Supplementary Information

The Biodiversity and Geochemistry of Cryoconite Holes in Queen Maud Land, East Antarctica

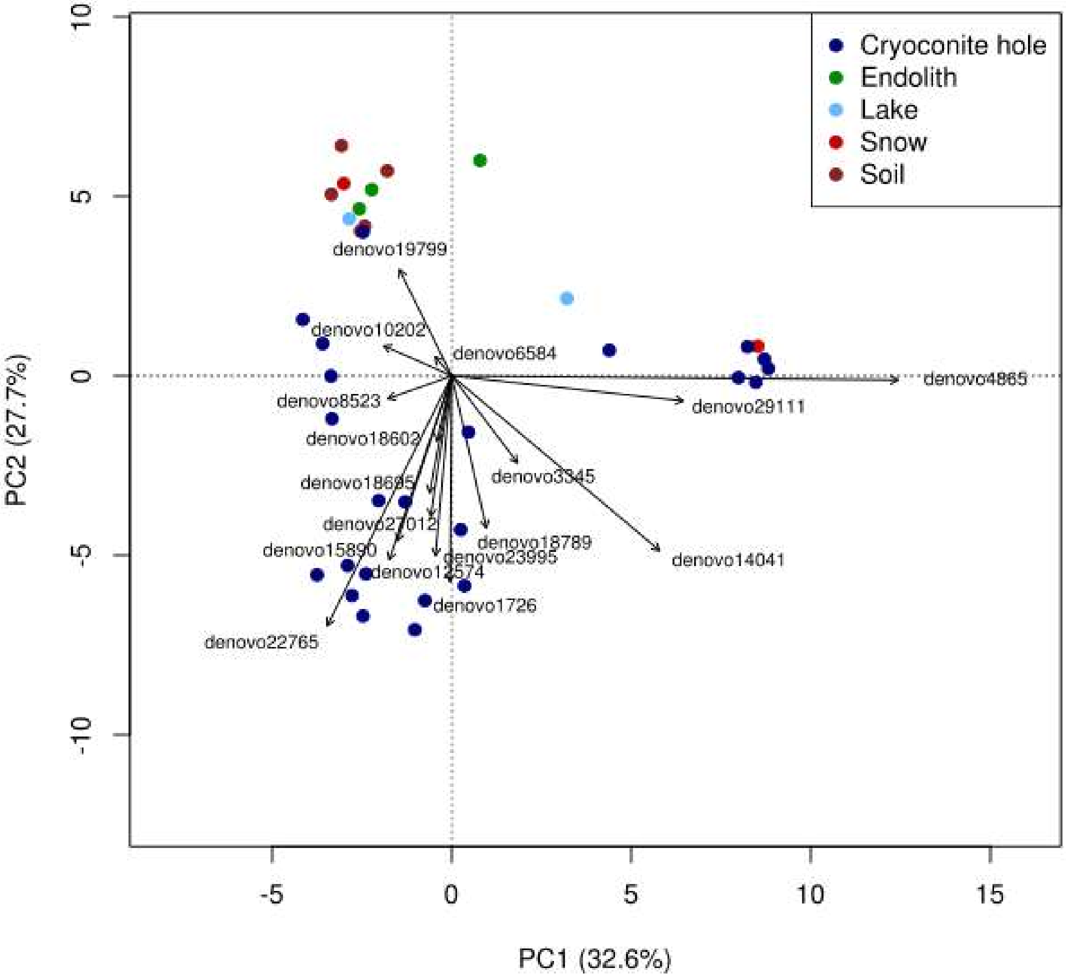

Figure S1. Principal component analysis of the bacterial OTUs. Samples cluster according to habitats.

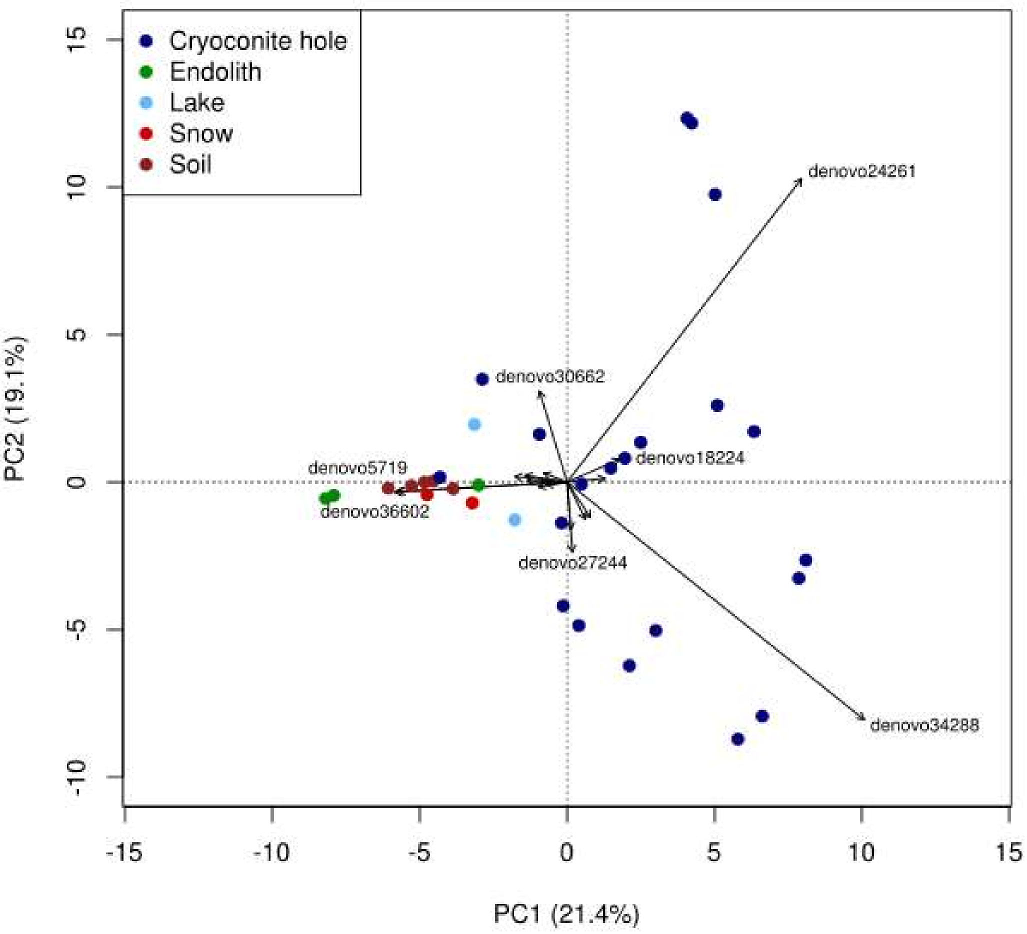

Figure S2. Principal component analysis of the eukaryotic OTUs. Samples cluster according to habitats.

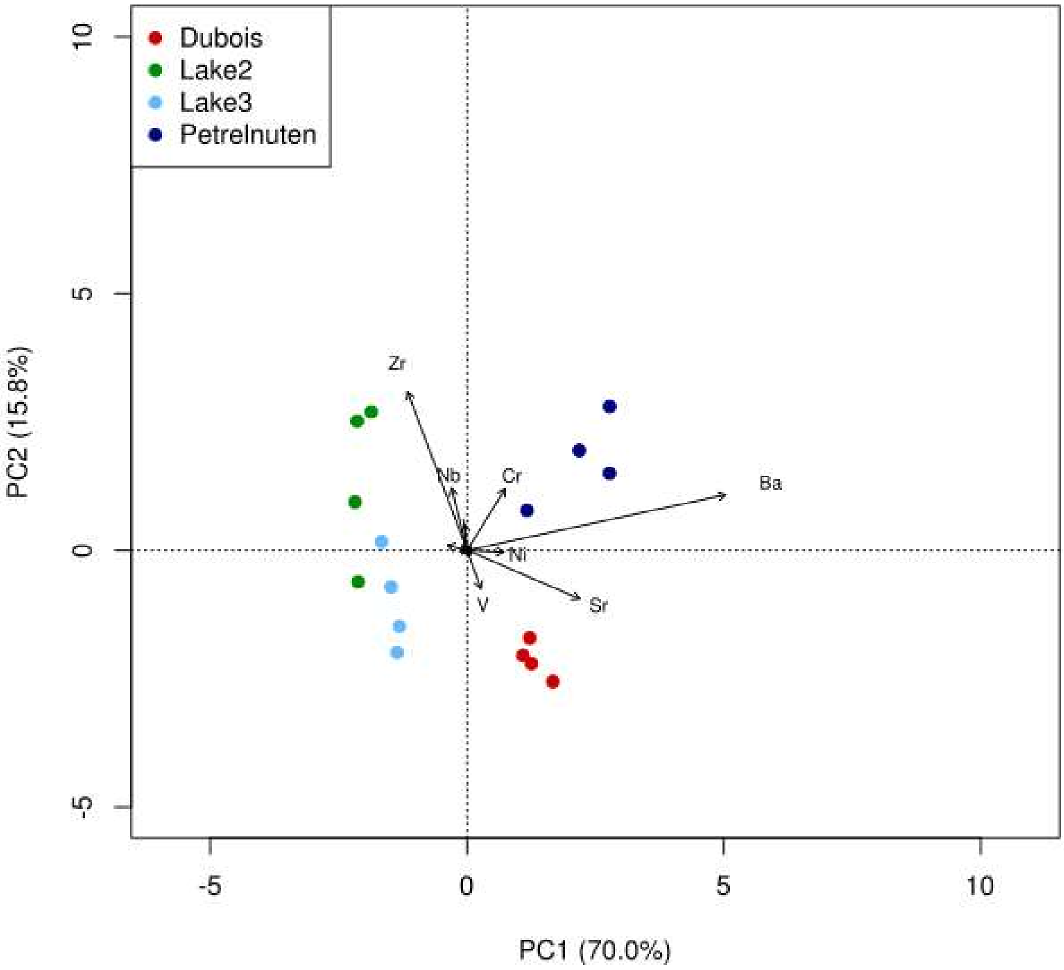

Figure S3. Principal component analysis of selected trace elements that cause the separation (primarily Zr, Ba and Sr).

