

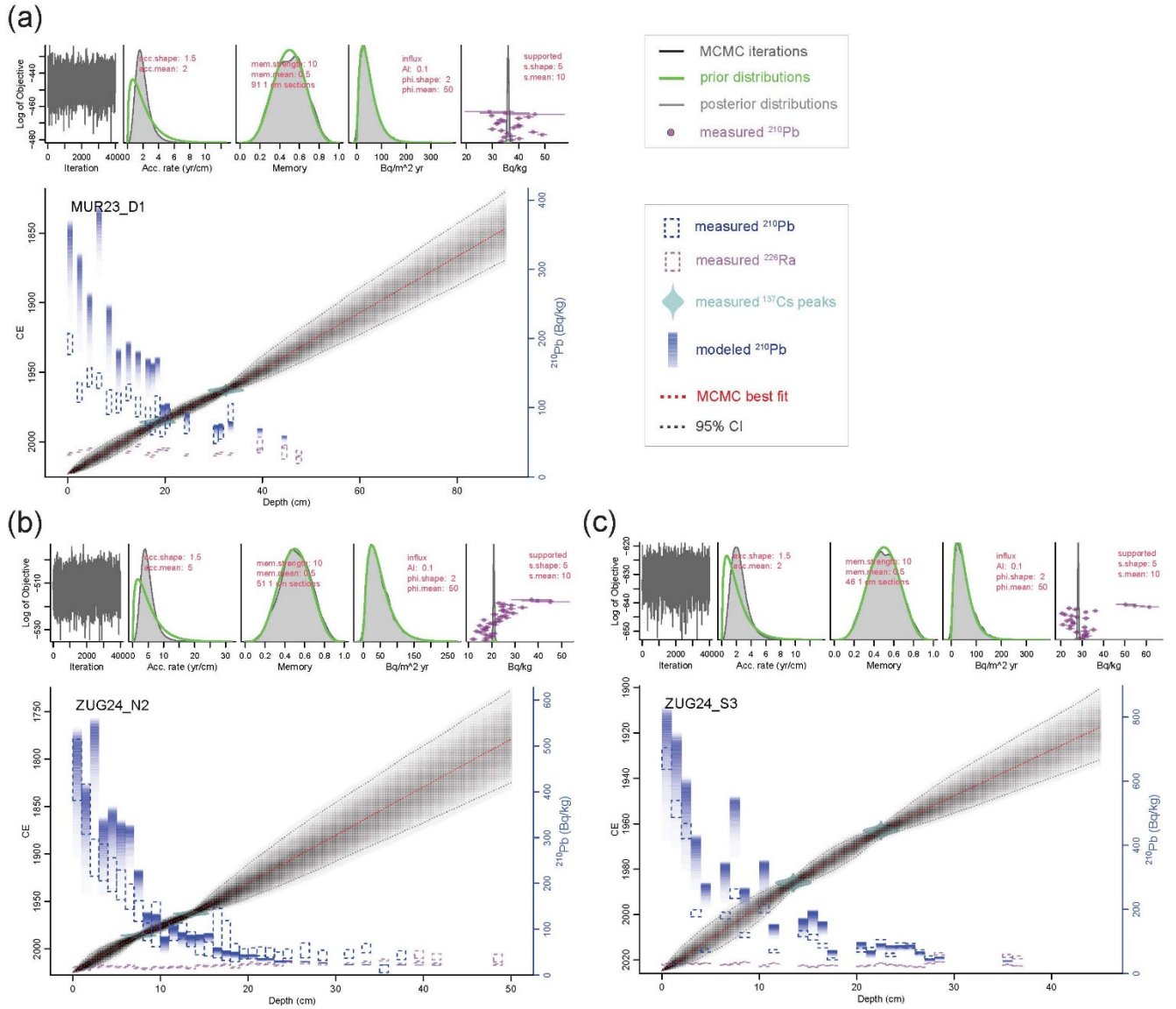


Figure S3: Age-depth model of the short cores from Murtensee (MUR23_D1) (a), the northern basin (ZUG24_N2) (b) and the southern basin (ZUG24_S3) (c) of Zugersee. The age-depth model was generated with the ‘rplum’ package (version 1.0.0; Aquino-López et al., 2018) in R. The upper panel indicates the rplum parameters, i.e., Markov Chain Monte Carlo (MCMC) random walk model iterations, prior and posterior distributions of sediment accumulation rates, memory, influx of unsupported ^{210}Pb , and supported ^{210}Pb . The lower panel illustrates the best fit estimate from MCMC iterations with 95% confidence intervals (CI) plotted with ^{210}Pb and ^{226}Ra measurements, ^{137}Cs peaks, and modeled ^{210}Pb values.

