

## Aberystwyth University

### *Microbial diversity on Icelandic glaciers and ice caps*

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## Supplementary Information

**Table S1:** Fatty acid composition of red snow samples. Fatty acid compounds are reported as percentage of total fatty acids. b=branched, A = Alkane.

Compound	C14:0	C15 b	C15:0	C16:4	C15 b	C16:1	C16:1	C16:1	C16:0	C18:3	C18:4	C18:2	C18:3	C18:1	C18:1	C21 A	C18:0	C20:5	C23 A	C20:0	C21:0	C22:0	C26 A	C27 A	C24:0
ICE-12_2	0	0	0	0	0	8	0	0	20	0	0	7	7	46	12	0	0	0	0	0	0	0	0	0	0
ICE-12_3	0	0	0	0	0	8	0	0	18	0	0	5	4	47	5	0	10	0	0	2	0	0	0	0	0
ICE-12_5	0	0	0	0	0	0	3	0	16	0	0	0	0	18	0	7	57	0	0	0	0	0	0	0	0
ICE-12_6	2	0	0	0	0	2	0	0	18	0	0	5	3	50	2	0	18	0	0	0	0	0	0	0	0
ICE-12_7	3	0	2	0	0	4	0	0	14	0	4	27	0	43	0	0	3	0	0	0	0	0	0	0	0
ICE-13_1	0	6	6	0	0	16	0	0	16	0	0	6	3	8	5	0	17	0	0	0	0	0	0	0	0
ICE-13_2	1	0	0	0	0	12	0	0	19	0	0	11	6	8	6	1	12	0	1	2	0	3	0	2	2
ICE-13_4	0	0	0	0	0	0	0	0	94	0	0	0	0	6	0	0	0	0	0	0	0	0	0	0	0
ICE-13_5	5	0	0	0	0	8	0	0	25	0	2	12	12	9	0	0	16	0	0	3	0	4	0	0	0
ICE-13_6	3	0	0	0	0	2	0	0	21	2	4	10	13	13	0	7	12	1	2	3	0	3	0	0	0
ICE-13_8	2	0	0	0	0	0	0	0	42	0	0	0	0	0	0	0	56	0	0	0	0	0	0	0	0
ICE-13_9	0	0	0	0	0	0	0	0	38	0	0	9	0	16	0	0	38	0	0	0	0	0	0	0	0
ICE-13_12	0	0	0	5	0	5	0	0	22	0	4	6	16	20	0	0	12	4	0	0	0	3	0	0	3
ICE-13_14	3	0	0	0	0	5	0	0	26	0	0	14	29	0	0	0	11	1	0	3	0	4	0	0	2
ICE-13_15	2	0	0	0	0	0	0	0	26	0	0	4	5	16	0	3	17	0	4	5	0	6	1	4	4
ICE-13_16	4	0	0	0	0	2	0	0	24	2	5	14	13	15	0	0	10	2	0	2	2	2	0	0	2
ICE-13_18	2	0	0	0	0	4	0	0	25	0	0	9	6	16	0	0	30	0	0	2	1	3	0	0	2
ICE-13_19	2	0	0	0	0	2	0	0	33	0	0	3	3	5	0	0	49	0	0	2	0	2	0	0	0
ICE-13_21	1	0	0	6	1	1	0	1	27	0	0	7	16	21	0	0	9	0	0	3	0	4	0	0	2
ICE-13_24	8	0	0	0	0	2	0	0	28	0	0	7	7	16	0	2	12	0	2	4	0	6	0	1	3

**Table S2:** Counts of OTUs matching eukaryotes, algae (*Chloroplastida*) and bacteria, clustered at 99%, 97% and 95% similarities after removal of singletons.

	99 %	97 %	95 %
<b>All eukaryotes</b>	4,170	2,811	1,901
<b>Chloroplastida</b>	807	567	395
<b>Bacteria</b>	1,591	1,733	1,500

Table S3: Distribution of OTUs clustered at 99%, 97% and 95% similarities aligned and assigned to eukaryotes. Values are the relative abundance of the taxa in percentage of total sequences and table shows taxa with >0.1% abundance.

OTU similarity	Drangajökull ICE12.2.3			Laugafell ICE12.4			Hofsjökull ICE12.6.7			Vatnajökull ICE13.14.15			Langjökull ICE13.16.18			Langjökull ICE13.19		
	99%	97%	95%	99%	97%	95%	99%	97%	95%	99%	97%	95%	99%	97%	95%	99%	97%	95%
Archaeplastida; Chloroplastida	32.3	45.3	46.3	32.6	35.9	30.6	63.9	60.6	56.3	59.9	56.6	57.3	2.6	9.7	10.2	1.8	4.5	5.3
Opisthokonta; Fungi	29.8	27.0	23.4	54.7	53.5	46.8	17.9	19.7	18.3	39.7	41.4	41.7	97.4	89.9	89.1	98.2	94.9	94.7
SAR; Alveolata	0.2	0.1	0.1	11.6	6.3	5.9	1.6	2.6	2.6	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
SAR; Rhizaria	37.7	27.6	30.2	1.2	4.2	16.7	16.4	16.5	21.7	0.0	1.5	0.4	0.0	0.2	0.6	0.0	0.7	0.0
SAR; Stramenopiles	0.0	0.0	0.0	0.0	0.0	0.0	0.2	0.6	1.1	0.4	0.6	0.5	0.0	0.2	0.1	0.0	0.0	0.0
Zeuk77; uncultured eukaryote	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0

OTU similarity	Snaefellsjökull ICE13.21.24			Eyafjallajökull ICE13.4.5.6			Mýrdalsjökull ICE13.8.9			Eyafjallajökull ICE14.1			Eyafjallajökull ICE14.2			Eyafjallajökull ICE14.3		
	99%	97%	95%	99%	97%	95%	99%	97%	95%	99%	97%	95%	99%	97%	95%	99%	97%	95%
Archaeplastida; Chloroplastida	8.1	7.8	5.5	35.9	29.8	27.5	21.4	19.7	20.3	21.1	17.3	16.4	66.0	57.9	55.4	43.9	35.4	33.2
Opisthokonta; Fungi	91.9	87.4	87.9	63.4	67.0	70.0	78.6	78.7	76.6	12.2	12.1	12.0	10.5	12.0	11.5	4.7	6.6	7.7
SAR; Alveolata	0.0	0.0	0.2	0.0	0.0	0.0	0.0	0.0	0.0	19.6	16.3	15.6	1.5	1.8	1.9	4.2	3.7	3.6
SAR; Rhizaria	0.0	4.8	6.4	0.0	2.0	0.5	0.0	1.6	3.1	0.0	0.0	0.5	0.0	0.0	1.1	0.0	0.0	0.3
SAR; Stramenopiles	0.0	0.0	0.0	0.7	1.1	2.0	0.0	0.0	0.0	46.3	54.3	55.4	21.5	28.1	29.7	47.0	53.9	54.7
Zeuk77; uncultured eukaryote	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.8	0.0	0.1	0.4	0.2	0.3	0.2	0.4	0.5

**Table S4:** Distribution of OTUs clustered at 99%, 97% and 95% similarities aligned and assigned to algal sequences (*Chloroplastida*). Values are the relative abundance of the taxa in percentage of total sequences and table shows taxa with >0.05% abundance.

OTU similarity	Drangajökull ICE12.2.3			Laugafell ICE12.4			Hofsjökull ICE12.6.7			Vatnajökull ICE13.14.15			Langjökull ICE13.16.18			Langjökull ICE13.19		
	99%	97%	95%	99%	97%	95%	99%	97%	95%	99%	97%	95%	99%	97%	95%	99%	97%	95%
<b>Chlorophyceae; Chloromonas cf. alpina CCCryo 033-99</b>	0.0	0.2	0.5	0.0	1.7	2.6	0.5	0.8	1.0	0.0	0.0	1.5	3.4	2.2	2.7	0.0	0.0	0.0
<b>Chlorophyceae; Chloromonas nivalis CCCryo 005-99</b>	3.2	14.9	1.4	0.0	6.7	6.5	0.0	0.2	0.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	2.6
<b>Chlorophyceae; Chloromonas polyptera</b>	32.8	27.8	43.3	21.1	23.3	29.9	4.5	5.1	4.8	25.0	14.3	13.6	33.3	31.1	32.7	52.4	36.1	28.2
<b>Chlorophyceae; Chloromonas tughillensis</b>	2.5	4.6	5.7	0.0	1.7	1.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
<b>Chlorophyceae; uncultured Chlamydomonadaceae</b>	8.9	1.4	0.0	7.9	3.3	0.0	0.0	0.0	0.0	6.3	0.0	0.0	0.0	0.0	0.0	4.8	0.0	0.0
<b>Chlorophyceae; uncultured Chlamydomonadaceae</b>	33.4	34.5	32.3	36.8	43.3	37.7	0.5	0.5	0.4	0.0	2.0	1.5	0.0	0.7	0.7	0.0	5.6	5.1
<b>Chlorophyceae; uncultured Chlamydomonadaceae</b>	0.6	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
<b>Trebouxiophyceae; Chloroidium</b>	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
<b>Trebouxiophyceae; Coccomyxa</b>	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	4.5	0.0	0.0	0.0	0.0	0.0	0.0
<b>Trebouxiophyceae; Prototheca cutis</b>	0.0	0.0	0.0	0.0	0.0	1.3	0.0	0.2	0.8	0.0	0.0	0.0	62.1	65.2	63.3	42.9	58.3	64.1
<b>Trebouxiophyceae; Raphidonema nivale CCCryo 130-01</b>	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
<b>Trebouxiophyceae; Raphidonema pyrenoidifera</b>	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
<b>Trebouxiophyceae; Raphidonema sempervirens</b>	18.5	16.6	17.0	34.2	20.0	20.8	94.6	93.3	92.7	68.8	53.1	45.5	1.1	0.7	0.7	0.0	0.0	0.0
<b>Trebouxiophyceae; Trebouxia usneae</b>	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	15.2	0.0	0.0	0.0	0.0	0.0	0.0
<b>Trebouxiophyceae; uncultured</b>	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	30.6	18.2	0.0	0.0	0.0	0.0	0.0	0.0



**Table S5:** Distribution of OTUs clustered at 99%, 97% and 95% similarities aligned and assigned to bacterial sequences. Values are the relative abundance of the taxa in percentage of total sequences and table shows taxa with >0.01% abundance.