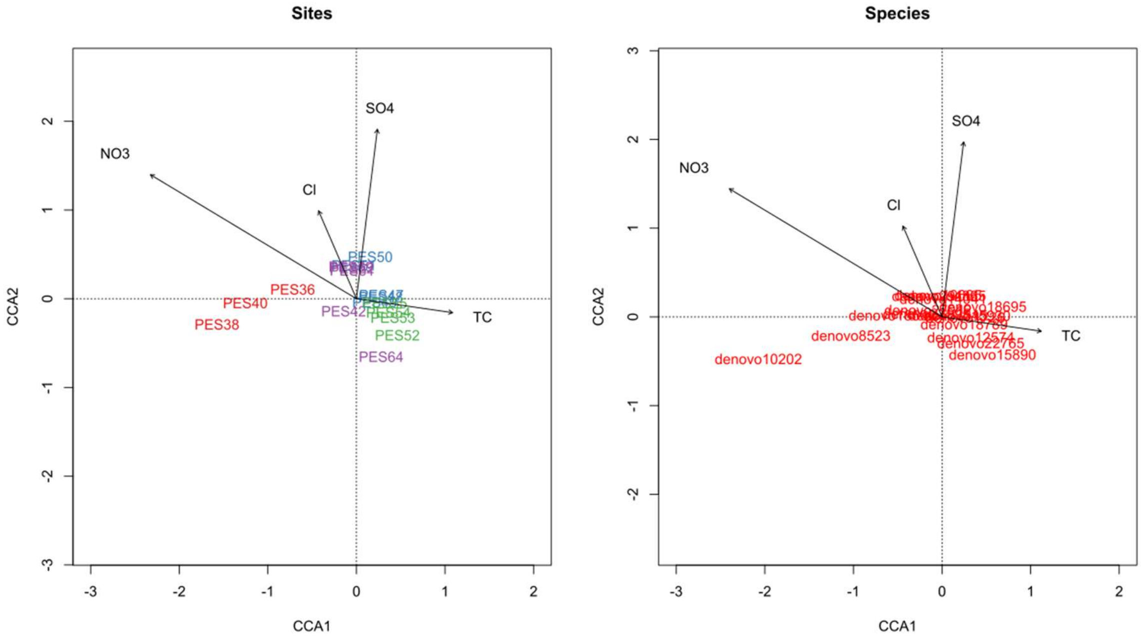

Figure S4. Partial canonical correspondence analysis of the bacterial abundances and all non-collinear environmental variables (i.e., after identification and exclusion of redundant predictor variables) and without spatial effects. Samples from Lake 3 in Utsteinen clustered with higher nitrate concentration and samples from Dubois with a higher TC abundance. Otherwise no clear trends could be observed.

Table S1. Number of sequences before and after quality control for bacterial and eukaryotic sequences, respectively.

	16S		18S	
Sample ID	**Before quality filtering**	**After quality filtering**	**Before quality filtering**	**After quality filtering**
PES17_36	79285	71418	112519	112201
PES17_38	115832	111434	44238	44166
PES17_39	128336	123761	31865	31789
PES17_40	107580	104609	27128	27074
PES17_42	225182	218495	103515	103323
PES17_43	219156	213095	67378	67199
PES17_47	82531	79949	60130	59998
PES17_48	123666	120275	64459	64306
PES17_49	163446	158674	126366	126115
PES17_50	107304	104667	158362	158063
PES17_51	95033	93296	-	-
PES17_52	113682	110463	119486	119205
PES17_53	126238	122760	72656	72461
PES17_54	120805	117807	181725	181281
PES17_55	112134	108809	146821	146408
PES17_56	193142	187986	154063	153724
PES17_59	226518	220298	32560	32444
PES17_60	186567	182136	213031	212325
PES17_61	143702	140104	155784	155222
PES17_62	104661	102291	-	-
PES17_63	114068	111261	101205	100998
PES17_64	101054	98423	70930	70674
PES17_65	117504	113810	192746	192282
Total	3107426	3015821	2236967	2231258

Table S2. Distribution of 97% clustered bacterial OTUs assigned to the lowest possible taxonomic level. Values are the relative abundance of the taxa in percentage of total sequences and presented are all OTUs with >0.1% abundance.

Phylum	Class	Order; Family; Genus; Species	PES36	PES38	PES39	PES40	PES42	PES43	PES47	PES48	PES49	PES50	PES51	PES52
Acidobacteria	[Chloracido-bacteria]	RB41; Ellin6075	2.5	0.1	0	0	0.6	1.2	3.7	7.7	0.9	0.3	0.3	17.3
Actinobacteria	Acidimicrobiia	Acidimicrobiales; C111	0	<0.05	0	0	7.4	3.1	6.1	3.2	5.9	3.8	3.3	8.5
		Actinomycetales	1.1	1.0	0.2	1.3	4.5	1.4	12.9	9.7	4.4	7.4	4.4	7.9
		Actinomycetales; Geodermatophilaceae	0.5	0.7	1.2	3.1	2.3	0.6	1.9	2.3	1.1	6.2	3.6	0.6
		Actinomycetales; Intrasporangiaceae	0	0	0	0	0	0	0	0	0.2	6.0	4.0	0
		Actinomycetales; Kineosporiaceae	0	3.9	2.8	1.3	0	0	0	0	0	0	0	0
		Actinomycetales; Microbacteriaceae	2.4	0.1	5.5	0.1	0.1	0.1	0.0	0.0	0.1	0.1	0.1	0.1
		Actinomycetales; Microbacteriaceae; Yonghaparkia	1.8	4.0	1.0	4.2	9.5	12.3	3.9	6.4	5.9	22.5	14.0	5.8
		Actinomycetales; Nocardioidaceae	4.5	17.7	17.4	27.9	7.2	2.9	2.1	3.7	3.7	4.4	10.6	5.1
		Actinomycetales; Nocardioidaceae; Aeromicrobium	0.5	0.2	0.9	0.9	0.2	0.1	<0.05	<0.05	0.2	0.2	0.3	0.0
		Actinomycetales; Sporichthyaceae	1.2	17.3	9.5	17.4	8.6	1.5	7.7	6.9	9.2	13.6	17.4	6.4
	Thermoleo-philia	Gaiellales; AK1AB1_02E	0	0	<0.05	0	1.1	0.9	0.2	0.2	0.1	0.1	1.1	0.3
		Solirubrobacterales; Patulibacteraceae	0.4	0.9	0.8	2.5	0	0	0	<0.05	0	0	<0.05	0.1
Bacteriodetes	Cytophagia	Cytophagales	0	0	0	0	0.1	3.3	0	0	0	0	0	0.1
		Cytophagales; Cyclobacteriaceae	0	0	0	0	<0.05	0.4	3.1	3.9	2.7	0.5	0.3	2.1

		Cytophagales; Cytophagaceae; Hymenobacter	2.7	25.2	25.1	12.6	0.5	0.5	0.9	5.3	4.3	1.4	0.5	0.6
		Cytophagales; Cytophagaceae; Spirosoma	0.3	0	0	<0.05	6.6	4.8	0.5	0.9	0.8	0.1	0.3	0.3
	Flavo- bacteriia	Flavobacteriales; Flavobacteriaceae; Flavobacterium	0.5	0	0	0	0.5	5.3	0	0	0	6.7	1.4	0
	Sphingo- bacteriia	Sphingobacteriales; Sphingobacteriaceae	0	0	0	0.0	0.0	0	0.1	1.1	0.0	0.0	0.1	0
	[Rhodo- thermi]	[Rhodothermales]; Rhodothermaceae; Rubricoccus	0.1	<0.05	0	0.0	1.7	1.5	0.0	0.3	<0.05	0.4	0.2	0
		[Saprospirales]; Chitinophagaceae	1.0	<0.05	0	0	6.9	3.1	0	0	0.7	0.1	1.0	0.8
		[Saprospirales]; Chitinophagaceae; Segetibacter	0	0	0	0	1.9	1.3	0	0	0.3	0.1	0.4	0.1
Chloroflexi	Thermo- microbia	JG30-KF-CM45	0	0	0	0	0.1	0.9	<0.05	<0.05	0	0.1	0.1	1.1
Cyanobacteria	Oscillatorio- phycideae	Chroococcales; Xenococcaceae	2.5	<0.05	<0.05	0.1	4.1	21.1	1.0	0.2	0.0	2.6	0.8	0.5
		Oscillatoriales; Phormidiaceae; Phormidium	1.4	0.1	<0.05	0	0.4	0	4.1	9.8	17.4	1.2	0.5	9.4
	Synechococco- phycideae	Pseudanabaenales; Pseudanabaenaceae	0.6	0	<0.05	0	0	0	<0.05	<0.05	0	4.5	1.3	0.8
FBP			0.5	<0.05	<0.05	0.1	4.1	9.0	0.5	0.7	0.8	0.1	0.3	0.1

