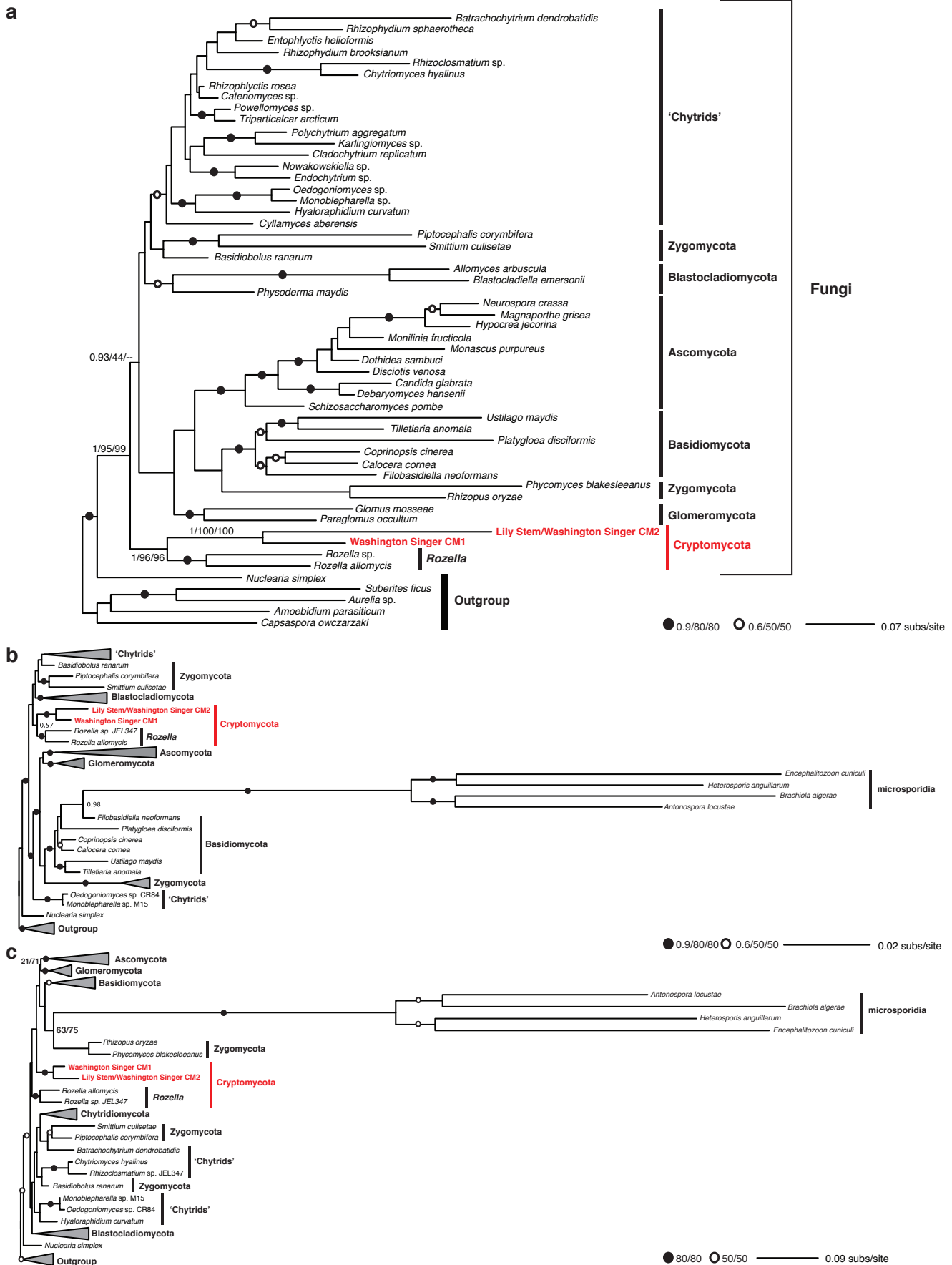
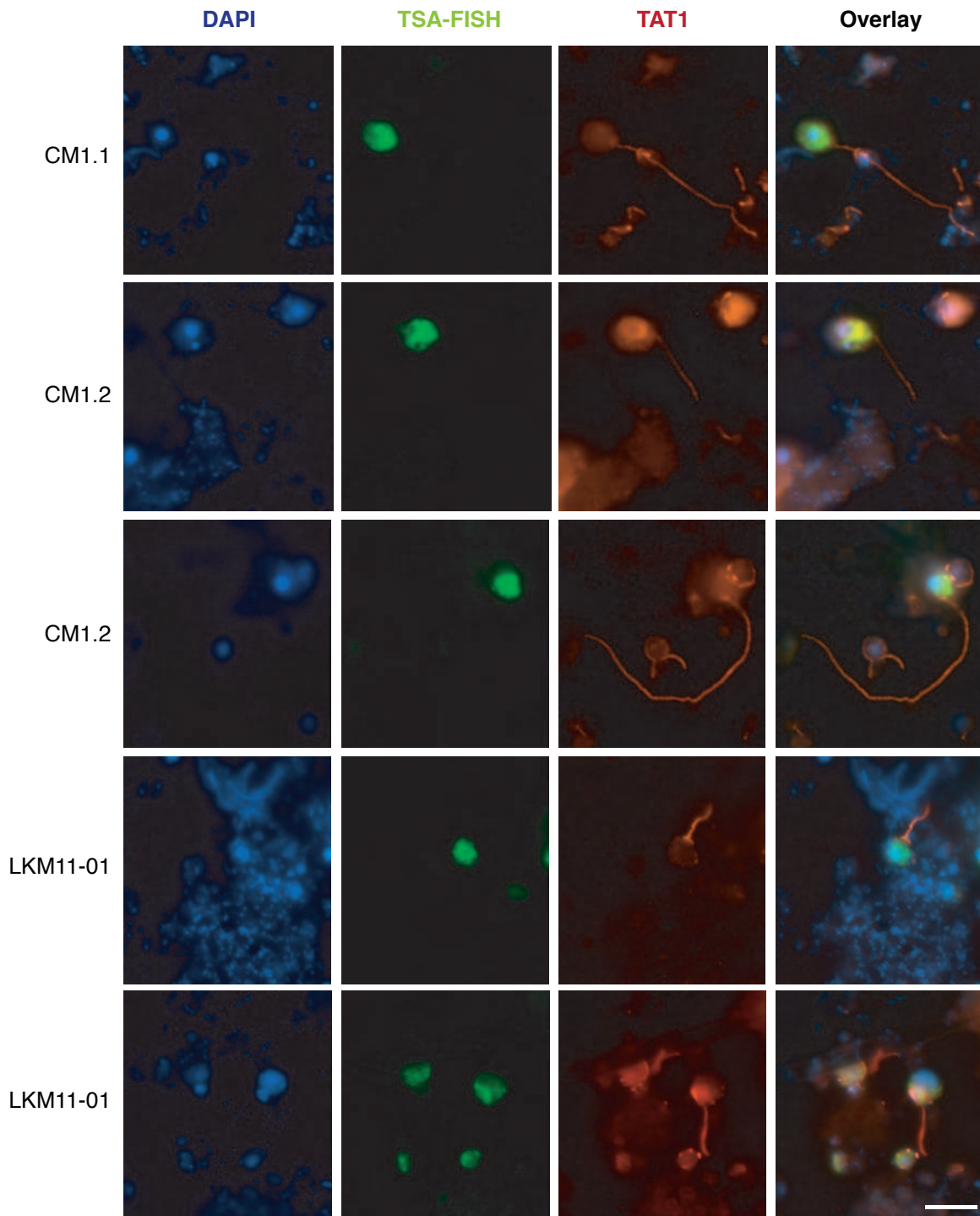


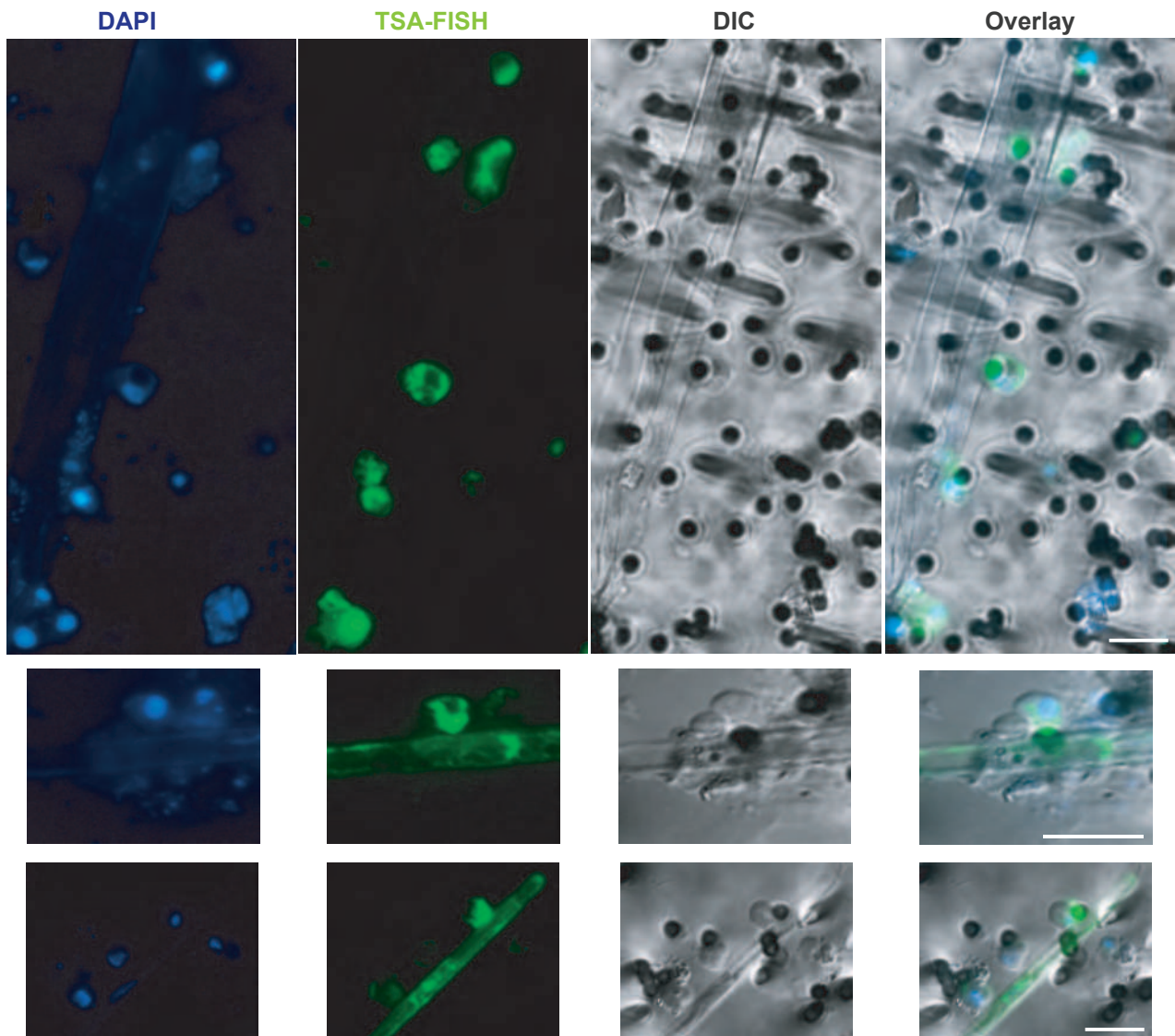
Supplementary Figure 1. Summary of the main findings of the paper. **a**, Standard working model of the fungal tree of life. **b**, Identification of a very large uncultured basal clade in the kingdom Fungi, marked in red and, with *Rozella*, named here as cryptomycota. This study therefore demonstrates that current models of fungal evolution and biodiversity, which are based on cultured microbes, have missed a huge fraction of the kingdom (perhaps even approaching one half). Furthermore, this group of microbes appears to grow without the defining fungal characteristics a chitin-rich cell wall (although this characteristic is also absent during the flagellated zoospore stage of many other chytrid fungi). Therefore these data challenge existing ideas of fungal biodiversity and current concepts regarding the adaptive features that drove the evolutionary diversification and ecological success of the fungal kingdom.