OTU similarity	Drangajökull ICE12.2.3			Laugafell ICE12.4			Hofsjökull ICE12.6.7			Vatnajökull ICE13.14.15			Langjökull ICE13.16.18			Langjökull ICE13.19		
	99%	97%	95%	99%	97%	95%	99%	97%	95%	99%	97%	95%	99%	97%	95%	99%	97%	95%
<b>Acidobacteria; Acidobacteriia</b>	0.6	0.4	0.3	0.0	0.0	0.0	0.0	0.1	0.2	0.0	0.0	0.2	0.0	0.2	0.0	0.0	0.0	0.0
<b>Actinobacteria; Actinobacteria</b>	10.7	6.0	5.6	0.8	2.6	2.8	1.2	0.9	1.4	0.0	0.3	1.4	3.6	4.1	3.4	26.4	15.9	14.6
<b>Bacteroidetes; Cytophagia</b>	0.2	0.1	0.0	10.0	5.4	4.8	1.2	1.4	1.1	0.0	2.3	1.8	0.0	0.0	0.4	0.0	0.7	0.6
<b>Bacteroidetes; Flavobacteriia</b>	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
<b>Bacteroidetes; Sphingobacteriia</b>	23.6	18.8	18.3	0.0	0.0	0.0	50.1	32.2	29.3	0.0	0.0	0.0	0.9	0.2	0.2	0.5	0.7	0.9
<b>Bacteroidetes; Saprospirae</b>	8.0	24.1	26.6	49.2	28.5	26.8	29.5	38.4	37.1	0.0	0.0	0.0	1.8	1.4	1.3	2.0	3.8	4.8
<b>Chlorobi; Ignavibacteria</b>	8.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
<b>Cyanobacteria;</b>	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	2.7	11.7	0.0	0.0	0.5	0.0	0.0	0.3
<b>Cyanobacteria; Nostocophycideae</b>	0.0	0.0	0.0	0.0	0.2	0.2	0.0	0.0	0.0	57.1	30.8	14.6	0.0	0.0	0.0	0.0	0.0	0.0
<b>Cyanobacteria; Oscillatoriothycideae</b>	0.0	0.0	0.0	0.0	0.0	0.2	0.0	0.0	0.0	21.4	9.0	16.2	0.9	0.5	0.5	0.0	0.0	0.0
<b>Cyanobacteria; Synechococcophycideae</b>	0.0	0.5	0.4	0.8	0.5	0.6	0.0	0.0	0.0	0.0	3.7	5.9	0.0	0.0	0.2	0.0	0.0	0.2
<b>Firmicutes; Bacilli</b>	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.1
<b>Gemmatimonadetes; Gemmatimonadetes</b>	0.2	0.1	0.1	0.0	0.5	0.7	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.1
<b>Proteobacteria; Alphaproteobacteria</b>	46.4	42.0	41.4	0.8	5.4	8.1	6.2	6.6	7.5	21.4	49.5	44.6	3.6	11.6	12.1	3.4	5.1	6.0
<b>Proteobacteria; Betaproteobacteria</b>	1.6	4.9	4.1	38.3	56.2	55.1	11.5	20.1	22.9	0.0	0.3	0.9	86.5	80.3	79.3	66.0	71.9	71.1
<b>Proteobacteria; Gammaproteobacteria</b>	0.6	1.3	1.1	0.0	0.0	0.2	0.3	0.1	0.3	0.0	0.0	1.4	2.7	1.8	2.2	1.8	1.6	1.4
<b>Bacteria; WPS-2</b>	0.2	0.9	0.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.3	0.2	0.0	0.0	0.0	0.0	0.0	0.0



**Table S6:** Distribution of OTUs clustered at 99%, 97% and 95% similarities aligned and assigned to archaeal sequences. Values are the relative abundance of the taxa in percentage of total sequences.

	Laugafell			Hofsjökull			Vatnajökull			Langjökull			Langjökull			Snaefellsjökull		
	ICE12.4			ICE12.6.7			ICE13.14.15			ICE13.16.18			ICE13.16.19			ICE13.21.24		
OTU similarity	99%	97%	95%	99%	97%	95%	99%	97%	95%	99%	97%	95%	99%	97%	95%	99%	97%	95%
Crenarchaeota; MBGA	0.2	0.0	1.7	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	2.1	1.3	0.0	0.1	0.0	0.2	0.4
Crenarchaeota; Thaumarchaeota; Cenarchaeales; Cenarchaeaceae	0.6	2.8	3.3	0.0	0.7	1.8	1.4	7.7	8.6	0.3	1.1	1.5	0.0	2.4	3.3	0.6	4.2	6.0
Crenarchaeota; Thaumarchaeota; Cenarchaeales; SAGMA-X	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.5	0.0	0.0	0.0	1.6	0.0	0.0	0.0
Crenarchaeota; Thaumarchaeota; Nitrososphaerales; Nitrososphaeraceae	99.3	96.5	91.7	33.3	27.6	29.4	98.6	92.0	91.3	99.7	98.1	92.3	98.7	97.6	94.2	99.4	95.6	93.1
Euryarchaeota; Methanobacteria; Methanobacteriales; MSBL1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Euryarchaeota; Methanomicrobia; Methanosarcinales; Methanosarcinaceae	0.0	0.0	0.0	66.7	71.6	68.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0

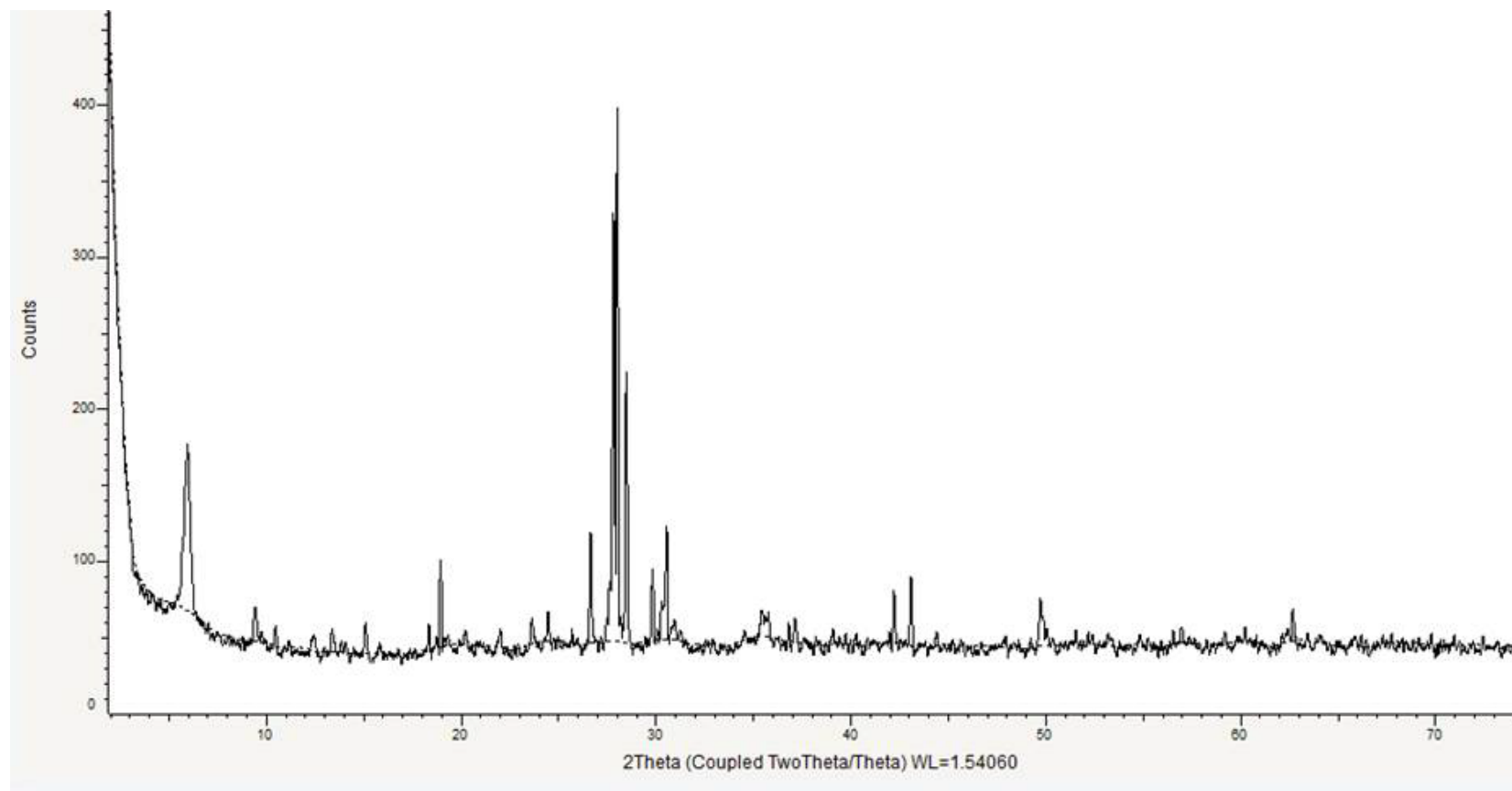
	Eyafjallajökull			Eyafjallajökull			Eyafjallajökull		
	ICE14.1			ICE14.2			ICE14.3		
OTU similarity	99%	97%	95%	99%	97%	95%	99%	97%	95%
Crenarchaeota; MBGA	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Crenarchaeota; Thaumarchaeota; Cenarchaeales; Cenarchaeaceae	0.0	0.0	0.9	0.0	0.0	2.1	0.0	0.0	4.9
Crenarchaeota; Thaumarchaeota; Cenarchaeales; SAGMA-X	0.0	0.0	0.0	15.4	18.1	17.5	0.0	0.0	0.0
Crenarchaeota; Thaumarchaeota; Nitrososphaerales; Nitrososphaeraceae	99.9	100.0	99.0	72.3	78.6	77.2	99.9	99.9	95.8
Euryarchaeota; Methanobacteria; Methanobacteriales; MSBL1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Euryarchaeota; Methanomicrobia; Methanosarcinales; Methanosarcinaceae	0.0	0.0	0.0	0.0	3.2	3.2	0.0	0.0	0.0



