Erica Toth  
Methods

Materials and Methods:

Quality Control  
 In order to clean up the data and insure good quality data, I used FastQC. I removed any sequences that had a quality score below 27 and cut them off after 370 base pairs. I also used this program to remove overrepresented sequences and deduplicate.

Analyses  
 Mothur is being used to analyze the sequence data. It was used to generate taxonomy files and summaries, as well as relative abundance files and biom files to use in PICRUSt. However, there have been some issues with generating the biom files so that I can do a functional analysis, and I’ve been in contact with Dr. Schloss and his associates to try to determine a solution.