

Structure and function of the peatland prokaryotic microbiome

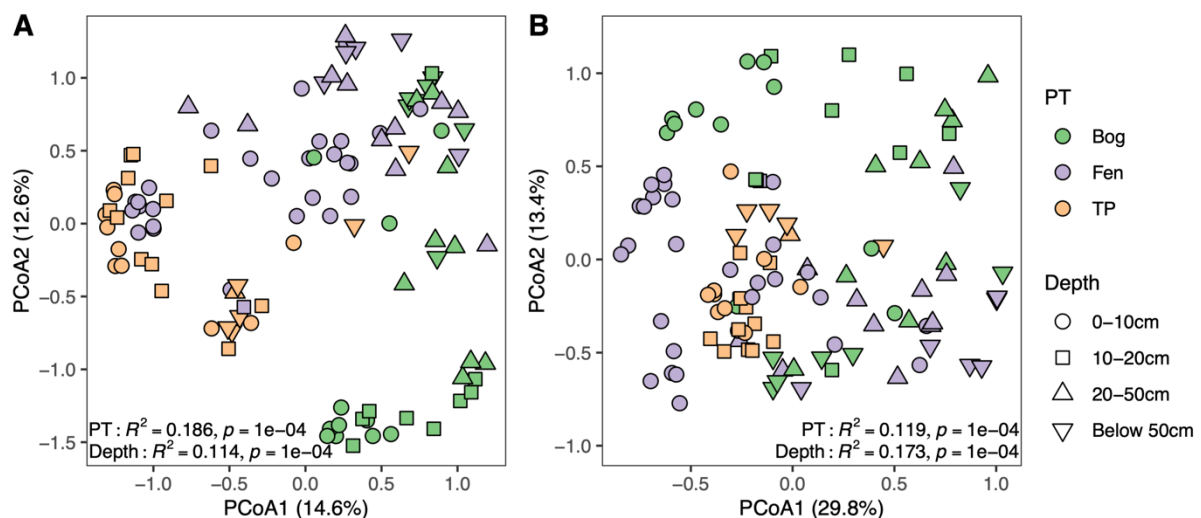
Supplementary figures

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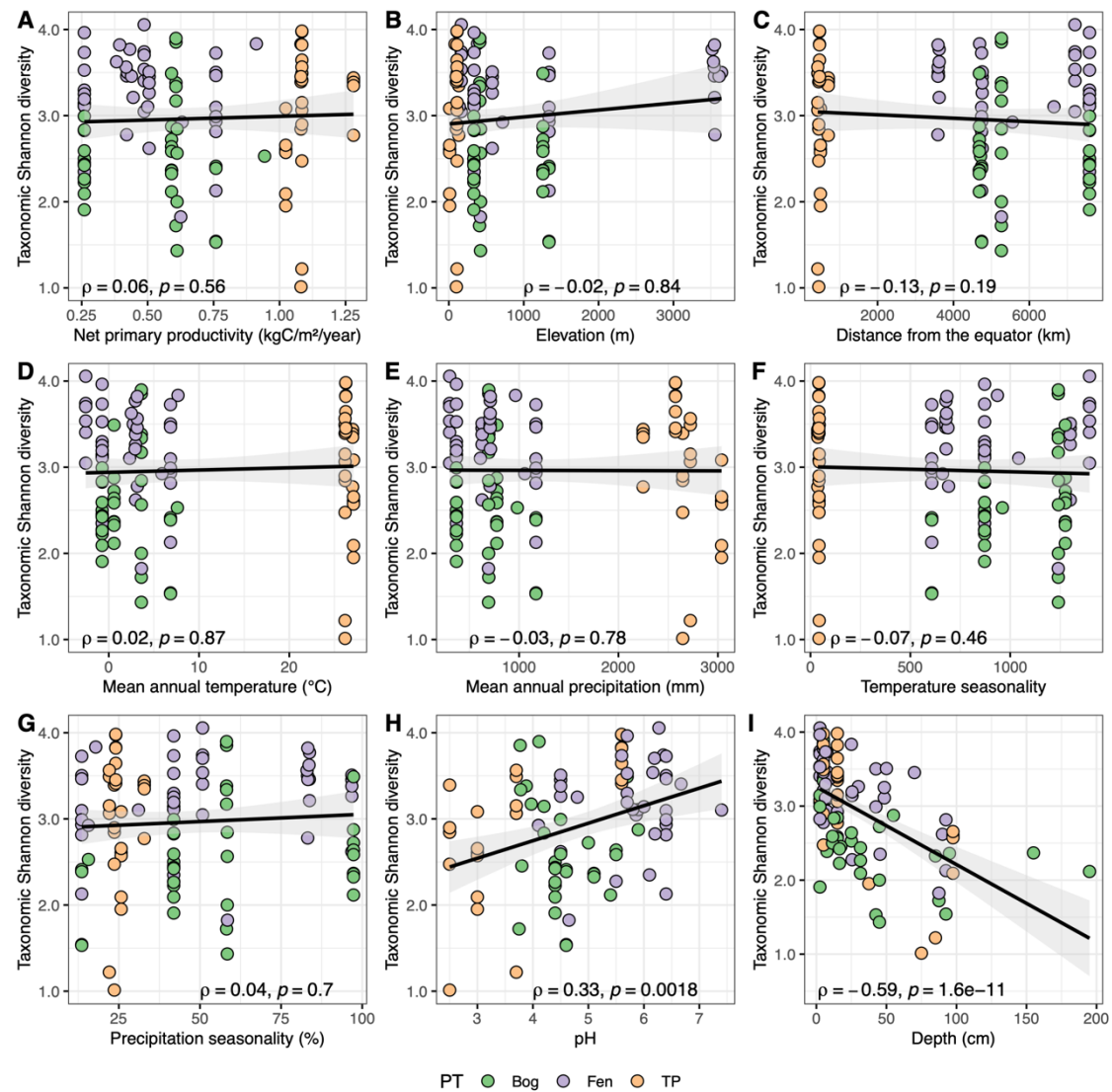
