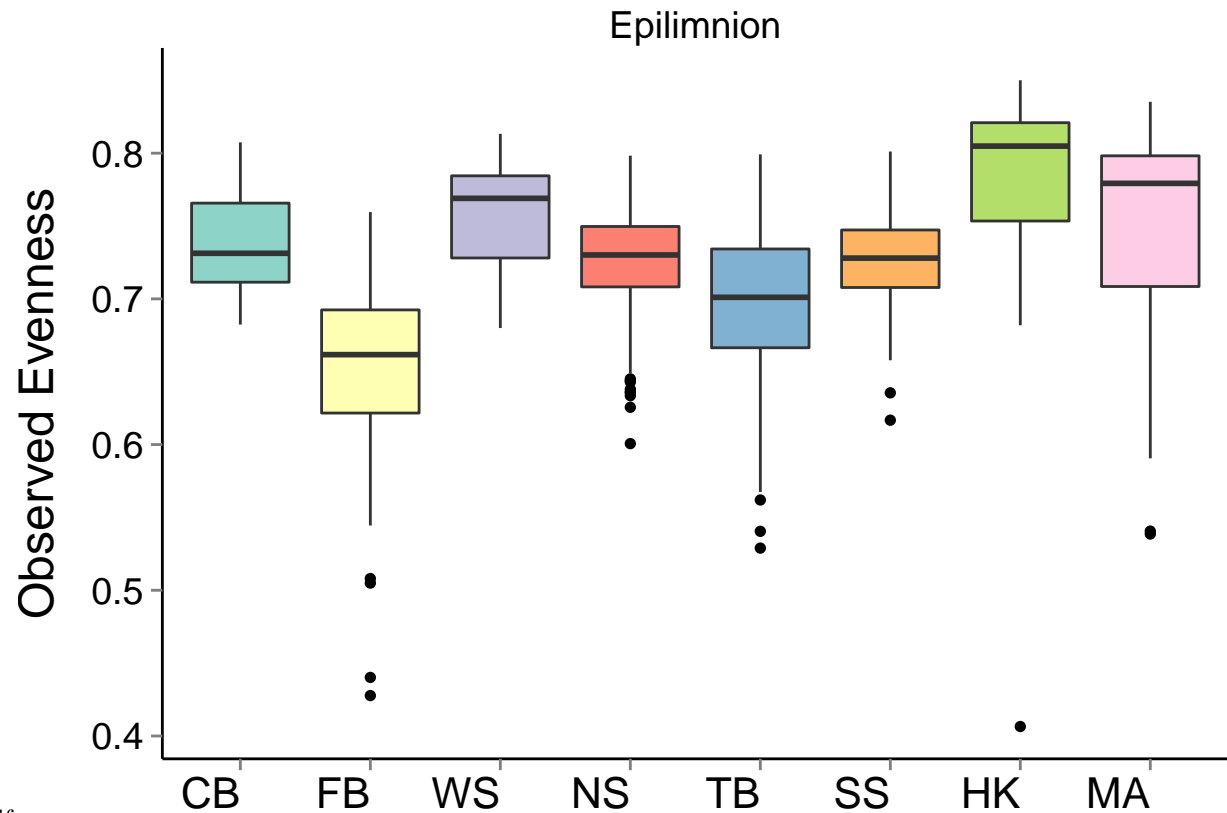


# Supplemental Figures

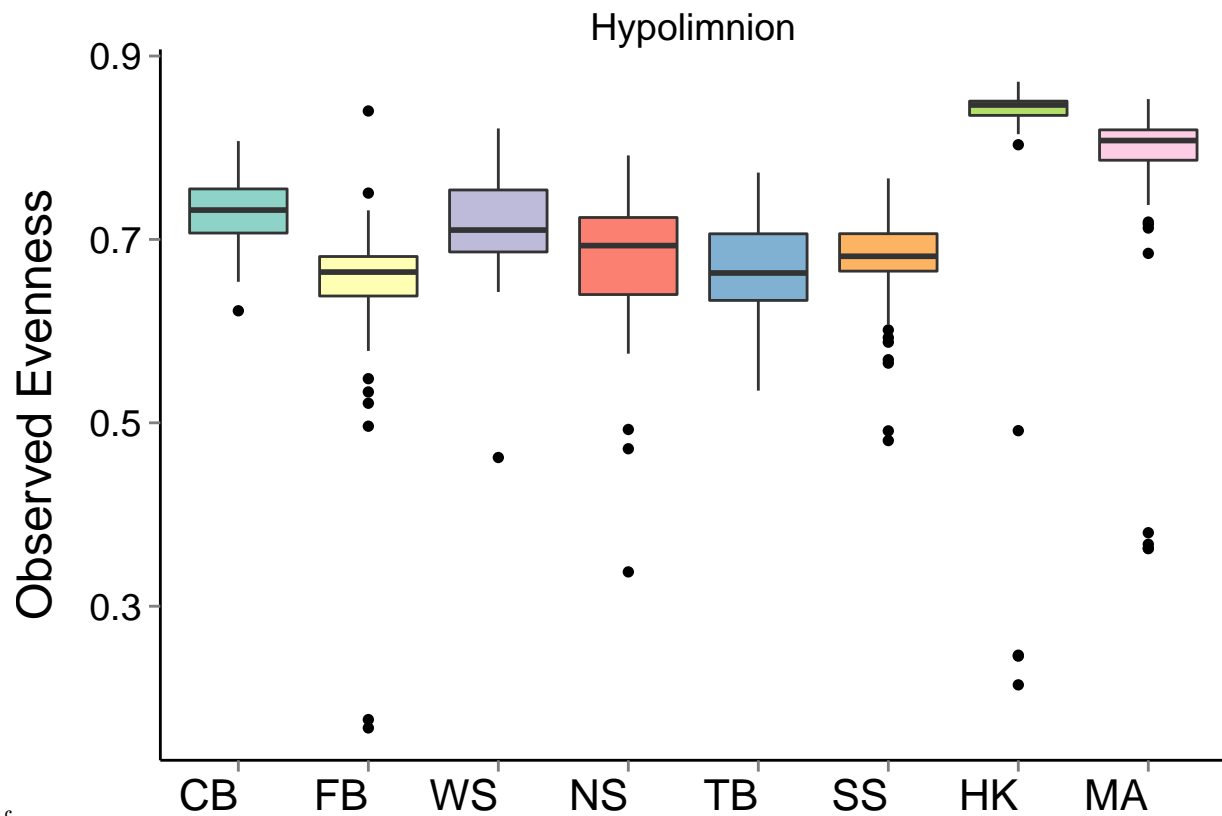
Alexandra Linz

Thursday, January 28, 2016

Supplemental figures accompanying the paper “Seasonal mixing frequency and historical mixing regime determine hypolimnion bacterial community dynamics in bog lakes”

