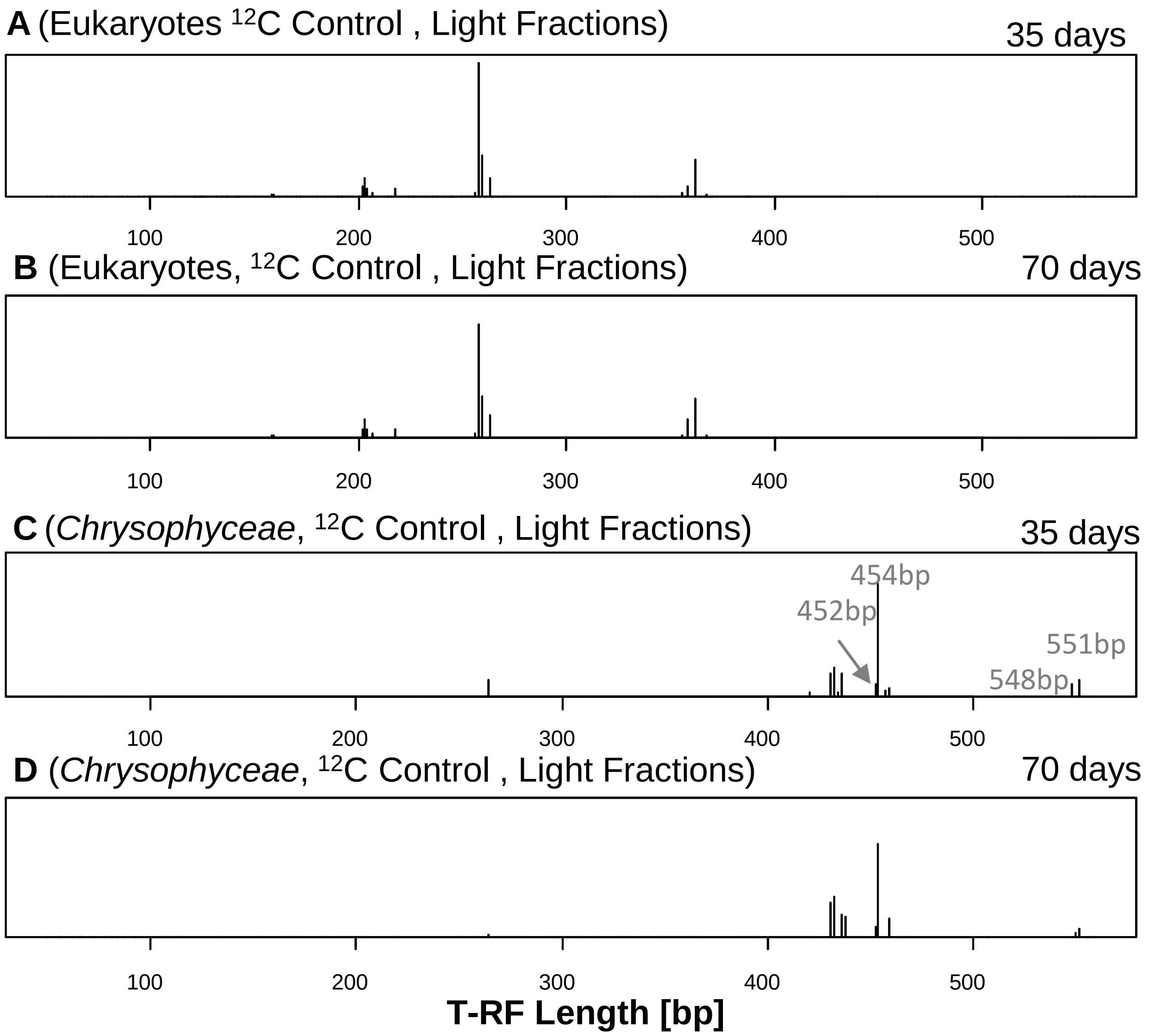

Fig. S1. T-RFLP patterns of Eukaryotes (A and B) and *Chrysophyceae* (C and D) in light fractions of gradients of the ^{12}C control treatments. Grey numbers, TRFs that have similar but different sizes than those that represented ^{13}C-labelled phylotypes of *Chrysophyceae* (Fig. 2).

Table S1. Selected protistan phylotypes of the 18S rRNA libraries derived from pooled “light” and “heavy” RNA fractions using eukaryote specific primers.

Phylogenetic group		**Range of % Similarity**[a]	**Start**[b]		**70 days**[b]	
			anoxic	**oxic**	**anoxic**	**oxic**
Alveolata (Ciliophora)	Oligohymenophorea; Peritrichia	99				57
	Litostomatea; Haptoria; Spathidiidae	98-99	1		3	
	Spirotrichea; Stichotrichia; Oxytrichidae	99	1			
Alveolata	Apicomplexa; Eimeriidae	97-99	3	9	7	1
	Colpodellidae	90		1		
Amoebozoa	Euamoebida	95-99	9		3	4
	Euamoebida; Tubulinida	86			1	
	Euamoebida; Tubulinida; Hartmannellidae	94-99	5		4	
	Centramoebida; Balamuthiidae	86	2			
	Mycetozoa; Dictyostelium	100	1			
Chlorophyta	Trebouxiophyceae	96-100	6	6	12	5
	Chlorophyceae; Sphaeropleales	98-99		2	1	1
	Chlorophyceae; Chlamydomonadales	97-99	12	13	5	5
	Chlorophyceae; Pseudotetracystis	99	1		2	2
	Chlorophyceae; Scenedesmaceae	98-100	26	17	21	15
	Chlorophyceae; Dictyococcus	99	1			
	Chlorophyceae; Radiococcus	99	1			
	Ulvophyceae	99		1		

[a], sequence similarity to the next related sequence in the nucleotide database of Genbank.