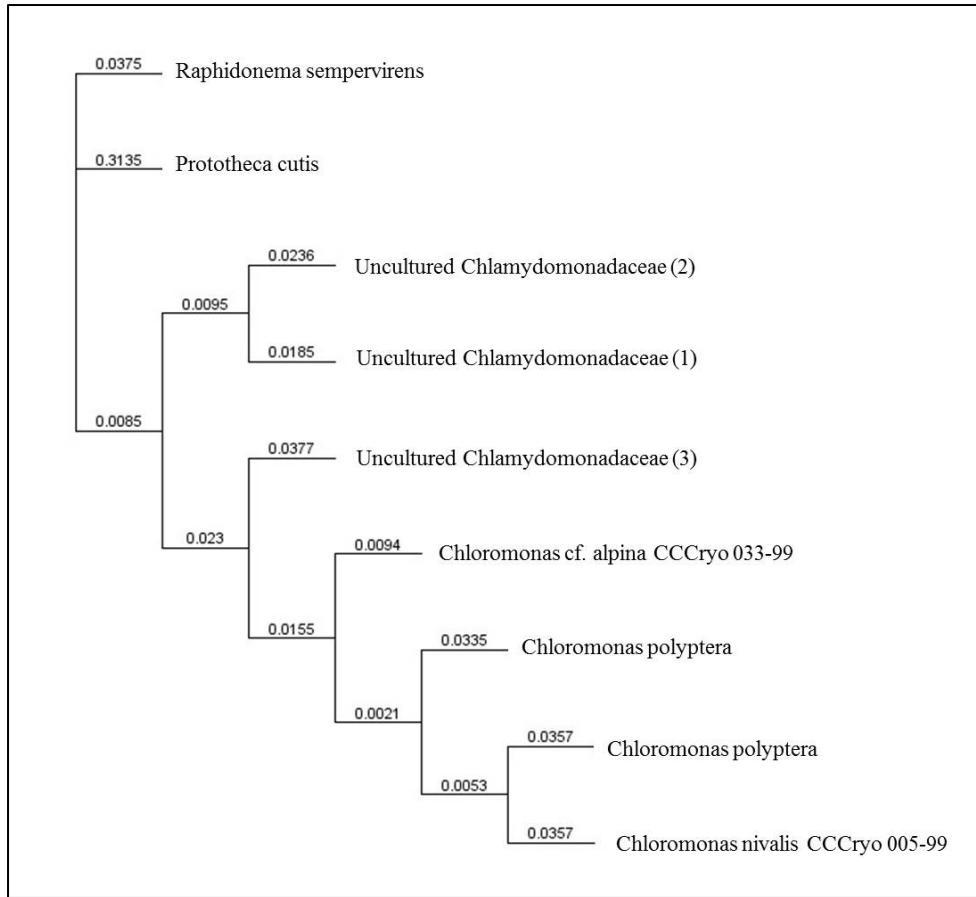
**Table S7:** Output of the PHREEQC geochemical modelling shown for one representative sample (ICE-13\_15, Vatnajökull).

Phase	SI	1=SUPERSATURATED; 0=UNDERSATURATED	log IAP	log KT	Formula
Albite	-9.3	0	-5.97	3.33	NaAlSi3O8
Albite_high	-10.79	0	-5.97	4.82	NaAlSi3O8
Albite_low	-9.3	0	-5.97	3.33	NaAlSi3O8
Analcime	-8.28	0	-1.1	7.18	Na.96Al.96Si2.04O6:H2O
Anorthite	-16.31	0	14.92	31.23	CaAl2(SiO4)2
Beidellite-Mg	-3.6	0	4.26	7.87	Mg.165Al2.33Si3.67O10(OH)2
Beidellite-Na	-4.34	0	3.47	7.81	Na.33Al2.33Si3.67O10(OH)2
Boehmite	0.74	1	10.1	9.37	AlO2H
Brucite	-12.36	0	5.73	18.09	Mg(OH)2
Ca-Al_Pyroxene	-21.23	0	20.43	41.66	CaAl2SiO6
Chalcedony	-1.19	0	-5.51	-4.32	SiO2
Clinochlore-14A	-44.5	0	32.32	76.82	Mg5Al2Si3O10(OH)8
Clinochlore-7A	-48.09	0	32.32	80.41	Mg5Al2Si3O10(OH)8
Cristobalite(alpha)	-1.51	0	-5.51	-4	SiO2
Cristobalite(beta)	-2.03	0	-5.51	-3.49	SiO2
Diaspore	1.18	1	10.1	8.92	AlHO2
Diopside	-22.5	0	0.44	22.93	CaMgSi2O6
Enstatite	-12.35	0	0.22	12.57	MgSiO3
Fayalite	-17.01	0	4.45	21.46	Fe2SiO4
Fe(OH)2	-10.45	0	4.98	15.44	Fe(OH)2
Fe(OH)3	-5.59	0	1.41	7	Fe(OH)3
FeO	-10.25	0	4.98	15.23	FeO
Forsterite	-25.13	0	5.95	31.08	Mg2SiO4
Gibbsite	0.73	1	10.1	9.38	Al(OH)3
Goethite	-0.12	0	1.41	1.53	FeOOH
Hedenbergite	-21.74	0	-0.31	21.43	CaFe(SiO3)2
Hematite	0.67	1	2.82	2.15	Fe2O3
Hercynite	-9.17	0	25.19	34.36	FeAl2O4
Kaolinite	0.13	1	9.19	9.06	Al2Si2O5(OH)4
Laumontite	-12.38	0	3.9	16.27	CaAl2Si4O12:4H2O
Lawsonite	-11.04	0	14.92	25.96	CaAl2Si2O7(OH)2:H2O
Magnetite	-6.1	0	7.8	13.9	Fe3O4
Monticellite	-26.69	0	5.95	32.64	CaMgSiO4
Montmor-Ca	-6.08	0	-2.33	3.74	Ca.165Mg.33Al1.67Si4O10(OH)2
Montmor-Mg	-6.01	0	-2.34	3.67	Mg.495Al1.67Si4O10(OH)2
Montmor-Na	-6.75	0	-3.13	3.62	Na.33Mg.33Al1.67Si4O10(OH)2
Mordenite	-10.66	0	-16.56	-5.9	Ca.2895Na.361Al.94Si5.06O12:3.468H2O

<b>Mordenite-dehy</b>	-27.42	0	-16.56	10.86	Ca.2895Na.361Al.94Si5.06O12
<b>Nontronite-Ca</b>	-1.81	0	-13.13	-11.31	Ca.165Fe2Al.33Si3.67H2O12
<b>Nontronite-H</b>	-1.68	0	-14.07	-12.39	H.33Fe2Al.33Si3.67H2O12
<b>Nontronite-Mg</b>	-1.82	0	-13.13	-11.3	Mg.165Fe2Al.33Si3.67H2O12
<b>Nontronite-Na</b>	-2.56	0	-13.92	-11.36	Na.33Fe2Al.33Si3.67H2O12
<b>Periclase</b>	-18.01	0	5.73	23.74	MgO
<b>Pyrophyllite</b>	-3.54	0	-1.84	1.71	Al2Si4O10(OH)2
<b>Quartz</b>	-0.9	0	-5.51	-4.62	SiO2
<b>SiO2(am)</b>	-2.4	0	-5.51	-3.11	SiO2



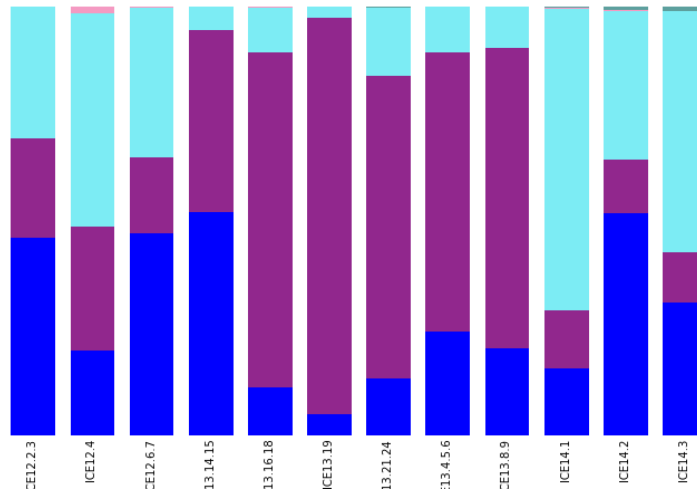
**Figure S1:** XRD pattern of one representative sample (ICE-13\_15, Vatnajökull) and typical for all Iceland samples showing the main mineral components quartz, feldspars, pyroxene and olivine and minor contributions from clays, basaltic glass and hematite.



**Figure S2:** Phylogenetic tree of main algal species showing the inferred evolutionary relationships between the main algal species in our samples. Based on their 18S rRNA sequences they are closely related (89-92% similarity) to other *Chloromonas* species found.