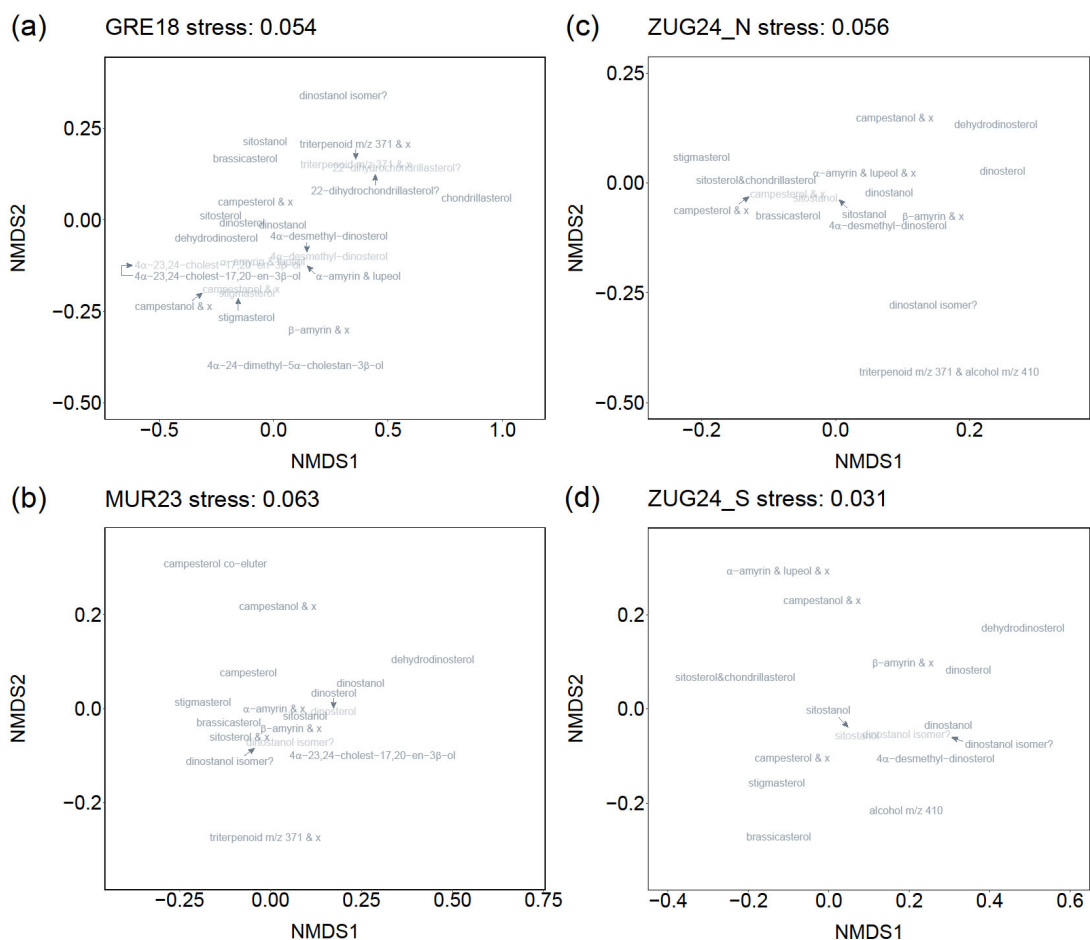


Figure S4: Non-metric-multidimensional scaling (NMDS) of relative concentrations of phytosterols and terrestrial triterpenoids in Greifensee (GRE18) (a), Murtensee (MUR23) (b), and the northern basin (ZUG24_N) (c) and the southern basin (ZUG24_S) (d) of Zugersee. Only the first and second dimensions are shown. For better visualization, the exact position of some compounds is indicated by arrows and/or the respective compound name. The term ‘& x’ refers to co-elution of specific alcohols with an unknown compound. ‘m/z’ refers to peaks in the mass to charge ratio of unknown compounds.

