Supplementary Information

Supplementary Information Text

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Code	Name	Longitude	Latitude	Altitude	Depth (max)
ABB	Abbaye	5.912	46.531	910	19.5
AIG	Aiguebelette	5.800	45.553	374	71.0
ALA	Alate	1.406	42.776	1868	10.0
ARA	Arratille	-0.175	42.801	2247	12.0
AYD	Aydat	2.986	45.664	825	15.0
AYE	Ayes	1.064	42.844	1694	10.0
BAL	Balcère	2.053	42.590	1765	14.0
BAE	Barroude	0.144	42.731	2355	9.0
BAR	Barterand	5.744	45.790	295	15.0
BES	Besse	2.359	44.192	245	10.0
BLA	Blanchemer	6.977	48.018	984	15.0
BON	Bonlieu	5.873	46.587	803	14.0
BOR	Bordères	0.461	42.860	1765	18.0
BOU	Bourget	5.869	45.742	231	147.0
CHA	Chalain	5.790	46.671	490	32.0
CHE	Chéserys	6.900	45.985	2135	6.0
COR	Corbeaux	6.904	47.991	887	27.0
CRE	Crégut	2.677	45.409	900	26.0
ESP	Espingo	0.495	42.729	1882	8.0
ETI	Etival	5.804	46.504	795	10.0
LAG	Gardelle	1.432	42.647	2387	27.0
GEN	Gentau	-0.488	42.848	1950	20.0
GER	Gérardmer	6.852	48.070	660	38.0
GOD	Godivelle	2.917	45.387	1239	44.0
GUE	Guéry	2.822	45.616	1246	20.0
ILA	Ilay	5.898	46.627	778	32.0
ISA	Isaby	0.023	42.951	1562	6.0
LAM	Lamoura	5.981	46.395	1156	9.0
LAN	Landie	2.766	45.422	1000	21.0
LEM	Léman	6.492	46.444	372	309.0
LON	Longemer	6.951	48.070	736	34.0
MAI	Maix	7.075	48.476	678	15.0
MAR	Marion	-1.548	43.468	50	22.8
MTC	Mont Coua	6.639	45.318	2797	10.0
MOU	Mouriscot	-1.558	43.456	21	10.0
NAN	Nantua	5.587	46.162	475	43.0
PAR	Parentis	-1.174	44.355	19	20.0
PEY	Peyrelade	0.114	42.943	1919	28.0
POR	Port Bielh	0.187	42.873	2313	19.0
ROU	Roumazet	1.435	42.634	2163	10.0
ROS	Rousses	6.089	46.505	1059	18.0
SAI	Saint-Point	6.318	46.820	850	42.0
SEV	Serviere	2.859	45.646	1200	29.0
SOU	Soucarrane	1.434	42.626	2291	10.0
GOU	Tazenat	2.990	45.980	630	66.0
VAL	Val	5.815	46.627	520	25.0
VED	Verdet	6.955	45.576	2736	12.0
VER	Vert	6.753	45.950	1266	9.0

