Supplemental Information
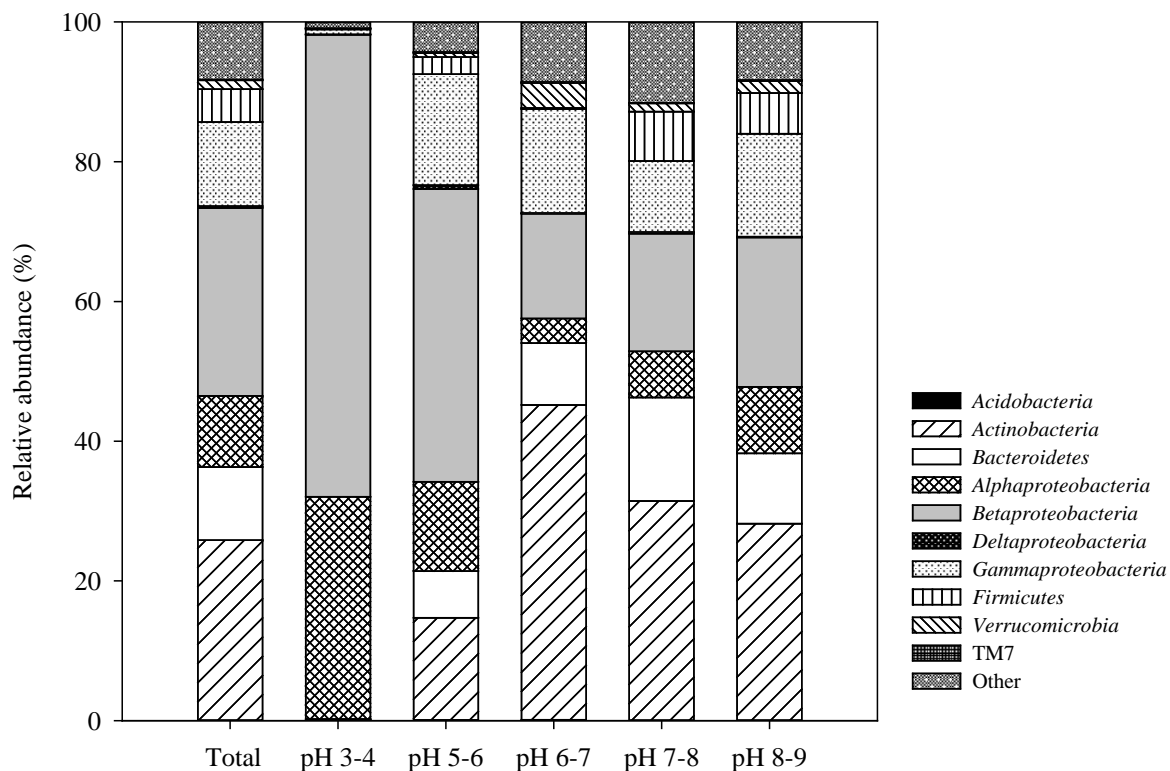