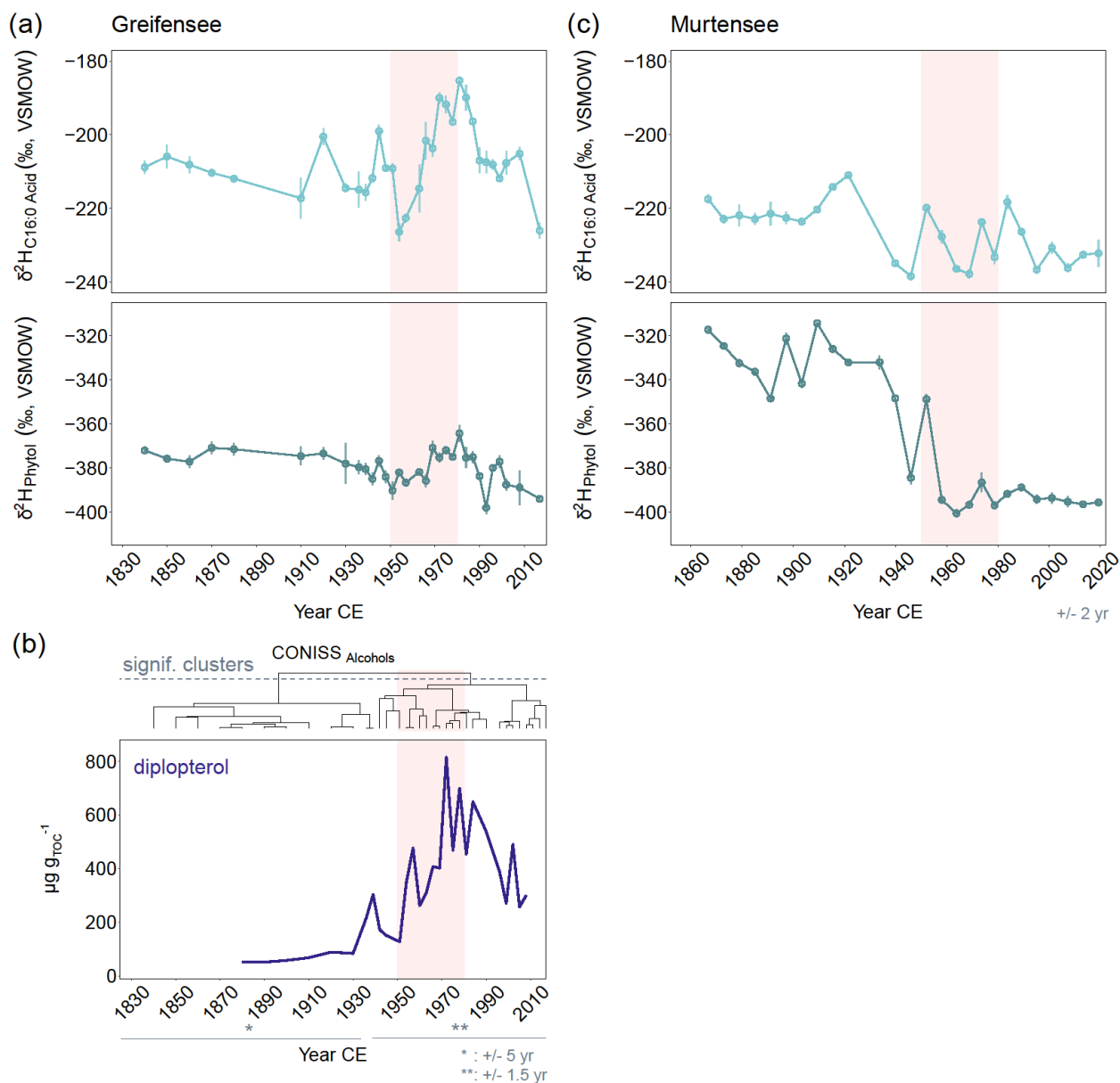


Figure S5: Time series of $\delta^2\text{H}_{\text{C16:0 Acid}}$ and $\delta^2\text{H}_{\text{Phytol}}$ values (a) and diplopterol concentrations (b) in Greifensee and $\delta^2\text{H}_{\text{C16:0 Acid}}$ and $\delta^2\text{H}_{\text{Phytol}}$ values in Murtensee (c). Diplopterol concentrations in (b) are plotted along a CONISS cluster dendrogram of relative alcohol distributions. Red background shading indicates the period of maximum eutrophication (~ 1950 to 1980 CE). VSMOW: Vienna Standard Mean Ocean Water.

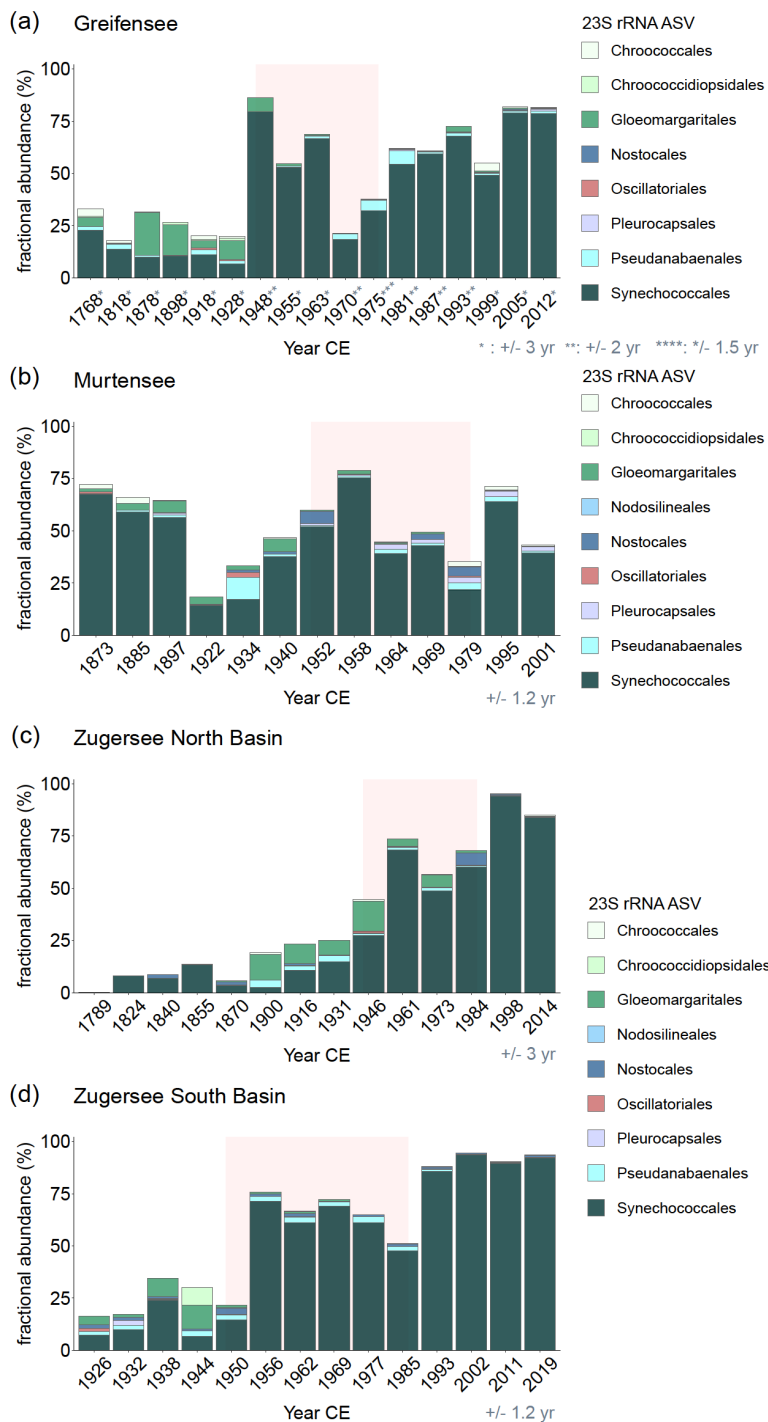
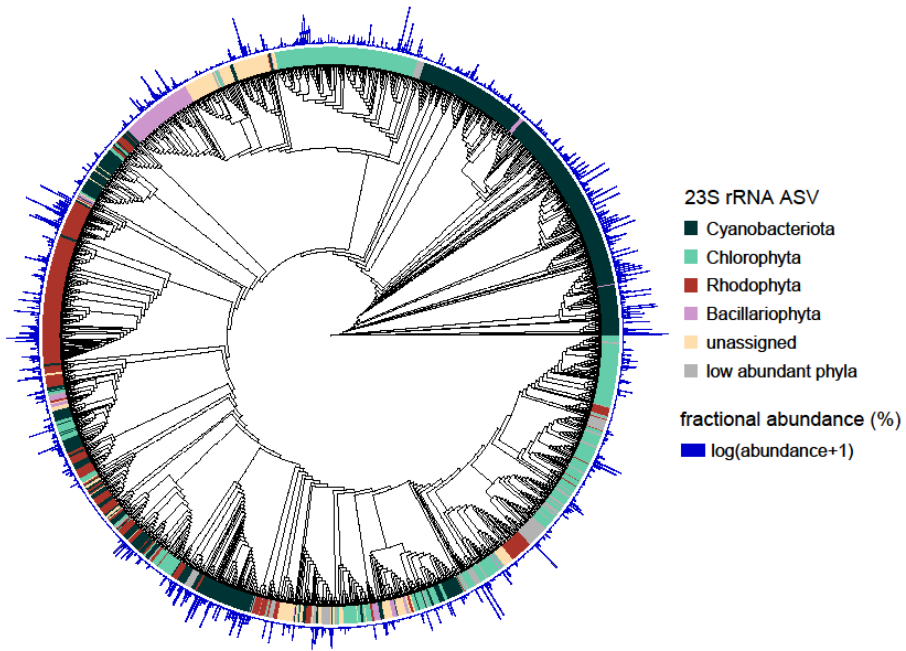


