

SERVICE REPORT

Metagenomics Profiling Data Report

SV00001

SERVICE REPORT

Customer: John Doe
Company/Institute: ABC University
Version 1: January 1, 2020

Performed by:
Norgen Biotek Corp.
3430 Schmon Pkwy, Thorold, ON
Canada L2V 4Y6

TABLE OF CONTENTS

Report Summary	3
Metagenomics Data Analysis Workflow Used	4
Sources of Metagenomics Reference Sequences	4
Downloading Your Files	4
Structure of Files Provided	5
Sample Raw Read File Information	5
Quantification of DNA used for Metagenomics	5
Total reads and OTU count	6
Metagenomics Analysis	7
Help and Technical Support	8

Report Summary

Client Name	John Doe
Norgen Order Number	SV00001
Number of Samples to Process	6 Samples
Sample Type	Stool (Human)
Sequencing Service Provided	16s V4 metagenomics
Sequencing Platform	Illumina MiSeq®
Sequencing Platform Reagent	MiSeq® Reagent Nano Kit v2 (500 Cycles)
Product Used for Library Preparation	Norgen's 16S V4 Library Preparation Kit for Illumina

Date and Time of Release of Report: January 1, 2020

Report Prepared by: Dr. Mohamed El-Mogy **Date:** January 1, 2020

Report Approved by: Dr. Yousef Haj-Ahmad **Date:** January 1, 2020

Metagenomics Data Analysis Workflow Used

Mothur (v1.43.0)

Link: <https://www.mothur.org/>

Sources of Metagenomics Reference Sequences

Small RNA Species	Reference or Database Sequences Used
16s rRNA	Silvia 138

Downloading Your Files

All files pertaining to this service have been uploaded to our servers. These files will be available for up to 1 month after the completion of the project. Please make sure to download all files before then.

To access your files, visit the link below and enter the user name and password provided. Click the [Download](#) button to start the download. If you have any issues accessing the files, please contact us for help.

Please note that all fields are case-sensitive.

Download Link:	<code>https:\\services.norgenbiotek.com\\sv00001</code>
Username:	user-sv00001
Password:	hG7*jg**m
Expiration:	April 1, 2020


Structure of Files Provided


Inside the UBS hard drive provided, you will find the following file structure that contains the analysis results.

Raw Reads

 Contains compressed original FASTQ file of each sample

Metagenomics Analysis

 Processed Data for metagenomics analysis

 Mapping summary for genus and phylum. Provided in
*.processed.tx.GENUS.cons.taxonomy and *.processed.tx.PHYLUM.cons.taxonomy

Sample Raw Read File Information

Norgen ID	Sample ID	Index 1	Associated R1 FASTQ File Name	Index 2	Associated R2 FASTQ File Name
SV00001-0001	1	N701	SV10001-0001_S1_R1_001	N707	SV10001-0001_S1_R2_001
SV00001-0002	2	N702	SV00001-0002_S2_R1_001	N708	SV00001-0002_S2_R2_001
SV00001-0003	3	N703	SV00001-0003_S3_R1_001	N709	SV00001-0003_S3_R2_001
SV00001-0004	4	N704	SV00001-0004_S4_R1_001	N710	SV00001-0004_S4_R2_001
SV00001-0005	5	N705	SV00001-0005_S5_R1_001	N711	SV00001-0005_S5_R2_001
SV00001-0006	6	N706	SV00001-0006_S6_R1_001	N712	SV00001-0006_S6_R2_001

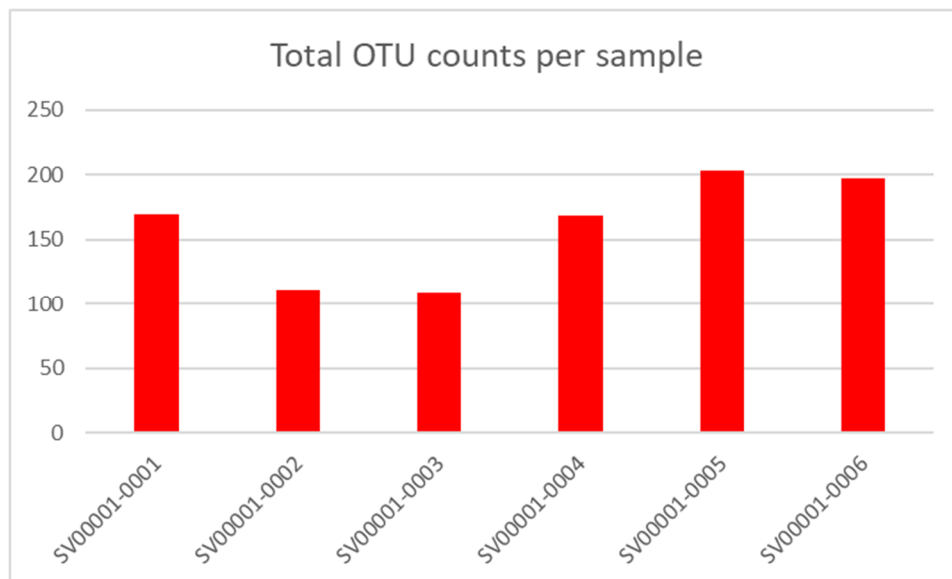
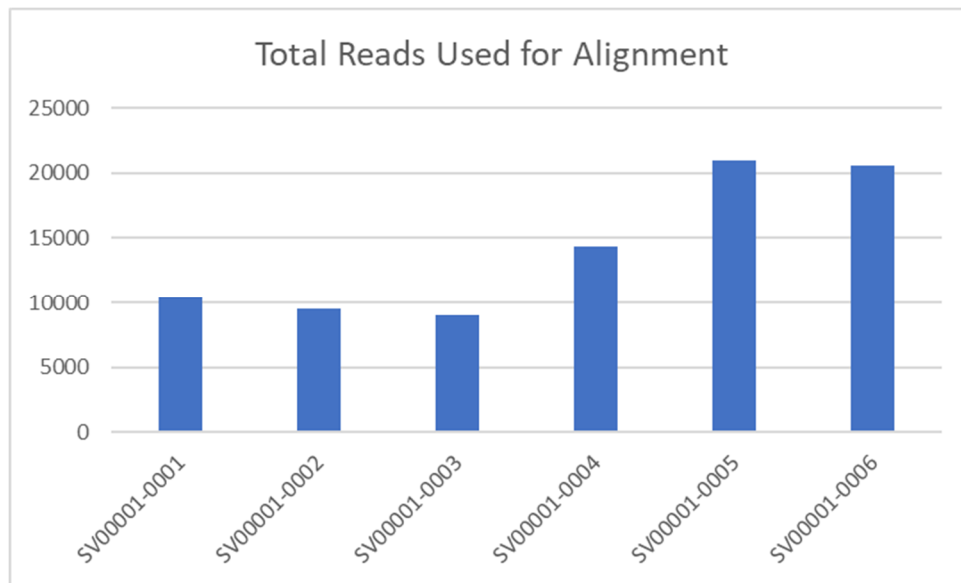
Quantification of DNA used for Metagenomics

