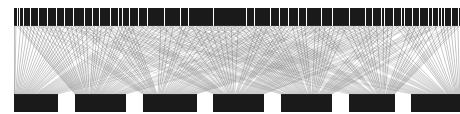
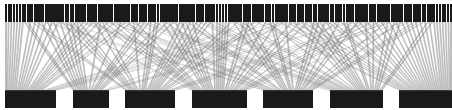


A higher connectance

connectance

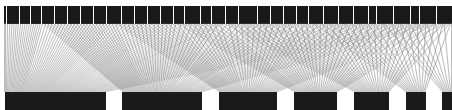
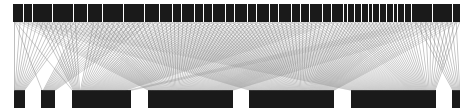
B lower connectance



C higher generality
(same connectance as **A**)

generality

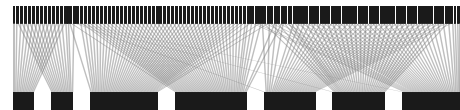
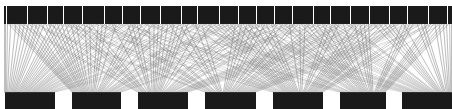
D lower generality
(same connectance as **A**)



E lower nestedness temperature

nestedness

F higher nestedness temperature
(same connectance as **E**)



G higher modularity

modularity

H lower modularity
(same connectance as **G**)

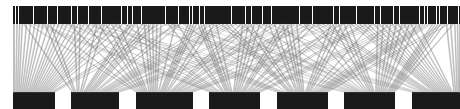
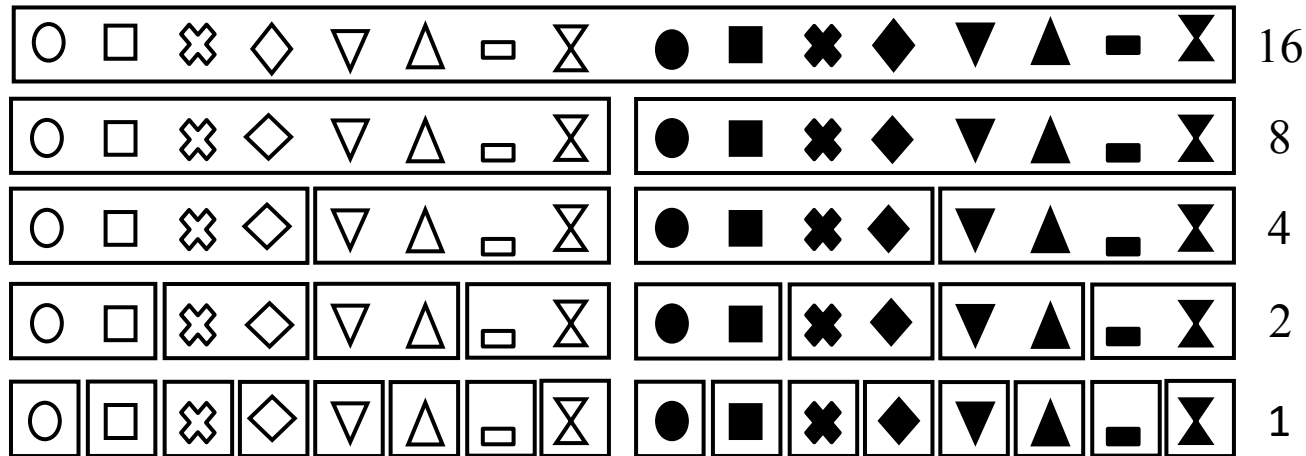


Figure S1: Conceptual bipartite networks with equal numbers of higher- and lower level partners, visualizing differences in connectance (A, B), generality (C, D), nestedness (E, F), and modularity (G, H).