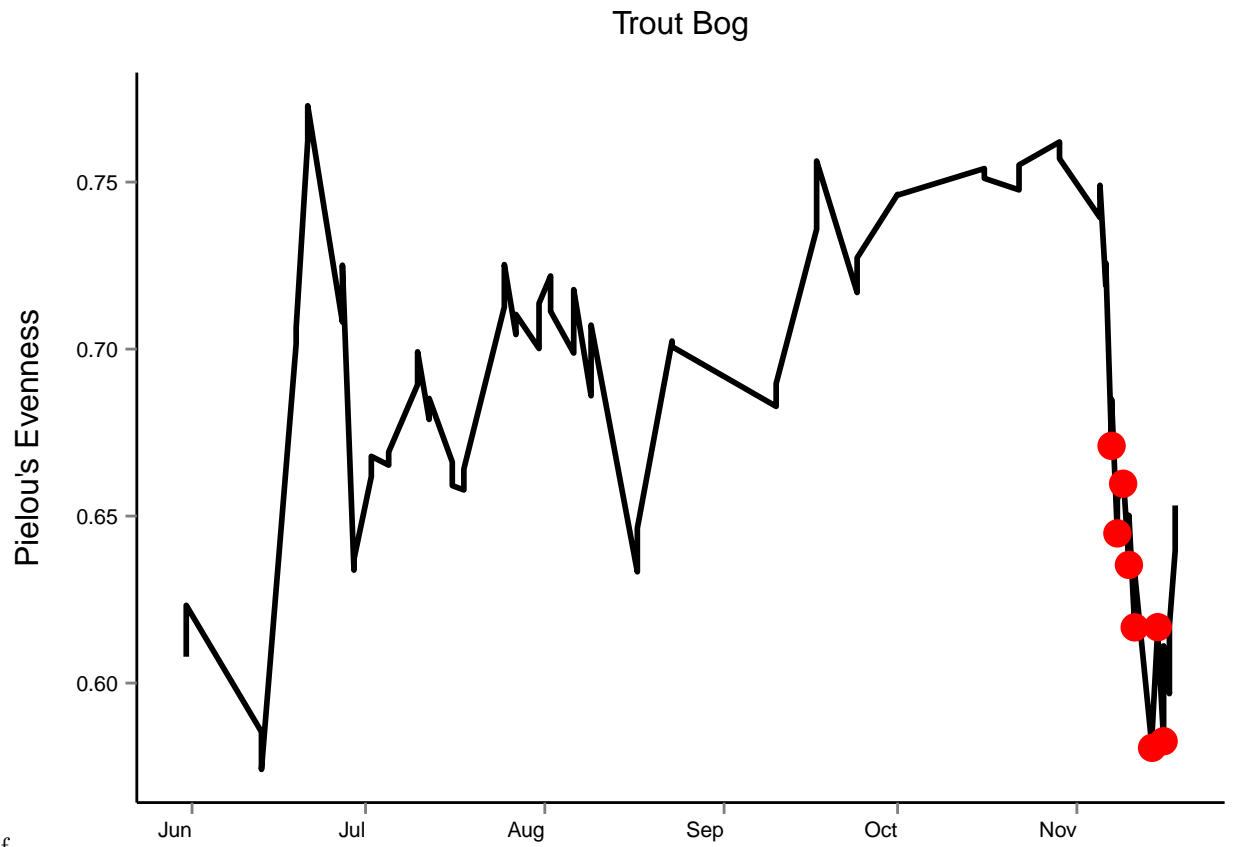


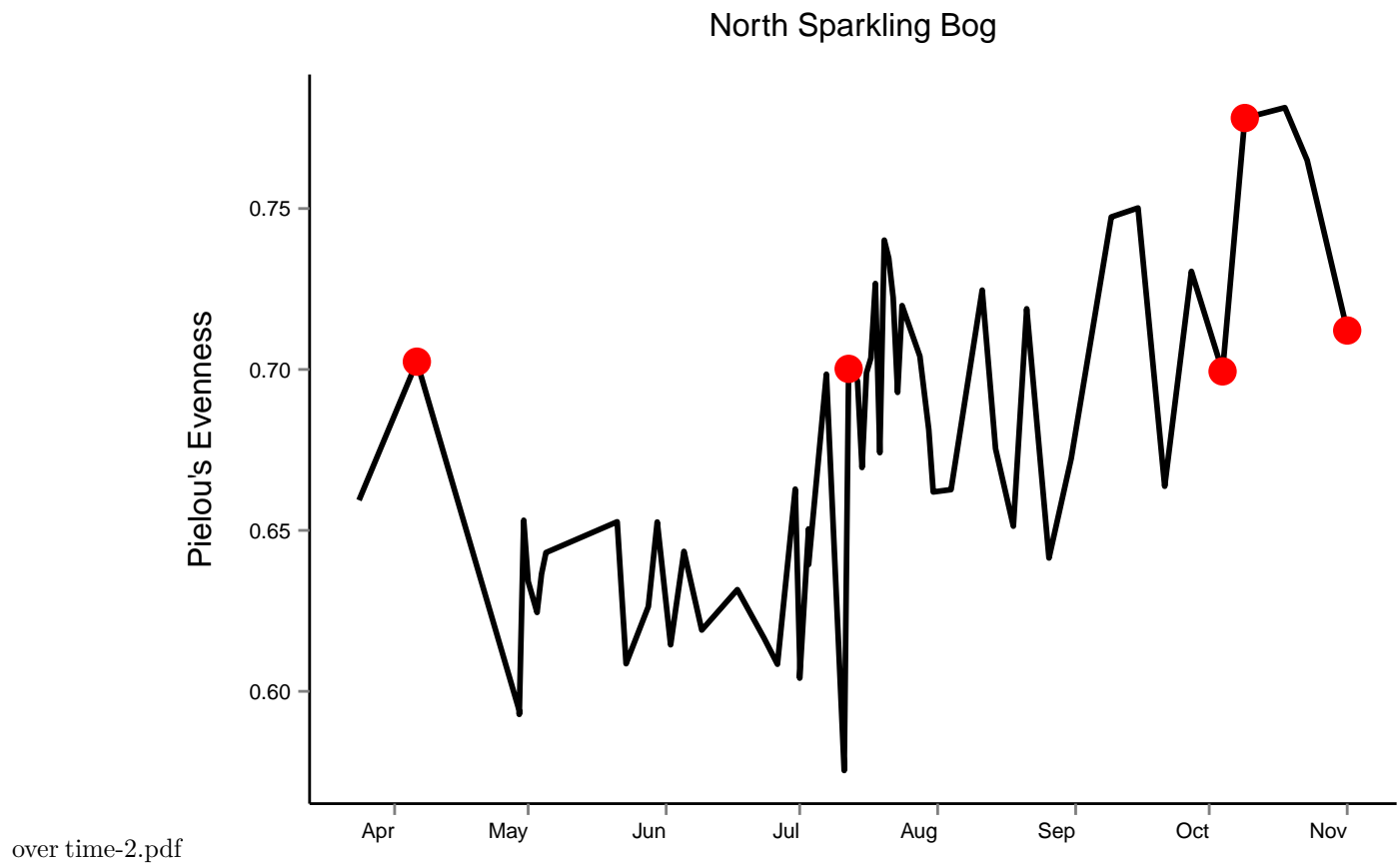
between bogs-1.pdf



between bogs-2.pdf

Figure S1. Evenness by lakes. Pielou's Evenness metric was used to measure the evenness of each sample and grouped by lake. While most pairs of lakes are significantly different in richness in both layers, no trend of increasing or decreasing evenness with depth is observed. However, the evenness in the hypolimnia of both meromictic lakes is significantly greater than all other lakes in this study.





**Figure S2. Evenness over time.** Evenness decreases during the Trout Bog 2007 fall mixing event, as is observed for richness. During the North Sparkling Bog artificial mixing event in 2008, evenness decreases but quickly recovers, with no drop in evenness during the fall mixing event for that year.