Table S1. List of the lakes included in the study with their three-letter code, geographic coordinates (decimal degrees; WGS84), altitude (meters) and maximum depth (meters).
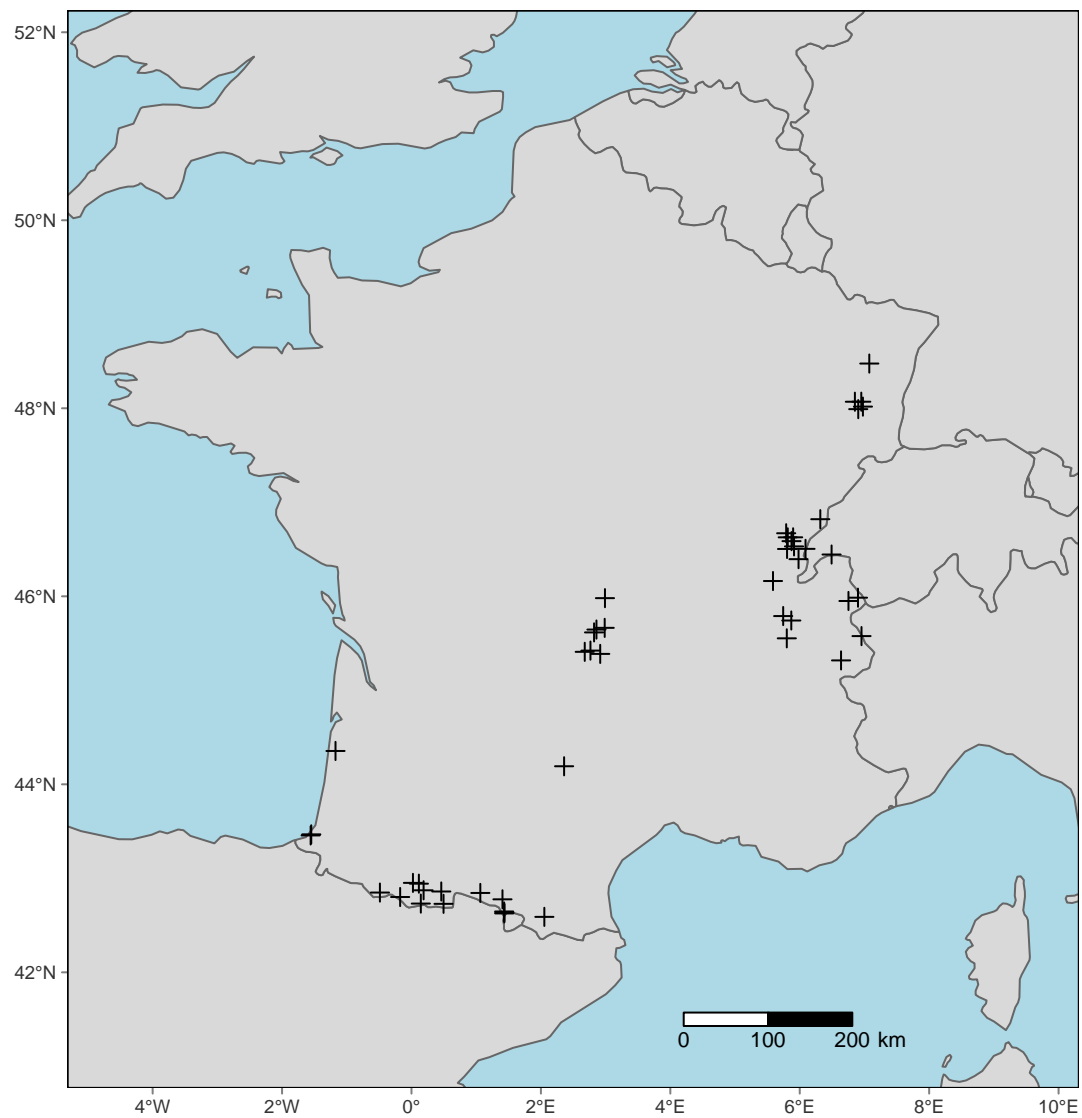
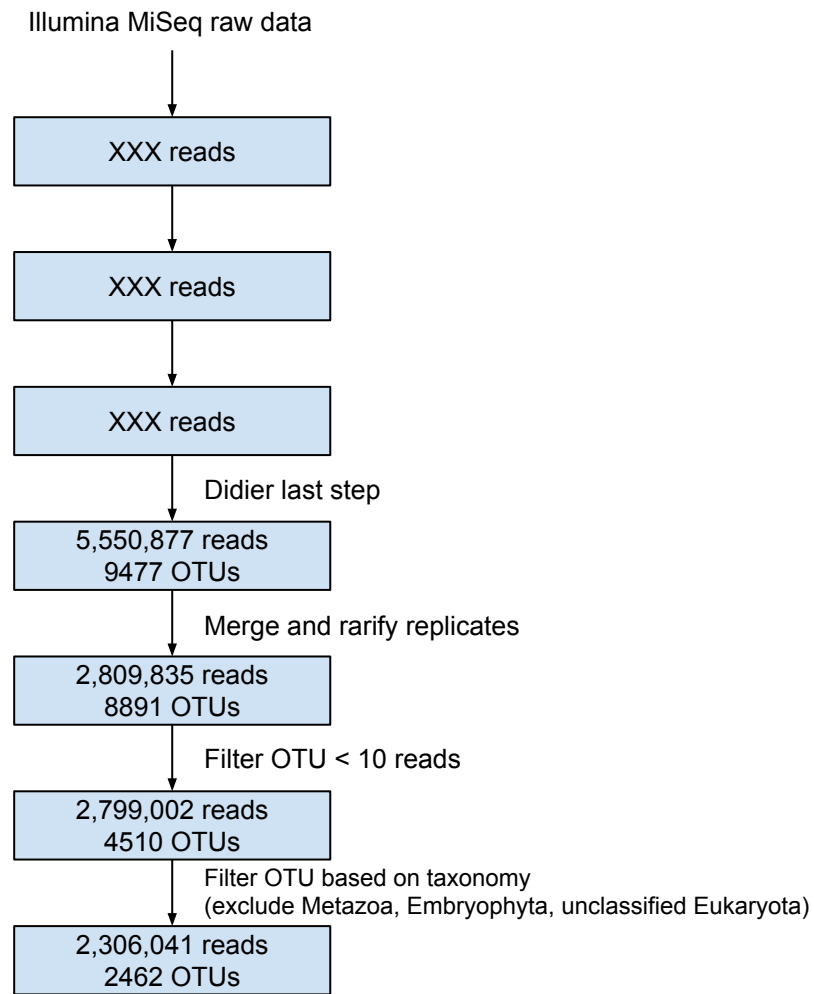**Figure S1.** Map of the 48 lakes included in the study.

