

Supplementary material:

Figure S1: Location of the treatment plots in the Merlot vineyard.

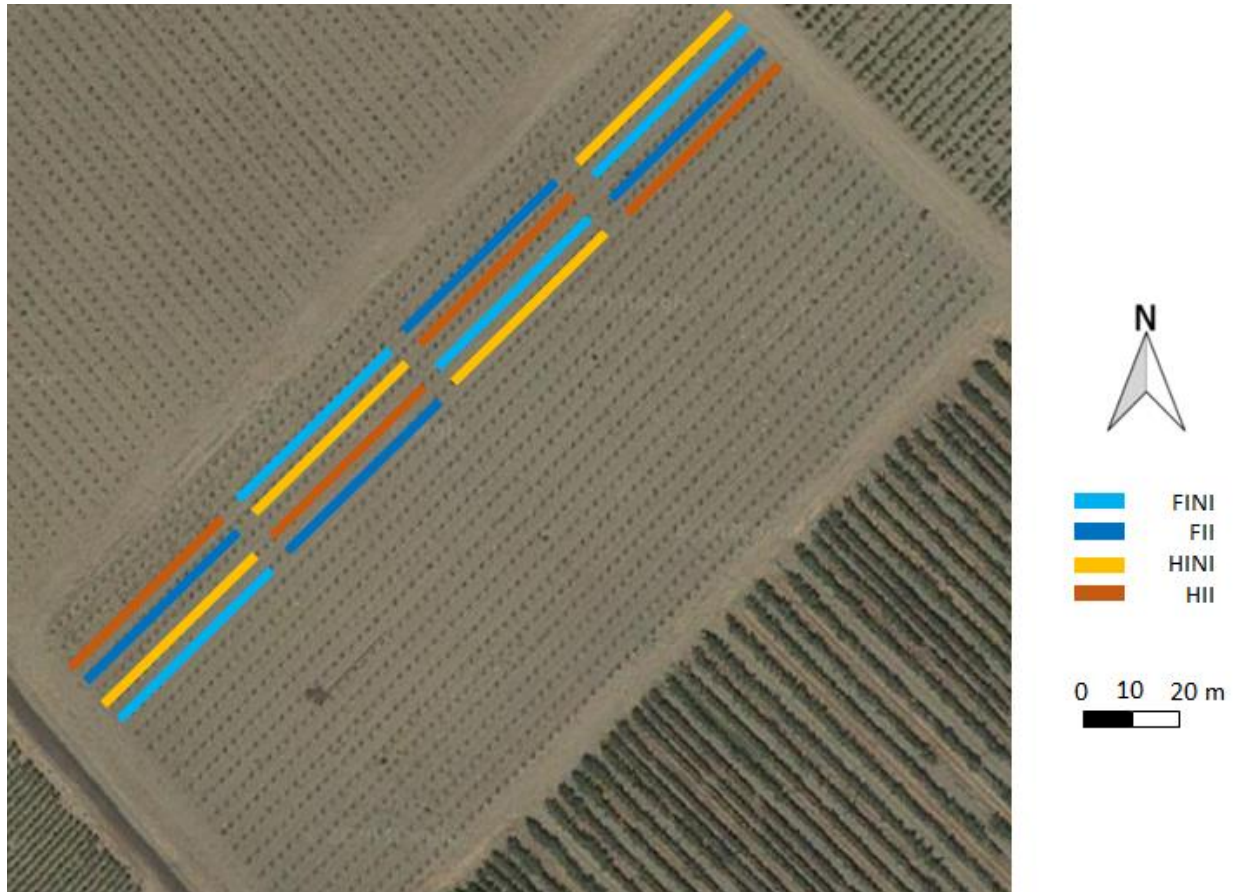


Figure S2: Number of OTUs shared among the different treatments (NT, FINI, FII, HINI and HII plots) for bacteria (A) and fungi (B) kingdoms. The numbers in the shaded overlapping zones indicate how many of the OTUs of the total number of OTUs (non shaded-non overlapping number) were shared among sample types.

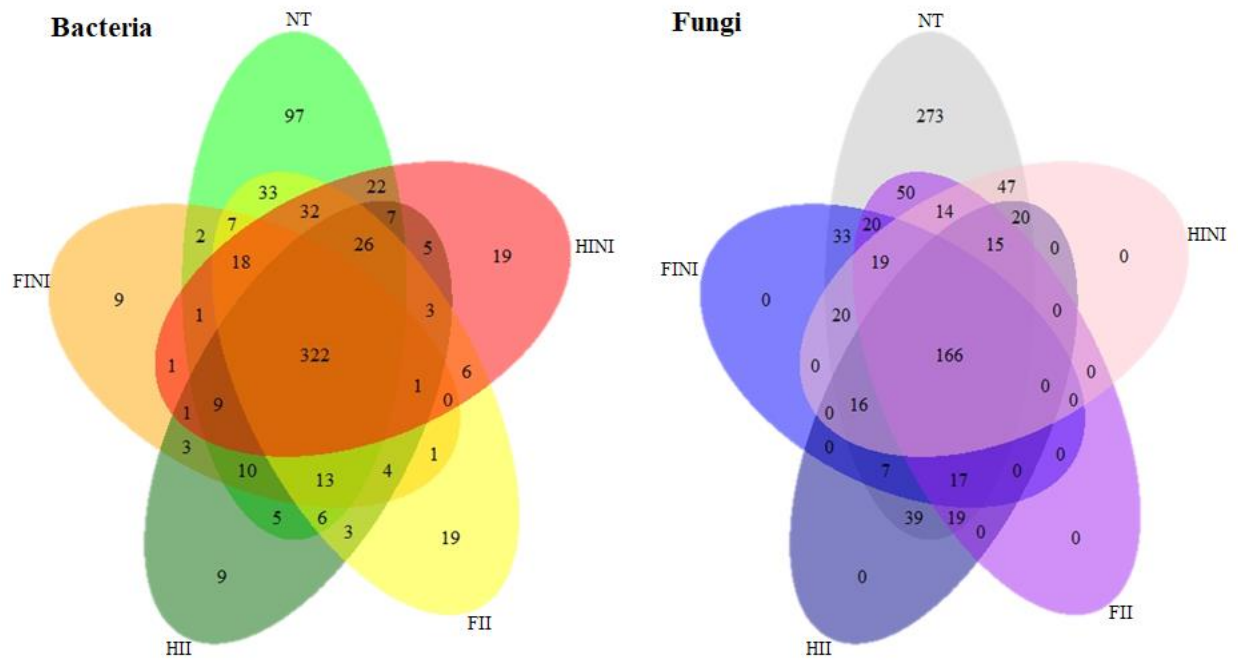


Figure S3: Relationships between the Shannon (A) and inverse of Simpson (B) indexes for bacterial and fungal communities found in plots before (NT) and after treatments, different irrigation amounts (FI, Full Irrigated or HI, Half Irrigated), and AMF inoculation (I, inoculated; or NI, non-inoculated). For each treatment, straight lines correspond to the linear regression lines and the 95% confidence interval.