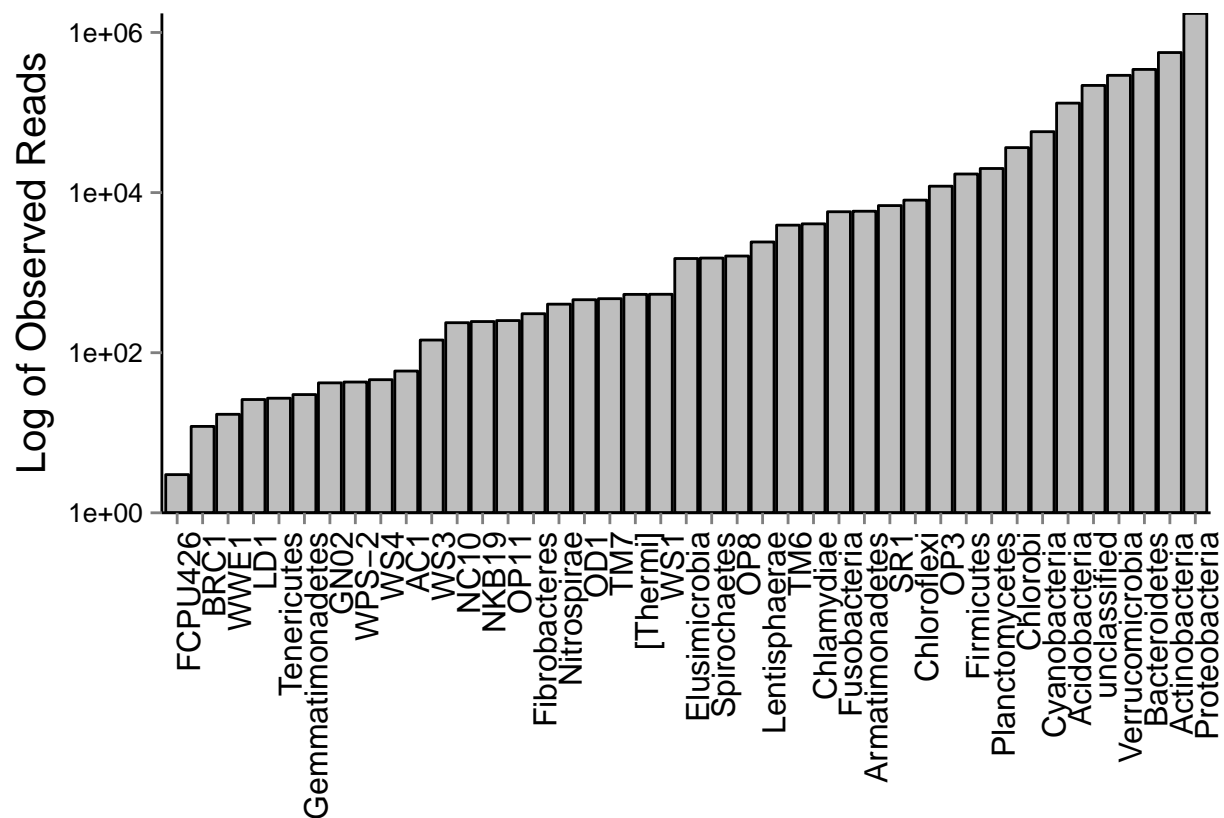


Figure S3. Forty phyla were identified over the entire NTL-MO time series. See Table 1 for lake abbreviations; the third letter indicates the sampling depth as “E” for epilimnion and “H” for hypolimnion. A) The most abundant phyla were Proteobacteria, Actinobacteria, Bacteroidetes, and Verrucomicrobia. Reads that could not be classified into a phylum were the fourth most abundant category. Candidate phyla members such as OP3 and SR1 are present in this dataset.