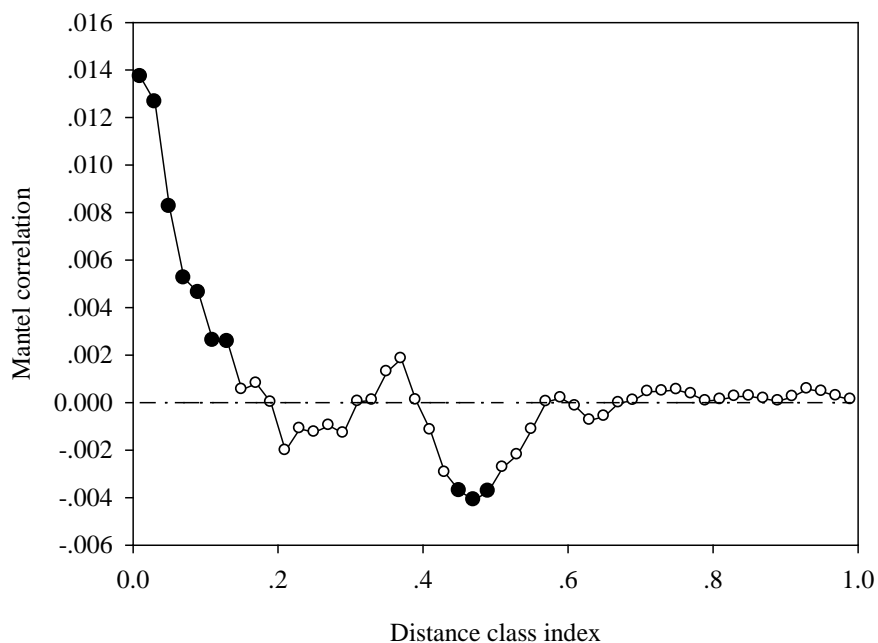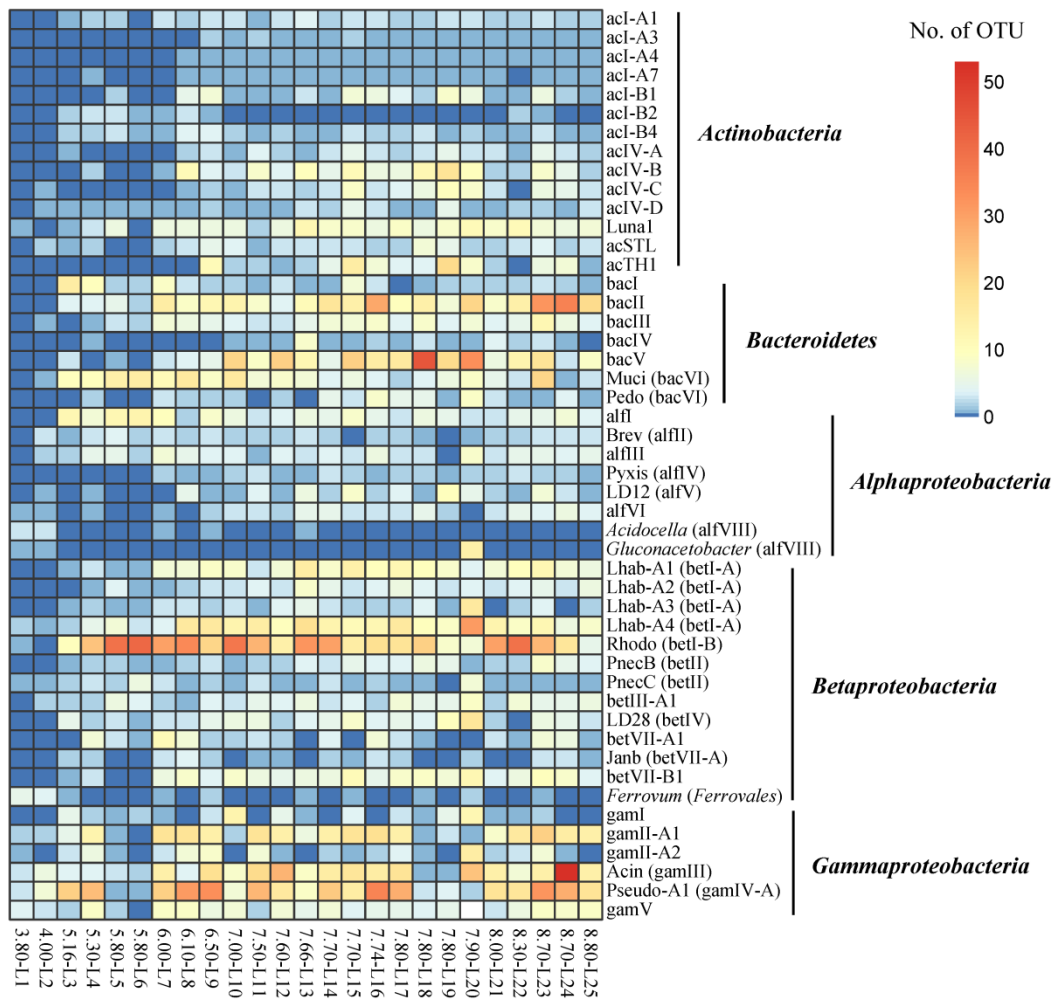