Proteobacteria	Alphaproteobacteria	Caulobacterales; Caulobacteraceae; Mycoplana	0	0	0	0	<0.05	0.1	2.4	0.5	0.6	0.2	0.1	0.1
		Rhodobacterales; Rhodobacteraceae; Rubellimicrobium	0	0	0	0	4.8	1.9	3.3	2.9	2.3	2.6	1.0	0.9
		Rhodospirillales; Acetobacteraceae	0.1	0	0.1	0.7	5.0	1.3	0.1	0.1	0.5	1.0	0.6	0.2
		Rhodospirillales; Acetobacteraceae; Roseococcus	0.5	0	0	0	0.1	0.7	3.0	3.1	0.9	1.5	0.5	0.9
		Sphingomonadales; Sphingomonadaceae	0	<0.05	0.1	0	0.2	0.2	0	0	<0.05	0.1	0.1	0.1
		Sphingomonadales; Sphingomonadaceae; Kaistobacter	7.9	7.4	14.6	15.2	16.1	3.9	19.1	20.6	10.6	4.7	16.3	0.7
	Betaproteobacteria	Burkholderiales; Comamonadaceae	5.5	0.1	1.2	0.5	0.6	1.2	0.6	1.2	0.9	0.2	0.6	0.6
		Burkholderiales; Comamonadaceae	3.6	15.2	15.0	11.1	1.4	0.9	0.3	0.4	1.4	0.3	1.8	0.5
		Burkholderiales; Comamonadaceae; Hydrogenophaga	0.1	0	0	<0.05	<0.05	0.1	0.0	0.2	<0.05	2.5	0.6	<0.05
		Burkholderiales; Oxalobacteraceae	0.0	4.0	0.4	0.6	1.2	0	0	0	0	0	0	0
		Burkholderiales; Oxalobacteraceae; Janthinobacterium	1.0	<0.05	0	0	<0.05	0	0	0	0	0	0.1	0
	Gamma-proteo- bacteria	Xanthomonadales; Xanthomonadaceae	0.4	<0.05	0	0	0.7	5.6	0.1	0	<0.05	0.1	0.1	0.4
		Xanthomonadales; Xanthomonadaceae; Lysobacter	0	0	0	0	0.3	0.6	1.6	1.3	1.3	0.5	0.7	0.8
		Xanthomonadales; Xanthomonadaceae; Thermomonas	<0.05	0	0	0	0.1	1.0	15.3	2.6	17.8	3.2	5.0	17.2

Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales; Verrucomicrobiaceae	0.6	<0.05	<0.05	<0.05	1.1	5.6	4.0	3.1	3.9	0.6	0.7	2.3
		Verrucomicrobiales; Verrucomicrobiaceae	0.5	0	0	0	0	0	0.9	1.0	0.6	0.1	0.0	3.7
		[Chthoniobacterales]; [Chthoniobacteraceae]; DA101	0	<0.05	0	0	0	0	0.8	0.5	0.6	0.1	0.1	3.8
Unassigned			55.4	3.0	4.4	0.4	0.2	1.8	0.2	0.1	0.1	0.1	5.5	<0.05

Table S2. continued.

Phylum	Class	Order; Family; Genus; Species	PES53	PES54	PES55	PES56	PES59	PES60	PES61	PES62	PES63	PES64	PES65
Acidobacteria	**[Chloracido-bacteria]**	RB41; Ellin6075	12.4	11.2	7.1	1.6	0	0	0	0	<0.05	<0.05	3.5
Actinobacteria	**Acidimicrobiia**	Acidimicrobiales; C111	3.7	3.8	1.6	2.5	1.1	1.0	2.0	1.0	2.6	2.6	0.4
		Actinomycetales	6.2	11.5	13.3	9.3	0.3	0.6	1.4	2.3	1.7	1.4	0.2
		Actinomycetales; Geodermatophilaceae	0.6	0.9	1.6	1.5	0.2	0.3	0.3	0.3	1.1	0.2	0.7
		Actinomycetales; Intrasporangiaceae	0	0	0	0	0	0	0	0	0	0	0
		Actinomycetales; Kineosporiaceae	0	0	0	0	0	0	0	0	0	0	0
		Actinomycetales; Microbacteriaceae	0.1	<0.05	<0.05	0.1	0.5	0.4	0.2	0.3	0.3	0.1	1.7
		Actinomycetales; Microbacteriaceae; Yonghaparkia	5.2	7.1	6.6	8.7	18.9	19.7	19.3	16.7	18.7	16.0	5.7
		Actinomycetales; Nocardioidaceae	3.9	4.3	2.9	2.1	3.7	3.2	2.4	2.4	2.6	1.6	1.9
		Actinomycetales; Nocardioidaceae; Aeromicrobium	0.2	0.0	0.2	0.0	0.0	0	0	0	<0.05	0	1.2
		Actinomycetales; Sporichthyaceae	7.3	8.8	12.1	8.0	2.2	2.6	3.2	2.9	2.3	0.9	1.2
	Th er	Gaiellales; AK1AB1_02E	0.5	0.3	0.2	0.1	0	0	0	0	0	0	0.1

		Solirubrobacterales; Patulibacteraceae	0.2	0.1	0.1	0.0	0	0	0	0	0	0	<0.05
Bacteriodetes	**Cytophagia**	Cytophagales	0.1	0.2	0.1	<0.05	0	0	0	0	0	0	0
		Cytophagales; Cyclobacteriaceae	0.2	1.0	<0.05	0.9	0	0	0	0	0.0	1.2	0
		Cytophagales; Cytophagaceae; Hymenobacter	2.0	2.4	2.0	5.3	9.1	6.1	5.0	4.9	4.9	2.9	5.4
		Cytophagales; Cytophagaceae; Spirosoma	2.4	0.8	1.0	2.2	0.1	0.1	0.2	0.1	0.6	0	0.2
	Flavobacterii	Flavobacteriales; Flavobacteriaceae; Flavobacterium	0	0	0	0	0	0	0	0	0	15.3	0.6
	Sphingobacteria	Sphingobacteriales; Sphingobacteriaceae	0	0	0	0	0	0	0	0	0	3.1	0
	[Rhodothermi]	[Rhodothermales]; Rhodothermaceae; Rubricoccus	<0.05	<0.05	0.1	0.1	0	0	0	0	0.1	0.3	0.8
		[Saprospirales]; Chitinophagaceae	0.6	0.8	2.9	5.1	<0.05	<0.05	0	0	0	0	1.0
		[Saprospirales]; Chitinophagaceae; Segetibacter	0.1	0.2	0.3	<0.05	0	0	0	0	0	0	1.8
Chloroflexi	**Thermomicrobia**	JG30-KF-CM45	0.1	0.4	0.1	0.1	0	0	0	0	0	0.1	0.4
Cyanobacteria	**Oscillatoriophycideae**	Chroococcales; Xenococcaceae	1.7	4.7	6.5	7.0	45.9	48.2	40.9	52.8	43.2	0.3	0.3
		Oscillatoriales; Phormidiaceae; Phormidium	18.9	20.2	20.0	15.0	0	0	0	0	<0.05	27.8	38.0