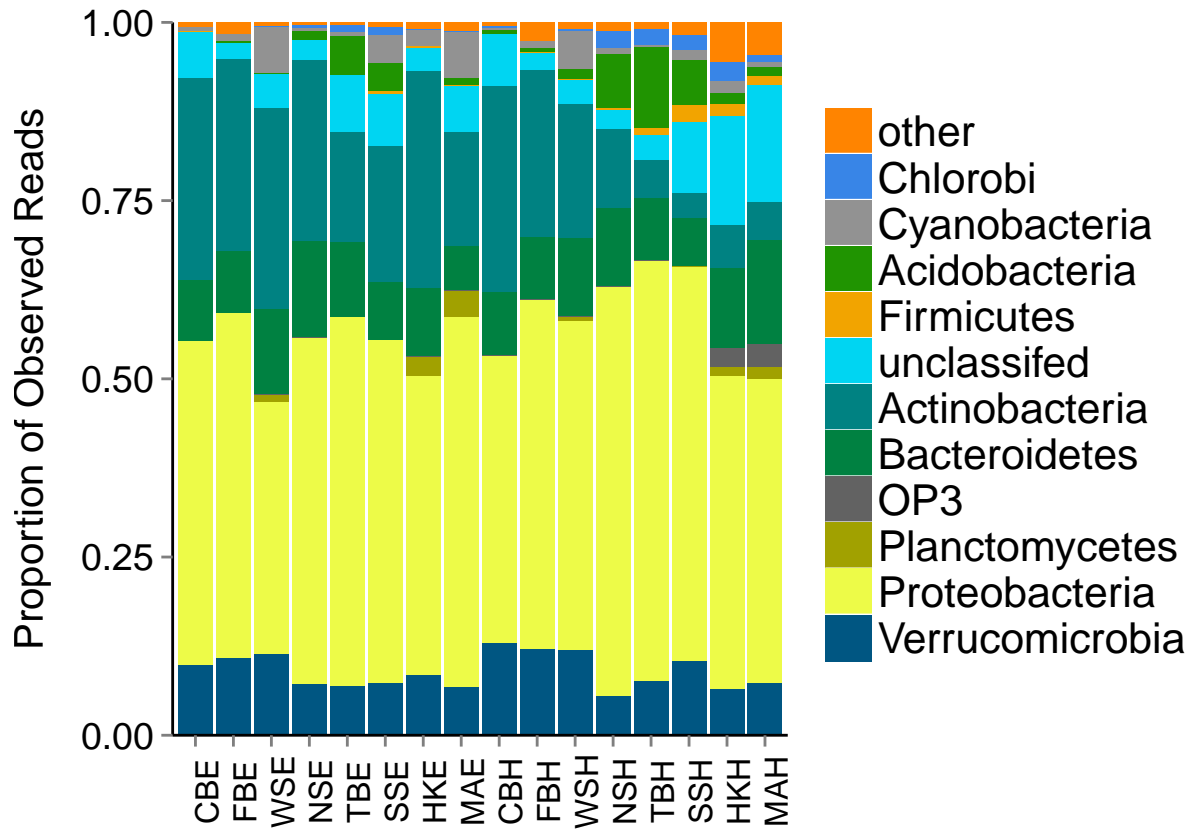
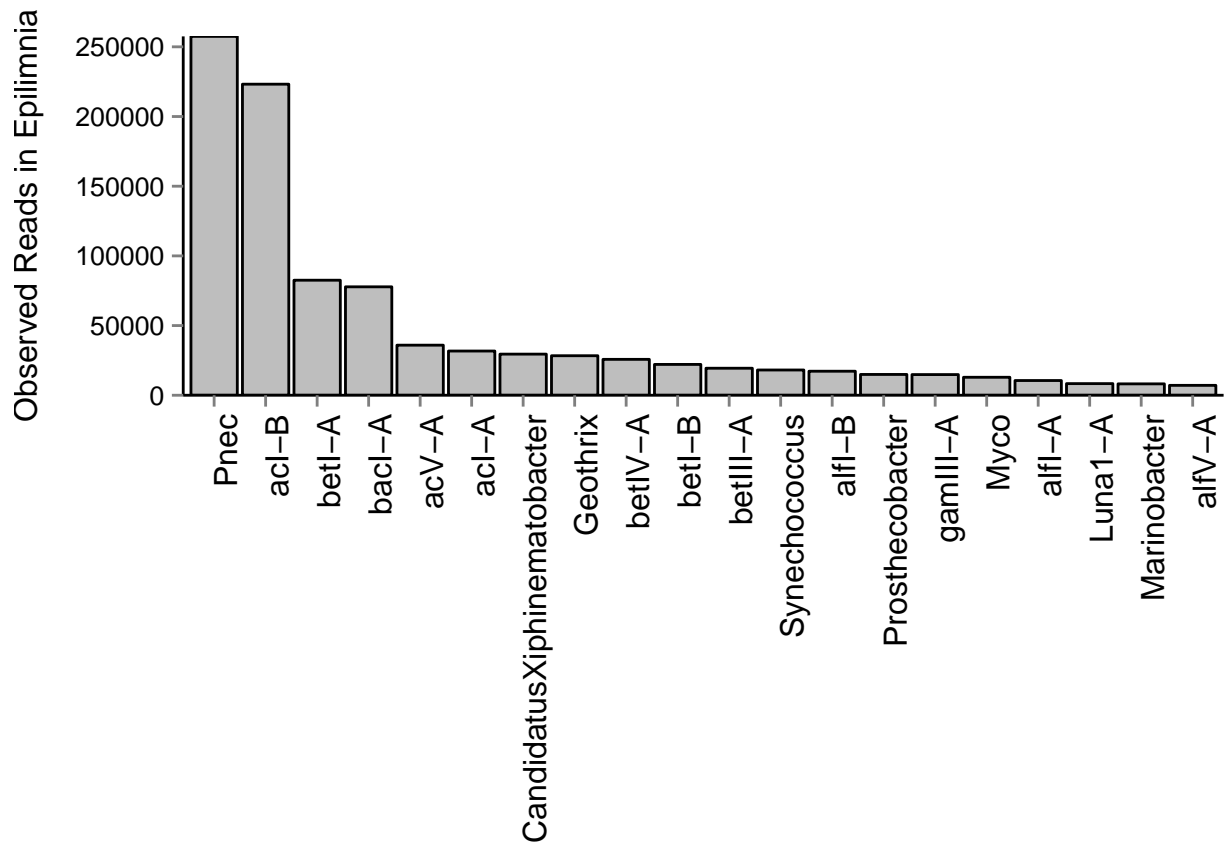


Figure S4. Phylum-level community differences were compared between layers and lakes. Epilimnion samples were relatively similar across all lakes, with the exception of the presence of Planctomyces in HKE and MAE, the epilimnia of the two meromictic lakes included in this study. Hypolimnion samples showed a trend of decreasing Actinobacteria with total lake depth, while the numbers of unclassified bacteria and other phyla (those comprising less than 8,000 reads in the dataset) increase with total lake depth. The sampled communities in hypolimnia of dimictic lakes (NSH, TBH, and SSH) contained higher levels of Acidobacteria than the other categories.