FIG S1 Relative abundances of the dominant bacterial taxa in all lakes combined (Total) and divided into different pH categories. The predominant phyla (subphyla) across all lakes were *Betaproteobacteria*, *Actinobacteria*, *Gammaproteobacteria*, *Bacteroidetes*, and *Alphaproteobacteria*.

FIG S2 Pearson's correlation resulting from the Mantel correlogram (9999 permutations) between the pairwise matrix of OTU niche distances and OTU phylogenetic distances. The phylogenetic signal in habitat associations was indicated by significant correlations ($P < 0.05$, filled circles). A significantly positive relationship between bacterioplankton ecological differences and phylogenetic distance was detected across relatively short phylogenetic distances.

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FIG S3 Heat map describing the number of OTUs within each main lineage or clade of

bacterioplankton communities (Y axis) across the pH gradient (X axis). Overall

bacterioplankton communities tended to be more phylogenetically distant to each other in

more acidic lakes.

TABLE S1 Summary of the relevant site characteristics of the investigated lakes and of the pyrosequencing results.

No.	Lake name	Location	No. of sequences	Accession no.	pH	TOC (mg·L⁻¹)	TP (mg·L⁻¹)	TFe (mg·L⁻¹)	TN (mg·L⁻¹)	NOₓ⁻ (mg·L⁻¹)	Conductivity (µS·cm⁻¹)	Area (km²)
L1	No name 1	56.020°N,9.089°E	24561	SRS518504	3.80	0.50	0.01	0.55	0.62	0.43	317.00	0.01
L2	No name 2	56.018°N,9.087°E	23257	SRS518506	4.00	0.37	0.01	0.24	0.59	0.29	208.00	0.10
L3	Vejlbo Mose	56.154°N,9.554°E	22490	SRS517772	5.16	31.90	0.17	0.87	2.04	0.02	297.00	0.03
L4	Brude Sø	56.054°N,9.681°E	28200	SRS518415	5.30	8.81	0.21	0.25	1.14	0.01	65.00	0.02
L5	No name 3	56.035°N,9.094°E	29014	SRS518503	5.80	2.99	0.03	0.97	1.44	1.36	238.00	0.16
L6	Ræv Sø	56.025°N,9.444°E	29426	SRS518524	5.80	3.14	0.02	0.02	0.30	0.01	59.00	0.06
L7	No name 4	56.020°N,9.095°E	31825	SRS518505	6.00	7.48	0.02	0.33	0.31	0.01	154.00	0.03
L8	No name 5	56.041°N,9.074°E	21136	SRS518502	6.10	4.93	0.01	3.54	0.31	0.01	320.00	0.12
L9	Kalgård Sø	56.013°N,9.453°E	30692	SRS518507	6.50	4.79	0.01	0.02	0.32	0.02	60.00	0.09
L10	Tranevig Sø	56.146°N,9.517°E	28582	SRS518498	7.00	14.60	0.05	3.07	1.08	0.02	332.00	0.03
L11	Slåen Sø	56.123°N,9.618°E	19817	SRS518645	7.50	2.41	0.01	0.02	0.02	0.23	266.00	0.18
L12	Silkeborg Langsø	56.170°N,9.522°E	31271	SRS518500	7.60	5.35	0.08	3.23	1.05	0.15	208.00	0.43
L13	Søby Sø	56.048°N,9.070°E	27043	SRS518501	7.66	3.50	0.02	0.08	0.35	0.05	183.00	0.73
L14	Nedenskov Sø	56.011°N,9.679°E	28017	SRS518416	7.70	5.63	0.03	0.02	0.51	0.10	373.00	0.10
L15	Lyng Sø	56.159°N,9.545°E	27026	SRS518499	7.70	7.68	0.24	0.27	2.35	0.03	230.00	0.10
L16	Karl Sø	56.013°N,9.543°E	22793	SRS518420	7.74	6.56	0.01	0.01	1.40	0.23	351.00	0.07
L17	Blid Sø	56.048°N,9.665°E	19739	SRS518414	7.80	5.61	0.02	0.02	0.52	0.01	186.00	0.05
L18	Ørn Sø	56.155°N,9.521°E	20818	SRS518423	7.80	2.73	0.06	51.00	1.17	0.49	397.00	0.42
L19	Torup Sø	56.015°N,9.432°E	21222	SRS518508	7.80	4.75	0.06	0.02	1.00	0.20	203.00	0.18
L20	Kvind Sø	56.027°N,9.497°E	22192	SRS518421	7.90	5.47	0.12	0.45	2.58	0.81	308.00	0.17
L21	Almind Sø	56.154°N,9.539°E	26795	SRS518422	8.00	2.37	0.01	0.05	0.28	0.03	205.00	0.53
L22	Væng Sø	56.036°N,9.655°E	27593	SRS518079	8.30	4.01	0.09	0.21	0.75	0.00	274.00	0.15
L23	Hampen Sø	56.020°N,9.388°E	21224	SRS518569	8.70	5.17	0.03	0.08	0.41	0.00	99.00	0.76
L24	Ring Sø	55.965°N,9.596°E	19168	SRS518418	8.70	5.81	0.13	0.06	0.80	0.12	277.00	0.23
L25	Stigsholm Sø	55.977°N,9.490°E	34881	SRS518419	8.80	4.86	0.06	0.17	1.95	1.48	236.00	0.22