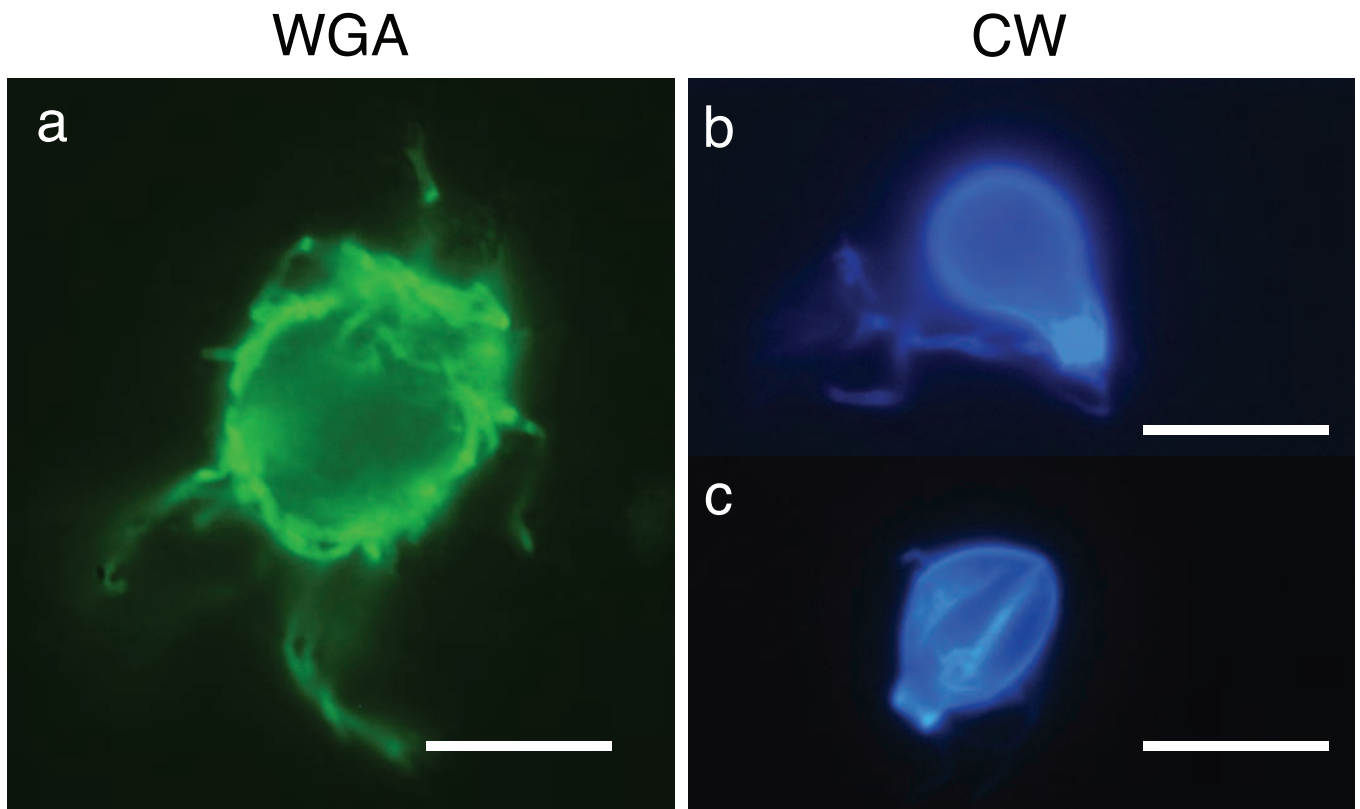
Supplementary Figure 2. Phylogenetic analysis of the SSU-5.8S-LSU alignment demonstrating the branching position of the cryptomycota. a. The phylogeny was calculated from an alignment of 54 sequences and 1,877 nucleotide alignment characters and demonstrates strong support for the placement of the novel clade as a sister group to *Rozella*. Node support values are labelled using the same convention as Fig. 1. **b.** Bayesian phylogeny based on SSU-LSU alignment with four microsporidia sequences added (58 sequences and 1,072 DNA characters – character number is reduced from **a** because of alignment of divergent microsporidia sequences). **c.** PhyML (fast Maximum Likelihood) tree topology with 1000 bootstrap values using PhyML and Log-Det distance methods calculated from the same alignments as **b**. These phylogenetic analyses followed the same procedure as described for the analyses shown in **a** and described in the methods section. Key topology support values are shown, however all other bootstrap values are notated with symbols: nodes supported by 0.9 posterior probability or greater and 80% bootstrap support or greater by both methods are marked with a black dot; nodes supported by 0.6 posterior probability or greater and 50% bootstrap support or greater by both methods are marked with a ringed circle.



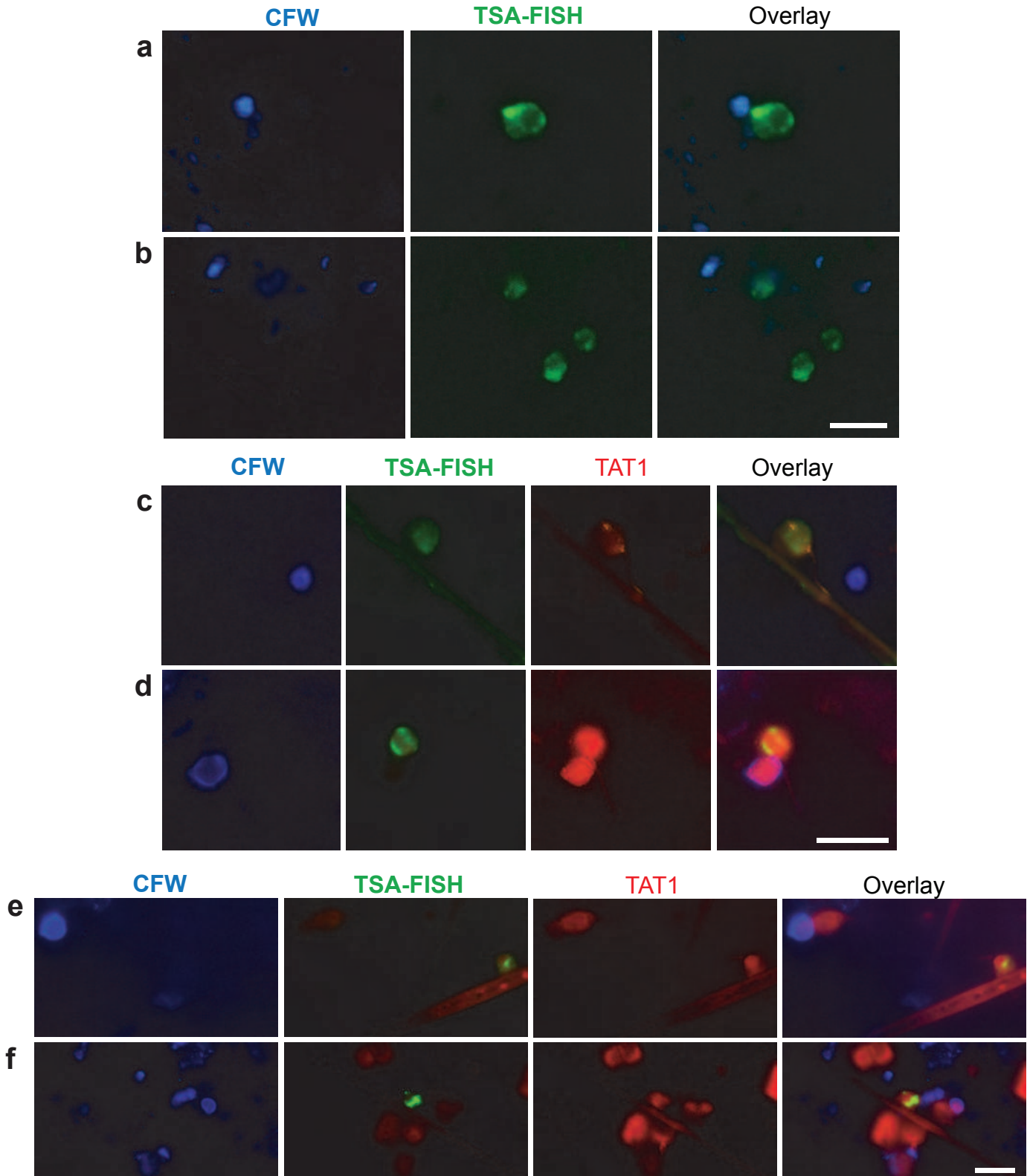
Supplementary Figure 3. Series of micrographs depicting flagellated TSA-FISH targeted cryptomycota cells. TAT1, an antibody for α -tubulin, was used to reveal the presence of a flagellum on cryptomycota cells. The probe used for each hybridisation is indicated on the left, this reveals that all three sub-groups have a flagellated stage for part of their lifecycle. Scale bar = 10 μ m.



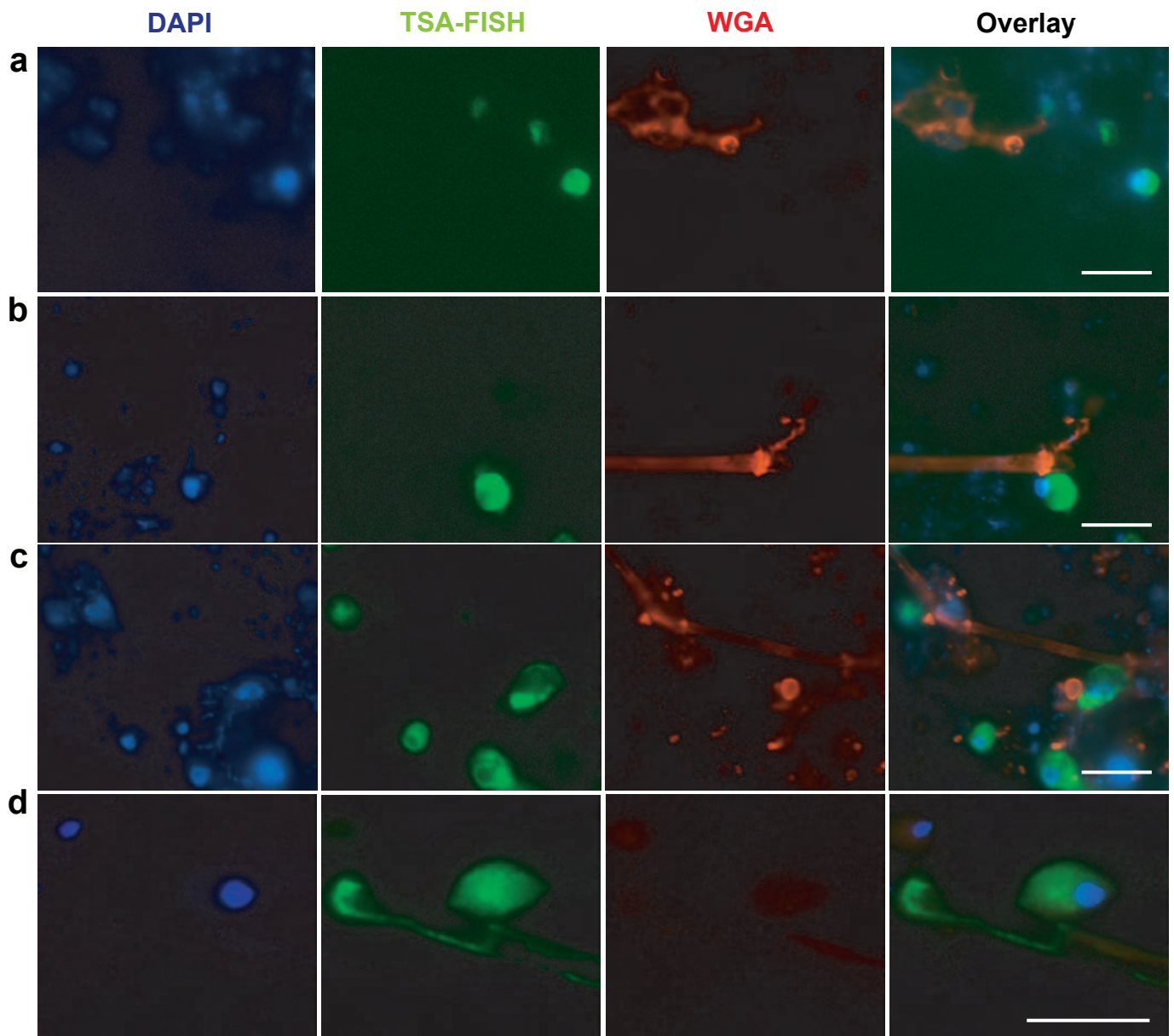
Supplementary Figure 4. Micrographs depicting TSA-FISH targeted cells seemingly attached to cells sampled from the wider environmental community. Column 1 shows the discrete DAPI stained nucleus, column 2 the TSA-FISH targeted cryptomycota cells, column 3 a bright field image showing the wider community of cells on the filter, and column 4 the images overlaid. Scale bar = 10 μm .