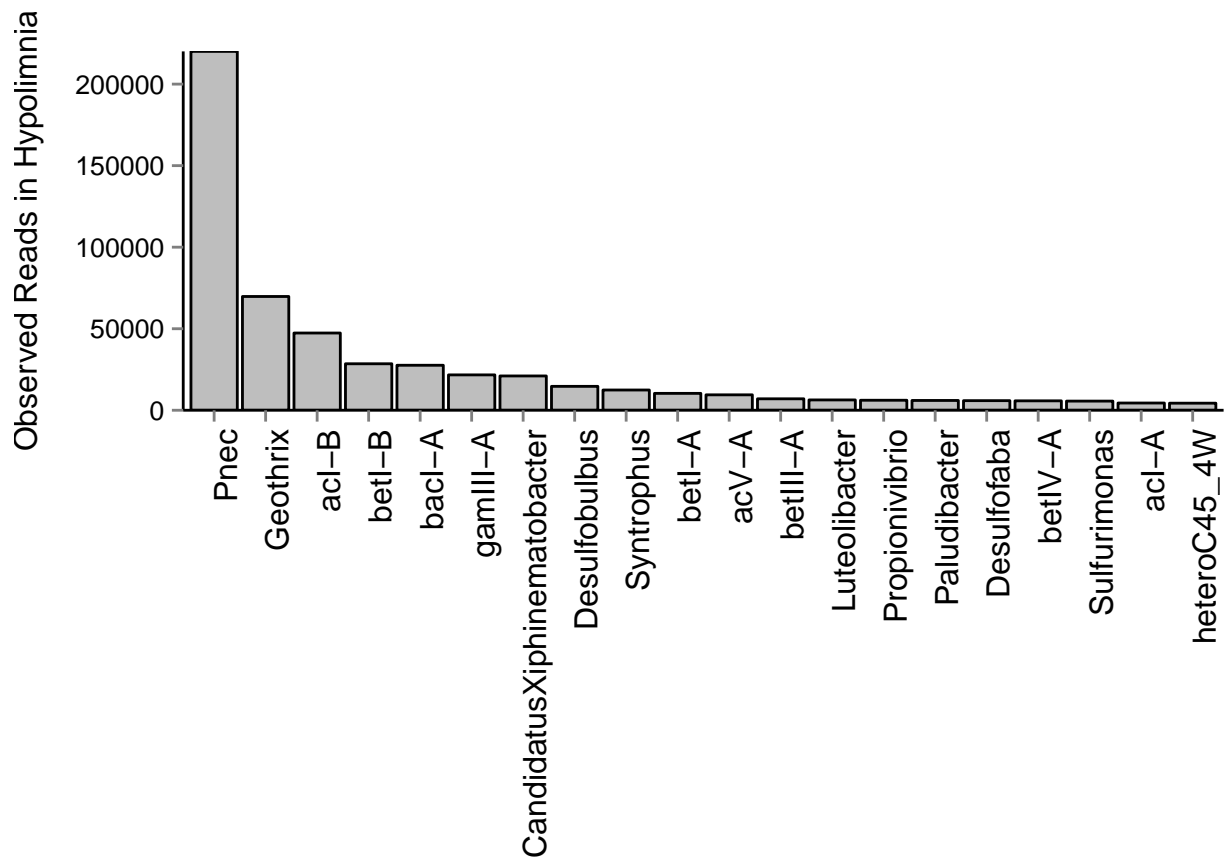
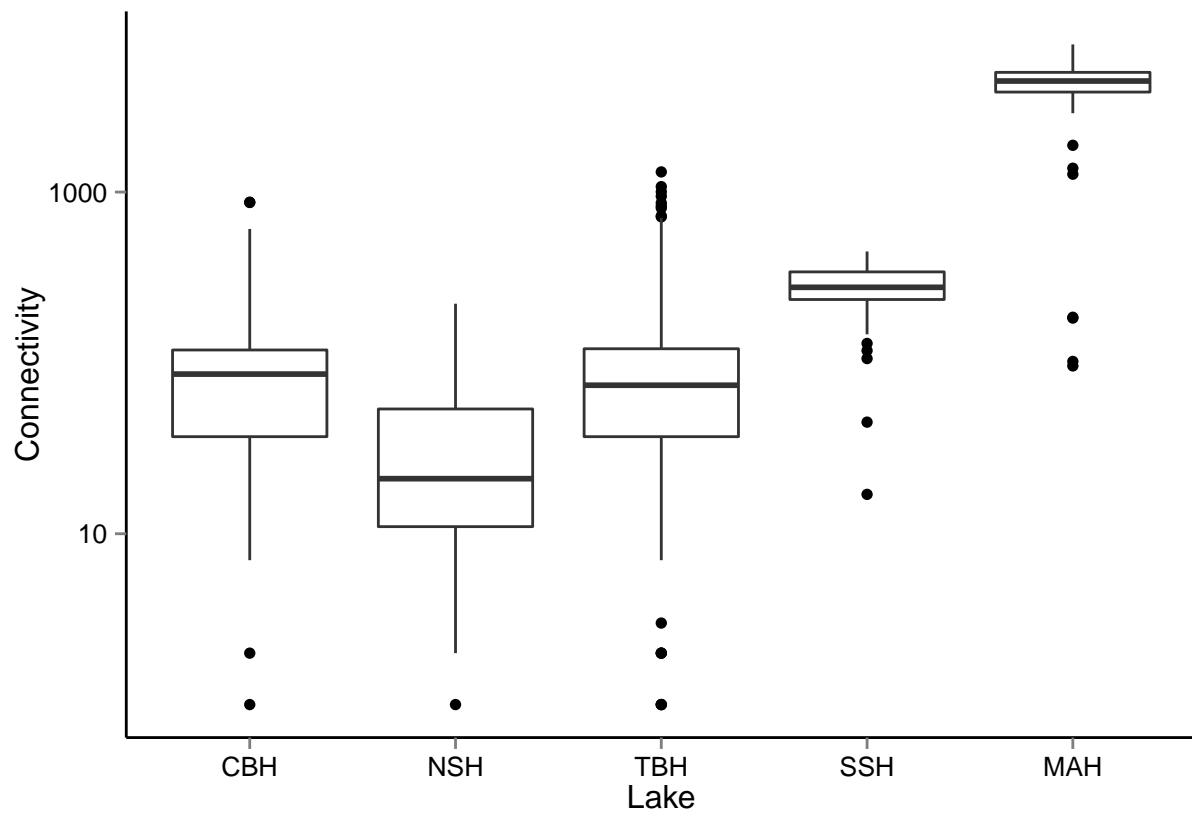


Figure S5. Rank abundance of the 20 most abundant clades in epilimnia samples. Total reads in all epilimnia samples have been summed for each clade-level group. Names represent the last classified level of taxonomic information for that clade; for example, the designation “Bacteria” indicates that clades unclassified at the phylum level are the fifth most abundant group in these samples. The most abundant groups in epilimnia are Pnec, acI-B, betI-A, and bacI-A.