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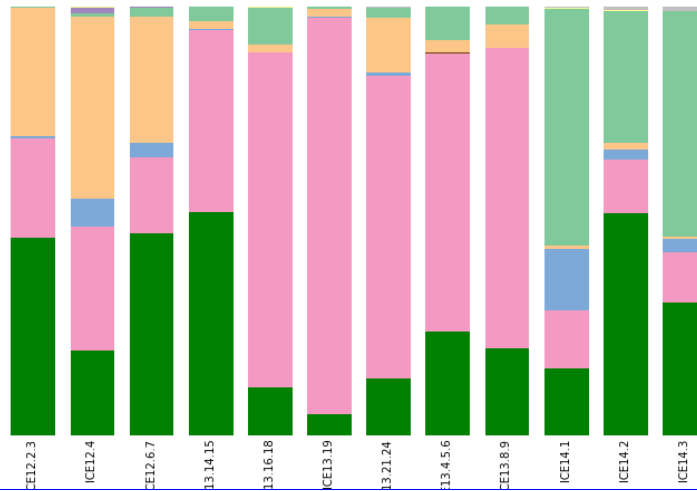


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Legend		Total	ICE12.2.3	ICE12.4	ICE12.6.7	ICE13.14.15	ICE13.16.18	ICE13.19	ICE13.21.24	ICE13.4.5.6	ICE13.8.9	ICE14.1	ICE14.2	ICE14.3
count	%	count	%	%	%	%	%	%	%	%	%	%	%	%
Eukaryota: Amoebozoa	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota: Archaeplastida	3	28.1%	46.0%	19.8%	47.2%	52.0%	11.1%	5.0%	13.4%	24.1%	20.2%	15.7%	51.9%	31.0%
Eukaryota: Centrohelida	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota: Kathablepharidae	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota: Opisthokonta	5	43.8%	23.2%	29.0%	17.7%	42.4%	78.1%	92.5%	70.5%	65.1%	70.2%	13.3%	12.4%	11.6%
Eukaryota: RTSiin25	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota: SAR	3	27.6%	30.7%	49.6%	34.9%	5.6%	10.5%	2.5%	15.8%	10.7%	9.6%	70.3%	34.6%	56.3%
Eukaryota: Zeuk77	0	0.2%	0.1%	1.6%	0.2%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.5%	0.2%	0.1%
No blast hit: Other	0	0.2%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.3%	0.0%	0.0%	0.2%	0.9%	1.0%

Taxonomy Summary, Current Level:

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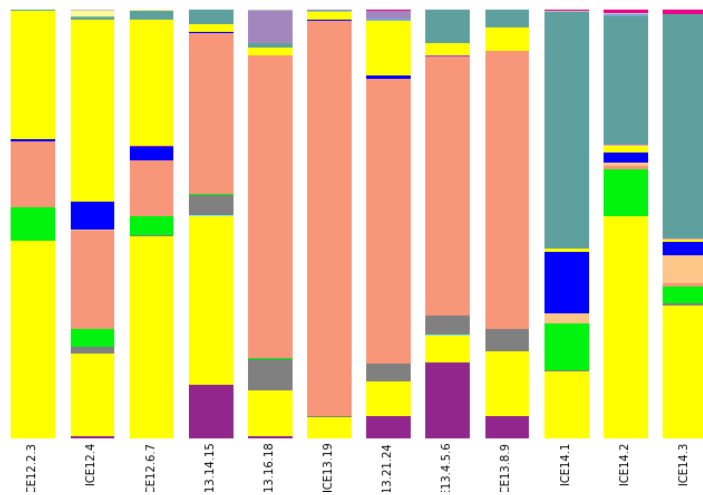


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Legend		Total	ICE12.2.3	ICE12.4	ICE12.6.7	ICE13.14.15	ICE13.16.18	ICE13.19	ICE13.21.24	ICE13.4.5.6	ICE13.8.9	ICE14.1	ICE14.2	ICE14.3
count	%	count	%	%	%	%	%	%	%	%	%	%	%	%
Eukaryota: Amoebozoa: Conosa	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota: Amoebozoa: Discosoa	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota: Amoebozoa: Lobosa	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota: Archaeplastida: Chloroplastida	3	28.1%	46.0%	19.8%	47.2%	52.0%	11.1%	5.0%	13.4%	24.1%	20.2%	15.7%	51.9%	31.0%
Eukaryota: Archaeplastida: Rhodophyceae	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota: Centrohelida: Heterophryidae	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota: Kathablepharidae: Roombia	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota: Opisthokonta: Fungi	5	43.8%	23.2%	29.0%	17.7%	42.4%	78.1%	92.5%	70.5%	65.1%	70.2%	13.3%	12.4%	11.6%
Eukaryota: Opisthokonta: Holozoa	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota: Opisthokonta: Metazoa	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota: Opisthokonta: uncultured	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota: RTSiin25: uncultured_Eimeriidae	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota: RTSiin25: uncultured_freshwater_eukaryote	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota: SAR: Alveolata	0	2.7%	0.5%	6.3%	3.4%	0.3%	0.1%	0.1%	0.8%	0.2%	0.0%	14.4%	2.4%	3.3%
Eukaryota: SAR: Rhizaria	1	10.9%	30.1%	42.5%	29.2%	1.9%	1.7%	1.9%	12.7%	2.7%	5.3%	0.9%	1.4%	0.5%
Eukaryota: SAR: Stramenopiles	2	14.0%	0.1%	0.8%	2.3%	3.4%	8.8%	0.5%	2.3%	7.9%	4.3%	55.0%	30.7%	52.4%
Eukaryota: Zeuk77: uncultured_Oxytrichidae	0	0.1%	0.1%	1.4%	0.2%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota: Zeuk77: uncultured_eukaryote	0	0.1%	0.0%	0.2%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.4%	0.2%	0.1%
No blast hit: Other	0	0.2%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.3%	0.0%	0.0%	0.2%	0.9%	1.0%

Taxonomy Summary, Current Level:

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Legend	Taxonomy	Total count	%	ICE12.2.3	ICE12.4	ICE12.6.7	ICE13.14.15	ICE13.16.18	ICE13.19	ICE13.21.24	ICE13.4.5.6	ICE13.8.9	ICE14.1	ICE14.2	ICE14.3
Eukaryota__Amoebozoa__Conosa__	<a href="#">Schizoplasmodiida</a>	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota__Amoebozoa__Conosa__	<a href="#">Soliformovum</a>	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota__Amoebozoa__Discosia__	<a href="#">Fibellinia</a>	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota__Amoebozoa__Lobosa__	<a href="#">Tubulinea</a>	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota__Archaeplastida__Chloroplastida__	<a href="#">Charophyta</a>	0	3.5%	0.0%	0.6%	0.0%	12.4%	0.5%	0.0%	5.2%	17.6%	5.3%	0.0%	0.0%	0.0%
Eukaryota__Archaeplastida__Chloroplastida__	<a href="#">Chlorophyta</a>	3	24.6%	46.0%	19.2%	47.2%	39.5%	10.6%	5.0%	8.2%	6.4%	14.9%	15.7%	51.8%	30.9%
Eukaryota__Archaeplastida__Chloroplastida__	<a href="#">uncultured</a>	0	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%
Eukaryota__Archaeplastida__Rhodophyceae__	<a href="#">Comosopogonales</a>	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota__Centrohelida__Heterophryidae__	<a href="#">Heterophrys</a>	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota__Kathablepharidae__	<a href="#">Roombia</a>	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota__Kathablepharidae__	<a href="#">Roombia truncata</a>	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota__Opisthokonta__Fungi__	<a href="#">Ascomycota</a>	0	2.4%	0.0%	1.4%	0.1%	4.9%	7.2%	0.2%	4.0%	4.5%	5.3%	0.2%	0.0%	0.0%
Eukaryota__Opisthokonta__Fungi__	<a href="#">Basal fungi</a>	0	3.6%	7.9%	4.4%	4.5%	0.1%	0.4%	0.0%	0.0%	0.0%	0.0%	10.9%	10.9%	3.9%
Eukaryota__Opisthokonta__Fungi__	<a href="#">Basidiomycota</a>	4	37.1%	15.3%	22.8%	13.1%	37.5%	70.5%	92.2%	66.6%	60.5%	64.9%	0.1%	0.7%	0.8%
Eukaryota__Opisthokonta__Fungi__	<a href="#">LKM11</a>	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota__Opisthokonta__Fungi__	<a href="#">LKM18</a>	0	0.8%	0.0%	0.4%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	2.1%	0.8%	6.4%
Eukaryota__Opisthokonta__Fungi__	<a href="#">Nucleiomycea</a>	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota__Opisthokonta__Holozoa__	<a href="#">Choanomonada</a>	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota__Opisthokonta__Metazoa__	<a href="#">Annelida</a>	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota__Opisthokonta__Metazoa__	<a href="#">Arthropoda</a>	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota__Opisthokonta__Metazoa__	<a href="#">Cnidaria</a>	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota__Opisthokonta__Metazoa__	<a href="#">Gastrotricha</a>	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota__Opisthokonta__Metazoa__	<a href="#">Nematoda</a>	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota__Opisthokonta__Metazoa__	<a href="#">Platyhelminthes</a>	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota__Opisthokonta__Metazoa__	<a href="#">Porifera</a>	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota__Opisthokonta__Metazoa__	<a href="#">Rotifera</a>	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota__Opisthokonta__Metazoa__	<a href="#">Tardigrada</a>	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota__Opisthokonta__uncultured__	<a href="#">uncultured_Sarcosomataceae</a>	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota__RTSiiin25__uncultured__	<a href="#">Eimeriidae:Other</a>	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota__RTSiiin25__uncultured__	<a href="#">freshwater_eukaryote:Other</a>	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota__SAR__	<a href="#">Alveolata__Aglicomplexa</a>	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota__SAR__	<a href="#">Alveolata__Ciliophora</a>	0	2.6%	0.5%	6.3%	3.1%	0.3%	0.1%	0.1%	0.8%	0.2%	0.0%	14.4%	2.4%	3.3%
Eukaryota__SAR__	<a href="#">Alveolata__Dinoflagellata</a>	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota__SAR__	<a href="#">Alveolata__NIF-4C10</a>	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota__SAR__	<a href="#">Alveolata__Protalycolata</a>	0	0.0%	0.0%	0.0%	0.3%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota__SAR__	<a href="#">Rhizaria__Cercosoa</a>	1	10.9%	30.1%	42.5%	29.2%	1.9%	1.7%	1.9%	12.7%	2.7%	5.3%	0.9%	1.4%	0.5%
Eukaryota__SAR__	<a href="#">Stramenopiles__Bicosoecida</a>	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota__SAR__	<a href="#">Stramenopiles__CCI40</a>	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.3%	0.0%
Eukaryota__SAR__	<a href="#">Stramenopiles__Chrysophyceae</a>	2	13.1%	0.1%	0.6%	2.3%	3.4%	1.1%	0.0%	0.0%	7.8%	4.3%	55.0%	30.0%	52.4%
Eukaryota__SAR__	<a href="#">Stramenopiles__Diatomea</a>	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota__SAR__	<a href="#">Stramenopiles__Fusigmatales</a>	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota__SAR__	<a href="#">Stramenopiles__Labyrinthulomycetes</a>	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota__SAR__	<a href="#">Stramenopiles__Peronosporomycetes</a>	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota__SAR__	<a href="#">Stramenopiles__Synurales</a>	0	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.4%	0.0%	0.0%	0.0%	0.4%	0.0%
Eukaryota__SAR__	<a href="#">Stramenopiles__TKR07M_92</a>	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota__SAR__	<a href="#">Stramenopiles__Xanthophyceae</a>	0	0.0%	0.0%	0.2%	0.0%	0.0%	0.0%	0.2%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota__SAR__	<a href="#">Stramenopiles__uncultured_eukaryote</a>	0	0.8%	0.0%	0.0%	0.0%	0.0%	7.6%	0.3%	1.9%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota__Zeuk77__uncultured__	<a href="#">Oxytrichidae:Other</a>	0	0.1%	0.1%	1.4%	0.2%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota__Zeuk77__uncultured__	<a href="#">eukaryote:Other</a>	0	0.1%	0.0%	0.2%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.4%	0.2%	0.1%
No blast hit:Other:Other:Other		0	0.2%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.3%	0.0%	0.0%	0.2%	0.9%	1.0%