Tree species	Type	No.	Tree species	Type	No.
<i>Castanea henryi</i> (Skan) Rehd. & Wils.	EcM	5 x 5	<i>Cyclobalanopsis glauca</i> (Thunb.) Oerst.	EcM	5 x 5
<i>Nyssa sinensis</i> Oliver	AM	5 x 5	<i>Quercus fabri</i> Hance	EcM	5 x 5
<i>Liquidambar formosana</i> Hance	AM	5 x 5	<i>Rhus chinensis</i> Mill.	AM	5 x 5
<i>Sapindus saponaria</i> Linn.	AM	5 x 5	<i>Schima superba</i> Gardner & Champion	AM	5 x 5
<i>Choerospondias axillaris</i> (Roxb.) Burt & Hill	AM	5 x 5	<i>Castanopsis eyrei</i> (Champ.) Tutcher / <i>C. carlesii</i> (Hemsl.) Hay.	EcM	5 x 5
<i>Triadica sebifera</i> (L.) Small	AM	5 x 5	<i>Cyclobalanopsis myrsinifolia</i> (Blume) Oerst.	EcM	5 x 5
<i>Quercus serrata</i> Murray	EcM	5 x 5	<i>Lithocarpus glaber</i> (Thunb.) Nakai	AM	5 x 5
<i>Castanopsis sclerophylla</i> (Lindl.) Schott.	EcM	5 x 5	<i>Koelreuteria bipinnata</i> Franch.	AM	5 x 5
Number of soil samples		200	Number of soil samples		200

Figure S2. Broken-stick-design of the experimental forest plots. Plot design presented for the biodiversity and ecosystem functioning (BEF) experiment China, study site A. The 16 species mix was sub-divided in two times eight species mixtures. These were likewise partitioned into four, two and one tree species communities. Tree species are shown as symbols. Similarity of symbols was only chosen to emphasize the experimental design and does not imply any similarities or dissimilarities of tree species traits. No.: Number of samples.

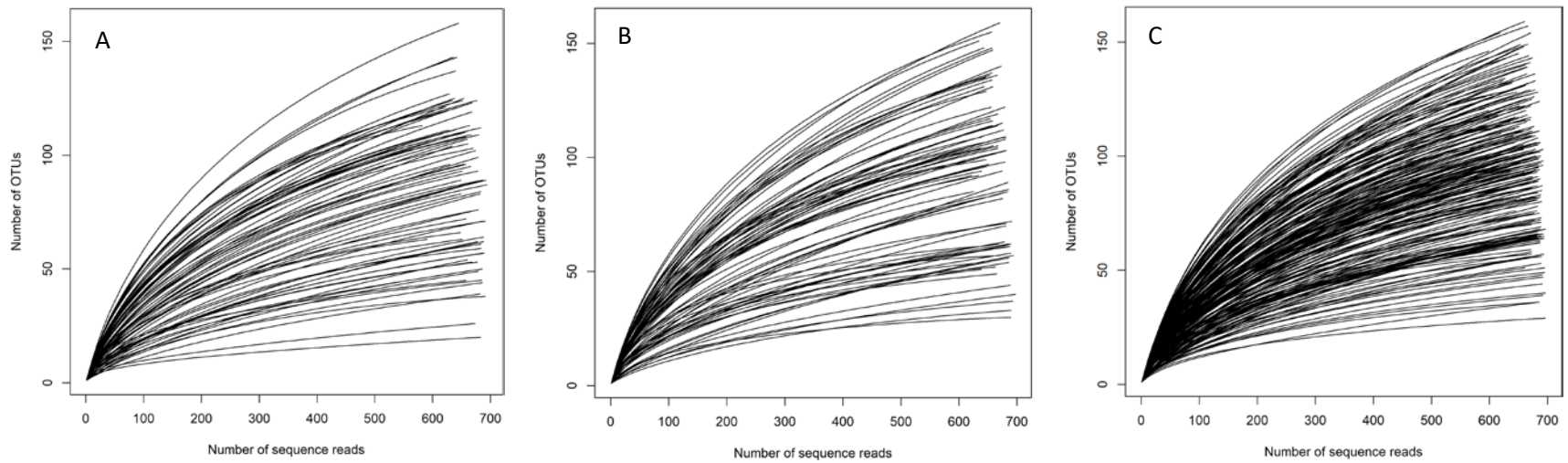


Figure S3. Rarefaction curves of monoculture (A) two tree species mixtures (B) high tree diversity mixtures (4, 8 or 16 tree species mixtures).