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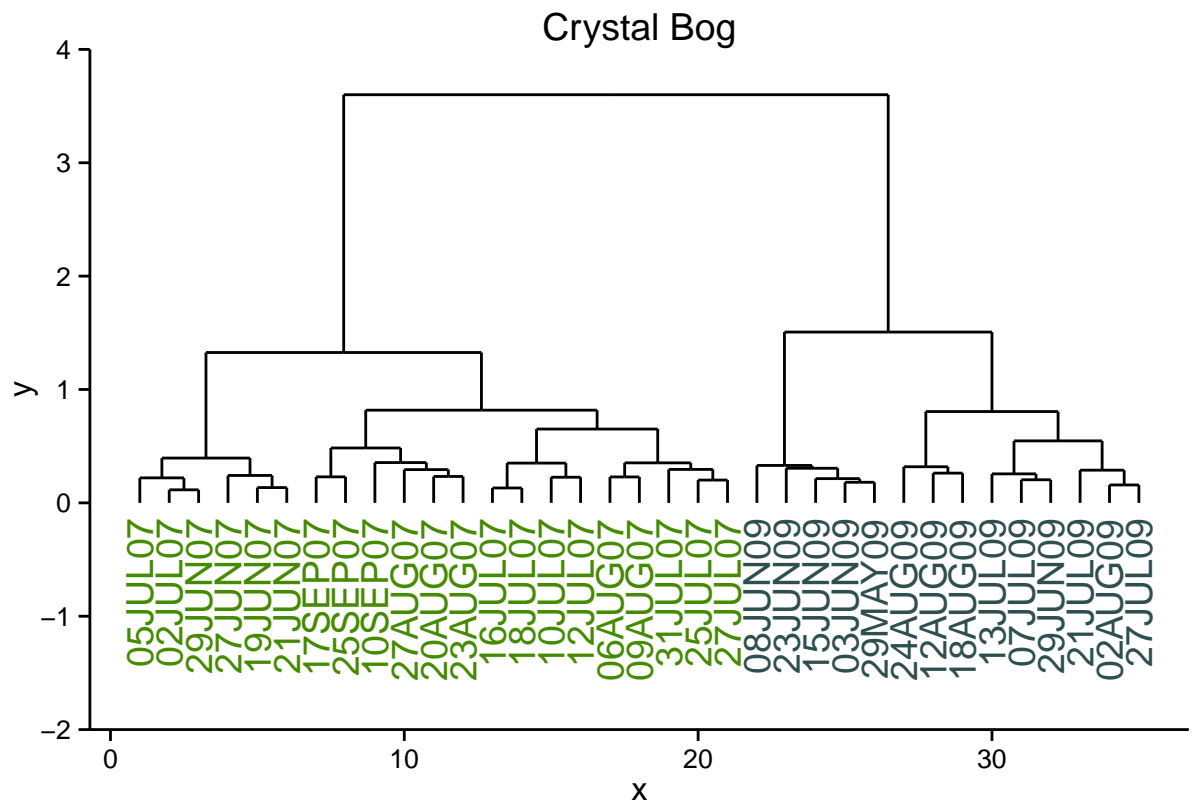
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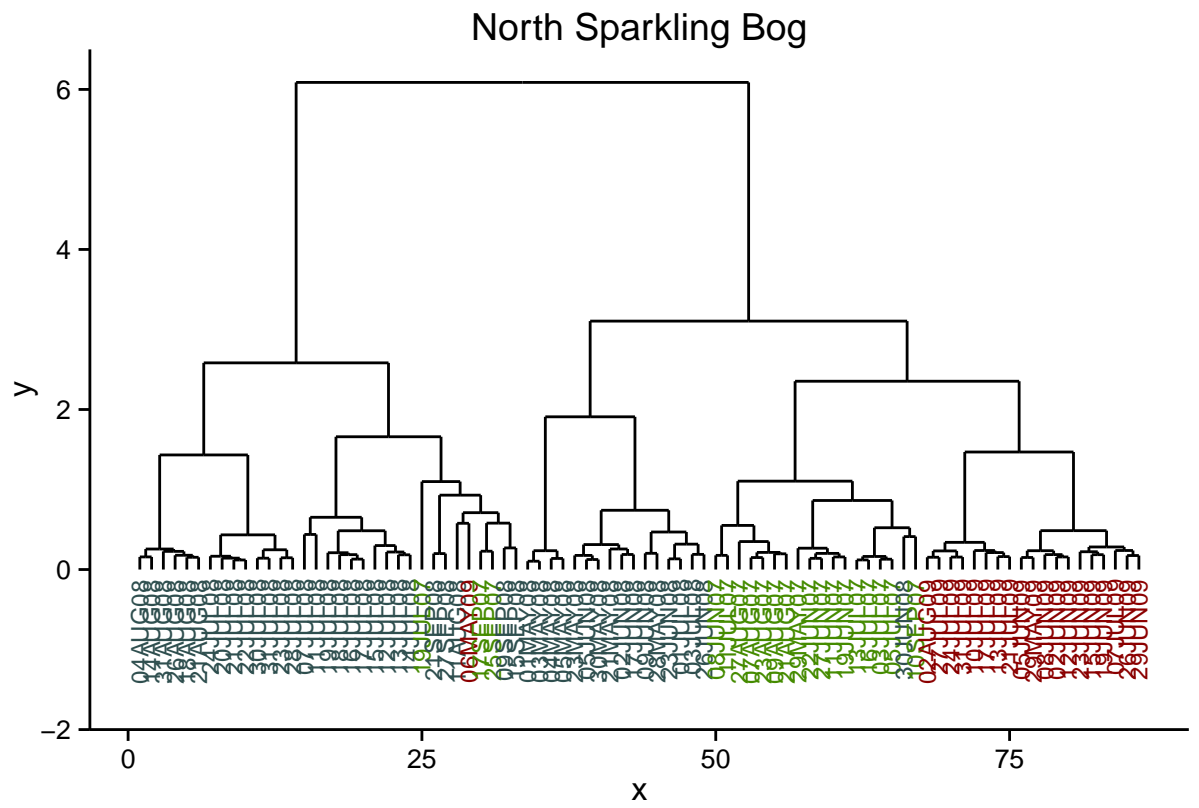


