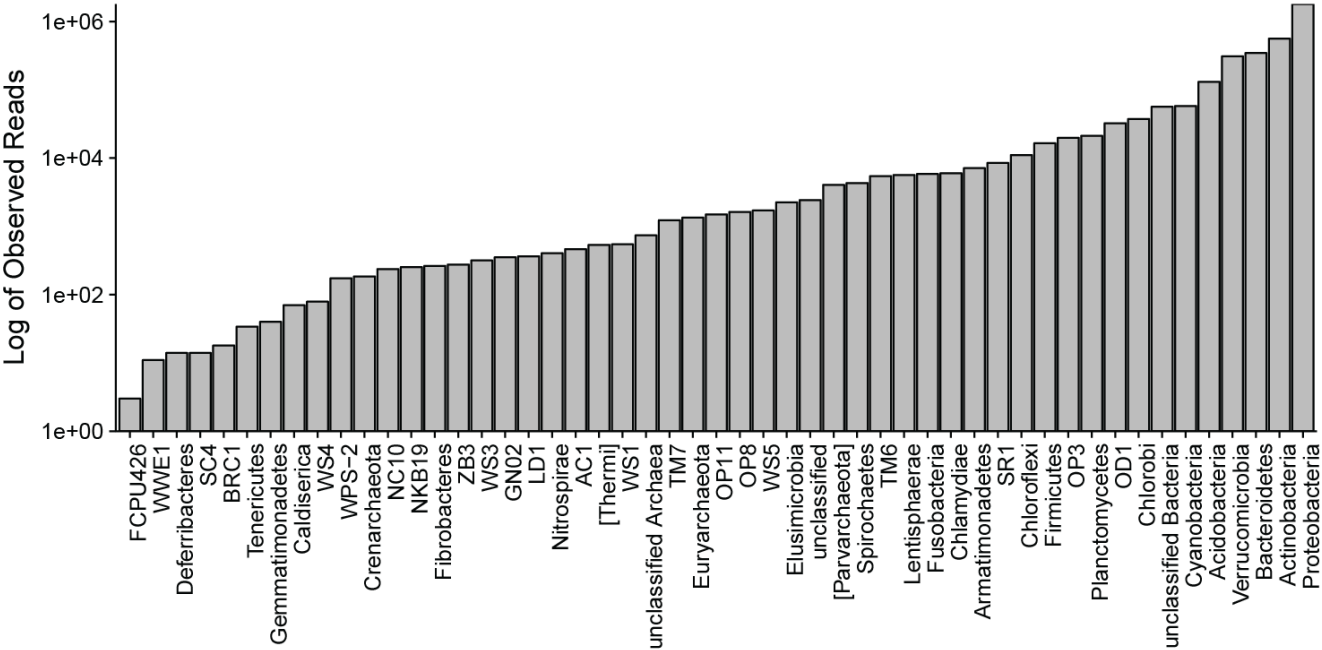


1 Supplemental Figures



2 Figure S1. Phylum rank abundance in entire dataset.

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Table S1. Means and standard deviations in the number of taxa by lake and layer.

