Supplementary information.

Methods.

Chemical characterization.

Pore water nitrate, ammonium, and sulfate concentrations were determined by chemiluminescence detection, colorimetry, and ion chromatography respectively (see supplemental material for details). Breifly, dissolved nitrate + nitrite (NO_x^-) and nitrite (NO_2^-) were determined by chemiluminescence detection after reduction to NO gas using a Thermo model 42i NO_x analyzer (Thermo Scientific). Nitrate + nitrite were reduced using an acidic $VnCl_2$ solution (2), and nitrite was reduced using an acidic iodide solution (3). Dissolved ammonium (NH_4^+) was determined by the colorimetric method of Bower and Holm-Hansen (1).

References:

1. **Bower, C. E., and T. Holmhansen.** 1980. A Salicylate-Hypochlorite Method for Determining Ammonia in Seawater. Canadian Journal of Fisheries and Aquatic Sciences **37:**794-798.
2. **Braman, R. S., and S. A. Hendrix.** 1989. Nanogram Nitrite and Nitrate Determination in Environmental and Biological-Materials by Vanadium(Iii) Reduction with Chemi-Luminescence Detection. Anal Chem **61:**2715-2718.
3. **Garside, C.** 1982. A chemiluminescent technique for the determination of nanomolar concentrations of nitrate and nitrite in sea-water. Marine Chemistry **11:**159-167.

Table S2 Environmental variables explaining the bacterial and archaeal community spatial turnover at 0 cm, 30cm, 75cm, and the all system, identified by distance-based linear model combined with a forward model-selection procedure. P values < 0.05 are highlighted in red, with the 3 taxa positively correlated with these environmental gradients. Prop. = proportion of variation explained; Cumul. = cumulated proportion of variation explained.

	Variables	**Adj R^2**	**P**	**Prop.**	**Cumul.**	**Positively correlated taxa**
0 cm	Chaemedaphne	0.12	0.03	0.26	0.26	Chaemedaphne: Sinobacteraceae_450 Chthoniobacter_542 Methylacidiphilales_537
	Aroma1635	0.21	0.07	0.21	0.47	
	eNP	0.34	0.12	0.20	0.67	
	Aliphat2920	0.39	0.36	0.13	0.80	
	A16S_d	0.40	0.49	0.11	0.90	
30 cm	Chaemedaphne	0.09	0.02	0.19	0.19	Chaemedaphne: Verrucomicrobiales_547 Syntrophobacteraceae_436 Aeropyrum_14
	Total_BA	0.16	0.08	0.16	0.35	
	Aliphat2920	0.21	0.14	0.13	0.48	
	A16S_d	0.26	0.21	0.11	0.59	
	eNP	0.30	0.29	0.10	0.69	
75 cm	A16S_d	0.10	0.03	0.23	0.23	A16S: Acidobacteria_39 Koribacter_41 Deltaproteobacteria_403
	Oacids1726	0.17	0.09	0.18	0.41	
	PHOS	0.23	0.22	0.15	0.56	
	eCP	0.24	0.45	0.12	0.67	
	Carbohyd1035	0.31	0.32	0.13	0.80	
All systems	CNratio	0.20	0.00	0.23	0.23	CNratio: Opitutus_539 Acetobacteraceae_330 Sphingobacteriales_111 A16S: Acidobacteria_39 Syntrophobacter_437 Rhodoplanes_317
	A16S_d	0.26	0.00	0.09	0.32	
	eCP	0.27	0.28	0.03	0.36	
	Chaemedaphne	0.27	0.29	0.03	0.39	
	Aroma1635	0.28	0.28	0.03	0.42	

Table S3 Environmental variables explaining the fungal community spatial turnover at 0 cm, 20cm, 30cm, and the all system, identified by distance-based linear model combined with a forward model-selection procedure. P values < 0.05 are highlighted in red.

	Variable	Adj R^2	P	Prop.	Cumul.
0 cm	Aroma1635	0.07	0.08	0.17	0.17
	D-Wratio	0.13	0.09	0.15	0.32
	eCP	0.15	0.33	0.11	0.44
	Carbohyd1035	0.19	0.33	0.11	0.55
	Aliphat2920	0.22	0.32	0.11	0.65
20 cm	PHOS	0.07	0.08	0.17	0.17
	Chaemedaphne	0.09	0.32	0.12	0.29
	CNratio	0.13	0.24	0.13	0.42
	Total_BA	0.18	0.23	0.12	0.54
	D-Wratio	0.24	0.26	0.12	0.66
30 cm	Aliphat2920	0.11	0.03	0.22	0.22
	PHOS	0.15	0.21	0.15	0.37
	D-Wratio	0.22	0.17	0.14	0.51
	CNratio	0.26	0.32	0.12	0.63
	Total_BA	0.34	0.25	0.12	0.75
All systems	CNratio	0.02	0.05	0.06	0.06
	Chaemedaphne	0.05	0.05	0.06	0.12
	PHOS	0.09	0.01	0.07	0.19
	eCP	0.13	0.01	0.06	0.25
	Aroma1635	0.15	0.10	0.05	0.30