Supplementary Figure 5. Confirmation that chytrids build fungal cell walls detectable using cell wall stains. The chytrid *Blastocladiella emersonii* was used as a fungal cell wall detection control. A culture sample was fixed using the standard FISH protocol as described in the methods and imaged using wheat germ agglutinin-488 (WGA) (a) and calcofluor white (CW) (b, c). Scale bars are 10 μm .



Supplementary Figure 6. Micrographs depicting the absence of a chitinous cell wall from LKM11-01 cryptomycota cells during the cyst, flagellate, and attached stages of the lifecycle, as detected by calcofluor white. Counterstaining with calcofluor white (a non-specific fluorochrome stain which binds to chitin and cellulose) reveals the cryptomycota cells are lacking a chitin and cellulose rich cell wall during the free-living (i.e. cyst or zoospore, a-b), zoospore (c), cyst (d), and attached (e-f) stages of their lifecycle. Images e and f were taken using a different microscope and filter set used to minimise green fluorescence background but the green filter range is affected by red cross-talk from the TAT1 signal. Scale bar = 10 μ m.



Supplementary Figure 7. Micrographs depicting absence of a chitinous cell wall from cryptomycota cells during the free-living (i.e. cyst or zoospore, a-c), and attached phases (d) of the lifecycle. Counter-staining with wheatgerm agglutinin (which binds to N-acetylglucosamine and N-acetylneuraminic acid (sialic acid) residues, the former of which is a monomeric unit of the polymer chitin). Scale bar = 10 μm .

Supplementary Table 1. Details of GenBank environmental sequences putatively clustering with the cryptomycota.

Chimaeric sequences are noted. All sequences <1350 bp and with evidence of chimaeras were excluded from further analyses (shaded grey). The remaining sequences were used in phylogenetic analyses (Fig. 1a). *Sequence name as denoted in GenBank (<http://blast.ncbi.nlm.nih.gov>).

Sequence name*	Accession Number	Sequence	Authors	Notes
WS_CM2	FJ687265	1467	This study.	Washington Singer, Pond water, University of Exeter, UK.
LS_CM2	FJ687267	1590	This study.	Scraping from lily stem, submerged in pond, lake district, UK.
WS_CM1	FJ687268	2546	This study.	Washington Singer, Pond water, University of Exeter site, UK.
Uncultured fungus clone F27_31 18S ribosomal	EU811620	707	Bastian F., Alabouvette C.;	Excluded - too short and/or does not cross the CM1/2

RNA gene, partial sequence.					probe/primer sites
Uncultured fungus clone FRBA4_A07 18S ribosomal RNA gene, partial sequence.	FJ482760	717		Bradley D.J., Martiny J.B.H.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured fungus clone FRBA4_C07 18S ribosomal RNA gene, partial sequence.	FJ482746	718		Bradley D.J., Martiny J.B.H.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured fungus clone FRBA4_E04 18S ribosomal RNA gene, partial sequence.	FJ482748	718		Bradley D.J., Martiny J.B.H.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured fungus clone FRBA4_H03 18S ribosomal RNA gene, partial sequence.	FJ482751	718		Bradley D.J., Martiny J.B.H.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured fungus clone FRBA4_H05 18S	FJ482752	718		Bradley D.J., Martiny J.B.H.;	Excluded - too short and/or does not cross the CM1/2

ribosomal RNA gene, partial sequence.					probe/primer sites
Uncultured fungus clone FRBA4_H10 18S ribosomal RNA gene, partial sequence.	FJ482753	718		Bradley D.J., Martiny J.B.H.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured fungus clone FRPA5_C01 18S ribosomal RNA gene, partial sequence.	FJ482837	718		Bradley D.J., Martiny J.B.H.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured fungus clone FRPA5_H03 18S ribosomal RNA gene, partial sequence.	FJ482884	718		Bradley D.J., Martiny J.B.H.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured fungus clone BRPA1_C04 18S ribosomal RNA gene, partial sequence.	FJ483077	718		Bradley D.J., Martiny J.B.H.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured fungus clone FRPA1_E12 18S	FJ483185	718		Bradley D.J., Martiny J.B.H.;	Excluded - too short and/or does not cross the CM1/2

ribosomal RNA gene, partial sequence.					probe/primer sites
Uncultured fungus clone FRBA4_B06 18S ribosomal RNA gene, partial sequence.	FJ482728	719		Bradley D.J., Martiny J.B.H.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured fungus clone FRBA4_F05 18S ribosomal RNA gene, partial sequence.	FJ482739	719		Bradley D.J., Martiny J.B.H.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured fungus clone FRBA4_G04 18S ribosomal RNA gene, partial sequence.	FJ482742	719		Bradley D.J., Martiny J.B.H.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured fungus clone FRBA4_H04 18S ribosomal RNA gene, partial sequence.	FJ482743	719		Bradley D.J., Martiny J.B.H.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured fungus clone FRPA5_A10 18S	FJ482826	719		Bradley D.J., Martiny J.B.H.;	Excluded - too short and/or does not cross the CM1/2

ribosomal RNA gene, partial sequence.					probe/primer sites
Uncultured fungus clone FRPA5_B05 18S ribosomal RNA gene, partial sequence.	FJ482832	719		Bradley D.J., Martiny J.B.H.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured fungus clone FRPA5_B08 18S ribosomal RNA gene, partial sequence.	FJ482835	719		Bradley D.J., Martiny J.B.H.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured fungus clone FRPA5_C08 18S ribosomal RNA gene, partial sequence.	FJ482842	719		Bradley D.J., Martiny J.B.H.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured fungus clone FRPA5_C09 18S ribosomal RNA gene, partial sequence.	FJ482843	719		Bradley D.J., Martiny J.B.H.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured fungus clone FRPA5_C10 18S	FJ482844	719		Bradley D.J., Martiny J.B.H.;	Excluded - too short and/or does not cross the CM1/2

ribosomal RNA gene, partial sequence.					probe/primer sites
Uncultured fungus clone FRPA5_D02 18S ribosomal RNA gene, partial sequence.	FJ482846	719		Bradley D.J., Martiny J.B.H.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured fungus clone FRPA5_D03 18S ribosomal RNA gene, partial sequence.	FJ482847	719		Bradley D.J., Martiny J.B.H.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured fungus clone FRPA5_D04 18S ribosomal RNA gene, partial sequence.	FJ482848	719		Bradley D.J., Martiny J.B.H.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured fungus clone FRPA5_D09 18S ribosomal RNA gene, partial sequence.	FJ482851	719		Bradley D.J., Martiny J.B.H.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured fungus clone FRPA5_E05 18S	FJ482856	719		Bradley D.J., Martiny J.B.H.;	Excluded - too short and/or does not cross the CM1/2

ribosomal RNA gene, partial sequence.					probe/primer sites
Uncultured fungus clone FRPA5_E11 18S ribosomal RNA gene, partial sequence.	FJ482859	719		Bradley D.J., Martiny J.B.H.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured fungus clone FRPA5_F08 18S ribosomal RNA gene, partial sequence.	FJ482866	719		Bradley D.J., Martiny J.B.H.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured fungus clone FRPA5_G09 18S ribosomal RNA gene, partial sequence.	FJ482879	719		Bradley D.J., Martiny J.B.H.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured fungus clone FRPA5_G11 18S ribosomal RNA gene, partial sequence.	FJ482881	719		Bradley D.J., Martiny J.B.H.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured fungus clone FRPA5_H04 18S	FJ482885	719		Bradley D.J., Martiny J.B.H.;	Excluded - too short and/or does not cross the CM1/2

ribosomal RNA gene, partial sequence.					probe/primer sites
Uncultured fungus clone FRPA5_H05 18S ribosomal RNA gene, partial sequence.	FJ482886	719		Bradley D.J., Martiny J.B.H.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured fungus clone BRPA1_C02 18S ribosomal RNA gene, partial sequence.	FJ483058	719		Bradley D.J., Martiny J.B.H.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured fungus clone BRPA4_B09 18S ribosomal RNA gene, partial sequence.	FJ483134	719		Bradley D.J., Martiny J.B.H.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured fungus clone BRPA4_E01 18S ribosomal RNA gene, partial sequence.	FJ483135	719		Bradley D.J., Martiny J.B.H.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured fungus clone BRPA4_E02 18S	FJ483150	719		Bradley D.J., Martiny J.B.H.;	Excluded - too short and/or does not cross the CM1/2

ribosomal RNA gene, partial sequence.					probe/primer sites
Uncultured eukaryote clone F3g 18S ribosomal RNA gene, partial sequence.	AY222617	720		Green S.J., Freeman S., Hadar Y., Minz D.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured fungus clone E10_FRBA3 18S ribosomal RNA gene, partial sequence.	FJ482598	721		Bradley D.J., Martiny J.B.H.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites and evidence of chimaera
Uncultured fungus clone FRBA4_C12 18S ribosomal RNA gene, partial sequence.	FJ482720	721		Bradley D.J., Martiny J.B.H.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured fungus clone FRPA5_A01 18S ribosomal RNA gene, partial sequence.	FJ482820	721		Bradley D.J., Martiny J.B.H.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured fungus clone FRPA5_F01 18S	FJ482860	721		Bradley D.J., Martiny J.B.H.;	Excluded - too short and/or does not cross the CM1/2

