



Figure S1. Geographical localization of sampling sites.

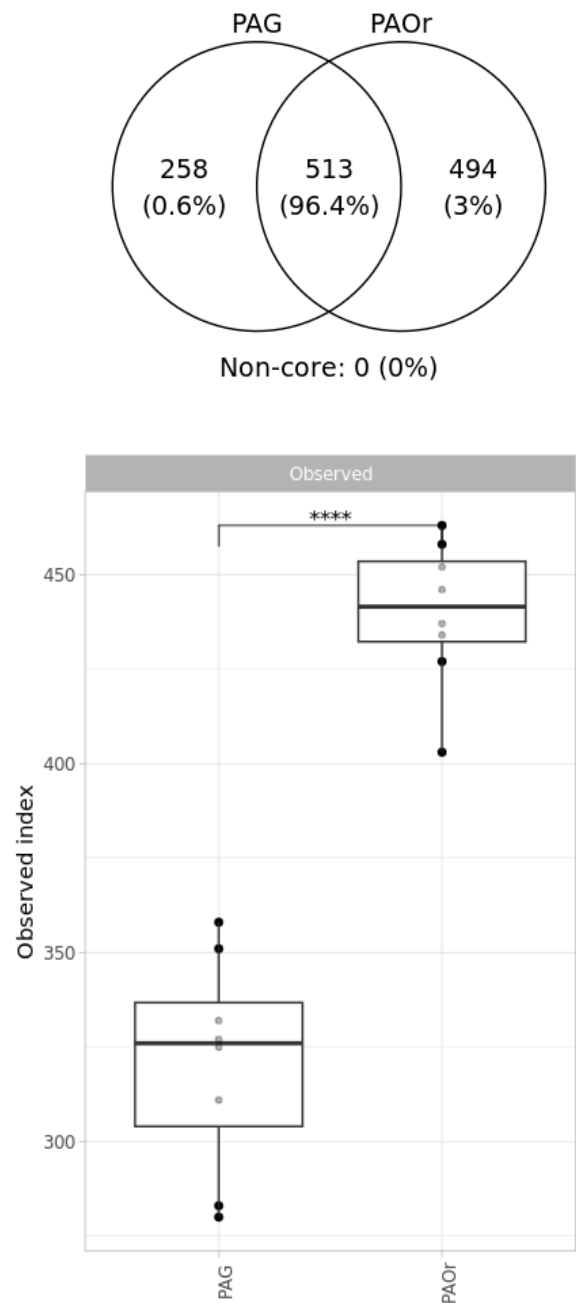
PAG/PAOr - Pimpirev glacier, Western Antarctica, South Shetland archipelago, Livingstone Island

IGAN – Igan glacier, Polar Ural

Mush - Mushketova glacier, Severnaya Zemlya

Garabashi/Shkelda – glaciers from the Central Caucasus

Map is adapted after https://upload.wikimedia.org/wikipedia/commons/c/cf/A_large_blank_world_map_with_oceans_marked_in_blue.PNG