Figure S6: Relative abundance of cyanobacterial 23S rRNA amplicon sequence variants (ASVs) in Greifensee (a), Murtensee (b) and the northern basin (c) and southern basin (d) of Zugersee plotted on the taxonomic order level. In the north basin of Zugersee (c), Spirulinales were detected but not included due to their low abundance (0.013 %). Red background shading indicates the period of maximum eutrophication (~1950 to 1980 CE).



40 **Figure S7: Phylogenetic tree from cyanobacterial and plastid 23S rRNA amplicon sequence variants (ASV) based on their relative abundance in Greifensee, Murtensee, Zugersee and Lac Neuchâtel. Taxonomic assignments occurred based on the National Center for Biotechnology Information (NCBI) reference database and the tree was generated with the ‘ggtree’ package (Yu et al., 2017; Yu et al., 2018; Yu, 2020; Xu et al., 2022), the ‘ggtreeExtra’ package (Xu et al., 2021) and the ‘treeio’ package (Wang et al., 2020) in R.**

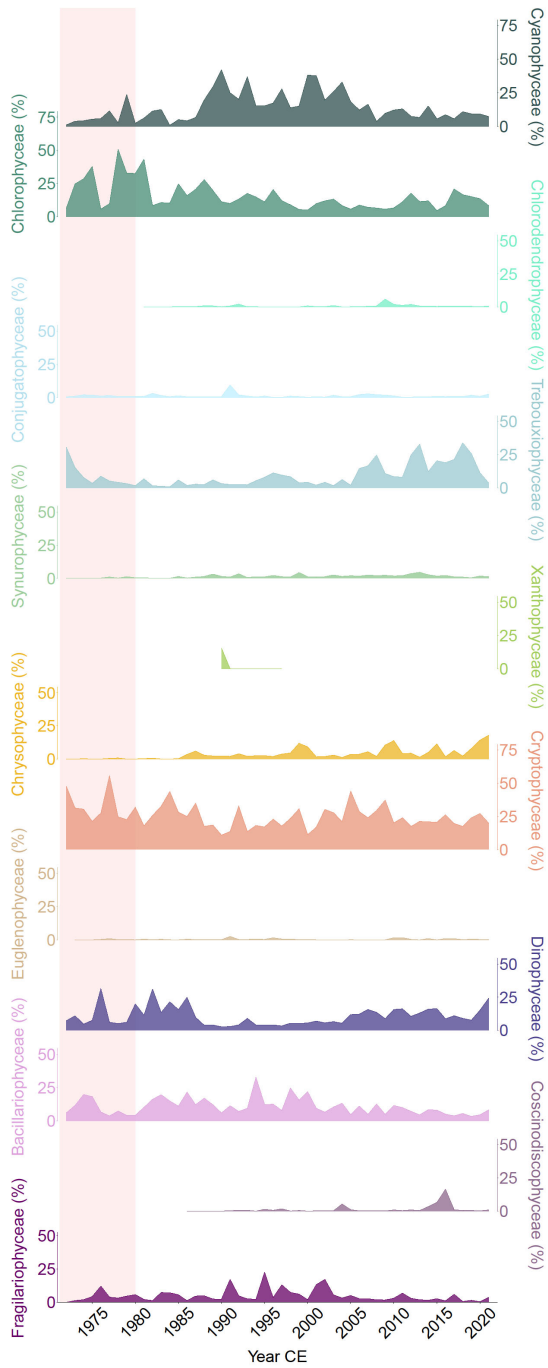


Figure S8: Time series of the relative biovolume of phytoplankton classes ($\mu\text{m}^3\text{L}^{-1}$) in Greifensee derived from mean annual cell counts in the water column from Bürgi et al. (2003) and Merz et al. (2023). Algal classes comprising less than 10 % of the biovolume in all samples are not shown. Red background shading indicates the period of maximum eutrophication (~ 1950 to 1980 CE).

