Data summary PMNM coral and symbiont isotope analysis

I. C:N in host and symbiont fractions

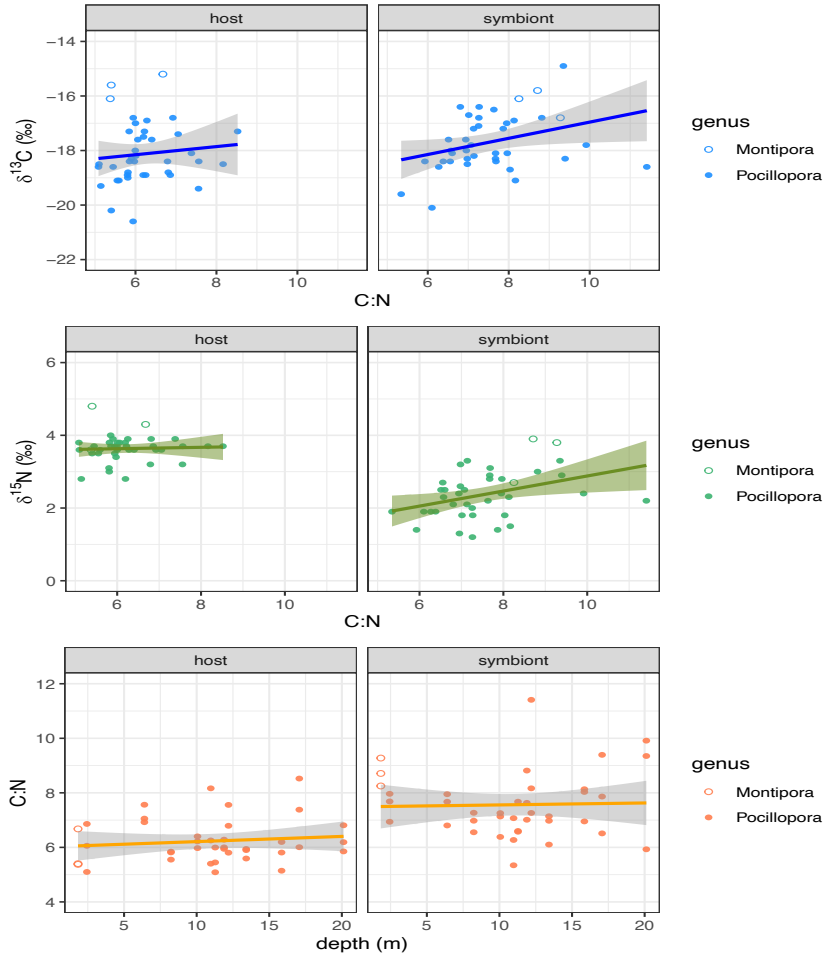

Figure 1. Diagnostic plots and examining C:N patterns

Overview: These figures (Figure 1A-C) have both *Montipora* and *Pocillopora* presented to see overall patterns and see how data processing and holobionts are affecting isotope values.

Overall, there is a positive trend for C:N and d13C in the samples, which can indicate a degree of skeletal carbonate contamination in the samples (which drive increased d13C values [ie., closer to zero]). However, I see this as unlikely, considering we filtered samples through nitex mesh (20 um) and the pattern is largely driven by a few outliers the symbiont-d13C values.

In addition, there is a positive trend in C:N and d15N of the symbionts, which reinforces that there is a biologically relevant reason for increasing in C:N correlating with increased d13C and d15N. However, we do not see a change in C:N with depth, which might have been important.

Take home: the analysis and processing were done well and we see positive patterns between C:N and carbona and nitrogen values, although this trend a few samples. I'm not concerned and think we can move past this QA/QC, although comparing this to Mario's data would be a good idea.

