

Unravelling large-scale patterns and drivers of biodiversity in dry rivers

Foulquier et al.

Supplementary figures and tables

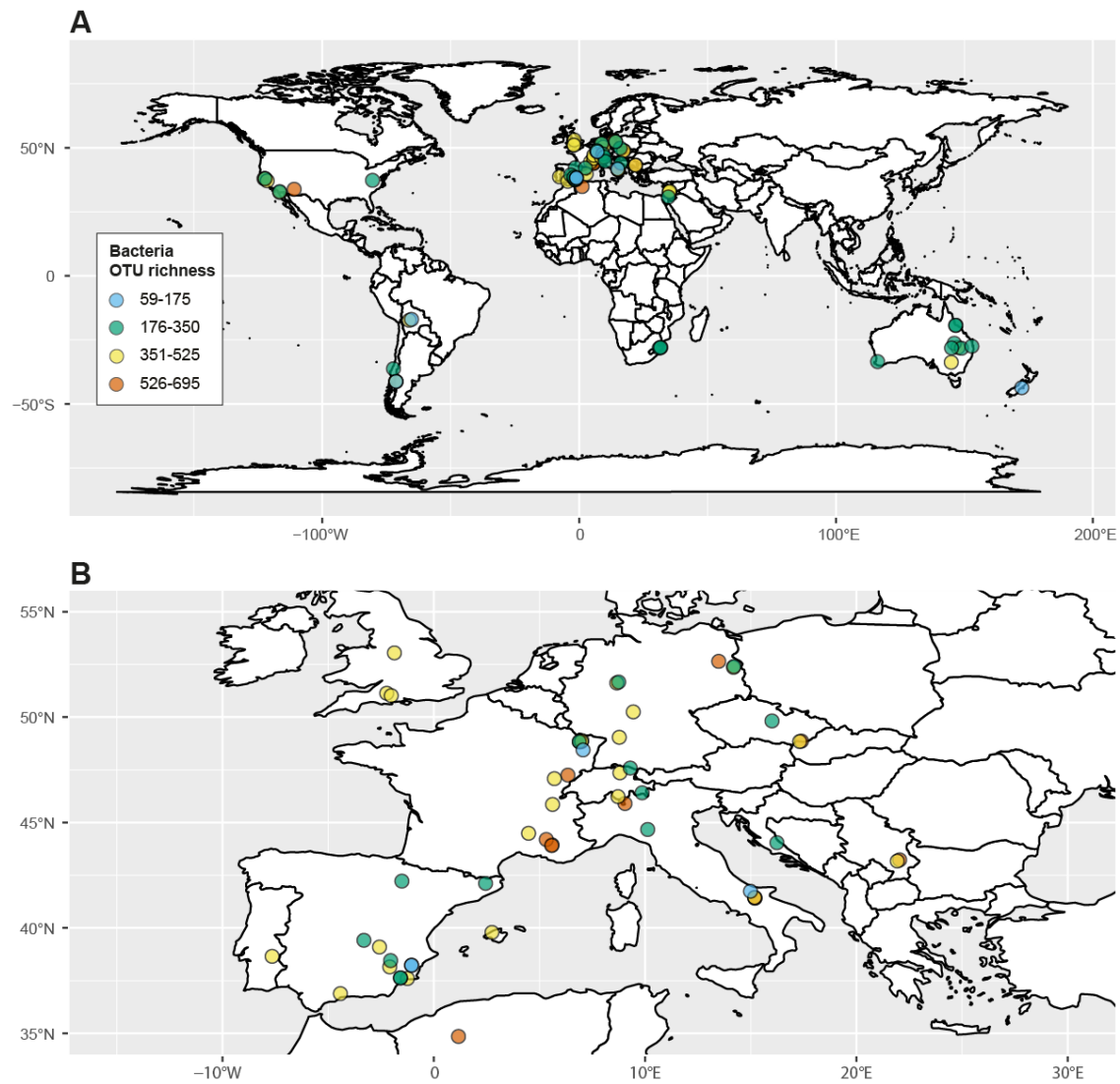


Fig. S1: Bacteria OTU richness: (A) all sampled dry riverbeds (n=84) and (B) within the most densely sampled area.

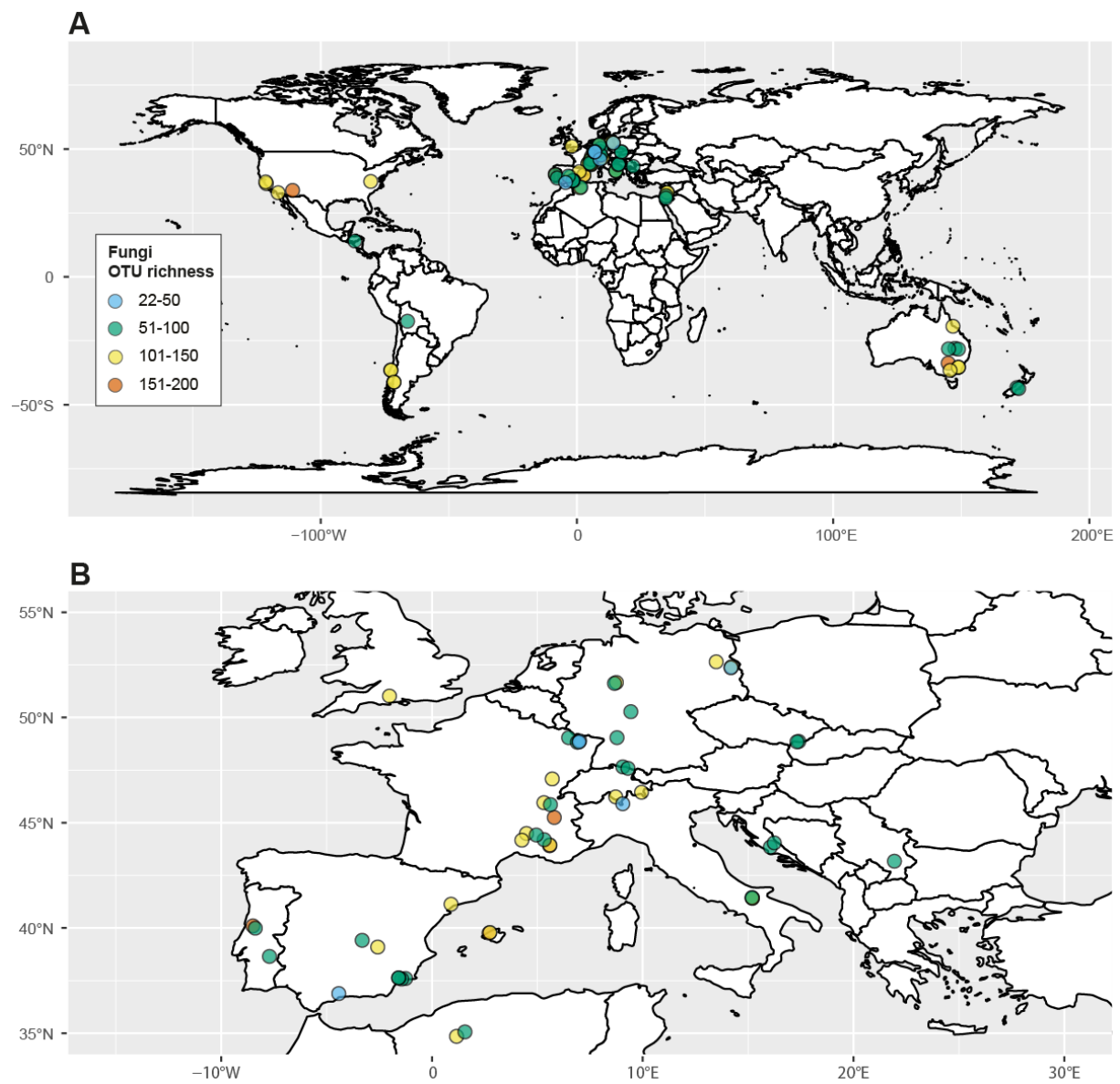


Fig. S2: Fungi OTU richness: (A) all sampled dry riverbeds (n=76) and (B) within the most densely sampled area.

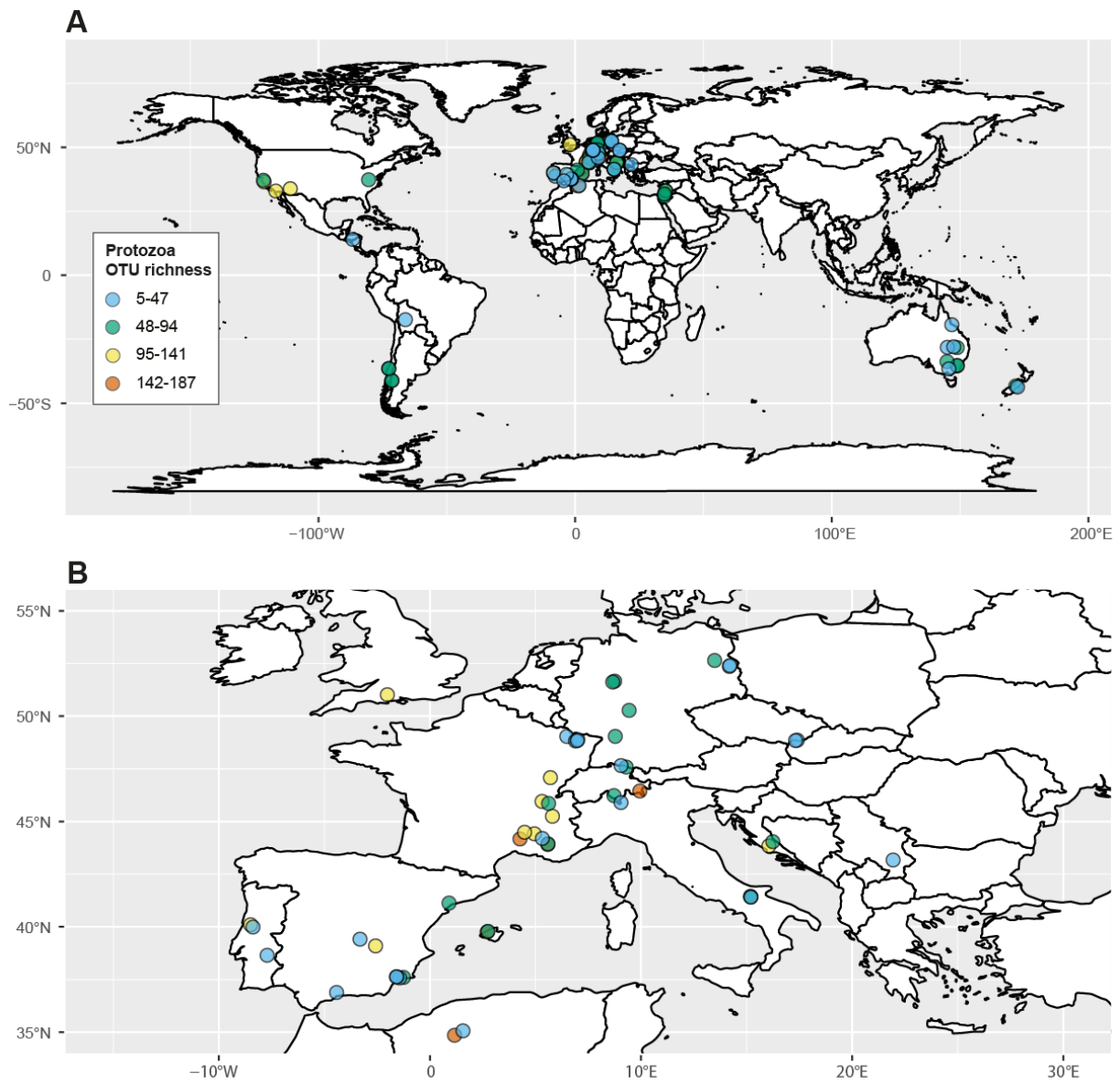


Fig. S3: Protozoa OTU richness: (A) all sampled dry riverbeds (n=76) and (B) within the most densely sampled area.