	Synechococco- phycideae	Pseudanabaenales; Pseudanabaenaceae	12.0	4.4	6.9	12.3	0	0	0	0	0	0	0
FBP			0.2	0.1	0.1	0.1	<0.05	<0.05	<0.05	<0.05	0.1	2.0	<0.05
Proteobacteria	**Alphaproteobacteria**	Caulobacterales; Caulobacteraceae; Mycoplana	0	<0.05	0	0.1	0	0	0	0	0.1	3.8	3.8
		Rhodobacterales; Rhodobacteraceae; Rubellimicrobium	0.9	1.1	0.6	1.2	0.3	0.3	0.5	0.1	0.9	0.7	0.5
		Rhodospirillales; Acetobacteraceae	0.6	0.3	0.3	0.5	0.1	0.1	0.1	<0.05	0.6	0.2	0.2
		Rhodospirillales; Acetobacteraceae; Roseococcus	0.5	1.1	0.3	1.7	0.0	<0.05	0.0	<0.05	1.2	2.9	0.5
		Sphingomonadales; Sphingomonadaceae	0.3	0.1	0.1	0.1	0	0	<0.05	0	0.0	<0.05	8.9
		Sphingomonadales; Sphingomonadaceae; Kaistobacter	5.5	4.1	3.1	6.0	2.7	2.3	5.3	3.0	3.9	2.4	1.8
	Betaproteo- bacteria	Burkholderiales; Comamonadaceae	0.7	0.5	0.3	0.5	0.1	0.1	0.3	0.2	1.2	0.2	1.2
		Burkholderiales; Comamonadaceae	0.7	0.8	1.8	0.3	0.1	<0.05	<0.05	<0.05	0.1	<0.05	1.3
		Burkholderiales; Comamonadaceae; Hydrogenophaga	0	0	0	0	<0.05	<0.05	0.1	0.1	0.4	3.9	1.3
		Burkholderiales; Oxalobacteraceae	0	0	0	0	0	0	0	0	0	0	0
		Burkholderiales; Oxalobacteraceae; Janthinobacterium	0	0	0	0	0	0	0	0	0	0	4.8
	Gamma- proteobacteria	Xanthomonadales; Xanthomonadaceae	0.3	0.7	0.7	1.7	10.8	12.2	17.1	11.1	11.9	1.0	0.2
		Xanthomonadales; Xanthomonadaceae; Lysobacter	2.3	0.8	0.5	0.3	1.6	1.5	0.7	0.2	0.3	0.6	0.2
		Xanthomonadales; Xanthomonadaceae; Thermomonas	4.4	3.2	1.1	2.1	0	0	0	0	0.0	8.0	0
Verrucomicrobia	**Verruco-**	Verrucomicrobiales; Verrucomicrobiaceae	1.2	1.2	0.6	0.2	<0.05	<0.05	<0.05	<0.05	<0.05	0.1	0.4

		Verrucomicrobiales; Verrucomicrobiaceae	1.4	1.4	0.3	2.1	0	0	0	0	0	0.3	4.3
		[Chthoniobacterales]; [Chthoniobacteraceae]; DA101	2.9	1.6	1.0	1.4	0	0	0	0	0	0.1	4.8
Unassigned			<0.05	0.1	3.7	0.0	2.2	1.3	1.1	1.7	1.1	0.2	0.8

Table S3. The core bacterial taxa present in all cryoconite hole samples at >1% relative abundance.

Phylum	**Class**	**Order**	**Family; Genus; Species**	**OTU ID**	**PES36**	**PES38**	**PES39**	**PES40**	**PES42**	**PES43**	**PES47**	**PES48**	**PES49**	**PES50**	**PES51**	**PES52**
Actinobacteria	Actinobacteria	Actinomycetales		denovo1726	0.2	<0.05	0.2	1.1	4.1	1.3	12.0	8.8	4.0	6.8	3.6	7.2
			Geodermatophilaceae	denovo19685	0.1	0.6	1.0	2.7	2.1	0.5	1.7	2.1	1.0	5.7	2.9	0.5
			Microbacteriaceae; Yonghaparkia	denovo14041	0.3	3.5	0.9	3.7	8.7	11.3	3.6	5.8	5.4	20.7	11.2	5.3
			Nocardioidaceae	denovo18602	0.7	14.5	12.6	17.4	3.5	1.4	0.8	1.4	1.2	1.8	4.4	0.6
			Sporichthyaceae	denovo23995	0.2	15.0	8.3	15.4	7.9	1.4	7.2	6.3	8.5	12.6	13.9	5.9
			Nocardioidaceae	denovo15045	0	<0.05	0.1	0.5	1.0	0.3	0.1	0.2	0.3	0.3	1.0	3.2
			Nocardioidaceae	denovo22480	0	<0.05	0.1	0.9	1.4	0.4	0.2	0.3	0.4	0.4	1.7	0.2
			Sporichthyaceae	denovo3326	<0.05	<0.05	<0.05	<0.05	0.2	<0.05	0.1	0.1	0.1	0.2	<0.05	0.1
Cyanobacteria	Oscillatoriophycideae	Chroococcales	Xenococcaceae	denovo4865	0.5	<0.05	<0.05	<0.05	3.7	19.1	0.9	0.1	<0.05	2.4	0.7	0.5
FBP				denovo15099	<0.05	<0.05	<0.05	0.1	3.2	5.1	<0.05	<0.05	<0.05	<0.05	0.3	0.1
Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae; Kaistobacter	denovo27012	1.5	6.4	12.7	13.4	10.8	2.7	14.7	15.1	9.0	3.9	12.9	0.5
		Rhodospirillales	Acetobacteraceae	denovo19929	<0.05	<0.05	0	0.6	4.6	1.2	0.1	0.1	0.4	0.9	0.5	0.2

	Betaproteo- bacteria	Burkholderiales	Xenococcaceae	denovo6584	1.1	0.1	1.0	0.4	0.6	1.1	0.6	1.1	0.9	0.2	0.5	0.5

Table S3. continued.

Phylum	Class	Order	Family; Genus; Species	OTU ID	PES53	PES54	PES55	PES56	PES59	PES60	PES61	PES62	PES63	PES64	PES65
Actinobacteria	Actinobacteria	Actinomycetales		denovo1726	5.8	10.9	12.2	8.7	0.3	0.5	1.3	2.2	1.5	1.3	0.2
			Geodermatophilaceae	denovo19685	0.6	0.9	1.5	1.4	0.2	0.2	0.2	0.3	1.1	0.2	0.6
			Microbacteriaceae; Yonghaparkia	denovo14041	4.8	6.8	6.0	8.1	17.8	19.0	18.6	16.1	17.5	14.6	4.8
			Nocardioidaceae	denovo18602	1.2	1.3	1.1	0.7	1.0	1.0	0.8	0.9	0.9	0.7	0.9
			Sporichthyaceae	denovo23995	6.8	8.4	11.1	7.4	2.1	2.5	3.0	2.8	2.2	0.8	1.0
			Nocardioidaceae	denovo15045	1.7	1.9	0.8	0.5	<0.05	<0.05	<0.05	<0.05	0.1	0.1	0.2
			Nocardioidaceae	denovo22480	0.5	0.4	0.4	0.2	<0.05	<0.05	<0.05	<0.05	0.1	0.2	0.3
			Sporichthyaceae	denovo3326	0.1	<0.05	<0.05	0.2	0.2	0.1	0.1	0.1	0.1	<0.05	<0.05
Cyanobacteria	Oscillatoriop-phycideae	Chroococcales	Xenococcaceae	denovo4865	1.6	4.5	5.9	6.4	42.6	46.0	39.1	50.7	39.8	0.2	0.3
FBP				denovo15099	0.1	0.1	0.1	<0.05	<0.05	<0.05	<0.05	<0.05	0.1	<0.05	<0.05
Proteobacteria	Alphaproteobacteria	Sphingo-monadales	Sphingomonadaceae; Kaistobacter	denovo27012	3.9	3.2	2.4	4.2	1.8	1.6	3.7	2.0	2.4	1.5	1.4
		Rhodo-spirillales	Acetobacteraceae	denovo19929	0.5	0.3	0.2	0.4	0.1	0.1	0.1	<0.05	0.6	0.2	0.2
	Betaproteo-bacteria	Burkholderiales	Xenococcaceae	denovo6584	0.6	0.5	0.3	0.4	0.1	0.1	0.3	0.2	1.1	0.2	1.0

Table S3. continued: continued. The NCBI hits of core bacterial taxa.

Phylum	Class	Order	Family; Genus; Species	OTU ID	Best NCBI hit	Accession number	Similarity [%]
Actinobacteria	Actinobacteria	Actinomycetales		denovo1726	Uncultured actinobacterium	FJ490312.1	99
			Geodermatophilaceae	denovo19685	Blastococcus sp.	EU704838.1	99
			Microbacteriaceae; Yonghaparkia	denovo14041	Leifsonia sp.	KT965169.1	99
			Nocardioidaceae	denovo18602	Nocardioides sp.	KY386518.1	99
			Sporichthyaceae	denovo23995	Uncultured actinobacterium	EU931108.1	99
			Nocardioidaceae	denovo15045	Nocardioides sp.	GQ420967.1	99
			Nocardioidaceae	denovo22480	Nocardioides sp.	GQ420967.1	97
			Sporichthyaceae	denovo3326	Leifsonia sp.	KT965169.1	96
Cyanobacteria	Oscillatorio-phycideae	Chroococcales	Xenococcaceae	denovo4865	Uncultured cyanbacterium	HQ230210.1	99
FBP				denovo15099	Uncultutred endolithic bacterium	AB374370.1	99
Proteobacteria	Alphaproteobacteria	Sphingo-monadales	Sphingomonadaceae; Kaistobacter	denovo27012	Sphingomonas sp.	MF002313.1	99
		Rhodo-spirillales	Acetobacteraceae	denovo19929	Uncultured bacterium	FR667548.1	97
	Betaproteo-bacteria	Burkholderiales	Comamonadaceae	denovo6584	Polaromonas sp.	KF414342.1	99

Table S4. Taxonomic identification of the discriminating OTUs in the principal component analysis (Figure 3).