Significant effects: *Pocillopora* only: C.N vs. d13C, C.N vs. d15N

II. d13C and d15N in host and symbiont fractions

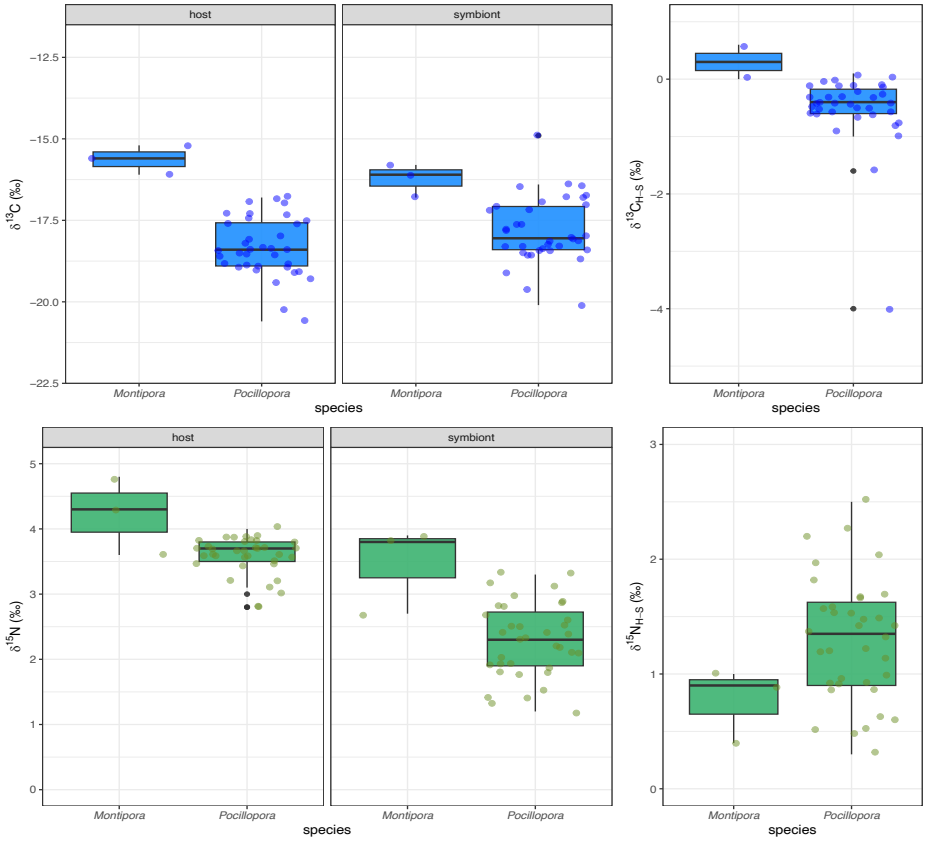

Figure 2. Host and symbiont d13C (*top*) and d15N values (*bottom*) and difference in host symbiont values for *Montipora* and *Pocillopora*.

Overview: This is pooled isotope values across all sampling location. We see *Montipora* (even at a very low sample size) is distinct from *Pocillopora*, motivating excluding this species from further analysis, and high degrees of heterotrophic reliance in Pocillopora.

Using the d13C, we see *Pocillopora* has a more negative values in hosts and symbionts compared to *Montipora*. This is likely driven by (1) fewer symbionts and greater fractionation, (2) and greater reliance on heterotrophy. The latter point is emphasized by the greater (and more negative) difference in host and symbiont for *Pocillopora*.

Using d15N values, we see the same pattern. There are clear differences in the two species, and lower d15N values for the host and symbiont in *Pocillopora*. Interestingly, we see higher d15N values in *Montipora* and its symbionts (albeit with low replication). However, we see a much more positive difference in d15N host-symbiont, again emphasizing differences in nutrient cycling in the two corals and a greater reliance on heterotrophy in *Pocillopora*, even if *Montipora* is showing signs of higher d15N in the host.

Take home: *Pocillopora* shows more negative d13C and d15N values, compared to *Pocillopora*. The exact drivers of this are not clear, but we see a consistent pattern of greater differences between hosts and symbiont d13C and d15N which are in agreement with high rates of heterotrophy.