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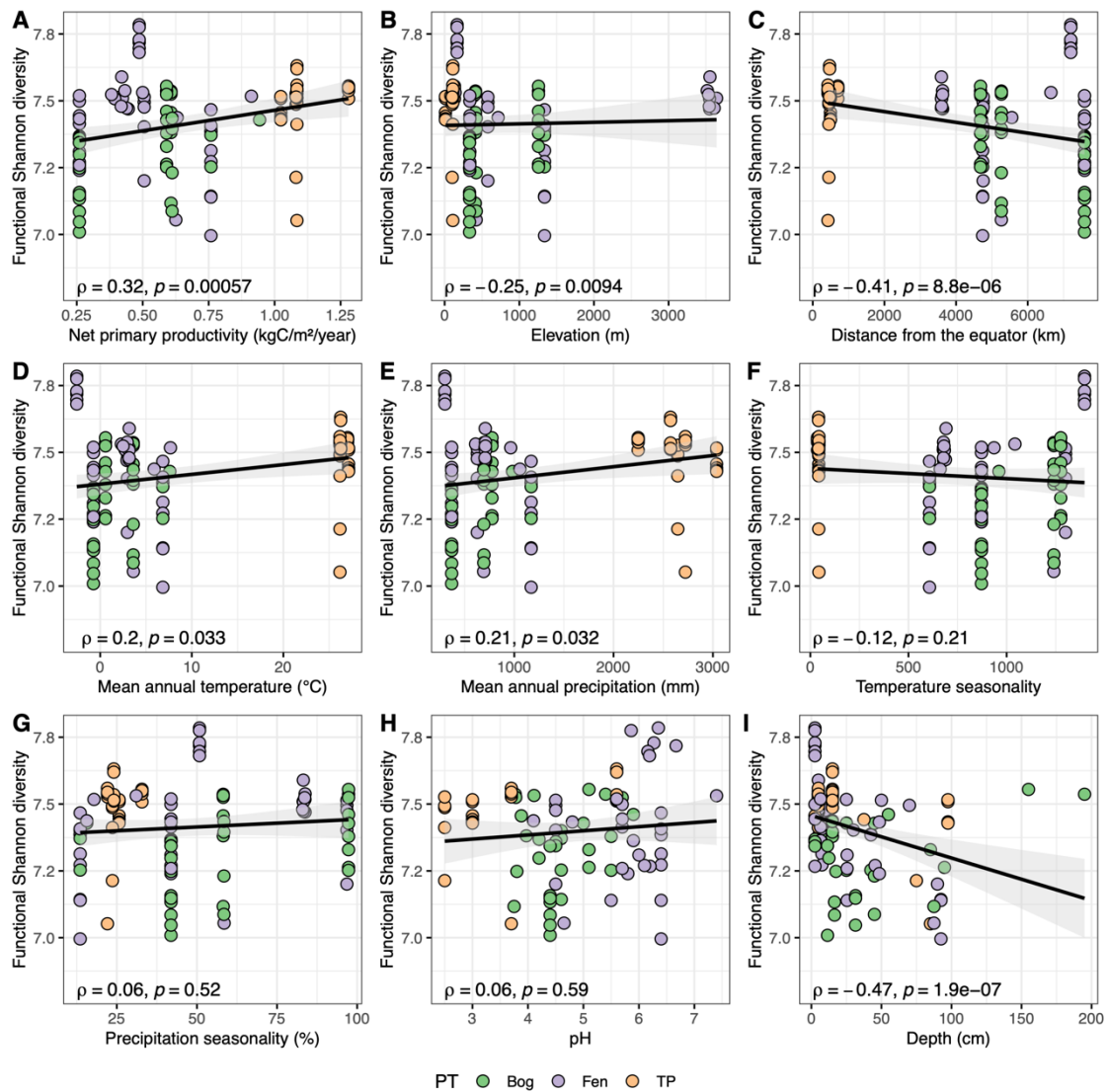
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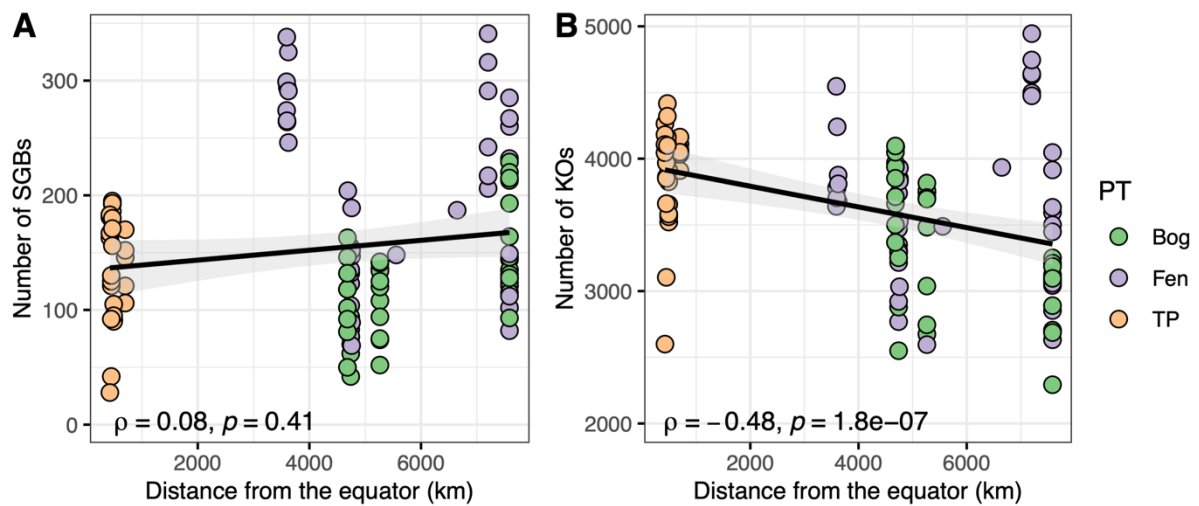
Supplementary Fig. 1. Principal coordinates analysis (PCoA) plots of (A) taxonomic and (B) functional beta diversity based on the Jaccard (presence/absence) distance metric. Values on the axes represent the percent variations explained. PERMANOVA statistics are provided on the plots. PT, peatland type; TP, tropical peatland.



