November 5 meeting agenda

- 1. Review proposal revisions
 - a. Introduction
 - b. Random forest
 - i. Markers are input; telling us different things with different inputs so its telling us two ways
 - c. Does intention for each aim connect better with the broad question
 - i. Sentence that
 - d. Research objectives
 - i. Redundancy is ok because each part is marked individually. About 1 page is ok
 - e. Overall comments & suggestions since last week

2. Revised figures

- a. Aim 1 alpha diversity
 - i. Remade figures with revised parameters; addition of indicator taxa
 - ii. Theme.classic; geom_points in box plot overlayed (looks nicer); increase Y-axis
 - iii. Take max value and *0.5
- b. Aim 2 alpha diversity
- c. Aim 1 & 2 beta diversity
 - i. Add ellipsoids for clusters
- d. Aim 3: core microbiome analysis
 - i. Changed to 0.01 and 0.5 (prevalence); plot that was asked by chris
 - ii. Taxa barplot analysis: get good overview with rare species instead of core microbiome (unique microbes that are highly prevalent and shared between/different between groups); look at all the ASV's but also could show bottom most rare species (top 80 and bottom 20 as separate plots)
 - iii. Save coremicrobiome as back up if nothing else works out
- 3. Moving forward
 - a. DeSeq
 - b. Literature interpretation for revised figures

Action Items for next meeting

- 1. Theme.classic; geom points in box plot overlayed (looks nicer); increase Y-axis
- 2. Dpi = 300
- 3. Figures
 - a. Aim 1 alpha diversity + beta + indicator species (significance built in)
 - i. Eli aesthetic fixes. Otherwise done.
 - ii. Eli Indicator species.
 - b. Aim 2 beta diversity + indicator species (significance built in)

- i. Caro to send code to chris.
- ii. Caro Indicator species.
- c. Core microbiome/taxa barplots
 - i. Asha
 - ii. Highlight first 3 columns that are unique in old,PMS
- d. DeSEQ + PICRUSt2 (depending on data if it can be included together)
 - i. Poppy + Eli + Burak
 - ii. LDEX2: better for microbiome data
 - iii. Get list of microbes and log fold change; can order it and see which ones are similar from two algorithms to confirm that groups are different
 - iv. Old PMS NS + Old PMS smoker
 - 1. Justification of why we're doing this; age related or more smoking related. Go off of data
- e. Project = niche markers that can be used for random forest