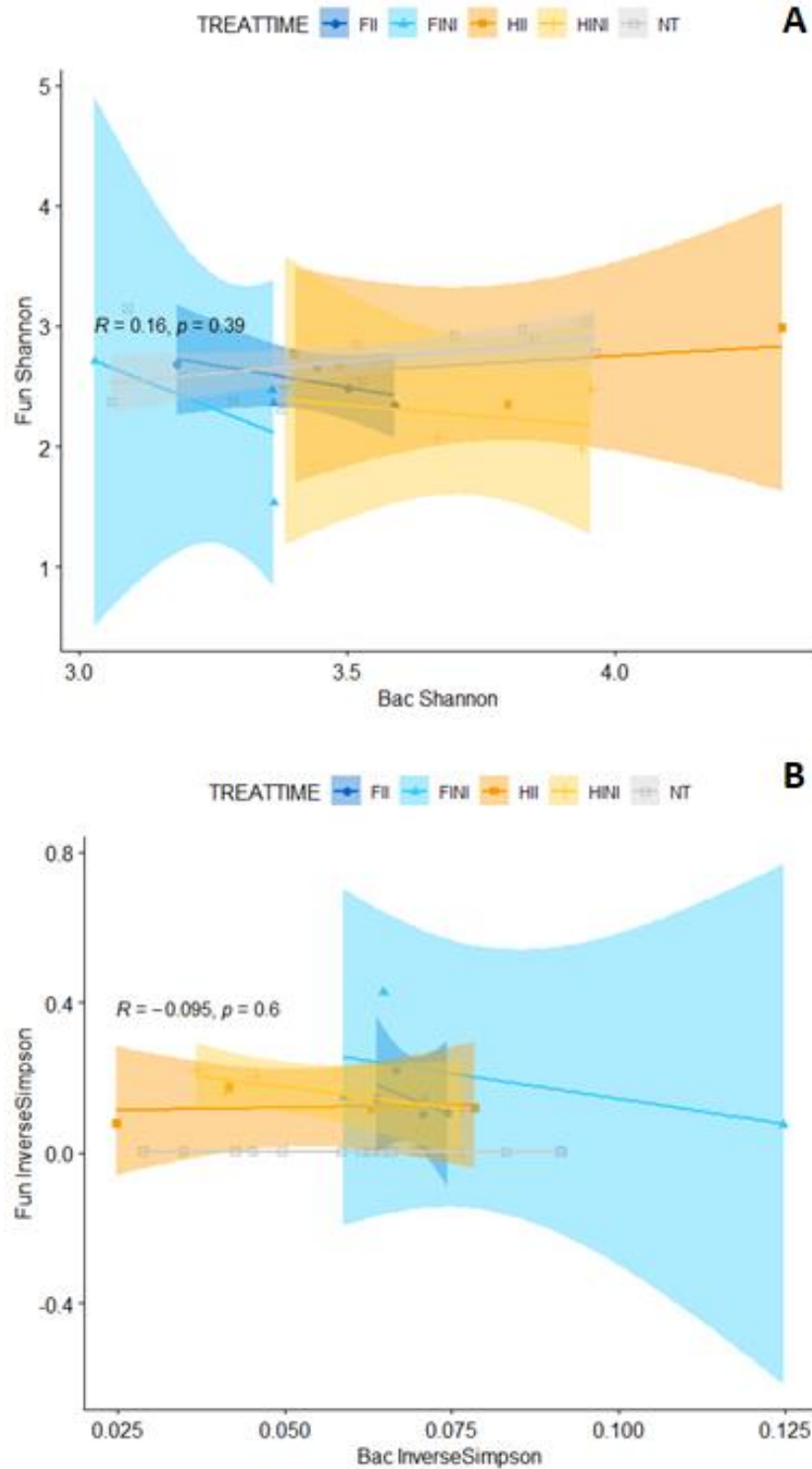


Figure S4. Heat tree with the taxonomy hierarchy of Proteobacteria phylum. Size and colors of nodes and edges are correlated with the abundance of organisms in each treatment. Green and brown were used to present higher or lower abundance, when comparing two conditions based on the different irrigation amounts (FI, Full Irrigated or HI, Half Irrigated), and AMF inoculation (I, inoculated; or NI, non-inoculated).