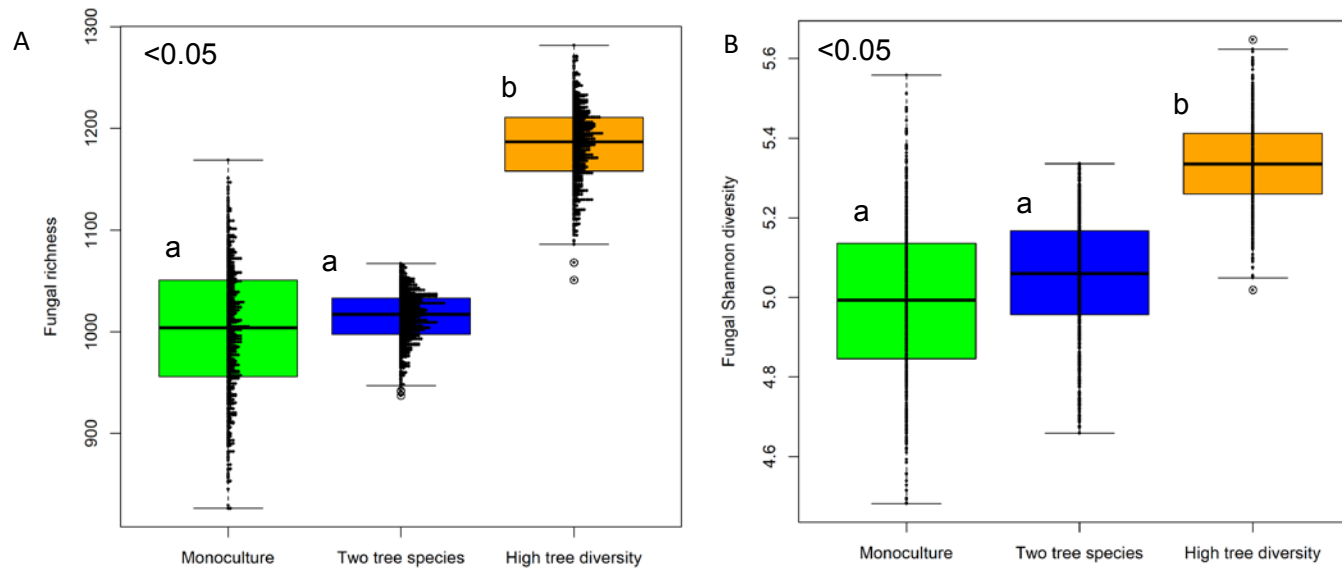


Figure S4. Fungal richness (A) and fungal Shannon diversity (B) across the 576 subsampling permutations.

