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Supplement of

Co-occurrence patterns in aquatic bacterial communities across changing permafrost landscapes

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Supplementary information (SI)

SI Figures

SI Figure 1: UPGMA clustering based on unweighted UniFrac distances among bacterial community samples. Color refers to valley identity with SAS: brown, KWK: purple, BGR: green, NAS: orange, RBL: blue. The complete names of the valleys are given in the main text.

SI Figure 2: Rank abundance curve of the bacterial communities originating from the 5 different valleys. Color refers to valley identity with SAS: brown, KWK: purple, BGR: green, NAS: orange, RBL: blue. The complete names of the valleys are given in the text.

SI Figure 3: Taxonomic uniqueness as determined by the local contribution to β - diversity (LCBD) among the different sampled valleys. The solid black horizontal and vertical lines represent the mean and standard deviation respectively.

SI Figure 4: Heatmap representation of habitat preference of the 2166 bacterial OTUs detected in the dataset. Habitat preference was determined by point biserial correlation.

SI Figure 5: Association networks between co-occurring bacterial OTUs and with the abiotic and biotic local conditions based on maximum interaction coefficient (MIC). Significant associations (MIC> 0.44, $P_{fdr}<0.03$) are presented. The color of the edges refers to the strengths of the relationship between two nodes and is proportional to MIC values with black lines corresponding to strong links). The size of the nodes is proportional to node degree that is the number of connection that a node has with other nodes. The associations between the major bacterial classes (bacterial OTUs colored by taxonomy) and with abiotic (white nodes) and biotic (black nodes) variables are presented in panel A. Panel B presents the association between the different environmental variables (colored by variable) and with bacterial OTUs.

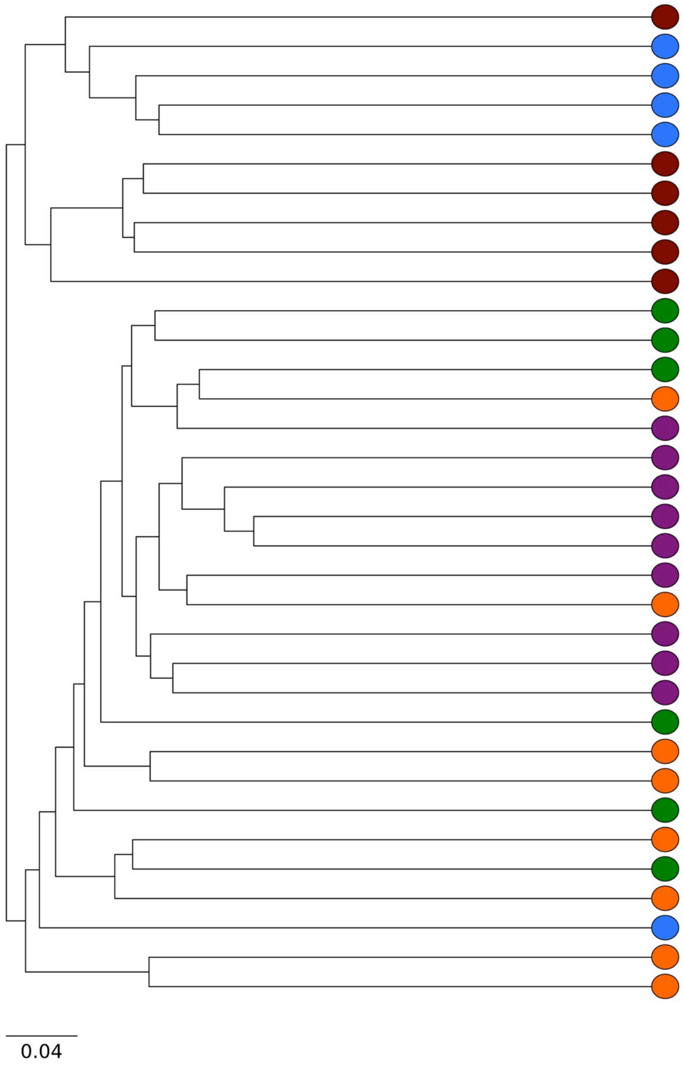
SI Figure 6: Association networks between co-occurring bacterial OTUs and with the abiotic and biotic local conditions based on maximum interaction coefficient (MIC). Panel A presents all significant associations (MIC> 0.44, $P_{fdr}<0.03$) between the bacterial OTUs. Impact of the removal of bacterial hubs (most connected nodes) on the topology of the association network is presented in panels B. Node color corresponds to the type of variable with grey referring to bacterial OTUs, white to abiotic variables and black to biotic variables.

