

FIG S1 Rarefaction curves using the 0% RDP Classifier confidence dataset for the (A) Oklahoma control and warming samples and (B) Alaska control and warming samples in the shallow (0 to -20 cm) and deep (-20 to -50 cm) soil layers.

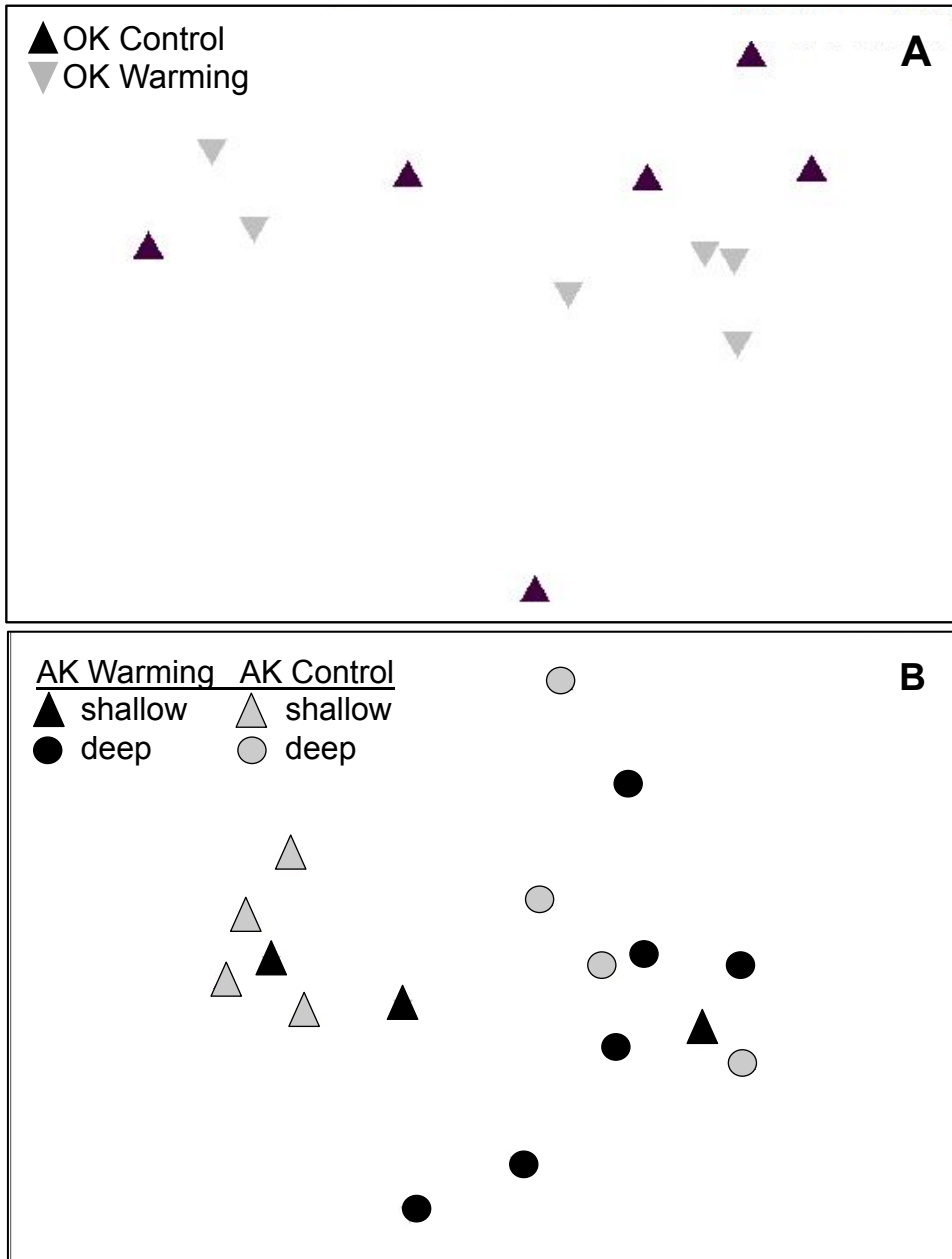


FIG S2 NMDS ordinations based on Bray-Curtis dissimilarity matrices for (A) Oklahoma control versus warming samples (2D stress=0.07) and (B) Alaska CiPEHR samples for shallow (0 to -20 cm) versus deep (-20 to -50 cm) and warming versus control.

