

Table S1. Primer pairs described in the text and PCR conditions used in this study.

Assay	Target	Primer pair	T _m °C	Reference
PCR + cloning qPCR	General Bacteria 16S rRNA	341F (5'-CCTACGGGAGGCAGCAG-3') 907R (5'-CCGCAATTCCTTTRAGTTT-3')	57 (58 qPCR*)	Muyzer <i>et al.</i> , 1993 Lane <i>et al.</i> , 1985
PCR + cloning qPCR	Planctomycetes 16S rRNA	Pla352F (5'-GGCTGCAGTCGAGRATCT-3') Pla920R (5'-TGTGTGAGCCCCCGTCAA-3')	58 (61 qPCR**)	Pollet <i>et al.</i> , 2011

PCR conditions: 95°C 5 min; 40 × [95°C 1 min, T_m 40 s, 72°C 1 min]; 72°C 5 min.

qPCR conditions: 95°C 4 min; 40 × [95°C 30 s, T_m 40 s, 72°C 30 s]; 80°C 25 s.

*qPCR efficiency 100%; R₂=0.999

**qPCR efficiency 85%; R₂=0.998

Table S2. Distribution of percentage of reads of the 16S rRNA gene amplicon pyrosequencing in the Saxnäs Mosse and the Obukhovskoye peat bogs.

Saxnäs Mosse	12 cm	18 cm	24 cm	30 cm	42 cm
Acidobacteria	60.5	51.4	54.8	47.6	30.0
Planctomycetaceae <i>Isosphaera</i>	0.7	1.8	6.0	6.1	0.0
Planctomycetaceae others:	4.0	2.5	0.7	1.1	0.4
- <i>Gemmata</i>	0.0	0.1	0.0	0.0	0.0
- Pir4 lineage	0.0	0.0	0.1	0.0	0.0
- <i>Schlesneria</i>	0.2	0.0	0.0	0.0	0.0
- <i>Singulisphaera</i>	0.1	0.1	0.0	0.0	0.0
- <i>Zavarzinella</i>	0.3	0.0	0.0	0.0	0.0
- uncultured	3.4	2.3	0.6	1.1	0.4
Alphaproteobacteria Rhizobiales	9.1	7.0	3.5	2.0	2.3
Alphaproteobacteria Rhodospirillales	4.6	3.3	0.7	0.7	0.1
Deltaproteobacteria Syntrophobacterales	0.43	5.9	8.3	23.0	5.7
Verrucomicrobia	8.2	15.9	13.2	5.8	5.1
Thaumarchaeota terrestrial group	0.05	0.28	0.28	0.81	36.6
Thaumarchaeota MCG	0.00	0.00	0.03	0.3	6.3
Actinobacteria	1.4	1.0	0.05	0.06	0.3

Obukhovskoye	5-10 cm	10-20 cm	20-30 cm	30-40 cm	40-50 cm
Acidobacteria	12.4	21.1	46.4	19.0	38.3
Planctomycetaceae <i>Isosphaera</i>	7.7	4.6	3.0	52.7	12.6
Planctomycetaceae others:	4.6	4.0	5.6	1.2	6.2
- <i>Gemmata</i>	0.4	0.1	0.1	0.0	0.1
- <i>Planctomyces</i>	0.3	0.7	1.2	0.2	0.7
- <i>Schlesneria</i>	0.1	0.0	0.1	0.0	0.0
- <i>Singulisphaera</i>	0.8	0.5	0.2	0.1	3.8
- <i>Zavarzinella</i>	0.1	0.0	0.3	0.1	0.0
- uncultured	2.9	2.7	3.8	0.9	1.7
Alphaproteobacteria Rhizobiales	23.9	18.0	15.4	7.4	11.6
Alphaproteobacteria Rhodospirillales	2.9	0.8	1.2	0.3	1.2
Deltaproteobacteria Syntrophobacterales	0.0	0.0	0.2	0.2	0.3
Verrucomicrobia	3.3	2.0	2.4	1.2	4.0
Thaumarchaeota terrestrial group	0.0	0.0	0.0	0.0	0.1
Thaumarchaeota MCG	0.0	0.0	0.0	0.0	0.1
Actinobacteria	29.3	40.1	17.0	14.5	10.8

Table S3. Percentage of total bacterial reads attributed to members of the Planctomycetaceae family in the Saxnäs Mosse and the Obukhovskoye peat bogs.

Saxnäs Mosse				
Depth (cm)	% 16S rRNA reads Planctomycetaceae Isosphaera*	% 16S rRNA reads Planctomycetaceae others*	% 16S rRNA reads Planctomycetaceae TOTAL*	% Planctomycete cells**
10-12	0.7	4.0	4.7	15.1
16-18	1.8	2.5	4.3	2.3
22-24	6.0	0.7	6.7	5.8
28-30	6.1	1.1	7.2	2.8
40-42	0.0	0.4	0.4	1.4

Obukhovskoye				
Depth (cm)	% 16S rRNA reads Planctomycetaceae Isosphaera*	% 16S rRNA reads Planctomycetaceae others*	% 16S rRNA reads Planctomycetaceae TOTAL*	% Planctomycete cells**
5-10	7.7	4.6	12.3	8.8
10-20	4.6	4.0	8.6	3.9
20-30	3.0	5.6	8.6	3.5
30-40	52.7	1.2	53.9	27.1
40-50	12.6	6.2	18.8	9.5

*Percentage of 16S rRNA gene reads obtained from the pyrosequencing analysis as shown in Table S2.