SI Tables

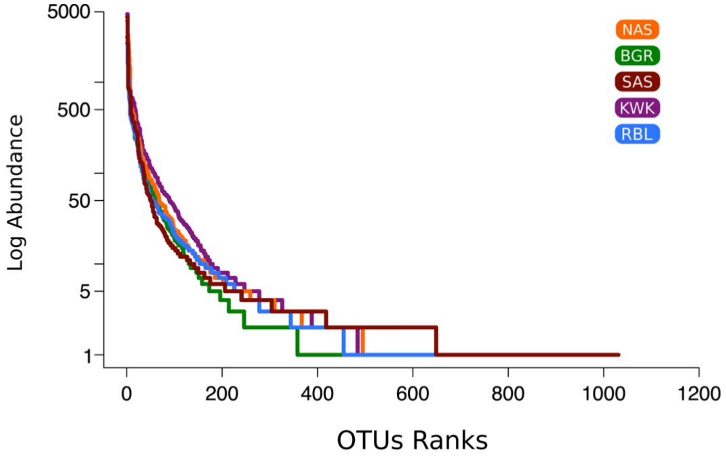
SI Table 1: Bacterial phylogenetic structure, taxonomic uniqueness and abundance across the sampling sites. N taxa represent the total number of detected taxa and PSR, PSE PD refer to phylogenetic species richness, evenness and diversity respectively. NRI corresponds to Net Relatedness Index. LCBD and BA refer to local contribution to beta-diversity and bacterial abundance (10^6 cells ml^{-1}) respectively.

SI Table 2: Taxonomic identity of network ‘hubs’. Top 24 is presented, which corresponds to 10% of total nodes number in the network. Taxonomic assignment was realized at a 97% similarity threshold. RA refers to relative abundance (% of total reads)