Taxonomy Summary. Current Level:

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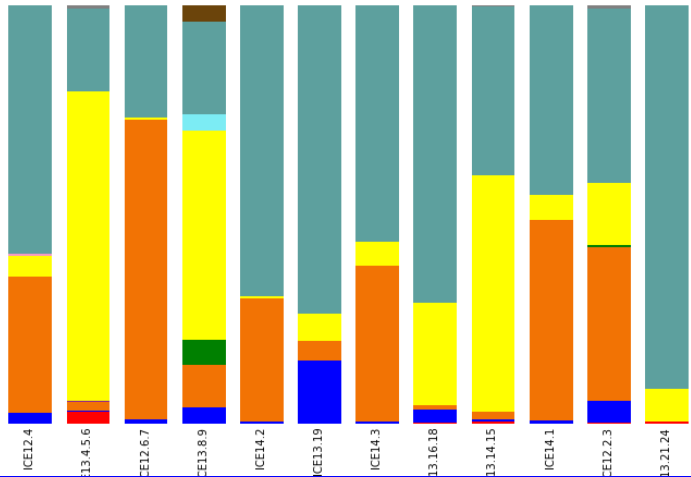




Eukaryota_SAR; Rhizaria; Cercozoa; Thecofilosea; uncultured	0	0.3%	0.6%	1.8%	0.7%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%
Eukaryota_SAR; Rhizaria; Cercozoa; uncultured; Cercozoa	0	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota_SAR; Rhizaria; Cercozoa; uncultured; uncultured_Eimeriidae	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota_SAR; Rhizaria; Cercozoa; uncultured; uncultured_cercozoan	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota_SAR; Rhizaria; Cercozoa; uncultured; uncultured_eukaryote	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota_SAR; Rhizaria; Cercozoa; uncultured; uncultured_eukaryotic_picoplankton	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota_SAR; Stramenopiles; Bicosoecida; P34.6; Bicosoecida	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota_SAR; Stramenopiles; Bicosoecida; Silvanidae; PSA11SP2005	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota_SAR; Stramenopiles; CCI40; uncultured_marine_eukaryote; Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.3%	0.0%
Eukaryota_SAR; Stramenopiles; Chrysophyceae; CCMP1899; Chrysophyceae_sp_176	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota_SAR; Stramenopiles; Chrysophyceae; CCMP1899; Ochromonas	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota_SAR; Stramenopiles; Chrysophyceae; CCMP1899; uncultured_marine_stramenopile	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota_SAR; Stramenopiles; Chrysophyceae; Chromulinales; Chromulina	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota_SAR; Stramenopiles; Chrysophyceae; Chromulinales; Chrysamoeba	0	0.0%	0.0%	0.4%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota_SAR; Stramenopiles; Chrysophyceae; Chromulinales; Chrysochaete	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota_SAR; Stramenopiles; Chrysophyceae; Chromulinales; LG31-02	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota_SAR; Stramenopiles; Chrysophyceae; Chromulinales; Spumella	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota_SAR; Stramenopiles; Chrysophyceae; Chrysocapsales; Chrysocapsa	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota_SAR; Stramenopiles; Chrysophyceae; Chrysocapsales; Hydrurus	2	13.0%	0.1%	0.2%	2.2%	3.4%	1.1%	0.0%	0.0%	7.8%	4.3%	55.0%	30.0%	52.3%	
Eukaryota_SAR; Stramenopiles; Chrysophyceae; LG21-05; uncultured_eukaryote	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota_SAR; Stramenopiles; Chrysophyceae; LG21-05; uncultured_marine_eukaryote	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota_SAR; Stramenopiles; Chrysophyceae; Ochromonadales; Ochromonas	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota_SAR; Stramenopiles; Chrysophyceae; Ochromonadales; Paraphysomonas	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota_SAR; Stramenopiles; Chrysophyceae; uncultured_eukaryote; Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota_SAR; Stramenopiles; Diatomea; Bacillariophytina; Bacillariophyceae	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota_SAR; Stramenopiles; Eustigmatales; Nannochloropsis; uncultured_marine_eukaryote	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota_SAR; Stramenopiles; Labryinthulomycetes; Thraustochytriales; Schizochytrium	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota_SAR; Stramenopiles; Peronosporomycetes; Aphanomyces; uncultured_Saprolegniales	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota_SAR; Stramenopiles; Peronosporomycetes; Lagenidium; Lagenidium_caudatum	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota_SAR; Stramenopiles; Peronosporomycetes; Ochromonadales; environmental_sample; Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota_SAR; Stramenopiles; Peronosporomycetes; Phytophthora; Halophytophthora	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota_SAR; Stramenopiles; Peronosporomycetes; Phytophthora; uncultured_soil_fungus	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota_SAR; Stramenopiles; Peronosporomycetes; Saprolegnia; Saprolegnia_sp_SAP1	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota_SAR; Stramenopiles; Synurales; Synura; Synura_uvella	0	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.4%	0.0%	0.0%	0.0%	0.0%	0.4%	0.0%
Eukaryota_SAR; Stramenopiles; TKR07M.82; uncultured_eukaryote; Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota_SAR; Stramenopiles; Xanthophyceae; Tribonematales; Botrydiopsis	0	0.0%	0.0%	0.2%	0.0%	0.0%	0.0%	0.2%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota_SAR; Stramenopiles; uncultured_eukaryote; Other; Other	0	0.8%	0.0%	0.0%	0.0%	0.0%	7.6%	0.3%	1.9%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota_Zeuk77; uncultured_Oxytrichidae; Other; Other; Other	0	0.1%	0.1%	1.4%	0.2%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Eukaryota_Zeuk77; uncultured_eukaryote; Other; Other; Other	0	0.1%	0.0%	0.2%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.4%	0.2%	0.1%	
No blast hit; Other; Other; Other; Other	0	0.2%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.3%	0.0%	0.0%	0.2%	0.9%	1.0%	

Taxonomy Summary. Current Level:

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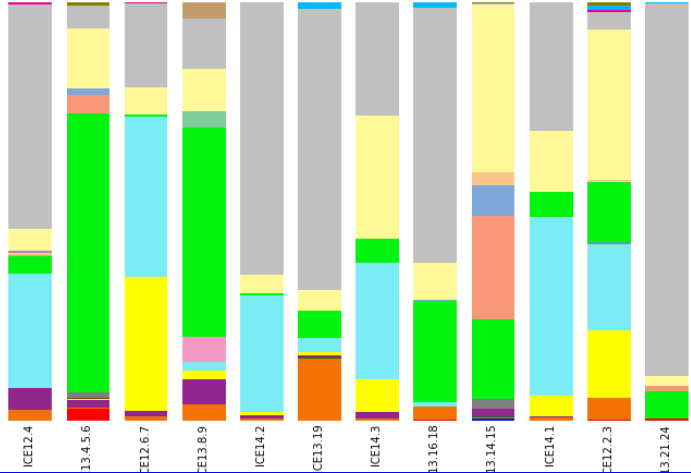


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Legend	Taxonomy	Total	ICE12.4	ICE13.4.5.6	ICE12.6.7	ICE13.8.9	ICE13.8.9	ICE14.2	ICE13.19	ICE14.3	ICE13.16.18	ICE13.14.15	ICE14.1	ICE12.2.3	ICE13.21.24
		count	%	%	%	%	%	%	%	%	%	%	%	%	%
k_Bacteria;p	Acidobacteria	0	0.4%	0.0%	2.9%	0.1%	0.0%	0.0%	0.0%	0.0%	0.2%	0.5%	0.0%	0.3%	0.5%
k_Bacteria;p	Actinobacteria	0	2.8%	2.7%	0.3%	0.9%	4.0%	0.5%	15.0%	0.6%	3.1%	0.5%	0.8%	5.1%	0.0%
k_Bacteria;p	Bacteroidetes	3	22.9%	32.4%	2.1%	71.6%	10.0%	29.3%	4.9%	37.2%	1.2%	1.9%	47.8%	36.8%	0.1%
k_Bacteria;p	Chlorobi	0	0.5%	0.0%	0.0%	0.0%	6.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.4%	0.0%
k_Bacteria;p	Chloroflexi	0	0.0%	0.0%	0.2%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p	Cyanobacteria	3	21.0%	5.0%	74.0%	0.6%	50.0%	0.8%	6.4%	5.7%	24.4%	56.4%	6.1%	14.9%	7.7%
k_Bacteria;p	Firmicutes	0	0.3%	0.0%	0.0%	0.0%	4.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p	Gemmatimonadetes	0	0.0%	0.5%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%
k_Bacteria;p	Proteobacteria	6	51.5%	59.5%	19.9%	26.8%	22.0%	69.4%	73.6%	56.5%	71.1%	40.4%	45.3%	41.6%	91.6%
k_Bacteria;p	Spirochaetes	0	0.3%	0.0%	0.0%	0.0%	4.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteria;p	WPS-2	0	0.2%	0.0%	0.7%	0.0%	0.0%	0.0%	0.0%	0.0%	0.3%	0.0%	0.8%	0.1%	