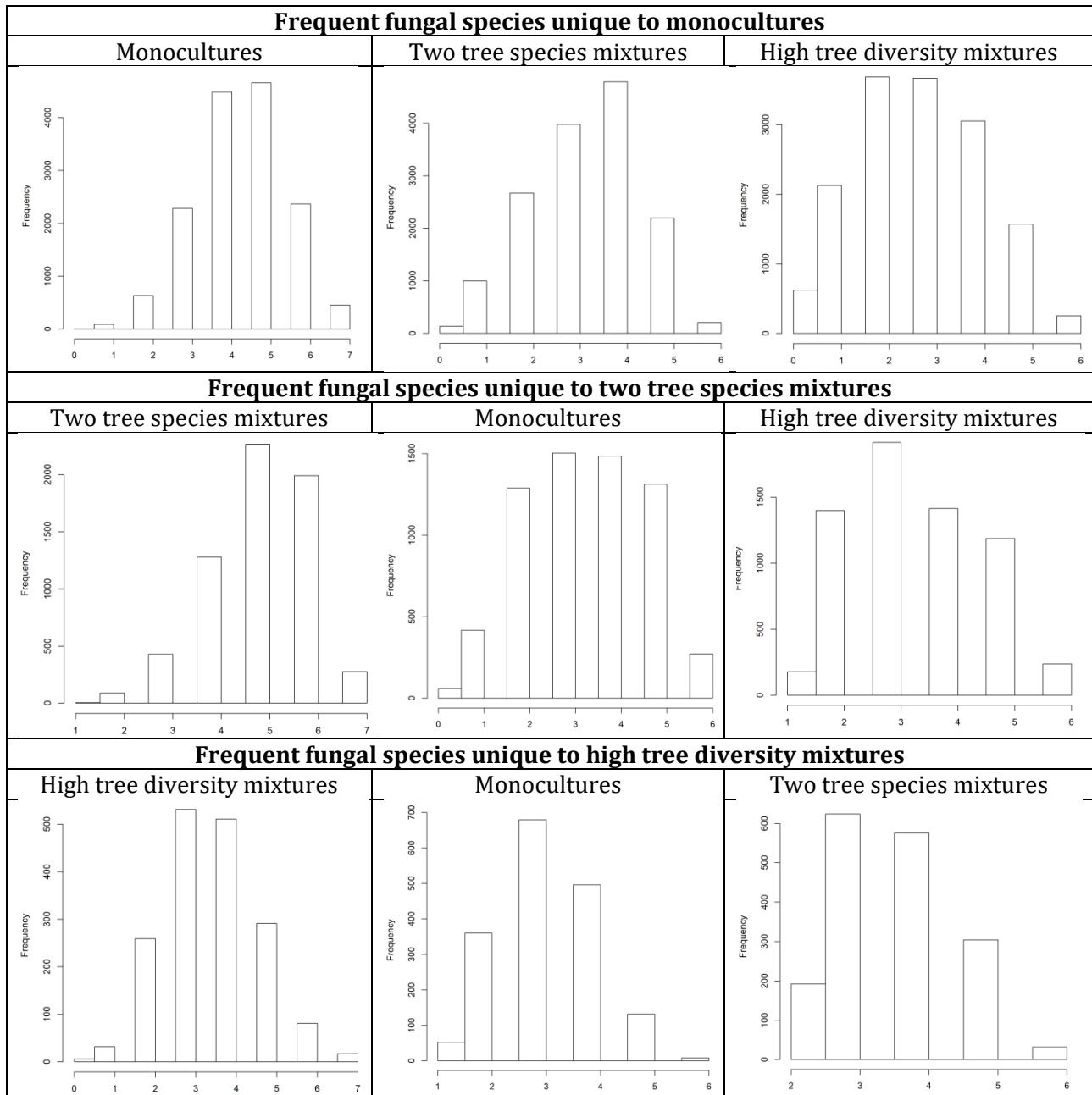


Figure S5. Histograms visualizing occurrence patterns of unique frequent fungal OTUs of one tree diversity level across all tree diversity levels. Frequent fungal OTUs were defined as those occurring on all seven plots in at least one permutation.

Table S1. Network characteristics for tree-fungal bipartite analysis based on co-occurrence. Network metrics (A) were compared between the tree diversity levels, while network nestedness (B) was compared against a null model. Networks were calculated for all possible link thresholds (one to five out of five samples) in which co-occurrence was observed. The Kruskal-Wallis test was applied to test for a significant difference of each network characteristic, the p value is reported. Median values of the 576 subsampling routines are given for the three tree diversity levels and below stated whether the Kruskal-Wallis test for multiple comparisons was significant (T=TRUE) or not (F=FALSE) for the group comparisons (indicated by numbers).