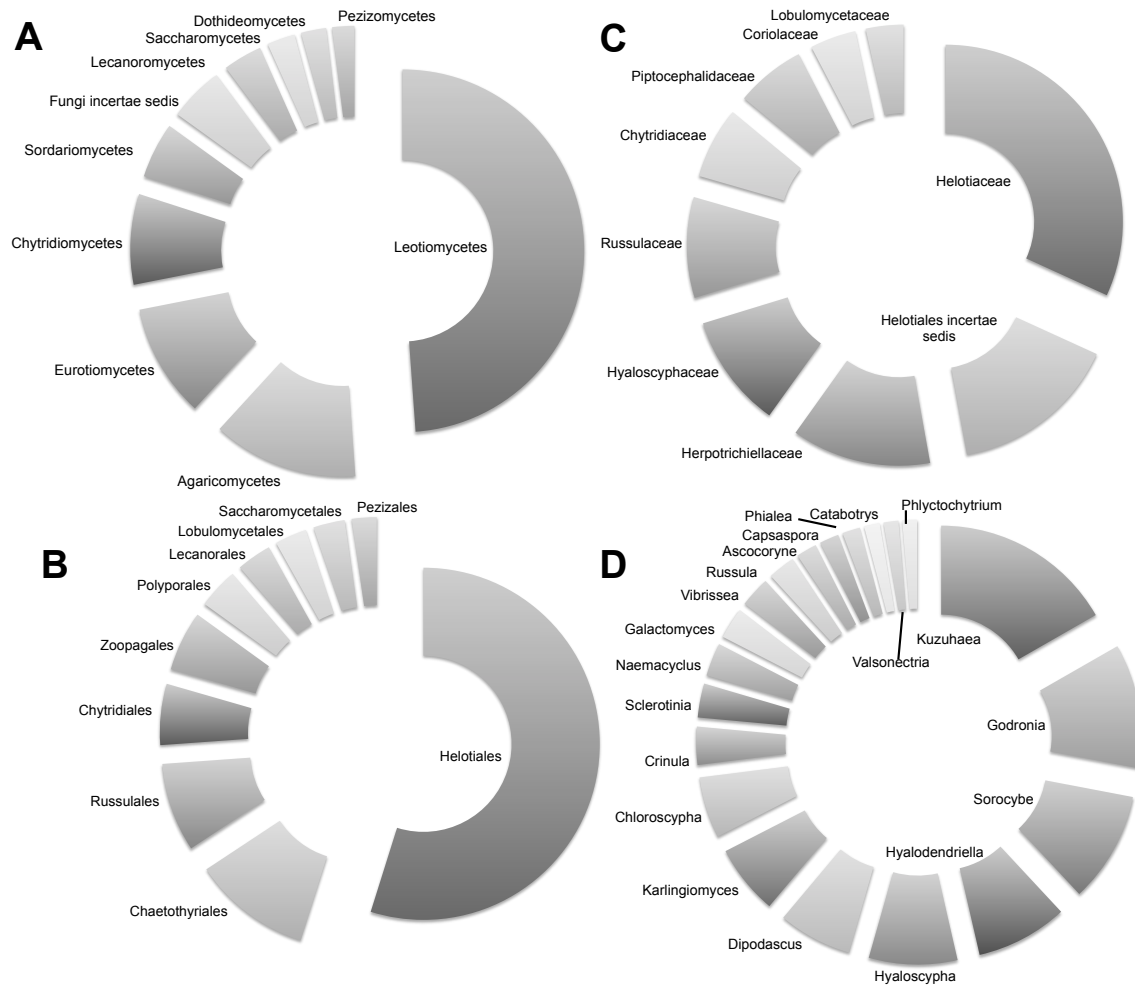


FIG S3 Composition of the top 10 taxa at the (A) class, (B) order, (C) family levels and top 20 taxa at the (D) genus level for the shallow (0 to -20 cm) layers of the Alaska CiPEHR samples. Total percent of all sequences is (A) 90.9%, (B) 78.4%, (C) 68.9% and (D) 72.0%.

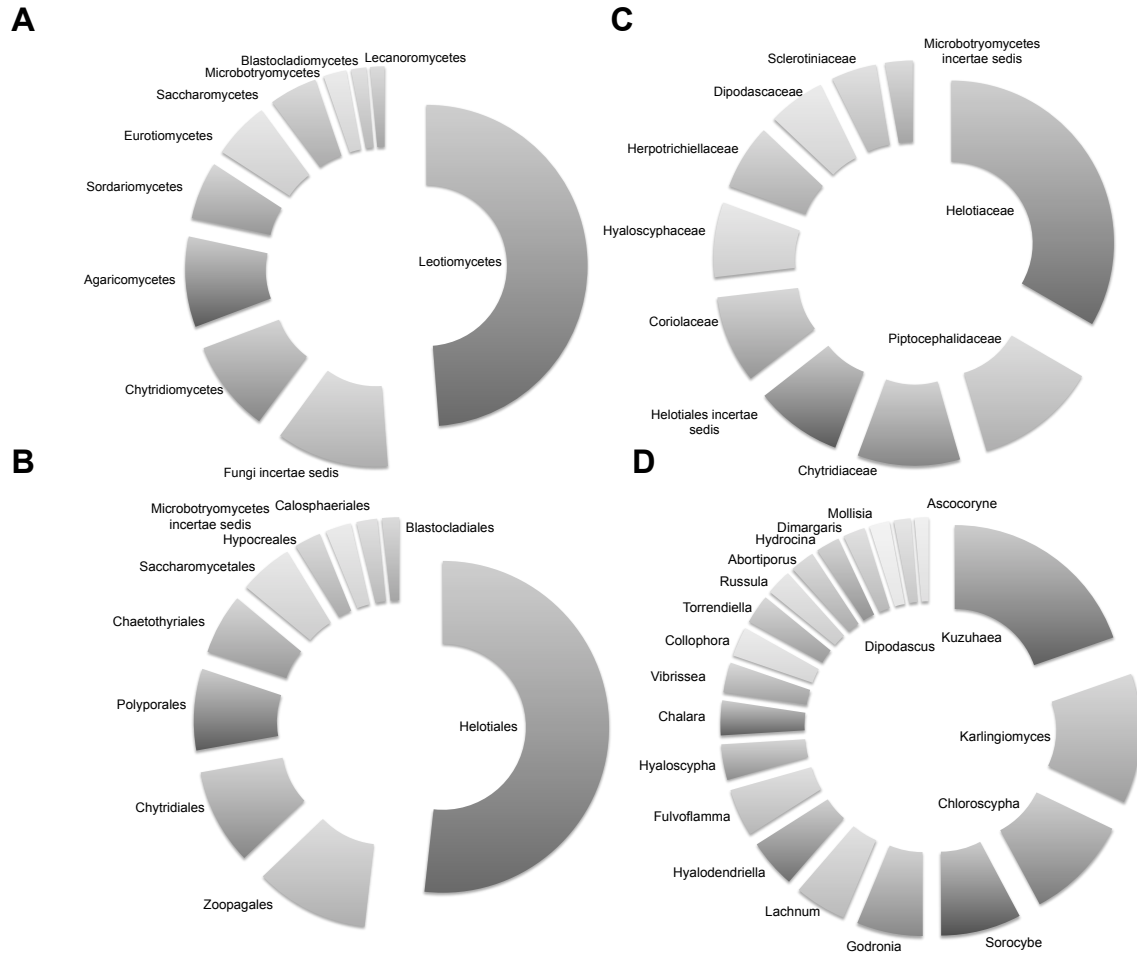


FIG S4 Composition of the top 10 taxa at the (A) class, (B) order, (C) family levels and top 20 taxa at the (D) genus level for the deep (-20 to -50 cm) layers of the Alaska CiPEHR samples. Total percent of all sequences is (A) 90.5%, (B) 83.7%, (C) 75.8% and (D) 73.6%.