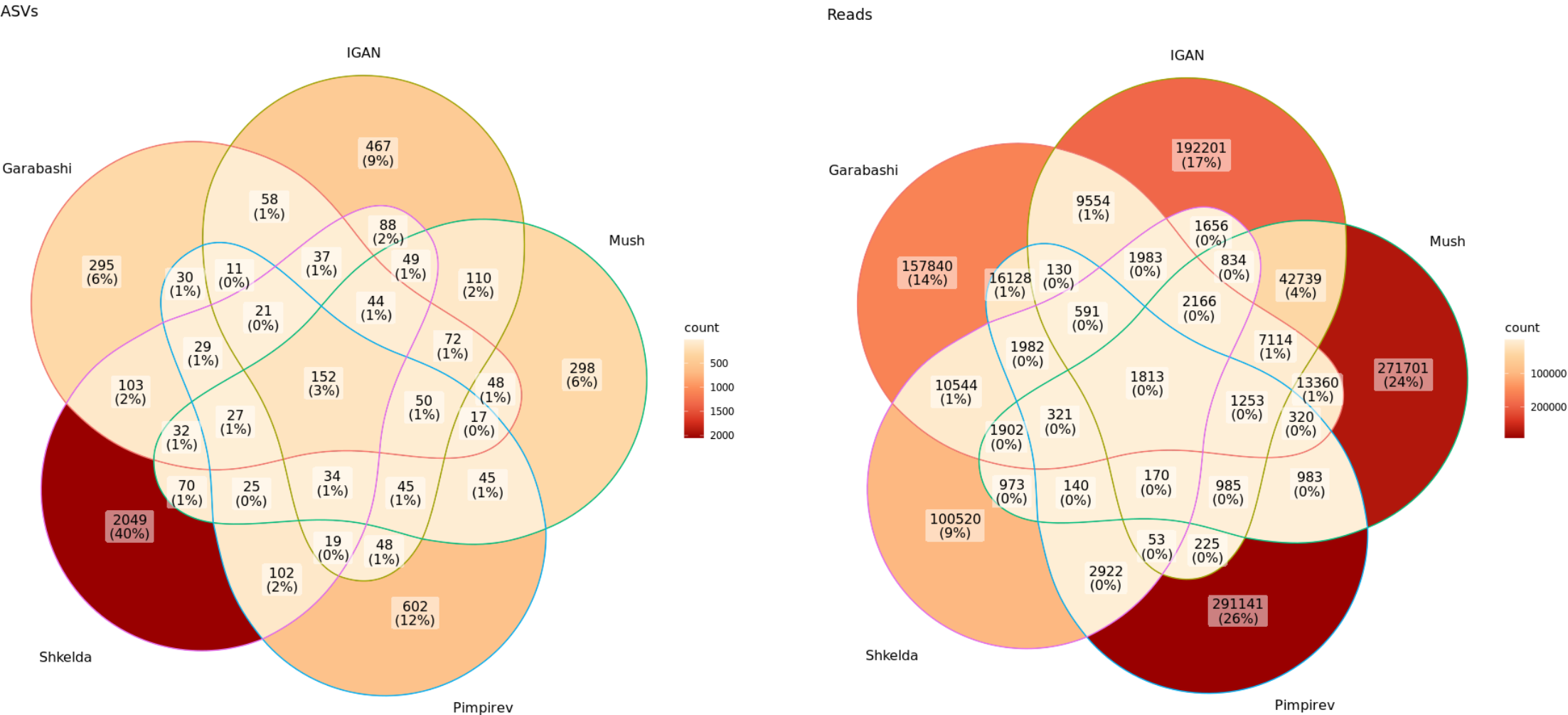


Bacteria; Cyanobacteriota -	38.3	32
Bacteria; Bacteroidota -	19.8	17.4
Bacteria; Pseudomonadota -	16.9	18.5
Bacteria; Actinobacteriota -	9.6	10.3
Bacteria; Gemmatimonadota -	4.9	3.7
Bacteria; Acidobacteriota -	3.3	4.5
Bacteria; Planctomycetota -	2.4	4.3
Bacteria; Chloroflexota -	1.5	2.1
Bacteria; Verrucomicrobiota -	1	1.8
Bacteria; Patescibacteria -	0.4	1.8
Bacteria; Myxococcota -	0.7	1.3
Bacteria; Bdellovibrionota -	0.6	0.9
Bacteria; Abditibacteriota -	0.2	0.4
Remaining taxa (16) -	0.4	1
	PAG -	PAOr -

Figure S2. Differences between PAG and PAOr sites:
 (A) Richness
 (B) ASV count
 (C) Heatmap of the major phyla

PAG/PAOr - Pimpirev glacier, Western Antarctica, South Shetland archipelago, Livingstone Island

Figure S3. Common ASVs (left) and reads (right) count between samples of cryoconite microbiomes.