OTU ID	Phylum	Class	Order	Family	Genus	Species	Best NCBI hit	Accession number	Similarity [%]
denovo1726	Actinobacteria	Actinobacteria	Actinomycetales	-	-	-	Uncultured actinobacterium	FJ490312.1	99
denovo3345	Bacteriodetes	Cytophagia	Cytophagales	Cytophagaceae	*Hymenobacter*	-	Uncultured Bacteriodetes	KC442558.1	98
denovo4865	Cyanobacteria	Oscillatoriophycideae	Chroococcales	Xenococcaceae	-	-	Uncultured cyanbacterium	HQ230210.1	99
denovo6584	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	-	-	Polaromonas sp.	KF414342.1	99
denovo8523	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	-	-	Uncultured Comamonadaceae	GQ454852.1	99
denovo10202	Bacteriodetes	Cytophagia	Cytophagales	Cytophagaceae	*Hymenobacter*	-	Hymenobacter sp. R-36490	FR682723.1	99
denovo12574	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	*Thermomonas*	-	Uncultured Gammaproteobacterium	FR749755.1	99
denovo14041	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	*Yonghaparkia*	-	Leifsonia sp.	KT965169.1	99
denovo15890	Acidobacteria	[Chloracidobacteria]	RB41	Ellin6075	-	-	Uncultured Blastocatella sp.	LT625222.1	99
denovo15930	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	*Rubellimicrobium*	-	Rubellimicrobium sp	JQ401336.1	99
denovo18602	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	-	-	Nocardioides sp.	KY386518.1	99
denovo18695	Cyanobacteria	Synechococcophycideae	Pseudanabaenales	Pseudanabaenaceae	-	-	Leptolyngbya sp. LEGE 07075	HM217080.1	98
denovo18789	Actinobacteria	Acidimicrobiia	Acidimicrobiales	C111	-	-	Uncultured Actinobacterium	EF628488.1	99
denovo19685	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophilaceae	-	-	Blastococcus sp.	EU704838.1	99
denovo19799	Acidobacteria	[Chloracidobacteria]	RB41	Ellin6075	-	-	Uncultured acidobacterium	JQ402009.1	99
denovo22765	Cyanobacteria	Oscillatoriophycideae	Oscillatoriales	Phormidiaceae	*Phormidium*	-	Phormidium sp. CCALA 846	GQ504034.1	99
denovo23995	Actinobacteria	Actinobacteria	Actinomycetales	Sporichthyaceae	-	-	Agrococcus sp.	KF029486.1	99

Table S5. Distribution of 99% clustered eukaryotic OTUs assigned to the lowest possible taxonomic level. Values are the relative abundance of the taxa in percentage of total sequences and presented are all OTUs with >0.1% abundance.

				PES36	PES38	PES39	PES40	PES42	PES43	PES47	PES48	PES49	PES50	PES52
Archaeplastida	Chloroplastida	Charophyta	Brassicales; Brassica; Brassica oleracea var. capitata	0.6	<0.05	0	0	0	0	0	0	0	0	0
			Poales; Triticum; Triticum aestivum	0.6	0	0	0	0	<0.05	0	<0.05	0	0	<0.05
			Phragmoplastophyta; Zygnematophyceae; Mesotaenium sp. AG-2009-1	4.4	0.1	0.1	0	0	0	<0.05	<0.05	<0.05	<0.05	0
		Chlorophyta	Chlorophyceae; Chlorococcum oleofaciens; Chlorococcum oleofaciens	0.2	0	<0.05	0	<0.05	0.2	0	0	0	<0.05	78.8
			Trebouxiophyceae; Actinastrum hantzschii; Actinastrum hantzschii	1.9	<0.05	95.3	96.3	0.1	0.5	18.1	89.4	1.0	21.9	7.0
			Trebouxiophyceae; uncultured Dunaliellaceae	30.1	0.2	0	0.2	0	0	0	0	0	0	0
			Trebouxiophyceae; uncultured eukaryote	4.7	0.1	0.0	0	0	<0.05	0.0	0.2	0	0	0
			Chlorodendrales; Tetraselmis; Tetraselmis subcordiformis	0	0	0	0	0.0	0	0	0	0	0	0.0
			Prasiolales; Prasiola; Prasiola furfuracea	37.6	0.2	0.1	0.0	0.1	0.0	<0.05	<0.05	0	0	0
			Prasiolales; Stichococcus; Stichococcus jenerensis	1.4	98.8	4.3	3.4	48.6	0.2	<0.05	<0.05	0.0	0.1	<0.05
	Rhodopycea		Bangiales; Pyropia; Pyropia fallax	1.3	<0.05	0.0	0.1	1.5	26.2	80.7	2.3	95.4	77.9	2.3
Excavata	Discoba	Discicristat	Tetramitia; AND12; Heterolobosea sp. OSA	0	0	0	0	0	<0.05	0	0.1	0	0	0
Opisthokonta	Holozoa	Metazoa	Bdelloidea; Adinetida; Hypsibius dujardini	3.7	0.1	0	0	0	0	0	0	0	0	<0.05
			Eutardigrada; Parachela; uncultured eukaryote	2.6	0.4	0	0	0	0	0	0.1	0	0	0

	Nucletmycea	Fungi	Eurotiomycetes; Eurotiales; Penicillium sp. NS051-06	0.8	0	0	0	0	0	0	0	0	0	0
			Eurotiomycetes; Eurotiales; Talaromyces radicus	0	0	0	0	0	0	0	0	0	0	0
			Saccharomycetes; Saccharomycetales; Saccharomyces cerevisiae Kyokai no. 7	0	0	0	0	0	<0.05	<0.05	<0.05	0	0	0
			Incertae Sedis; Hyaloraphidium; Hyaloraphidium curvatum	0	0	0	0	<0.05	0	0.1	0.2	0.1	0	0
			Incertae Sedis; Malassezia; uncultured eukaryote	4.0	0.1	0.1	0	<0.05	<0.05	0	0	0	0	<0.05
			Incertae Sedis; Malassezia; uncultured fungus	0	0	0	0	0	0	0	0.0	0	0	0
SAR	Alveolata	Ciliophora	Phyllopharyngea; Cyrtophoria; Colepidae environmental sample	0	0	0	0	0	0	0	0	0	0	0
	Rhizaria	Cercozoa	Glissomonadida; Heteromita; Cercozoa sp. B128	0.3	<0.05	0	0	29.1	<0.05	<0.05	0	0	0	0
			Glissomonadida; Heteromita; uncultured cercozoan	0	0	0	0	0.1	12.2	0	0	0.4	0	0
			Glissomonadida; Heteromita; uncultured eukaryote	0.5	0	0	0	0	0	0	0	0	<0.05	11.6
			Glissomonadida; uncultured eukaryote	0	0	0	0	0.8	57.4	0	0	0	0	0
			Thecofilosea; E-A1	0	0	0	0	0	0	0	0.0	0	0	0
			Thecofilosea; uncultured eukaryote	0	0	0	<0.05	19.7	3.3	1.1	7.5	3.1	0.1	0.3
	Stramenopiles	Ochrophyta	Chrysophyceae; uncultured eukaryote	1.4	0	0	0	0	0	0	<0.05	0	0	0
			Chrysocapsales; Hydrurus; uncultured Hydrurus	4.0	<0.05	0	0	0	<0.05	0	0	0	<0.05	<0.05
Unassigned				0	0	0	0	<0.05	0.1	0	0	0	0	0

Table S5. continued.

				PES53	PES54	PES55	PES56	PES59	PES60	PES61	PES63	PES64	PES65
Archaeplastida	Chloroplastida	Charophyta	Brassicales; Brassica; Brassica oleracea var. capitata	0	0.1	0	<0.05	0.2	0.4	1.3	0	0	0
			Poales; Triticum; Triticum aestivum	<0.05	0.2	0	0	15.3	60.6	30.8	<0.05	<0.05	0
			Phragmoplastophyta; Zygnematophyceae; Mesotaenium sp. AG-2009-1	<0.05	1.2	<0.05	<0.05	0.1	0.6	0.7	<0.05	0	0
		Chlorophyta	Chlorophyceae; Chlorococcum oleofaciens; Chlorococcum oleofaciens	1.1	0.3	0	0	3.1	0.2	0.2	7.0	28.1	0.1
			Trebouxiophyceae; Actinastrum hantzschii; Actinastrum hantzschii	6.7	35.1	2.4	28.6	0.1	0.2	<0.05	0.2	<0.05	0.6
			Trebouxiophyceae; uncultured Dunaliellaceae	0	0.1	0	0	0	0.0	0	0	0	0
			Trebouxiophyceae; uncultured eukaryote	0	0.1	0	<0.05	0.2	0.1	0.3	0	0	0
			Chlorodendrales; Tetraselmis; Tetraselmis subcordiformis	0.2	2.1	0	<0.05	0	0	0	0	0	<0.05
			Prasiolales; Prasiola; Prasiola furfuracea	0	0.1	0	<0.05	22.8	3.3	2.9	0.7	0	0.1
			Prasiolales; Stichococcus; Stichococcus jenerensis	0	0	<0.05	<0.05	0.0	0.3	0.5	0	<0.05	<0.05
	Rhodopycea		Bangiales; Pyropia; Pyropia fallax	5.4	19.1	4.3	30.0	30.7	6.9	14.2	85.7	0.9	0.9
Excavata	Discoba	Discicristat	Tetramitia; AND12; Heterolobosea sp. OSA	0	0	0	0	0	0	0	0	8.1	0.0
Opisthoko	Holozoa	Metazoa	Bdelloidea; Adinetida; Hypsibius dujardini	<0.05	0.1	0	0	0	<0.05	0.1	0	0	0
			Eutardigrada; Parachela; uncultured eukaryote	0	0.1	0	0	0	0	0	0	0	0