ribosomal RNA gene, partial sequence.					probe/primer sites
Uncultured fungus clone FRPA5_H09 18S ribosomal RNA gene, partial sequence.	FJ482889	721		Bradley D.J., Martiny J.B.H.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites and evidence of chimaera
Uncultured fungus clone E12_FRBA3 18S ribosomal RNA gene, partial sequence.	FJ482599	722		Bradley D.J., Martiny J.B.H.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites and evidence of chimaera
Uncultured fungus clone FRPA1_B09 18S ribosomal RNA gene, partial sequence.	FJ483152	723		Bradley D.J., Martiny J.B.H.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites and evidence of chimaera
Uncultured fungus gene for 18S rRNA, partial sequence, clone: S08fB07.	AB469118	724		Nagahama T., Takahashi E., Abdel- Wahab M.A., Miyazaki M., Horikoshi K.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured fungus clone H10_BRPA2 18S ribosomal RNA gene,	FJ482441	725		Bradley D.J., Martiny J.B.H.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites

partial sequence.				
Uncultured fungus clone C05_FRBA3 18S ribosomal RNA gene, partial sequence.	FJ482580	727	Bradley D.J., Martiny J.B.H.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites and evidence of chimaera
Uncultured fungus clone FRPA5_B07 18S ribosomal RNA gene, partial sequence.	FJ482834	732	Bradley D.J., Martiny J.B.H.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured eukaryote isolate Soil.06.17 18S ribosomal RNA gene, partial sequence.	AY099411	736	Jumpponen A., Neises D.L., Johnson L.C.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured fungus clone FRPA5_E10 18S ribosomal RNA gene, partial sequence.	FJ482858	736	Bradley D.J., Martiny J.B.H.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites and evidence of chimaera
Uncultured eukaryote clone Zeuk3 18S ribosomal RNA gene, partial	AY916572	740	Luo Q., Krumholz L.R., Najjar F.Z., Roe B.A., Peacock A.D., White D.C., Elshahed M.S.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites

sequence.					
Uncultured eukaryotic picoplankton clone VN14 18S ribosomal RNA gene, partial sequence.	DQ409102	772		Lepere C., Domaizon I., Debroas D.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured marine eukaryote clone MB10.47 18S ribosomal RNA gene, partial sequence.	EF539145	774		Cheung M.K., Wong C.K., Chu K.H.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured fungus clone control46 18S ribosomal RNA gene, partial sequence.	EF674478	780		Seena S., Barlocher F.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured eukaryote clone 121-O17 18S ribosomal RNA gene, partial sequence.	EF586117	792		Dopheide A., Lear G., Stott R., Lewis G.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured fungus clone Sey019 small subunit ribosomal RNA gene,	AY605190	794		Berney C., Fahrni J., Pawlowski J.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites

partialsequence.					
Uncultured fungus clone Sey052 small subunit ribosomal RNA gene, partialsequence.	AY605199	798		Berney C., Fahrni J., Pawlowski J.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured fungus clone EB5.113 18S ribosomal RNA geje, partial sequence.	EU143985	800		Chen M.J.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured fungus clone WLB50.79 18S ribosomal RNA gene, partial sequence.	EU144010	800		Chen M.J.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured fungus clone MLBM81.42 18S ribosomal RNA gene, partial sequence.	FJ410535	804		Chen M.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured eukaryote clone EBF6.14 18S ribosomal RNA gene,	FJ410641	804		Chen M.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites

partialsequence.					
Uncultured fungus clone	FJ410646	804		Chen M.;	Excluded - too short and/or
EBF11.30 18S ribosomal					does not cross the CM1/2
RNA gene, partial					probe/primer sites
sequence.					
Uncultured fungus clone	FJ410647	804		Chen M.;	Excluded - too short and/or
EBF11.41 18S ribosomal					does not cross the CM1/2
RNA gene, partial					probe/primer sites
sequence.					
Uncultured fungus clone	FJ410654	804		Chen M.;	Excluded - too short and/or
EBF16.56 18S ribosomal					does not cross the CM1/2
RNA gene, partial					probe/primer sites
sequence.					
Uncultured fungus clone	FJ410665	804		Chen M.;	Excluded - too short and/or
EBF30.121 18S ribosomal					does not cross the CM1/2
RNA gene, partial					probe/primer sites
sequence.					
Uncultured fungus clone	FJ410685	804		Chen M.;	Excluded - too short and/or
EBM14.31 18S ribosomal					does not cross the CM1/2
RNA gene, partial					probe/primer sites

sequence.					
Uncultured eukaryote clone 528-O45 18S ribosomal RNA gene, partial sequence.	EF586074	819	Dopheide A., Lear G., Stott R., Lewis G.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites	
Uncultured eukaryotic picoplankton clone BI109 18S ribosomal RNA gene, partial sequence.	EF196756	838	Lepere C., Domaizon I., Debroas D.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites and evidence of chimaera	
Uncultured marine eukaryote clone BL010320.33 18S ribosomal RNA gene, partial sequence.	AY426912	853	Massana R., Balague V., Pedros-Alio C.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites	
Uncultured eukaryotic picoplankton clone B910 18S ribosomal RNA gene, partial sequence.	EF196797	949	Lepere C., Domaizon I., Debroas D.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites	
Uncultured eukaryote clone BSR1LC06 16S	AY689720	969	Baeseman J., Walker J.J., Pace N.R., Silverstein J., Smith R.L.;	Excluded - too short and/or does not cross the CM1/2	

ribosomal RNA gene, partialsequence.					probe/primer sites
Uncultured eukaryote clone E_6N 18S ribosomal RNA gene, partial sequence.	FJ490225	980	Lacap D.C., Pointing S.B.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites	
Uncultured eukaryote clone BSR1LE07 16S ribosomal RNA gene, partialsequence.	AY689723	1003	Baeseman J., Walker J.J., Pace N.R., Silverstein J., Smith R.L.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites	
Uncultured eukaryote clone L73_ML_326 small subunit ribosomal RNA gene, partial sequence.	FJ353892	1014	Amaral-Zettler L.A., Rocca J.D., Lamontagne M.G., Dennett M.R., Gast R.J.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites	
Uncultured fungus clone EMPE7 small subunit ribosomal RNA gene, partialsequence.	AF372715	1042	Dawson S.C., Pace N.R.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites	
Uncultured eukaryote clone F02_SE4A 18S	FJ592434	1076	Costello E.K., Halloy S.R.P., Reed S.C., Sowell P., Schmidt S.K.;	Excluded - too short and/or does not cross the CM1/2	

ribosomal RNA gene, partialsequence.					probe/primer sites
Uncultured eukaryote clone C07_SE1A 18S ribosomal RNA gene, partialsequence.	FJ592330	1086		Costello E.K., Halloy S.R.P., Reed S.C., Sowell P., Schmidt S.K.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured eukaryote clone IAFDv110 18S ribosomal RNA gene, partialsequence.	AY835696	1090		Laurin V., Labbe N., Parent S., Juteau P., Villemur R.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites and evidence of chimaera
Uncultured marine eukaryote clone GoC5_H04 small subunit ribosomal RNA gene, partial sequence.	FJ153728	1114		Stock A., Juergens K., Bunge J.A., Stoeck T.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites and evidence of chimaera
Uncultured marine eukaryote clone GoC6_F01 small subunit ribosomal RNA gene, partial sequence.	FJ153737	1136		Stock A., Juergens K., Bunge J.A., Stoeck T.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites and evidence of chimaera

Uncultured marine eukaryote clone GoC5_A03 small subunit ribosomal RNA gene, partial sequence.	FJ153710	1148	Stock A., Juergens K., Bunge J.A., Stoeck T.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites and evidence of chimaera
Uncultured fungus clone BRKC111 small subunit ribosomal RNA gene, partial sequence.	AF372714	1164	Dawson S.C., Pace N.R.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Bacillariophyta sp. RS19 clone A1 18S ribosomal RNA gene, partial sequence.	EF432533	1168	Beaudoin D.J., Gast R.J., Conte M.A., Cummings M.P.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites and evidence of chimaera
Uncultured marine eukaryote clone GoC4_G06 small subunit ribosomal RNA gene, partial sequence.	FJ153704	1187	Stock A., Juergens K., Bunge J.A., Stoeck T.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites and evidence of chimaera
Uncultured eukaryote clone EPK_B_G7 18S	DQ104595	1194	Strap J.L., Colwell F.S., Crawford R.L.;	Excluded - too short and/or does not cross the CM1/2

ribosomal RNA gene, partialsequence.					probe/primer sites
Uncultured eukaryote clone EUKDPK41 18S ribosomal RNA gene, partialsequence.	DQ104599	1210		Strap J.L., Colwell F.S., Crawford R.L.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured eukaryote clone EUKDPK65 18S ribosomal RNA gene, partialsequence.	DQ104605	1229		Strap J.L., Colwell F.S., Crawford R.L.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured eukaryote clone JMYED32 18S ribosomal RNA gene, partialsequence.	FJ810615	1237		Yagi J.M., Madsen E.L.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured fungus clone LEM108 small subunit ribosomal RNA gene, partialsequence.	AF372716	1238		Dawson S.C., Pace N.R.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites and evidence of chimaera
Uncultured eukaryote clone JMYED29 18S	FJ810613	1241		Yagi J.M., Madsen E.L.;	Excluded - too short and/or does not cross the CM1/2

ribosomal RNA gene, partial sequence.					probe/primer sites
Uncultured eukaryote clone EfeReC63 18S ribosomal RNA gene, partial sequence.	FJ810604	1245		Yagi J.M., Madsen E.L.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites and evidence of chimaera
Uncultured eukaryotic picoplankton clone P34.11 18S ribosomal RNA gene, partial sequence.	AY642711	1264		Lefranc M., Thenot A., Debroas D.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured fungus clone BAQK11 small subunit ribosomal RNA gene, partial sequence.	AF372717	1271		Dawson S.C., Pace N.R.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured fungus gene for 18S rRNA, partial sequence, clone: S08B40.	AB468674	1293		Nagahama T., Takahashi E., Miyazaki M., Horikoshi K.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured fungus gene for 18S rRNA, partial sequence, clone: S08B38.	AB468672	1328		Nagahama T., Takahashi E., Miyazaki M., Horikoshi K.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites