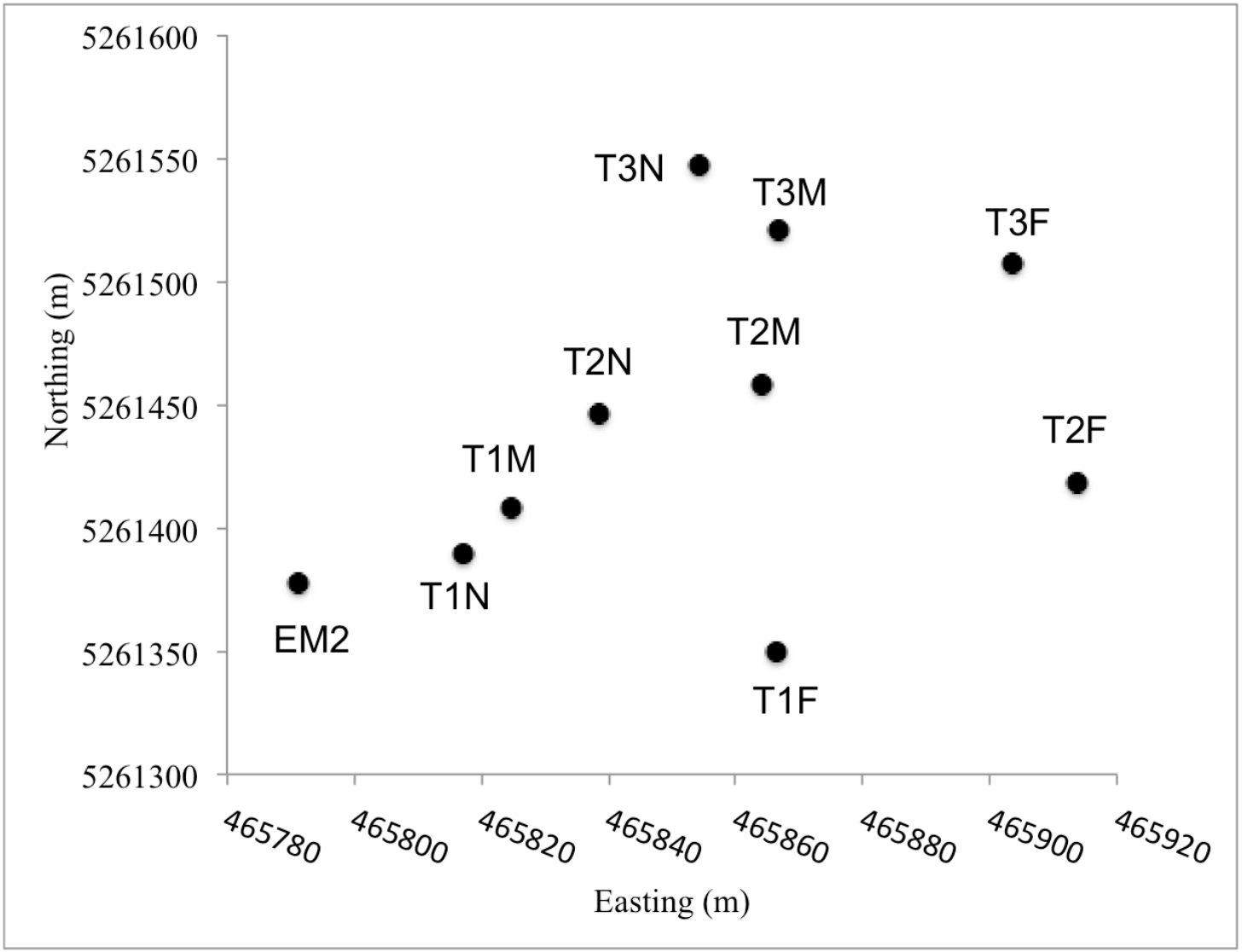

Fig. S1 S1 bog sites in the Marcell Experimental Station of northern Minnesoda, USA. In the S1 bog, samples were taken from 10 sites, including EM2, near (N), mid (M), and far (F) sites of each transect (T1 – T3). Bog Lake fen (47° 30' 22.62", -93° 29' 20.46”) is about 2 miles from the S1 bog and not shown here.