SI Fig. 1

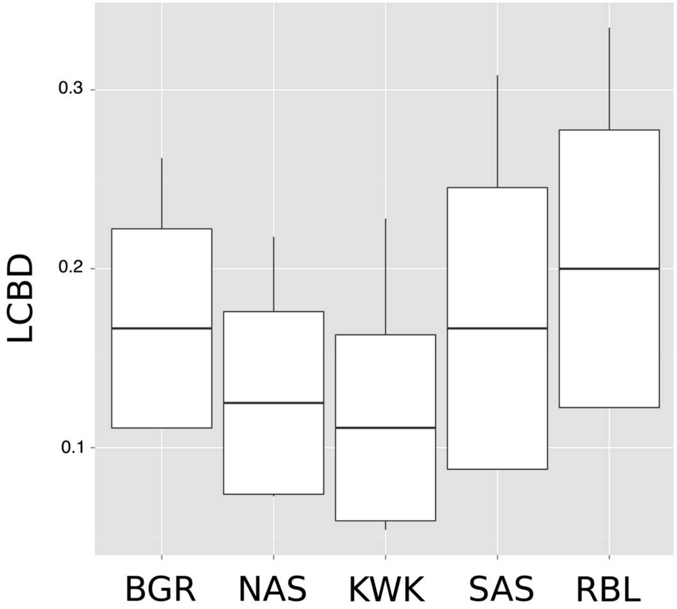


SI Fig. 2

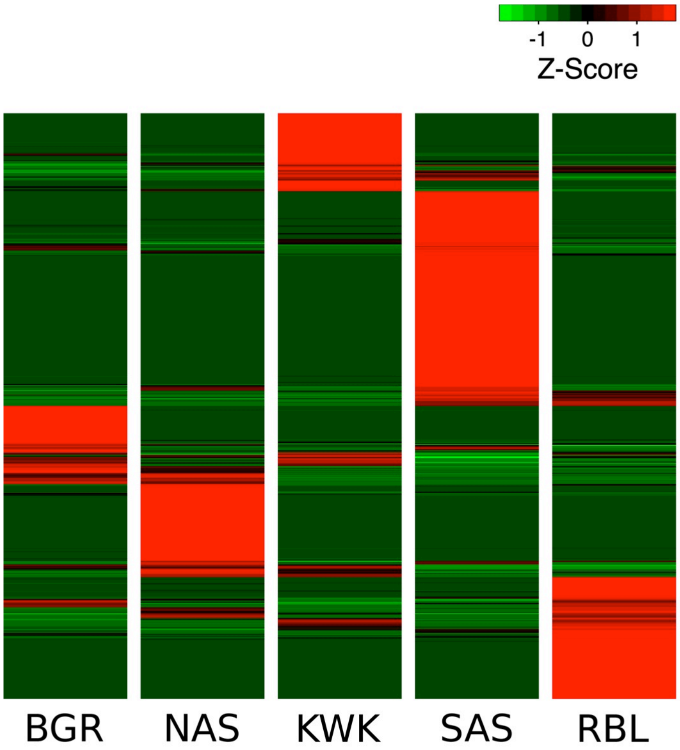


5000
500
50
5
1
Log Abundance
0
200
400
600
800
1000
1200
OTUs Ranks
NAS
BGR
SAS
KWK
RBL

