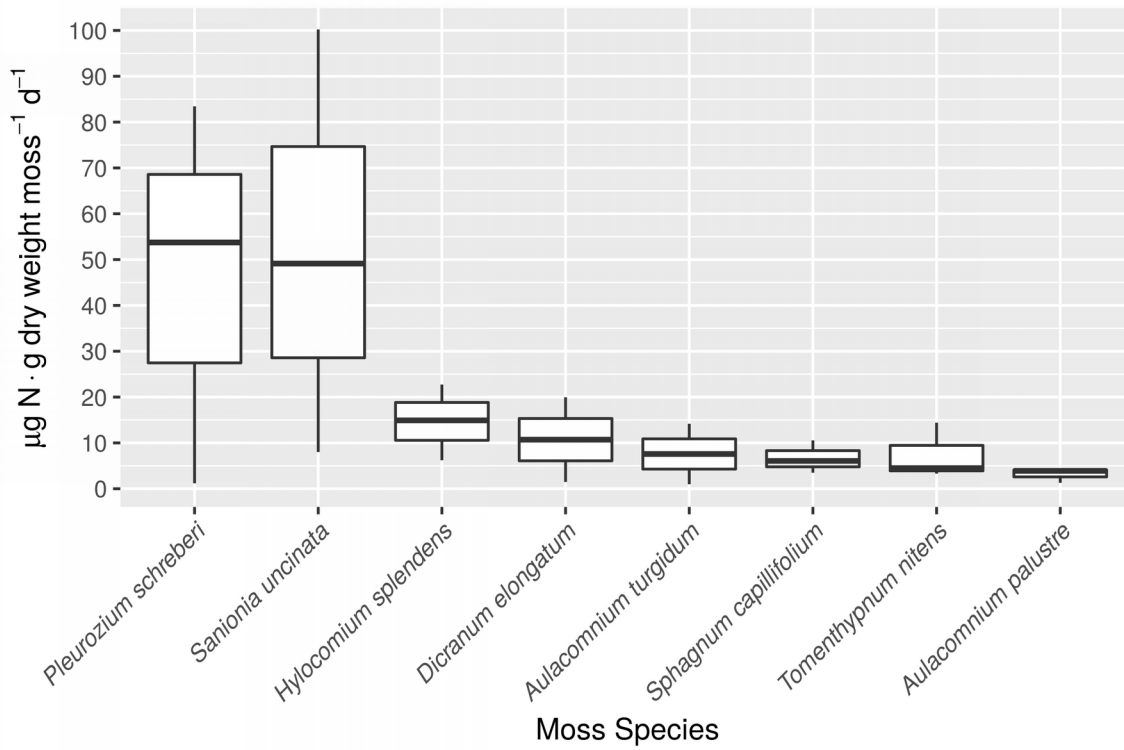
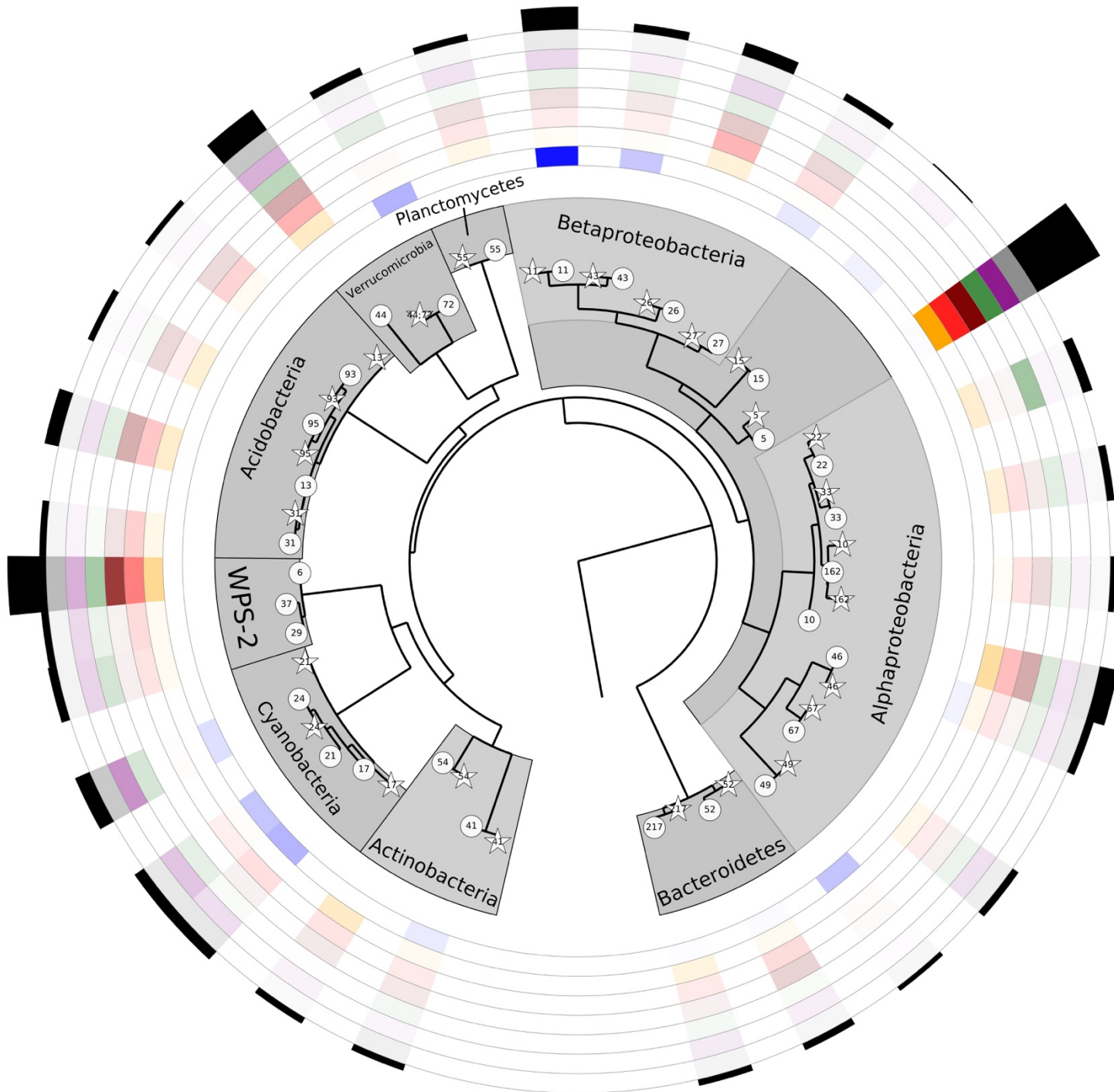