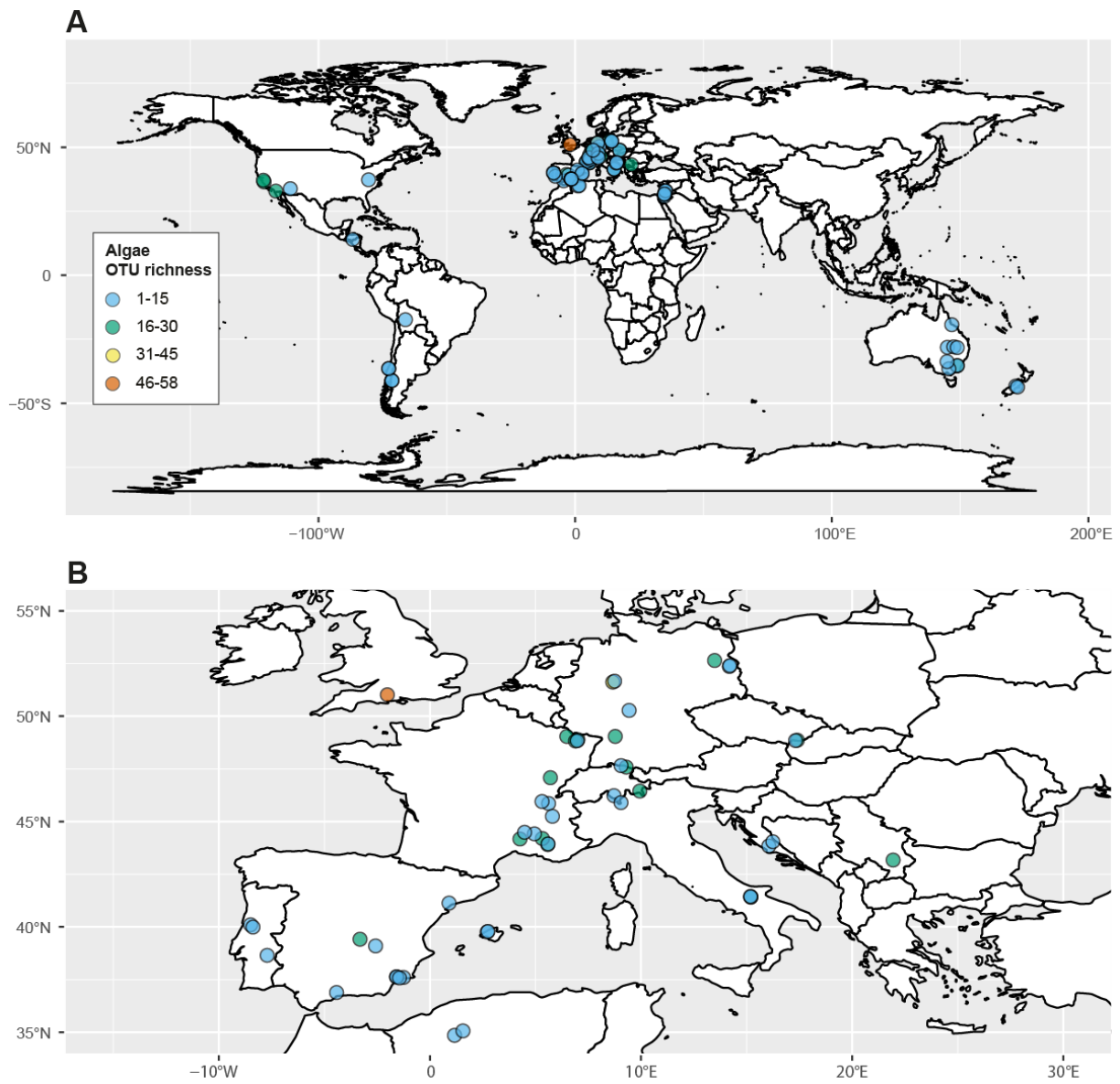


Fig. S4: Algae OTU richness: (A) all sampled dry riverbeds (n=76) and (B) within the most densely sampled area.

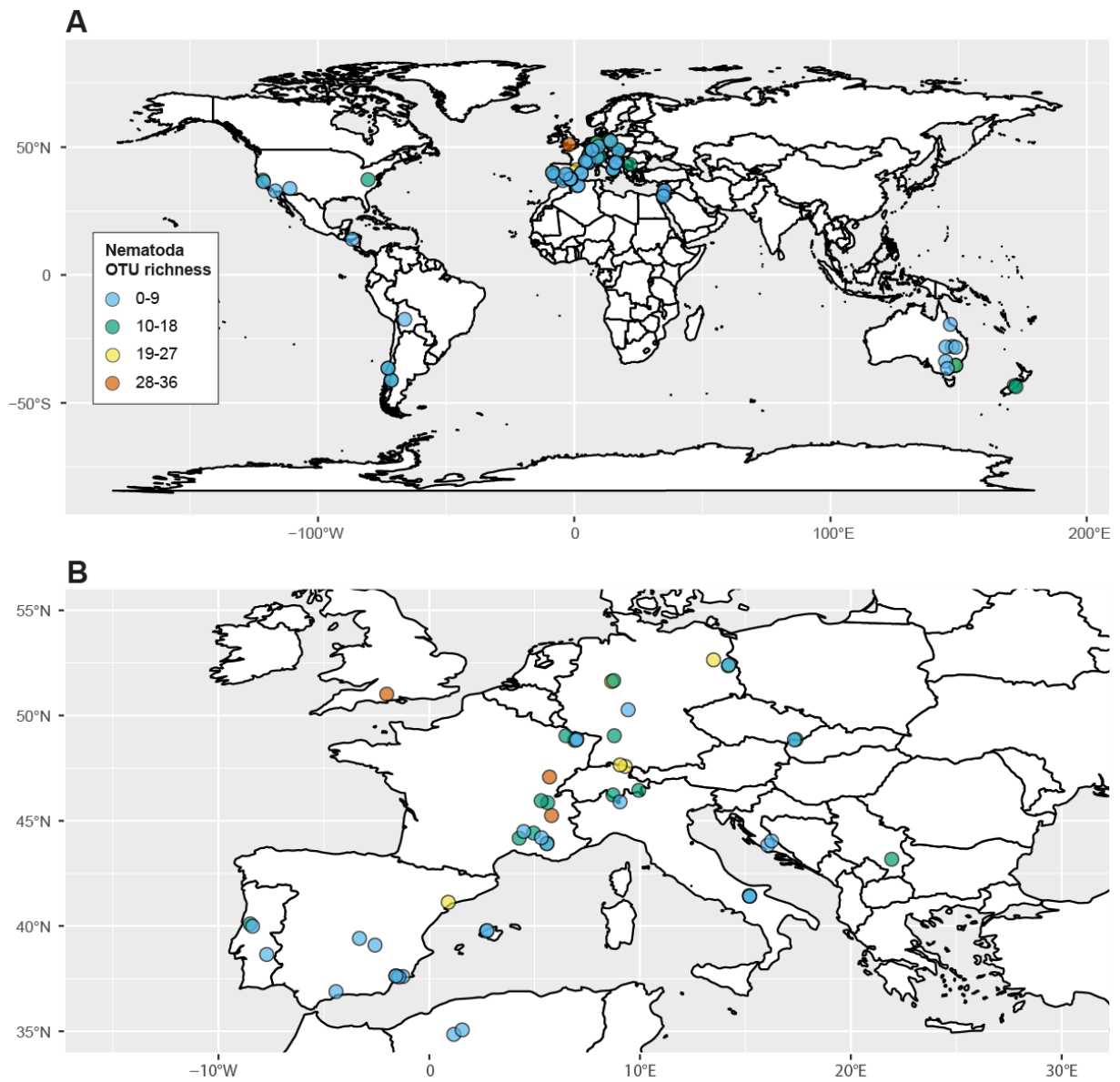


Fig. S5: Nematoda OTU richness: (A) all sampled dry riverbeds (n=76) and (B) within the most densely sampled area.

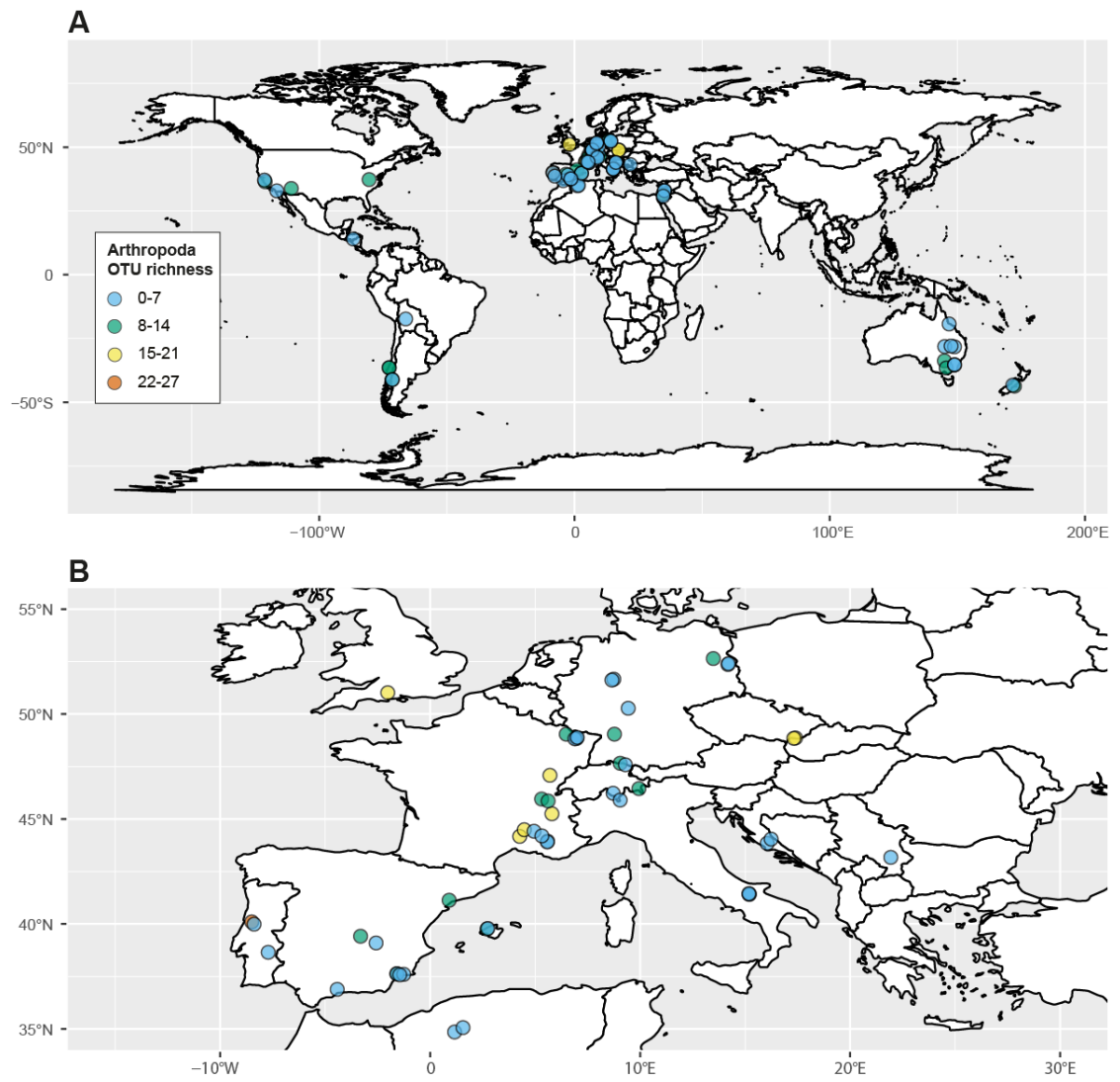


Fig. S6: Arthropoda OTU richness: (A) all sampled dry riverbeds (n=76) and (B) within the most densely sampled area.