	<u>Epilimnion</u>		<u>Hypolimnion</u>	
	Mean	Standard Deviation	Mean	Standard deviation
<i>Crystal Bog (CB)</i>	129	28	148	31
<i>Forestry Bog (FB)</i>	109	32	145	57
<i>West Sparkling Bog (WS)</i>	150	45	182	56
<i>North Sparkling Bog (NS)</i>	143	33	178	40
<i>Trout Bog (TB)</i>	148	38	186	38
<i>South Sparkling Bog (SS)</i>	191	57	191	54
<i>Hell's Kitchen (HK)</i>	199	67	397	124
<i>Mary Lake (MA)</i>	259	67	477	110

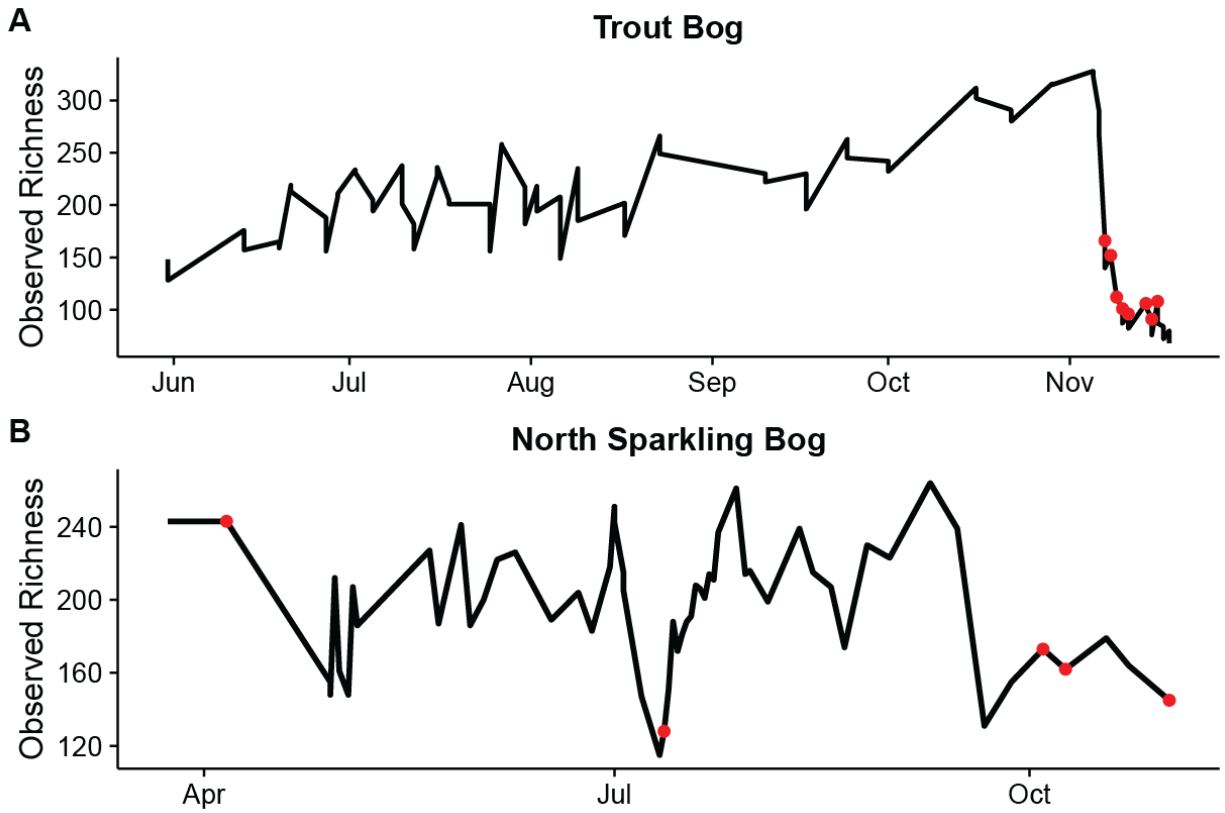
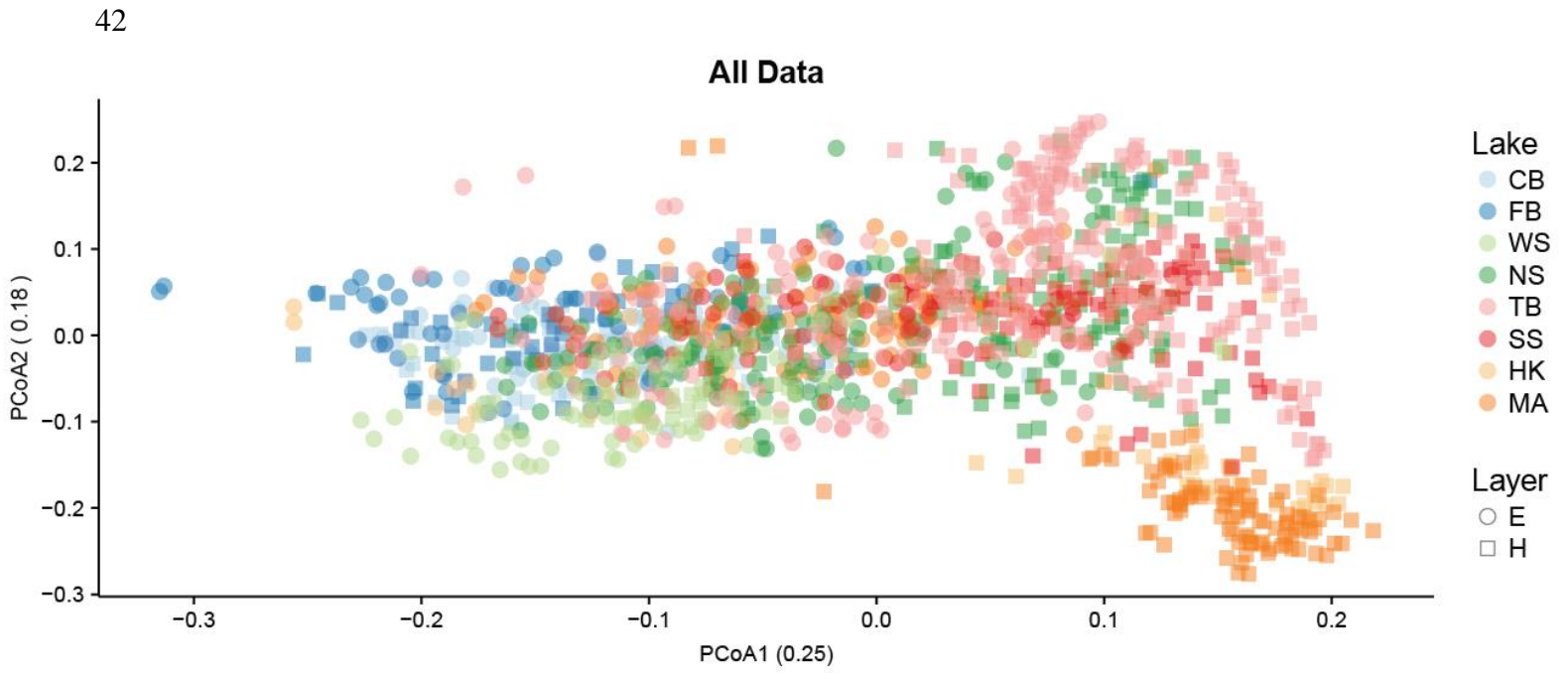


Figure S2. Richness over time during mixing events.



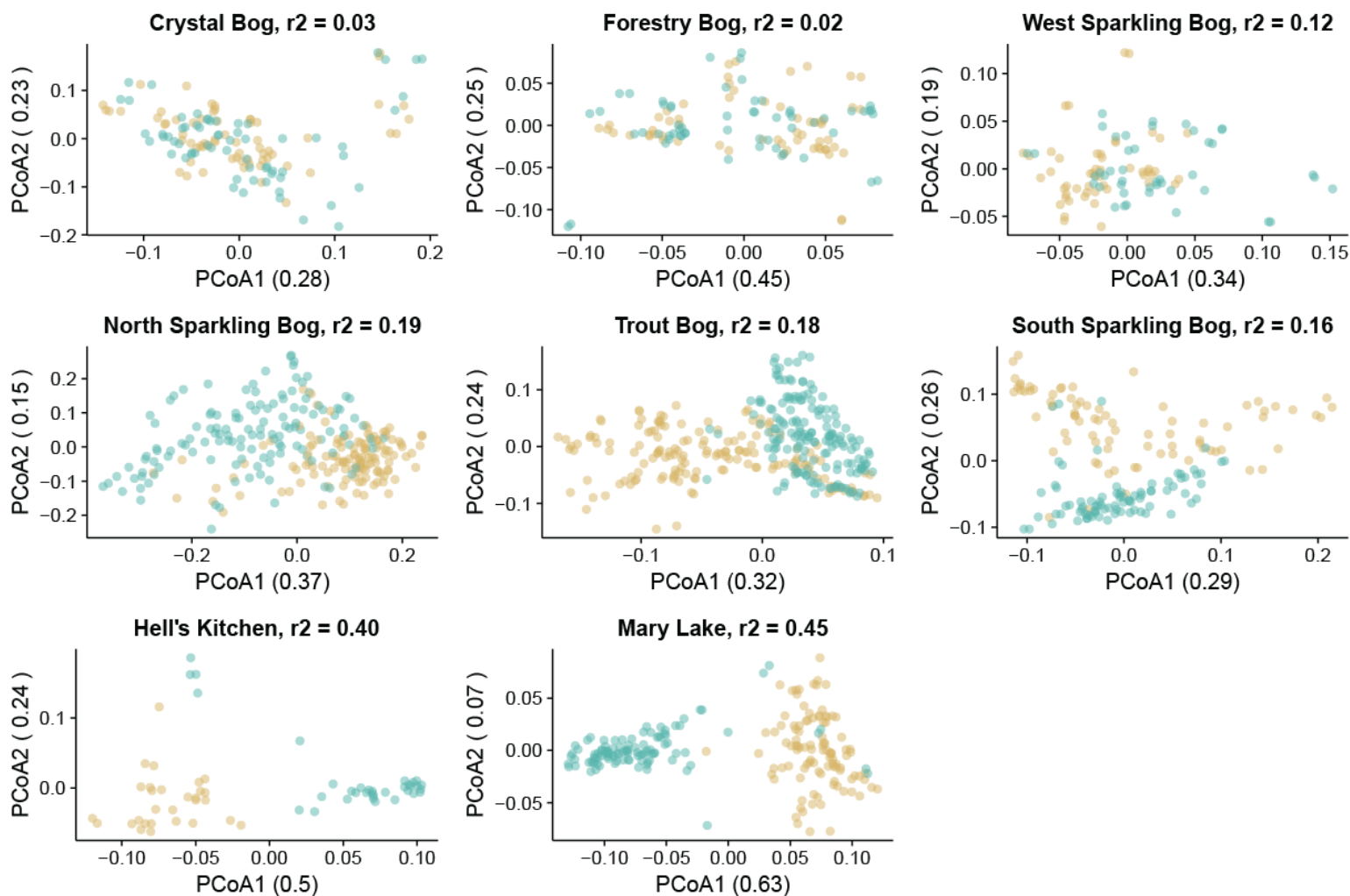
43 **Figure S3. PCoA of all data points with a layer designation.**