**Percentage of planctomycete cells respect to the total bacterial cells assuming that the average 16S rRNA copy number per bacterial cell is 3.6 (Schloss et al., 2009), and that planctomycetes have an average of 2.5 copies of 16S rRNA gene per genome (considering 2 copies present in *Pirellula marina* and *Planctomyces* species, and 3 copies in *Isosphaera pallida*; Ribosomal RNA Operon Copy Number Database; Klappenbach et al., 2001). See Fig. S4 for details.

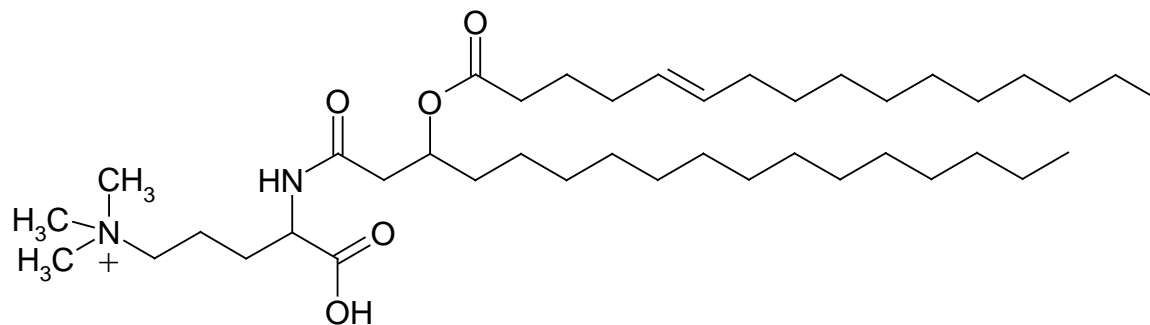
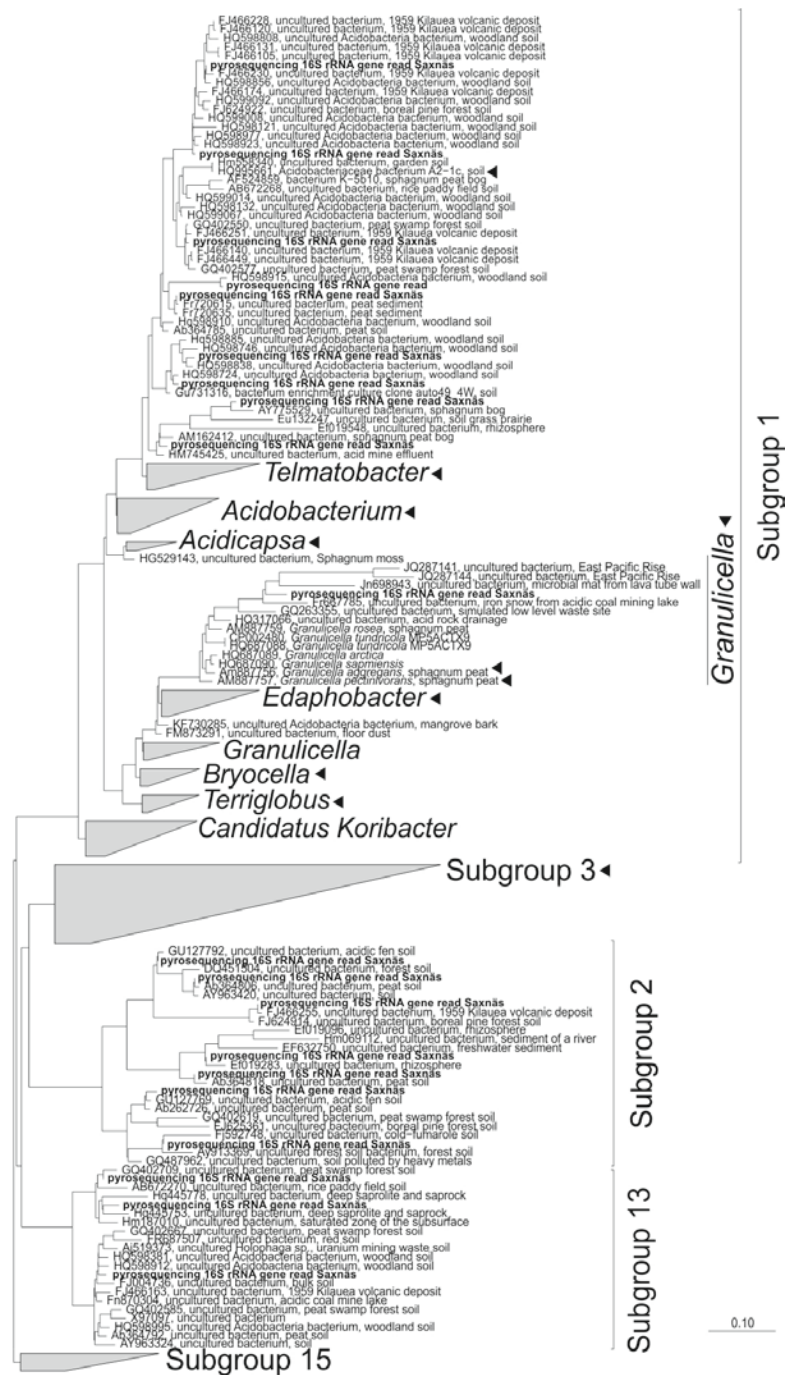