	Nucletmycea	Fungi	Eurotiomycetes; Eurotiales; Penicillium sp. NS051-06	<0.05	<0.05	0	0	0.8	2.2	1.6	0	0	0
			Eurotiomycetes; Eurotiales; Talaromyces radicus	0	0	0	0	1.7	3.8	1.1	<0.05	0	0
			Saccharomycetes; Saccharomycetales; Saccharomyces cerevisiae Kyokai no. 7	0	0.1	0	0	5.2	13.3	17.9	<0.05	0	0
			Incertae Sedis; Hyaloraphidium; Hyaloraphidium curvatum	0	0	0	0	0	0	0.2	0.1	31.2	0.1
			Incertae Sedis; Malassezia; uncultured eukaryote	0.1	0.7	0	0	1.0	1.7	2.0	0	0	0
			Incertae Sedis; Malassezia; uncultured fungus	0	0.1	0	0	0.2	0.8	2.5	0	0	0
SAR	Alveolat	Ciliophor	Phyllopharyngea; Cyrtophoria; Colepidae environmental sample	0	0	0	0	0.0	0	0	0	2.5	29.5
	Rhizaria	Cercozoa	Glissomonadida; Heteromita; Cercozoa sp. B128	0	0	<0.05	0	0	<0.05	0	0	0	0.0
			Glissomonadida; Heteromita; uncultured cercozoan	0	0	0	0	0	<0.05	0.0	0	8.4	0.6
			Glissomonadida; Heteromita; uncultured eukaryote	4.1	26.1	<0.05	10.3	0	<0.05	0	0	0.0	0
			Glissomonadida; uncultured eukaryote	0	0.1	0	0.0	0	<0.05	0.1	0	0.2	26.1
			Thecofilosea; E-A1	22.0	0.0	<0.05	2.6	0	0	0	0	0	<0.05
			Thecofilosea; uncultured eukaryote	60.5	13.3	93.2	28.2	2.8	0.4	0.9	6.0	20.4	41.9
	Strameno-	Ochrophyta	Chrysophyceae; uncultured eukaryote	<0.05	0.3	0	<0.05	0	0.2	0.2	0.0	0	0
			Chrysocapsales; Hydrurus; uncultured Hydrurus	<0.05	0.9	0	<0.05	0.1	0.4	0.6	<0.05	<0.05	0
Unassigned				0	<0.05	0	0.1	15.8	4.6	22.0	0.3	0	0

Table S6. The core eukaryotic taxa present in all cryoconite hole samples at >1% relative abundance.

OTU ID	PES36	PES38	PES39	PES40	PES42	PES43	PES47	PES48	PES49	PES50	PES52	PES53	PES54	PES55	PES56	PES59	PES60	PES61	PES63	PES64	PES65
denovo9728	1.4	<0.05	94.5	95.5	0.1	0.5	17.9	87.3	1.0	21.7	6.9	6.0	32.8	2.3	27.5	0.1	0.1	<0.05	0.1	<0.05	0.6
denovo13741	1.0	<0.05	<0.05	0.1	1.5	25.8	79.8	2.3	94.0	77.3	2.2	4.9	17.8	4.2	28.9	25.7	4.9	10.0	85.0	0.9	0.8

Table S6. continued. The closest NCBI hits of core Eukaryotic taxa.

OTU ID						NCBI	Accession number	Similarity [%]
denovo9728	Archaeplastida	Chloroplastida	Chlorophyta	Trebouxiophyceae	Actinastrum hantzschi	Chlorella sp.		100
denovo13741		Rhodophceae	Bangiales	Pyropia	Pyropia fallax	Porpyrax fallax, Ulothrix zonata		99

Table S7. Taxonomic identification of the discriminating OTUs in the principal component analysis (Figure 5).

OTU ID	**Unranked**	**Division**	**Class**	**Order**	**Family**	**Genus**	**Species**	**Best NCBI hit**	**Similarity [%]**
denovo5719	Rhizaria	Cercozoa	Sarcomonadea	Glissomonadida	Heteromitidae	*Heteromita*		Unculutred eukaryote clone	99
denovo7317	Rhizaria	Cercozoa	Thecofilosea					Rhogostoma cylindrica	99
denovo9728	Archaeplastida	Chlorophyta	Trebouxiophyceae	Chlorellales	Chlorellaceae	*Actinastrum*	*Actinastrum hantzschi*	Chlorella sp.	100
denovo10938	Archaeplastida	Charophyta	Spermatophyta	Poales	Poaceae	*Triticum*	*Triticum aestivum*	Triticum aestivum, Uncultured fungal clone	100
denovo12309	Archaeplastida	Chlorophyta	Trebouxiophyceae	Prasiolales	Prasiolaceae	*Stichococcus*	*Stichococcus jenerensis*	Chlorella spp./Raphidonema spp./Stichococcus spp.	99
denovo13741	Archaeplastida	Rhodophyta	Bangiophyceae	Bangiales	Bangiaceae	*Pyropia*	*Pyropia fallax*	Porpyrax fallax, Ulothrix zonata	99
denovo18224	Rhizaria	Cercozoa	Thecofilosea					No blast hit	
denovo24261	Archaeplastida	Rhodophyta	Bangiophyceae	Bangiales	Bangiaceae	*Pyropia*	*Pyropia fallax*	Porpyrax fallax, Ulothrix zonata	99
denovo27244	Metazoa	Rotifera	Bdelloidea	Adinetida	Adinetidae	*Adineta*	*Adineta vaga*	Adineta vaga	99
denovo30662	Fungi	Ascomycota	Lecanoromycetes	Acarosporales	Acarosporaceae	*Acarospora*	*Acarospora peliscypha*	Acarospora spp.	99
denovo34288	Fungi	Ascomycota	Thelebolaceae	Thelebolales	Thelebolaceae	*Thelebolus*	*Thelebolus stercoreus*	Thelebolus spp.	99
denovo30662	Fungi	Ascomycota	Lecanoromycetes	Acarosporales	Acarosporaceae	*Acarospora*	*Acarospora peliscypha*	Acarospora spp.	99

denovo29111	Archaeplastida	Chlorophyta	Chlorophyceae	Chlorococcales	Chlorococcaceae	*Chlorococcum*	*Chlorococcum oleofaciens*	Chlorococcum spp./Pleurastrum spp./Macrochloris spp.	99

Table S8. Overview of solid total carbon (TC), total organic carbon (TOC), total nitrogen (N), total organic nitrogen (TON), thermogravimetry, thermovaporization and pyrolysis analyses.

Sample	Location	TC [%]	TOC [%]	TN [%]	TON [%]	Total mass loss in TGA [%]	TOC [%]	Thermovaporization (300°C) Live C [mg/g TOC]	Pyrolysis (300–600°C) Labile C [mg/g TOC]
PES36	Lake 3	0.12	0.02	0.01	<0.01	0.52	0.017	0	58
PES37	Lake 3	0.12	0.09	0.01	<0.01	-			
PES38	Lake 3	0.02	b.d.	<0.01	<0.01	0.78			
PES39	Lake 3	0.02	0.02	<0.01	<0.01	0.95			
PES40	Lake 3	0.02	0.03	<0.01	<0.01	0.63			
PES47	Lake 2	0.10	0.05	<0.01	<0.01	0.47			
PES48	Lake 2	0.22	0.05	0.01	<0.01	1.00			
PES49	Lake 2	0.13	0.10	<0.01	<0.01	1.02	0.095	0	55
PES50	Lake 2	0.04	0.08	<0.01	<0.01	0.21			
PES51	Lake 2	0.03	0.02	<0.01	<0.01	0.62			
PES52	Dubois	0.05	0.03	<0.01	<0.01	1.12			
PES53	Dubois	0.03	0.04	<0.01	<0.01	0.61			
PES54	Dubois	0.07	0.03	<0.01	<0.01	0.65			
PES55	Dubois	0.05	0.05	<0.01	<0.01	0.78	0.047	0	74
PES56	Dubois	0.03	0.04	<0.01	<0.01	0.42			
PES42	Petrelnuten	0.06	0.03	<0.01	<0.01	0.61			
PES43	Petrelnuten	0.11	0.08	<0.01	<0.01	-			
PES59	Petrelnuten	0.12	0.03	0.01	<0.01	0.35			
PES60	Petrelnuten	0.13	0.12	<0.01	<0.01	-			
PES61	Petrelnuten	0.08	0.12	<0.01	<0.01	0.33	0.123	0	17
PES62	Petrelnuten	0.10	0.14	<0.01	<0.01	0.88	0.136	0	5
PES63	Petrelnuten	0.24	0.10	0.01	<0.01	0.35	0.103	0	10
PES64	Petrelnuten	0.16	0.23	0.01	<0.01	0.96	0.229	0	19
PES65	Petrelnuten	0.14	0.12	0.01	<0.01	0.98			

Table S9. Chemical composition of cryoconite sediments (expressed as oxides) from X-ray fluorescence (XRF) analysis.