Figure S2. Tracking of the number of DNA reads and OTUs during the filtering and data pre-processing steps.
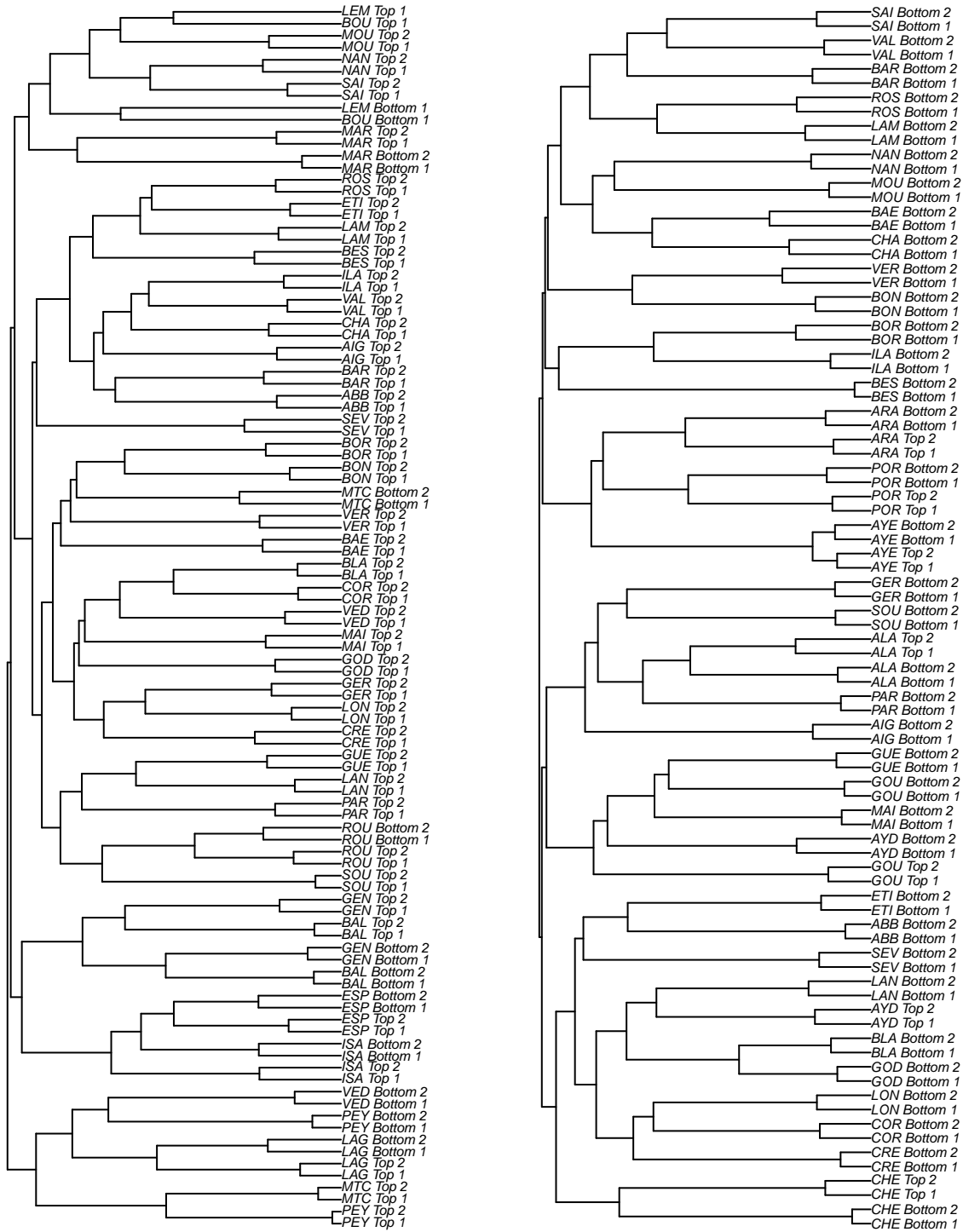
Figure S3. Hierarchical clustering of the OTU matrix (Bray Curtis dissimilarity) including the technical replicates. The code of each sample corresponds to the combination of the lake (three-letter code; see Supplementary Table S1), stratum (Top or Bottom) and replicate number (1 or 2 except for Bourget and Léman that have only one replicate). For better readability, the tree has been divided in two parts.
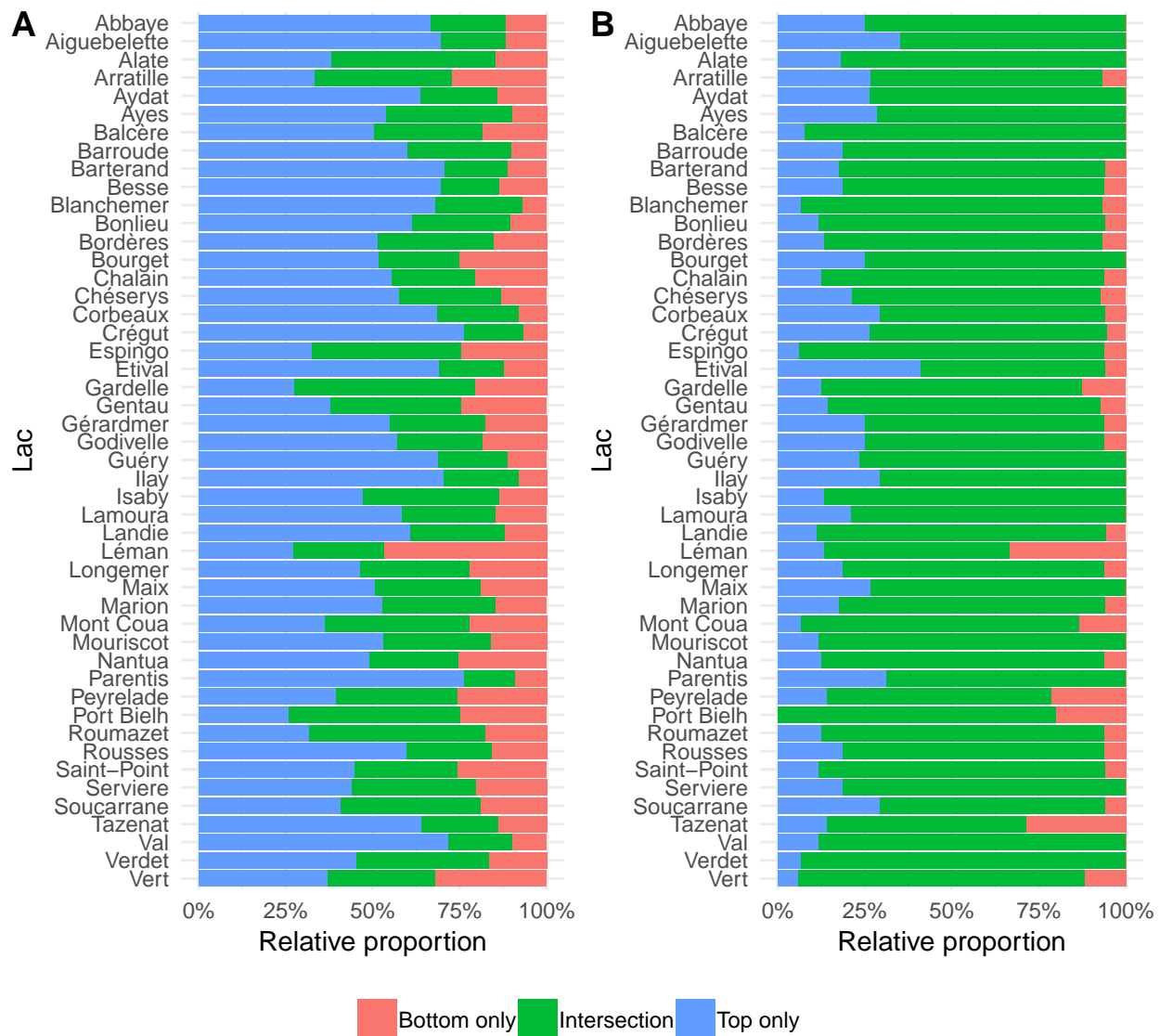