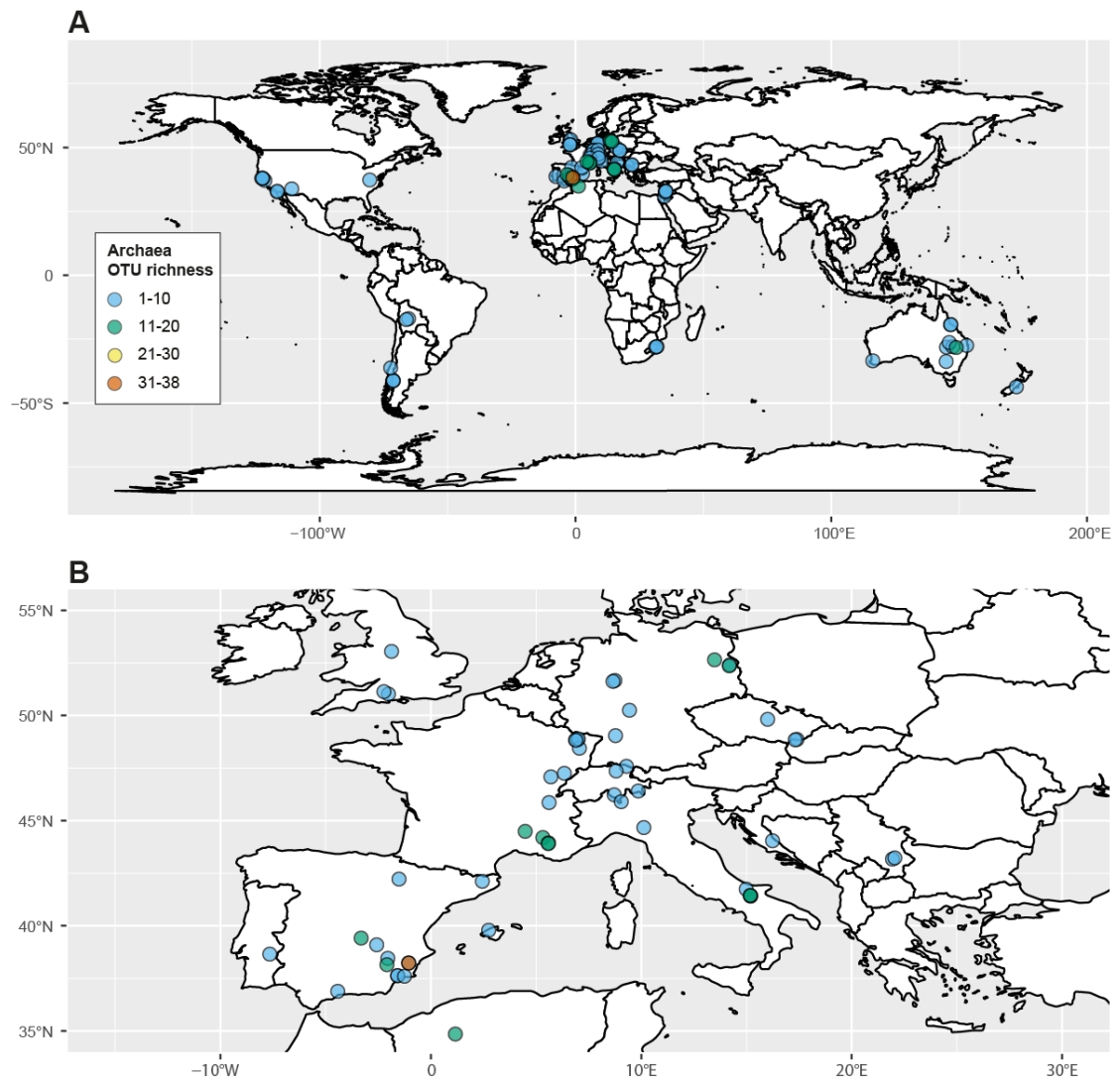


Fig. S7: Archaea OTU richness: (A) all sampled dry riverbeds (n=84) and (B) within the most densely sampled area.

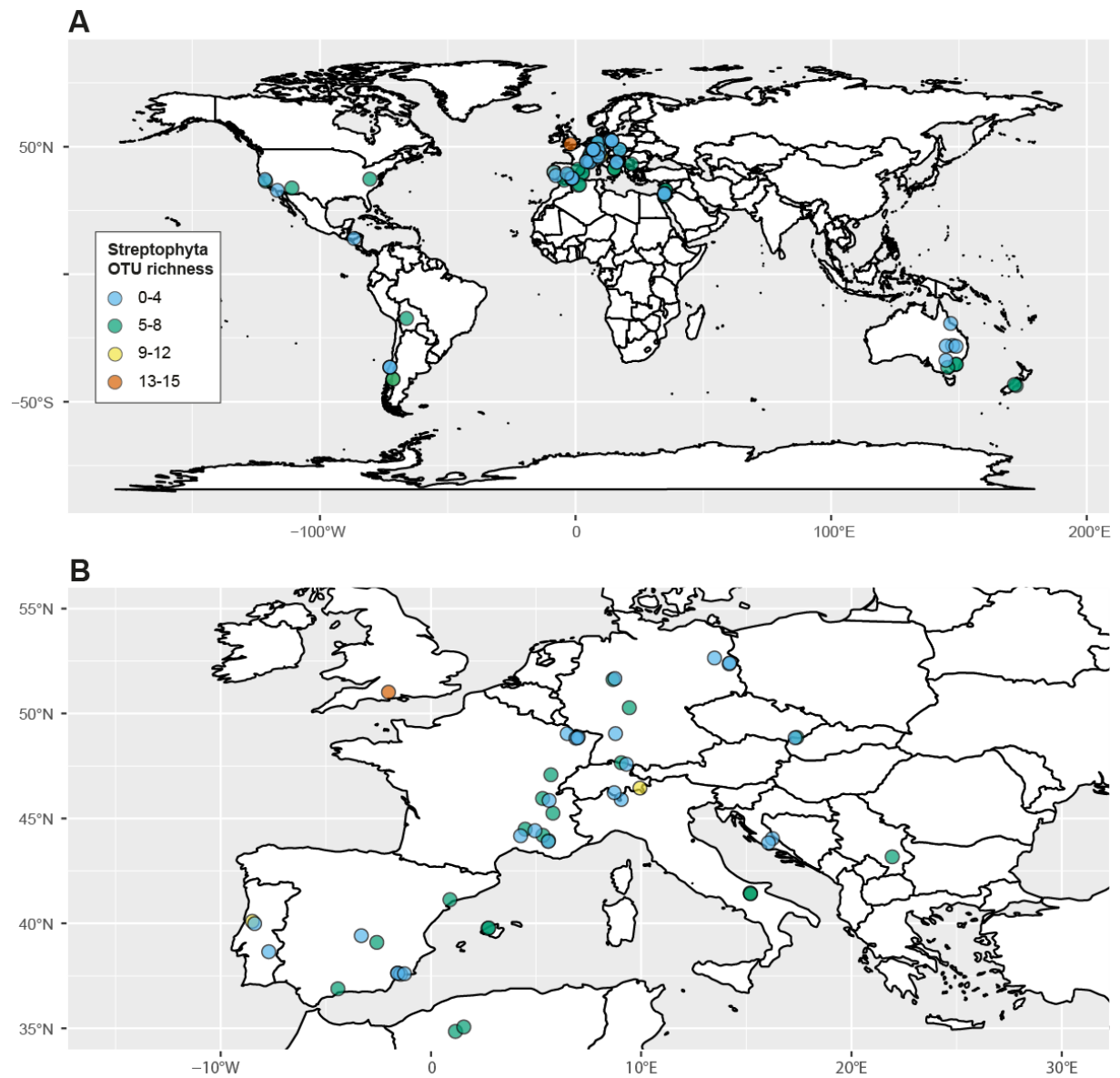


Fig. S8: Streptophyta OTU richness in (A) all sampled dry riverbeds (n=76) and (B) within the most densely sampled area.

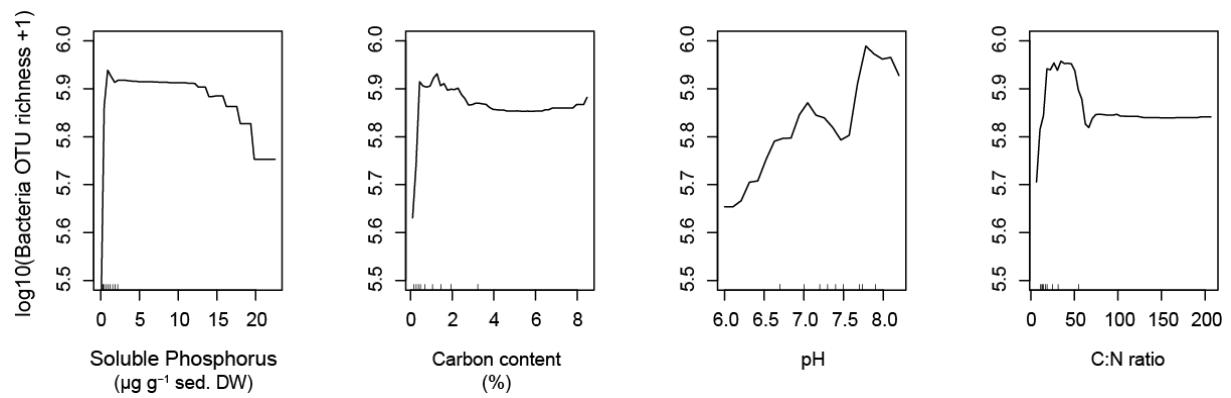


Fig. S9: Partial dependence plot of Bacteria OTU richness. The plots show the contribution of predictor variables to $\log_{10}(x+1)$ OTU richness as a function of the predictors (i.e. when all other predictors are held at their mean). Hash marks on x axes indicate the deciles of the predictor variables. Predictors are shown in order of decreasing importance (%IncMse) from left to right.

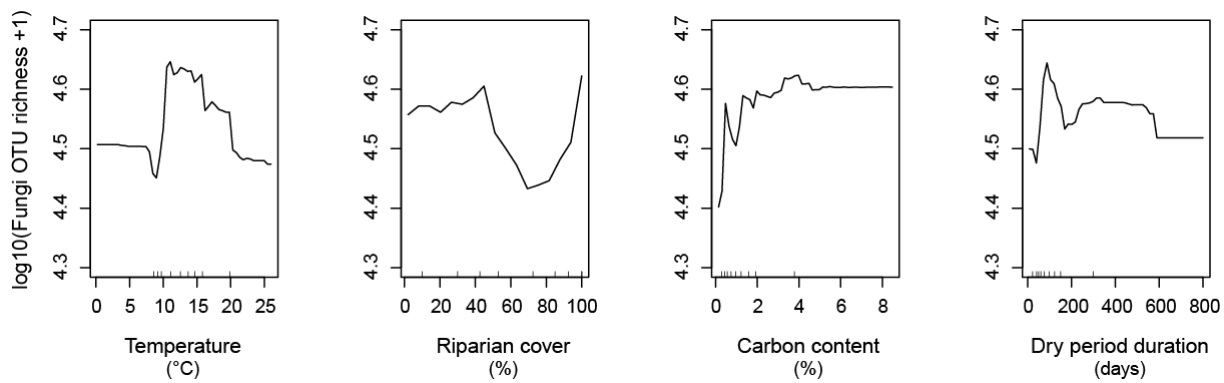


Fig. S10: Partial dependence plot of Fungi OTU richness. See Fig. S9 for further details.

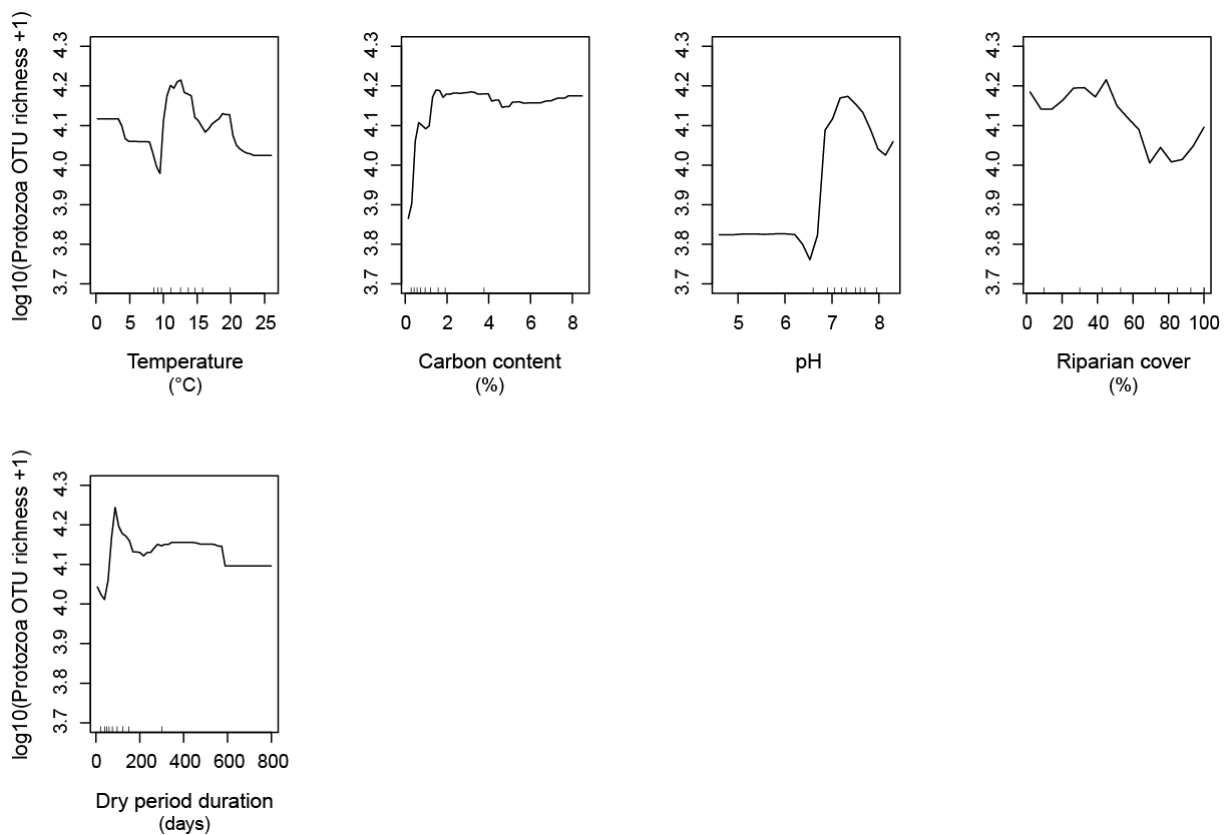


Fig. S11: Partial dependence plot of Protozoa OTU richness. See Fig. S9 for further details.

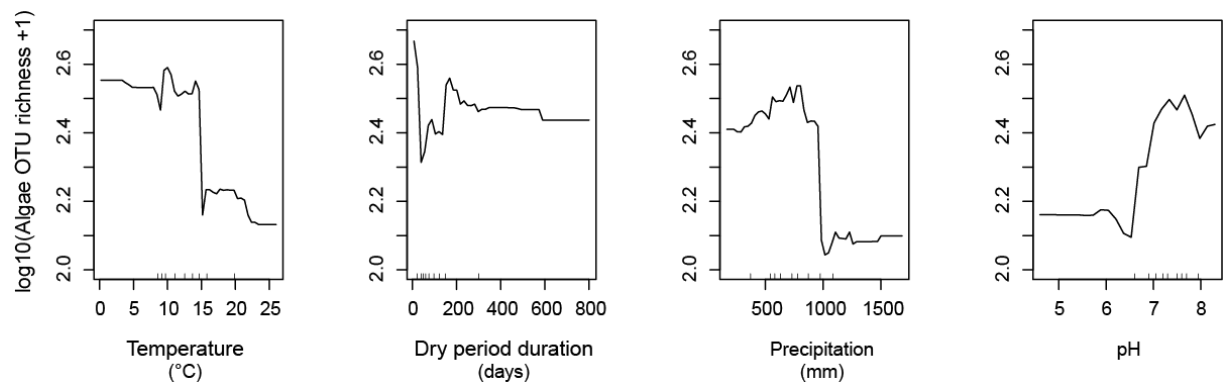


Fig. S12: Partial dependence plot of Algae OTU richness. See Fig. S9 for further details.

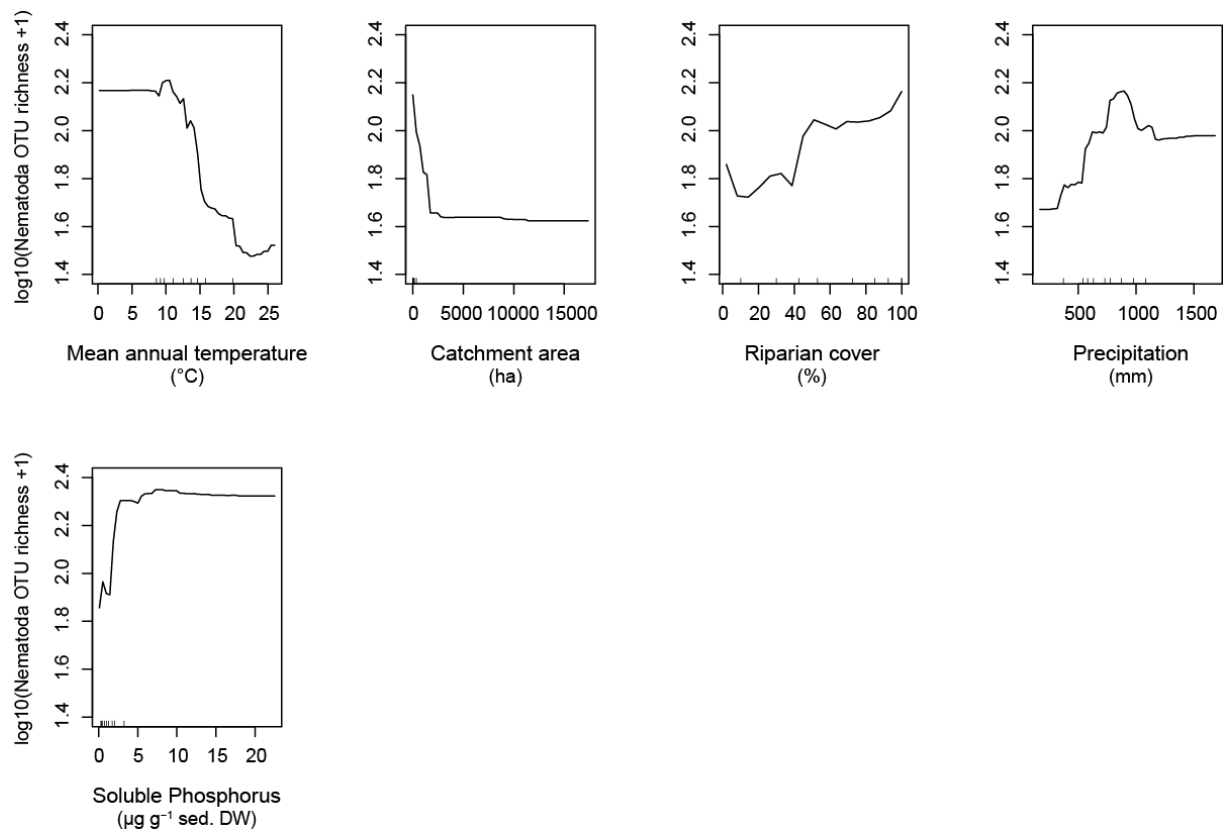


Fig. S13: Partial dependence plot of Nematoda OTU richness. See Fig. S9 for further details.

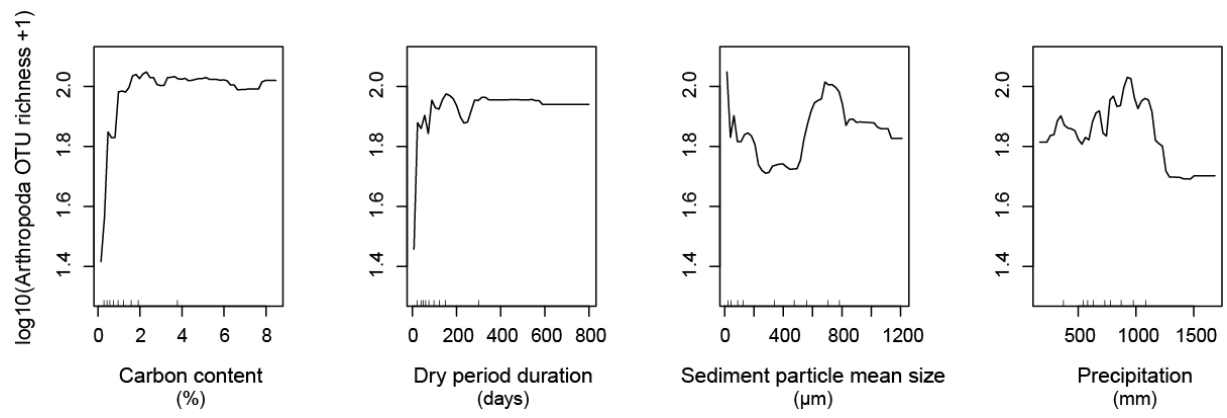


Fig. S14: Partial dependence plot of Arthropoda OTU richness. See Fig. S9 for further details.