Taxonomy Summary. Current Level:

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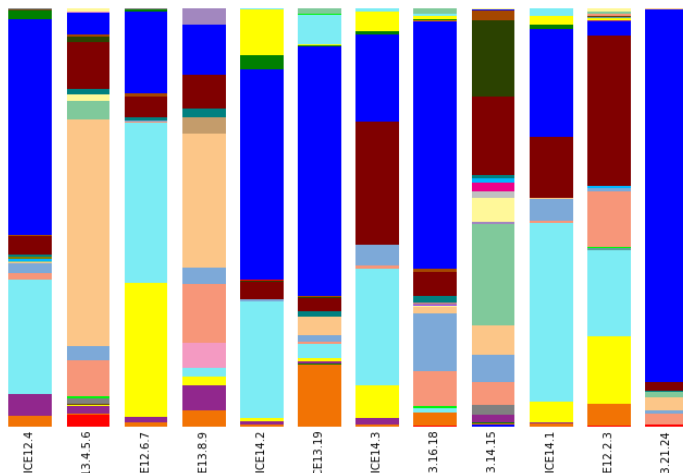


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Legend	Taxonomy	Total	ICE12.4	ICE13.4.5.6	ICE12.6.7	ICE13.8.9	ICE14.2	ICE13.19	ICE14.3	ICE13.16.18	ICE13.14.15	ICE14.1	ICE12.2.3	ICE13.21.24		
		count	%	%	%	%	%	%	%	%	%	%	%	%		
k_Bacteria;p	Acidobacteria;c_Acidobacteria	0	0.3%	0.0%	2.9%	0.1%	0.0%	0.0%	0.0%	0.0%	0.2%	0.0%	0.0%	0.3%	0.5%	
k_Bacteria;p	Acidobacteria;c_Solibactera	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	
k_Bacteria;p	Actinobacteria;c_Actinobacteria	0	2.8%	2.5%	0.3%	0.9%	4.0%	0.5%	14.9%	0.6%	3.1%	0.3%	0.8%	5.1%	0.0%	
k_Bacteria;p	Actinobacteria;c_Thermoleophila	0	0.0%	0.2%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.3%	0.0%	0.0%	0.0%	
k_Bacteria;p	Bacteroidetes;c_Cytophagia	0	1.6%	5.2%	1.8%	1.4%	6.0%	0.7%	0.7%	1.6%	0.0%	1.9%	0.1%	0.1%	0.1%	
k_Bacteria;p	Bacteroidetes;c_Sphingobacteria	1	5.4%	0.0%	0.2%	32.0%	2.0%	0.8%	0.6%	7.6%	0.2%	0.0%	5.0%	16.1%	0.0%	
k_Bacteria;p	Bacteroidetes;c_Saprosirae	2	15.9%	27.3%	0.1%	38.2%	2.0%	27.8%	3.6%	28.0%	1.0%	0.0%	42.7%	20.6%	0.0%	
k_Bacteria;p	Chlorobi;c_Ignavibacteria	0	0.5%	0.0%	0.0%	0.0%	6.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	
k_Bacteria;p	Chlorobi;c_SJA28	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.4%	0.0%	
k_Bacteria;p	Chloroflexi;c_Ktesonobacteria	0	0.0%	0.0%	0.2%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	
k_Bacteria;p	Cyanobacteria;c_	0	0.3%	0.0%	1.4%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	2.2%	0.0%	0.0%	0.0%	
k_Bacteria;p	Cyanobacteria;c_Nostocplast	2	17.0%	4.3%	66.5%	0.6%	50.0%	0.8%	6.4%	5.7%	24.1%	19.0%	6.1%	14.5%	6.4%	
k_Bacteria;p	Cyanobacteria;c_Nostocophyceae	0	2.6%	0.2%	4.6%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	24.9%	0.0%	0.0%	1.4%	
k_Bacteria;p	Cyanobacteria;c_Oscillatorophyceae	0	0.8%	0.0%	1.4%	0.0%	0.0%	0.0%	0.0%	0.0%	0.3%	7.3%	0.0%	0.0%	0.0%	
k_Bacteria;p	Cyanobacteria;c_Synechococophyceae	0	0.3%	0.5%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	3.0%	0.0%	0.4%	0.0%	
k_Bacteria;p	Firmicutes;c_Bacilli	0	0.3%	0.0%	0.0%	0.0%	4.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	
k_Bacteria;p	Gemmatimonadetes;c_Gemmatimonadetes	0	0.0%	0.5%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	
k_Bacteria;p	Proteobacteria;c_Alphaproteobacteria	2	14.7%	5.2%	14.3%	6.6%	10.0%	4.4%	4.8%	29.4%	8.8%	40.1%	14.7%	36.0%	2.5%	
k_Bacteria;p	Proteobacteria;c_Betaproteobacteria	4	36.3%	53.8%	5.4%	20.0%	12.0%	64.9%	67.3%	27.1%	60.9%	0.3%	30.6%	4.2%	89.1%	
k_Bacteria;p	Proteobacteria;c_Deltaproteobacteria	0	0.1%	0.5%	0.1%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.3%	0.0%	
k_Bacteria;p	Proteobacteria;c_Gammaproteobacteria	0	0.4%	0.0%	0.1%	0.1%	0.0%	0.1%	1.5%	0.1%	1.4%	0.0%	0.0%	1.1%	0.1%	
k_Bacteria;p	Spirochaetes;c_Spirochaetes	0	0.3%	0.0%	0.0%	0.0%	4.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	
k_Bacteria;p	WPS-2;c_	0	0.2%	0.0%	0.7%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.3%	0.0%	0.8%	0.1%

Taxonomy Summary. Current Level:

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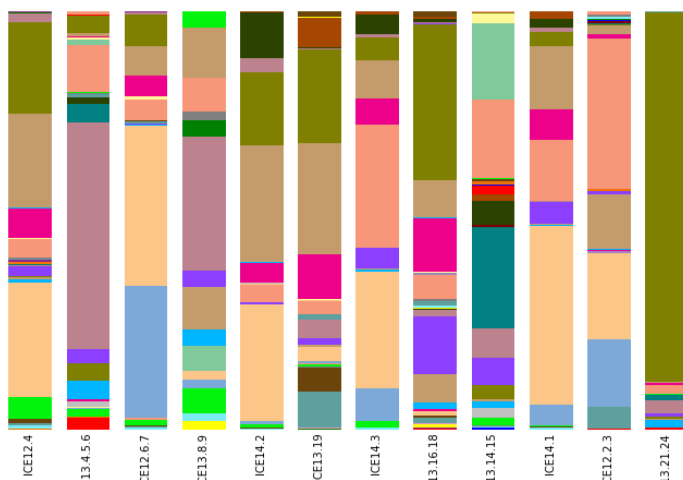