	antarctica	caucasus				polar ural	severnaya zemlya
Bacteria; Pseudomonadota-	17.6	27.7	27.6	34.7	15.1	33	18
Bacteria; Cyanobacteriota-	35.2	25.1	16.3	0.8	0.1	0.5	20.3
Bacteria; Bacteroidota-	18.6	19.8	15.6	13.9	2.7	23.1	10
Bacteria; Actinobacteriota-	9.9	7.2	16.7	15.8	15.1	7.8	11.1
Bacteria; Acidobacteriota-	3.9	5.5	3.5	8.4	17.2	5.1	6.7
Bacteria; Patescibacteria-	1.1	1.5	2	1	0.1	6	10.2
Bacteria; Chloroflexota-	1.8	3.4	2.8	4.7	0.5	0	7.5
Bacteria; Planctomycetota-	3.4	1.4	2.4	2.6	4.6	4.9	1.7
Bacteria; Gemmatimonadota-	4.3	0.8	2.3	6.5	0.8	1.3	1.6
Bacteria; Bacillota-	0.2	1.7	0.5	1.4	9.2	7.5	0.5
Bacteria; Myxococcota-	1	2.6	4	1.2	3.6	2.1	1.5
Bacteria; Verrucomicrobiota-	1.4	0.2	2.8	4.7	10.4	1.1	0.1
Bacteria; Armatimonadota-	0.1	1.5	0.6	0.4	0.1	1.8	4
Bacteria; WPS-2-	0	0	0	0	0	0.5	5.7
Bacteria; Bdellovibrionota-	0.8	0.4	1.5	0.4	0	1.3	0.7
Archaea; Thermoproteota-	0	0	0.3	0.1	10.8	0	0
Bacteria; Thermodesulfobacteriota-	0	0.1	0	0.3	0.2	3	0
Bacteria; Nitrospirota-	0	0	0.1	2.2	0.8	0	0
Bacteria; RCP2-54-	0	0	0	0.1	3.8	0	0
Bacteria; Deinococcota-	0	0.6	0.4	0.1	0	0	0.2
Bacteria; Methyломirabilota-	0	0	0	0.1	2.7	0	0
Bacteria; Fibrobacterota-	0.1	0.2	0	0	0	0.6	0
Bacteria; Abditibacteriota-	0.3	0.1	0.6	0.1	0	0	0
Bacteria; Entotheonellaeota-	0	0	0	0	1.4	0	0
Bacteria; SAR324_clade(Marine_group_B)-	0.2	0	0	0	0	0	0
Bacteria; Latescibacterota-	0	0	0	0.3	0.1	0	0
Bacteria; NB1-j-	0	0	0	0	0.5	0	0
Bacteria; FCPU426-	0	0	0	0	0	0.1	0
Bacteria; Elusimicrobiota-	0	0	0	0.1	0	0	0
Bacteria; Dependuntiae-	0	0	0	0.1	0	0	0
Remaining taxa (12)-	0.1	0	0	0.1	0.1	0.1	0
	Pimpirev	Garabashi	Mud	Shkelda	Soil	IGAN	Mush

Figure S4. Heatmap of the major phyla in the dataset



Figure S5. P-values for differences in phylum composition between cryoconite samples. Violet – difference is significant (p-value < 0,05), yellow – not significant (p-value > 0,05),

	antarctica	caucasus				polar ural	severnaya zemlya
Cyanobacteriota; Phormidesmis_ANT.L52.6-	3.2	7.3	0.8	0.1	0	0.1	19.1
Bacteroidota; Ferruginibacter-	1.1	11.6	1.3	2.3	0	1.7	1.6
Cyanobacteriota; Tychonema_CCAP_1459-11B-	2	11.7	2.7	0.1	0	0	0