Figure S4. Proportion of OTUs (*A*) and taxonomic groups (*B*) specific to the bottom (Bottom only) and top (Top only) strata, or common to both strata (Intersection).
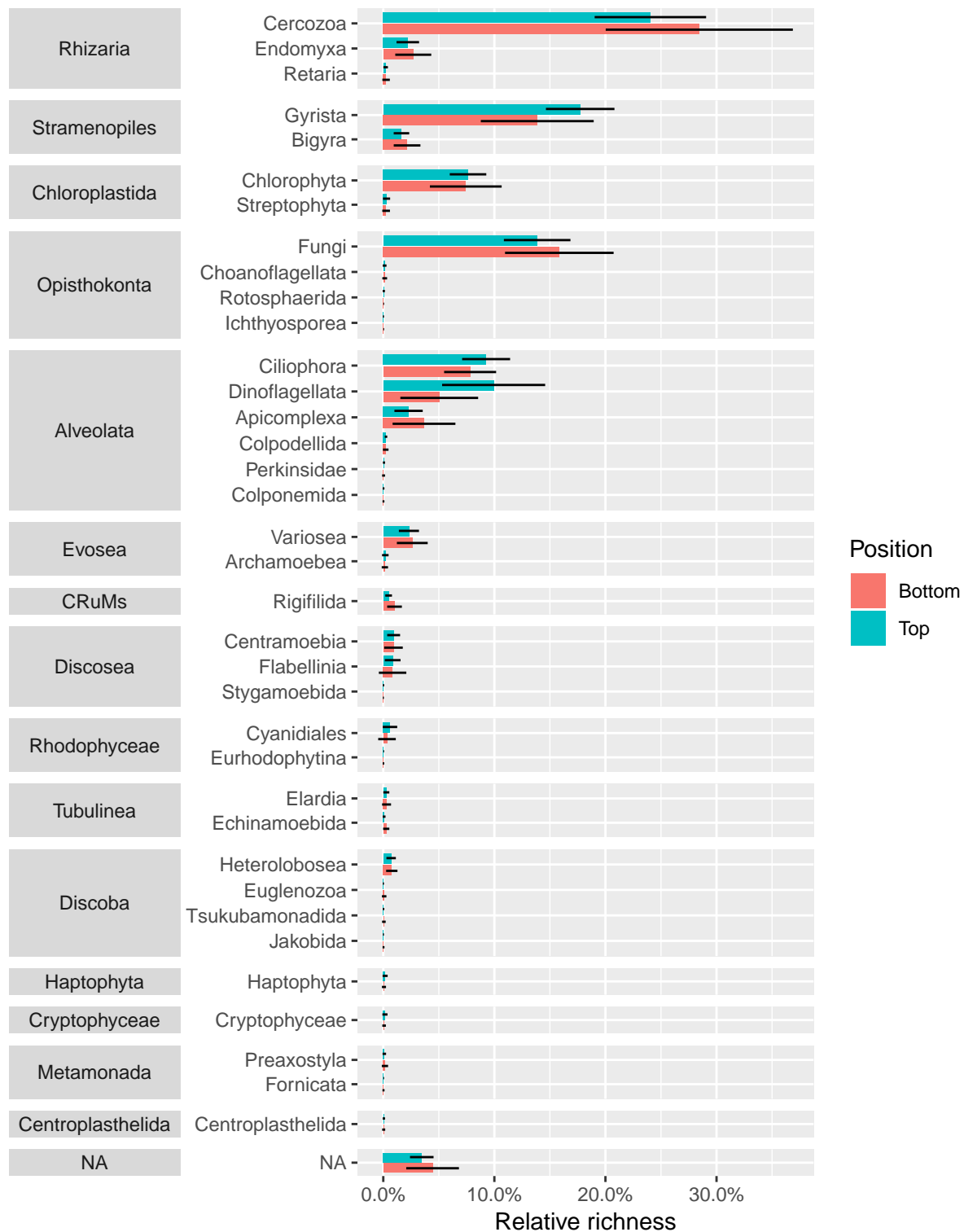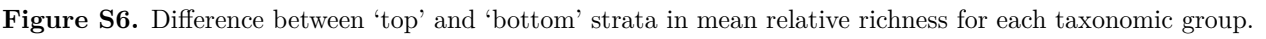
Figure S5. Mean relative richness (number of distinct OTUs) for each taxa computed for the bottom and the top samples across all lakes. Horizontal lines show the standard error.
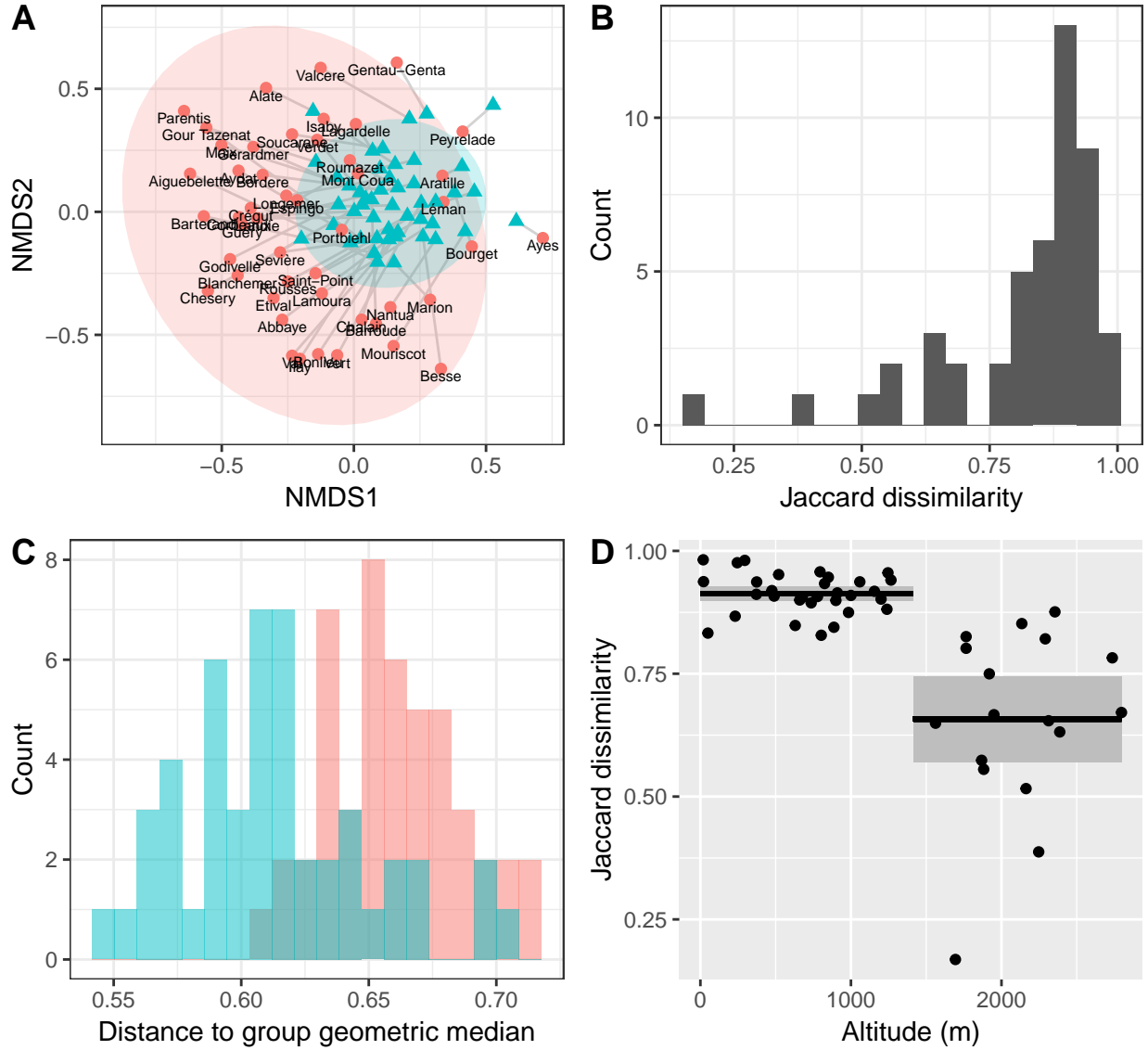
Figure S6. Difference between 'top' and 'bottom' strata in mean relative richness for each taxonomic group.