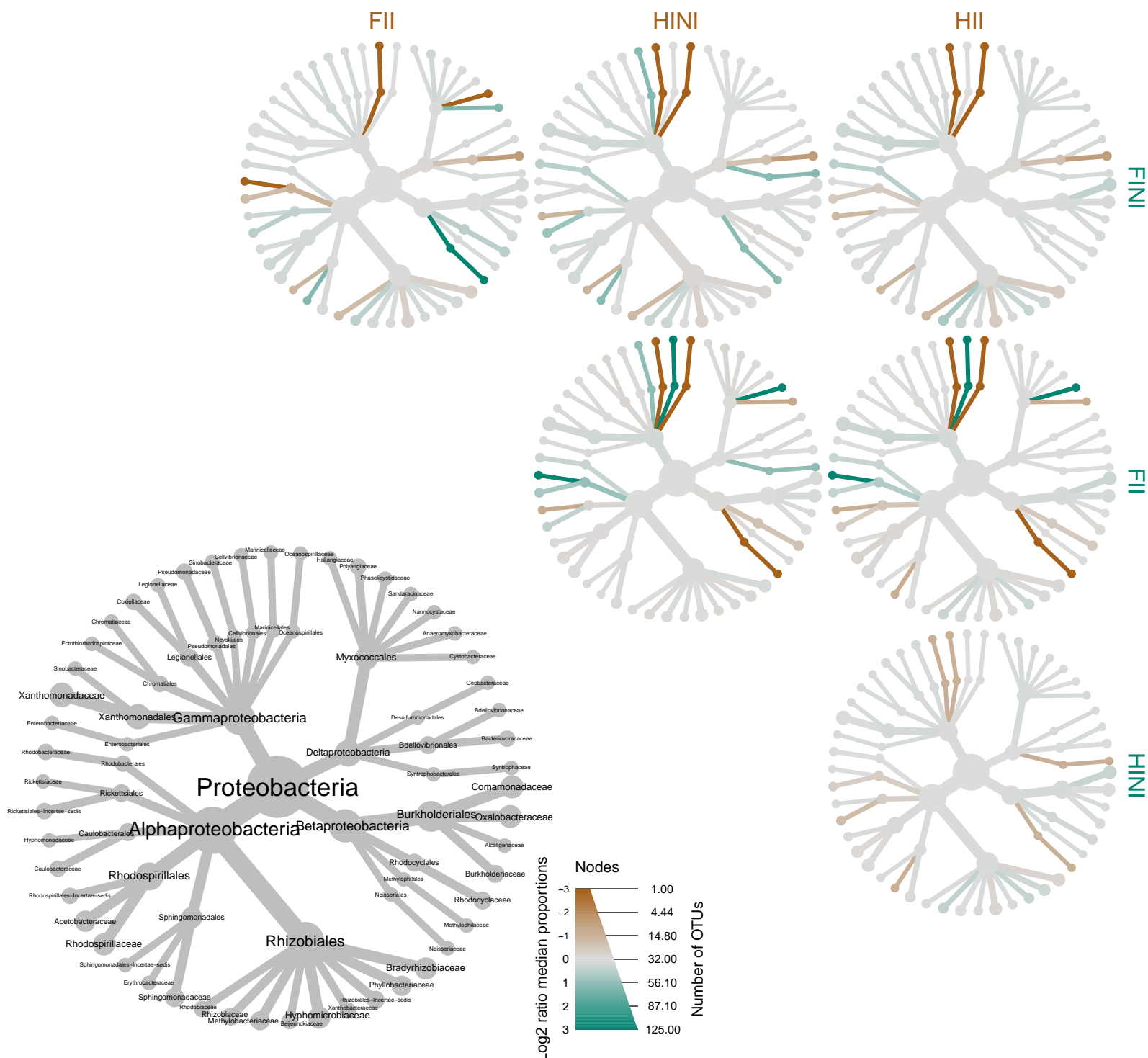


Figure S6. Heat tree with the taxonomy hierarchy of Firmicutes phylum. Size and colors of nodes and edges are correlated with the abundance of organisms in each treatment. Green and brown were used to present higher or lower abundance, when comparing two conditions based on the different irrigation amounts (FI, Full Irrigated or HI, Half Irrigated), and AMF inoculation (I, inoculated; or NI, non-inoculated).

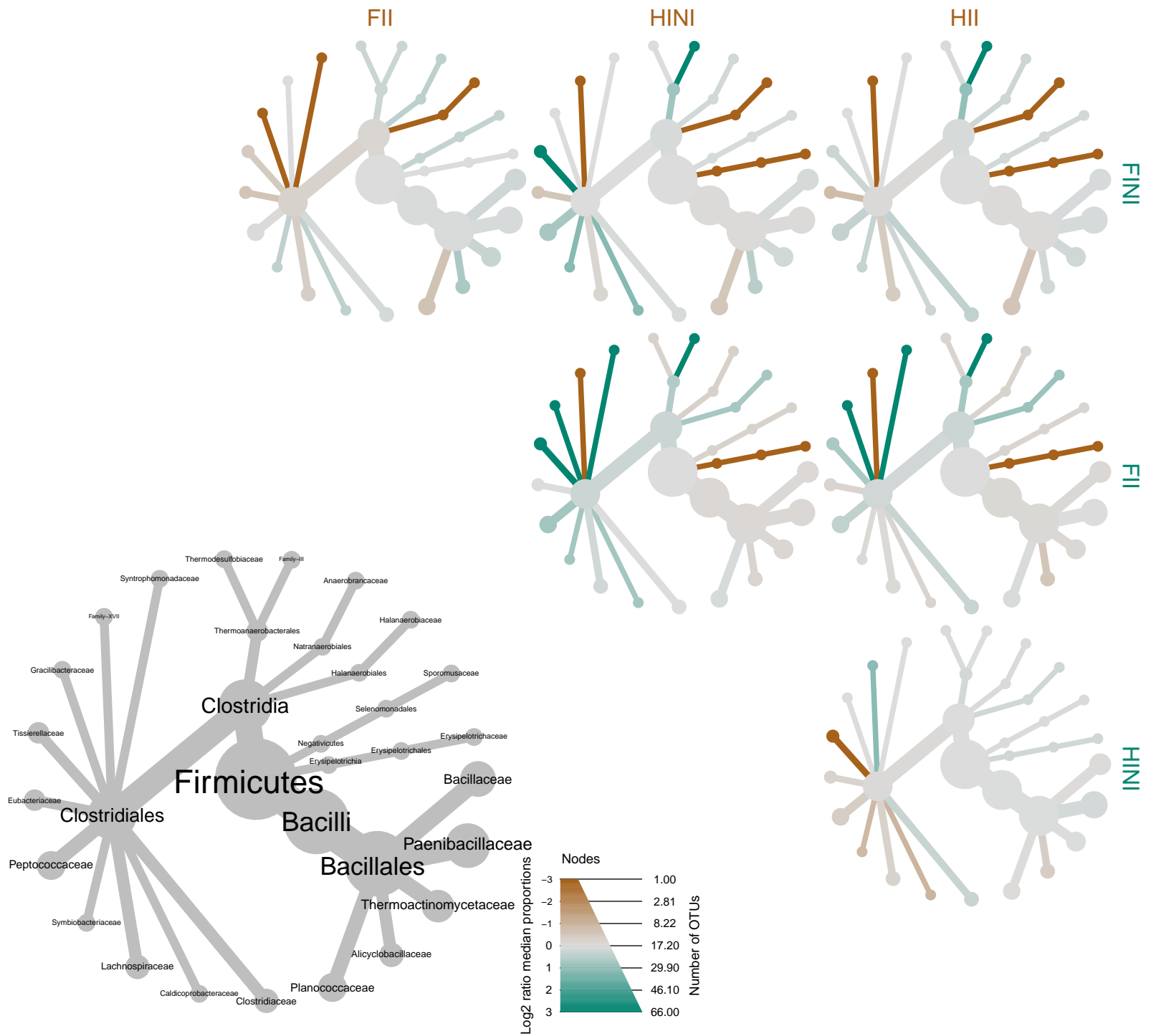


Figure S8. Heat tree with the taxonomy hierarchy of Ascomycota phylum. Size and colors of nodes and edges are correlated with the abundance of organisms in each treatment. Green and brown were used to present higher or lower abundance, when comparing two conditions based on the different irrigation amounts (FI, Full Irrigated or HI, Half Irrigated), and AMF inoculation (I, inoculated; or NI, non-inoculated).