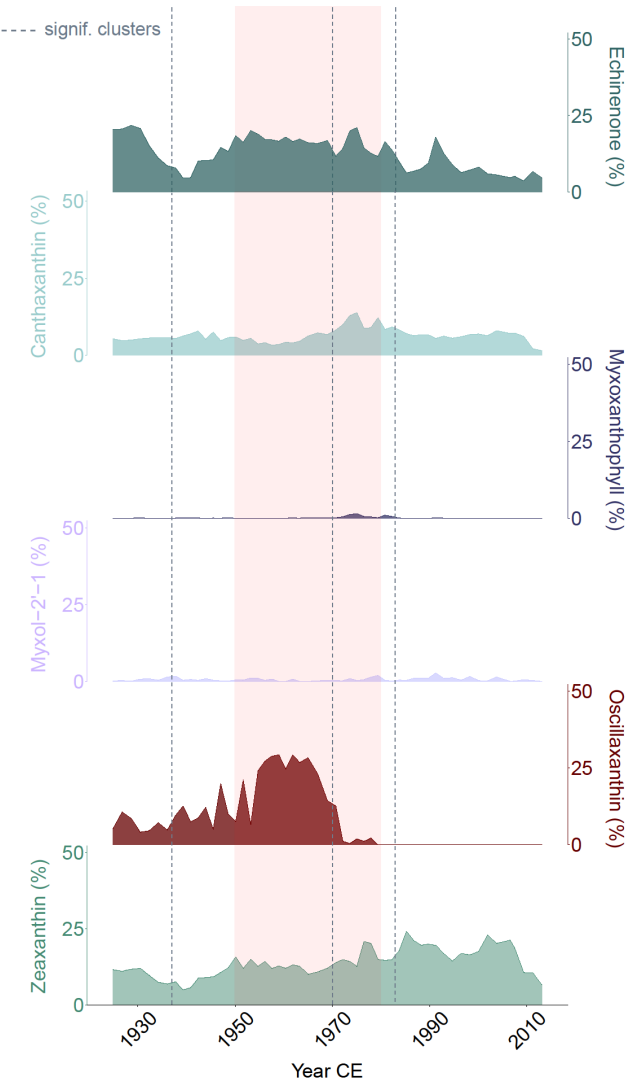


Figure S9: Time series of cyanobacterial xanthophylls (% of total algal xanthophylls) in Murtensee from Makri et al. (2019). Dashed lines indicate significant changes in CONISS clusters of sedimentary pigment distributions described by Makri et al. (2019). Red background shading indicates the period of maximum eutrophication (~ 1950 to 1980 CE).

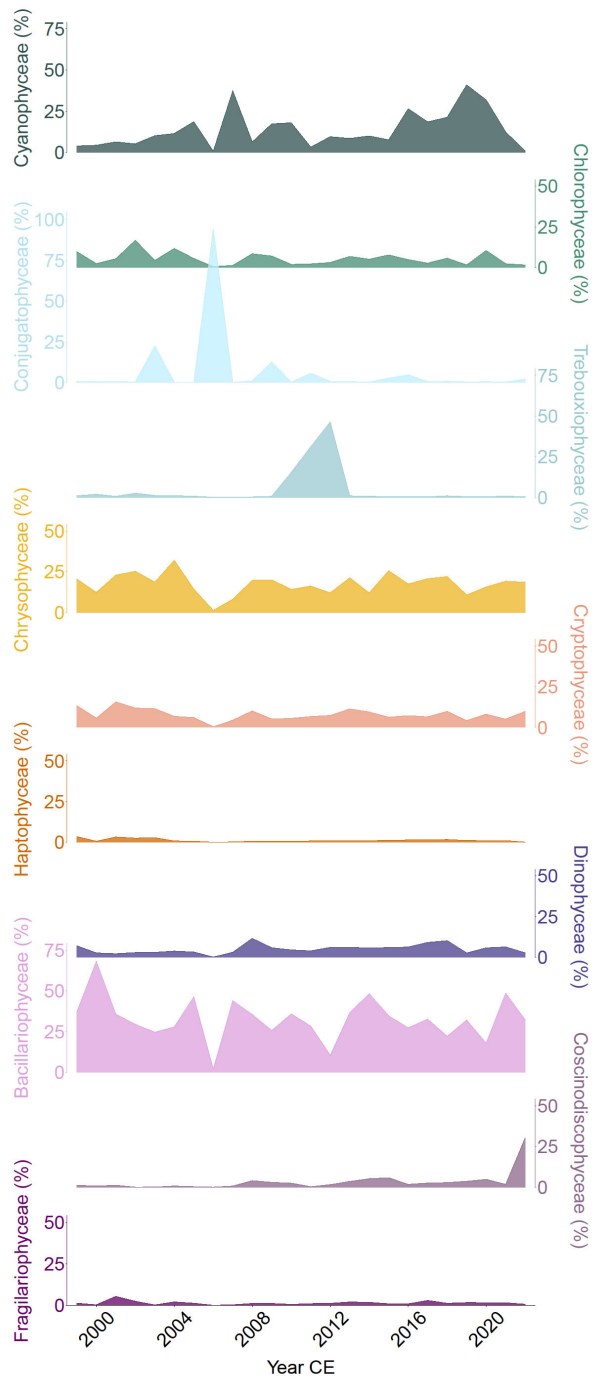


Figure S10: Time series of the relative biovolume of phytoplankton classes ($\mu\text{m}^3\text{L}^{-1}$) in Murtensee derived from mean annual cell counts in the water column from Merz et al. (2023). Algal classes comprising less than 10 % of the biovolume in all samples are not shown.