Figure S7. Community analyses reproduced with the Jaccard dissimilarity index. (*A*) NMDS of community compositions of the 'top' (blue triangles) and 'bottom' (red circles) samples with 95% confidence ellipses represented for each group. Grey lines connect 'top' and 'bottom' samples taken within the same lake. (*B*) Distribution of Jaccard index values computed for each lake between 'top' and 'bottom' samples . (*C*) Distribution of the distances between samples and group geometric median for 'top' (blue) and 'bottom' (red) samples. (*D*) Relationship between lake altitude and community dissimilarity (Jaccard index) between the 'top' and 'bottom' strata. Fitted regression tree model is represented by black lines (mean values). Grey shading represent the 95% confidence intervals around means.

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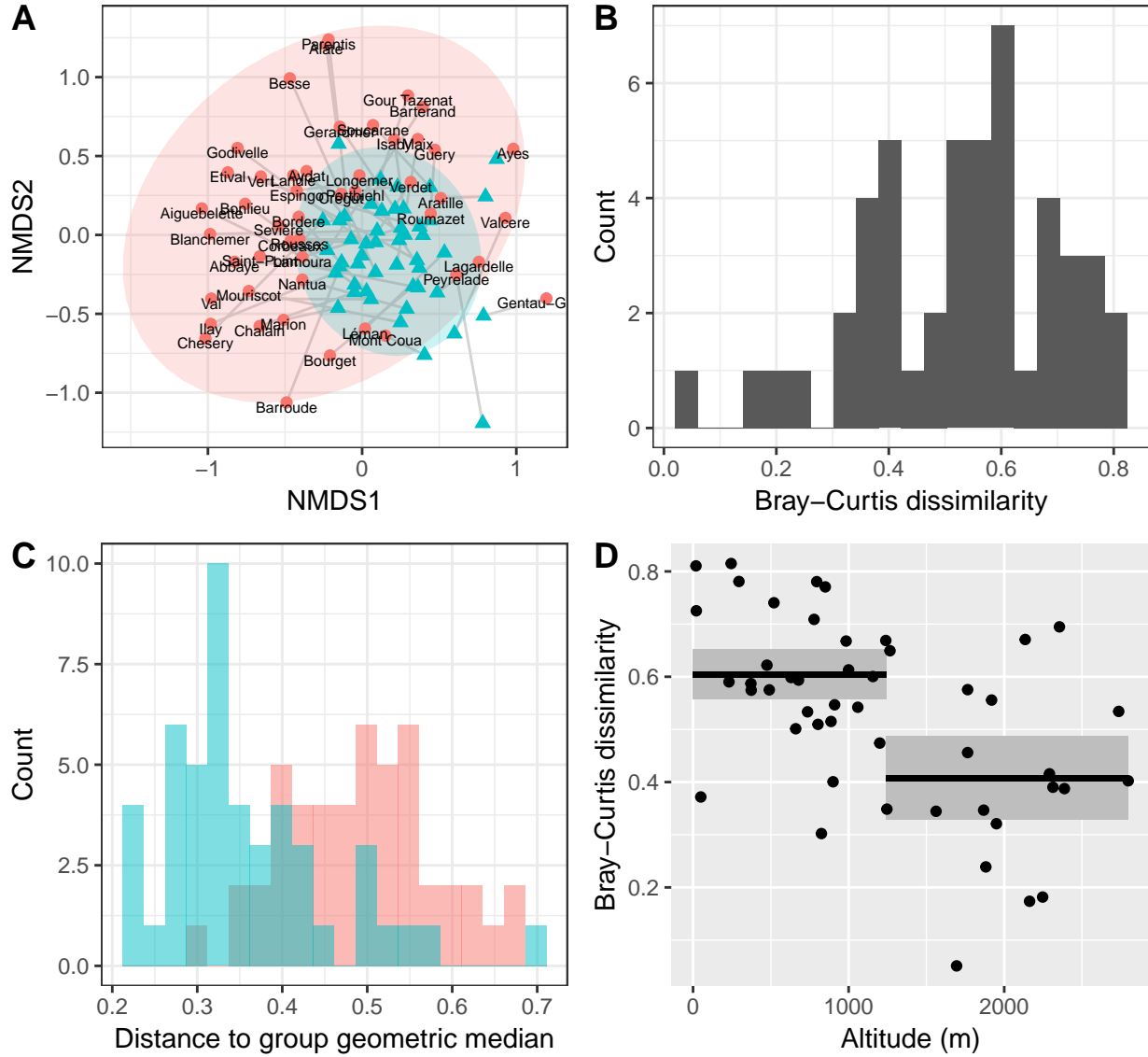
Figure S8. Community analyses reproduced with the taxonomy table. (*A*) NMDS of community compositions of the 'top' (blue triangles) and 'bottom' (red circles) samples with 95% confidence ellipses represented for each group. Grey lines connect 'top' and 'bottom' samples taken within the same lake. (*B*) Distribution of Bray-Curtis index values computed for each lake between 'top' and 'bottom' samples . (*C*) Distribution of the distances between samples and group geometric median for 'top' (blue) and 'bottom' (red) samples. (*D*) Relationship between lake altitude and community dissimilarity (Bray-Curtis index) between the 'top' and 'bottom' strata. Fitted regression tree model is represented by black lines (mean values). Grey shading represent the 95% confidence intervals around means.