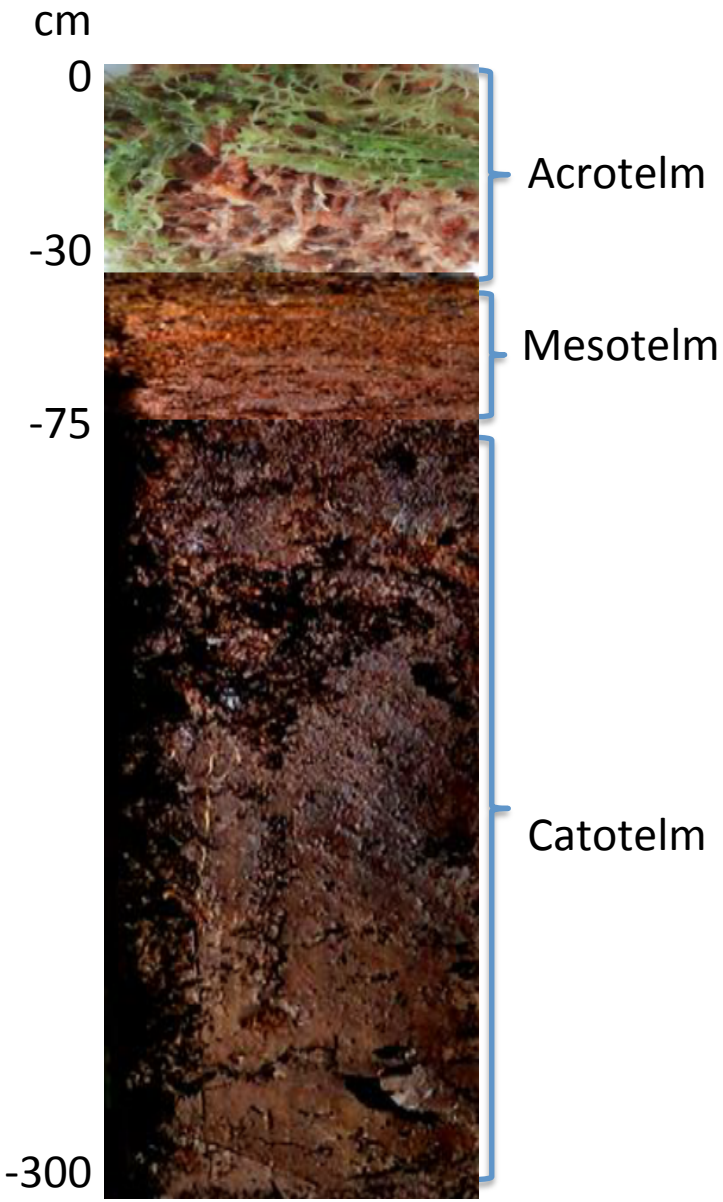

Fig. S2 Schematic diagram showing the three different layers identified in S1 bog and bog lake fen. Depth is not in scale.

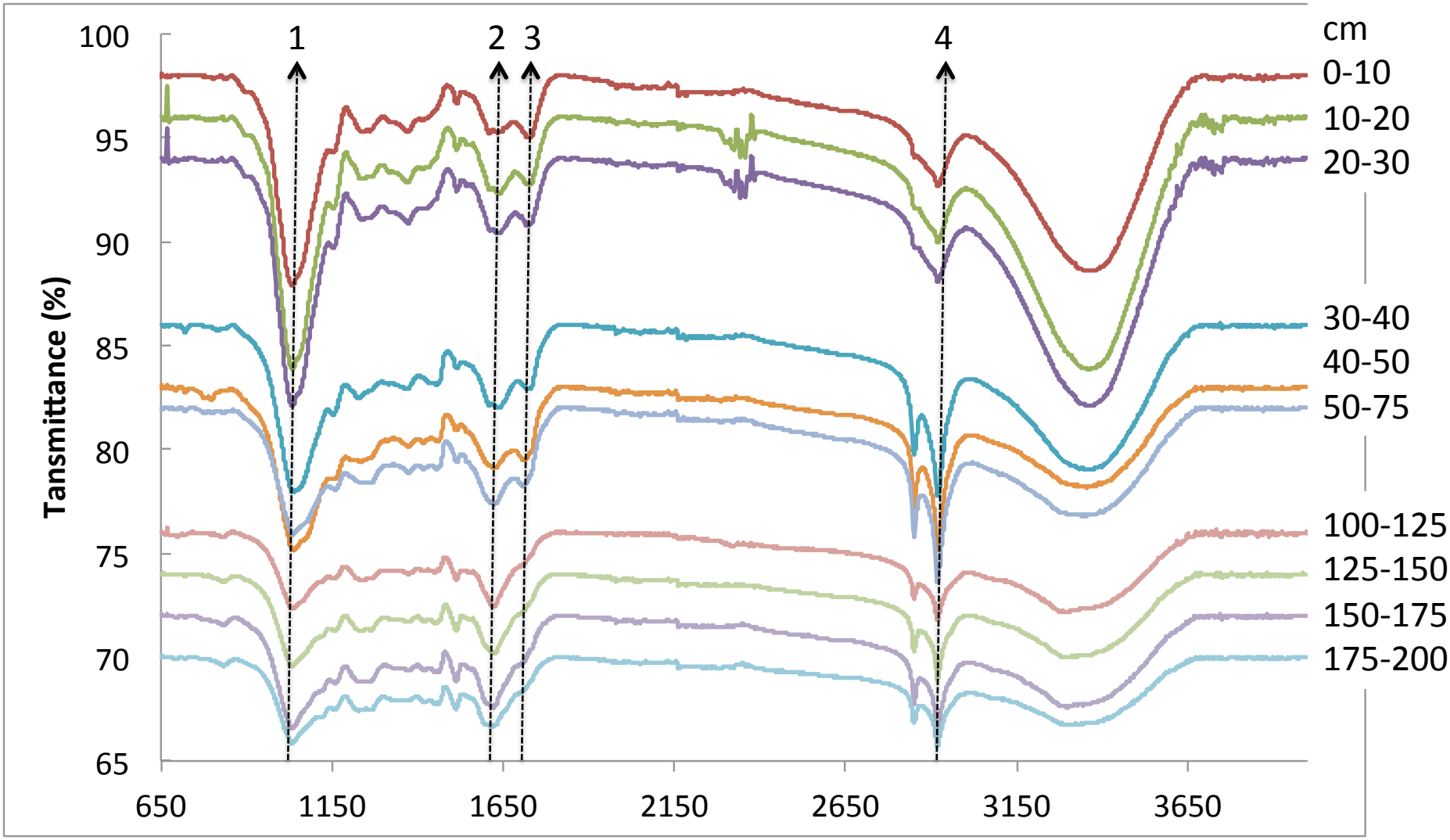

Fig. S3 Fourier-transform infrared spectra (FT-IR) across the depth profile from the T3F site. Peak numbers indicate (1) carbohydrates; (2) aromatic rings and C-O of quinine and amide groups; (3) represents organic acids ; and (4) aliphatics.

