT	O_MR	O_POT	P_MR	P_POT	SUB
B_POT	0.56						
O_POT			1				
P_POT					0.70		
SUB	1	1	1	1	0.81	1	

B birch, O oak, P pine; MR field plant mycorrhizosphere, BS bulk soil, POT pot plant mycorrhizosphere, SUB control pot substrate. Asterisks represent significant values ($p < 0.05$).

Table S21. PERMANOVA test output of pairwise comparisons between field plant mycorrhizosphere, pot plant mycorrhizosphere and control pot substrate based on the relative abundance of the most representative bacterial taxa.

Total sum of squares	1.474
Within-group sum of squares	0.2391
F	11.19
P	0.0001

Table S22. PERMANOVA p-values of pairwise comparisons field plant mycorrhizosphere, pot plant mycorrhizosphere and control pot substrate based on the relative abundance of the most representative bacterial taxa.

	B_MR	B_POT	O_MR	O_POT	P_MR	P_POT	SUB
B_POT	0.10						
O_POT			0.10				
P_POT					0.10		
SUB	0.10	0.10	0.10	0.10	0.10	0.10	

B birch, O oak, P pine; MR field plant mycorrhizosphere, BS bulk soil, POT pot plant mycorrhizosphere, SUB control pot substrate. Asterisks represent significant values ($p < 0.05$).