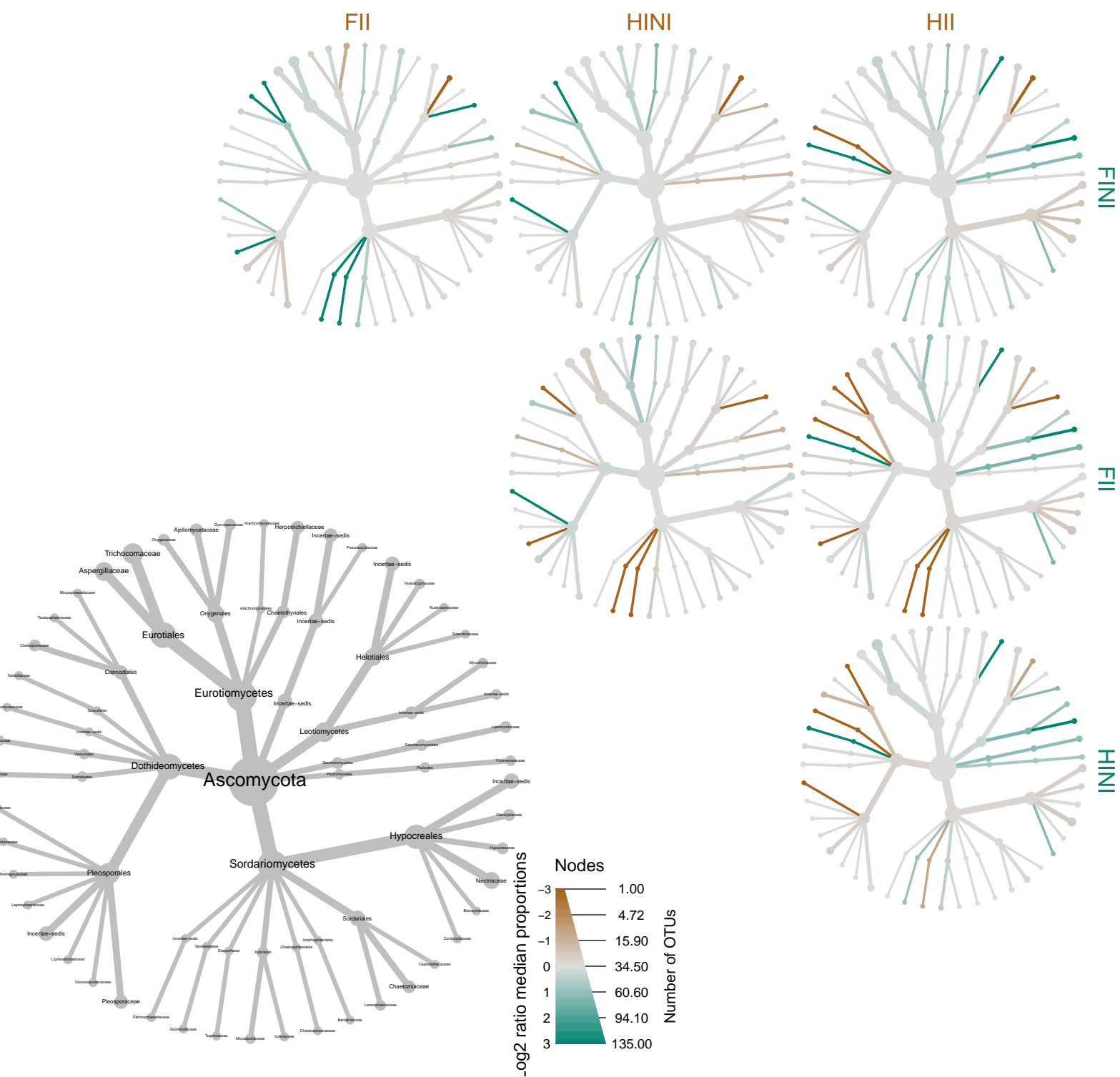


Figure S9. Heat tree with the taxonomy hierarchy of Basidiomycota phylum. Size and colors of nodes and edges are correlated with the abundance of organisms in each treatment. Green and brown were used to present higher or lower abundance, when comparing two conditions based on the different irrigation amounts (FI, Full Irrigated or HI, Half Irrigated), and AMF inoculation (I, inoculated; or NI, non-inoculated).