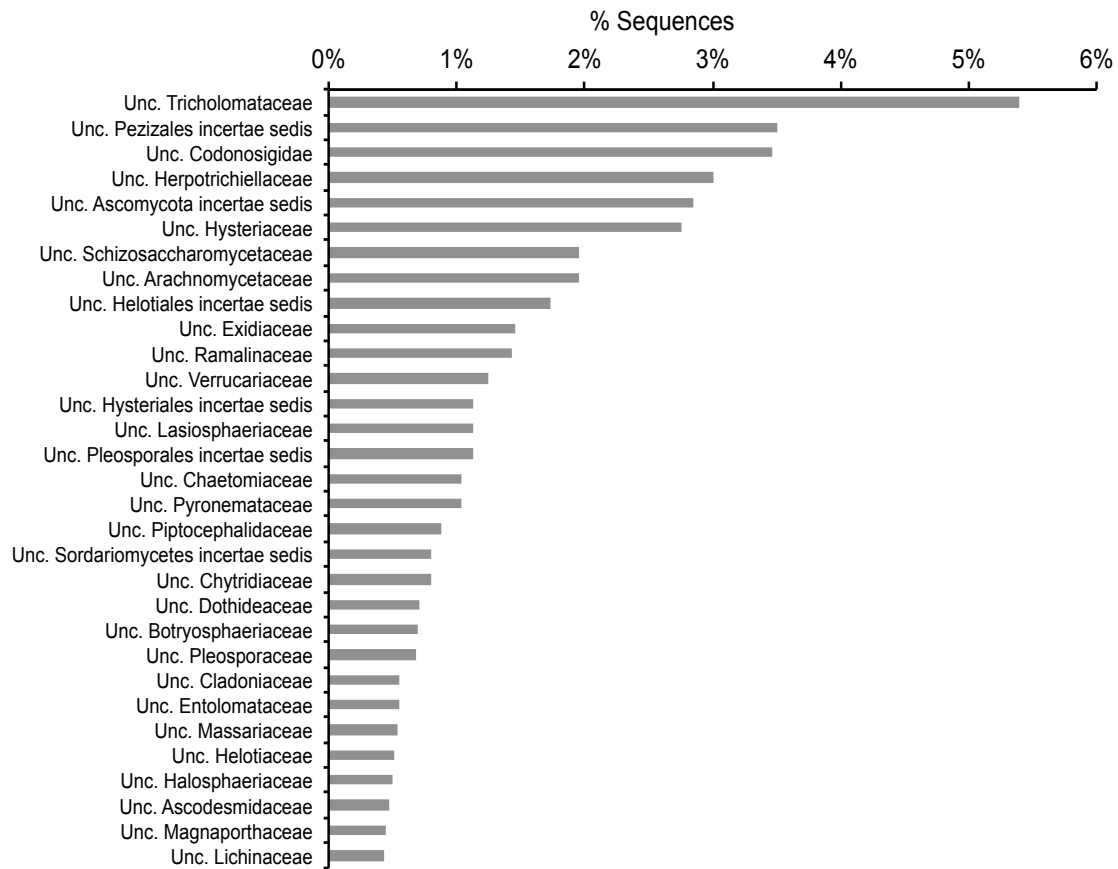


FIG S5 Composition and relative abundance of the unclassified genera as defined by a RDP fungal classifier confidence level <50% in the Oklahoma tallgrass prairie samples within the listed unclassified family bins.