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		Total	ICE12.4	ICE13.4.5.6	ICE12.6.7	ICE13.8.9	ICE14.2	ICE13.19	ICE14.3	ICE13.16.18	ICE13.14.15	ICE14.1	ICE12.2.3	ICE13.21.24
Legend	Taxonomy	count	%	%	%	%	%	%	%	%	%	%	%	%
k_Bacteriap_Acidobacteria;c_Acidobacteria;o_Acidobacteriales		0	0.3%	0.0%	2.9%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.3%	0.5%
k_Bacteriap_Acidobacteria;c_Solibacteres;o_Solibacterales		0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.5%	0.0%	0.0%
k_Bacteriap_Actinobacteria;c_Actinobacteria;o_Actinomycetales		0	2.8%	2.5%	0.3%	0.9%	4.0%	0.5%	14.9%	0.6%	3.1%	0.3%	0.8%	5.1%
k_Bacteriap_Actinobacteria;c_Thermoleophilia;o_Gaiellales		0	0.0%	0.2%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.3%	0.0%	0.0%
k_Bacteriap_Bacteroidetes;c_Cytophagia;o_Cytophagales		0	1.6%	5.2%	1.8%	1.4%	6.0%	0.7%	0.7%	1.6%	0.0%	1.9%	0.1%	0.1%
k_Bacteriap_Bacteroidetes;c_Sphingobacteria;o_Sphingobacteriales		1	5.4%	0.0%	0.2%	32.0%	2.0%	0.8%	0.6%	7.6%	0.2%	0.0%	5.0%	16.1%
k_Bacteriap_Bacteroidetes;c_Saprospirae;o_Saprospirales		2	15.9%	27.3%	0.1%	38.2%	2.0%	27.8%	3.6%	28.0%	1.0%	0.0%	42.7%	20.6%
k_Bacteriap_Chlorobici;Ignavibacteria;o_Ignavibacteriales		0	0.5%	0.0%	0.0%	0.0%	6.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteriap_Chlorobici;SJA28;o_		0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.4%
k_Bacteriap_Chloroflexi;Ktedonobacteria;o_Thermogemmatisporales		0	0.0%	0.0%	0.2%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteriap_Cyanobacteria;c_		0	0.3%	0.0%	1.4%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	2.2%	0.0%	0.0%
k_Bacteriap_Cyanobacteria;c_Chloroplast;o_		0	0.1%	0.0%	0.4%	0.0%	0.0%	0.1%	0.0%	0.0%	0.5%	0.0%	0.1%	0.4%
k_Bacteriap_Cyanobacteria;c_Chloroplast;o_Chlorophyta		1	4.6%	1.6%	8.6%	0.4%	14.0%	0.1%	0.4%	0.7%	8.3%	5.4%	0.5%	13.2%
k_Bacteriap_Cyanobacteria;c_Chloroplast;o_Strametophiles		0	3.7%	2.5%	3.4%	0.2%	4.0%	0.5%	1.7%	4.9%	13.9%	6.5%	5.2%	0.7%
k_Bacteriap_Cyanobacteria;c_Chloroplast;o_Siretophyta		1	8.5%	0.2%	54.2%	0.0%	32.0%	0.1%	4.3%	0.0%	1.4%	7.0%	0.2%	0.1%
k_Bacteriap_Cyanobacteria;c_Nostocophycidae;o_Nostocales		0	2.5%	0.2%	4.6%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	24.4%	0.0%	1.4%
k_Bacteriap_Cyanobacteria;c_Nostocophycidae;o_Silgonematales		0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.5%	0.0%	0.0%	0.0%
k_Bacteriap_Cyanobacteria;c_Oscillatoriothycidae;o_Chroococcales		0	0.6%	0.0%	1.4%	0.0%	0.0%	0.0%	0.0%	0.0%	0.3%	0.0%	0.0%	0.0%
k_Bacteriap_Cyanobacteria;c_Oscillatoriothycidae;o_Oscillatoriales		0	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	1.6%	0.0%	0.0%
k_Bacteriap_Cyanobacteria;c_Synechococophycidae;o_Pseudanabaenales		0	0.2%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	1.9%	0.0%	0.0%
k_Bacteriap_Cyanobacteria;c_Synechococophycidae;o_Synechococcales		0	0.2%	0.5%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	1.1%	0.0%	0.4%	0.0%
k_Bacteriap_Firmicutes;c_Bacilli;o_Bacillales		0	0.3%	0.0%	0.0%	0.0%	4.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteriap_Gemmatimonadetes;c_Gemmatimonadetes;o_Gemmatimonadales		0	0.0%	0.5%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.1%
k_Bacteriap_Proteobacteria;c_Alphaproteobacteria;o_		0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.3%	0.0%	0.0%	0.0%	0.0%
k_Bacteriap_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales		0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.3%	0.0%	0.0%	0.0%	0.0%
k_Bacteriap_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales		0	0.7%	0.7%	1.3%	0.8%	2.0%	0.0%	1.1%	0.0%	1.5%	0.8%	0.1%	0.4%
k_Bacteriap_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales		1	11.8%	4.3%	11.2%	4.8%	8.0%	4.2%	3.3%	29.3%	5.9%	18.7%	14.6%	35.7%
k_Bacteriap_Proteobacteria;c_Alphaproteobacteria;o_Rickettsiales		0	1.6%	0.0%	1.3%	0.0%	0.0%	0.1%	0.1%	0.0%	0.0%	18.2%	0.0%	0.0%
k_Bacteriap_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales		0	0.5%	0.2%	0.4%	0.9%	0.0%	0.2%	0.3%	0.0%	0.7%	2.4%	0.0%	0.1%
k_Bacteriap_Proteobacteria;c_Betaproteobacteria;o_		0	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteriap_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales		4	33.1%	51.8%	5.3%	19.5%	12.0%	50.4%	69.8%	20.8%	59.2%	0.3%	25.6%	3.4%
k_Bacteriap_Proteobacteria;c_Betaproteobacteria;o_Ellin6067		0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.3%	0.0%	0.0%	0.0%
k_Bacteriap_Proteobacteria;c_Betaproteobacteria;o_Gallionellales		0	0.7%	2.0%	0.0%	0.4%	0.0%	3.4%	0.2%	0.9%	0.2%	0.0%	1.0%	0.0%
k_Bacteriap_Proteobacteria;c_Betaproteobacteria;o_IS44		0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.2%	0.0%
k_Bacteriap_Proteobacteria;c_Betaproteobacteria;o_Methylophilales		0	1.6%	0.0%	0.0%	0.0%	0.0%	10.8%	0.1%	4.7%	0.7%	0.0%	2.2%	0.4%
k_Bacteriap_Proteobacteria;c_Betaproteobacteria;o_Rhodocyclales		0	0.9%	0.0%	0.1%	0.1%	0.0%	0.3%	7.2%	0.6%	0.5%	0.0%	1.8%	0.1%
k_Bacteriap_Proteobacteria;c_Betaproteobacteria;o_SCI-84		0	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteriap_Proteobacteria;c_Deltaproteobacteria;o_MBNT15		0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%
k_Bacteriap_Proteobacteria;c_Deltaproteobacteria;o_Myxococcales		0	0.0%	0.2%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.2%
k_Bacteriap_Proteobacteria;c_Deltaproteobacteria;o_Spirochaetales		0	0.0%	0.2%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteriap_Proteobacteria;c_Gammaproteobacteria;o_		0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.2%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteriap_Proteobacteria;c_Gammaproteobacteria;o_Legionellales		0	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.7%
k_Bacteriap_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales		0	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.8%
k_Bacteriap_Proteobacteria;c_Gammaproteobacteria;o_Thiotrichales		0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.2%	0.0%	0.0%	0.0%	0.1%
k_Bacteriap_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales		0	0.3%	0.0%	0.0%	0.1%	0.0%	0.1%	1.3%	0.0%	1.2%	0.0%	0.0%	0.4%
k_Bacteriap_Spirochaetes;c_Spirochaetales;o_Spirochaetales		0	0.3%	0.0%	0.0%	0.0%	4.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteriap_WPS-2;c_		0	0.2%	0.0%	0.7%	0.0%	0.0%	0.0%	0.0%	0.0%	0.3%	0.0%	0.8%	0.1%

Taxonomy Summary, Current Level:

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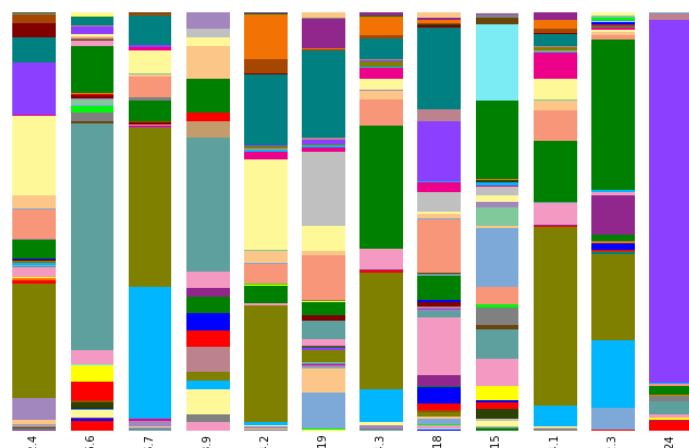
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		Total	ICE12.4	ICE13.4.5.6	ICE12.6.7	ICE13.8.9	ICE14.2	ICE13.19	ICE14.3	ICE13.16.18	ICE13.14.15	ICE14.1	ICE12.2.3	ICE13.21.24
Legend	Taxonomy	count	%	%	%	%	%	%	%	%	%	%	%	%