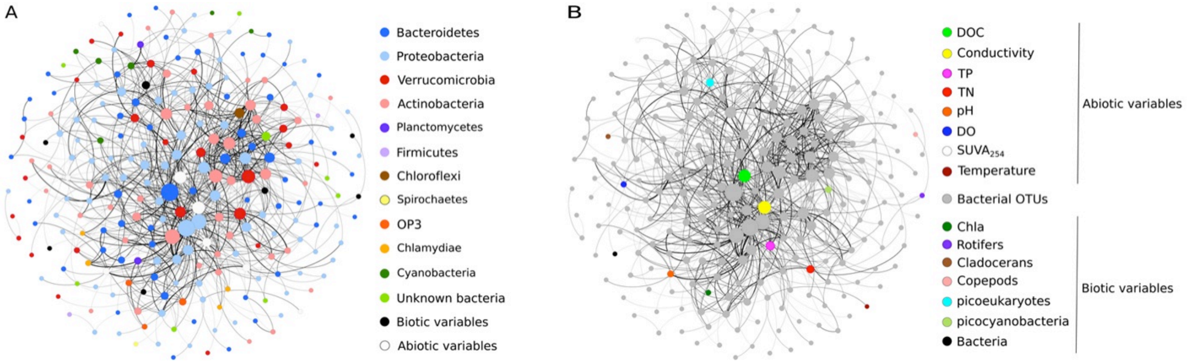
SI Fig. 3



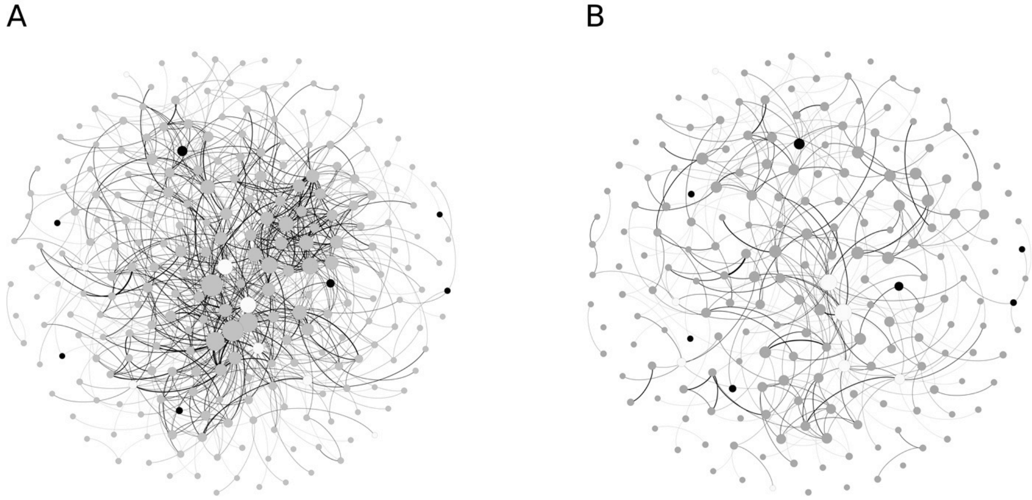
SI Fig. 4



SI Fig. 5


A
Bacteroidetes
Proteobacteria
Verrucomicrobia
Actinobacteria
Planctomycetes
Firmicutes
Chloroflexi
Spirochaetes
OP3
Chlamydiae
Cyanobacteria
Unknown bacteria
Biotic variables
Abiotic variables
B
DOC
Conductivity
TP
TN
pH
DO
SUVA$_{254}$
Temperature
Abiotic variables
Bacterial OTUs
Chla
Rotifers
Cladocerans
Copepods
picoeukaryotes
picocyanobacteria
Bacteria
Biotic variables

SI Fig. 6



SI Table 1

Landscape and sites	N Taxa	PSR	PSE	PD	NRI	LCBD	BA
Discontinous							
BGR2	168	150.6	0.8	24.8	2.2	0.14	1.3
BGR17	120	108.7	0.7	21.9	1.0	0.21	8.7
BGR33	126	112.8	0.7	22.7	2.2	0.26	1.9
BGR40	224	200.1	0.8	27.2	2.2	0.15	1.2
BGR7	187	166.5	0.8	28.0	1.9	0.13	2.9
BGRh	200	180.6	0.8	30.7	1.1	0.12	3.9
NASa	286	256.1	0.8	37.4	3.3	0.12	1.7
NASb	223	201.1	0.5	32.4	3.7	0.22	1.0
NASc	119	103.3	0.8	16.3	1.7	0.09	13.5
NASd	154	135.9	0.8	20.9	0.9	0.11	4.3
NASe	123	110.4	0.7	22.4	2.2	0.08	19.3
NASg	192	171.9	0.8	25.6	2.0	0.07	6.0
NASh	289	258.1	0.8	36.5	2.3	0.17	8.4
NASi	104	92.9	0.7	18.5	2.0	0.15	8.4
Sporadic							
KWK1	180	156.2	0.8	24.0	2.1	0.08	6.2
KWK11	204	158.9	0.8	29.3	1.1	0.13	2.7
KWK12	190	157.7	0.9	26.6	1.4	0.15	1.9
KWK17	242	182.0	0.7	32.3	2.5	0.08	1.6
KWK19	203	157.8	0.8	27.1	2.0	0.05	1.8
KWK22	157	129.6	0.7	22.6	2.4	0.08	2.2
KWK33	202	160.3	0.8	27.7	2.8	0.10	1.8
KWK6	229	185.3	0.9	33.4	2.1	0.23	4.7
KWK7	170	141.2	0.8	24.8	1.9	0.11	2.4
SAS-S1	267	238.9	0.8	39.8	2.5	0.21	5.9
SAS-S2	365	328.9	0.8	51.7	2.6	0.12	1.1
SAS-S5	389	349.4	0.8	53.7	1.9	0.12	1.8
SAS-S8	277	250.9	0.6	41.4	2.9	0.15	2.5
SAS-N2	329	293.8	0.7	46.3	2.3	0.10	3.5
SAS-N3	192	174.0	0.8	35.7	1.2	0.31	30.0
Rock-basin lakes							
IQUAL	204	183.7	0.7	31.2	2.3	0.33	1.9
CAR	287	260.9	0.8	36.9	2.9	0.15	4.2
OLSH	248	223.7	0.8	37.3	2.8	0.19	3.5
PAC	286	260.3	0.9	37.9	3.1	0.14	4.2
WP1	155	138.2	0.6	23.5	1.3	0.18	2.0