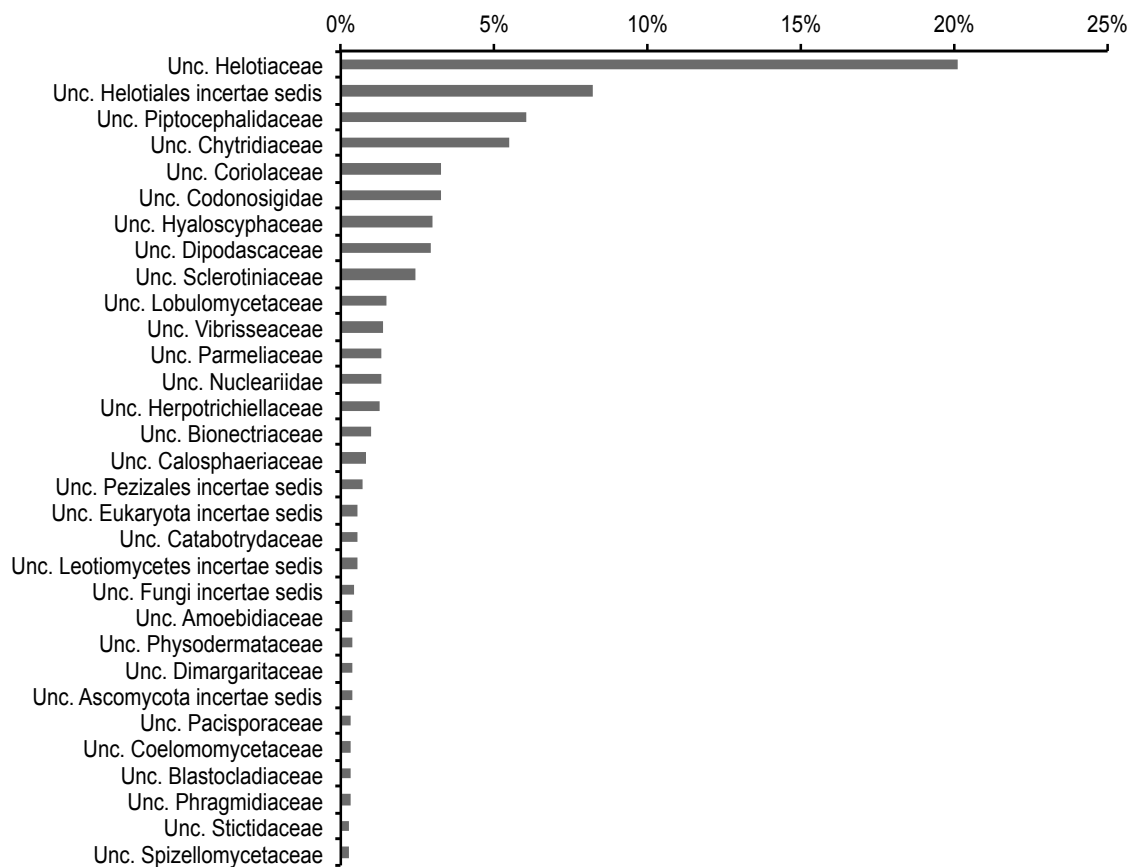


FIG S6 Composition and relative abundance of the unclassified genera as defined by a RDP fungal classifier confidence of <50% in the Alaska samples within the listed unclassified family bins.