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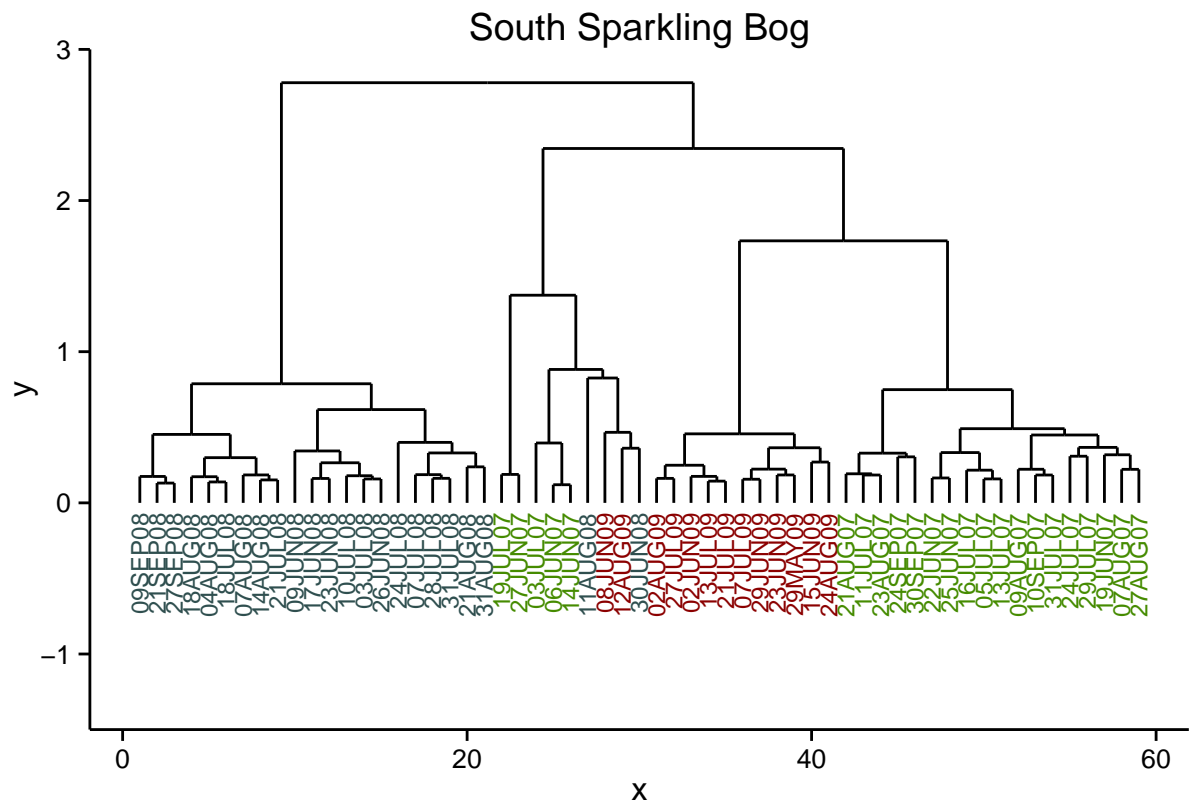
**Figure S6. Connectivity between hypolimnia.** Connectivity was measured as the number of edges connecting each OTU multiplied by the abundance of that OTU in a given sample, then summed for the given sample. When the amount of connectivity is compared for lakes with multiple years of sampling, Mary Lake has higher connectivity, followed by South Sparkling Bog. The only lakes that are not significantly different are CBH and TBH.



of all bogs-1.pdf



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####Figure S7. Hierarchical clustering of samples over years. This analysis was performed on hypolimnia with multiple years of sampling. All hypolimnia except for that of Mary Lake show strong clustering patterns by year (see main figures)