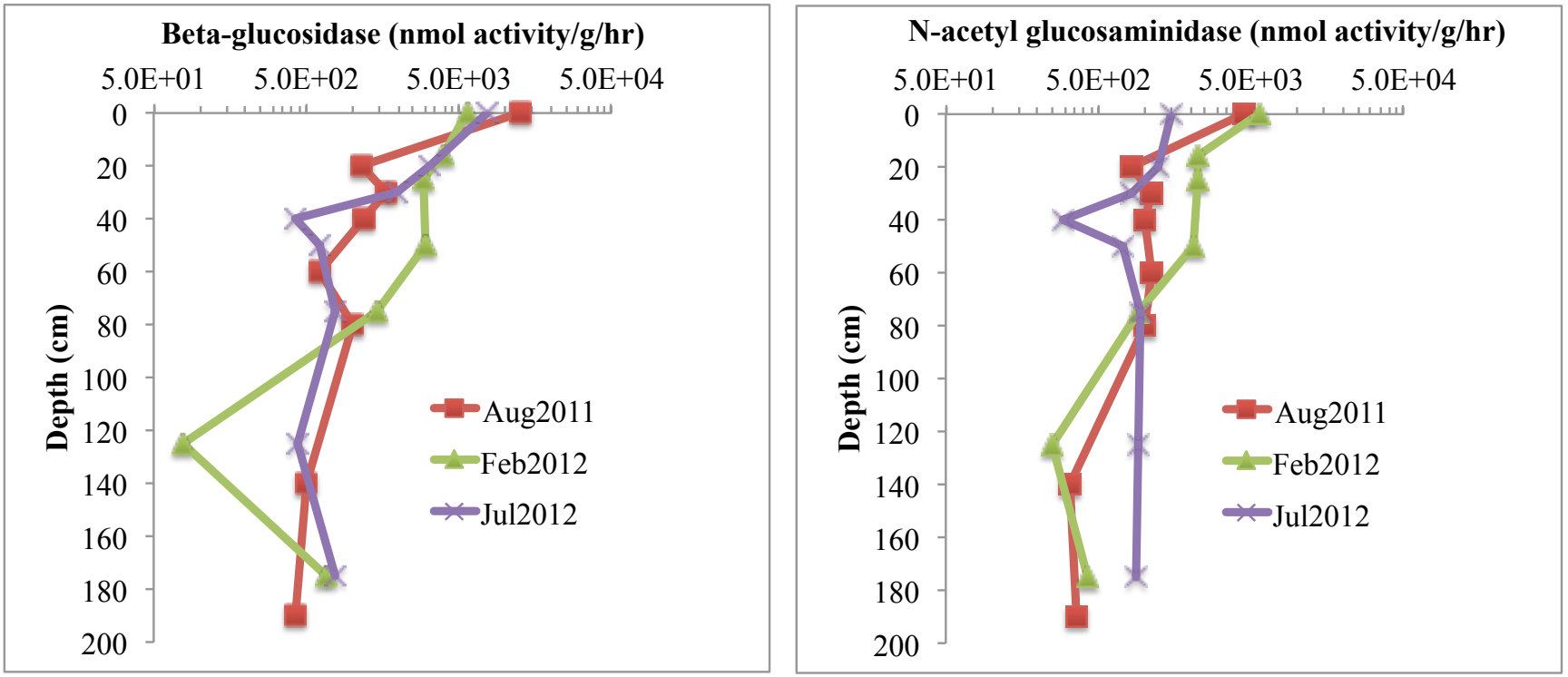

Fig. S4 Seasonal comparison of β-glucosidase (cellulose degradation) and N-acetyl glucosaminidase (Chitin degradation) across depths in the EM2 bog site.

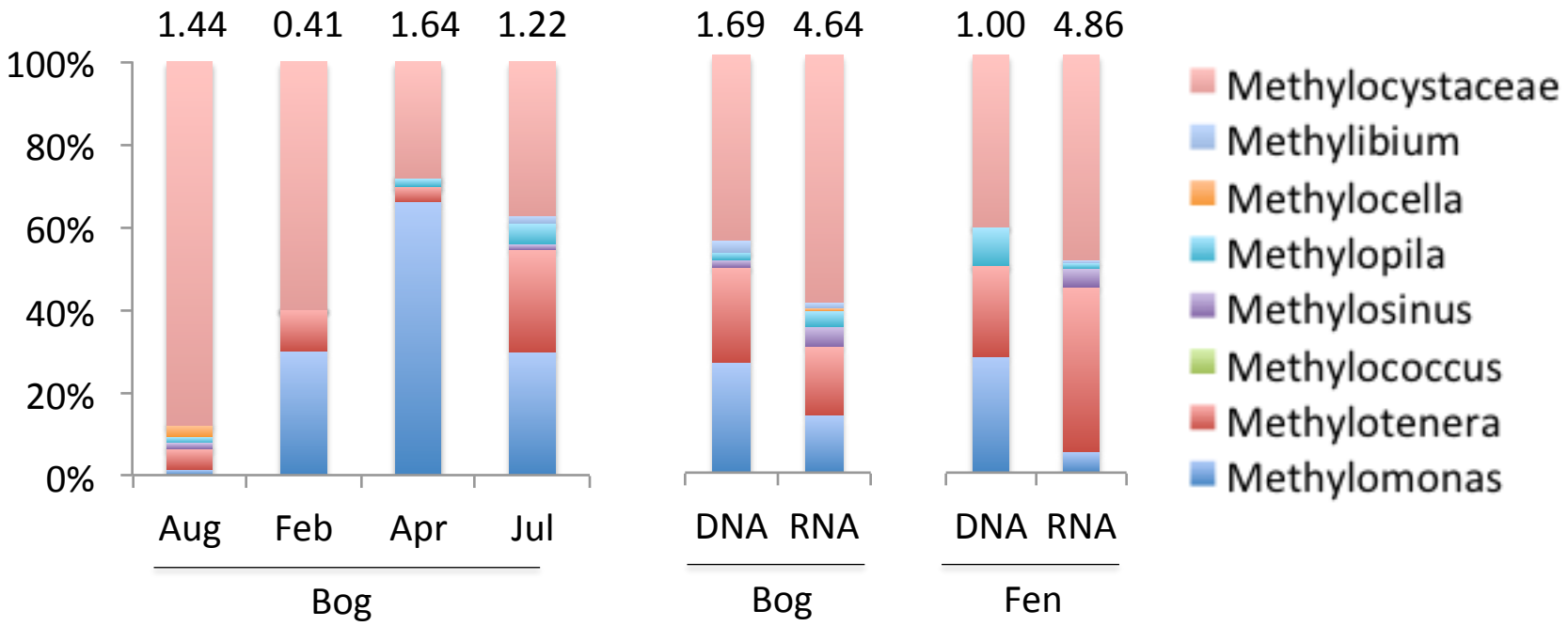

Fig. S5 Temporal variation in methanotrophic community in the surface layer of peat (0-30cm) in bog. Parallel comparison between DNA- and RNA-derived methanotrophic community is shown for both the bog EM2 site and the fen site. Data are averaged from all sites of each sampling season. Number on top of each bar indicates the total percentage of methanotrophs in the whole microbial community. Mythylocystaceae here are sequences unclassified to the genus level.

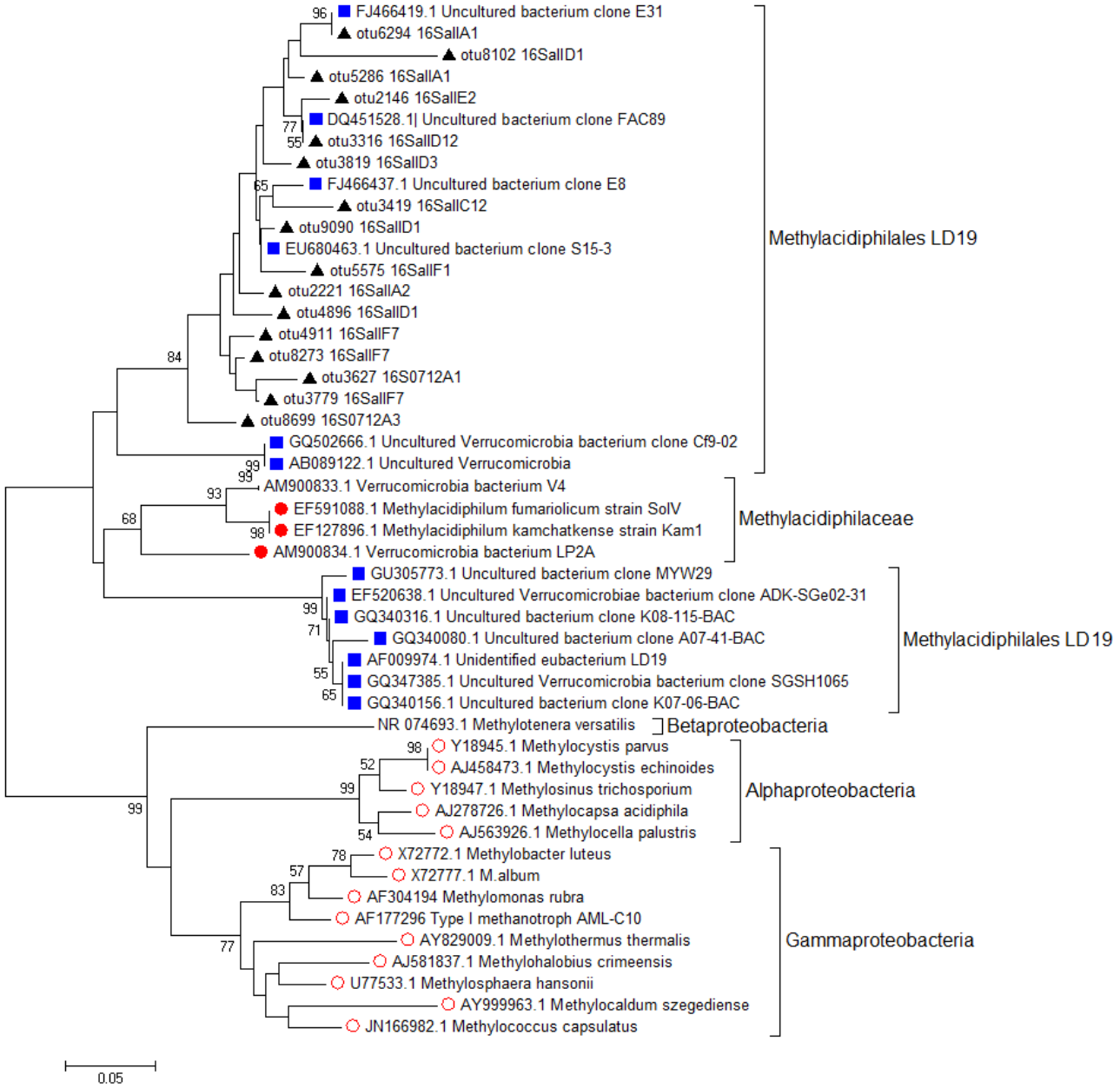

Fig. S6 Neighbor-joining tree of proteobacterial methanotrophs (open circle), cultured methanotrophs belonging to Verrucomicrobia (closed circle), environmental sequences affiliated with Methylacidiphilales family LD19 from the Greengenes database (square), and OTUs of this study (triangle) affiliated with Methylacidiphilales.