Uncultured fungus gene for 18S rRNA, partial sequence, clone: S08B39.	AB468673	1328	Nagahama T., Takahashi E., Miyazaki M., Horikoshi K.;	Excluded - too short and/or does not cross the CM1/2 probe/primer sites
Uncultured eukaryotic picoplankton clone PG5.28 18S ribosomal RNA gene, partial sequence.	AY642731	1366	Lefranc M., Thenot A., Debroas D.;	Included in phylogenetic analysis (Fig. 1a)
Uncultured eukaryotic picoplankton clone G5.3 18S ribosomal RNA gene, partial sequence.	AY642721	1369	Lefranc M., Thenot A., Debroas D.;	Included in phylogenetic analysis (Fig. 1a)
Uncultured alveolate clone G40 18S small subunit ribosomal RNA gene, partial sequence.	EU910606	1398	Zajack H.A., Biddanda B.A., Nold S.C.;	Included in phylogenetic analysis (Fig. 1a)
Uncultured Banisveld eukaryote clone P1-3m12 18S ribosomal RNA gene, partial sequence.	EU091838	1399	Roling W.F.M., Brad T., Braster M.;	Included in phylogenetic analysis (Fig. 1a)
Uncultured Banisveld	EU091850	1400	Roling W.F.M., Brad T., Braster M.;	Included in phylogenetic

eukaryote clone P2-3m3 18S ribosomal RNA gene, partialsequencd.					analysis (Fig. 1a)
Uncultured Banisveld eukaryote clone P1-3m9 18S ribosomal RNA gene, partialsequence.	EU091835	1401		Roling W.F.M., Brad T., Braster M.;	Included in phylogenetic analysis (Fig. 1a)
Uncultured Banisveld eukaryote clone P6-3m3 18S ribosomal RNA gene, partialsequence.	EU091872	1406		Roling W.F.M., Brad T., Braster M.;	Included in phylogenetic analysis (Fig. 1a)
Uncultured Banisveld eukaryote clone P4-3m5 18S ribosomal RNA gene, parthalsequence.	EU091865	1417		Roling W.F.M., Brad T., Braster M.;	Included in phylogenetic analysis (Fig. 1a)
Uncultured Banisveld eukaryote clone P1-3m3 18S ribosomal RNA gene, partialsequence.	EU091829	1423		Roling W.F.M., Brad T., Braster M.;	Included in phylogenetic analysis (Fig. 1a)
Uncultured Banisveld	EU091851	1423		Roling W.F.M., Brad T., Braster M.;	Included in phylogenetic

eukaryote clone P2-3m4 18S ribosomal RNA gene, partial sequence.					analysis (Fig. 1a)
Uncultured Banasveld eukaryote clone P2-3m5 18S ribosomal RNA gene, Partial Sequence.	EU091852	1424		Roling W.F.M., Brad T., Braster M.;	Included in phylogenetic analysis (Fig. 1a)
Uncultured opisthokont clone PRS2_4E_06 small subunit ribosomal RNA, partial sequence.	FJ976649	1428		Lara E., Moreira D., Lopez Garcia P.;	Included in phylogenetic analysis (Fig. 1a)
Uncultured rhizosphere zygomycete partial 18S rRNA gene, clone RSC- CHU-43	AJ506017	1495		Hussels C.;	Included in phylogenetic analysis (Fig. 1a)
Uncultured rhizosphere zygomycete partial 18S rRNA gene, clone RSC- CHU-42	AJ506016	1496		Hussels C.;	Included in phylogenetic analysis (Fig. 1a)
Uncultured rhizosphere	AJ506030	1496		Hussels C.;	Included in phylogenetic

zygomycete partial 18S rRNA gene, clone RSC- CHU-59					analysis (Fig. 1a)
Uncultured fungus clone CV1_B2_34 small subunit ribosomal RNA gene, partial sequence.	AY821997	1542		Slapeta J., Moreira D., Lopez- Garcia P.;	Included in phylogenetic analysis (Fig. 1a)
Unidentified eukaryote 18S ribosomal RNA, clone LKM46, partial	AJ130857	1567		van Hannen E.J., Mooij W., van Agterveld M.P., Gons H.J., Laanbroek H.J.;	Included in phylogenetic analysis (Fig. 1a)
Unidentified eukaryote 18S ribosomal RNA, clone LKM11, partial	AJ130849	1594		van Hannen E.J., Mooij W., van Agterveld M.P., Gons H.J., Laanbroek H.J.;	Included in phylogenetic analysis (Fig. 1a)
Unidentified eukaryote 18S ribosomal RNA, clone LKM15, partial	AJ130850	1602		van Hannen E.J., Mooij W., van Agterveld M.P., Gons H.J., Laanbroek H.J.;	Included in phylogenetic analysis (Fig. 1a)
Uncultured fungus clone CH1_S2_50 small subunit ribosomal RNA gene, partial sequence.	AY821991	1612		Slapeta J., Moreira D., Lopez- Garcia P.;	Included in phylogenetic analysis (Fig. 1a)

Uncultured eukaryote clone kor_110904_24 18S ribosomal RNA gene, partial sequence	FJ157332	1635	Kormas <i>et al.</i> ,	Included in phylogenetic analysis (Fig. 1a)
Uncultured eukaryote gene for SSU rRNA, partial sequence, clone: NAMA KO-36.	AB252776	1638	Takishita K., Tsuchiya M., Kawato M., Oguri K., Kitazato H., Maruyama T.;	Included in phylogenetic analysis (Fig. 1a)
Uncultured eukaryote clone Joinv23 18S ribosomal RNA gene, partial sequence.	FJ577832	1646	Poitelon J.-B., Joyeux M., Welte B., Duguet J.-P., Peplies J., DuBow M.S.;	Included in phylogenetic analysis (Fig. 1a)
Uncultured marine fungus clone FAS_48 18S small subunit ribosomal RNA gene, partial sequence.	GQ120147	1658	Jebaraj C.S., Raghukumar C., Stoeck T.;	Excluded - evidence of chimaera
Uncultured eukaryote gene for SSU rRNA, partial sequence, clone: NAMA KO-37.	AB252777	1662	Takishita K., Tsuchiya M., Kawato M., Oguri K., Kitazato H., Maruyama T.;	Included in phylogenetic analysis (Fig. 1a)

Uncultured fungus clone BAQA254 small subunit ribosomal RNA gene, partial sequence.	AF372713	1662	Dawson S.C., Pace N.R.;	Included in phylogenetic analysis (Fig. 1a)
Uncultured eukaryote clone Ivry06 18S ribosomal RNA gene, partial sequence.	FJ577810	1662	Poitelon J.-B., Joyeux M., Welte B., Duguet J.-P., Peplies J., DuBow M.S.;	Excluded - evidence of chimaera
Uncultured fungus clone BAQA64 small subunit ribosomal RNA gene, partial sequence.	AF372718	1669	Dawson S.C., Pace N.R.;	Included in phylogenetic analysis (Fig. 1a)
Uncultured fungus clone BAQA15 small subunit ribosomal RNA gene, partial sequence.	AF372796	1669	Dawson S.C., Pace N.R.;	Excluded - evidence of chimaera
Uncultured fungus clone BAQA04 small subunit ribosomal RNA gene, partial sequence.	AF372712	1678	Dawson S.C., Pace N.R.;	Included in phylogenetic analysis (Fig. 1a)

Uncultured eukaryote clone dpeuk6 18S ribosomal RNA gene, partial sequence.	AY916638	1683	Luo Q., Krumholz L.R., Najjar F.Z., Roe B.A., Peacock A.D., White D.C., Elshahed M.S.;	Included in phylogenetic analysis (Fig. 1a)
Uncultured eukaryote clone wwueuk6 18S ribosomal RNA gene, partial sequence.	AY916644	1683	Luo Q., Krumholz L.R., Najjar F.Z., Roe B.A., Peacock A.D., White D.C., Elshahed M.S.;	Included in phylogenetic analysis (Fig. 1a)
Uncultured eukaryote clone Zeuk2 18S ribosomal RNA gene, partial sequence.	AY916571	1689	Luo Q., Krumholz L.R., Najjar F.Z., Roe B.A., Peacock A.D., White D.C., Elshahed M.S.;	Included in phylogenetic analysis (Fig. 1a)
Uncultured eukaryote clone Zeuk1 18S ribosomal RNA gene, partial sequence.	AY916573	1691	Luo Q., Krumholz L.R., Najjar F.Z., Roe B.A., Peacock A.D., White D.C., Elshahed M.S.;	Excluded - evidence of chimaera
Uncultured eukaryote clone Zeuk79 18S ribosomal RNA gene, partial sequence.	AY916588	1691	Luo Q., Krumholz L.R., Najjar F.Z., Roe B.A., Peacock A.D., White D.C., Elshahed M.S.;	Excluded - evidence of chimaera

Uncultured eukaryote clone Zeuk5 18S ribosomal RNA gene, partial sequence.	AY916570	1699	Luo Q., Krumholz L.R., Najjar F.Z., Roe B.A., Peacock A.D., White D.C., Elshahed M.S.;	Excluded - evidence of chimaera
Uncultured eukaryote gene for SSU rRNA, partial sequence, clone: DSGM-64.	AB275064	1718	Takishita K., Yubuki N., Kakizoe N., Inagaki Y., Maruyama T.;	Included in phylogenetic analysis (Fig. 1a)
Uncultured eukaryote gene for small subunit rRNA, partial sequence, clone: TAGIRI-23.	AB191431	1719	Takishita K., Miyake H., Kawato M., Maruyama T.;	Included in phylogenetic analysis (Fig. 1a)
Uncultured fungus clone PFB3AU2004 18S ribosomal RNA gene, partial sequence.	DQ244018	1734	Lefevre E., Bardot C., Noel C., Carrias J.-F., Sime-Ngando T., Viscogliosi E., Amblard C.;	Included in phylogenetic analysis (Fig. 1a)
Uncultured fungus clone PFB12AU2004 18S ribosomal RNA gene,	DQ244016	1736	Lefevre E., Bardot C., Noel C., Carrias J.-F., Sime-Ngando T., Viscogliosi E., Amblard C.;	Included in phylogenetic analysis (Fig. 1a)

partialsequence.				
Uncultured fungus clone PFD5AU2004 18S ribosomal RNA gene, partialsequence.	DQ244017	1741	Lefevre E., Bardot C., Noel C., Carrias J.-F., Sime-Ngando T.,Viscogliosi E., Amblard C.;	Included in phylogenetic analysis (Fig. 1a)
Uncultured eukaryote clone RT5iin3 18S ribosomal RNA gene, completesequences.	AY082996	1757	Amaral Zettler L.A., Gomez F., Zettler E., Keenan B.G., Amils R.,Sogin M.L.;	Included in phylogenetic analysis (Fig. 1a)
Uncultured fungus clone PFB7SP2005 18S ribosomal RNA gene, partialsequence.	EU162635	1757	Lefevre E., Roussel B., Amblard C., Sime-Ngando T.;	Excluded as highly similar to other sequences from the same library
Eimeriidae environmental sample clone Amb_18S_1035 18S ribosomal RNA gene, partial sequence.	EF023454	1761	Lesaulnier C.C., Papamichail D., McCorkle S.R., Ollivier B., Skiena S.,Taghavi S., Zak D.R., van der Lelie D.;	Included in phylogenetic analysis (Fig. 1a)
Eimeriidae environmental sample clone	EF023474	1761	Lesaulnier C.C., Papamichail D., McCorkle S.R., Ollivier B., Skiena	Excluded as highly similar to other sequences from

Amb_18S_1059 18S ribosomal RNA gene, partial sequence.			S., Taghavi S., Zak D.R., van der Lelie D.;	the same library
Eimeriidae environmental sample clone Amb_18S_1083 18S ribosomal RNA gene, partial sequence.	EF023493	1761	Lesaulnier C.C., Papamichail D., McCorkle S.R., Ollivier B., Skiena S., Taghavi S., Zak D.R., van der Lelie D.;	Excluded as highly similar to other sequences from the same library
Eimeriidae environmental sample clone Amb_18S_1135 18S ribosomal RNA gene, partial sequence.	EF023535	1761	Lesaulnier C.C., Papamichail D., McCorkle S.R., Ollivier B., Skiena S., Taghavi S., Zak D.R., van der Lelie D.;	Excluded as highly similar to other sequences from the same library
Eimeriidae environmental sample clone Amb_18S_855 18S ribosomal RNA gene, partial sequence.	EF023614	1761	Lesaulnier C.C., Papamichail D., McCorkle S.R., Ollivier B., Skiena S., Taghavi S., Zak D.R., van der Lelie D.;	Excluded as highly similar to other sequences from the same library
Eimeriidae environmental sample clone	EF023682	1761	Lesaulnier C.C., Papamichail D., McCorkle S.R., Ollivier B., Skiena	Excluded as highly similar to other sequences from