Fig. S1. Trimethylornithine (TMO) lipid structure.



Fig. S2. Locations of peat sample collection in Russia ($58^{\circ} 14' N$, $38^{\circ} 12' E$) and Sweden ($56^{\circ} 51' 20.78'' N$, $13^{\circ} 27' 39.62'' E$).

Fig. S3. Phylogenetic tree including the representative pyrosequencing 16S rRNA gene reads (in bold) obtained from the Saxnäs Mosse peat bog samples and classified as Acidobacteria, and their closest relatives. Triangles indicate Acidobacteria strains or groups the lipid composition of which have been previously reported by Sinninghe Damsté et al., 2011.



Subgroup 1

Granulicella

Subgroup 3

Subgroup 2

Subgroup 13

Subgroup 15

0.10

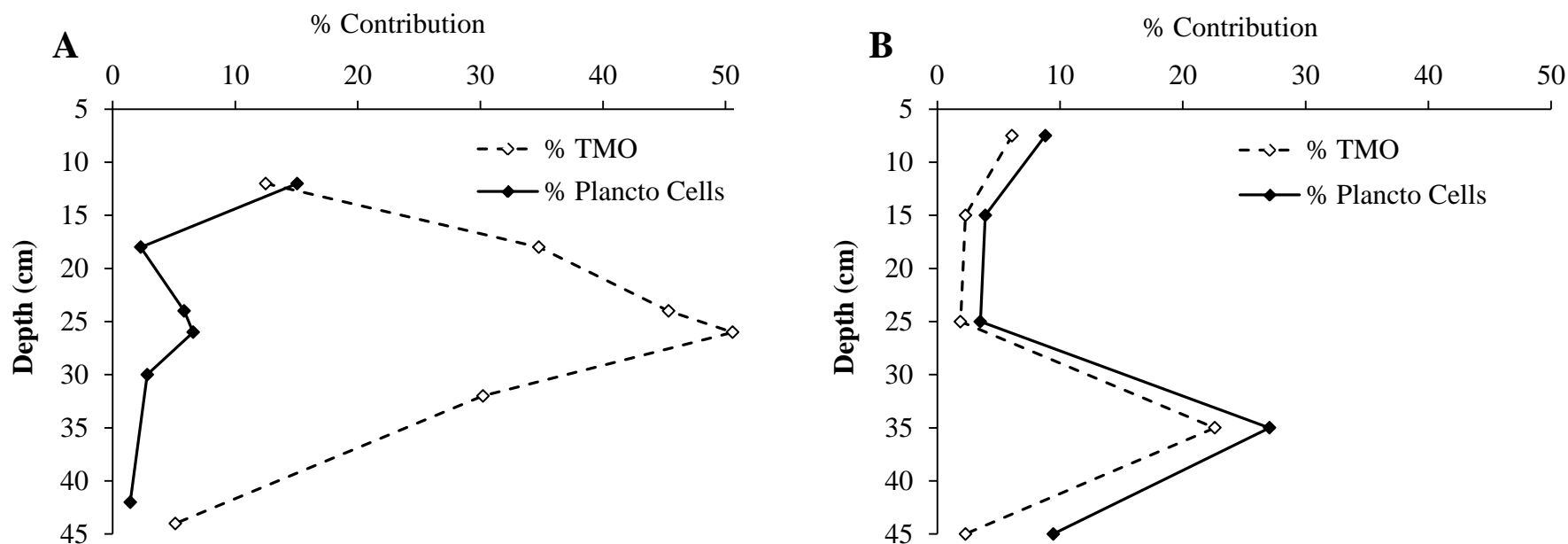


Fig. S4. Percent of total IPLs made up by trimethylornithine lipid (TMO) based on HPLC/MS base peak area; Planctomycete cells to total Bacterial cells based on the calculation of converting planctomycete and bacterial specific 16S rRNA gene copies to cell numbers in the (A) Saxnäs Mosse, and the (B) Obukhovskoye peat bogs. Total bacterial and planctomycete cell numbers were estimated assuming that the average 16S rRNA copy number per bacterial cell is 3.6 (Klappenbach et al., 2001), and that planctomyces have an average of 2.5 copies of 16S rRNA gene per genome (considering 2 copies present in *Pirellula marina* and *Planctomyces* species, and 3 copies in *Isosphaera pallida*; Ribosomal RNA Operon Copy Number Database; Göker et al., 2011).

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