Cyanobacteriota; Chamaesiphon_PCC-7430-	8.5	3.4	0	0.2	0	0.2	0.1
Pseudomonadota; Sphingomonas-	1.7	4.2	2.7	4	0.3	0.3	0.7
Pseudomonadota; Polaromonas-	1.5	5.9	0	1.5	0	1	0.8
Bacteroidota; Hymenobacter-	4.3	3.7	0.4	0.7	0	0.2	0.4
Acidobacteriota; Granulicella-	0	0	0	0	0	1.7	4.9
Gemmatimonadota; Gemmatimonas-	4.3	0.8	0.4	2	0	0.2	0.9
Pseudomonadota; Acidiphilium-	0	1.4	0	0.9	0	0.9	4
Cyanobacteriota; Phormidium_CYN64-	7	0	0.3	0	0	0	0
Actinobacteriota; Parafrigoribacterium-	0	0.4	0	0	0	2.8	2.3
Cyanobacteriota; Crinalium_SAG_22.89-	4.6	0	0.1	0.1	0	0	0
Actinobacteriota; hgcl_clade-	0	0	0	0	0	0.6	3.1
Bacteroidota; Paludibacter-	0	0.2	0	0	0	5.5	0
Actinobacteriota; Oryzihumus-	0	2.1	0	1.1	0	0.1	1.6
Chloroflexota; f_Ktedonobacteraceae_Seq13-	0	0	0	0	0	0	3.3
Pseudomonadota; Rhodoferax-	0.2	1.9	0	0.8	0	2.4	0
Bacteroidota; Mucilaginibacter-	0	0	0	0.1	0	3	1.2
Bacillota; Clostridium_sensu_stricto_9-	0	0.4	0	0.1	0	4.5	0
Acidobacteriota; Blastocatella-	1.9	1.8	0.6	0.6	0	0	0
Pseudomonadota; Ellin6067-	0.6	2.4	0	1.8	0	0	0
Pseudomonadota; Rhizobacter-	0.3	2.9	0.4	0.9	0	0.3	0
Cyanobacteriota; Chlorogloea_SAG_10.99-	3.2	0	0	0	0	0	0
Myxococcota; Pajaroellobacter-	0.2	1.3	0.3	0.1	0	1.1	0.8
Acidobacteriota; Candidatus_Solibacter-	0	0.7	0	0.2	0.1	0.4	1.7
Bacteroidota; Flavobacterium-	1.9	0.2	0.1	2	0	0	0
Chloroflexota; f_Ktedonobacteraceae_Seq29-	0	0	0	0	0	0	2.2
Bacteroidota; Solitalea-	0	0	0	0	0	0.6	1.9
Armatimonadota; Chthonomonas-	0	1.1	0.1	0.2	0	0.6	1.1
WPS-2; p_WPS-2_Seq25-	0	0	0	0	0	0.2	2
Pseudomonadota; f_Acetobacteraceae_Seq26-	0	0.3	0	0	0	0.4	1.6
Pseudomonadota; Novosphingobium-	0	0.3	0.2	1.6	0	1.1	0.4
Cyanobacteriota; o_RD011_Seq36-	2.5	0	0	0	0	0	0
Verrucomicrobiota; Candidatus_Udaeobacter-	0	0	0.1	2.4	4.1	0	0
Cyanobacteriota; f_Leptolyngbyaceae_Seq46-	2.3	0	0	0	0	0	0
Bacteroidota; f_env.OPS_17_Seq34-	0	0	0	0	0	0.6	1.4
Actinobacteriota; Aquipuribacter-	2.1	0	0.2	0	0	0	0
Planctomycetota; Pirellula-	1.5	0	0.5	0.5	0.7	0	0
Thermodesulfobacteriota; Citrif fermentans-	0	0	0	0	0	2.7	0
Remaining taxa (4005)-	44.8	34.1	88.5	75.7	94.3	67.1	42.6
	Pimpirev	Garabashi	Mud	Shkelda	Soil	IGAN	Mush