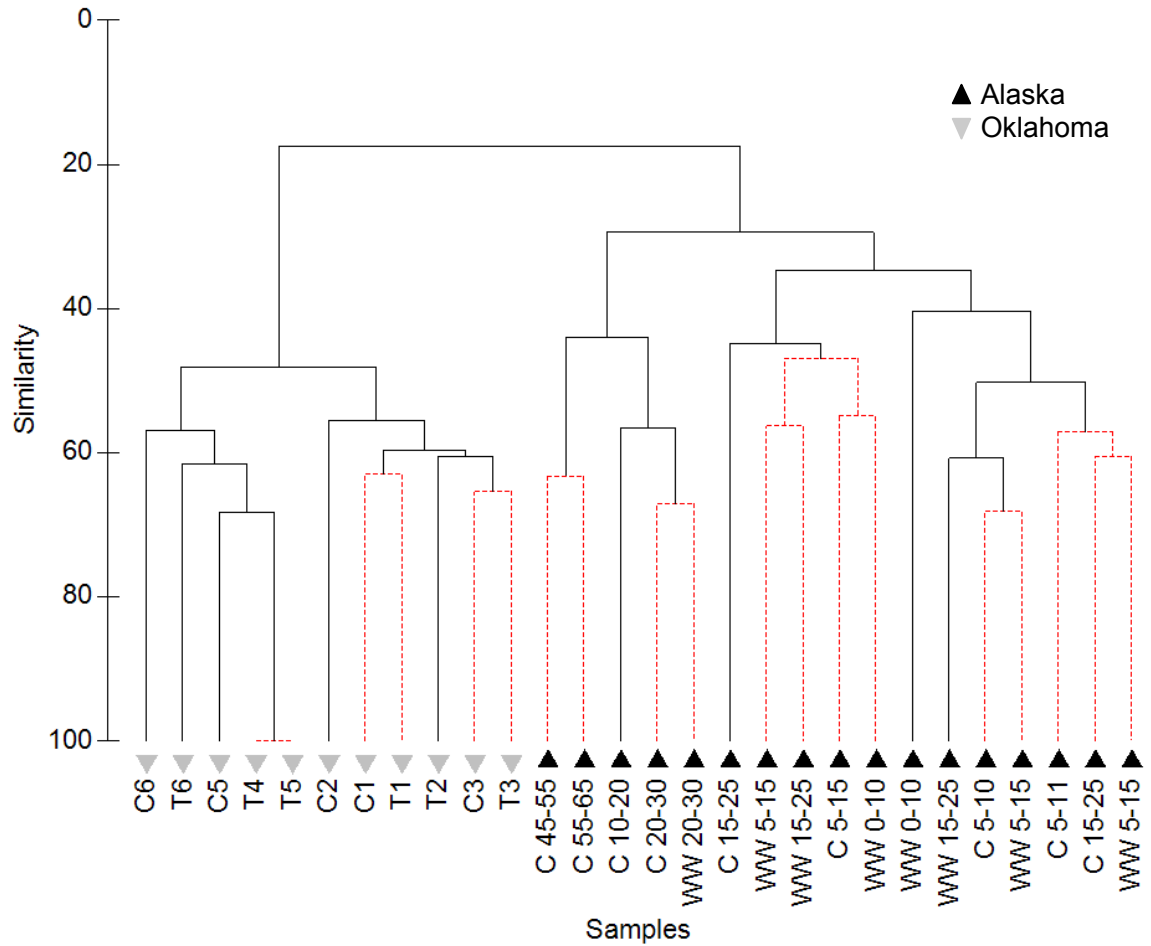


FIG S7 Cluster analysis using complete linkage clustering with similarity profile analysis (SIMPROF) differentiating the Alaska and Oklahoma fungal communities. Solid lines indicate significant (95% confidence) cluster placement.

TABLE S1 Average relative abundances of the most abundant fungal classes in the Alaska and Oklahoma samples. The far right column indicates the significance between treatments resulting from a two-tailed t-test. *=P<0.05, **=P<0.01.

CLASS	AK	OK	P
Leotiomyces	43%	5%	**
Agaricomycetes	8%	26%	**
Eurotiomyces	8%	17%	**
Sordariomyces	4%	15%	**
Dothideomycetes	1%	17%	**
Lecanoromycetes	4%	5%	
Chytridiomycetes	7%	1%	**
Fungi inc. sed.	7%	0%	**
Saccharomycetes	3%	0%	**
Schizosaccharomycetes	0.0%	1.9%	**
Blastocladiomycetes	1%	1%	
Taphrinomycetes	0.2%	1.3%	
Tremellomycetes	0.2%	0.9%	
Pneumocystidomycetes	0.0%	1.0%	
Ichthyospora	0.5%	0.3%	

TABLE S2 Average relative abundances of the most abundant fungal families in the Alaska and Oklahoma samples. The far right column indicates the significance between treatments resulting from a two-tailed t-test. *=P<0.05, **=P<0.01.

