

Supplementary material: Title of paper

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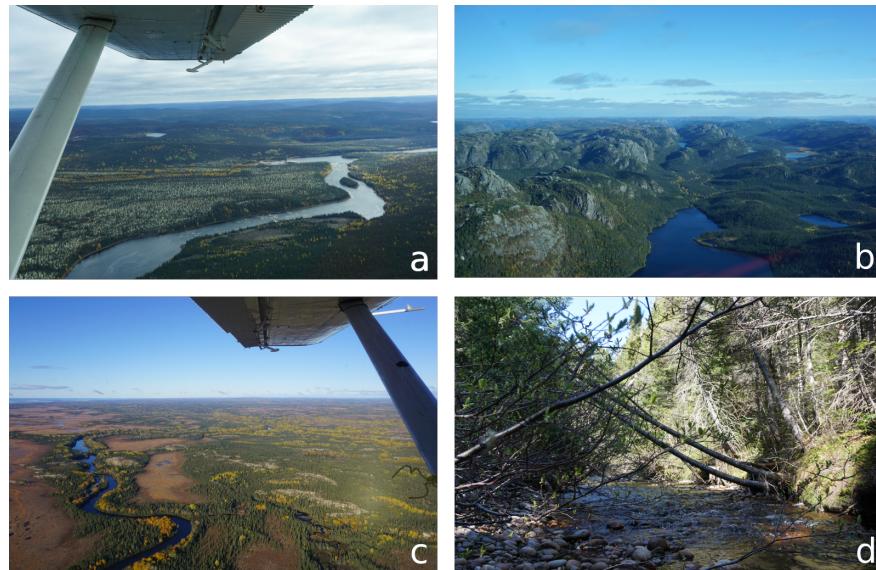
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The following file contains the supplementary material for the publication “Title of publication” (DOI:).

Supplementary Methods

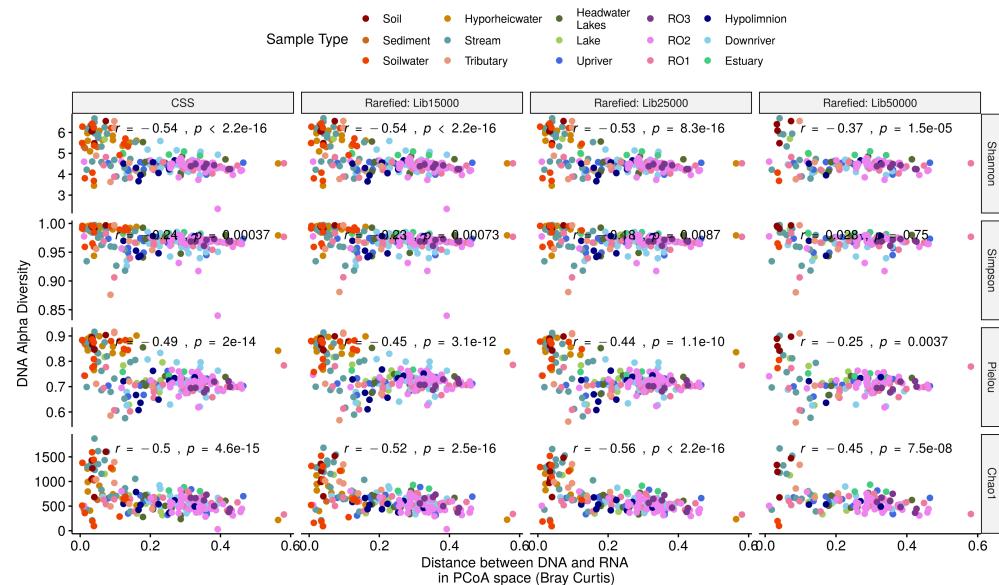
Supplementary Figures

Figure S1: Landscape within the La Romaine catchment



- (a) Northern area with shrubs and moss-lichen, (b) Mountainous section close to Reservoir 3, (c) Lower coastal plain with peatland areas, (d) Example of a sampled stream.