A	number						NODF		
	OTUs	modularity	connectance	fungal generality	fungal C score	mean shared fungal partners	B	median	Wilcox.p
1 co-occurrence	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001			
<u>Median</u>									
mono	1004	0.43	0.26	2.61	0.64	69.17	1 co-occurrence	Mono	27.83
two mix.	1017	0.41	0.27	2.73	0.63	77.98		Nullmodel	56.71
high	1187	0.46	0.24	2.39	0.67	66.67		Two mix.	29.42
1-2/1-3/2-3	F/T/T/	T/T/T/	T/T/T/	T/T/T/	T/T/T/	T/T/T/		Nullmodel	56.83
								High	24.61
								Nullmodel	56.66
2 co-occurrences	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001		Mono	22.18
<u>Median</u>								Nullmodel	54.74
mono	423	0.50	0.22	2.27	0.68	20.19	2 co-occurrences	Two mix.	23.67
two mix.	427	49	0.23	2.33	0.68	21.14		Nullmodel	53.87
high	550	0.55	0.21	2.06	0.72	20.71		High	17.8
1-2/1-3/2-3	F/T/T/	T/T/T/	T/T/T/	T/T/T/	F/T/T/	T/_F/T/		Nullmodel	54.24
								Mono	21.51
3 co-occurrences	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001		Nullmodel	57.6
<u>Median</u>								Two mix.	22.59
Mono	206	0.52	0.22	2.26	0.67	9.43	3 co-occurrences	Nullmodel	57.48
two mix.	198	0.51	0.22	2.33	0.68	9.57		High	15.66
high	251	0.58	0.2	2	0.74	8.48		Nullmodel	57.32
1-2/1-3/2-3	T/T/T/	F/T/T/	F/T/T/	T/T/T/	F/T/T/	F/T/T/		Mono	22.91
								Nullmodel	59.76
4 co-occurrences	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001		Two mix.	26.3
<u>Median</u>								Nullmodel	60.04
mono	96	0.51	0.22	2.35	0.65	4.83	4 co-occurrences	High	16.85
two mix.	83	0.49	0.23	2.53	0.63	4.86		Nullmodel	58.71
high	117	0.56	0.2	2.08	0.72	4.43		Mono	21.47
1-2/1-3/2-3	T/T/T/	T/T/T/	T/T/T/	T/T/T/	T/T/T/	F/T/T/		Nullmodel	59.63
								Two mix.	24.25
5 co-occurrences	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001		Nullmodel	58.67
<u>Median</u>								High	14.98
mono	45	0.52	0.22	2.33	0.66	2.19	5 co-occurrences	Nullmodel	59.37
two mix.	39	0.51	0.23	2.37	0.65	2.05			<0.001
high	56	0.58	0.2	1.95	0.72	1.9			<0.001
1-2/1-3/2-3	T/T/T/	F/T/T/	T/T/T/	F/T/T/	F/T/T/	T/T/_F/			

Network modularity: A high value indicates stronger connections within than between modules, **Network connectance:** Realized proportion of possible links, **Fungal generality:** Mean effective number of tree species per fungal species, **Mean number of shared fungal partners:** Mean number of fungal species that two tree species interact with, **Fungal C score:** Average degree of co-occurrence for all possible pairs of fungal OTUs. Values close to 1 indicate that there is evidence for disaggregation, e.g. through competition. Value close to 0 indicate aggregation of species (i.e. no repelling forces between species); **NODF:** nestedness metric (nestedness metric based on overlap and decreasing fill).

Table S2. Top 20 specialist fungal OTUs identified by maximum phi coefficient values.