SI Table 2

OTU ID	Degree	RA	Taxonomy
3	47	3.3	Bacteroidetes/ Sphingobacteria/ Sphingobacteriales/ Flexibacteraceae/ *Arcicella*
2426	45	1.7	Proteobacteria/ Betaproteobacteria/ Burkholderiales/ Comamonadaceae/ Caenimonas
1	39	6.2	Proteobacteria/ Betaproteobacteria/ Burkholderiales/ Comamonadaceae/ *Variovorax*
14	38	2.0	Actinobacteria/ Actinobacteria/ Actinomycetales/ ACK-M1
2	32	9.3	Actinobacteria/ Actinobacteria/ Actinomycetales/ ACK-M1
6	32	1.3	Verrucomicrobia/ Opitutae/ Puniceicoccales/ Puniceicoccaceae /*Pelagicoccus*
795	28	0.9	Actinobacteria/ Actinobacteria/ Actinomycetales/ ACK-M1
80	27	0.2	Proteobacteria/ Alphaproteobacteria/ Rhizobiales/ Beijerinckiaceae/ *Beijerinckia*
1709	26	1.8	Proteobacteria/ Betaproteobacteria/ Burkholderiales/ Comamonadaceae/ *Limnohabitans*
24	26	1.0	Verrucomicrobia/ Opitutae/ Puniceicoccales/ Puniceicoccaceae/ *Pelagicoccus*
25	26	0.8	Actinobacteria/ Actinobacteria/ Actinomycetales/ Mycobacteriaceae/ *Mycobacterium*
126	24	0.1	Actinobacteria/ Actinobacteria/ Actinomycetales/ ACK-M1
13	23	1.1	Proteobacteria/ Betaproteobacteria/ Burkholderiales/ Comamonadaceae/ *Curvibacter*
15	23	1.1	Verrucomicrobia/ Spartobacteria/ Spartobacteriales/ Spartobacteriaceae/ *CandidatusXiphinematobacter*
28	23	0.6	Actinobacteria/ Actinobacteria/ Acidimicrobiales/ CL500-29
44	23	0.3	Actinobacteria/ Actinobacteria/ Acidimicrobiales/ CL500-29
18	22	0.9	Bacteroidetes/ Sphingobacteria/ Sphingobacteriales/ Chitinophagaceae/ *Sediminibacterium*
35	22	0.4	Proteobacteria/ Alphaproteobacteria/ Rhizobiales/ Beijerinckiaceae/ *Beijerinckia*
453	22	0.4	Proteobacteria/ Betaproteobacteria/ Burkholderiales/ Burkholderiaceae/ *Polynucleobacter*
467	22	0.4	Bacteroidetes/ Sphingobacteria/ Sphingobacteriales/ Chitinophagaceae/ *Sediminibacterium*
43	21	0.3	Chloroflexi/ SOGA31
508	20	0.1	Proteobacteria/ Betaproteobacteria/ Burkholderiales/ Oxalobacteraceae/ *Herminiimonas*
1242	19	0.7	Proteobacteria/ Betaproteobacteria/ Burkholderiales/ Comamonadaceae/ *Limnohabitans*
50	19	0.2	Proteobacteria/ Alphaproteobacteria/ Rhodobacterales/ Rhodobacteraceae/ *Rhodobacter*