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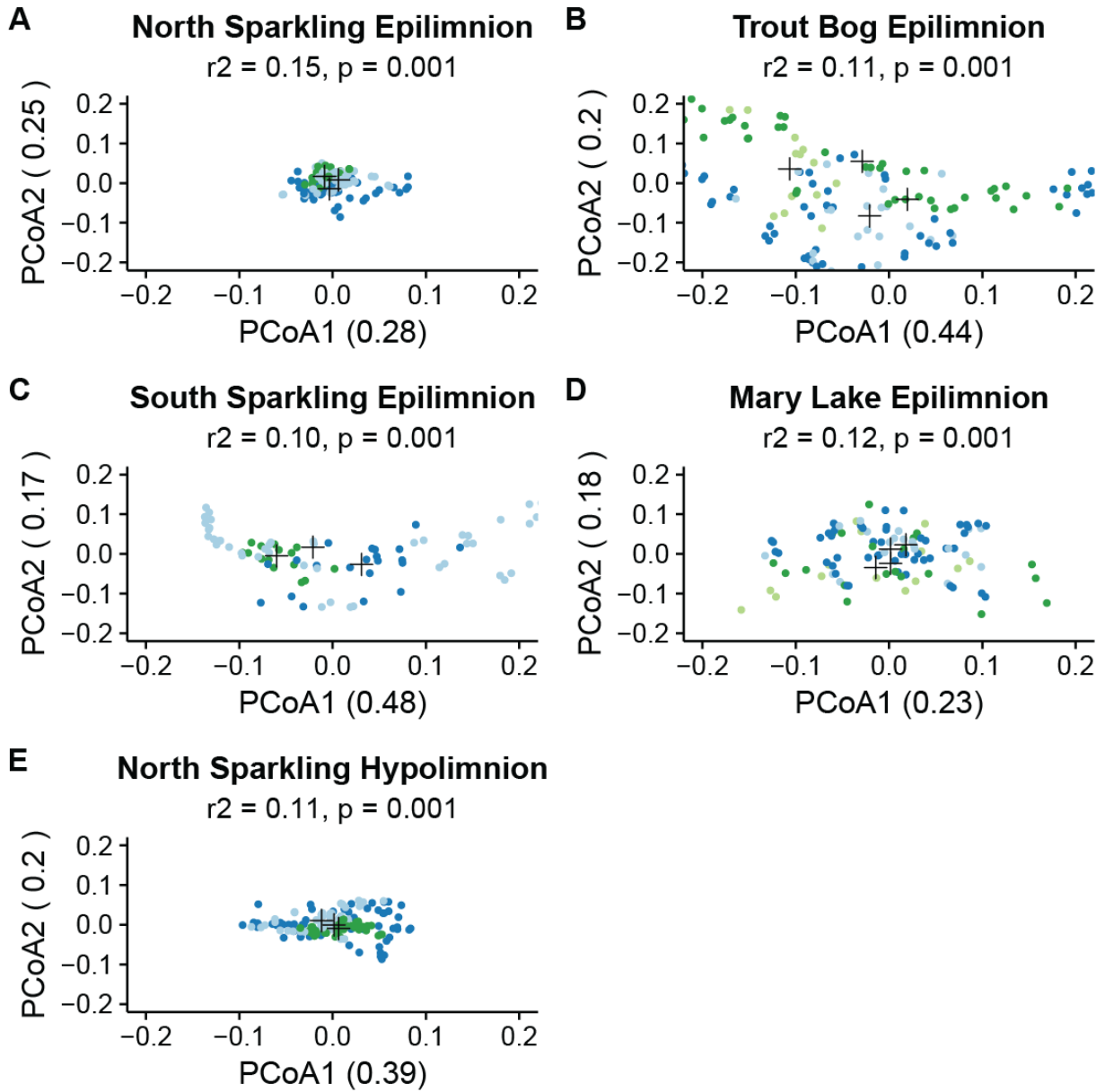
50 **Figure S4. Layers cluster within lakes.**

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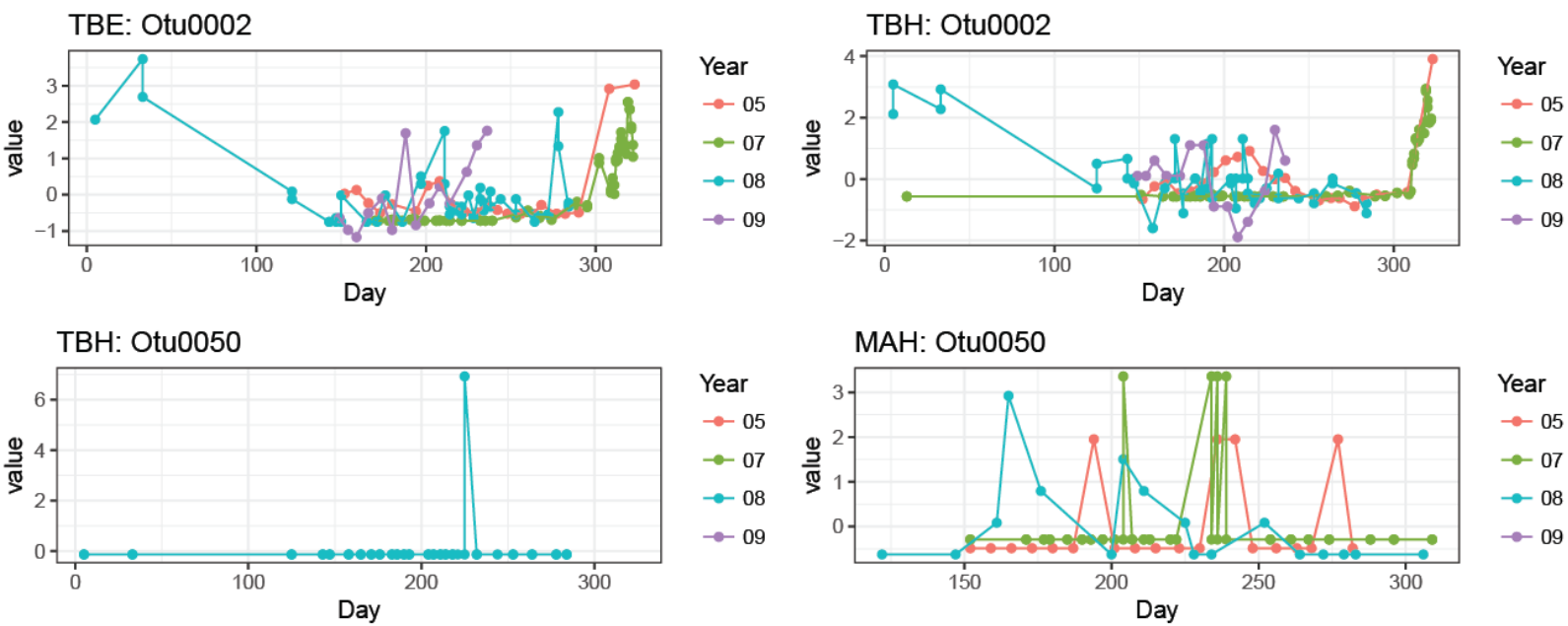
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56 **Figure S5. PCoA of extra epilimnia and hypolimnia by lake by year.**

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59 **Figure S6. Annual trends in OTUs.**

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```

80 library(OTUtable)          # You will need these three packages
81 library(ggplot2)
82 library(reshape2)
83 data(otu_table)            # Load the OTU table
84
85 # Write function to plot multiple years at once.