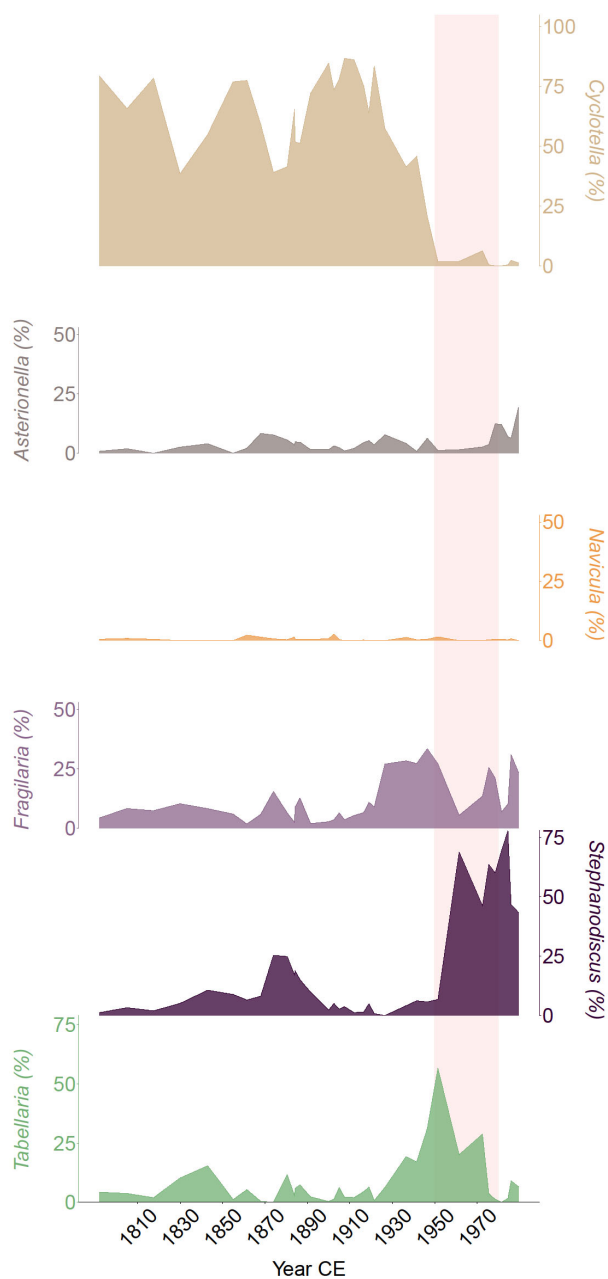


Figure S11: Time series of reconstructed diatom communities in the southern basin of Zugersee from AquaPlus (2001). The relative abundance of silica frustules from single diatom genera in the sediment record are plotted as trophic indicators. *Cyclotella* is interpreted as oligotrophic indicator, while *Stephanodiscus* and *Tabellaria* comprise rather eutrophic species (AquaPlus, 2001). Red background shading indicates the period of maximum eutrophication (~ 1950 to 1980 CE).

Table S1: Forward primers used in the first PCR for cyanobacterial and plastid 23S rRNA ASV library preparation. Primers were modified as phased amplicon primers with up to eight nucleotides attached to the beginning of the original primer sequence (Sherwood and Presting, 2007).

name	PCR1 forward primer	forward overhang
p23SrV_f1	TCGTCGGCAGCGTCAGATGTGTATAA GAGACAGGGACAGAAAGACCCTATG A*A	TCGTCGGCAGCGTCAGATGTGTATA AGAGACAG
p23SrV_f2	TCGTCGGCAGCGTCAGATGTGTATAA GAGACAGTGGACAGAAAGACCCTATG A*A	TCGTCGGCAGCGTCAGATGTGTATA AGAGACAG
p23SrV_f3	TCGTCGGCAGCGTCAGATGTGTATAA GAGACAGCTGGACAGAAAGACCCTAT GA*A	TCGTCGGCAGCGTCAGATGTGTATA AGAGACAG
p23SrV_f4	TCGTCGGCAGCGTCAGATGTGTATAA GAGACAGTCTGGACAGAAAGACCCTA TGA*A	TCGTCGGCAGCGTCAGATGTGTATA AGAGACAG
p23SrV_f5	TCGTCGGCAGCGTCAGATGTGTATAA GAGACAGATCTGGACAGAAAGACCCT ATGA*A	TCGTCGGCAGCGTCAGATGTGTATA AGAGACAG
p23SrV_f6	TCGTCGGCAGCGTCAGATGTGTATAA GAGACAGCATCTGGACAGAAAGACCC TATGA*A	TCGTCGGCAGCGTCAGATGTGTATA AGAGACAG
p23SrV_f7	TCGTCGGCAGCGTCAGATGTGTATAA GAGACAGACATCTGGACAGAAAGACC CTATGA*A	TCGTCGGCAGCGTCAGATGTGTATA AGAGACAG
p23SrV_f8	TCGTCGGCAGCGTCAGATGTGTATAA GAGACAGGACATCTGGACAGAAAGA CCCTATGA*A	TCGTCGGCAGCGTCAGATGTGTATA AGAGACAG