ORDER	AK	OK	P
Helotiaceae	19.6%	0.1%	*
Trichomonascaceae	0.0%	9.3%	
Hyaloscyphaceae	7.7%	0.7%	
Herpotrichiellaceae	8.0%	0.0%	
Hoehnelomycetaceae	0.0%	7.8%	
Arthoniaceae	0.0%	7.5%	
Piptocephalidaceae	6.9%	0.1%	
Massariaceae	0.0%	5.3%	**
Coelomomycetaceae	0.5%	3.8%	
Lecanoraceae	0.0%	4.2%	
Hysteriales inc. sed.	0.0%	3.9%	
Dipodascaceae	3.3%	0.0%	**
Coriolaceae	3.2%	0.1%	
Russulaceae	3.2%	0.1%	
Vibrisseaceae	1.4%	1.6%	
Parmeliaceae	2.4%	0.5%	
Exobasidiaceae	0.0%	2.9%	
Raveneliaceae	0.1%	2.1%	
Schizothyriaceae	0.0%	1.8%	
Pleosporales inc. sed.	0.2%	1.4%	
Pyxidiophoraceae	0.0%	1.5%	
Psoraceae	0.0%	1.4%	
Lobulomycetaceae	1.1%	0.2%	
Massarinaceae	0.0%	1.2%	**
Leotiomycetes inc. sed.	1.0%	0.1%	
Marasmiaceae	0.0%	1.0%	
Pezizales inc. sed.	0.5%	0.6%	
Chaetosphaerellaceae	0.0%	1.0%	**
Brachybasidiaceae	0.0%	1.0%	

TABLE S3 Top BLAST results to the ARB-SILVA database of the RDP unclassified sequences, based on <50% classifier confidence. Percent abundances are to the total RDP unclassified sequences. BLAST percent identities are shown. * indicates lack of presence of this genus in the current RDP fungal classifier database release 1.

	% abund.	% ID
<i>Serpula lacrymans</i>	22.2%	91.3%
<i>Cyberlindnera meyeriae</i> *	22.6%	88.1%
<i>Phaeosphaeria avenaria</i> f. sp. triticae	13.2%	92.2%
<i>Passalora perplexa</i>	5.1%	84.9%
<i>Gloeophyllum abietinum</i> *	3.7%	88.1%
<i>Chytridium</i> sp. JEL341	3.2%	96.6%
<i>Nowakowskiella</i> sp. JEL127	2.7%	88.0%
<i>Sordaria macrospora</i> k-hell	2.5%	94.1%
<i>Melanoleuca melaleuca</i>	2.4%	91.8%
<i>Geomyces destructans</i> 20631-21*	2.1%	92.4%
<i>Tuber melanosporum</i> (Perigord truffle)	3.0%	86.0%
<i>Saccharomyces cerevisiae</i> Lalvin QA23	1.8%	81.2%
<i>Puccinia striiformis</i> f. sp. tritici PST-130	1.6%	78.5%
<i>Trametes versicolor</i>	1.4%	96.2%
<i>Cladochytrium replicatum</i> ⁺	0.9%	86.1%
<i>Antrodia xanthan</i>	0.8%	93.2%
<i>Arthrobotrys oligospora</i> ATCC 24927*	0.8%	87.6%
<i>Kodamaea ohmeri</i>	0.8%	84.5%
<i>Epichloe festucae</i> F11	0.6%	88.1%
<i>Mycosphaerella graminicola</i> STIR04_1.1.2	0.6%	80.4%
<i>Epichloe glyceriae</i> E277	0.5%	92.6%
<i>Gloeophyllum sepiarium</i>	0.5%	86.7%
<i>Phlyctochytrium planicorne</i>	0.3%	88.3%
<i>Lecophagus</i> sp. ATCC 56071	0.3%	85.0%
<i>Synchytrium decipiens</i>	0.3%	78.0%
<i>Schizothyrium pomi</i>	0.3%	82.8%
<i>Fomes fomentarius</i>	0.3%	96.1%
TOTAL	94.5%	