Amb_18S_944 18S ribosomal RNA gene, partial sequence.			S., Taghavi S., Zak D.R., van der Lelie D.;	the same library
Eimeriidae environmental sample clone	EF023706	1761	Lesaulnier C.C., Papamichail D., McCorkle S.R., Ollivier B., Skiena	Excluded as highly similar to other sequences from
Amb_18S_984 18S ribosomal RNA gene, partial sequence.			S., Taghavi S., Zak D.R., van der Lelie D.;	the same library
Eimeriidae environmental sample clone	EF023799	1761	Lesaulnier C.C., Papamichail D., McCorkle S.R., Ollivier B., Skiena	Excluded as highly similar to other sequences from
Amb_18S_1243 18S ribosomal RNA gene, partial sequence.			S., Taghavi S., Zak D.R., van der Lelie D.;	the same library
Eimeriidae environmental sample clone	EF024044	1761	Lesaulnier C.C., Papamichail D., McCorkle S.R., Ollivier B., Skiena	Excluded as highly similar to other sequences from
Amb_18S_1526 18S ribosomal RNA gene, partial sequence.			S., Taghavi S., Zak D.R., van der Lelie D.;	the same library
Eimeriidae environmental sample clone	EF023637	1762	Lesaulnier C.C., Papamichail D., McCorkle S.R., Ollivier B., Skiena	Excluded as highly similar to other sequences from

Amb_18S_883 18S ribosomal RNA gene, partial sequence.				S., Taghavi S., Zak D.R., van der Lelie D.;	the same library
Eimeriidae environmental sample clone	EF023661	1762		Lesaulnier C.C., Papamichail D., McCorkle S.R., Ollivier B., Skiena	Excluded as highly similar to other sequences from
Amb_18S_915 18S ribosomal RNA gene, partial sequence.				S., Taghavi S., Zak D.R., van der Lelie D.;	the same library
Uncultured alveolate clone PAA9SP2005 18S ribosomal RNA gene, partial sequence.	EU162624	1762		Lefevre E., Roussel B., Amblard C., Sime-Ngando T.;	Excluded - evidence of chimaera
Eimeriidae environmental sample clone	EF024492	1763		Lesaulnier C.C., Papamichail D., McCorkle S.R., Ollivier B., Skiena	Included in phylogenetic analysis (Fig. 1a)
Elev_18S_791 18S ribosomal RNA gene, partial sequence.				S., Taghavi S., Zak D.R., van der Lelie D.;	
Uncultured eukaryotic picoplankton clone P34.42 18S ribosomal RNA gene,	AY642700	1764		Lefranc M., Thenot A., Debroas D.;	Included in phylogenetic analysis (Fig. 1a)

partial sequence.

Eimeriidae environmental sample clone Amb_18S_485 18S ribosomal RNA gene, partial sequence.	EF023192	1765	Lesaulnier C.C., Papamichail D., McCorkle S.R., Ollivier B., Skiena S., Taghavi S., Zak D.R., van der Lelie D.;	Excluded - evidence of chimaera
Eimeriidae environmental sample clone Elev_18S_792 18S ribosomal RNA gene, partial sequence.	EF024493	1766	Lesaulnier C.C., Papamichail D., McCorkle S.R., Ollivier B., Skiena S., Taghavi S., Zak D.R., van der Lelie D.;	Included in phylogenetic analysis (Fig. 1a)
Uncultured fungus clone PFB5SP2005 18S ribosomal RNA gene, partial sequence.	EU162634	1768	Lefevre E., Roussel B., Amblard C., Sime-Ngando T.;	Excluded - evidence of chimaera
Uncultured alveolate clone I34 18S small subunit ribosomal RNA gene, partial sequence.	EU910604	1770	Zajack H.A., Biddanda B.A., Nold S.C.;	Included in phylogenetic analysis (Fig. 1a)
Nucleariidae environmental	EF023360	1777	Lesaulnier C.C., Papamichail D.,	Excluded - evidence of

sample clone			McCorkle S.R., Ollivier B., Skiena	chimaera
Amb_18S_686 18S			S., Taghavi S., Zak D.R., van der	
ribosomal RNA gene,			Lelie D.;	
partial sequence.				
Eimeriidae environmental	EF023366	1777	Lesaulnier C.C., Papamichail D.,	Excluded - evidence of
sample clone			McCorkle S.R., Ollivier B., Skiena	chimaera
Amb_18S_694 18S			S., Taghavi S., Zak D.R., van der	
ribosomal RNA gene,			Lelie D.;	
partial sequence.				
Uncultured fungus clone	DQ244011	1782	Lefevre E., Bardot C., Noel C.,	Included in phylogenetic
PFA12AU2004 18S			Carrias J.-F., Sime-Ngando	analysis (Fig. 1a)
ribosomal RNA gene,			T., Viscogliosi E., Amblard C.;	
partial sequence.				
Uncultured eukaryote	EF024082	1784	Lesaulnier C.C., Papamichail D.,	Excluded - evidence of
clone Amb_18S_6171 18S			McCorkle S.R., Ollivier B., Skiena	chimaera
ribosomal RNA gene,			S., Taghavi S., Zak D.R., van der	
partial sequence.			Lelie D.;	
Uncultured Boletaceae	EF024361	1784	Lesaulnier C.C., Papamichail D.,	Excluded - evidence of
clone Elev_18S_1012 18S			McCorkle S.R., Ollivier B., Skiena	chimaera
ribosomal RNA gene,			S., Taghavi S., Zak D.R., van der	

partialsequence.			Lelie D.;	
Uncultured Boletaceae	EF024374	1784	Lesaulnier C.C., Papamichail D.,	Excluded - evidence of
clone Elev_18S_1027 18S			McCorkle S.R., Ollivier B., Skiena	chimaera
ribosomal RNA gene,			S.,Taghavi S., Zak D.R., van der	
partialsequence.			Lelie D.;	
Uncultured Boletaceae	EF024438	1784	Lesaulnier C.C., Papamichail D.,	Excluded - evidence of
clone Elev_18S_1103 18S			McCorkle S.R., Ollivier B., Skiena	chimaera
ribosomal RNA gene,			S.,Taghavi S., Zak D.R., van der	
partialsequence.			Lelie D.;	
Uncultured Boletaceae	EF024524	1784	Lesaulnier C.C., Papamichail D.,	Excluded - evidence of
clone Elev_18S_832 18S			McCorkle S.R., Ollivier B., Skiena	chimaera
ribosomal RNA gene,			S.,Taghavi S., Zak D.R., van der	
partialsequence.			Lelie D.;	
Uncultured fungus partial	AM114814	1786	Moon-van der Staay S.Y., Tzeneva	Included in phylogenetic
18S rRNA gene, clone			V.A., van der Staay G.W.M., Smidt	analysis (Fig. 1a)
WIM27			H.,de Vos W.M., Hackstein J.H.P.;	
Dicksoniaceae	EF023829	1792	Lesaulnier C.C., Papamichail D.,	Excluded - evidence of
environmental sample			McCorkle S.R., Ollivier B., Skiena	chimaera
clone Amb_18S_1278 18S			S.,Taghavi S., Zak D.R., van der	
ribosomal RNA gene,			Lelie D.;	

partial sequence.				
Dicksoniaceae	EF023907	1792	Lesaulnier C.C., Papamichail D., McCorkle S.R., Ollivier B., Skiena S., Taghavi S., Zak D.R., van der Lelie D.;	Excluded - evidence of chimaera
environmental sample clone Amb_18S_1363 18S ribosomal RNA gene, partial sequence.				
Uncultured eukaryote	EF025006	1792	Lesaulnier C.C., Papamichail D., McCorkle S.R., Ollivier B., Skiena S., Taghavi S., Zak D.R., van der Lelie D.;	Excluded - evidence of chimaera
clone Elev_18S_5091 18S ribosomal RNA gene, partial sequence.				
Dicksoniaceae	EF023209	1796	Lesaulnier C.C., Papamichail D., McCorkle S.R., Ollivier B., Skiena S., Taghavi S., Zak D.R., van der Lelie D.;	Excluded - evidence of chimaera
environmental sample clone Amb_18S_504 18S ribosomal RNA gene, partial sequence.				
Eimeriidae environmental sample clone Elev_18S_1213 18S ribosomal RNA gene, partial sequence.	EF024722	1800	Lesaulnier C.C., Papamichail D., McCorkle S.R., Ollivier B., Skiena S., Taghavi S., Zak D.R., van der Lelie D.;	Excluded - evidence of chimaera

Uncultured Sarcosomataceae clone Amb_18S_575 18S ribosomal RNA gene, partial sequence.	EF023269	1804	Lesaulnier C.C., Papamichail D., McCorkle S.R., Ollivier B., Skiena S., Taghavi S., Zak D.R., van der Lelie D.;	Excluded as highly similar to other sequences from the same library
Eimeriidae environmental sample clone Amb_18S_405 18S ribosomal RNA gene, partial sequence.	EF023121	1826	Lesaulnier C.C., Papamichail D., McCorkle S.R., Ollivier B., Skiena S., Taghavi S., Zak D.R., van der Lelie D.;	Included in phylogenetic analysis (Fig. 1a)
Eimeriidae environmental sample clone Amb_18S_397 18S ribosomal RNA gene, partial sequence.	EF023117	1835	Lesaulnier C.C., Papamichail D., McCorkle S.R., Ollivier B., Skiena S., Taghavi S., Zak D.R., van der Lelie D.;	Included in phylogenetic analysis (Fig. 1a)
Dicksoniaceae environmental sample clone Amb_18S_1218 18S ribosomal RNA gene, partial sequence.	EF023777	1849	Lesaulnier C.C., Papamichail D., McCorkle S.R., Ollivier B., Skiena S., Taghavi S., Zak D.R., van der Lelie D.;	Excluded - evidence of chimaera

Supplementary Table 2. Probe and primer details. (Non TSA-FISH probes are in grey)

Name	Sequence (5'-3')	5'- Fluorophor e	Total number of cells observed	Target clade	Target sequences with 100% match	Notes (where possible binding site relative to <i>E. coli</i> is also listed)
CM1.1	GTGAGT CGGGCT TTTTGC	HRP	98	CM1	LKM11 (AJ130849) CV1_B2_34 (AY821997) Washington singer CM1 (FJ687268) BAQA04 (AF372712) BAQA254 (AF372713) Zeuk2 (AY916571)	TSA-FISH probe and forward PCR primer, binds to position 152-169 LKM11 CM SSU sequence (AJ130849). Minimum two mismatches with all non-target database SSU sequences. Addition of group-specific helper probes was used.
CM1.2	GTAAGG CTCGGTT CCCTAG	HRP	58	CM1 (- LKM11)	CV1_B2_34 (AY821997) Washington singer CM1 (FJ687268) BAQA04 (AF372712) BAQA254 (AF372713) Zeuk2 (AY916571)	TSA-FISH probe binds to position 651-669 BAQA04 (AF372712) CM1 SSU sequence. Minimum two mismatches with all non-target database SSU sequences. Addition of group-specific helper

CM1.3	CAGTACA	HRP	CM1 (- LKM11, CV1_B2_34,	Washington singer CM1
	CCCAGT		BAQA04, BAQA254, Zeuk2)	(FJ687268)
	GGGCG			
CM1.4	CACCCA	HRP	CM1 (- LKM11, CV1_B2_34,	Washington singer CM1
	GTGGGC		BAQA04, BAQA254, Zeuk2)	(FJ687268)
	GACCAG			

probes was used.

TSA-FISH probe binds to position 480-497 Washington singer CM1 (FJ687268)

SSU sequence. Minimum two mismatches with all non-target database SSU sequences.

Consistently negative over replicate samples, different freshwater environments and stringency variations.