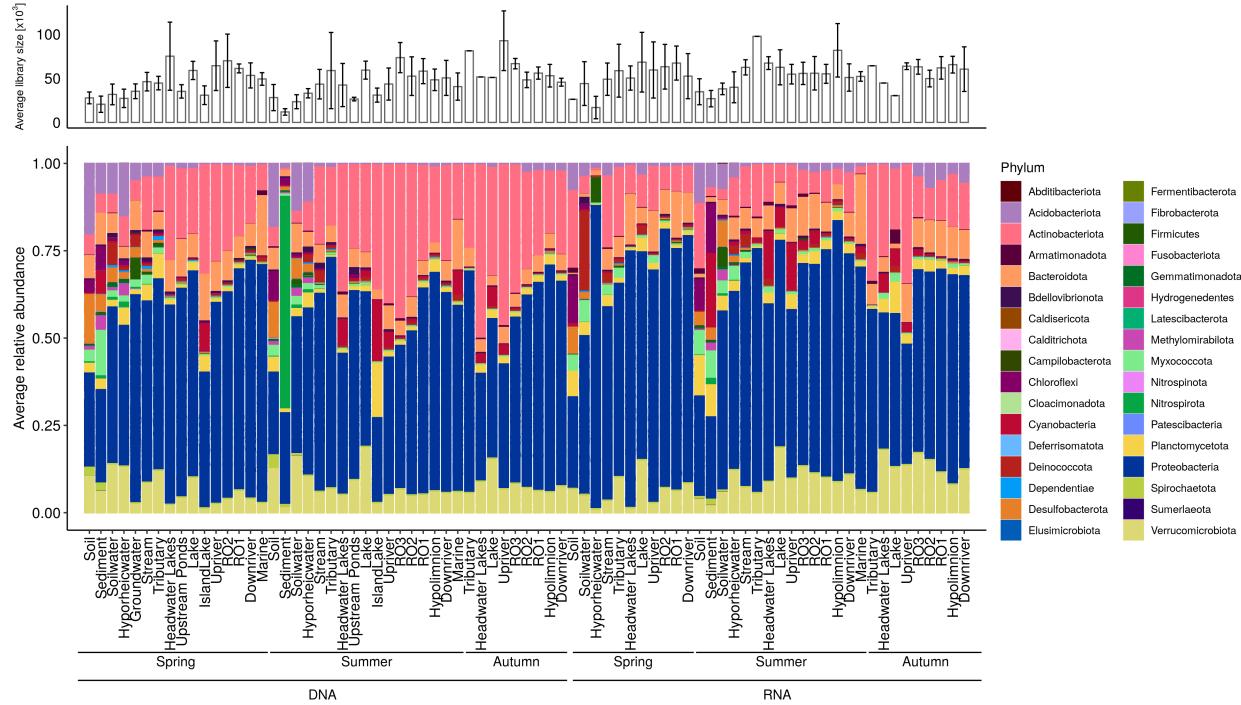
Figure S2: No substantial effect of data transformation methods on alpha-diversity estimations



Comparing the effect of used method on the relation between DNA alpha diversity indices and the distance between DNA and RNA of the same samples within PCoA space. Rows represent different alpha diversity indices: Shannon-Wiener index (H'), Simpson's index (λ), Pielou's evenness (J) and Chao1 richness estimator.

CSS = cumulative sum scaling, all remaining three subsequent columns are rarefied datasets with the applied minimum library size threshold indicated after “Lib”.

Figure S3: Taxonomic composition of sample types



Given are averages of phyla found across sample types. Upper panel shows average library sizes across sample types. Error bars indicate the standard deviation from the mean.

Supplementary Tables

Table S1: Number of samples per sample type.

Number of samples are given per sample type. RO stands for reservoir.

	Nucleic Acid Type																	
	Soil	Sediment	Solwater	Hyporheicwater	Groundwater	Stream	Tributary	Headwater Lakes	Upstream Ponds	Lake	Uptiver	RO3	RO2	ROI	Hypolimnion	Downriver	Estuary	Sum
DNA	33	22	44	17	4	34	9	17	10	16	22	7	63	25	9	43	20	395
RNA	8	4	13	14	0	18	5	8	0	11	12	7	43	25	9	21	4	202