21 **TABLE S2** Relative weight of the predictor environmental variables to the relative abundances of the different phyla in multiple regression. The

22 relative weight was estimated by using a Heuristic method. The relative weight means the proportionate contribution each environmental variable

23 makes to R^2, considering both its unique contribution and its contribution when combined with other variables.

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Index	pH	TOC (mg·L⁻¹)	TP (mg·L⁻¹)	TFe (mg·L⁻¹)	TN (mg·L⁻¹)	NO_x^- (mg·L⁻¹)	Conductivity (μS·cm⁻¹)	Area (km²)
Alphaproteobacteria	57.25%	1.56%	2.07%	3.10%	3.84%	17.26%	9.53%	5.38%
Betaproteobacteria	76.22%	1.70%	5.81%	2.60%	3.39%	2.23%	0.74%	7.32%
Acidobacteria	66.41%	12.80%	1.32%	0.41%	1.93%	2.65%	4.15%	10.33%
Actinobacteria	65.83%	1.09%	2.24%	11.67%	6.25%	0.91%	5.38%	6.63%
Bacteroidetes	30.14%	2.72%	3.41%	9.66%	14.32%	17.08%	7.55%	15.10%
Gammaproteobacteria	19.08%	2.69%	14.95%	7.81%	18.43%	8.28%	6.22%	22.52%

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26 **TABLE S3** Multiple regression on distance matrices (MRM) of community composition relative to geographical distance and distance of

27 standardized environmental parameters. The environmental parameters were selected by the BIOENV procedure in the vegan package in R. G:

28 geographical distance; E: environmental distance.

Factors	Taxonomic composition	Phylogenetic composition
	pH, TOC	pH, TOC
Pure E	38.27%	46.20%
Pure G	2.24%	3.72%
Shared effect	9.66%	13.03%
Residuals	49.83%	37.05%

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