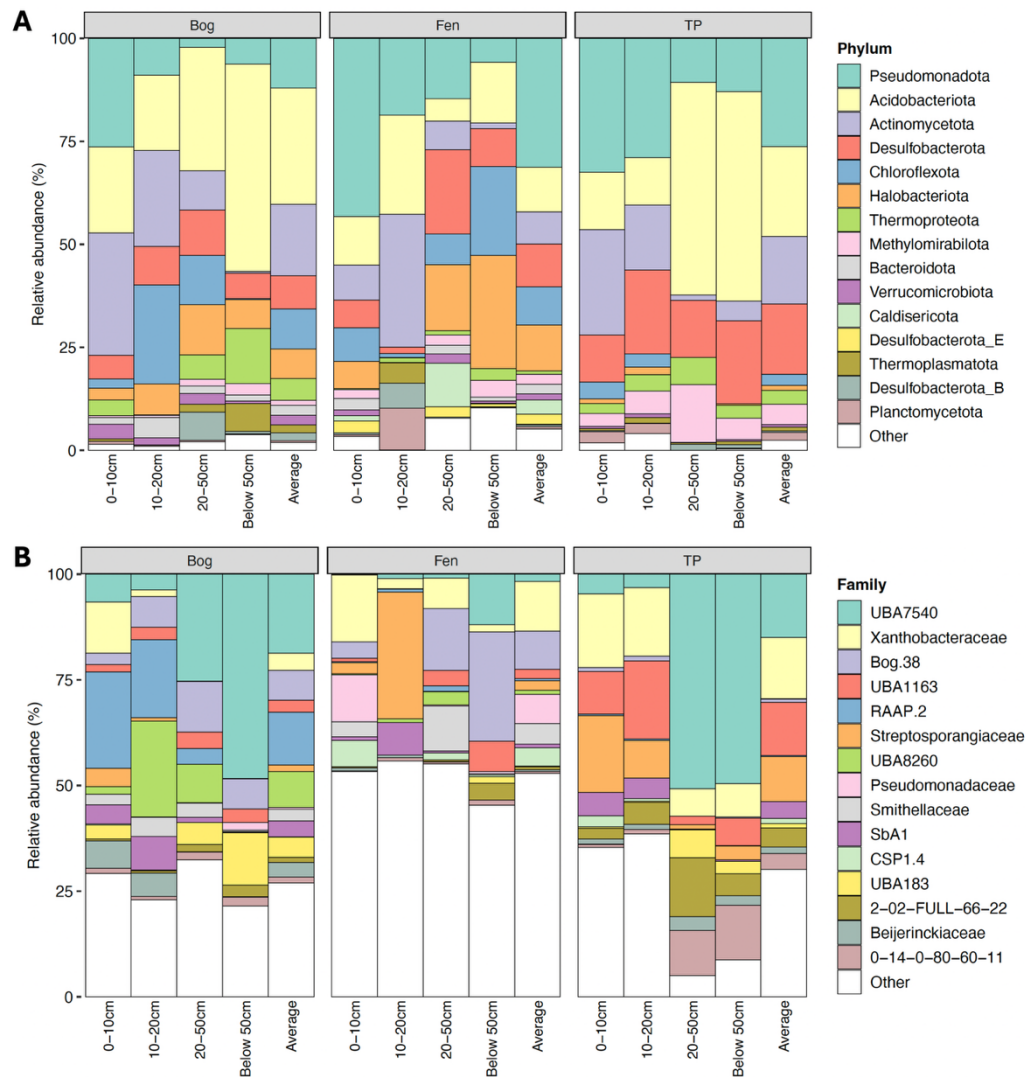
Supplementary Fig. 2. Spearman's correlations between taxonomic alpha diversity and continuous variables. Grey areas around the regression lines represent regions of 95% confidence interval. Panel H was based on a subset with available pH data ($n = 88$). PT, peatland type; TP, tropical peatland.