Supplemental Information:

Figure S1: Nitrogen fixation rates measured for each moss species. Rates are in units of $\mu\text{g N} \cdot \text{g dry weight moss}^{-1} \text{d}^{-1}$.





- Sequenced phylotype
- ☆ Nearest isolated relative

Rings

- Sanionia uncinata*
- Dicranum elongatum*
- Aulacomnium turgidum*
- Pleurozium schreberi*
- Sphagnum capillifolium*
- Aulacomnium palustre*
- Tomenthypnum nitens*
- Total Mean Relative Abundance

Figure S2: A phylogenetic tree of the top 30 phylotypes (circles) and their nearest isolated relatives (stars). The top 30 phylotypes represented here account for 35% of the 16S rRNA gene reads in the dataset. Each inner colored ring represents a different species of moss, from the inside ring to the outer ring they are: *Sanionia uncinata* (blue), *Dicranum elongatum*. (yellow), *Aulacomnium turgidum* (bright red), *Pleurozium schreberi* (dark red), *Sphagnum capillifolium* (green), *Aulacomnium palustre* (purple), *Tomenthypnum nitens* (gray). The opacity of the colored rings represents the relative abundance (log transformed and scaled between 0 and 1) of the different phylotypes within in each host moss species. The black outer ring represents the total relative abundance of each phylotype across all species (also log transformed and scaled between 0 and 1).

Figure S3: Comparison of the relative abundances of the top 8 phyla in the amplicon sequencing and Metaxa2-derived shotgun metagenomic sequences. Despite the different methods used to infer bacterial community composition, the abundances of the phyla were similar.