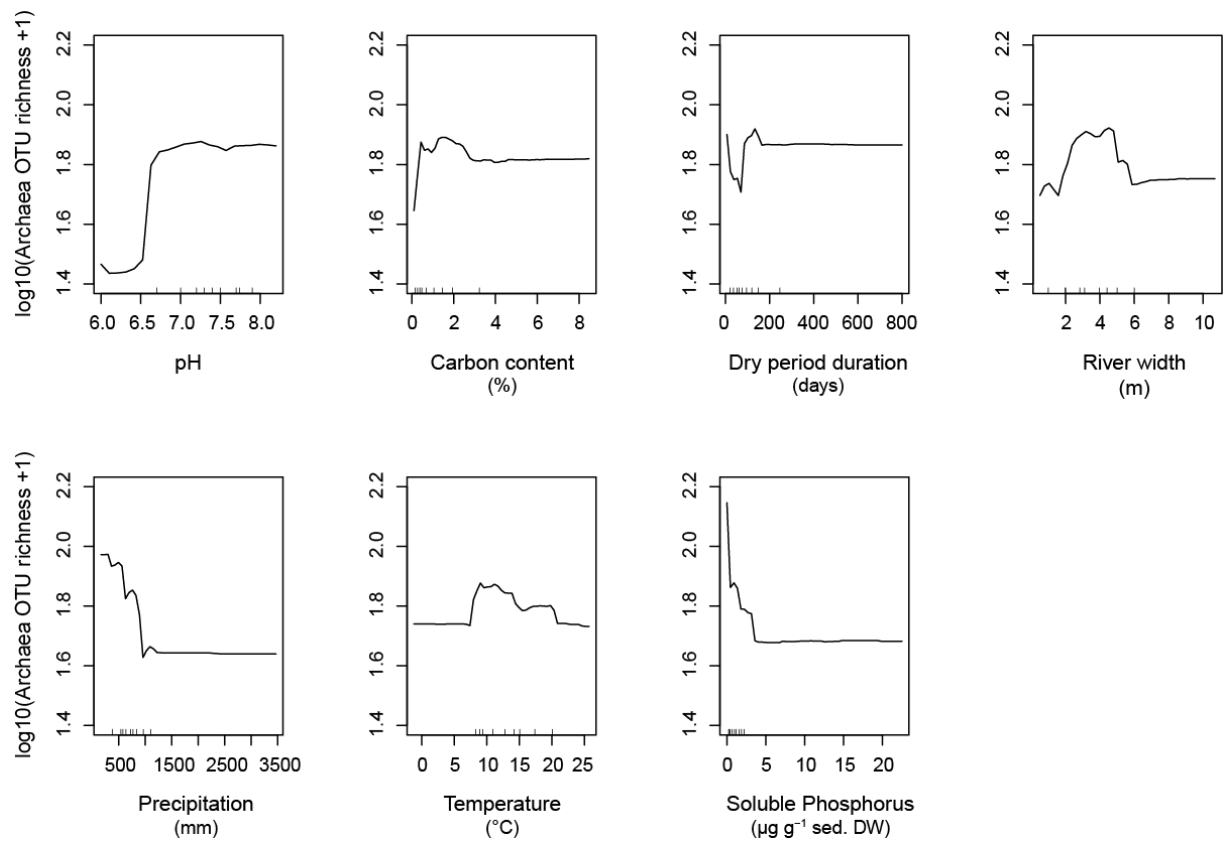


Fig. S15: Partial dependence plot of Archaea OTU richness. See Fig. S9 for further details.

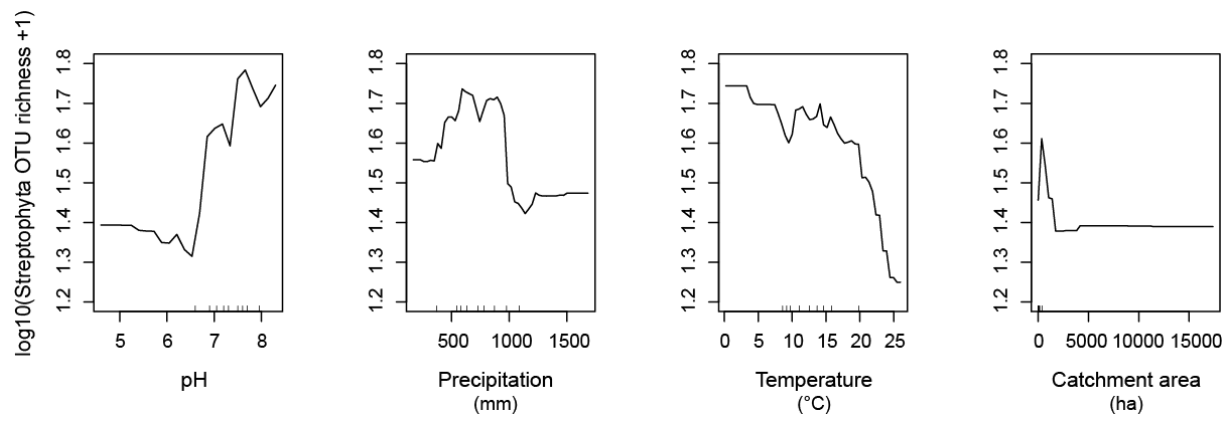


Fig. S16: Partial dependence plot of Streptophyta OTU richness. See Fig. S9 for further details.

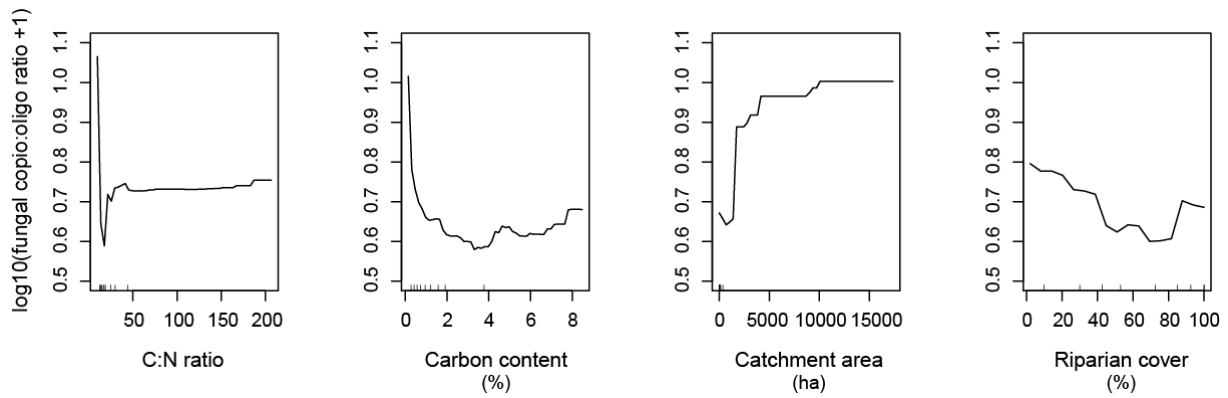


Fig. S17: Partial dependence plot of the relative abundance of fungal copiotrophic and oligotrophic OTUs indicating the contribution of predictor variables to $\log_{10}(\text{copio:oligo ratio} + 1)$ as a function of the predictors (i.e. when the other contributing predictors are held at their mean). Hash marks at the bottom of the plot indicate the deciles of the predictor variables. Predictors are shown in order of decreasing importance (%IncMse) from the left to the right.

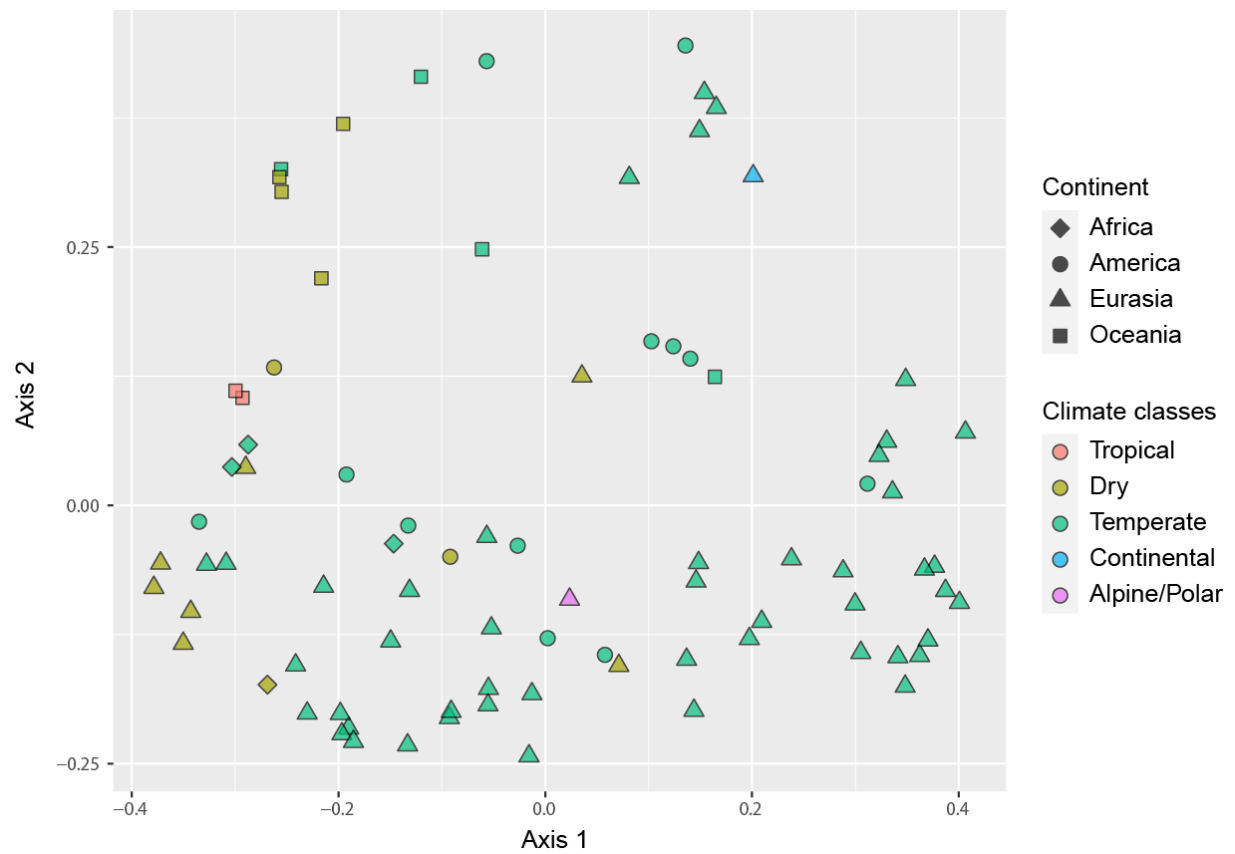


Fig. S18: Principal coordinate analysis ordination of Bacteria community composition on four continents and in five climate classes based on Bray-Curtis distances between all pairs of samples.

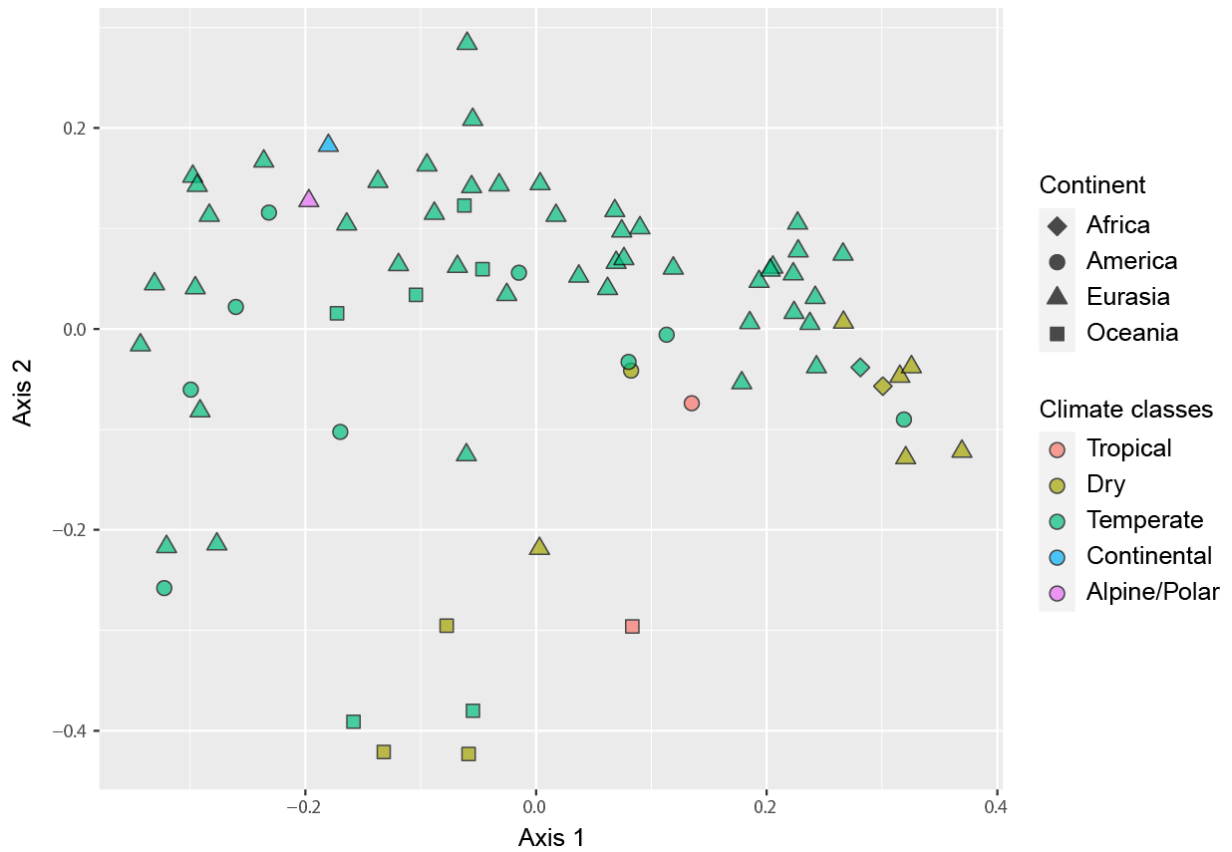


Fig. S19: Principal coordinate analysis ordination of Fungi community composition on four continents and in five climate classes based on Bray-Curtis distances between all pairs of samples.