86 annual_trends <- function(lake, otu){
87   bog <- bog_subset(lake, otu_table)
88   year1 <- year_subset("05", bog)
89   year2 <- year_subset("07", bog)
90   year3 <- year_subset("08", bog)
91   year4 <- year_subset("09", bog)
92
93   # Since sites have different years sampled, these if statements identify which years are present
94   if(dim(year1)[2] > 0){
95     # Once years present are identified, normalize and combine into a single table
96     year1 <- zscore(year1)
97     year2 <- zscore(year2)
98     year3 <- zscore(year3)
99     year4 <- zscore(year4)
100
101     ztable <- cbind(year1, year2, year3, year4)
102   }else if(dim(year1)[2] == 0 & dim(year3)[2] > 0){
103     year2 <- zscore(year2)
104     year3 <- zscore(year3)
105     year4 <- zscore(year4)
106
107     ztable <- cbind(year2, year3, year4)
108   }else if(dim(year1)[2] == 0 & dim(year3)[2] == 0 & dim(year4)[2] > 0){
109     year2 <- zscore(year2)
110     year4 <- zscore(year4)
111
112     ztable <- cbind(year2, year4)
113   }else{
114     ztable <- zscore(year2)
115   }
116   # Format the final table
117   ztable <- melt(ztable)
118   ztable$Year <- substr(ztable$Var2, start = 9, stop = 10)
119   ztable$Day <- format(extract_date(ztable$Var2), format = "%j")
120
121   # Save the results for plotting
122   plot <- ggplot(data = ztable[which(ztable$Var1 == otu), ], aes(x = Day, y = value, group = Year, color = Year)) +
123   geom_point() + geom_line() + theme_bw() + labs(title = paste(lake, otu, sep = ": "))
124   return(plot)
125 }
126
127 # Example Usage – 3 letter site code includes 1st 2 for site (see Table 1) and letter 3 for layer (E = epilimnion, H =
128 hypolimnion. OTU designation is case sensitive, and number must contain 4 digits.
129 plot_this <- annual_trends("TBE", "Otu0012")
130 plot_this
131 # You may get warning messages about points being removed. That means the OTU was not present in those points
132 # If all points were removed and no plot is produced, it was not present in that site
133
134
135

```

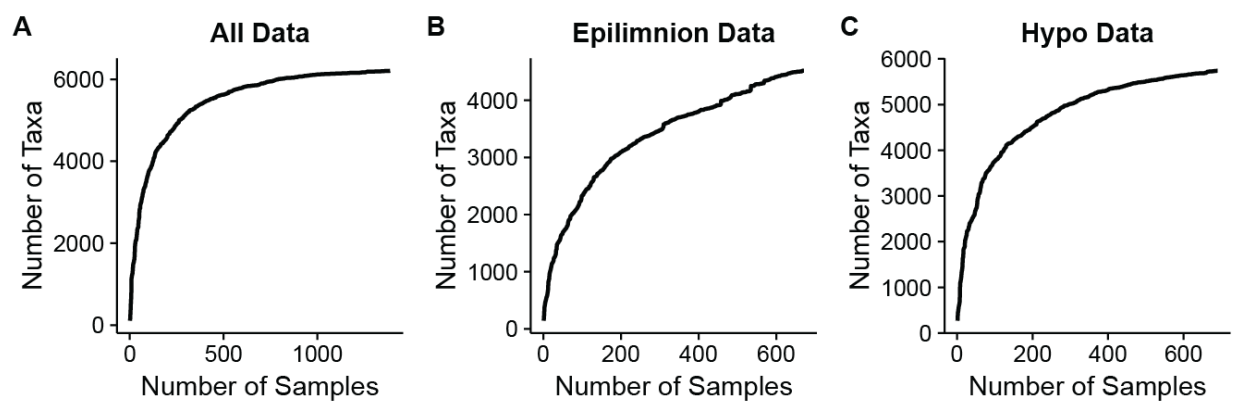



Figure S7. Rarefaction curves.