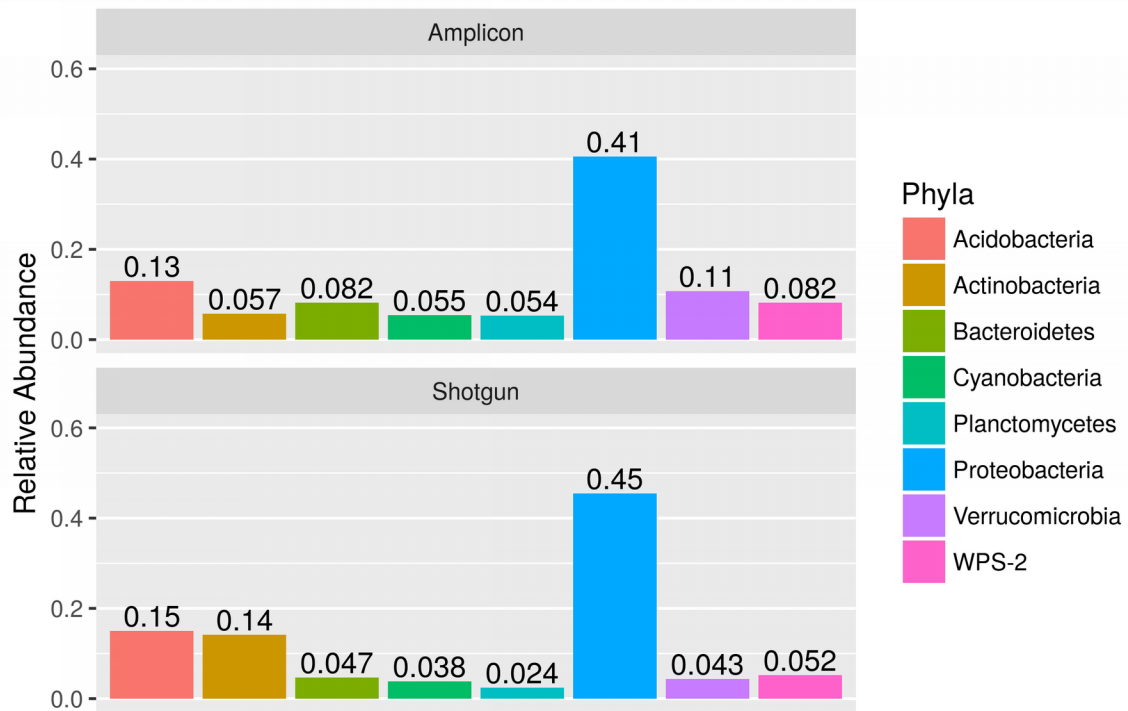


Table S1: Voucher specimen information for each moss sample

Taxon	Authority	Collector	Collection # (site-species #)	Herbarium
<i>Aulacomnium palustre</i>	(Hedw.) Schwägr.	M. Mack	1-3	FLAS
<i>Aulacomnium palustre</i>	(Hedw.) Schwägr.	M. Mack	2-3	FLAS
<i>Aulacomnium palustre</i>	(Hedw.) Schwägr.	M. Mack	3-3	FLAS
<i>Aulacomnium turgidum</i>	(Wahlenb.) Schwägr.	M. Mack	1-6	FLAS
<i>Aulacomnium turgidum</i>	(Wahlenb.) Schwägr.	M. Mack	2-6	FLAS
<i>Aulacomnium turgidum</i>	(Wahlenb.) Schwägr.	M. Mack	3-6	FLAS
<i>Dicranum elongatum</i>	Schleich. ex Schwägr.	M. Mack	1-8	FLAS
<i>Dicranum elongatum</i>	Schleich. ex Schwägr.	M. Mack	3-8	FLAS
<i>Pleurozium schreberi</i>	(Brid.) Mitt.	M. Mack	1-2	FLAS
<i>Pleurozium schreberi</i>	(Brid.) Mitt.	M. Mack	2-2	FLAS
<i>Pleurozium schreberi</i>	(Brid.) Mitt.	M. Mack	3-2	FLAS
<i>Sanionia uncinata</i>	(Hedw.) Loeske	M. Mack	1-4	FLAS
<i>Sanionia uncinata</i>	(Hedw.) Loeske	M. Mack	2-4	FLAS
<i>Sanionia uncinata</i>	(Hedw.) Loeske	M. Mack	3-4	FLAS
<i>Sphagnum capillifolium</i>	(Ehrh.) Hedw.	M. Mack	1-7	FLAS
<i>Sphagnum capillifolium</i>	(Ehrh.) Hedw.	M. Mack	2-7	FLAS
<i>Sphagnum capillifolium</i>	(Ehrh.) Hedw.	M. Mack	3-7	FLAS
<i>Tomentypnum nitens</i>	(Hedw.) Loeske	M. Mack	1-5	FLAS
<i>Tomentypnum nitens</i>	(Hedw.) Loeske	M. Mack	2-5	FLAS
<i>Tomentypnum nitens</i>	(Hedw.) Loeske	M. Mack	3-5	FLAS
<i>Hylcomium splendens</i>	(Hedw.) Shimp	M. Mack	1-1	FLAS
<i>Hylocomium splendens</i>	(Hedw.) Shimp	M. Mack	2-1	FLAS
<i>Hylocomium splendens</i>	(Hedw.) Shimp	M. Mack	3-1	FLAS