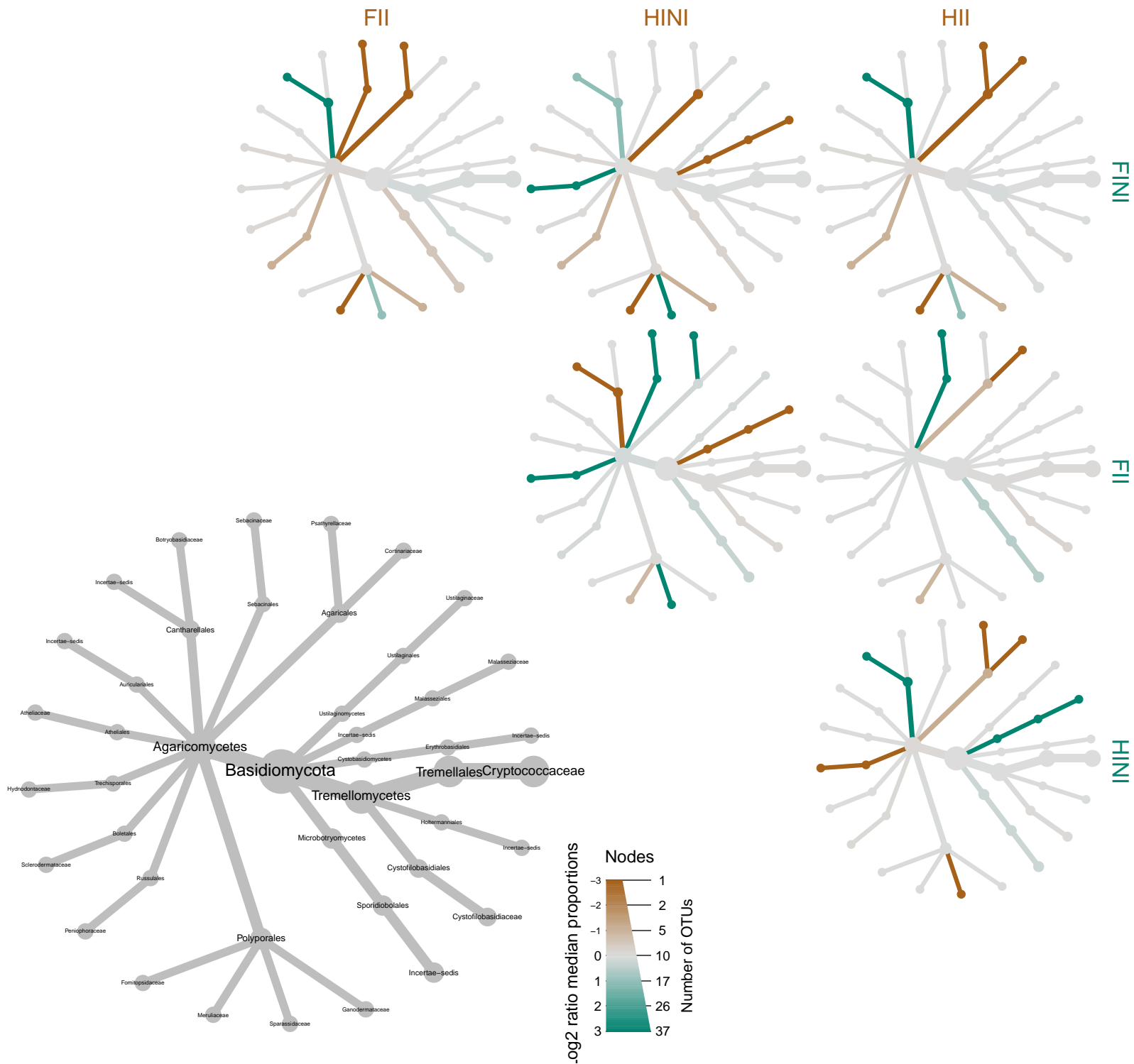


Figure S10. Heat tree with the taxonomy hierarchy of Zygomycota phylum. Size and colors of nodes and edges are correlated with the abundance of organisms in each treatment. Green and brown were used to present higher or lower abundance, when comparing two conditions based on the different irrigation amounts (FI, Full Irrigated or HI, Half Irrigated), and AMF inoculation (I, inoculated; or NI, non-inoculated).

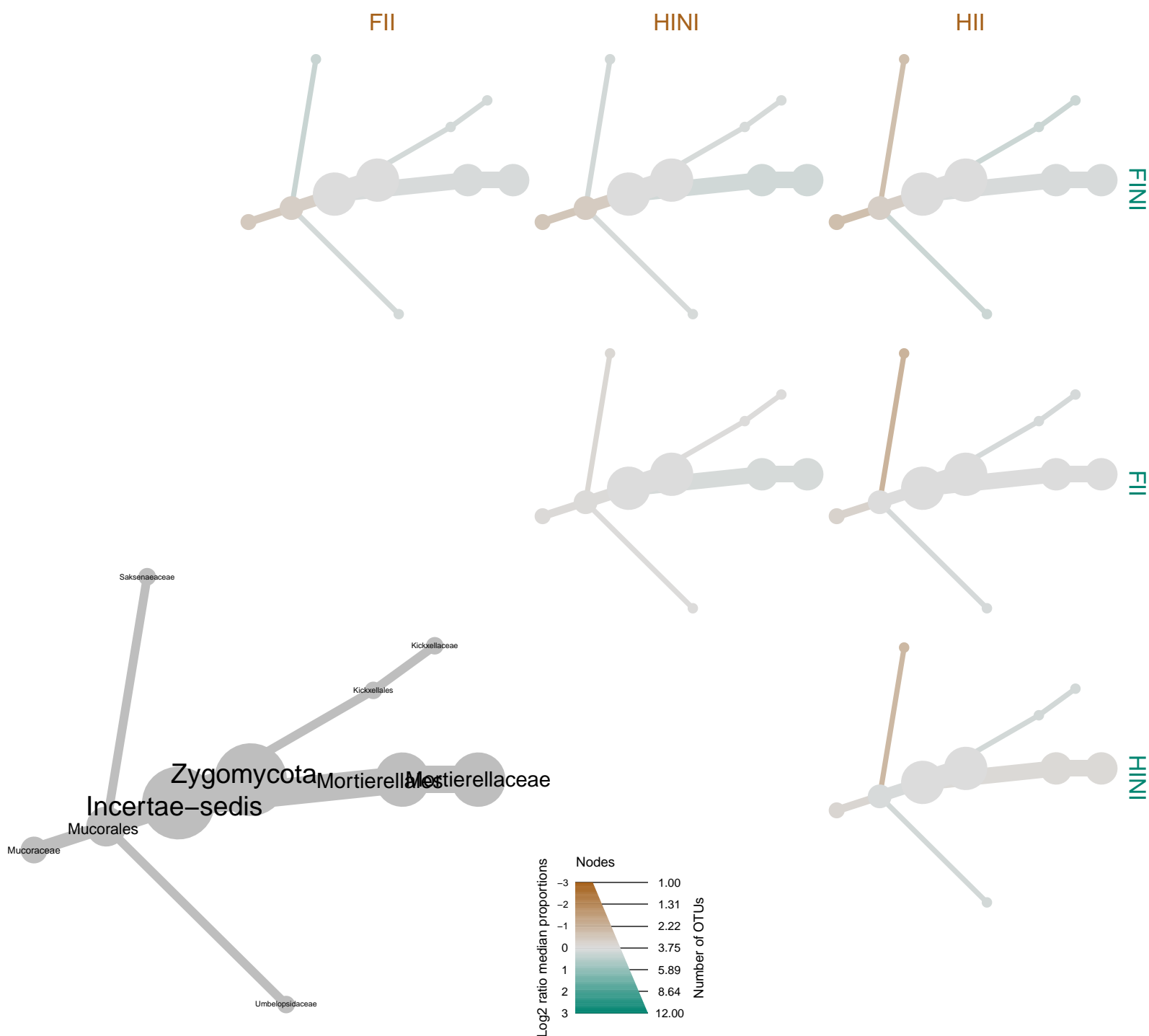


Table S1: Relationships between the Shannon and inverse of Simpson indices for bacterial and fungal communities within each not treated (NT) or treated plots subjected to different irrigation amounts (FI, Full Irrigated or HI, Half Irrigated), and AMF inoculation (I, inoculated; or NI, non-inoculated). R values, t values, degrees of freedom (df) and p-values of the regression study (Pearson correlation) conducted are reported.