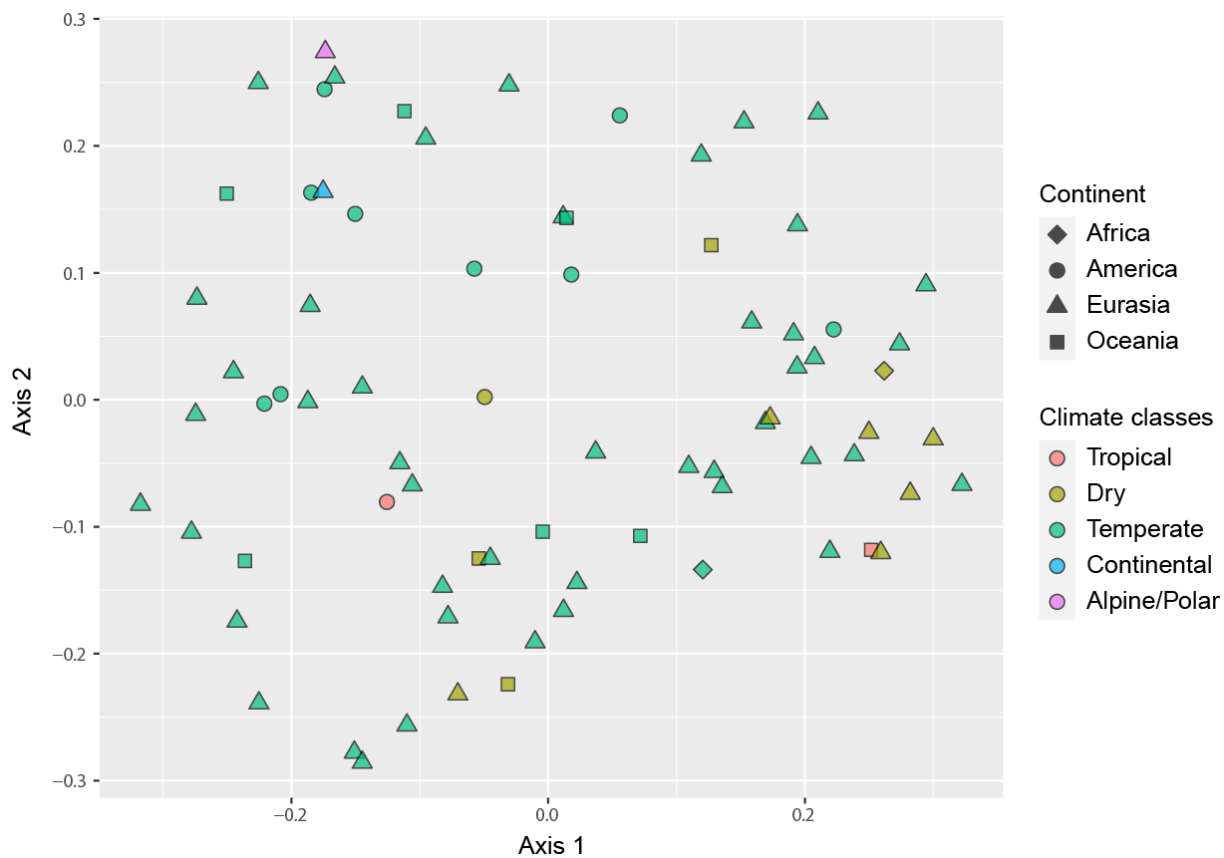


Fig. S20: Principal coordinate analysis ordination of Protozoa community composition on four continents and in five climate classes based on Bray-Curtis distances between all pairs of samples.

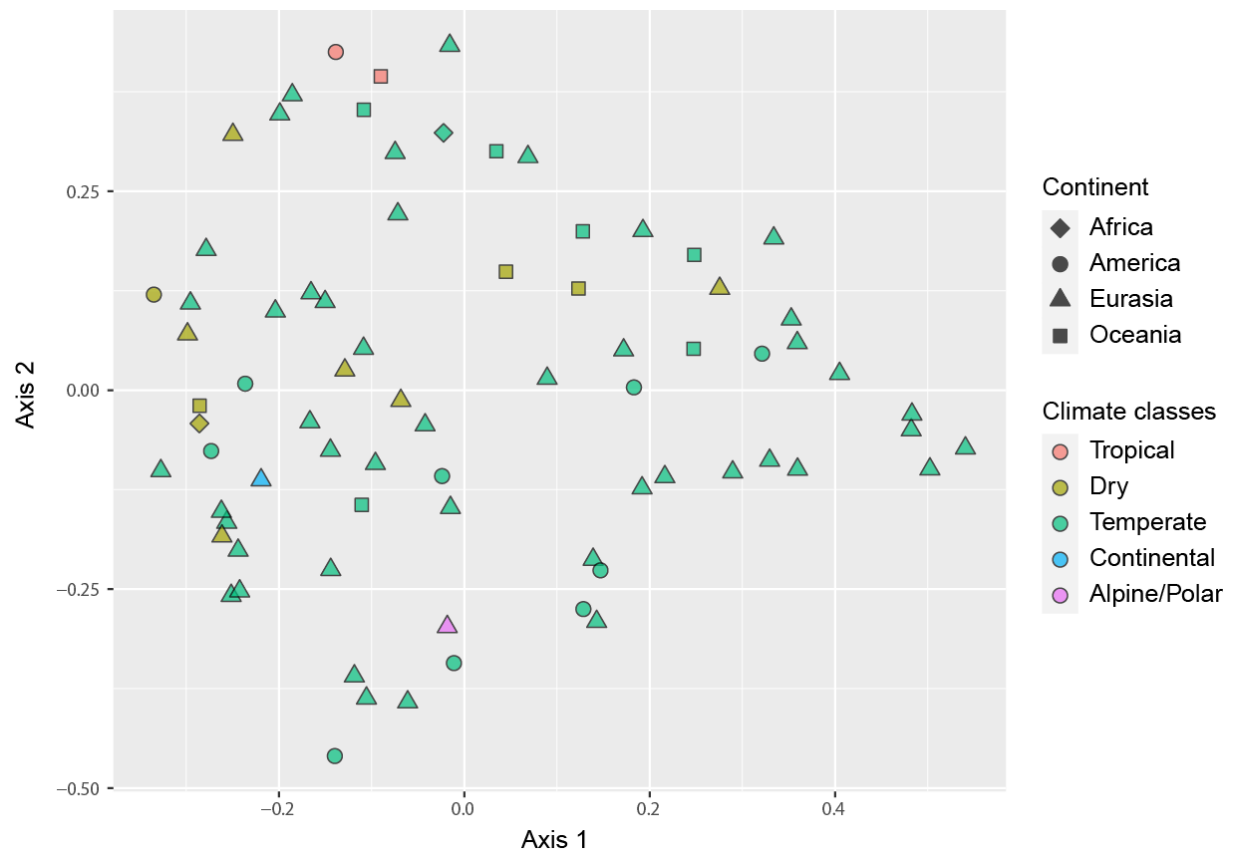


Fig. S21: Principal coordinate analysis ordination of Algae community composition on four continents and in five climate classes based on Bray-Curtis distances between all pairs of samples.

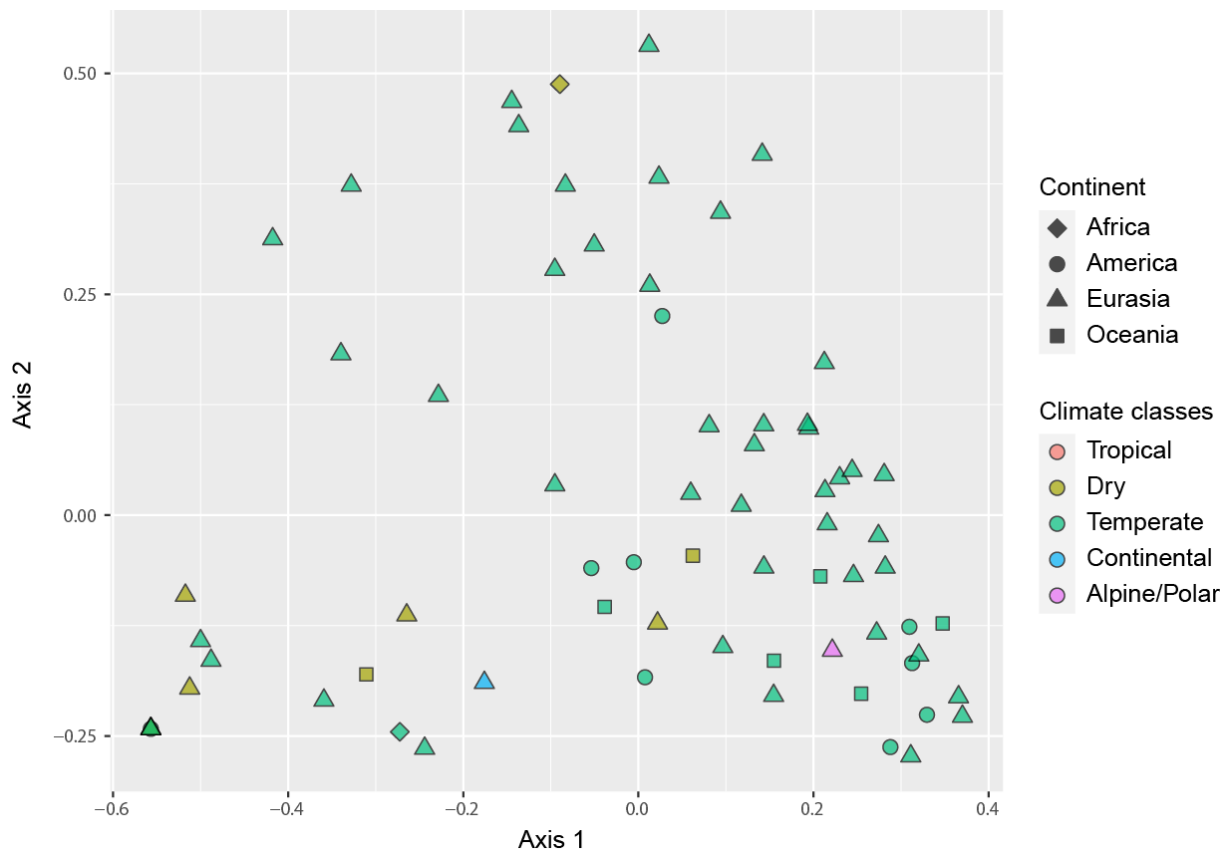


Fig. S22: Principal coordinate analysis ordination of Nematoda community composition on four continents and in five climate classes based on Bray-Curtis distances between all pairs of samples.