Sample	Location	SiO2 [%]	TiO2 [%]	Al2O3 [%]	Fe2O3 [%]	MnO [%]	MgO [%]	CaO [%]	Na2O [%]	K2O [%]	P2O5 [%]	LOI Tiegel [%]	Sum [%]
PES36	Lake 3	63.6	0.495	15.8	5.81	0.093	1.43	2.55	3.31	5.84	0.053	0.63	99.67
PES38	Lake 3	58.6	0.679	16.4	8.44	0.135	2.22	3.78	3.36	5.05	0.060	0.83	99.57
PES39	Lake 3	55.8	0.933	15.9	10.65	0.174	3.06	4.91	3.01	3.93	0.080	1.14	99.57
PES40	Lake 3	62.6	0.410	17.0	5.02	0.082	1.29	2.18	3.50	7.01	0.044	0.66	99.72
PES47	Lake 2	68.5	0.372	14.1	4.77	0.073	0.45	1.64	3.24	5.99	0.053	0.49	99.61
PES48	Lake 2	72.2	0.224	13.2	3.00	0.044	0.18	0.94	3.13	5.75	0.028	1.01	99.66
PES49	Lake 2	65.7	0.435	15.0	5.30	0.082	0.77	1.91	3.56	5.81	0.071	0.99	99.63
PES50	Lake 2	73.4	0.150	12.9	2.33	0.034	0.05	0.64	2.83	6.18	0.014	1.25	99.82
PES52	Dubois	65.9	0.529	15.0	4.90	0.088	1.94	3.63	3.56	3.04	0.143	0.90	99.65
PES53	Dubois	67.5	0.310	16.1	3.09	0.059	1.12	2.90	3.95	3.86	0.080	0.71	99.62
PES54	Dubois	68.3	0.355	15.1	3.16	0.063	1.24	3.13	3.54	3.88	0.098	0.81	99.63
PES55	Dubois	67.4	0.447	15.3	3.90	0.066	1.41	2.79	3.63	3.77	0.123	0.85	99.65
PES62	Petrelnuten	68.4	0.325	14.7	3.81	0.059	0.78	2.26	3.39	5.23	0.055	0.48	99.42
PES63	Petrelnuten	67.0	0.421	14.7	4.67	0.069	0.95	2.53	3.48	5.12	0.067	0.41	99.45
PES64	Petrelnuten	64.4	0.524	14.8	5.51	0.092	1.82	3.64	3.33	4.20	0.095	0.91	99.37
PES65	Petrelnuten	60.6	0.857	14.1	8.42	0.137	2.97	4.83	3.16	2.97	0.098	1.21	99.34

Table S9. continued.

Sample	Location	Ba [ppm]	Cr [ppm]	Ga [ppm]	Nb [ppm]	Ni [ppm]	Rb [ppm]	Sr [ppm]	V [ppm]	Y [ppm]	Zn [ppm]	Zr [ppm]
PES36	Lake 3	243	118	25	16	<10	149	78	84	30	82	510
PES38	Lake 3	247	89	27	22	14	133	105	124	46	117	290
PES39	Lake 3	227	72	25	23	17	109	123	171	45	130	448
PES40	Lake 3	272	63	24	12	<10	172	79	71	29	85	233
PES47	Lake 2	204	167	26	29	<10	171	56	14	49	112	796
PES48	Lake 2	167	209	24	17	<10	156	39	<10	28	70	488
PES49	Lake 2	257	109	27	29	<10	171	93	22	50	116	906
PES50	Lake 2	147	250	21	13	<10	157	30	16	20	51	299
PES52	Dubois	785	202	21	<10	24	116	366	73	28	77	214
PES53	Dubois	996	113	20	<10	<10	120	391	42	17	49	138

PES54	Dubois	840	129	20	<10	13	121	336	39	21	52	172
PES55	Dubois	785	144	19	<10	13	133	324	55	23	61	191
PES62	Petrelnuten	1751	180	21	23	12	122	267	30	36	89	338
PES63	Petrelnuten	1758	321	22	28	18	114	251	43	41	98	453
PES64	Petrelnuten	1361	327	23	22	24	113	289	75	43	104	433
PES65	Petrelnuten	861	318	22	36	30	97	265	110	61	158	333

Table S10. Aqueous concentrations of nutrients and simple organics as analyzed by Ion Chromatography (IC) in μgL^{-1}.

Sample	Location	NO_3^{2-}	PO_4^{3-}	SO_4^{2-}	Cl^-	F^-	Oxalate	Formic acid	Acetate	Propionate	Butyrate	Valerate
PES 36	Lake 3	1.24	<0.2	5.29	3.02	0.48	<0.2	<0.1	1.71	<0.1	<0.1	<0.1
PES 38	Lake 3	1.81	<0.2	7.66	10.38	0.35	<0.2	0.30	2.97	0.43	<0.1	<0.1
PES 40	Lake 3	2.25	<0.2	10.86	5.47	0.36	<0.2	0.23	6.91	0.34	<0.1	<0.1
PES 47	Lake 2	0.32	<0.2	5.18	4.25	0.40	<0.2	0.11	1.50	0.45	<0.1	<0.1
PES 48	Lake 2	0.10	<0.2	4.13	2.92	0.79	<0.2	0.19	1.88	0.48	<0.1	<0.1
PES 49	Lake 2	0.55	<0.2	8.64	9.29	0.59	<0.2	0.16	4.56	0.58	<0.1	<0.1
PES 50	Lake 2	1.43	<0.2	67.79	19.68	3.40	0.71	0.22	1.02	0.14	<0.1	<0.1
PES 51	Lake 2	1.33	<0.2	46.45	10.62	1.29	<0.2	0.12	1.13	0.13	<0.1	<0.1
PES 52	Dubois	0.14	<0.2	6.32	4.32	0.16	<0.2	0.12	0.98	0.37	<0.1	<0.1
PES 53	Dubois	0.30	<0.2	10.66	4.19	0.24	<0.2	0.21	2.47	0.71	<0.1	<0.1
PES 54	Dubois	<0.02	<0.2	12.87	5.88	0.13	<0.2	0.12	1.39	0.30	<0.1	<0.1
PES 55	Dubois	0.37	<0.2	11.44	1.60	0.22	<0.2	<0.1	1.45	0.20	<0.1	<0.1
PES 42	Petrelnuten	0.54	<0.2	1.56	1.17	0.20	<0.2	0.73	6.13	1.02	0.20	0.22
PES 59	Petrelnuten	0.28	<0.2	2.42	1.44	0.18	1.17	0.36	2.53	0.37	<0.1	<0.1
PES 61	Petrelnuten	2.30	0.85	5.35	1.51	0.34	1.61	0.36	17.37	0.35	0.15	<0.1
PES 62	Petrelnuten	0.55	2.09	5.86	1.23	0.22	1.88	0.13	1.22	0.17	<0.1	<0.1
PES 64	Petrelnuten	0.45	0.25	11.69	5.12	0.32	1.46	0.17	2.25	0.24	<0.1	<0.1

Supplementary Data S1: Output of the PCA of bacterial OTUs.

```
Partitioning of variance:

              Inertia Proportion

Total          15747          1

Unconstrained   15747          1


Eigenvalues, and their contribution to the variance


Importance of components:

                           PC1       PC2       PC3       PC4       PC5       PC6       PC7       PC8       PC9
PC10     PC11     PC12     PC13     PC14     PC15     PC16

Eigenvalue           6793.2866 4678.3590 1.414e+03 1.028e+03 531.99097 404.11167 345.20355
191.92975 1.026e+02 76.465707 66.640577 56.009731 28.149296 12.864986 1.078e+01
5.5524155

Proportion Explained     0.4314     0.2971 8.976e-02 6.528e-02    0.03378    0.02566    0.02192
0.01219 6.516e-03  0.004856  0.004232  0.003557  0.001788  0.000817 6.847e-04 0.0003526

Cumulative Proportion    0.4314     0.7285 8.183e-01 8.835e-01    0.91733    0.94300    0.96492
0.97711 9.836e-01  0.988479  0.992711  0.996268  0.998056  0.998873 9.996e-01 0.9999101

                          PC17

Eigenvalue           1.416e+00

Proportion Explained  8.991e-05

Cumulative Proportion 1.000e+00


Scaling 2 for species and site scores

* Species are scaled proportional to eigenvalues

* Sites are unscaled: weighted dispersion equal on all dimensions

* General scaling constant of scores:  24.26073



Species scores
```