Table S2: Genome Bins Passing Quality Filter

Genome bins were assessed for completeness and contamination using CheckM (see paper). Briefly, completeness and contamination are calculated based on the percentage of conserved single-copy marker genes in a bin and the number of duplicates of each single-copy marker genes in each bin. The marker genes used in this assessment were chosen based on the inferred lineage of each bin. The 7 genomes that were identified as being greater than 70% complete and less than 10% contaminated (duplicates) were considered as passing quality filter, and are listed in the table below. The genome sizes were estimated by using the number of base pairs in each bin and the percent completion estimate.

Genome Bin	Classification	Percent complete	Percent contaminated	Estimated Genome Size (Mbp)
61	Cyanobacteria	96.51	4.11	8.88
29	WPS-2	89.51	4.82	3.88
44	WPS-2	88.79	1.83	4.34
33	WPS-2	84.46	7.82	3.41
54	Acidobacteria	82.66	9.44	7.61
53	Cyanobacteria	72.52	2.85	9.8
49	Alphaproteobacteria	70.49	6.46	4.04

Table S3: Nearest isolated relatives of abundant bacterial phylotypes identified from the sampled moss species.

Phylotype	Relative Abundance	RDP ID	RDP Similarity Score	RDP Sequence Name	GreenGenes-assigned taxonomy
Phylotype_5	0.07	S000995323	0.94	Steroidobacter denitrificans (T); FS; EF605262	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Xanthomonadales; f__Sinobacteraceae; g__; s__
Phylotype_6	0.04	S002350837	0.82	Thermosinus carboxydivorans; type strain: DSM 14886; FR749974	k__Bacteria; p__WPS-2; c__; o__; f__; g__; s__
Phylotype_10	0.02	S003312544	0.94	Endobacter medicaginis (T); M1MS02; JQ436923	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodospirillales; f__Acetobacteraceae; g__; s__
Phylotype_11	0.02	S000627892	1	Rhizobacter fulvus (T); Gsoil 322; AB245356	k__Bacteria; p__Proteobacteria; c__Betaproteobacteria; o__Burkholderiales; f__Comamonadaceae; g__Methylibium; s__
Phylotype_13	0.01	S000941899	0.98	Granulicella aggregans (T); type strain: TPB6028; AM887756	k__Bacteria; p__Acidobacteria; c__Acidobacteriia; o__Acidobacteriales; f__Acidobacteriaceae; g__; s__
Phylotype_15	0	S000011435	1	Pseudomonas graminis; HhSaOsb; AF511514	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; s__viridiflava
Phylotype_17	0.01	S004215061	1	Nostoc sp. Protopannaria pezizoides UK120 cyanobiont; KF359684	k__Bacteria; p__Cyanobacteria; c__Nostocophycideae; o__Nostocales; f__Nostocaceae; g__Nostoc; s__
Phylotype_21	0.01	S000457688	1	Nostoc commune; SO-42; AB098071	k__Bacteria; p__Cyanobacteria; c__Nostocophycideae; o__Nostocales; f__Nostocaceae; g__Nostoc; s__