Significant differences: *Pocillopora* alone: host vs. symbiont d13C, d15N, C:N

III. Drivers of change in d13C and d15N

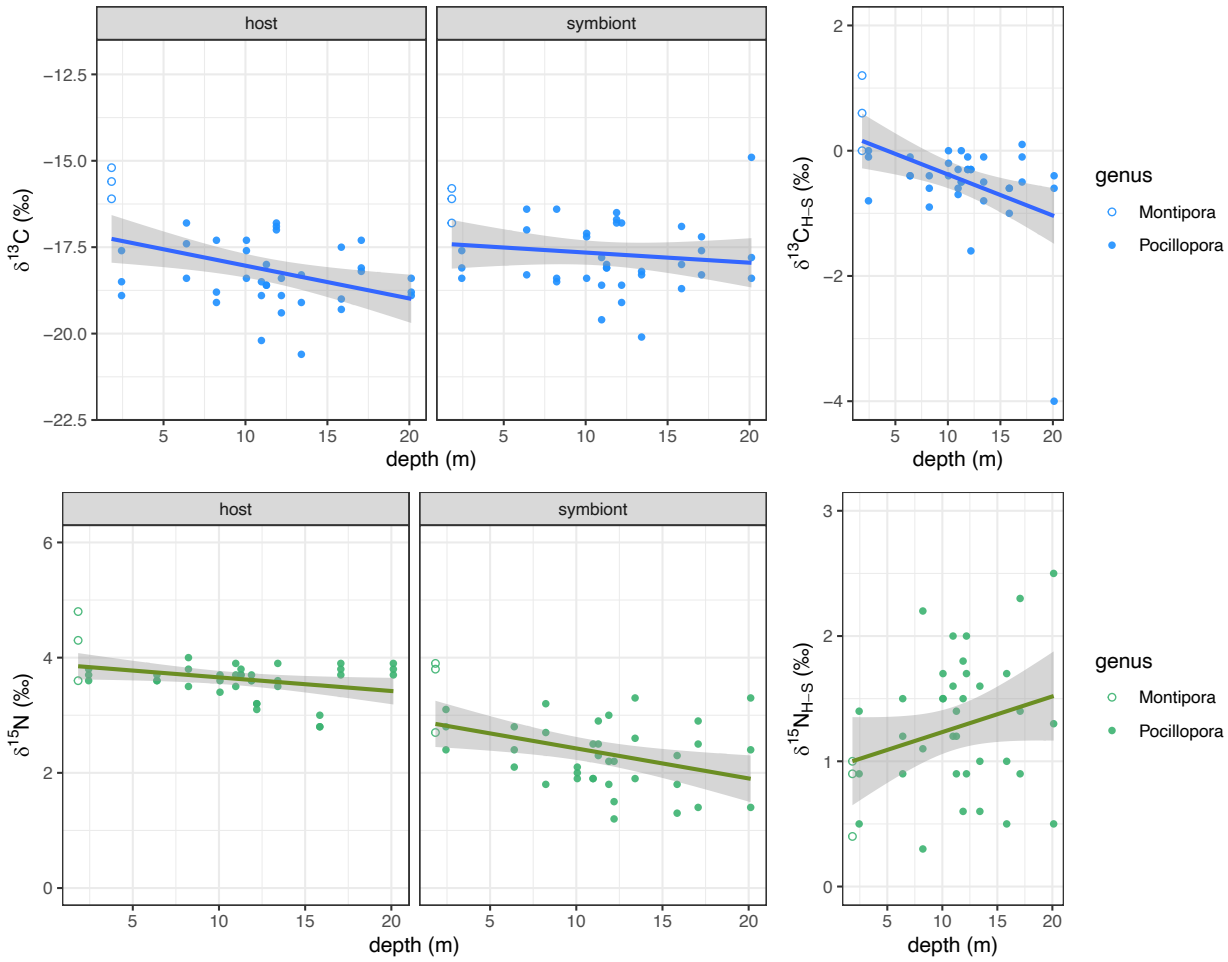

Figure 3. Pooled *Montipora* and *Pocillopora* d13C and d15N values across depths.

Overview: Depth is important in shaping carbon isotope values as it relates to changes in photon flux, photosynthetic rates, and therefore 13C discrimination. We see a pattern with decreasing host (d13C) and symbiont (d15N) values with depth, which also correspond to increased heterotrophy (determined from change in host and symbiont values).

In the pooled data, we have stronger patterns for these depth association, since the highest d13C and d15N values observed are in *Montipora*, which were in shallow backreef habitats. This helps us understand why isotope values of the host and symbiont (when pooled across habitats) were as high as they were. When we remove *Montipora*, most effects are NS, but there are marginal trends across the dataset. n the values found in the shallow.

Take home: There are trends in the depth x isotope data, but not enough replication and or low sample size to draw large conclusions about depth dependence here.
Significant trend: *Pocillopora* only d13C host-symbiont x depth (p=0.053).