	Fungal_guild	Phylum	Class	Order	Family	Genus
Otu00046	Ectomycorrhizal	Basidiomycota	Agaricomycetes	Agaricales	Hymenogastraceae	Hymenogaster
Otu00561	Ectomycorrhizal	Basidiomycota	Agaricomycetes	Agaricales	Entolomataceae	Entoloma
Otu01026	Ectomycorrhizal	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	Tomentella
Otu01059	Unknown	Rozellomycota	GS11	NA	NA	NA
Otu01081	Unknown	NA	NA	NA	NA	NA
Otu01112	Ectomycorrhizal	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	Tomentella
Otu01197	Unknown	Rozellomycota	GS11	NA	NA	NA
	Orchid					
Otu01234	Mycorrhizal	Basidiomycota	Agaricomycetes	Cantharellales	Tulasnellaceae	Epulorhiza
Otu01639	Saprotroph	Ascomycota	Archaeorhizomycetes	Archaeorhizomycetales	Archaeorhizomycetaceae	Archaeorhizomyces
Otu01746	Unknown	Ascomycota	Leotiomycetes	Helotiales	NA	NA
Otu01872	Saprotroph	Mucoromycota	NA	Mortierellales	Mortierellaceae	Mortierella
Otu01993	Ectomycorrhizal	Basidiomycota	Agaricomycetes	Cantharellales	Ceratobasidiaceae	Ceratobasidium
Otu02009	Unknown	Ascomycota	Eurotiomycetes	NA	NA	NA
Otu02292	Ectomycorrhizal	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	Tomentella
Otu02384	Unknown	Ascomycota	Xylonomycetes	GS34	NA	NA
Otu02663	Saprotroph	Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae	Clavaria
Otu02893	Saprotroph	Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Penicillium
Otu03239	Unknown	Ascomycota	NA	NA	NA	NA
Otu03384	Ectomycorrhizal	Basidiomycota	Agaricomycetes	Agaricales	Entolomataceae	Entoloma
Otu04209	Ectomycorrhizal	Basidiomycota	Agaricomycetes	Sebacinales	Sebacinaceae	Sebacina

Table S3. Frequent fungal OTUs at all three tree diversity treatments (monocultures, two tree species mixtures and high tree diversity mixtures). Frequent fungal species were defined as fungal OTUs appearing at least once on all seven plots of one subsampling permutation.

	Fungal_guild	Kingdom	Phylum	Class	Order	Family
Otu00002	Saprotroph	Fungi	Ascomycota	Archaeorhizomycetes	GS31	NA
Otu00003	Saprotroph	Fungi	Basidiomycota	Geminibasidiomycetes	Geminibasidiales	Geminibasidiaceae
Otu00005	Saprotroph	Fungi	Ascomycota	Eurotiomycetes	Eurotiales	Trichocomaceae
Otu00009	Saprotroph	Fungi	Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae
Otu00012	Unknown	Fungi	Ascomycota	Leotiomycetes	Helotiales	NA
Otu00019	Saprotroph	Fungi	Mucoromycota	NA	Mortierellales	Mortierellaceae
Otu00034	Saprotroph	Fungi	Basidiomycota	Agaricomycetes	Trechisporales	Hydnodontaceae
Otu00038	Arbuscular Mycorrhizal	Fungi	Glomeromycota	Glomeromycetes	Glomerales	Glomeraceae
Otu00068	Unknown	Fungi	NA	NA	NA	NA
Otu00080	Plant Pathogen	Fungi	Ascomycota	Dothideomycetes	Capnodiales	Cladosporiaceae
Otu00084	Saprotroph	Fungi	Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae
Otu00203	Saprotroph	Fungi	Basidiomycota	Agaricomycetes	Agaricales	Clavariaceae
Otu00211	Unknown	Fungi	Basidiomycota	Agaricomycetes	Agaricales	NA
Otu00273	Saprotroph	Fungi	Mucoromycota	NA	Mortierellales	Mortierellaceae
Otu00298	Plant Pathogen	Fungi	Ascomycota	Sordariomycetes	Xylariales	Sporocadaceae