TSA-FISH probe binds to position 475-492 Washington singer CM1 (FJ687268)

SSU sequence. Minimum one mismatch with all non-target database SSU sequences (a small number of environmental sequences have a single

CM1.5 CAAAAGC HRP
GACATCC
ACCG

CM1 (- CV1_B2_34)

LKM11 (AJ130849)
Washington singer CM1
(FJ687268)
BAQA04 (AF372712)
BAQA254 (AF372713)
Zeuk2 (AY916571)

mismatch). Consistently negative over replicate samples, different freshwater environments and stringency variations.

TSA-FISH probe binds to position 1010-1027 LKM11 CM SSU sequence (AJ130849). Minimum two mismatches with all non-target database SSU sequences.

Consistently negative over replicate samples, different freshwater environments and stringency variations. Addition of group specific helper probes was also tried.

CM2 GTCCCG HRP
CAGAGTT
CTCAC

CM2

Lily Stem CM2 (FJ687267)

TSA-FISH probe and forward PCR primer binds to position 1165-1182 LS-CM2 SSU sequence (FJ687267). Minimum two mismatches with all non-target

CM- TACGCC HRP
 R001gp1 CCCACAT
 TGTTA

CM3 (not shown on Fig. 1 but
 binds equivalent range of
 sequence range to probe
 LKM11-01 which is shown on
 Fig. 1)

LKM46 (AJ130857)
 Pg5.28 (AY642731)
 PFB12AU2004 (DQ244016)
 PFD5AU2004 (DQ244017)
 P1-3m9 (EU091835)
 P1-3m12 (EU091838)
 PFB3AU2004 (DQ244018)
 P2-3m3 (EU091850)

database SSU sequences.

Consistently negative over
 replicate samples, different
 freshwater environments and
 stringency variations. Addition of
 group specific helper probes was
 also tried.

TSA-FISH probe, binds to position
 452-469 LKM46 CM SSU
 sequence (AJ130857). Minimum
 one mismatch with all non-target
 database SSU sequences (a small
 number of environmental
 sequences have a single
 mismatch). Consistently negative
 over replicate samples, different
 freshwater environments and
 stringency variations.

CM- AACAAAA HRP
 R002gp2 TAAGACG

CM3 (not shown on Fig. 1 but
 binds equivalent range of

LKM46 (AJ130857)
 Pg5.28 (AY642731)

TSA-FISH probe, binds to position
 452-469 LKM46 CM SSU

	GAG		sequence range to probe	PFB12AU2004 (DQ244016)	sequence (AJ130857). Minimum
			LKM11-01 which is shown on	PFD5AU2004 (DQ244017)	one mismatch with all non-target
			Fig. 1)	P1-3m9 (EU091835)	database SSU sequences (a small
				P1-3m12 (EU091838)	number of environmental
				PFB3AU2004 (DQ244018)	sequences have a single
				P2-3m3 (EU091850)	mismatch). Consistently negative
					over replicate samples, different
					freshwater environments and
					stringency variations.
CM-	CATTACA	HRP	CM3 (not shown on Fig. 1 but	LKM46 (AJ130857)	TSA-FISH probe, binds to position
R003gp3	TCAGACT		binds equivalent range of	Pg5.28 (AY642731)	600-617 LKM46 CM SSU
	ACGA		sequence range to probe	PFB12AU2004 (DQ244016)	sequence (AJ130857) binding site
			LKM11-01 which is shown on	PFD5AU2004 (DQ244017)	relative to <i>E. coli</i> is 579. Minimum
			Fig. 1)	P1-3m9 (EU091835)	two mismatches with all non-target
				P1-3m12 (EU091838)	database SSU sequences.
				PFB3AU2004 (DQ244018)	Consistently negative over
				P2-3m3 (EU091850)	replicate samples, different
					freshwater environments and
					stringency variations.

LKM11-01	TACTGTC	HRP	>1000	LKM11-01 (equivalent to CM3)	LKM46 (AJ130857)	TSA-FISH probe designed by
	ACTACCT				Pg5.28 (AY642731)	Mangot <i>et al.</i> , 2009, binds to
	CGCC				PFB12AU2004 (DQ244016)	position 432-449 LKM46 CM SSU
					PFD5AU2004 (DQ244017)	sequence (AJ130857). This probe
					P1-3m9 (EU091835)	has at least one mismatch with all
					P1-3m12 (EU091838)	non-target database SSU
					PFB3AU2004 (DQ244018)	sequences; a small number of
					P2-3m3 (EU091850)	sequences have a single
						mismatch, this mismatch differs
						between three groups. These are
						a) a scattering of filamentous,
						non-flagellate, 'higher fungi' with
						chitin cell walls, b) a small
						subgroup of biflagellate
						photosynthetic green algae, and c)
						small sub-clade of <i>Flamella</i>
						pseudopodial amoebae, which are
						multi-nucleate and cell size >20
						µm. Based on the morphologies of
						the LKM11-01 cells observed false

LKM11-02 TGGTCCT HRP
CAAACCA
AC

A subsection of CM1 +
additional sequences in
cryptomycota clade (sequence
range not illustrated on Fig. 1)

LKM11 (AJ130849)
BAQA04 (AF372712)
BAQA254 (AF372713)
Zeuk2 (AY916571)
P34.42 (AY642700)
P2-3m4 (EU091851)
PRS2_4E_06 (FJ976649)

positives for these groups can be
excluded.

TSA-FISH probe (Mangot *et al.*,
2009), binds to position 800-825
LKM11 CM SSU sequence
(AJ130849). Minimum two
mismatches with all non-target
database SSU sequences.

Consistently negative over
replicate samples, different
freshwater environments and
stringency variations.

CM-R006 CGATCC HRP
GCGCAG
TTATCA

CM4 (not shown on Fig. 1)

Joinv23 (FJ577832)
P4-3m5 (EU091865)
RT5iin3 (AY082996)

TSA-FISH probe, binds to position
193-210 Joinv23 CM SSU
sequence (AJ130857) binding site
relative to *E. coli* is 194. Minimum
one mismatch with all non-target
database SSU sequences (a small
number of environmental
sequences have a single

Rappemo	CTCTCTC	HRP
nad plastid	TTCTCAG	
probe	AGAG	

CM1.1h1	CCCGAA	n/a
	GGCATT	
	GGTTTTT	
CM1.1h2	YYTAATA	n/a
	AATACAG	
	CCCT	
CM1.1h3	GTATTAG	n/a
	YTCTAGA	
	ATTA	
CM1.1h4	ACGGTTA	n/a
	TCCAAGT	

mismatch). Consistently negative over replicate samples, different freshwater environments and stringency variations.

Negative control probe originally designed to rappemonad (Kim *et al.*, 2011) plastids but consistently negative for cryptomycota-like cells in all experiments

Helper probe for CM1.1 probe, binds to position 192-210 LKM11 CM SSU sequence (AJ130849).
 Helper probe for CM1.1 probe, binds to position 172-187 LKM11 CM SSU sequence (AJ130849).
 Helper probe for CM1.1 probe, binds to position 132-149 LKM11 CM SSU sequence (AJ130849).
 Helper probe for CM1.1 probe, binds to position 112-129 LKM11

	AGTA		CM SSU sequence (AJ130849).
CM1.2h1	TCAAGCR	n/a	Helper probe for CM1.2 probe,
	TAAGCCT		binds to position 738-755 LKM11
	GCTT		CM SSU sequence (AJ130849).
CM1.2h2	AACACTC	n/a	Helper probe for CM1.2 probe,
	TAATTTTC		binds to position 723-735 LKM11
	YTCA		CM SSU sequence (AJ130849).
CM1.2h3	CRCCGA	n/a	Helper probe for CM1.2 probe,
	AGCACR		binds to position 677-691 LKM11
	RCTAGY		CM SSU sequence (AJ130849).
CM1.2h4	CCCGAA	n/a	Helper probe for CM1.2 probe,
	GGTGAG		binds to position 658-673 LKM11
	GCGCR		CM SSU sequence (AJ130849).
CM1.5h1	TGCGAC	n/a	Helper probe for CM1.5 probe,
	CATACTC		binds to position 1070-1087
	CCCCC		LKM11 CM SSU sequence
			(AJ130849).
CM1.5h2	AACCCAA	n/a	Helper probe for CM1.5 probe,
	AAAYTTT		binds to position 1050-1067

	GATT		LKM11 CM SSU sequence (AJ130849).
CM1.5h3	TCGTAAG	n/a	Helper probe for CM1.5 probe, binds to position 1030-1047
	GTGCCG		
	ATGGA		LKM11 CM SSU sequence (AJ130849).
CM1.5h4	CCCTAGT	n/a	Helper probe for CM1.5 probe, binds to position 990-1007 LKM11
	CGGCAT		
	AGTTT		CM SSU sequence (AJ130849).
CM1.5h5	GGTTAAG	n/a	Helper probe for CM1.5 probe, binds to position 970-987 LKM11
	ACTACGA		
	CGGT		CM SSU sequence (AJ130849).
CM2.1h1	CAAACCTT	n/a	Helper probe for CM2 probe, binds to position 1205-1222 LS-
	CCGACT		
	GCTAT		CM2 SSU sequence (FJ687267).
CM2.1h2	GCAGTC	n/a	Helper probe for CM2 probe, binds to position 1202-1185 LS-
	AGTCCCT		
	CTAAG		CM2 SSU sequence (FJ687267).
CM2.1h3	TGCCAAC	n/a	Helper probe for CM2 probe, binds to position 1145-1162 LS-
	TAGTTAG		

	CAGG		CM2 SSU sequence (FJ687267).
CM2.1h4	AAGGTCT	n/a	Helper probe for CM2 probe,
	CGTTCGT		binds to position 1125-1142 LS-
	TATC		CM2 SSU sequence (FJ687267).
AU2	TTTCGAT	n/a	Forward PCR primer
	GGTAGG		(Vandenkoornhuysse <i>et al.</i> , 2002)
	ATAGDG		
	G		
AU4	RTCTCAC	n/a	Reverse PCR primer
	TAAGCCA		(Vandenkoornhuysse <i>et al.</i> , 2002)
	TTC		
1520r	CTGCAG	n/a	Reverse PCR primer (Lefèvre <i>et</i>
	GTTCCACC		<i>al.</i> , 2007)
	TAC		
28Sr1	5'-	n/a	Reverse PCR primer (Bass <i>et al.</i> ,
	CGGTACT		2007)
	TGTTCGC		
	TATCGG-		

3'

Supplementary Table 3. Sampling sites. (Grey rows were negative samples for FISH using LKM11-01, CM1.1 and CM1.2)

Sampling location	Date of Sampling	Volume filtered	GPS
Eutrophic freshwater Washington Singer pond (surface/watercolumn wading sample)	03/06/08	1500 ml	$\lambda = 50.733,$ $\varphi = -3.537$
Eutrophic freshwater Washington Singer pond (surface/watercolumn wading sample)	06/08/08	200 ml	$\lambda = 50.733,$ $\varphi = -3.537$
Eutrophic freshwater Washington Singer pond (surface/watercolumn wading sample)	31/05/09	200 ml	$\lambda = 50.733,$ $\varphi = -3.537$
Eutrophic freshwater Washington Singer pond (surface/watercolumn wading sample)	05/08/08	500 ml	$\lambda = 50.733,$ $\varphi = -3.537$
Eutrophic freshwater Washington Singer pond (surface/watercolumn wading sample)	13/11/08	200 ml	$\lambda = 50.733,$ $\varphi = -3.537$
Eutrophic freshwater Washington Singer pond (surface/watercolumn wading sample)	29/10/09	1000 ml	$\lambda = 50.733,$ $\varphi = -3.537$
Eutrophic freshwater Washington Singer pond (surface/watercolumn wading sample)	03/11/09	500 ml	$\lambda = 50.733,$ $\varphi = -3.537$
Eutrophic freshwater Washington Singer pond (surface/watercolumn wading sample)	29/10/09	600 ml	$\lambda = 50.733,$ $\varphi = -3.537$
Eutrophic freshwater Washington Singer pond	03/11/09	600 ml	$\lambda = 50.733,$