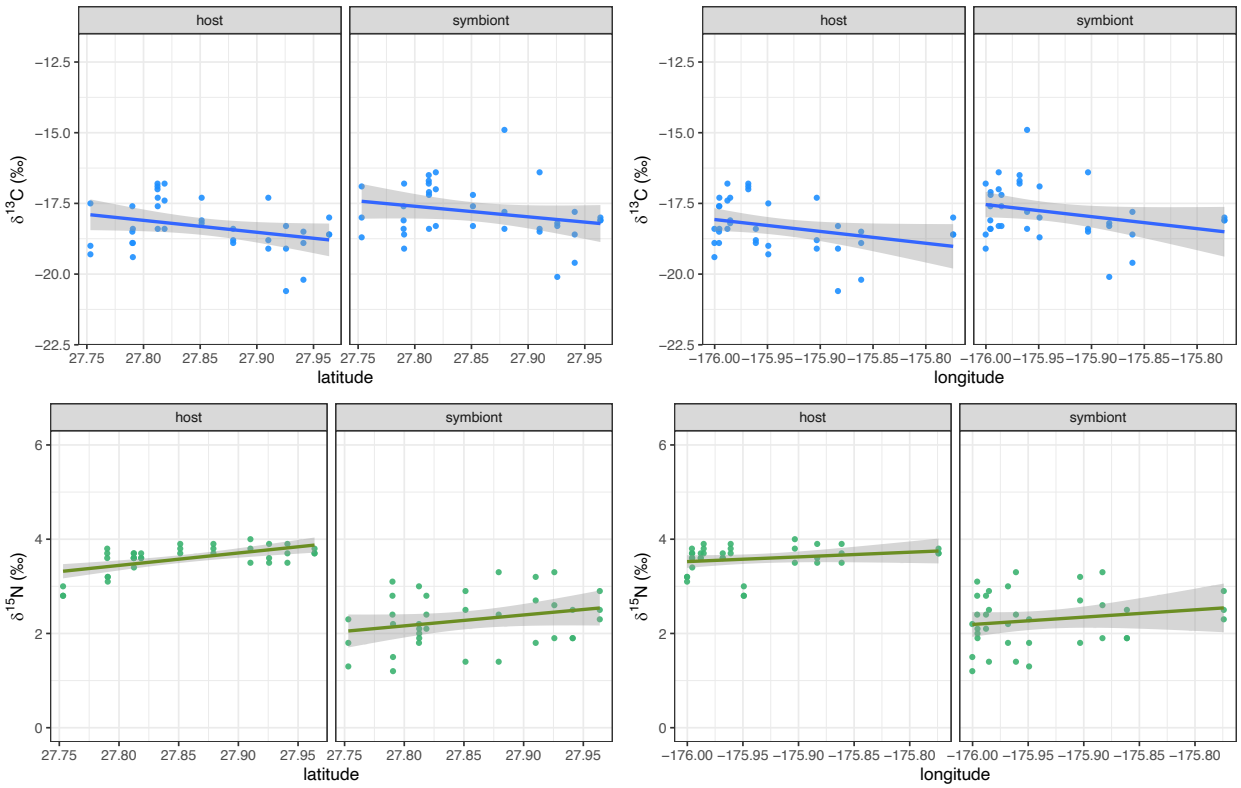

Figure 4. *Pocillopora* d13C and d15N values across latitude (*left*) and longitude (*bottom*).

Overview: Spatial patterns exist in isotope values across latitude, longitude for d13C and d15N, but the explanatory power is limited.

Spatial patterns across PHA exist for *Pocillopora* isotopes values. While these patterns are not strong, they are important in considering spatial differences in nutrition and isotope values which are also influenced by depth.

Take home: patterns exist in host, but they are weak. However, latitude and or longitude might be important in an analysis of covariance (ANCOVA) with depth as a covariate (or visa vera).

Significant trends: latitude effects on d13C host and symbiont ($p<0.08$). Longitude shows marginal trend for host d15N ($p=0.051$). No pattern for host-symbiont for carbon or nitrogen.