Table S2: Reverse primers used in the first PCR for cyanobacterial and plastid 23S rRNA ASV library preparation. Primers were modified as phased amplicon primers with up to eight nucleotides attached to the beginning of the original primer sequence (Sherwood and Presting, 2007).

name	PCR1 reverse primer	reverse overhang
p23SrV_r1	GTCTCGTGGGCTCGGAGATGTGTATA AGAGACAGTCAGCCTGTTATCCCTAG A*G	GTCTCGTGGGCTCGGAGATGTGTAT AAGAGACAG
p23SrV_r2	GTCTCGTGGGCTCGGAGATGTGTATA AGAGACAGGTCAGCCTGTTATCCCTA GA*G	GTCTCGTGGGCTCGGAGATGTGTAT AAGAGACAG
p23SrV_r3	GTCTCGTGGGCTCGGAGATGTGTATA AGAGACAGAGTCAGCCTGTTATCCCT AGA*G	GTCTCGTGGGCTCGGAGATGTGTAT AAGAGACAG
p23SrV_r4	GTCTCGTGGGCTCGGAGATGTGTATA AGAGACAGTAGTCAGCCTGTTATCCC TAGA*G	GTCTCGTGGGCTCGGAGATGTGTAT AAGAGACAG
p23SrV_r5	GTCTCGTGGGCTCGGAGATGTGTATA AGAGACAGCTAGTCAGCCTGTTATCC CTAGA*G	GTCTCGTGGGCTCGGAGATGTGTAT AAGAGACAG
p23SrV_r6	GTCTCGTGGGCTCGGAGATGTGTATA AGAGACAGGCTAGTCAGCCTGTTATC CCTAGA*G	GTCTCGTGGGCTCGGAGATGTGTAT AAGAGACAG
p23SrV_r7	GTCTCGTGGGCTCGGAGATGTGTATA AGAGACAGAGCTAGTCAGCCTGTTAT CCCTAGA*G	GTCTCGTGGGCTCGGAGATGTGTAT AAGAGACAG
p23SrV_r8	GTCTCGTGGGCTCGGAGATGTGTATA AGAGACAGCAGCTAGTCAGCCTGTT ATCCCTAGA*G	GTCTCGTGGGCTCGGAGATGTGTAT AAGAGACAG

85 **Table S3: Mass spectra of alcohol TMS-derivatives. Reported retention times (RT) are on a Rxi-5ms column (60 m x 25 mm x 25 μ m) (Restek) (method details in main text). MW: Molecular Weight. TMS: Trimethylsilyl.**

RT (min)	Chemical structure	IUPAC name	Trivial name	MW TMS	Other M+ ions
58.79	C ₂₇ H ₄₆ O	cholest-5-en-3 β -ol	cholesterol	458	73, 129, 213, 329, 368
59.07	C ₂₇ H ₄₈ O	5 α -cholestan-3 β -ol	cholestanol	460	75, 107, 215, 355, 445
59.95	C ₂₈ H ₄₆ O	24-methylcholesta-5,22-dien-3 β -ol	brassicasterol	470	69, 129, 255, 380
61.68	C ₂₈ H ₄₈ O	ergost-5-en-3-ol, (3 β ,24R)	campesterol	472	73, 129, 343, 382
62.11	C ₂₈ H ₅₀ O	5 α -campestan-3 β -ol	campestanol	474	75, 215, 289, 369, 459
62.74	C ₂₉ H ₄₈ O	(22E,24S)-24-ethylcholesta-5,22-dien-3 β -ol	stigmasterol	484	83, 129, 213, 255, 351, 394
62.92	C ₂₉ H ₅₀ O	23,24-dimethyl-5 α -cholest-22E-en-3 β -ol	4 α -desmethyl-dinosterol	486	69, 83, 257, 345, 374
63.37			alcohol m/z 486	486	73, 117, 135, 147, 281
63.68	C ₂₈ H ₄₈ O	5- α -ergost-7-en-3- β -ol	fungisterol	472	75, 213, 255, 367
64.68	C ₂₉ H ₅₀ O	24-ethylcholest-5-en-3 β -ol	sitosterol	486	43, 73, 129, 255, 357, 381, 396, 471
64.68	C ₂₉ H ₄₈ O	24 β -ethylcholesta-7,22-dien-3 β -ol	chondrillasterol	484	75, 147, 213, 255, 343
65.11	C ₂₉ H ₅₂ O	5 α -stigmastan-3 β -ol	sitostanol	488	75, 215, 383, 398, 473
65.27	C ₂₉ H ₅₀ O	4 α -24-dimethyl-5 α -cholestan-3 β -ol	4 α -24-dimethyl-5 α -cholestan-3 β -ol	486	75, 229, 359, 398, 473
65.46	C ₃₀ H ₅₀ O	olean-12-en-3 β -ol	β -amyrin	498	73, 190, 203, 218
65.97	C ₃₀ H ₄₈ O	4 α -23,24-trimethyl-5 α -cholest-5,22-E-dien-3 β -ol	dehydrodinosterol	498	69, 139, 269, 368
66.20	C ₃₀ H ₅₂ O	4 α -23,24-trimethyl-5 α -cholest-22-E-dien-3 β -ol	dinosterol	500	69, 139, 271, 359, 388