Taxonomy	0	0.3%	0.0%	2.9%	0.1%	0.0%	0.0%	0.0%	0.2%	0.0%	0.3%	0.5%
k_Bacteriap_Acidobacteria;c_Acidobacteria;o_Acidobacteriales;f_Acidobacteriaceae	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteriap_Acidobacteria;c_Solibacteres;o_Solibacterales;f_	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteriap_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_	0	0.0%	0.2%	0.2%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%
k_Bacteriap_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Frankiaceae	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%
k_Bacteriap_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Geodermatophilaceae	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.3%	0.0%	0.0%	0.0%
k_Bacteriap_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Kinopsoraceae	0	0.2%	0.0%	0.0%	0.0%	2.0%	0.0%	0.0%	0.9%	0.0%	0.0%	0.0%
k_Bacteriap_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Microbacteriaceae	0	0.4%	0.9%	0.0%	0.4%	2.0%	0.2%	0.2%	0.4%	0.0%	0.3%	0.5%
k_Bacteriap_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Nocardiaceae	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.2%	0.0%	0.0%	0.0%
k_Bacteriap_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Pseudonocardaceae	0	1.3%	0.5%	0.1%	0.2%	0.0%	0.0%	8.7%	0.0%	1.2%	0.0%	1.1%
k_Bacteriap_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Sporichthyaceae	0	0.7%	0.9%	0.0%	0.4%	0.0%	0.4%	5.7%	0.2%	0.5%	0.0%	0.3%
k_Bacteriap_Actinobacteria;c_Thermoleophilia;o_Gaillales;f_	0	0.0%	0.2%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.3%	0.0%
k_Bacteriap_Bacteroidetes;c_Cytophagia;o_Cytophagales;f_Cytophagaceae	0	1.6%	5.2%	1.8%	1.4%	6.0%	0.7%	0.7%	1.6%	0.0%	1.9%	0.1%
k_Bacteriap_Bacteroidetes;c_Sphingobacterii;o_Sphingobacteriales;f_	0	0.0%	0.0%	0.0%	0.4%	0.0%	0.0%	0.2%	0.0%	0.0%	0.0%	0.0%
k_Bacteriap_Bacteroidetes;c_Sphingobacterii;o_Sphingobacteriales;f_Sphingobacteriaceae	1	5.3%	0.0%	0.2%	31.6%	2.0%	0.8%	0.4%	7.6%	0.2%	0.0%	5.0%
k_Bacteriap_Bacteroidetes;c_[Saprospirae]o_[Saprospirales]f_Chitinophagaceae	2	15.9%	27.3%	0.1%	38.2%	2.0%	27.8%	3.6%	28.0%	1.0%	0.0%	42.7%
k_Bacteriap_Chlorobici;Ignavibacteriia;o_Ignavibacteriales;f_Ignavibacteriaceae	0	0.5%	0.0%	0.0%	0.0%	6.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteriap_Chlorobici;SJA28;o_f_	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.4%
k_Bacteriap_Chloroflexi;Ktedonobacteriia;o_Thermogemmatissporales;f_Thermogemmatissporaceae	0	0.0%	0.0%	1.2%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteriap_Cyanobacteria;o_f_	0	0.3%	0.0%	0.4%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	2.2%	0.0%
k_Bacteriap_Cyanobacteria;c_Chloroplasto;f_	0	0.1%	0.0%	0.4%	0.0%	0.0%	0.1%	0.0%	0.0%	0.5%	0.0%	0.1%
k_Bacteriap_Cyanobacteria;c_Chloroplasto;Chlorophyta;f_	0	1.2%	0.7%	4.4%	0.2%	4.0%	0.1%	0.0%	0.5%	1.5%	1.6%	0.1%
k_Bacteriap_Cyanobacteria;c_Chloroplasto;Chlorophyta;f_Chlamydomonadaceae	0	2.7%	0.7%	0.1%	0.1%	10.0%	0.0%	0.4%	0.3%	6.7%	0.5%	0.4%
k_Bacteriap_Cyanobacteria;c_Chloroplasto;Chlorophyta;f_Trebouxiothyceae	0	0.7%	0.2%	4.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	3.3%	0.0%
k_Bacteriap_Cyanobacteria;c_Chloroplasto;Stramenopiles;f_	0	3.7%	2.5%	3.4%	0.2%	4.0%	0.5%	1.7%	4.9%	13.9%	6.5%	5.2%
k_Bacteriap_Cyanobacteria;c_Chloroplasto;Streptophyta;f_	1	8.5%	0.2%	54.2%	0.0%	32.0%	0.1%	4.3%	0.0%	1.4%	7.0%	0.2%
k_Bacteriap_Cyanobacteria;c_Nostocophycidae;o_Nostocales;f_Nostocaceae	0	2.8%	0.2%	4.6%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	24.4%	0.0%
k_Bacteriap_Cyanobacteria;c_Nostocophycidae;o_Sigonematales;f_Rivulariaceae	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.5%	0.0%	0.0%
k_Bacteriap_Cyanobacteria;c_Oscillatoriothycidae;o_Chroococcales;f_Xenococcaceae	0	0.6%	0.0%	1.4%	0.0%	0.0%	0.0%	0.0%	0.0%	0.3%	5.7%	0.0%
k_Bacteriap_Cyanobacteria;c_Oscillatoriothycidae;o_Oscillatoriales;f_Phormidiaceae	0	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	1.6%	0.0%
k_Bacteriap_Cyanobacteria;c_Synechococphyceae;o_Pseudanabaenales;f_Pseudanabaenaceae	0	0.2%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	1.9%	0.0%
k_Bacteriap_Cyanobacteria;c_Synechococphyceae;o_Synechococcales;f_Acaryochloridaceae	0	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.3%	0.0%	0.0%
k_Bacteriap_Cyanobacteria;c_Synechococphyceae;o_Synechococcales;f_Chamaesiphonaceae	0	0.1%	0.5%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.8%	0.0%	0.4%
k_Bacteriap_Firmicutes;c_Bacilli;o_Bacillales;f_Alicyclobacillaceae	0	0.3%	0.0%	0.0%	0.0%	4.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%
k_Bacteriap_Gemmatimonadetes;o_Gemmatimonadetes;o_Gemmatimonadales;f_Ellin5301	0	0.0%	0.5%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.1%
k_Bacteriap_Proteobacteria;c_Alphaproteobacteria;o_f_	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.3%	0.0%	0.0%	0.0%
k_Bacteriap_Proteobacteria;c_Alphaproteobacteria;o_Caulobacteriales;f_Caulobacteraceae	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.3%	0.0%	0.0%
k_Bacteriap_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Bejeriaceae	0	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteriap_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Bradyrhizobiaceae	0	0.3%	0.5%	0.7%	0.6%	0.0%	0.0%	1.1%	0.0%	1.2%	0.0%	0.1%
k_Bacteriap_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiaceae	0	0.1%	0.0%	0.0%	0.2%	0.0%	0.0%	0.1%	0.0%	0.0%	0.5%	0.0%
k_Bacteriap_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Methyllobacteriaceae	0	0.2%	0.2%	0.2%	0.0%	2.0%	0.0%	0.0%	0.0%	0.3%	0.0%	0.0%
k_Bacteriap_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Methylocystaceae	0	0.1%	0.0%	0.3%	0.0%	0.0%	0.0%	0.0%	0.0%	0.3%	0.0%	0.4%
k_Bacteriap_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Acetobacteraceae	1	11.8%	4.3%	11.2%	4.8%	8.0%	4.2%	3.3%	29.3%	5.9%	18.7%	14.5%
k_Bacteriap_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Rhodospirillaceae	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteriap_Proteobacteria;c_Alphaproteobacteria;o_Rickettsiales;f_	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.1%	0.0%	0.0%	0.0%	0.0%
k_Bacteriap_Proteobacteria;c_Alphaproteobacteria;o_Rickettsiales;f_mitochondria	0	1.6%	0.0%	1.3%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	18.2%	0.0%
k_Bacteriap_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.5%	0.0%	0.0%	0.0%
k_Bacteriap_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae	0	0.4%	0.2%	0.4%	0.9%	0.0%	0.2%	0.3%	0.0%	0.2%	2.4%	0.0%
k_Bacteriap_Proteobacteria;c_Betaproteobacteria;o_f_	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteriap_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_	1	4.6%	7.2%	0.4%	4.8%	0.0%	4.7%	10.7%	6.3%	12.9%	0.0%	7.1%
k_Bacteriap_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Burkholderiaceae	0	0.1%	0.2%	0.0%	0.1%	0.0%	0.2%	0.0%	0.0%	0.2%	0.0%	0.0%
k_Bacteriap_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Commonadaceae	1	11.0%	22.3%	0.7%	7.1%	12.0%	28.0%	26.5%	9.2%	8.8%	0.0%	15.3%
k_Bacteriap_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Oxalobacteraceae	2	17.4%	22.1%	4.2%	7.5%	0.0%	17.5%	22.6%	5.3%	37.3%	0.3%	3.2%
k_Bacteriap_Proteobacteria;c_Betaproteobacteria;o_Ellin6067;f_	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.3%	0.0%	0.0%
k_Bacteriap_Proteobacteria;c_Betaproteobacteria;o_Gallionellales;f_Gallionellaceae	0	0.7%	2.0%	0.0%	0.4%	0.0%	3.4%	0.2%	0.9%	0.2%	0.0%	1.0%
k_Bacteriap_Proteobacteria;c_Betaproteobacteria;o_IS44;f_	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.2%
k_Bacteriap_Proteobacteria;c_Betaproteobacteria;o_Methylotrophiales;f_	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.4%
k_Bacteriap_Proteobacteria;c_Betaproteobacteria;o_Methylotrophiales;f_Methylotrophaceae	0	1.5%	0.0%	0.0%	0.0%	0.0%	10.8%	0.1%	4.7%	0.7%	0.0%	2.2%
k_Bacteriap_Proteobacteria;c_Betaproteobacteria;o_Rhodocyclales;f_Rhodocyclaceae	0	0.9%	0.0%	0.1%	0.1%	0.0%	0.3%	7.2%	0.6%	0.5%	0.0%	1.8%
k_Bacteriap_Proteobacteria;c_Betaproteobacteria;o_SC-I84;f_	0	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteriap_Proteobacteria;c_Deltaproteobacteria;o_MBNT15;f_	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%
k_Bacteriap_Proteobacteria;c_Deltaproteobacteria;o_Myxococcales;f_Haliangiaceae	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%
k_Bacteriap_Proteobacteria;c_Deltaproteobacteria;o_Myxococcales;f_Polyangiaceae	0	0.0%	0.2%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%
k_Bacteriap_Proteobacteria;c_Deltaproteobacteria;o_Spiracillales;f_	0	0.0%	0.2%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteriap_Proteobacteria;c_Gammaproteobacteria;o_f_	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.2%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteriap_Proteobacteria;c_Gammaproteobacteria;o_Legionellales;f_Coxiellaceae	0	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.7%	0.0%
k_Bacteriap_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Pseudomonadaceae	0	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteriap_Proteobacteria;c_Gammaproteobacteria;o_Thiotrichales;f_Thiotrichaceae	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.2%	0.0%	0.0%	0.1%
k_Bacteriap_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Sinobacteraceae	0	0.2%	0.0%	0.0%	0.1%	0.0%	0.1%	1.3%	0.0%	1.2%	0.0%	0.0%
k_Bacteriap_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.4%
k_Bacteriap_Spirochaetes;c_Spirochaetes;o_Spirochaetales;f_Spirochaetaeae	0	0.3%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteriap_WPS-2;c_o_f_	0	0.2%	0.0%	0.7%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.3%	0.0%

Taxonomy Summary. Current Level:

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Legend	Taxonomy	Total	ICE12.4	ICE13.4.5.6	ICE12.6.7	ICE13.8.9	ICE14.2	ICE13.19	ICE14.3	ICE13.16.18	ICE13.14.15	ICE14.1	ICE12.2.3	ICE13.21.24
		count	%	%	%	%	%	%	%	%	%	%	%	%
k_Bacteriap_Acidobacteria;c_Acidobacteriia;o_Acidobacteriales;f_Acidobacteriaceae;g_		0	0.3%	0.0%	2.3%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.3%	0.4%
k_Bacteriap_Acidobacteria;c_Acidobacteriia;o_Acidobacteriales;f_Granulicella		0	0.1%	0.0%	0.5%	0.0%	0.0%	0.0%	0.0%	0.0%	0.2%	0.0%	0.0%	0.1%
k_Bacteriap_Acidobacteria;c_Acidobacteriia;o_Acidobacteriales;f_Acidobacteriaceae;g_Terriglobus		0	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteriap_Acidobacteria;c_Solibacteres;o_Solibacterales;f_g_		0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.5%	0.0%	0.0%	0.0%
k_Bacteriap_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_g_		0	0.0%	0.2%	0.2%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteriap_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Frankiaceae;g_		0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteriap_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Geodermatophilaceae;g_		0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
k_Bacteriap_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Kinosporaceae;g_		0	0.2%	0.0%	0.0%	0.0%	2.0%	0.0%	0.0%	0.0%	0.3%	0.0%	0.0%	0.0%
k_Bacteriap_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Microbacteriaceae;g_		0	1.1%	0.2%	0.0%	0.1%	0.0%	0.1%	0.1%	0.3%	0.0%	0.0%	0.1%	0.0%
k_Bacteriap_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Mycetocola		0	0.0%	0.5%	0.0%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%