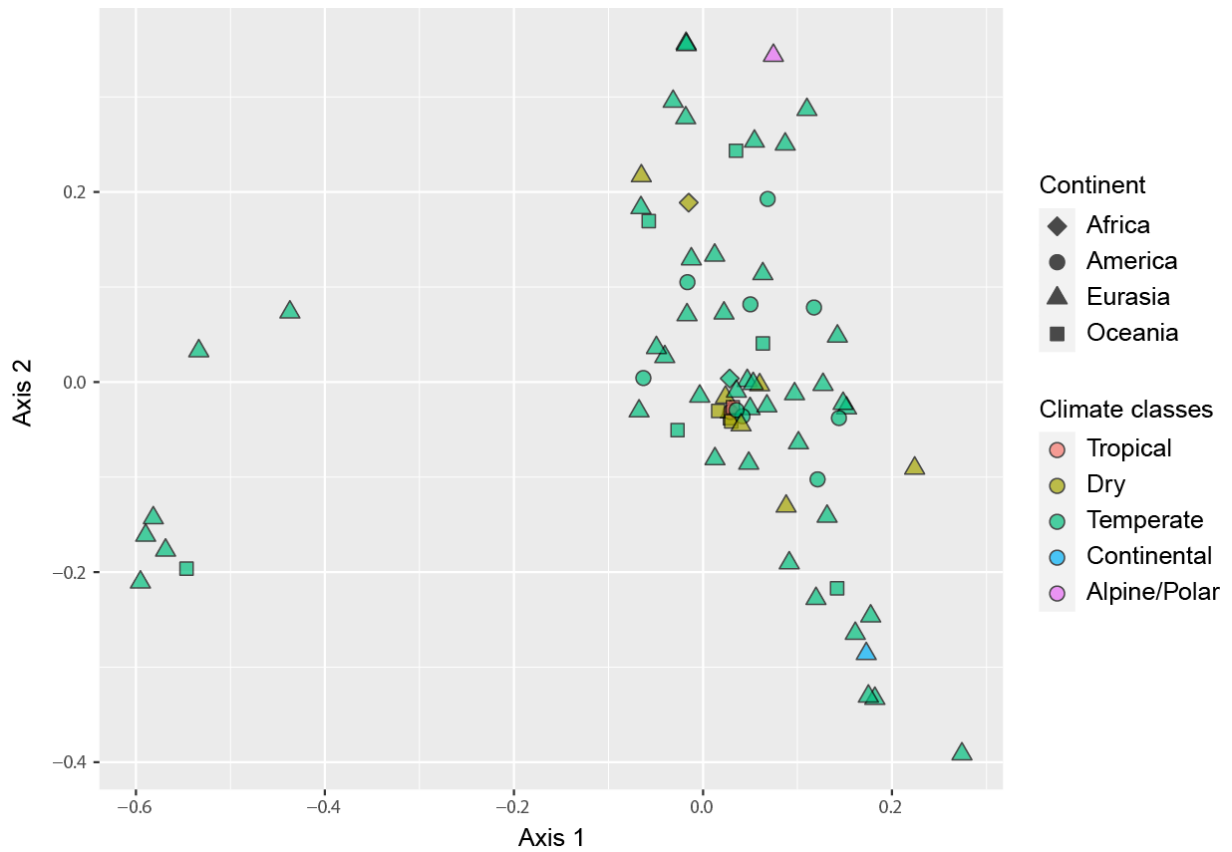


Fig. S23: Principal coordinate analysis ordination of Arthropoda community composition on four continents and in five climate classes based on Bray-Curtis distances between all pairs of samples.

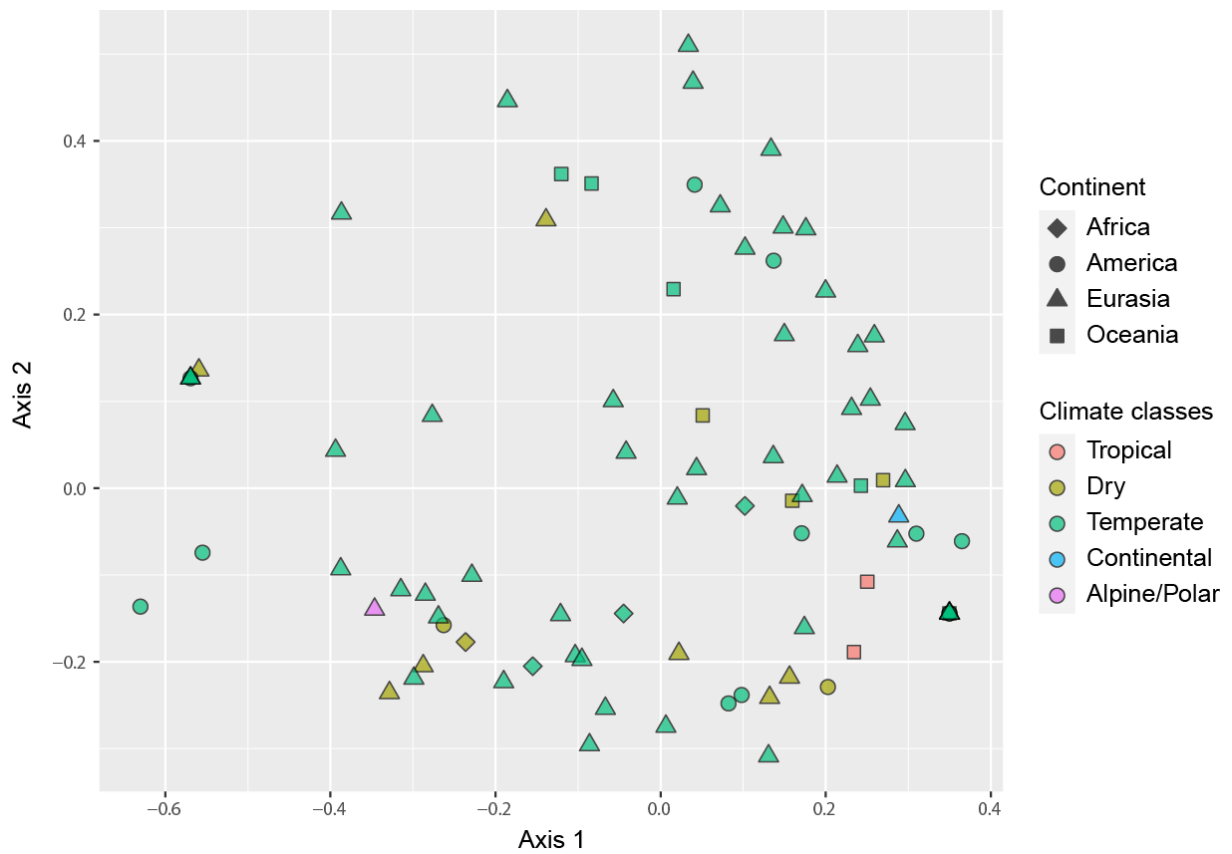


Fig. S24: Principal coordinate analysis ordination of Archaea community composition on four continents and in five climate classes based on Bray-Curtis distances between all pairs of samples.

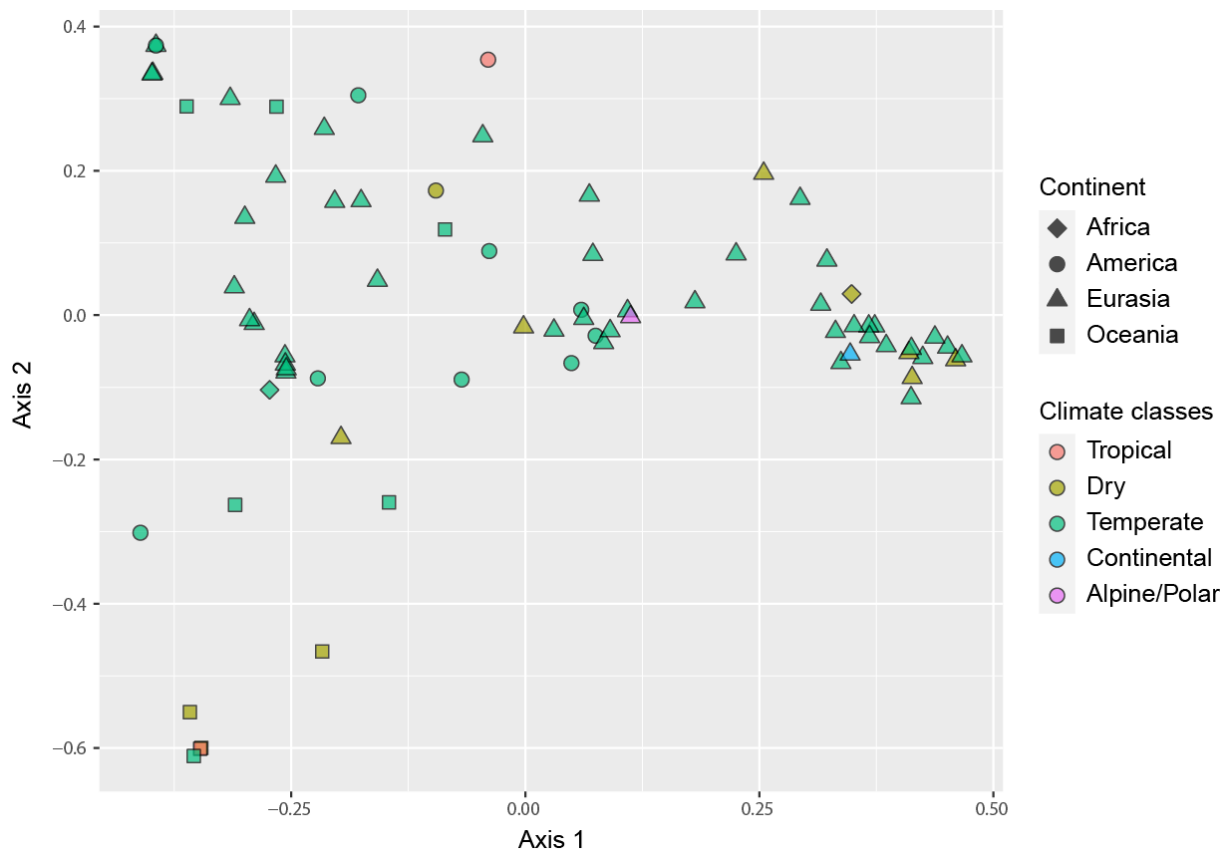


Fig. S25: Principal coordinate analysis ordination of Streptophyta community composition on four continents and in five climate classes based on Bray-Curtis distances between all pairs of samples.