Phylotype_22	0.01	S000443861	0.96	Acidocella sp. M21; AY765998	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodospirillales; f__Acetobacteraceae; g__Acidocella; s__
Phylotype_24	0.01	S000749734	1	Gloeotrichia echinulata PYH6; AM230703	k__Bacteria; p__Cyanobacteria; c__Nostocophycideae; o__Nostocales; f__Nostocaceae; g__ ; s__
Phylotype_26	0.01	S000398336	1	Paraburkholderia glathei; Hg5; AY154370	k__Bacteria; p__Proteobacteria; c__Betaproteobacteria; o__Burkholderiales; f__Burkholderiaceae; g__Burkholderia
Phylotype_27	0.01	S000415015	0.97	Derxia gummosa; IAM 14990; AB089481	k__Bacteria; p__Proteobacteria; c__Betaproteobacteria; o__Burkholderiales; f__ ; g__ ; s__
Phylotype_29	0.01	S000891994	0.79	Carboxydocella ferrireducens; 019; EF092457	k__Bacteria; p__WPS-2; c__ ; o__ ; f__ ; g__ ; s__
Phylotype_31	0.01	S000941902	0.97	Granulicella rosea (T); type strain: T4; AM887759	k__Bacteria; p__Acidobacteria; c__Acidobacteriia; o__Acidobacteriales; f__Acidobacteriaceae; g__ ; s__
Phylotype_33	0.01	S001093906	0.99	Acidisoma tundrae (T); type strain: WM1; AM947652	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodospirillales; f__Acetobacteraceae; g__Acidisoma; s__
Phylotype_37	0.01	S000543874	0.75	Paenibacillus terrae; MH72; AJ318910	k__Bacteria; p__WPS-2; c__ ; o__ ; f__ ; g__ ; s__
Phylotype_41	0.01	S000126222	1	Antarctic bacterium R- 9112; AJ441003	k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Actinomycetales; f__Microbacteriaceae; g__Salinibacterium; s__
Phylotype_43	0.01	S001291898	1	Leptothrix sp. PW10C; AB480712	k__Bacteria; p__Proteobacteria; c__Betaproteobacteria; o__Burkholderiales; f__Comamonadaceae; g__ ; s__
Phylotype_44	0.02	S000515723	0.86	bacterium Ellin507; AY960770	k__Bacteria; p__Verrucomicrobia; c__[Methylacidiphilae]; o__Methylacidiphilales; f__ ; g__ ; s__

Phylotype_46	0.01	S000143080	1	Bradyrhizobium sp. 1; AY238503	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Bradyrhizobiaceae; g__Bradyrhizobium; s__
Phylotype_49	0	S000017317	1	Sphingomonas sp. BF14; BF14 (bright yellow group 1 colony type) = DSM 9257; Z23157	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Sphingomonadales; f__Sphingomonadaceae; g__Sphingomonas; s__echinoides
Phylotype_52	0.01	S001588687	0.99	Mucilaginibacter mallensis (T); type strain: MP1X4; FN400859	k__Bacteria; p__Bacteroidetes; c__Sphingobacteriia; o__Sphingobacteriales; f__Sphingobacteriaceae; g__; s__
Phylotype_54	0.01	S000515720	1	bacterium Ellin504; AY960767	k__Bacteria; p__Actinobacteria; c__Thermoleophilia; o__Solirubrobacterales; f__Conexibacteraceae; g__; s__
Phylotype_55	0.01	S000403461	0.97	bacterium Ellin5111; AY234528	k__Bacteria; p__Planctomycetes; c__Planctomycetia; o__Gemmatales; f__Isosphaeraceae; g__; s__
Phylotype_67	0.01	S000395297	0.98	bacterium Ellin340; AF498722	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhizobiales; f__Methylocystaceae; g__; s__
Phylotype_72	0.01	S000515723	0.98	bacterium Ellin507; AY960770	k__Bacteria; p__Verrucomicrobia; c__[Spartobacteria]; o__[Chthoniobacteriales]; f__[Chthoniobacteraceae]; g__Chthoniobacter; s__
Phylotype_93	0	S002223179	1	Granulicella paludicola; LCBR1; FR716684	k__Bacteria; p__Acidobacteria; c__Acidobacteriia; o__Acidobacteriales; f__Acidobacteriaceae; g__Granulicella; s__paludicola
Phylotype_95	0.01	S003805061	0.98	Granulicella paludicola; Colony1; KC924939	k__Bacteria; p__Acidobacteria; c__Acidobacteriia; o__Acidobacteriales; f__Acidobacteriaceae; g__; s__
Phylotype_162	0.01	S000650671	0.96	Acetobacteraceae bacterium MP03; AM162403	k__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodospirillales; f__Acetobacteraceae; g__; s__

Phylotype_217	0.01	S002232422	0.98	Mucilaginibacter sp. HME6636; HM638228	k__Bacteria; p__Bacteroidetes; c__Sphingobacteriia; o__Sphingobacteriales; f__Sphingobacteriaceae; g__; s__
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