[b], absolute abundance of phylotype in gene library.

Table S2 Fungal phylotypes of the 18S rRNA libraries derived from pooled "light" and "heavy" RNA fractions using eukaryote specific primers.

Phylogenetic Group		**Range of % Similarity**[a]	**Start**[b]		**70 days**[b]	
			Anoxic	**Oxic**	**Anoxic**	**Oxic**
Unknown Ascomycota		95-98	3.9			
Mitosporic Ascomycota		97-100	28.6	10.2	17.6	44.4
Saccharomycota		100		1.7		
Pezizomycotina; Dothideomycetes		98-100	7.8	5.1	11.8	
Pezizomycotina; Eurotiomycetes		99-100	2.6	8.5		3.7
Pezizomycotina; Laboulbeniomycetes		99	3.9		5.9	
Pezizomycotina; Pezizomycetes		94-98	1.3	3.4		
Pezizomycotina; Leotiomycetes		98-99			2.9	3.7
Pezizomycotina; Sordariomycetes	Verticillium	98-100	5.2	3.4		
	Hypocrea	99-100		8.5		
	Fusarium	98-99	3.9		5.9	
	Microascales	96-99	3.9	8.5	17.6	3.7
	Coniochaeta	98-100	2.6			
	Giberella	100		1.7		3.7
	Ophiocordiceps	99-100		6.8		7.4
	Lecythophora	98-100	16.9	18.6	14.7	14.8
	Chaetomiaceae	97-100	13	18.6		
	Lasiophaeris	98-100	1.3		8.8	
	Acremonium	95-100	5.2	5.1		7.4
	Melanospora	98-99			5.9	
	Ceratosystiopsis	97			2.9	
	Podospora	99			2.9	
	Cordiceps	99			2.9	
	Menispora	99				7.4
	Doratomyces	99				3.7

[a], sequence similarity to the next related sequence in the nucleotide database of Genbank.

[b], relative abundance of phylotype in gene library in percent.

Table S3. Assignment of T-RFs to detected phylotypes in 18S rRNA libraries using eukaryotic-specific primers. Analyzed were samples taken at 70 days from oxic treatments that were supplemented with [^{13}C-u]cellulose. These sequences are results of a second clone library. A more extensive library that was retrieved from combined "light" and "heavy" RNA fractions is shown in Table 1.

Clone	**T-RF [bp]**	**Next relative**	**% Sequence identity**[a]
D6	182	Uncultured Scolecobasidium clone LL76(mitosporic Ascomycota)	100
B8	203	Scotiellopsis terrestris (Chlorophyceae; Scenedesmaceae)	100
A10	205	Vischeria punctata UTEX 153 (Stramenopiles)	99
B10	217	Xanthonema sp. 735 (Stramenopiles)	99
F2	230	Ciliate	99
H1	249	Mayamaea atomus var. atomus (Stramenopiles)	99
G1	257	Lecythophora hoffmannii (Ascomycota; Lecythophora)	99
H6	262	Cryptococcus terreus (Basidiomycota)	100
D8	266	Hyphochytrium catenoides (Stramenopiles)	99
H3	342	Opisthonecta minima (Ciliophora; Peritrichia)	98
B12	343	Opisthonecta minima (Ciliophora; Peritrichia)	99
H2	344	Opisthonecta minima (Ciliophora; Peritrichia)	98
C2	362	Psathyrella candolleana AFTOL-ID 1507 (Basidiomycota)	99
F10	369	Pleurochloris meiringensis (Stramenopiles)	99
E6	369	Malawimonas jakobiformis (Malawimonadidae flagellates)	91
B11	370	Proleptomonas faecicola (Cercozoa)	100
F3	371	Malawimonas jakobiformis (Malawimonadidae flagellates)	96
F1	375	Uncultured Chytridiomycota clone T5P1AeC06 (Fungi; Chytridiomycetes)	88
A3	387	Hartmannellidae environmental clone Amb_18S_1090 (Amoebozoa)	99

[a], sequence similarity to the next related sequence in the nucleotide database of Genbank.

Table S4. Assignment of T-RFs to detected phylotypes in 18S rRNA libraries using *Chrysophyceae*-specific primers. Analyzed were samples taken at 70 days from oxic treatments that were supplemented with [^{13}C-u]cellulose.

Clone	**T-RF [bp]**	**Next relative**	**% Sequence identity**[a]
H12	263	Uncultured stramenopile clone MLBM27	99
G10	268	Ochromonas vasocystis strain CCMP2741	96
C11	300	Leukarachnion sp. ATCC PRA-24	92
A5	429	Chrysophyceae sp. CCCM41	99
B2	430	Chrysophyceae sp. CCCM41	99
A8	431	Synura curtispina strain CCMP847	94
C10	432	Mallomonas peroneides var. bangladeshica strain	94
A2	435	Chrysophyceae sp. CCCM41	98
D2	436	Chrysophyceae sp. CCCM41	93
D1	437	Spumella-like flagellate 1027	99
E5	438	Leukarachnion sp. ATCC PRA-24	95
G6	452	Soil flagellate AND30	98
D3	452	Spumella-like flagellate 1243	98
F11	453	Spumella-like flagellate 1243	98
D11	454	Leukarachnion sp. ATCC PRA-24	92
G9	457	Spumella-like flagellate 1243	98
G8	458	Leukarachnion sp. ATCC PRA-24	96
B5	465	Spumella-like flagellate JBNA46	97

[a], sequence similarity to the next related sequence in the nucleotide database of Genbank.