Taxa	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj
Apicomplexa	118.710	-1.872	0.357	-5.247	0.000	0.000
Archamoebea	4.679	0.000	0.803	0.000	1.000	1.000
Bigyra	560.970	-3.578	0.436	-8.215	0.000	0.000
Centramoebia	59.052	0.025	0.510	0.050	0.960	1.000
Centroplasthelida	0.303	0.340	1.223	0.278	0.781	0.932
Cercozoa	15513.087	-3.302	0.317	-10.401	0.000	0.000
Chlorophyta	819.373	0.344	0.308	1.117	0.264	0.444
Choanoflagellata	3.222	-1.050	0.781	-1.344	0.179	0.315
Ciliophora	1994.685	-1.032	0.295	-3.500	0.000	0.001
Colpodellida	23.103	1.799	0.458	3.930	0.000	0.000
Colponemida	0.276	-0.061	2.072	-0.029	0.977	1.000
Cryptophyceae	2.658	0.251	0.805	0.312	0.755	0.932
Cyanidiales	6.985	1.733	0.541	3.202	0.001	0.003
Dinoflagellata	1718.508	2.004	0.370	5.420	0.000	0.000
Echinamoebida	42.423	-5.601	0.820	-6.828	0.000	0.000
Elardia	7.976	-1.738	0.544	-3.194	0.001	0.003
Endomyxa	105.126	0.240	0.327	0.733	0.463	0.686
Euglenozoa	0.670	-3.186	1.141	-2.793	0.005	0.011
Eurhodophytina	0.125	-1.840	2.912	-0.632	0.527	0.723
Flabellinia	38.658	-0.877	0.539	-1.626	0.104	0.194
Fornicata	0.227	-2.442	2.556	-0.956	0.339	0.523
Fungi	3141.736	-1.165	0.338	-3.448	0.001	0.002
Gyrista	5675.728	-0.872	0.339	-2.573	0.010	0.021
Haptophyta	7.103	2.581	0.796	3.243	0.001	0.003
Heterolobosea	707.388	-4.135	0.549	-7.526	0.000	0.000
Ichthyosporea	0.106	-0.824	2.466	-0.334	0.738	0.932
Jakobida	0.187	-0.255	2.086	-0.122	0.903	0.997
Perkinsidae	0.624	0.100	0.850	0.118	0.906	0.997
Preaxostyla	1.331	-1.262	0.779	-1.621	0.105	0.194
Retaria	8.800	-2.232	0.638	-3.497	0.000	0.001
Rigifilida	1934.533	-3.696	0.634	-5.832	0.000	0.000
Rotosphaerida	0.428	1.526	1.424	1.071	0.284	0.457
Streptophyta	10.234	0.359	0.565	0.634	0.526	0.723
Stygamoebida	0.157	0.173	1.643	0.105	0.916	0.997
Tsukubamonadida	0.392	-0.349	1.206	-0.289	0.772	0.932
Variosea	1402.686	-2.252	0.455	-4.950	0.000	0.000
Undetermined (NA)	501.501	-2.292	0.361	-6.345	0.000	0.000

Table S2. Detailed results of the DESeq2 analysis conducted on data aggregated at the 2nd taxonomy rank of Adl et al. (2019). For each taxa, column *baseMean* indicates the average of the normalized count values, dividing by size factors, *lfcSE* is the standard error of the *log2FoldChange*, column *stat* is the Wald statistic, *pvalue* is the raw p-value and *padj* is the p-value corrected with the Benjamini & Hochberg method.