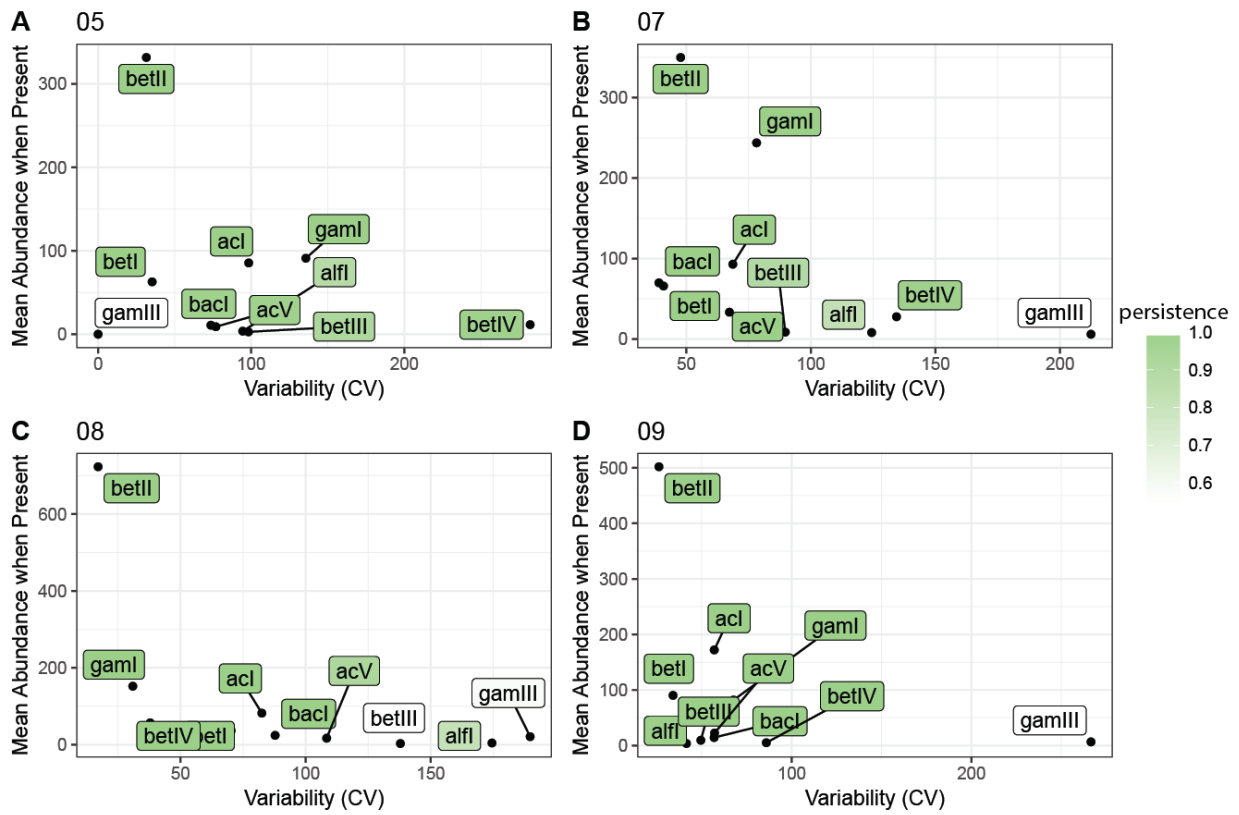


Figure S8. Lineage traits by year.