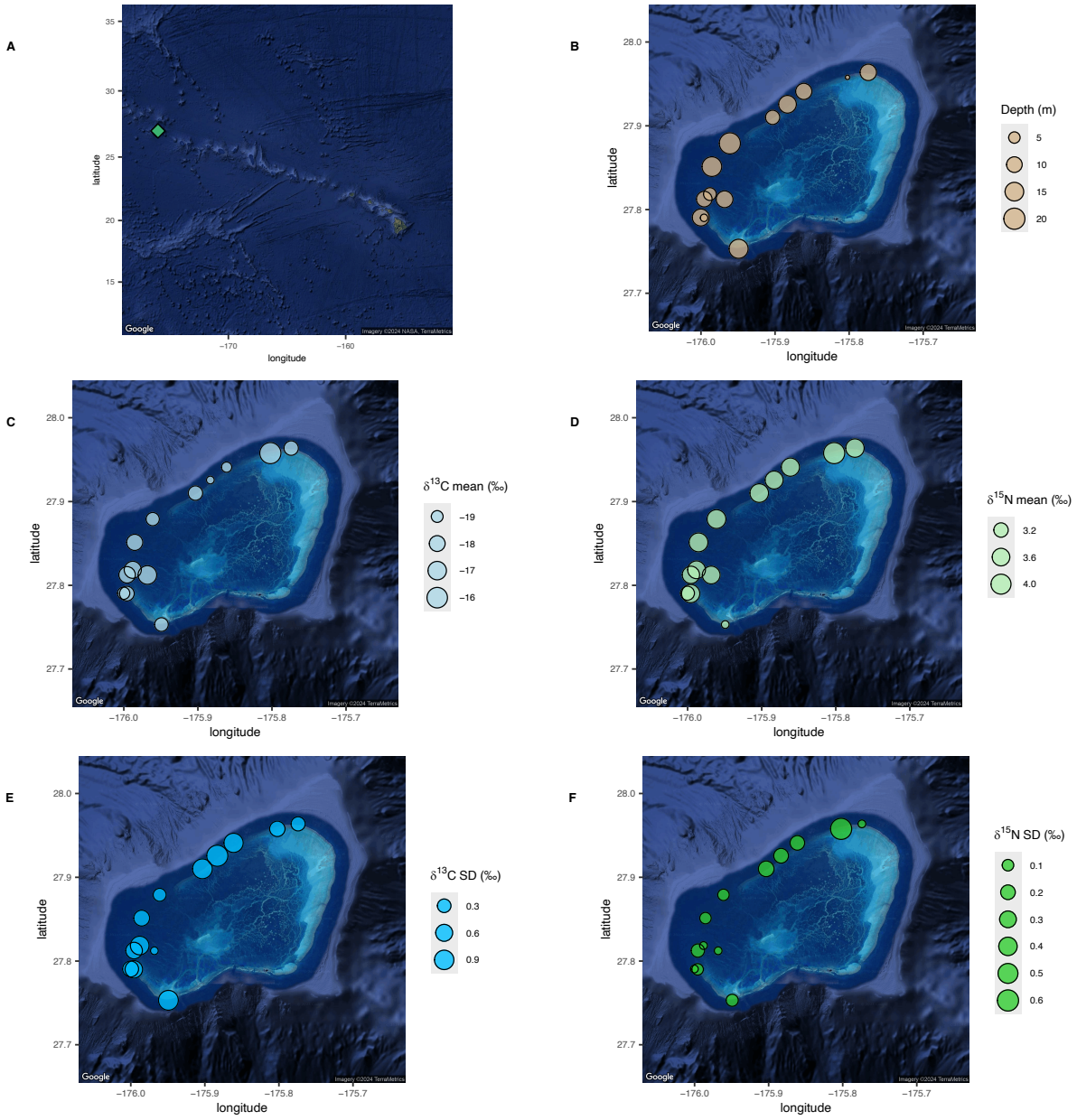

Figure 5. Maps showing *Pocillopora* sampling location and collection depths (*top panel*), host d13C and host d15N mean values (*middle panel*) and standard deviation (*bottom panel*). At each location, 3 corals were sampled.

<u>Take home</u>: patterns in carbon and isotope values across latitude and longitude are nested within depth changes. Accounting for these patterns will be important in determining the spatial effects on corals at PHA (and sources of nutrients).

It is notable that there is less variance in coral d15N samples at the western edge (lowest lat-long), and these values are generally lower than other locations, although this effect size is small. Possibly due to more oceanic influence?