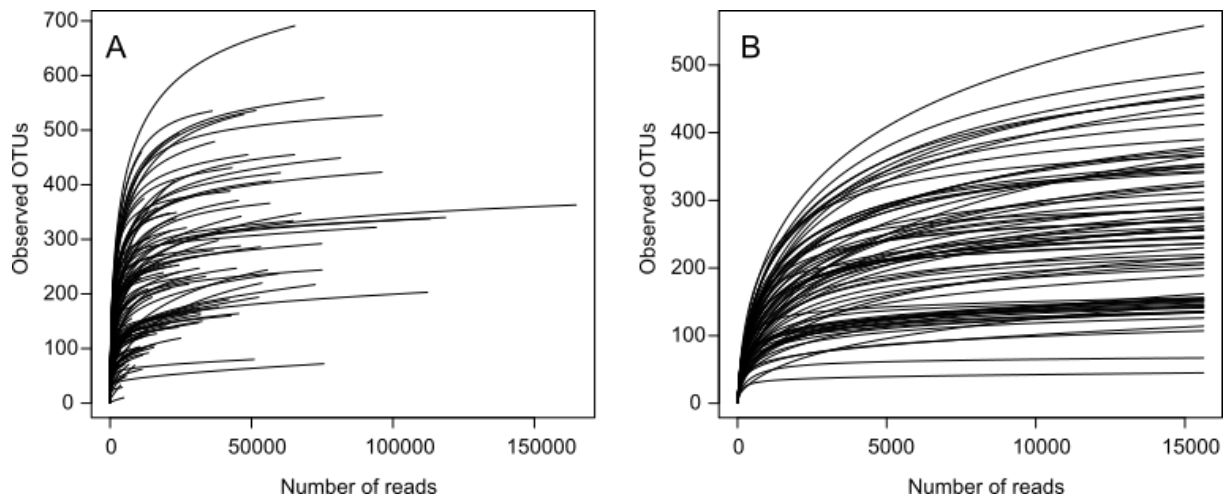


Fig. S26: Rarefaction curves showing Eukaryota OTU richness as a function of the number of reads (sample size) in each sample before (A) and after (B) rarefaction to 15624 reads for the 18S marker. Each curve corresponds to a sample.

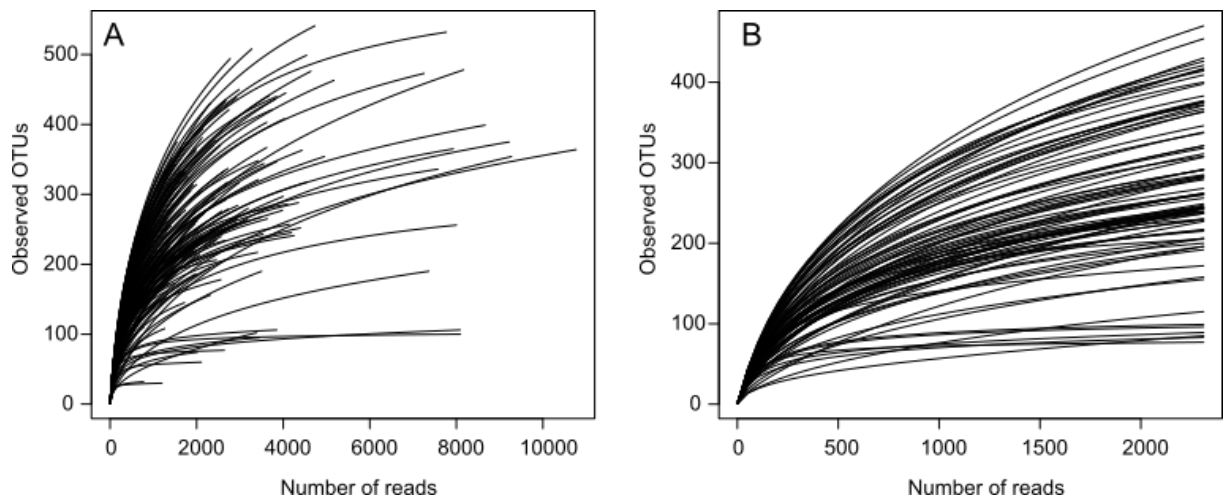


Fig. S27: Rarefaction curves showing Bacteria/Archaea OTU richness as a function of the number of reads (sample size) in each sample before (A) and after (B) rarefaction to 2311 reads for the 16S marker. Each curve corresponds to a sample.

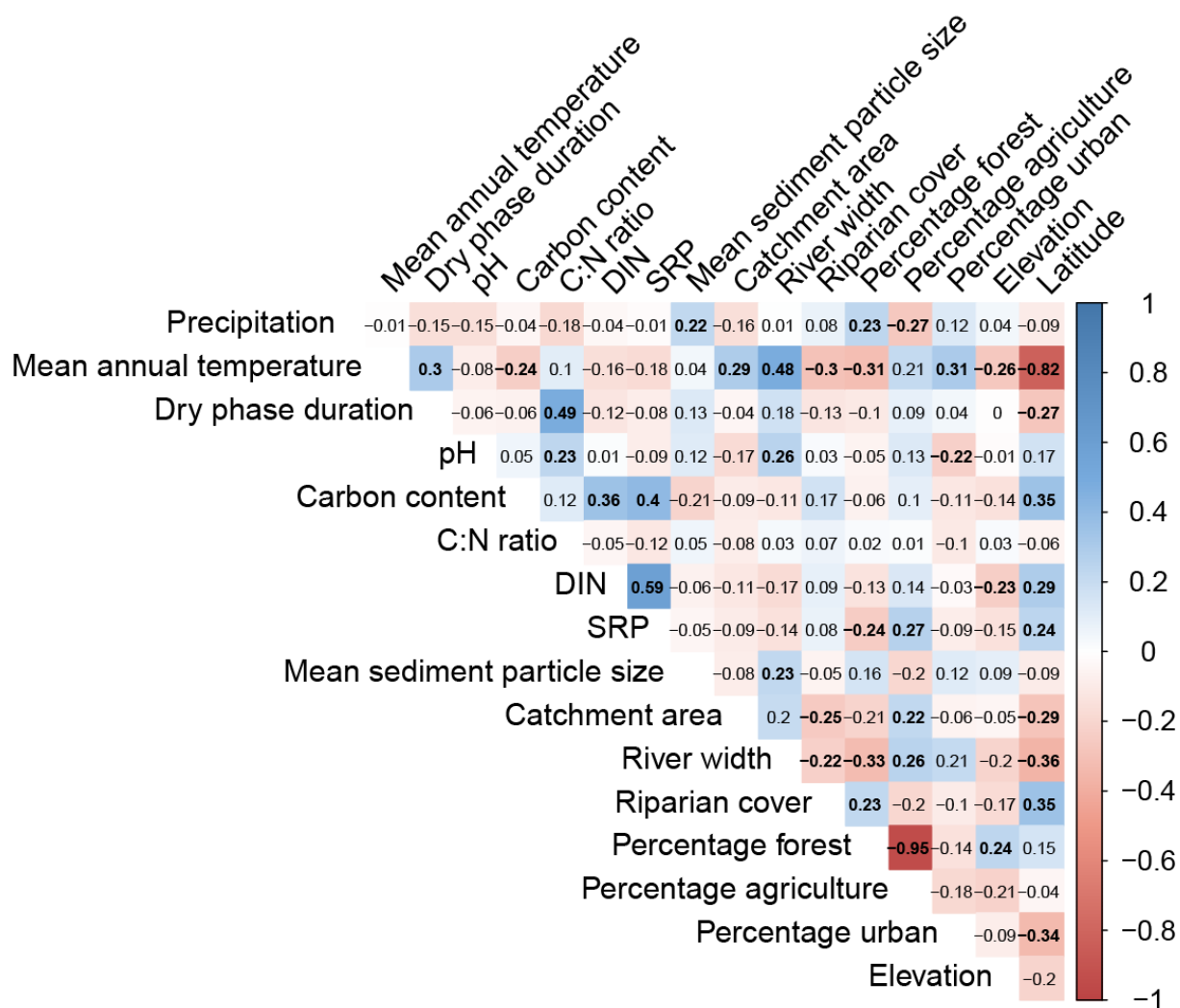


Fig. S28: Pearson correlation matrix of climatic, physicochemical, land-use and spatial variables (n=84). Significant correlation coefficient values (p<0.05) are indicated in bold. Source data are provided as a Source Data file.

Table S1: Summary statistics of physicochemical, land-use and climatic variables. Max, maximum; min, minimum; sed. DW, sediment dry weight; std. dev, standard deviation. Source data are provided as a Source Data file.

	Africa (n=4)				America (n=14)			
Variable	Mean	Std. dev.	Min	Max	Mean	Std. dev.	Min	Max
Carbon content (%)	0.36	0.52	0.1	1.1	0.96	1.2	0.1	4.1
C:N ratio	19	19	6.5	47	17	8.3	9.3	38
Dissolved inorganic nitrogen ($\mu\text{g g}^{-1}$ sed. DW)	2.7	1.5	0.56	3.9	5.6	3.3	0.84	12
Soluble reactive phosphorus ($\mu\text{g g}^{-1}$ sed. DW)	0.51	0.25	0.36	0.88	1.4	1.1	0.091	4.6
pH	7.5	0.24	7.3	7.8	6.8	0.51	6	7.6
Mean sediment particle size (μm)	604	165	400	771	364	291	24	815
Catchment area (km^2)	1616	2924	45	6000	19	36	0	132
River width (m)	6.5	2.4	5	10	2.3	1.7	0.5	5.7
Riparian cover (%)	19	8.5	10	30	69	31	10	100
Percentage forest (%)	41	27	20	80	80	27	20	100
Percentage urban (%)	14	18	0	40	8	12	0	37
Mean annual temperature ($^{\circ}\text{C}$)	18	2.7	14	20	13	4.8	5.8	25
Mean annual precipitation (mm)	711	225	377	870	940	749	430	3469
Dry-phase duration (days)	96	52	30	150	99	66	15	250

	Eurasia (n=56)				Oceania (n=10)			
Variable	Mean	Std. dev.	Min	Max	Mean	Std. dev.	Min	Max
Carbon content (%)	1.6	1.9	0.1	8.5	0.69	0.67	0.1	1.9
C:N ratio	32	38	9.5	207	22	16	11	64
Dissolved inorganic nitrogen ($\mu\text{g g}^{-1}$ sed. DW)	17	20	1.2	97	13	19	2.1	60
Soluble reactive phosphorus ($\mu\text{g g}^{-1}$ sed. DW)	1.8	2.9	0	16	2.8	6.9	0.063	23

pH	7.5	0.43	6.4	8.2	7.2	0.49	6.1	7.7
Mean sediment particle size (μm)	276	286	15	1210	366	301	20	768
Catchment area (km^2)	112	355	0.1	2557	3172	5427	1.1	17371
River width (m)	3.4	2	0.6	11	4.8	2.2	0.5	8
Riparian cover (%)	70	31	0	100	47	37	10	100
Percentage forest (%)	53	37	0	100	18	30	0	100
Percentage urban (%)	3.3	7.7	0	50	9.8	25	0	80
Mean annual temperature ($^{\circ}\text{C}$)	12	4.3	-1.2	26	19	3.8	12	24
Mean annual precipitation (mm)	724	267	168	1424	700	310	367	1245
Dry-phase duration (days)	125	176	7	800	147	119	15	312

Table S2: Number of samples, PCR replicates, reads and unique sequences (=operational taxonomic units, OTUs) for the Bacteria/Archaea (Bact02) and Eukaryota (Euka02) marker after each filtering step. PCR, polymerase chain reaction.

Filtering step	Bact02				Euka02			
	Samples	PCR replicates	Reads	OTUs	Samples	PCR replicates	Reads	OTUs
Raw data	177	531	6259902	2357163	177	531	19134518	1013900
Basic filter (singletons, length)	177	531	2921780	282351	177	531	13196993	234390
Removal of OTUs found in only 1 PCR replicate	177	530	2339063	80513	177	531	13196993	82161
obiclean	177	530	1303834	5751	177	531	9555919	4302
OTU clustering 97%	177	530	691283	2166	177	531	7989962	2692
Removal of dysfunctional PCRs	167	488	542701	2154	152	388	6761322	2676
Removal of contaminants and non-target taxa	167	488	466680	2117	152	388	4020797	2629