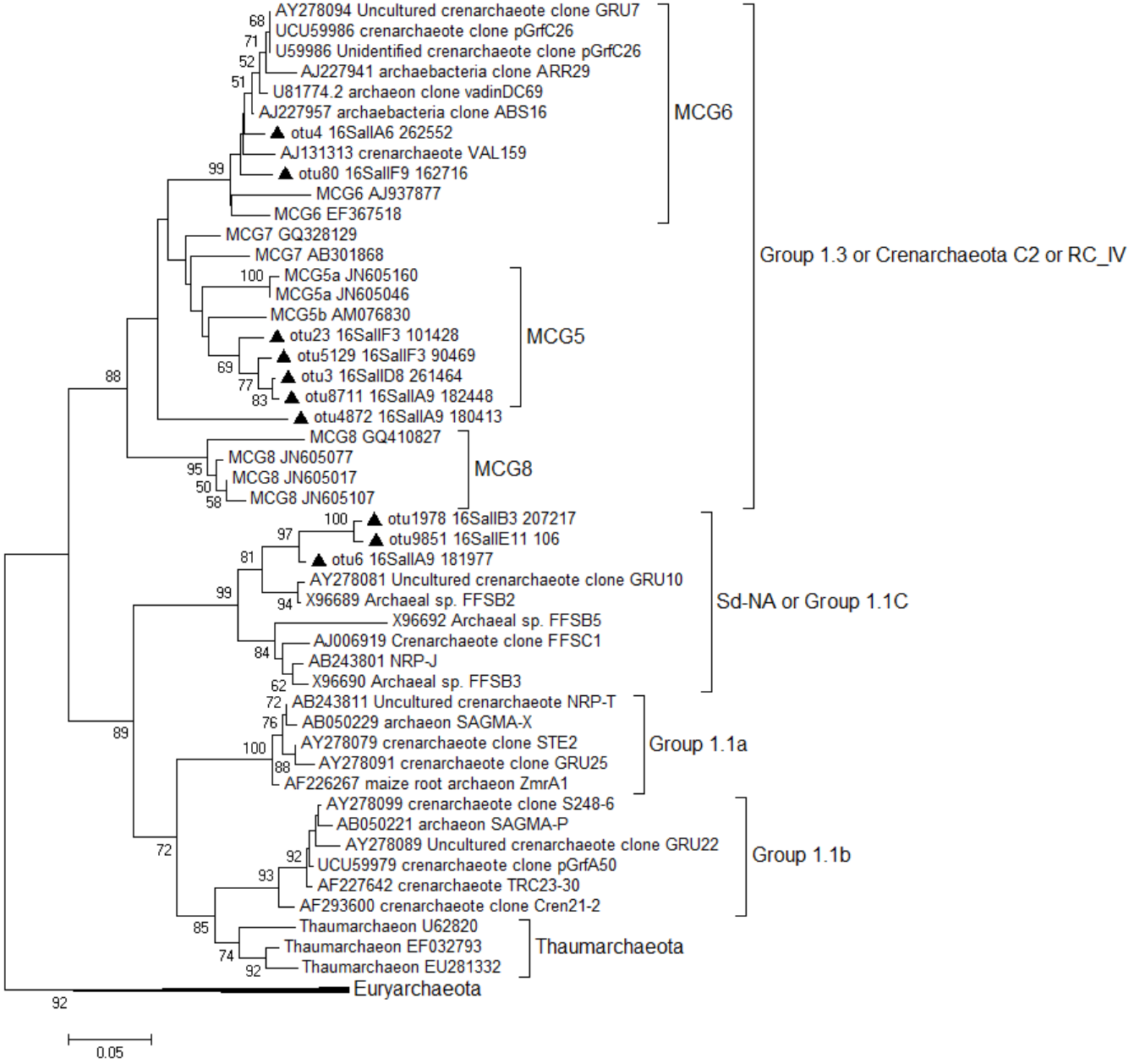

Fig. S7 Neighbor-joint tree of Crenarchaeal OTUs found in the MEF peatland (triangles) and representative sequences used to define several uncultivated Crenarchaeal groups. MCG = Miscellaneous Crenarchael Group. Crenarchaeota C2 and Sd-NA clades are defined based on Greengenes taxonomic framework (http://greengenes.lbl.gov/)

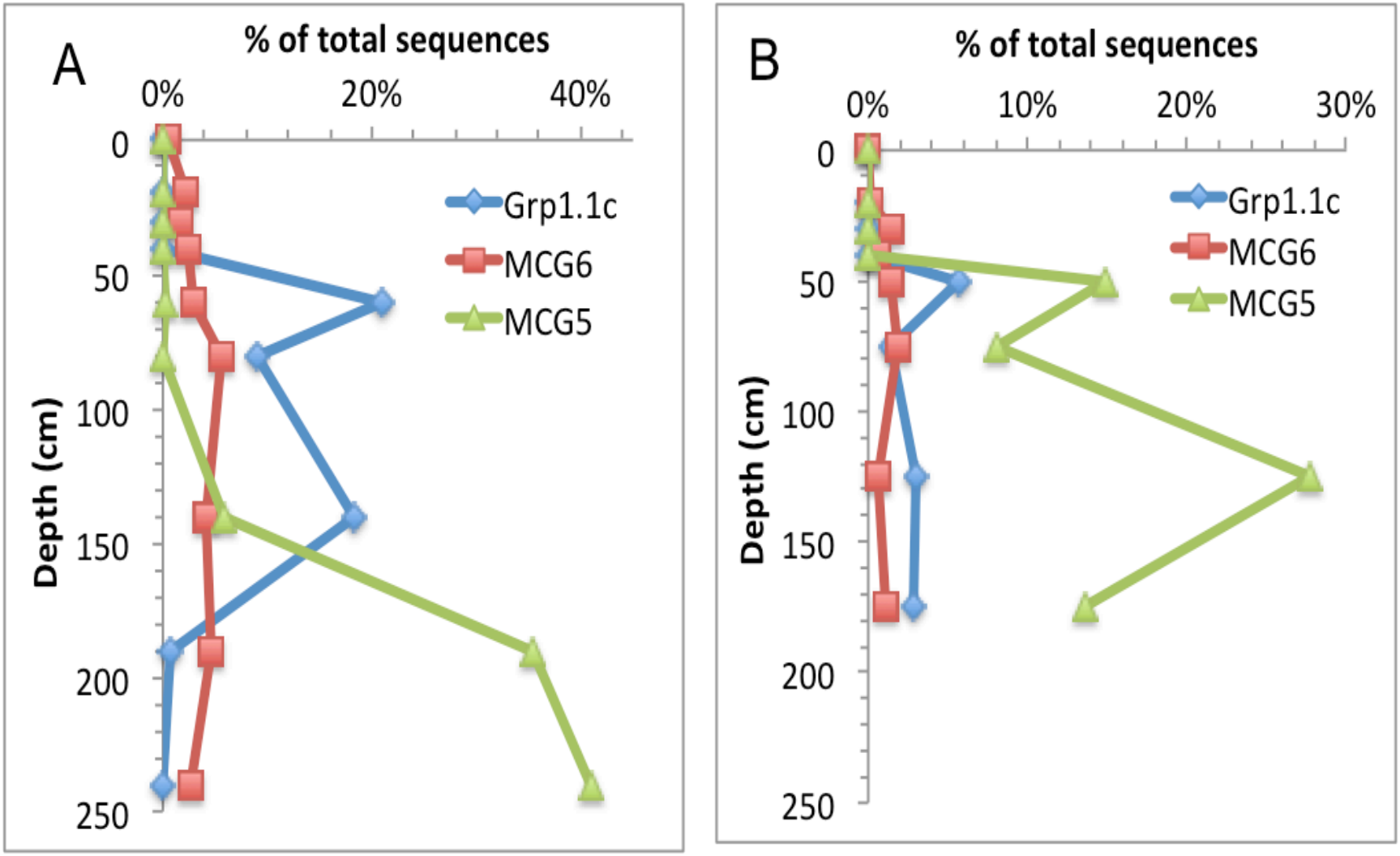

Fig. S8 Vertical distribution of 3 Crenarchaeal groups identified by 454 amplicon sequencing in bog (A) and fen (B) of the MEF peatland.

