**Background from Prior Steps**

**Experimental Design, Sampling, and Extraction Notes:**

**Target (R16S, ITS, shotgun):**

**Library structure:**

**Quality Control Considerations:**

Technical noise removal (critical for mapping):

Batch effects (y/n, evidence):

Reference genome quality:

**Amplicon Sequencing Results**

(remove if shotgun)

**ASV or OTU:**  
 Software used with version (Mothur, dada2, qiime2):  
 Databases used with versions:

Parameters (cut offs, etc):

Number of ASVs/OTUs produced:  
 Summary table of filtering (dada2):

**Taxonomy stack plots:**

**Shotgun Sequencing Results**

(remove if amplicon)

**Abundance or Presence/Absence?**

**Assembly (y/n, software and version):**  
 Binning software and version:  
 # of bins:  
 checkM results of bins:  
 reassembly (y/n, details):  
 final assembly stats (N50s, completeness, contamination, strain het.):

**Databases used with versions:**

**Krona screenshot:**

**Stack Plots:**

**Taxonomy Results**

**Strategy (Presence/Absence. Abundance):**

Software used (with versions):  
 common examples: EdgeR, DESeq2, Kraken, Bracken, Krona, KrakenTools, kraken\_biom, phyloseq

**Rarifaction curve:**

**MDS or other ordination:**

Software used:  
 Variation explained:  
 Noisiness of samples:  
 Plot:

**Alpha Diversity:**

Strategy (e.g. Shannon, Simpson, Chao1):  
 Software used (e.g. KrackenTools, kraken-biom, phyloseq)  
 Taxonomy filters:

Prevalence filters:

Plots:

**Beta Diversity:**

Strategy (e.g. Bray-Curtis, UniFrac, Aitchison):

Plots:  
  
  
**Comparison:**

Strategy (e.g. PERMANOVA, EdgeR, DESeq2, community signatures):  
 Findings:

Plots: