**FIG S1** The relative abundance of different sized RNA fragments in the sample Sa. (A) total RNA; (B) after treatment with the RiboMinus bacteria kit; (C) after treatment with the RiboMinus bacteria kit and the MICROBExpress kit; (D) after treatment with the RiboMinus bacteria kit, the MICROBExpress kit and the RiboMinus Eukaryote kit. 16S: 16S rRNA; 18S: 18S rRNA; 23S: 23S rRNA; 28S: 28S rRNA. Fluorescence is equivalent to the abundance of RNA fragments. Time is equivalent to size of fragments. The relative abundance of RNA fragments can be compared within and between treatments.
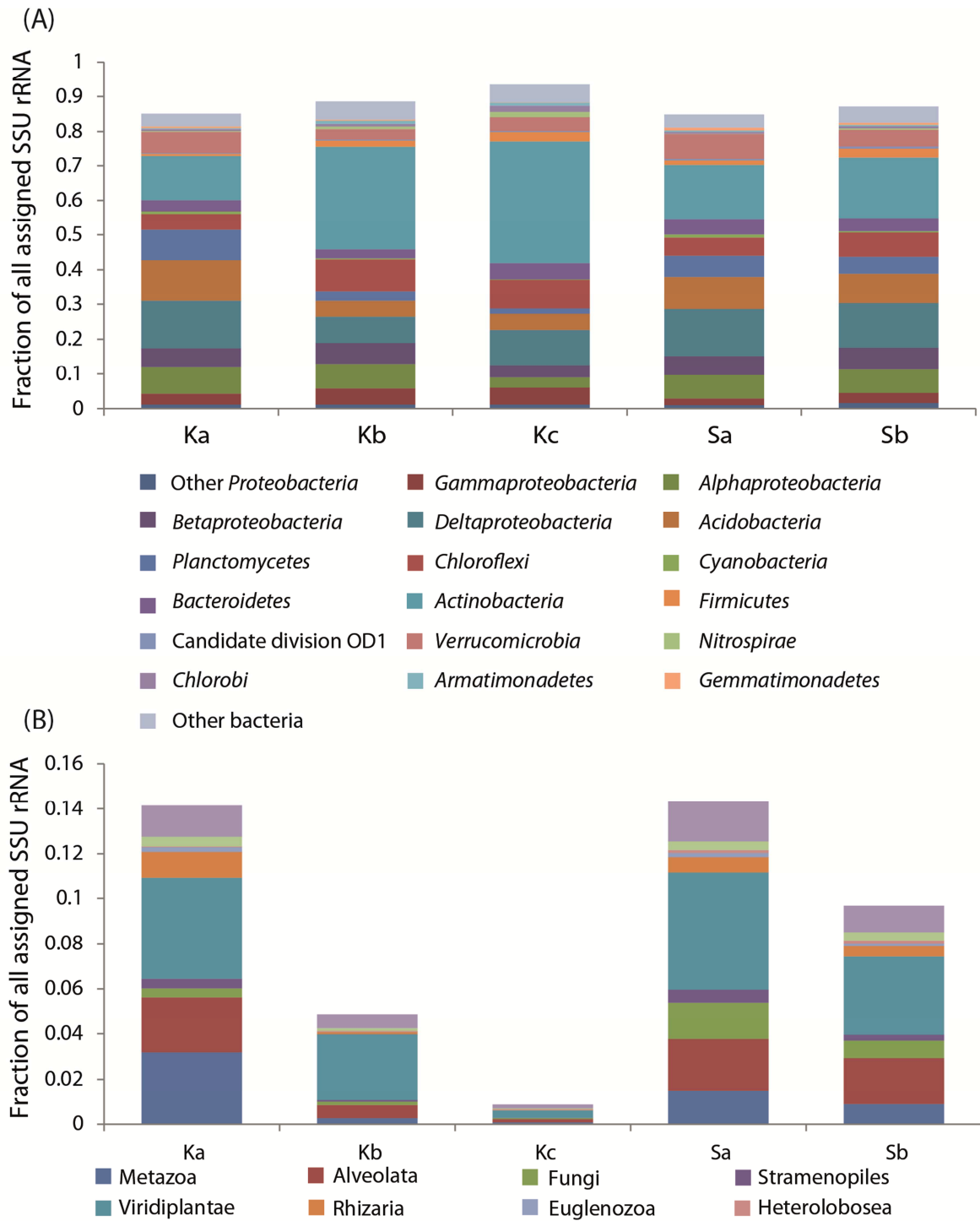
FIG S2 Bacteria (A) and Eukarya (B) community profiles based on 16S rRNA and 18S rRNA respectively, at the different depths of Knudsenheia (Ka, Kb, Kc) and Solvatn (Sa, Sb). Column sizes represent the fraction of all assigned sequences assigned to these taxa at phylum/class-level taxonomy. The taxon names from top left corresponds row by row with the columns from bottom to top.
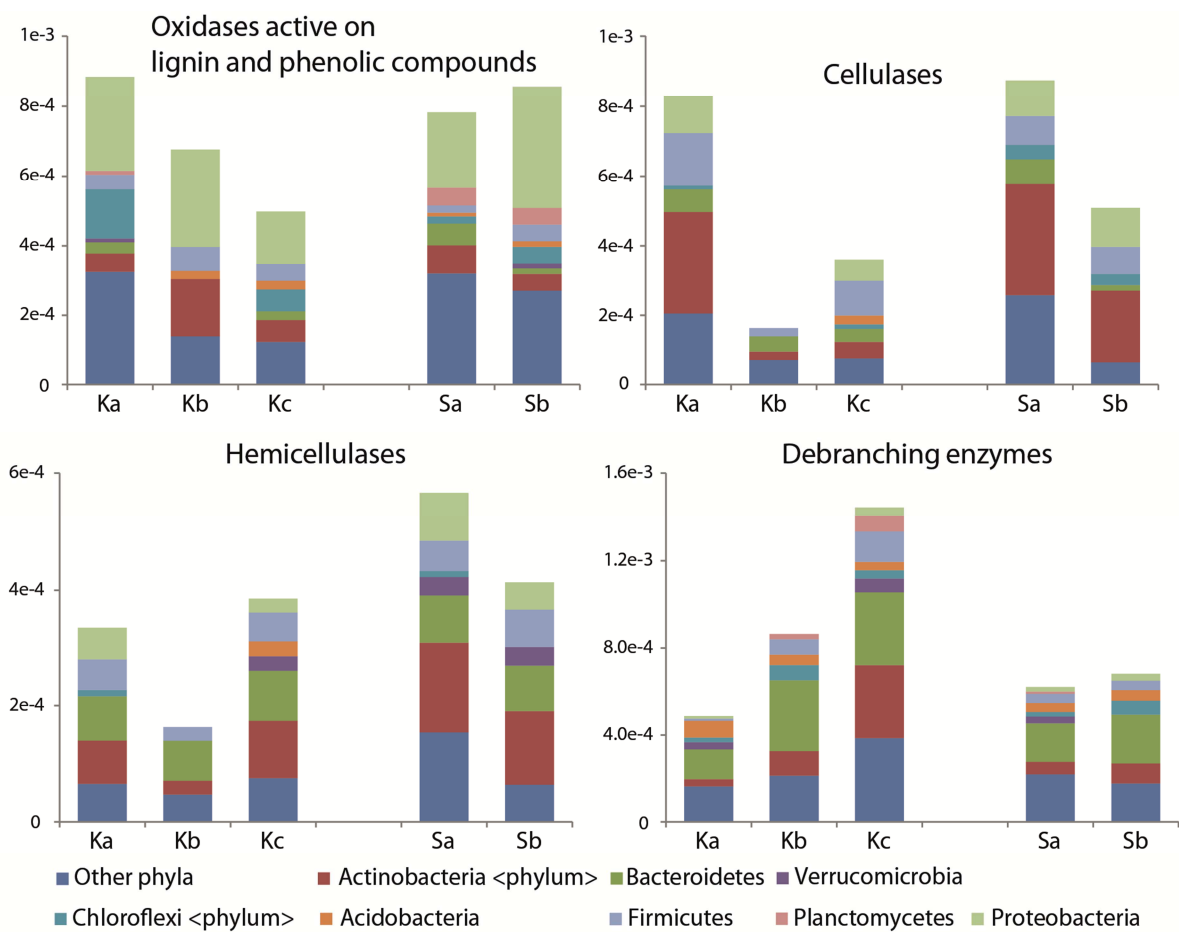
FIG S3 Taxonomic assignment of transcripts encoding oxidases, cellulases, endohemicellulases, and debranching enzymes. Protein family domains were identified by searches in the Pfam database. Sequences containing identified domains were taxonomically assigned using BLASTP (see Materials and methods).

TABLE S1 Nucleic acids extraction

Sample	Extracted nucleic acids (µg gdw^{-1})	Spectrophotometric measurement ratio 260/280	Spectrophotometric measurement ratio 260/230	Extracted RNA (µg gdw^{-1})	% RNA	cDNA synthesis efficiency (%)
Sa	526	1.9	1.9	185	35	29
Sb	375	2.0	1.8	80	21	2
Ka	574	2.0	1.7	135	24	>90
Kb	137	1.9	1.4	26	19	1
Kc	131	1.9	1.1	20	15	4

TABLE S2 mRNA enrichment by removal of rRNA molecules. *Sa 1 and Sa 2 were pooled to provide a larger pool after this step. One sample was terminated after each kit to provide material for analysis of kit specific effect on rRNA removal. RiboBac: RiboMinus Bacteria; MicEx: MICROBExpress; RibE: RiboMinus Eukaryote. See materials and methods for kit descriptions.

	First kit	Input µl	ng added	ng left	Removal	Second kit	Input µl	ng added	ng left	Additional removal	Kit	Input µl	ng input	ng left	Additional removal	Estimated total removal
S2a 1	RibBac	20	2378	1164	51.0 %	MicEx	13.5	1048	1004	2.0 %	RibEuk	11.5	3150	1870	16.8 %	69.9 %
S2a 2	RibBac	20	5647	2396	57.6 %	MicEx	13.5	2156	1919	4.7 %	RibEuk	*	*	*	*	*
S2a 3	RibBac	20	5647	2362	58.2 %	MicEx	13.5	2125	2007	2.3 %						
S2a 4	RibBac	20	5647	2415	57.2 %											
K1a 1	RibBac	20	5661	2474	56.3 %	MicEx	13.5	2227	2056	3.3 %	RibEuk	11.5	1713	995	17.1 %	76.7 %
K1a 2	RibBac	20	5661	2342	58.6 %	MicEx	13.5	2108	2082	0.5 %						
K1a 3	RibBac	20	5661	2302	59.3 %											

TABLE S3 RNA amplification using Message Amp II bacteria kit and cDNA synthesis to test applicability of amplified RNA.

	ng added	ng/µl output	µl	µg	Nanodrop 260/280 ratio	Nanodrop 260/230 ratio	ng input cDNA test	output cDNA test	Nanodrop 260/280 ratio	Nanodrop 260/230 ratio
S2a	12.5	481	150	72.15	2.83	2.53				
S2b	12.5	149	150	22.35	2.27	1.66				
K1a	12.5	531	150	79.65	2.72	2.11	1200	3072	1.92	2.32
K1b	12.5	101	150	15.15	2.52	2.17				
K1c	12.5	152	150	22.8	2.63	2.64				
K1a_e	12.5	141.5	150	21.225	2.18	2.37	1800	1500	1.81	1.49

TABLE S4 The number of mRNA transcripts encoding key enzymes for methane oxidation assigned to the methanotrophic genus *Methylobacter* (all assigned to *M. tundripaludum*) at the different depths of peat in Knudsenheia and Solvatn. In brackets, the fraction of reads assigned to that specific function in the *M. tundripaludum* genome, out of all assigned reads to any genome in the RefSeq database, is shown.

Predicted function	E.C.	Gene ID	Ka	Kb	Kc	Sa	Sb
Methane monooxygenase subunit C	1.14.18.3	*pmoC*	360 (1.21)	229 (1.67)	265 (0.97)	8 (0.02)	117 (0.55)
Methane monooxygenase subunit B	1.14.18.3	*pmoB*	116 (0.39)	102 (0.74)	143 (0.52)	2 (0.01)	24 (0.11)
Methane monooxygenase subunit A	1.14.18.3	*pmoA*	86 (0.29)	79 (0.58)	108 (0.40)	5 (0.02)	25 (0.12)
PQQ-dependent methanol dehydrogenase	1.1.1.244	*mxaIF*	18 (0.06)	13 (0.09)	7 (0.03)	0 (0)	4 (0.02)
PQQ-dependent aldehyde dehydrogenase	1.2.99.3	*aldh*	11 (0.04)	1 (0.01)	1 (0.004)	6 (0.02)	4 (0.02)
Formaldehyde-activating enzyme	4.2.1.147	*fae*	2 (0.01)	2 (0.01)	3 (0.01)	0 (0)	0 (0)
Formate dehydrogenase	1.2.1.2	*fdh*	14 (0.05)	7 (0.05)	16 (0.06)	1 (0)	3 (0.01)
Total assigned to *Methylobacter*	-	-	3671 (12.3)	2516 (18.3)	4181 (15.3)	451 (1.4)	832 (3.9)
Total assigned to *Methylococcaceae*	-	-	6448	4380	6927	1304	1761
Total assigned to any RefSeq genome	-	-	298697	137257	272563	321674	214568