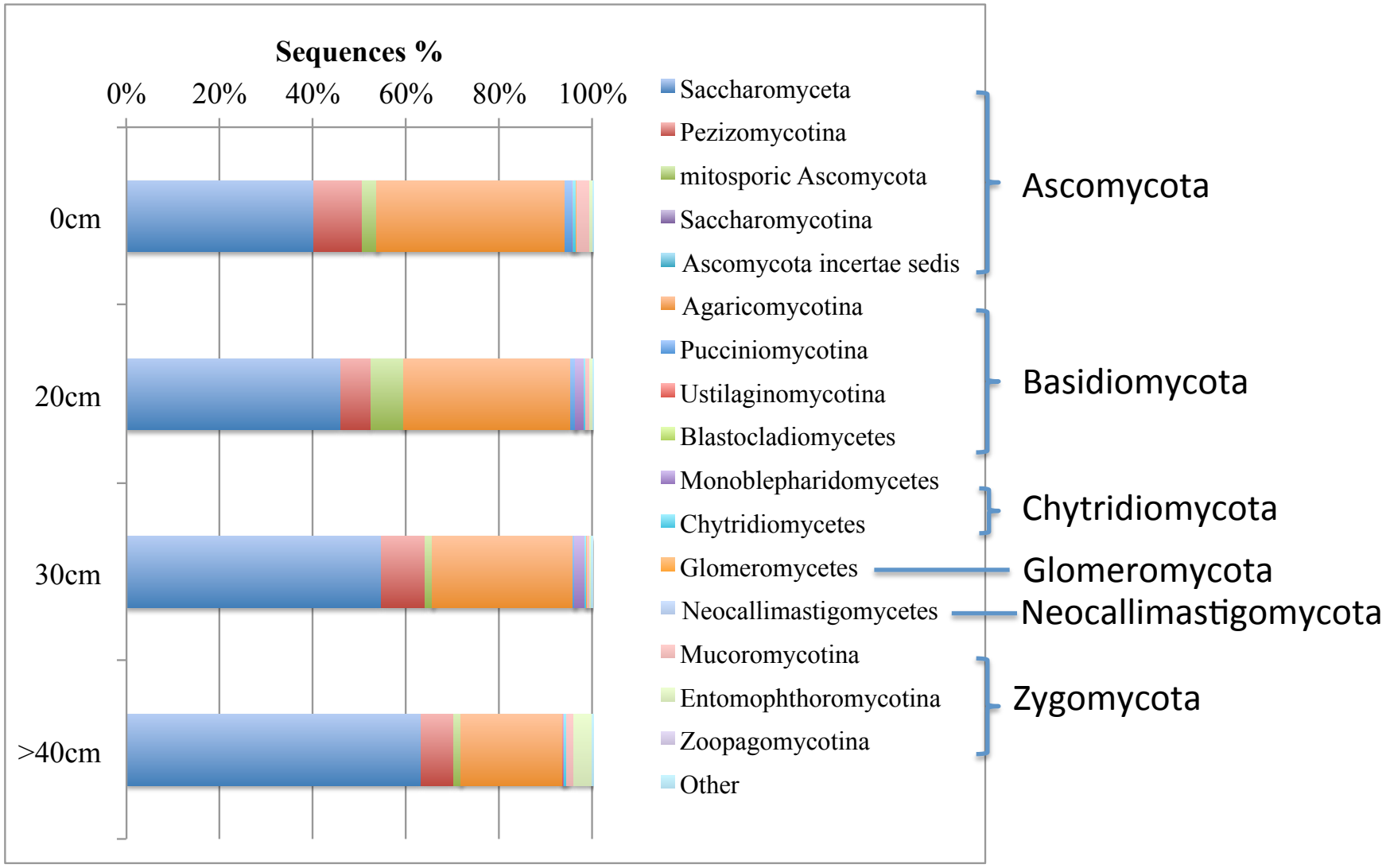

Fig. S9 Fungal community composition at a subphylum level. Data are averaged from all samples of different seasons.

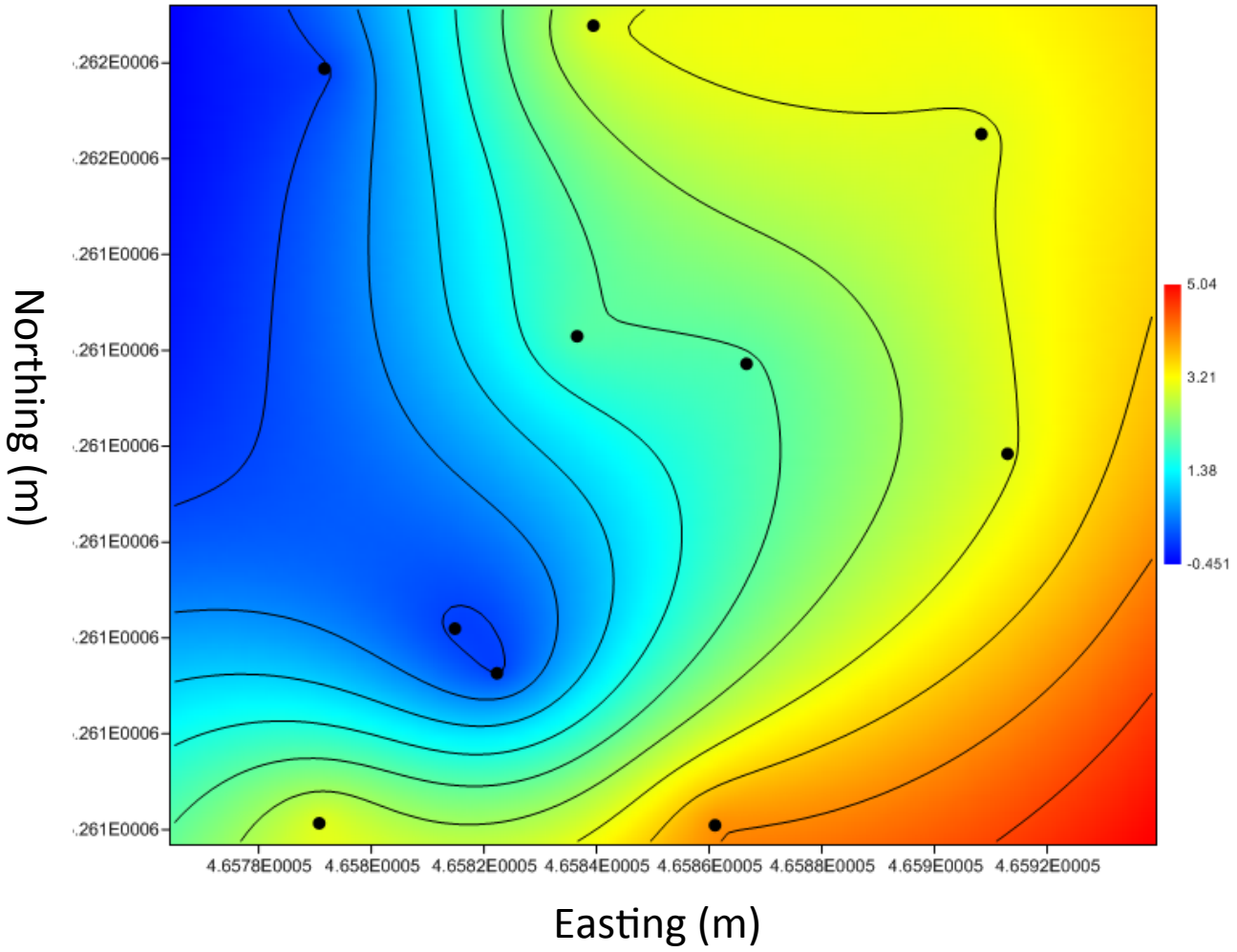

Fig. S10 Spatial distribution of *Chaemedaphne* count at the S1 bog.