Treatment	R	t	df	p-value
<i>Shannon entropy</i>				
NT	0.469	1.984	14	0.067
FINI	-0.580	-1.006	2	0.420
FII	-0.815	-1.992	2	0.185
HINI	-0.367	-0.558	2	0.633
HII	0.400	0.617	2	0.600
<i>Inverse of Simpson</i>				
NT	-0.443	-1.850	14	0.085
FINI	-0.524	-0.871	2	0.476
FII	-0.605	-1.076	2	0.395
HINI	-0.846	-2.245	2	0.154
HII	0.166	0.238	2	0.834

Table S2: Separation of phylum (A) or class (B) bacterial abundances between treatments by Kenward–Roger method and Tukey’s p-value adjustment ($P \leq 0.05$). Different letters within column, indicate significant differences as affected by not treated (NT) or subjected to different irrigation amounts (FI, Full Irrigated or HI, Half Irrigated), and AMF inoculation (I, inoculated; or NI, non-inoculated) and their combinations.

Table S2A:

Phylum	Contrast groups with Tukey's p value adjustment					LMEM	
	NT	FINI	FII	HINI	HII	F	p value
<i>Acidobacteria</i>	a	ab	b	ab	ab	3.03	0.032
<i>Actinobacteria</i>	b	ab	b	a	ab	4.8	0.003
<i>Armatimonadetes</i>	a	a	a	a	a	1.96	0.128
<i>Bacteroidetes</i>	ab	b	ab	ab	a	4.14	0.009
<i>Chloroflexi</i>	ab	ab	b	a	ab	3.42	0.019
<i>Firmicutes</i>	b	a	a	a	a	19.26	≤ 0.0001
<i>Gemmatimonadetes</i>	a	b	b	ab	b	10.41	≤ 0.0001
<i>Planctomycetes</i>	a	a	a	a	a	1.72	0.169
<i>Proteobacteria</i>	b	a	a	c	b	14.17	≤ 0.0001
<i>Verrucomicrobia</i>	a	a	a	a	a	1.53	0.219
Others	b	b	b	a	ab	7.99	≤ 0.0001

Table S2B:

Class	Contrast groups with Tukey's p value adjustment					LMEM	
	NT	FINI	FII	HINI	HII	F	p value
<i>Actinobacteria</i>	b	ab	b	a	ab	4.42	0.006
<i>Alphaproteobacteria</i>	b	a	a	c	b	9.53	≤ 0.0001
<i>Bacilli</i>	b	a	a	a	a	17.45	≤ 0.0001
<i>Betaproteobacteria</i>	ab	a	a	c	bc	7.96	≤ 0.001
<i>Gammaproteobacteria</i>	b	b	b	a	ab	9.54	≤ 0.0001
<i>Gemmatimonadetes</i>	a	b	b	ab	b	10.41	≤ 0.0001
<i>Planctomycetia</i>	a	a	a	a	a	1.78	0.157
<i>Rubrobacteria</i>	a	a	a	a	a	1.8	0.153
<i>Solibacteres</i>	a	ab	b	ab	ab	3.03	0.032
<i>Spartobacteria</i>	a	a	a	a	a	1.64	0.193
<i>Thaumarchaeota</i>	a	b	b	a	a	40.18	≤ 0.0001
<i>Thermoleophilia</i>	a	a	a	a	a	1.19	0.331
Others	ab	b	b	a	ab	5.03	0.003

Table S3: Separation of phylum (A) or class (B) fungal abundances between treatments by Kenward–Roger method and Tukey’s p-value adjustment ($P \leq 0.05$). Different letters within column, indicate significant differences as affected by not treated (NT) or subjected to different irrigation amounts (FI, Full Irrigated or HI, Half Irrigated), and AMF inoculation (I, inoculated; or NI, non-inoculated) and their combinations.

Table S3A:

Phylum	Contrast groups with Tukey's p value adjustment					LMEM	
	NT	FINI	FII	HINI	HII	F	p value
<i>Ascomycota</i>	a	ab	ab	b	ab	4.36	0.007
<i>Basidiomycota</i>	b	a	a	a	a	72.51	≥ 0.0001
<i>Zygomycota</i>	c	ab	a	bc	b	16.59	≥ 0.0001
Others	a	b	b	b	b	319.63	≥ 0.0001

Table S3B:

Class	Contrast groups with Tukey's p value adjustment					LMEM	
	NT	FINI	FII	HINI	HII	F	p value
<i>Agaricomycetes</i>	a	b	ab	ab	ab	4.26	0.008
<i>Dothideomycetes</i>	a	ab	ab	b	ab	5.07	0.003
<i>Eurotiomycetes</i>	a	a	a	a	a	1.46	0.241
<i>Leotiomycetes</i>	a	c	ab	b	ab	7.98	≤ 0.001
<i>Pezizomycetes</i>	a	a	a	a	a	2.18	0.093
<i>Saccharomycetes</i>	a	b	ab	ab	b	6.11	0.001
<i>Sordariomycetes</i>	a	ab	b	b	b	15.06	≤ 0.0001
<i>Tremellomycetes</i>	b	a	a	a	a	42.67	≤ 0.0001
Others	a	b	b	c	bc	36.67	≤ 0.0001

Table S4: Canonical correspondence analysis (CCA) for bacterial communities. ANOVA table of the CCA model (A), Eigenvalues and their contribution to the scaled Chi-square (B). Scores for species in the first two components (highest scores are shown), species scaled proportioned to eigenvalues (C).

Table S4A:

ANOVA				
	Df	ChiSquare	F	Pr(>F)
Model	6	0.22765	0.906	0.608

Table S4B:

Importance of components						
	CCA1	CCA2	CCA3	CCA4	CCA5	CCA6
Eigenvalue	0.1558	0.0287	0.01408	0.01318	0.01167	0.004231
Proportion explained	0.2576	0.04747	0.02328	0.0218	0.01931	0.006998
Cumulative proportion	0.2576	0.30512	0.3284	0.3502	0.36951	0.376504

Table S4C:

Species scores						
	CCA1	CCA2	CCA3	CCA4	CCA5	CCA6
<i>Nitrososphaera sp.</i>	0.90311	0.051796	0.05354	0.12737	0.005261	-0.04755
<i>Jatrophihabitans sp.</i>	0.840039	-0.17079	-0.14341	-0.23653	-0.20954	-0.08596
<i>Actinophytocola sp.</i>	0.816335	-0.05015	-0.02503	0.072079	-0.0816	0.115352
<i>Pseudonocardia sp.</i>	0.803977	0.070511	-0.06399	-0.088	0.043903	-0.01812
<i>Geodermatophilus sp.</i>	0.795144	-0.06155	-0.04005	-0.0704	-0.31164	-0.00122
<i>Actinomycetospora sp.</i>	0.783389	-0.05301	-0.03739	-0.06676	-0.07548	-0.00228
<i>Rugosimonospora acidiphila</i>	0.763093	0.249127	-0.05172	-0.10548	-0.00558	-0.03235
<i>Micromonospora hermanusense</i>	0.757079	-0.07651	-0.12834	-0.24113	0.123897	-0.07726
<i>Pilimelia sp.</i>	0.742563	0.162	-0.05302	-0.11957	-0.05318	-0.02341
<i>Lysobacter sp.</i>	0.741922	-0.9376	0.27309	0.35681	0.06597	0.127134
<i>Afipia sp.</i>	0.736507	-0.23968	-0.02602	-0.01671	-0.29163	0.172745
<i>Actinomadura bangladeshensis</i>	0.730014	0.105852	-0.16461	-0.3963	-0.04963	-0.12888
<i>Cellulomonas xylanilytica</i>	0.727358	-0.36363	-0.12005	-0.21129	-0.55435	0.068473
<i>Mycobacterium sp.</i>	0.69934	-0.10373	-0.06341	-0.47121	-0.11255	-0.12158
<i>Sporocytophaga sp.</i>	0.694234	-0.25704	-0.06803	-0.23426	-0.10568	0.173353
<i>Roseiflexus sp.</i>	0.692224	-0.02525	-0.06411	0.05317	0.027705	0.089307
<i>Blastococcus sp.</i>	0.682404	-0.16904	-0.07267	-0.12735	-0.2557	-0.05435
<i>Actinoallomurus liliacearum</i>	0.681606	0.055553	-0.08196	-0.19411	-0.24573	-0.01392
<i>Chitinophaga sp.</i>	0.651481	-0.19698	-0.04486	-0.31888	-0.20564	0.149745
<i>Opitutus sp.</i>	0.634364	-0.21628	-0.04987	-0.34872	-0.10618	-0.0653
<i>Pseudonocardia halophobica</i>	0.625778	-0.1957	-0.23561	-0.35158	-0.20011	0.087913
<i>Adhaeribacter sp.</i>	0.624527	-0.70378	0.102099	0.186241	-0.01492	0.113118
<i>Streptosporangium sp.</i>	0.619618	0.028435	-0.0078	0.063166	-0.1801	0.028091

<i>Streptomyces atratus</i>	0.610858	0.270358	-0.08153	0.053402	0.113615	0.088858
<i>Crossiella sp.</i>	0.605013	-0.1129	0.234968	0.412531	-0.143	0.03732
<i>Acidothermus sp.</i>	0.604694	0.145956	0.032827	0.097312	-0.12328	0.019451
<i>Pseudomonas brassicacearum</i>	0.599419	-0.44257	0.101634	0.171433	-0.21706	-0.04127
<i>Chryseolinea sp.</i>	0.584017	-0.23373	0.082954	0.08548	-0.49614	-0.3828
<i>Flavobacterium sp.</i>	0.576424	-0.3924	-0.07892	-0.24644	-0.12032	0.0838
<i>Sediminibacterium sp.</i>	0.575512	-0.24451	0.006759	-0.13939	-0.30003	-0.16434
<i>Actinoallomurus sp.</i>	0.568872	0.103537	0.038472	-0.09071	-0.02741	-0.0593
<i>Iamia sp.</i>	0.561461	0.069445	-0.05372	-0.32416	-0.1957	0.015219
<i>Marmoricola sp.</i>	0.546627	-0.16358	-0.29893	0.003933	-0.45004	0.088858
<i>Streptomyces sp.</i>	0.541773	0.122691	0.017125	0.063244	-0.187	0.00441
<i>Streptomyces phaeochromogenes</i>	0.539556	0.078553	-0.24487	-0.77926	-0.22819	0.237075
<i>Acidiphilium sp.</i>	0.516372	-0.23848	0.017026	0.157383	-0.2564	-0.01408
<i>Rhodopirellula sp.</i>	0.514133	-0.32655	0.028747	0.02222	-0.12991	0.078482
<i>Reyranella sp.</i>	0.489423	0.043458	-0.1318	-0.31596	-0.14176	0.029237
<i>Cupriavidus basilensis</i>	0.450702	-0.58379	0.251971	0.191967	0.276559	0.117796
<i>Labrys sp.</i>	0.438376	-0.00789	-0.14218	-0.14215	0.048079	-0.25277
<i>Polycladomyces sp.</i>	0.437634	-0.10789	0.124592	-0.22934	-0.30697	0.089599
<i>Nitrospira sp.</i>	0.432062	0.051167	-0.02968	-0.01631	0.172367	-0.03902
<i>Acidicaldus sp.</i>	0.426277	-0.03105	-0.12241	-0.0801	-0.25062	-0.09681
<i>Kaistobacter sp.</i>	0.422394	-0.64032	0.102711	-0.01616	0.046888	0.08476
<i>Geobacter sp.</i>	0.41423	-0.52195	0.035951	-0.13136	-0.1508	0.114173
<i>Sandaracinus sp.</i>	0.411317	-0.4303	-0.0215	-0.18697	-0.13011	-0.07674
<i>Arthrobacter cereus</i>	0.401652	0.168511	0.044562	0.039195	0.165427	0.0745
<i>Caldilinea sp.</i>	0.400044	-0.11916	-0.01428	0.076314	-0.19153	-0.00879
<i>Pirellula sp.</i>	0.39959	-0.03753	-0.04231	-0.03345	-0.12983	0.043535
<i>Pedosphaera sp.</i>	0.392142	0.064753	0.011451	-0.06564	-0.18035	0.036975

Table S5: Canonical correspondence analysis (CCA) for fungal communities. ANOVA table of the CCA model (A), Eigenvalues and their contribution to the scaled Chi-square (B). Scores for species in the first two components (highest scores are shown), species scaled proportioned to eigenvalues (C).

Table S5A:

ANOVA				
	Df	ChiSquare	F	Pr(>F)
Model	6	0.63028	0.793	0.864

Table S5B:

Importance of components						
	CCA1	CCA2	CCA3	CCA4	CCA5	CCA6
Eigenvalue	0.2657	0.11584	0.10115	0.06398	0.05351	0.0301
Proportion explained	0.1458	0.06358	0.05552	0.03512	0.02937	0.01652
Cumulative proportion	0.1458	0.20941	0.26492	0.30004	0.32941	0.34593

Table S5C:

Species scores						
	CCA1	CCA2	CCA3	CCA4	CCA5	CCA6
<i>Cryptococcus sp.</i>	1.11445	0.369036	0.85219	0.206592	-0.3235	0.117307
<i>Cladorrhinum sp.</i>	0.72235	0.317987	-0.12432	-0.52805	0.7938	-0.4051
<i>Penicillium citrinum</i>	0.6278	0.204333	-0.07052	0.688437	-0.5441	-1.4151
<i>Acrostalagmus luteoalbus</i>	0.60276	-0.2674	0.760029	0.692359	0.3234	-0.25102
<i>Cryptococcus fuscescens</i>	0.56284	0.008541	0.26487	0.168223	0.1596	-0.59571
<i>Neonectria sp.</i>	0.5587	-0.25211	0.704434	0.653559	0.333	-0.19386
<i>Tetracladium sp.</i>	0.52137	-0.29803	0.507676	0.409709	0.1025	-0.23154
<i>Coniolariaella ershadii</i>	0.5162	-0.01997	0.527921	0.385819	-0.0925	-0.09418
<i>Chaetomium sp.</i>	0.46664	-0.13988	0.66335	0.546768	0.2206	-0.28436
<i>Metarhizium anisopliae</i>	0.46504	0.345326	-0.52514	-0.5746	1.494	-0.48263
<i>Fusarium oxysporum</i>	0.40833	0.073049	0.058425	-0.32262	-0.116	0.131518
<i>Humicola grisea</i>	0.3833	0.378417	-0.02284	-0.24794	0.5765	-0.34542
<i>Hansfordia sp.</i>	0.37479	-0.05013	-0.41502	0.778428	0.8976	0.553268
<i>Peniophora sp.</i>	0.37108	-0.56695	0.50854	0.241481	0.1225	-0.06754
<i>Acremonium blochii</i>	0.34809	0.189951	0.25942	0.088453	0.2766	-0.00467
<i>Calycina claroflava</i>	0.3388	0.487644	0.48107	-0.13743	-0.474	0.838292
<i>Penicillium nodositatum</i>	0.3348	-0.1124	0.633723	-0.25831	-0.5275	-0.68092
<i>Dactylonectria estremocensis</i>	0.3228	-0.24038	0.065716	-0.67842	-0.4284	0.606488
<i>Penicillium ochrochloron</i>	0.27953	0.215827	-0.17022	-0.56202	0.3418	-1.05939
<i>Holtermannia corniformis</i>	0.27285	0.256185	0.420311	0.148273	-0.0208	-0.25956
<i>Cryptococcus podzolicus</i>	0.27124	0.162272	-0.15969	-0.12922	-0.0927	0.105592
<i>Cephalotheca sulfurea</i>	0.25635	-0.03941	-0.42956	0.111054	0.1225	-0.14599
<i>Scytalidium cuboideum</i>	0.25032	-0.17853	-0.33245	0.216152	0.5841	0.000858
<i>Scytalidium sp.</i>	0.20882	0.075278	-0.01714	0.124967	0.07061	0.192727

<i>Cryptococcus aerius</i>	0.19134	0.071912	-0.08592	0.260048	0.1436	-0.12786
<i>Venturia hystrioides</i>	0.1847	-0.02675	-0.06878	-0.40722	0.7753	-0.11931
<i>Mortierella rishiksha</i>	0.16504	-0.36623	-0.95523	-0.05554	-0.6483	-0.066
<i>Arachnomyces gracilis</i>	0.16501	-0.32828	-0.2074	0.836369	0.4482	0.170912
<i>Aspergillus amstelodami</i>	0.15459	-0.13999	-0.29212	0.590017	0.5816	0.54309
<i>Lecanicillium sp.</i>	0.1436	-0.88611	0.106287	-0.14634	-0.2268	0.210686
<i>Acremonium persicinum</i>	0.13505	0.303458	0.077052	-0.01712	-0.0489	-0.39946
<i>Lophiostoma sp.</i>	0.13158	0.000766	0.06781	-0.10491	-0.0726	0.030338
<i>Clonostachys rosea</i>	0.1299	0.271409	0.358792	-0.1997	0.05228	-0.22732
<i>Truncatella laurocerasi</i>	0.12811	0.17719	0.006564	-0.30468	0.4193	-0.14976
<i>Ganoderma brownii</i>	0.1161	-0.39575	0.096624	0.030226	0.5736	-0.04758
<i>Mortierella amoeboides</i>	0.08273	-0.27787	-0.3866	-0.3853	-0.0929	0.279037
					9.59E-	
<i>Cryptococcus phenolicus</i>	0.06974	0.034382	0.076743	0.026955	05	-0.07322
<i>Aspergillus austroafricanus</i>	0.06599	0.182446	-0.72365	0.771937	-0.3383	-0.52212
<i>Veronaeopsis simplex</i>	0.05568	-0.01419	-0.43392	-0.17827	0.191	-0.25153
<i>Alternaria atra</i>	0.04772	0.15823	0.08665	-0.1211	-0.1955	0.109611
<i>Podospora sp.</i>	0.04349	0.402698	0.047896	-0.04429	0.0452	-0.11608
<i>Metacordyceps chlamydosporia</i>	0.04242	0.191909	-0.29859	-0.37822	0.1638	-0.23786
<i>Spiromastix warcupii</i>	0.03242	-0.53109	-0.05011	-0.69589	-0.4098	0.103761
<i>Penicillium menonorum</i>	0.026	0.008825	0.063361	-0.08254	0.02202	-0.14104
<i>Cladophialophora sp.</i>	0.01671	0.262961	0.289349	-0.20773	-0.2603	0.664512
<i>Rhodotorula lamellibrachiae</i>	0.0166	0.134016	0.215551	0.567111	0.1564	0.056186
<i>Aspergillus wentii</i>	-0.0193	-0.5697	0.483928	0.032808	0.1285	0.454078
<i>Cryptococcus terreus</i>	-0.0301	-0.02635	0.016622	-0.02606	0.02417	-0.09928
<i>Hypocrea atroviridis</i>	-0.0341	0.43336	0.34215	-0.47482	-0.3226	-0.01758
<i>Aspergillus piperis</i>	-0.0542	-0.22666	0.581666	0.080866	0.1759	0.101951