(surface/watercolumn wading sample)			$\varphi = -3.537$
Eutrophic freshwater Washington Singer pond (submerged surface scrapings)	03/11/09	250 ml	$\lambda = 50.733,$ $\varphi = -3.537$
Eutrophic freshwater Washington Singer pond (surface/watercolumn wading sample)	01/12/09	900 ml	$\lambda = 50.733,$ $\varphi = -3.537$
Eutrophic freshwater Washington Singer pond (surface/watercolumn wading sample)	21/07/08	400 ml	$\lambda = 50.733,$ $\varphi = -3.537$
Oligotrophic freshwater Tottiford reservoir (surface/watercolumn wading sample)	28/01/10	850 ml	$\lambda = 50.632,$ $\varphi = -3.683$
Oligotrophic freshwater Tottiford reservoir (surface/watercolumn wading sample)	28/01/10	500 ml	$\lambda = 50.632,$ $\varphi = -3.683$
Oligotrophic freshwater Kennick reservoir (surface/watercolumn wading sample)	28/01/10	1000 ml	$\lambda = 50.65,$ $\varphi = -3.69$
Oligotrophic freshwater Kennick reservoir (surface/watercolumn wading sample)	28/01/10	500 ml	$\lambda = 50.65,$ $\varphi = -3.69$
Oligotrophic freshwater Trenchford reservoir (surface/watercolumn wading sample)	28/01/10	1000 ml	$\lambda = 50.630,$ $\varphi = -3.688$
Oligotrophic freshwater Trenchford reservoir (surface/watercolumn wading sample)	28/01/10	500 ml	$\lambda = 50.630,$ $\varphi = -3.688$

Coastal marine Sidmouth samples (surface/watercolumn wading sample)	8/07/08	~500 ml	$\lambda = 50.683,$ $\varphi = -3.233$
Coastal marine Seaton samples (surface/watercolumn wading sample)	8/07/08	~500 ml	$\lambda = 50.702,$ $\varphi = -3.066$
Coastal marine Budleigh Salterton samples (surface/watercolumn wading sample)	8/07/08	~500 ml	$\lambda = 50.623,$ $\varphi = -3.315$
Coastal marine Exmouth samples (surface/watercolumn wading sample)	8/07/08	~500 ml	$\lambda = 50.601,$ $\varphi = -3.402$
Eutrophic freshwater Priest Pot pond (epiphytic microbial community scraped from a submerged lily stem from)	--/09/02		$\lambda = 54.372,$ $\varphi = -2.990$

Supplementary Table 4. PCR amplification conditions

Protocol number	Amplification conditions*
1	Initial denaturation of 95 °C for 5 min. was followed by 30 cycles of 95 °C for 1 min., 55 °C for 1 min., and extension at 72 °C for 2 min., with a final extension at 72 °C for 10 min.
2	Initial denaturation of 95 °C for 5 min was followed by 35 cycles of 95 °C for 1 min., 58 °C for 1 min. and 72 °C for 3 min., with a final extension step of 72 °C for 10 min.
3	Initial denaturation of 95 °C for 5 min. was followed by 30 cycles of 95 °C for 1 min., 56 °C for 1 min., and 72 °C for 2 min., with a final extension step of 72 °C for 10 min

*General PCR mix. Each 25 μL reaction contained 1 μL of each primer (10 pM L^{-1}), 12.5 μL of Master Mix (Promega, containing 3 mM MgCl_2 , 400 μM of each dNTP, and 50 U/mL of Taq DNA polymerase), 9.5 μL of PCR water, and 1 μL of template DNA.

Supplementary Table 5. Details of sequences from identified species used to construct phylogenies

Species	GenBank Acc. SSU	Genank Acc. 5.8S	GenBank Acc. LSU
<i>Rozella sp.</i>	AY601707.1	AY997086.1	DQ273766.1
<i>Rozella allomycis</i>	AY635838.1	AY997087.1	DQ273803.1
<i>Filobasidiella neoformans</i>	AF356652.1	AF356652.1	AF356652.1
<i>Platyglaea disciformis</i>	DQ234563.1	DQ234556.1	AY629314.1
<i>Coprinopsis cinerea</i>	M92991.1	EU168109.1	EU168109.1
<i>Calocera cornea</i>	AY771610.1	AY701526.1	AY789083.1
<i>Ustilago maydis</i>	X62396.1	AF455508.1	AF455508.1
<i>Tilletiaria anomala</i>	AY803752.1	DQ234558.1	AY745715.1
<i>Phycomyces blakesleeanus</i>	AY635837.1	AY997071.1	DQ273800.1
<i>Rhizopus oryzae</i>	supercontig 3.6 [DNA] 2077734-2081500 http://www.broad.mit.edu/annotation/genome/rhizopus_oryzae/MultiHome.html		
<i>Candida glabrata</i>	AY198398.1	AY198398.1	AY198398.1

<i>Debaryomyces hansenii</i>	DQ534402.1	EF543259.1	EF543260.1
<i>Neurospora crassa</i>	FJ360521.1	FJ360521.1	FJ360521.1
<i>Magnaporthe grisea</i>	AB026819.1	AB026819.1	AB026819.1
<i>Hypocrea jecorina</i>	AF510497.1	AF510497.1	AF510497.1
<i>Monilinia fructicola</i>	AY544724.1	AY544683.1	DQ491506.1
<i>Dothidea sambuci</i>	AY544722.1	AY544681.1	DQ491505.1
<i>Monascus purpureus</i>	DQ782881.1	DQ782847.1	DQ782908.1
<i>Disciotis venosa</i>	AY544711.1	DQ491503.1	AY544667.1
<i>Schizosaccharomyces pombe</i>	Z19578.1	Z19578.1	Z19578.1
<i>Glomus mosseae</i>	AY635833.1	AY997053.1	DQ273793.1
<i>Paraglomus occultum</i>	DQ322629.1	AY997069.1	DQ273827.1
<i>Piptocephalis corymbifera</i> (extremely long branch excluded from SSU analysis)	AB016023.1	AY997073.1	AY546690.1

<i>Smittium culisetae</i>	D29950.1	AY997089.1	DQ273773.1
<i>Polychytrium aggregatum</i>	AY601711.1	AY997074.1	AY546686.1
<i>Karlingiomyces sp.</i>	AF164278.2	AY997056.1	DQ273814.1
<i>Rhizophydium brooksianum</i>	AY601710.1	AY997079.1	AY349086.1
<i>Powellomyces sp.</i>	AF164245.2	AY997075.1	DQ273776.1
<i>Triparticalcar arcticum</i>	DQ536480.1	AY997096.1	DQ273826.1
<i>Rhizophlyctis rosea</i>	AY635829.1	AY997078.1	DQ273787.1
<i>Catenomyces sp.</i>	AY635830.1	AY997033.1	DQ273789.1
<i>Basidiobolus ranarum</i>	AY635841.1	AY997030.1	DQ273807.1
<i>Cyllamyces aberensis</i>	DQ536481.1	AY997042.1	DQ273829.1
<i>Rhizoclostridium sp.</i>	AY601709.1	AY997076.1	DQ273769.1
<i>Chytrium hyalinus</i>	DQ536487.1	DQ536499.1	DQ273836.2
<i>Batrachochytrium dendrobatidis</i>	supercontig 1.14 [DNA] 187000-191314 (http://www.broad.mit.edu/annotation/genome/batrachochytrium_dendrobatidis/)		

<i>Entophlyctis helioformis</i>	AY635826.1	AY997048.1	DQ273784.1
<i>Oedogoniomyces sp.</i>	AY635839.1	AY997066.1	DQ273804.1
<i>Monoblepharella sp.</i>	AY546682	AY997060.1	AY546687.1
<i>Hyaloraphidium curvatum</i>	Y17504.1	AY997055	DQ273771.1
<i>Rhizophydium sphaerotheca</i>	AY635823.1	AY997082.1	DQ273781.1
<i>Allomyces arbuscula</i>	AY552524.1	AY997028.1	AY552525.1
<i>Blastocladiella emersonii</i>	AY635842.1	AY997032.1	DQ273808.1
<i>Nowakowskiella sp.</i>	AY635835.1	AY997065.1	DQ273798.1
<i>Endochytrium sp.</i>	AY635844.1	AY997044.1	DQ273816.1
<i>Cladochytrium replicatum</i>	AY546683.1	AY997037.1	AY546688
<i>Physoderma maydis</i>	DQ536489.1	AY997072.1	DQ273768.1
<i>Nuclearia simplex</i>	AF484687.1	AF484687.1	AY148095.1
<i>Suberites ficus</i>	AJ627184.1	AJ627184.1	AY026381.1

<i>Aurelia</i> sp.	EU276014.1	EU276014.1	EU276014.1
<i>Capsaspora owczarzaki</i>	AY363957.1	AY363957.1	AY724688.1
<i>Amoebidium parasiticum</i>	Y19155.1	AY997029.1	DQ273802.1
<i>Brachiola algerae</i> ¹	AM422905.1	AM422905.1	AM422905.1
<i>Heterosporis anguillarum</i> ¹	AF387331.1	AF387331.1	AF387331.1
<i>Antonospora locustae</i> ¹	AY376351	Contig 955 http://gmod.mbl.edu/perl/site/antonospora01	
<i>Encephalitozoon cuniculi</i> ¹	AJ005581	AJ005581	AJ005581
LS_CM2	FJ687267	-	-
WS_CM2	-	FJ687265	FJ687265
WS_CM1	FJ687268	FJ687268	FJ687268

¹Used for microsporidia phylogenetic analysis only (Supplementary Fig. 2b/c)

Supplementary Table 6. Environmental origin of cryptomycota cells depicted in figures.

Figure	TSA-FISH probe used	Origin of sample
Figure 1 (d)	CM1.1	Washington Singer Pond
	CM1.2	
	LKM11-01	
Figure 2 (a)	CM1.1	Washington Singer Pond
	LKM11-01	Trenchford Reservoir
Figure 2 (b)	CM1.1	Washington Singer Pond
	LKM11-01	Tottiford Reservoir
Figure 2 (c)	LKM11-01	Washington Singer Pond
		Trenchford Reservoir
Figure 2 (d)	LKM11-01	Trenchford Reservoir
		Tottiford Reservoir
Figure 2 (e)	CM1.1	Washington Singer Pond
	LKM11-01	

Supplementary Figure 3	CM1.1	Washington Singer Pond
	CM1.2	
	CM1.2	
	LKM11-01	
	LKM11-01	Trenchford Reservoir
Supplementary Figure 4	LKM11-01	Trenchford Reservoir
		Tottiford Reservoir
		Trenchford Reservoir
Supplementary Figure 6 (a)	LKM11-01	Washington Singer Pond
Supplementary Figure 6 (b)		
Supplementary Figure 6 (c)		Trenchford Reservoir
Supplementary Figure 6 (d)		Washington Singer Pond
Supplementary Figure 6 (e)		Trenchford Reservoir
Supplementary Figure 6 (f)		Tottiford Reservoir
Supplementary Figure 7 (a)	LKM11-01	Tottiford Reservoir

Supplementary Figure 7 (b)

Trenchford Reservoir

Supplementary Figure 7 (c)

Supplementary Figure 7 (d)

Washington Singer Pond