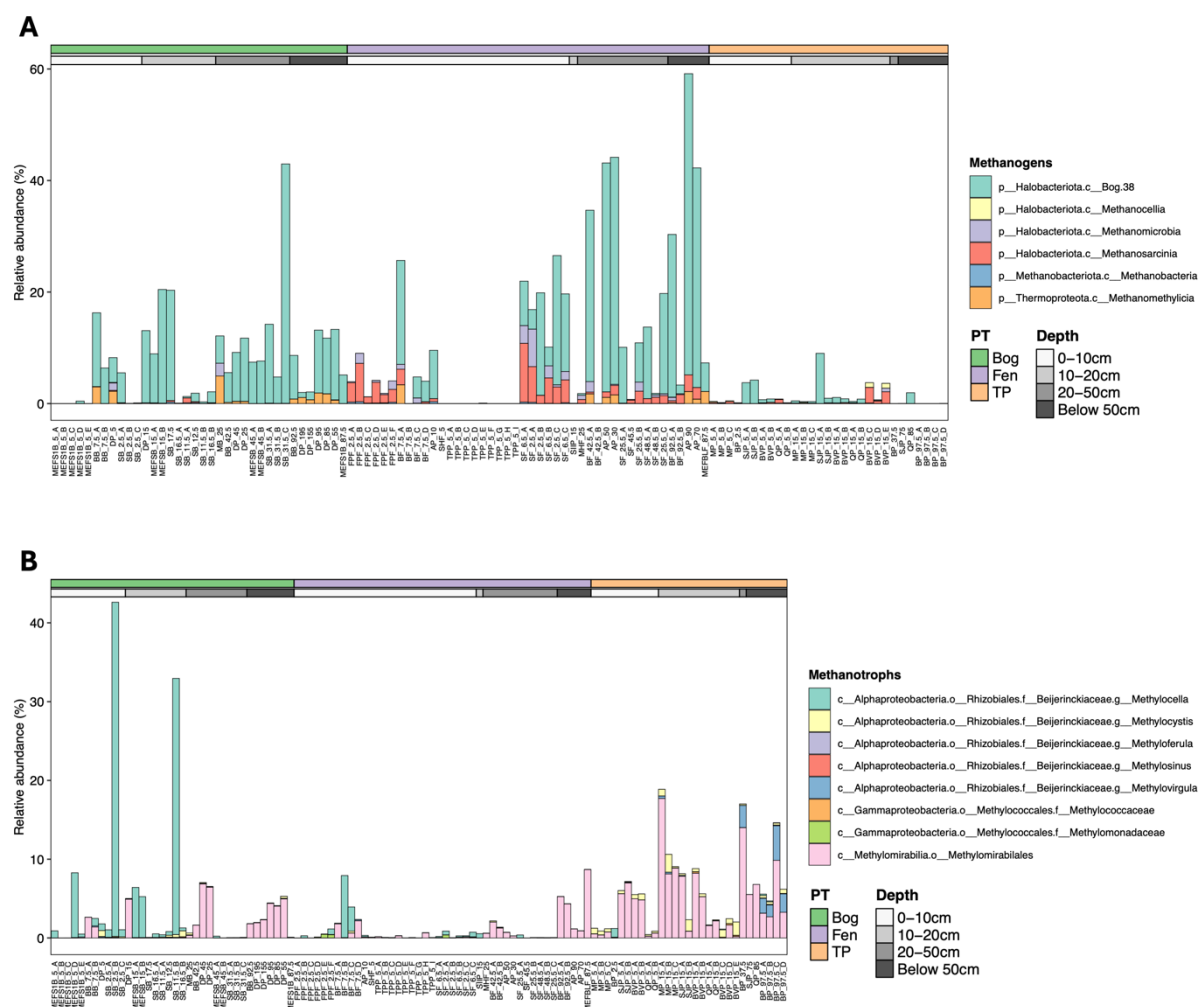
Supplementary Fig. 3. Spearman's correlations between functional alpha diversity and continuous variables. Grey areas around the regression lines represent regions of 95% confidence interval. Panel H was based on a subset with available pH data ($n = 88$). PT, peatland type; TP, tropical peatland.



Supplementary Fig. 4. Latitudinal diversity gradient analysis in taxa and function. Spearman's correlations between distance from the equator and **(A)** the number of species-level genome bins (SGBs) and **(B)** the number of KEGG orthologs (KOs). Grey areas around the regression lines represent regions of 95% confidence interval. PT, peatland type; TP, tropical peatland.



Supplementary Fig. 5. Taxonomic composition of the peatland microbiome aggregated by peatland type and depth. Stacked bar plots of the top 15 most abundant microbial **(A)** phyla and **(B)** families across depth in each peatland type. Also included in each facet is a bar representing the averaged values across all metagenomes from a particular peatland type. TP, tropical peatland.



Supplementary Fig. 6. Taxonomic composition of methanogens and methanotrophs. Stacked bar plots of **(A)** methanogenic classes and **(B)** methanotrophs across the 109 metagenomes. Metagenomes are annotated according to the peatland type (PT) and sampling depth. TP, tropical peatland.