Taxa	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj
Consumers	28997.670	-3.194	0.284	-11.232	0.000	0.000
Mixotrophs	1633.332	1.413	0.332	4.259	0.000	0.000
Parasites	1335.536	-0.929	0.218	-4.268	0.000	0.000
Photosynthetics	3342.250	0.656	0.281	2.335	0.020	0.023
Saprotrophs	943.798	-0.956	0.338	-2.827	0.005	0.007
Undetermined (NA)	1706.654	0.278	0.222	1.251	0.211	0.211

Table S3. Detailed results of the DESeq2 analysis conducted on data aggregated by trophic groups. For each group, column *baseMean* indicates the average of the normalized count values, dividing by size factors, *lfcSE* is the standard error of the *log2FoldChange*, column *stat* is the Wald statistic, *pvalue* is the raw p-value and *padj* is the p-value corrected with the Benjamini & Hochberg method.

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Dataset S1 (separate file).Type or paste legend here.

References

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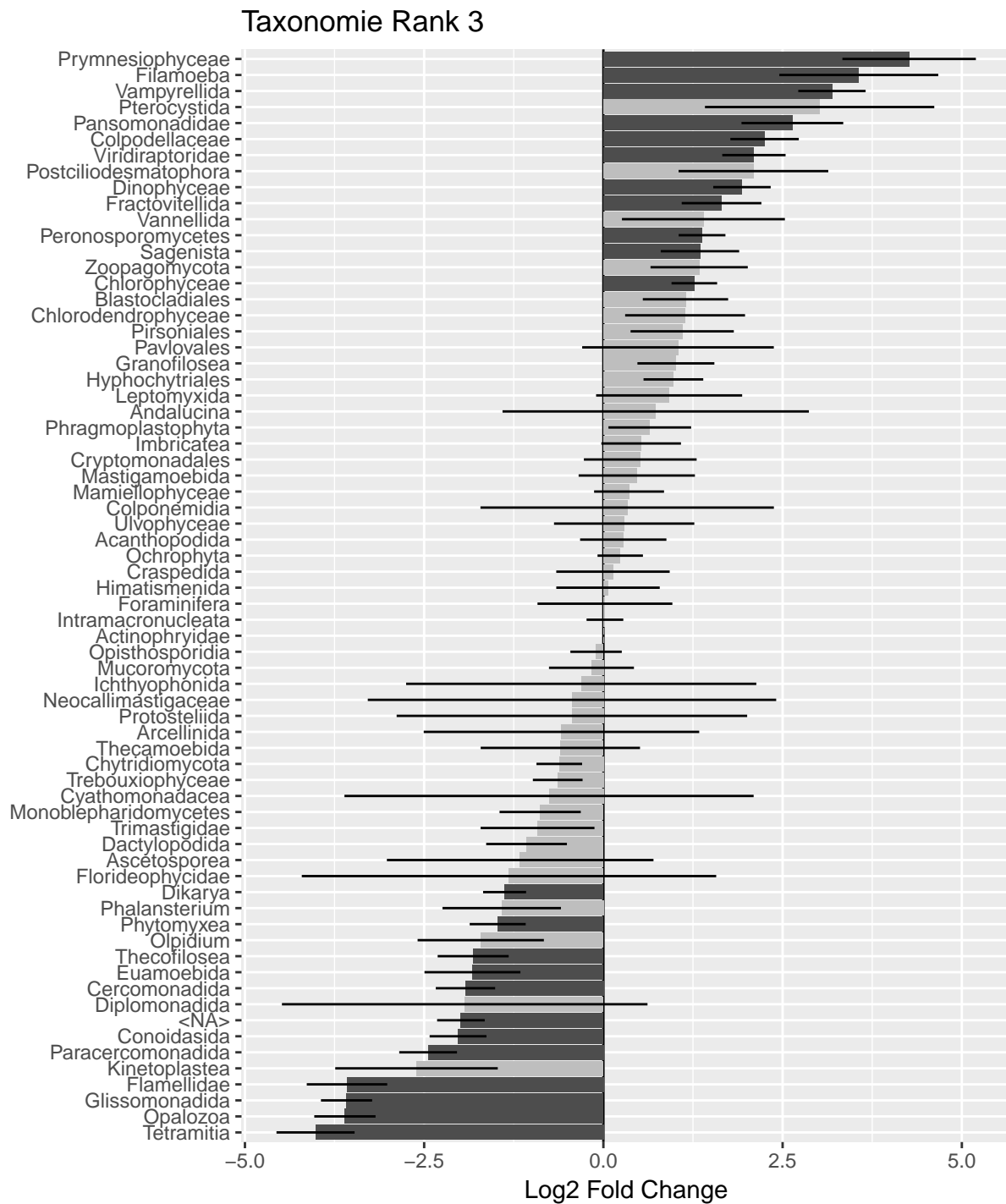
Taxonomie Rank 3

Figure S9. Results of the DESeq2 analysis conducted on data aggregated at the third taxonomy rank of Adl et al. (2019).