	PC1	PC2	PC3	PC4	PC5	PC6
denovo1726	1.9330	–3.3075	–2.744973	0.89041	–0.3236	0.37377
denovo3345	–1.0710	–1.4295	–0.829714	0.63621	0.7122	–0.71516
denovo4865	–11.2220	–2.0645	–0.714512	1.61216	–0.2443	–0.82563
denovo8523	2.1145	4.3312	–0.002888	0.96140	0.1050	–0.88119
denovo10202	1.7369	5.8445	0.292209	1.57188	–0.3297	–1.62305
denovo12574	3.4820	–3.5348	–1.728445	–2.31705	–0.9573	–1.91509
denovo14041	–3.6746	–1.8151	–1.220601	–0.48451	2.1839	–0.68703
denovo15890	3.0874	–3.6962	–0.710738	2.29696	–2.5047	–0.50447
denovo15930	0.4346	–1.5190	–1.400352	–1.04964	0.4520	0.45420
denovo18602	1.2955	4.1246	–0.830046	0.88979	0.5602	–0.73865
denovo18695	1.6246	–2.4502	–0.934114	3.50553	0.5347	1.32931
denovo18789	0.4817	–2.6949	–1.881208	–1.20691	–0.2353	–0.37626
denovo19685	0.9268	0.1985	–1.592742	0.05793	0.9241	0.65926
denovo22765	5.5384	–6.0109	3.455035	1.07373	1.9540	–1.21702
denovo23995	2.3194	1.2102	–3.190476	1.61198	1.0131	–0.63293
denovo27012	1.9544	1.9546	–2.696771	–0.89699	0.7428	0.07036
denovo29111	–5.9147	–1.1008	0.212286	0.39085	–0.1575	–0.99265

Site scores (weighted sums of species scores)

	PC1	PC2	PC3	PC4	PC5	PC6
PES36	0.7064	3.98609	9.33174	–3.77326	–9.48330	14.451
PES38	3.2222	11.50566	0.98320	4.14821	0.60878	–6.651
PES39	3.5435	11.99882	1.24401	3.15030	–3.00226	–3.458
PES40	3.2832	10.67471	–2.71133	2.72923	2.49249	–1.338
PES42	–0.1608	1.91838	–5.16052	–4.91939	3.22027	7.447
PES43	–4.9232	0.56563	–0.01738	–4.43271	–3.60905	2.009
PES47	3.9929	–2.70408	–7.09890	–7.17259	–6.52145	–1.398

PES48	4.3767	–2.40723	–3.31813	–2.18144	–0.72628	2.237
PES49	5.1712	–2.69284	–1.03963	–8.71273	4.86474	–8.135
PES50	0.9759	–1.11788	–7.33151	–0.43796	7.69668	7.047
PES51	2.2320	1.69301	–7.18152	–3.67781	3.75658	4.116
PES52	4.4278	–5.55594	–0.98030	–1.45140	–13.66172	–6.453
PES53	4.3186	–5.28861	0.57451	8.09853	–3.05366	1.652
PES54	3.0778	–5.70140	–0.38226	7.32414	–1.69439	–2.447
PES55	2.4506	–4.75291	0.08320	10.05463	1.29713	1.652
PES56	1.2654	–4.71465	–0.95717	7.60960	5.74090	3.116
PES59	–8.7342	–0.05903	1.39786	0.16083	–0.45844	–1.557
PES60	–9.1794	–0.32675	0.86797	0.84275	0.09254	–2.726
PES61	–8.7210	–0.43970	–0.97533	–0.07724	0.42860	–2.707
PES62	–9.1640	–0.47268	–0.21848	1.86899	–1.24315	–1.905
PES63	–8.2342	–0.63115	–0.71051	–0.38146	0.36328	–1.311
PES64	2.7418	–3.69534	9.33742	–8.05294	7.12704	–5.731
PES65	3.3307	–1.78212	14.26309	–0.71629	5.76468	2.089

Supplementary Data 2: Output of the PCA of the eukaryotic OTUs.

```
Partitioning of variance:

            Inertia Proportion

Total          15469          1

Unconstrained   15469          1


Eigenvalues, and their contribution to the variance


Importance of components:

                        PC1       PC2       PC3       PC4       PC5       PC6       PC7       PC8      PC9
PC10      PC11      PC12      PC13      PC14      PC15      PC16

Eigenvalue           3556.0027 3170.4533 2735.8550 1956.9294 1.135e+03 735.39034 664.64005
420.57004 323.2648 244.03926 161.29456 1.369e+02 1.168e+02 58.93167 35.539388 1.426e+01

Proportion Explained     0.2299    0.2050    0.1769    0.1265 7.339e-02    0.04754    0.04297
0.02719    0.0209    0.01578    0.01043 8.849e-03 7.551e-03  0.00381   0.002298 9.218e-04

Cumulative Proportion    0.2299    0.4348    0.6117    0.7382 8.116e-01    0.85915    0.90211
0.92930    0.9502    0.96598    0.97640 9.853e-01 9.928e-01  0.99661   0.998912 9.998e-01

                       PC17      PC18      PC19

Eigenvalue           2.1080097 4.405e-01 2.930e-02

Proportion Explained  0.0001363 2.848e-05 1.894e-06

Cumulative Proportion 0.9999696 1.000e+00 1.000e+00


Scaling 2 for species and site scores

* Species are scaled proportional to eigenvalues

* Sites are unscaled: weighted dispersion equal on all dimensions

* General scaling constant of scores:  23.58416



Species scores
```

```
            PC1      PC2     PC3       PC4       PC5      PC6
denovo630    0.21428  0.59621 –0.2311  0.486920 –1.566124  2.5029
denovo2262   0.28787  0.67569  0.6802 –0.526218  0.067123  0.2428
denovo5580   1.64674  0.61362  0.9724 –1.540197  0.169338 –0.3139
denovo6766  –0.21175  0.55173  0.2299  2.059635 –1.827537  2.4818
denovo7317  –1.51171  1.80307 –8.0330 –1.461693  1.864655 –0.1565
denovo7358  –0.02315  0.65206  0.6404 –0.353579  0.082539  0.2432
denovo9691   0.02972  1.38594  0.7367  1.592919  0.390766  0.3988
denovo9728  –8.38999 –4.83868  2.0418 –1.903572 –0.255986 –0.7586
denovo10529  1.73524  0.59058  1.0236 –2.146429  0.003463 –0.2367
denovo10938  2.95208  1.21416  1.7092 –3.762391 –0.042161 –0.2944
denovo12309 –1.23435  4.36815  3.1591  3.829199  2.896415 –1.3305
denovo13741  5.45465 –7.68878 –0.9051  2.347243  1.330446 –0.4851
denovo13822 –0.05318  1.08974 –1.5834  0.213848 –1.816457 –0.3682
denovo18417  0.70609  1.01138 –1.6878  1.647614 –3.979861 –3.0613
denovo21615  1.93243  0.42366  0.8629 –1.989633  0.096171 –0.3652
denovo27253 –0.42022 –0.53445  0.1142  0.001703 –0.509331  0.9990
denovo28736 –0.46569  0.03486 –1.5948 –0.489182  1.086853  0.2660
denovo29133  2.10434  0.88593  1.6992 –2.953475 –0.033885 –0.1408
denovo30251 –0.49077 –0.12643 –0.9470 –0.446115  0.734645  0.4070


Site scores (weighted sums of species scores)


        PC1      PC2     PC3      PC4      PC5       PC6
PES36    0.8848  4.2389  3.4155  –2.7643   0.17514   2.10197
PES38   –1.2094  9.8767  5.6640   8.1509   9.07234  –5.23181
PES39  –10.1635 –1.3921  4.9316  –2.5700  –0.62555  –3.56796
PES40  –10.1778 –1.7729  4.6998  –2.6251  –0.77559  –3.04725
PES42   –0.1265  8.2890  4.5611  10.5825   2.86929   3.02470
```

PES43	3.7570	–0.4121	–1.6422	6.0558	–11.86270	–10.83672
PES47	1.9263	–8.4653	0.7299	3.2262	1.78166	–0.56849
PES48	–8.3978	–3.6317	3.5739	–3.0306	–3.31781	0.67045
PES49	5.8685	–6.9895	–0.5386	5.5678	1.72984	2.41472
PES50	1.3569	–8.5337	0.6575	2.9057	2.49661	–1.81267
PES52	–1.6318	0.7390	0.4319	–0.7249	–0.53815	2.57969
PES53	–2.5479	1.8433	–10.1486	–3.0866	6.50475	2.17745
PES54	–2.7399	–4.2008	1.8805	0.1025	–3.96778	6.71029
PES55	–1.7059	3.2125	–11.6552	–2.6110	6.03782	0.77682
PES56	–2.7740	–3.9787	–5.9475	–1.5249	5.23123	–0.46331
PES59	7.7658	0.2901	2.9724	–6.7364	1.25232	–1.71041
PES60	6.3085	3.9234	4.4715	–9.9747	–0.62126	–0.78624
PES61	7.0495	2.9355	3.9362	–8.5098	0.05099	–1.14555
PES63	6.6609	–6.0380	–0.4312	3.9330	2.84985	–0.09898
PES64	0.6546	4.2428	–1.3518	2.9063	–9.02974	15.91727
PES65	–0.7583	5.8236	–10.2107	0.7278	–9.31328	–7.10397