Figure S6. Heatmap of the major genera in the dataset

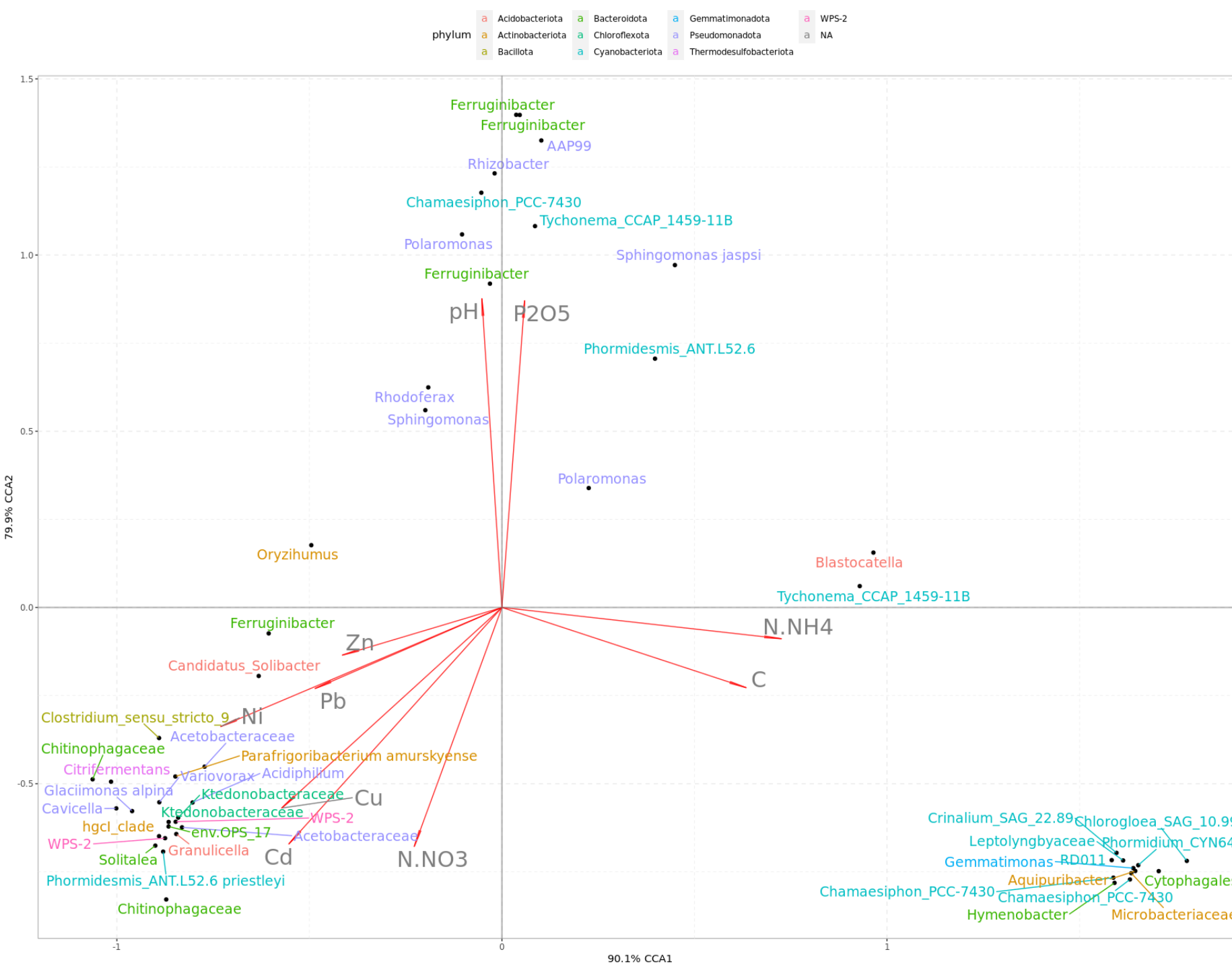


Figure S8. CCA for the pop ASVs in the cryoconite microbiomes

Currelation of the WGCNA clusters with soil characteristics

black	-0.19 (0.1203)	-0.17 (0.1562)	-0.24 (0.0520)	-0.28 (0.0228)	-0.3 (0.0122)	-0.094 (0.4435)	0.13 (0.2824)	0.56 (<0.001)	0.66 (<0.001)	0.69 (<0.001)	0.64 (<0.001)
blue	-0.26 (0.0306)	-0.25 (0.0419)	-0.27 (0.0261)	-0.35 (0.0039)	-0.37 (0.0019)	-0.078 (0.5272)	0.17 (0.1537)	0.78 (<0.001)	0.73 (<0.001)	0.9 (<0.001)	0.77 (<0.001)
green	-0.38 (0.0015)	-0.5 (<0.001)	-0.44 (<0.001)	-0.67 (<0.001)	-0.59 (<0.001)	0.54 (<0.001)	0.77 (<0.001)	0.76 (<0.001)	0.49 (<0.001)	0.36 (0.0027)	0.78 (<0.001)
pink	-0.18 (0.1426)	-0.32 (0.0069)	-0.27 (0.0268)	-0.44 (<0.001)	-0.34 (0.0047)	0.55 (<0.001)	0.61 (<0.001)	0.21 (0.0845)	-0.042 (0.7339)	-0.27 (0.0285)	0.22 (0.0730)
red	-0.21 (0.0812)	-0.35 (0.0039)	-0.34 (0.0047)	-0.52 (<0.001)	-0.43 (<0.001)	0.67 (<0.001)	0.75 (<0.001)	0.21 (0.0829)	-0.031 (0.8020)	-0.31 (0.0105)	0.29 (0.0177)
turq.	-0.39 (<0.001)	-0.28 (0.0193)	0.69 (<0.001)	0.75 (<0.001)	0.66 (<0.001)	0.034 (0.7858)	-0.56 (<0.001)	-0.25 (0.0424)	-0.32 (0.0087)	-0.26 (0.0342)	-0.2 (0.1058)
brown	0.78 (<0.001)	0.82 (<0.001)	-0.12 (0.3132)	0.24 (0.0477)	0.29 (0.0147)	-0.57 (<0.001)	-0.11 (0.3515)	-0.4 (<0.001)	-0.058 (0.6365)	0.045 (0.7147)	-0.54 (<0.001)
yellow	0.54 (<0.001)	0.53 (<0.001)	-0.16 (0.1823)	-0.24 (0.0483)	-0.27 (0.0251)	-0.46 (<0.001)	-0.41 (<0.001)	-0.51 (<0.001)	-0.29 (0.0177)	-0.21 (0.0905)	-0.54 (<0.001)
grey	0.12 (0.3359)	0.0026 (0.9829)	-0.51 (<0.001)	-0.48 (<0.001)	-0.4 (<0.001)	0.077 (0.5342)	0.57 (<0.001)	0.28 (0.0190)	0.32 (0.0086)	0.21 (0.0920)	0.35 (0.0030)
	PH	P2O5	C	K2O	N.NH4	N.NO3	Ni	Cu	Pb	Zn	Cd

Figure S9. WGCNA clustering of ASVs from cryoconite microbiomes according to their chemical composition.

Figure S10. Differences between PAG and PAOr sites:

(A) Heatmap of the major genera

(B) Significantly different microorganisms between ornitogenic (PAOr) and nonornitogenic (PAG) sites. Testing and normalization based on ANCOM-BC. Phylotypes grouped based on the genus, size of the panel was determined according to the abundances of the phylotypes.