Taxa	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj
Acanthopodida	6.539	0.277	0.602	0.460	0.645	0.832
Actinophryidae	0.000	0.000	0.000	0.000	1.000	1.000
Andalucina	0.315	0.730	2.137	0.342	0.733	0.911
Arcellinida	0.162	-0.585	1.921	-0.304	0.761	0.911
Ascetosporea	0.099	-1.161	1.859	-0.624	0.533	0.739
Blastocladiales	7.037	1.145	0.595	1.924	0.054	0.123
Cercomonadida	1099.959	-1.924	0.414	-4.647	0.000	0.000
Chlorodendrophyceae	4.602	1.140	0.836	1.363	0.173	0.309
Chlorophyceae	805.990	1.269	0.318	3.989	0.000	0.000
Chytridiomycota	953.254	-0.615	0.318	-1.933	0.053	0.123
Colpodellaceae	29.790	2.248	0.477	4.710	0.000	0.000
Colponemidia	0.278	0.332	2.046	0.162	0.871	0.947
Conoidasida	154.767	-2.027	0.396	-5.115	0.000	0.000
Craspedida	3.682	0.134	0.791	0.169	0.866	0.947
Cryptomonadales	1.846	0.514	0.786	0.654	0.513	0.727
Cyathomonadacea	0.180	-0.758	2.854	-0.266	0.791	0.911
Dactylopodida	42.577	-1.072	0.563	-1.903	0.057	0.123
Dikarya	133.764	-1.378	0.300	-4.592	0.000	0.000
Dinophyceae	2143.456	1.933	0.401	4.823	0.000	0.000
Diplomonadida	0.228	-1.934	2.550	-0.759	0.448	0.670
Euamoebida	8.566	-1.826	0.669	-2.730	0.006	0.020
Filamoeba	1.793	3.563	1.108	3.214	0.001	0.004
Flamellidae	1129.135	-3.576	0.561	-6.372	0.000	0.000
Florideophycidae	0.151	-1.317	2.891	-0.456	0.649	0.832
Foraminifera	0.380	0.022	0.941	0.023	0.982	0.996
Fractovitellida	208.734	1.648	0.556	2.966	0.003	0.010
Glissomonadida	3060.955	-3.583	0.357	-10.043	0.000	0.000
Granofilosea	92.481	1.011	0.537	1.885	0.059	0.123
Himatismenida	7.738	0.065	0.721	0.089	0.929	0.962
Hyphochytriales	2.624	0.977	0.417	2.344	0.019	0.054
Ichthyophonida	0.073	-0.309	2.442	-0.127	0.899	0.955
Imbricatea	70.927	0.527	0.555	0.948	0.343	0.556
Intramacronucleata	1588.647	0.021	0.256	0.084	0.933	0.962
Kinetoplastea	0.578	-2.607	1.133	-2.300	0.021	0.058
Leptomyxida	0.610	0.917	1.019	0.900	0.368	0.582
Mamiellophyceae	3.677	0.358	0.488	0.734	0.463	0.670
Mastigamoebida	4.899	0.466	0.811	0.574	0.566	0.770
Monoblepharidomycetes	2.755	-0.882	0.567	-1.557	0.120	0.226
Mucoromycota	198.441	-0.166	0.593	-0.281	0.779	0.911
Neocallimastigaceae	0.057	-0.438	2.849	-0.154	0.878	0.947
Ochrophyta	4430.828	0.235	0.317	0.742	0.458	0.670
Olpidium	0.487	-1.711	0.881	-1.942	0.052	0.123
Opalozoa	447.040	-3.605	0.427	-8.439	0.000	0.000
Opisthosporidia	110.830	-0.102	0.358	-0.285	0.776	0.911
Pansomonadidae	22.510	2.636	0.710	3.715	0.000	0.001
Paracercomonadida	321.360	-2.445	0.403	-6.070	0.000	0.000
Pavlovales	0.614	1.041	1.336	0.779	0.436	0.670
Peronosporomycetes	59.741	1.376	0.326	4.220	0.000	0.000
Phalansterium	0.602	-1.418	0.826	-1.716	0.086	0.167
Phragmoplastophyta	6.295	0.648	0.576	1.123	0.261	0.433
Phytomyxea	58.355	-1.474	0.391	-3.773	0.000	0.001
Pirsoniales	28.656	1.099	0.720	1.527	0.127	0.233

Taxa	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj
Postciliodesmatophora	1.154	2.093	1.044	2.004	0.045	0.118
Protosteliida	0.127	-0.439	2.445	-0.180	0.857	0.947
Prymnesiophyceae	4.581	4.265	0.931	4.581	0.000	0.000
Pterocystida	1.217	3.016	1.599	1.886	0.059	0.123
Sagenista	12.384	1.347	0.547	2.462	0.014	0.041
Tetramitia	651.639	-4.015	0.545	-7.372	0.000	0.000
Thecamoebida	0.536	-0.600	1.111	-0.540	0.589	0.785
Thecofilosea	3239.036	-1.816	0.495	-3.666	0.000	0.001
Trebouxiophyceae	47.430	-0.637	0.347	-1.838	0.066	0.132
Trimastigidae	1.414	-0.919	0.794	-1.157	0.247	0.421
Ulvophyceae	0.238	0.290	0.979	0.296	0.767	0.911
Vampyrellida	82.987	3.188	0.470	6.788	0.000	0.000
Vannellida	1.053	1.395	1.137	1.228	0.219	0.383
Viridiraptoridae	22.839	2.100	0.442	4.755	0.000	0.000
Zoopagomycota	24.499	1.336	0.678	1.969	0.049	0.123
Undetermined (NA)	3776.683	-1.987	0.332	-5.981	0.000	0.000

Table S5. Detailed results of the DESeq2 analysis conducted on data aggregated at the 3rd taxonomy rank of Adl et al. (2019). For each taxa, column *baseMean* indicates the average of the normalized count values, dividing by size factors, *lfcSE* is the standard error of the *log2FoldChange*, column *stat* is the Wald statistic, *pvalue* is the raw p-value and *padj* is the p-value corrected with the Benjamini & Hochberg method.