RT (min)	Chemical structure	IUPAC name	Trivial name	MW TMS	Other M+ ions
66.80	C ₃₀ H ₅₀ O	5 α -urs-12-en-3 β -ol	α -amyrin	498	73, 118, 189, 203, 207, 218
66.86	C ₂₇ H ₄₄ O	5 α -stigmast-7-en-3 β ol, (24S)	22-dihydrochondrilla sterol	486	75, 107, 145, 213, 255, 381
67.04	C ₃₀ H ₅₀ O	(3 β)-lup-20(29)-en-3-ol	lupeol	498	73, 95, 135, 189, 281
67.74	C ₂₇ H ₄₆ O	4 α -23-24-cholest-17(20)-en-3 β -ol	4 α -23-24-cholest-17(20)-en-3 β -ol	500	75, 95, 297, 359, 387
68.00			unknown triterpenoid m/z 371	486	75, 95, 189, 281, 371
68.78	C ₃₀ H ₅₄ O	4 α ,23,24-trimethyl-5 α -cholestan-3 β -ol	dinostanol	502	75, 95, 229, 373, 412, 487
70.71			sterol m/z 75 255 388 500	500	75, 255, 388, 500
71.89	C ₃₀ H ₅₀ O	(3 β)-lanosta-8,24-dien-3-ol	lanosterol?	498	73, 129, 145, 255, 393, 483
74.59	C ₃₀ H ₅₂ O	gammaceran-3 β -ol	tetrahymanol	485	69, 81, 95, 109, 123, 191, 395
75.39	C ₃₀ H ₅₂ O	hopan-22-ol	diplopterol	485	73, 131, 189, 395

References

- AquaPlus: Entwicklung des Gesamtphosphors im Zugersee anhand der im Sediment eingelagerten Kieselalgen, Bericht zuhanden des Amtes für Umweltschutz des Kantons Zug, 2001.
- Aquino-López, M. A., Blaauw, M., Christen, J. A., and Sanderson, N. K.: Bayesian Analysis of 210 Pb Dating, *J. Agric. Biol. Environ. Stat.*, 23, 317–333, <https://doi.org/10.1007/s13253-018-0328-7>, 2018.
- Bürgi, H. R., Bührer, H., and Keller, B.: Long-term changes in functional properties and biodiversity of plankton in Lake Greifensee (Switzerland) in response to phosphorus reduction, *Aquat. Ecosyst. Health and Manag.*, 6, 147–158, 2003.
- Makri, S., Lami, A., Lods-Crozet, B., and Loizeau, J. L.: Reconstruction of trophic state shifts over the past 90 years in a eutrophicated lake in western Switzerland, inferred from the sedimentary record of photosynthetic pigments, *J. Paleolimnol.*, 61, 129–145, <https://doi.org/10.1007/s10933-018-0049-5>, 2019.
- Merz, E., Saberski, E., Gilarranz, L. J., Isles, P. D. F., Sugihara, G., Berger, C., and Pomati, F.: Disruption of ecological networks in lakes by climate change and nutrient fluctuations, *Nat. Clim. Chang.*, 13, 389–396, <https://doi.org/10.1038/s41558-023-01615-6>, 2023.
- Sherwood, A. R. and Presting, G. G.: Universal primers amplify a 23S rDNA plastid marker in eukaryotic algae and cyanobacteria, *J. Phycol.*, 43, 605–608, <https://doi.org/10.1111/j.1529-8817.2007.00341.x>, 2007.
- Wang, L. G., Lam, T. T. Y., Xu, S., Dai, Z., Zhou, L., Feng, T., Guo, P., Dunn, C. W., Jones, B. R., Bradley, T., Zhu, H., Guan, Y., Jiang, Y., and Yu, G.: Treeio: An R Package for Phylogenetic Tree Input and Output with Richly Annotated and Associated Data, *Mol. Biol. Evol.*, 37, 599–603, <https://doi.org/10.1093/molbev/msz240>, 2020.
- Xu, S., Dai, Z., Guo, P., Fu, X., Liu, S., Zhou, L., Tang, W., Feng, T., Chen, M., Zhan, L., Wu, T., Hu, E., Jiang, Y., Bo, X., and Yu, G.: GgtreeExtra: Compact Visualization of Richly Annotated Phylogenetic Data, *Mol Biol Evol*, 38, 4039–4042, <https://doi.org/10.1093/molbev/msab166>, 2021.
- Xu, S., Li, L., Luo, X., Chen, M., Tang, W., Zhan, L., Dai, Z., Lam, T., Guan, Y., Yu, G.: Ggtree: A serialized data object for visualization of a phylogenetic tree and annotation data, *iMeta*, 4, e56, 2022.
- Yu, G.: Using ggtree to visualize data on tree-like structures. *Current Protocols in Bioinformatics*, 69, e96, 2020.
- Yu, G., Smith, D. K., Zhu, H., Guan, Y., and Lam, T. T. Y.: ggtree: an r package for visualization and annotation of phylogenetic trees with their covariates and other associated data, *Methods Ecol. Evol.* 8(1), 28–36. <https://doi.org/10.1111/2041-210X.12628>, 2017.
- Yu, G., Lam, T. T., Zhu, H., Guan, Y.: Two methods for mapping and visualizing associated data on phylogeny using ggtree, *Mol. Biol. Evolut.* 35, 3041–3043, 2018.