DNA isolated using Norgen's Stool DNA Isolation Kit (# 27600).

Sample ID	DNA ID	DNA Conc., ng/uL (NanoDrop)
SV00001-0001	SV00001-0001_0001-RNA	50.00
SV00001-0002	SV00001-0002_0002-RNA	60.00
SV00001-0003	SV00001-0003_0003-RNA	62.00
SV00001-0004	SV00001-0004_0004-RNA	58.00
SV00001-0005	SV00001-0005_0005-RNA	71.00
SV00001-0006	SV00001-0006_0006-RNA	63.00

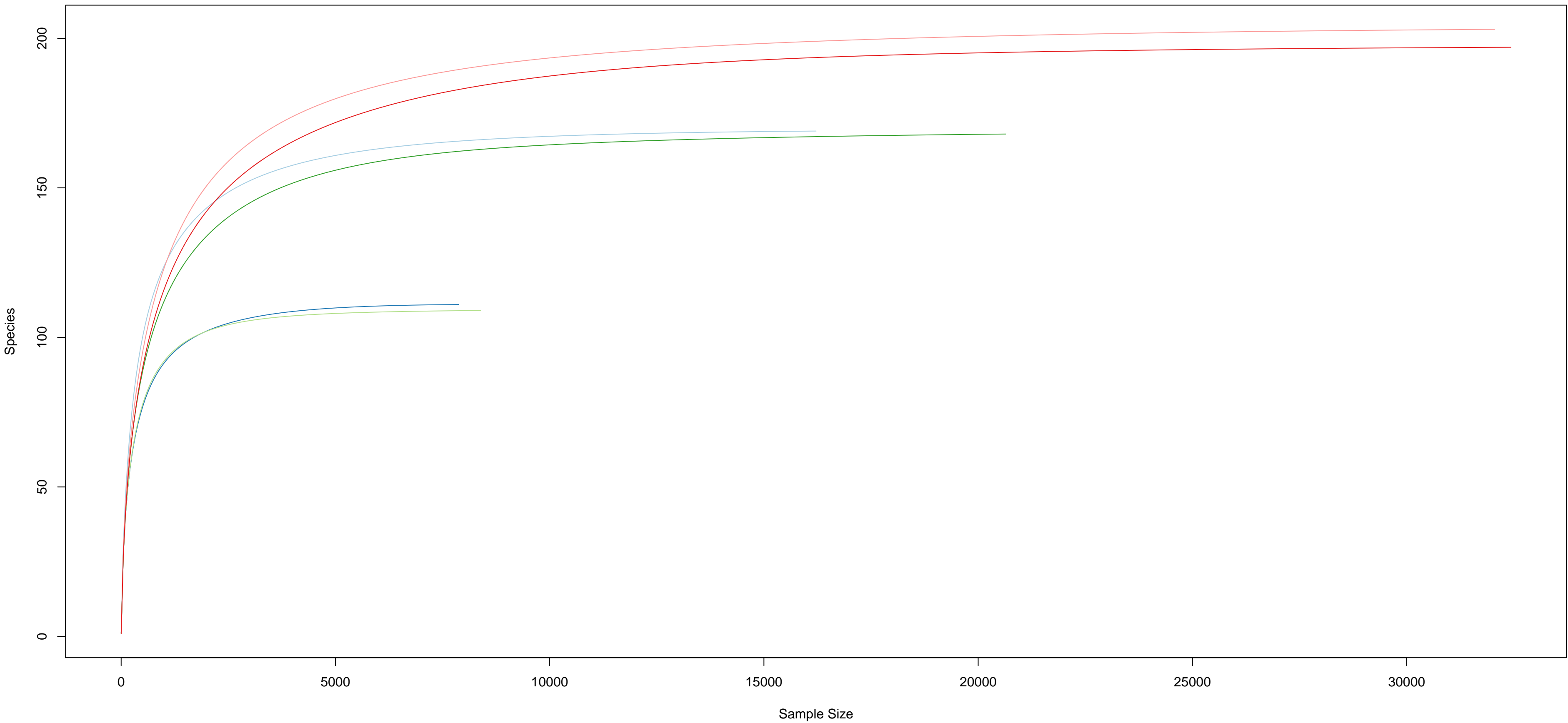
Amount of DNA is in line with observed yield of similar DNA samples. It meets the minimal requirement for library prep and sequencing.

Total reads and OTU count



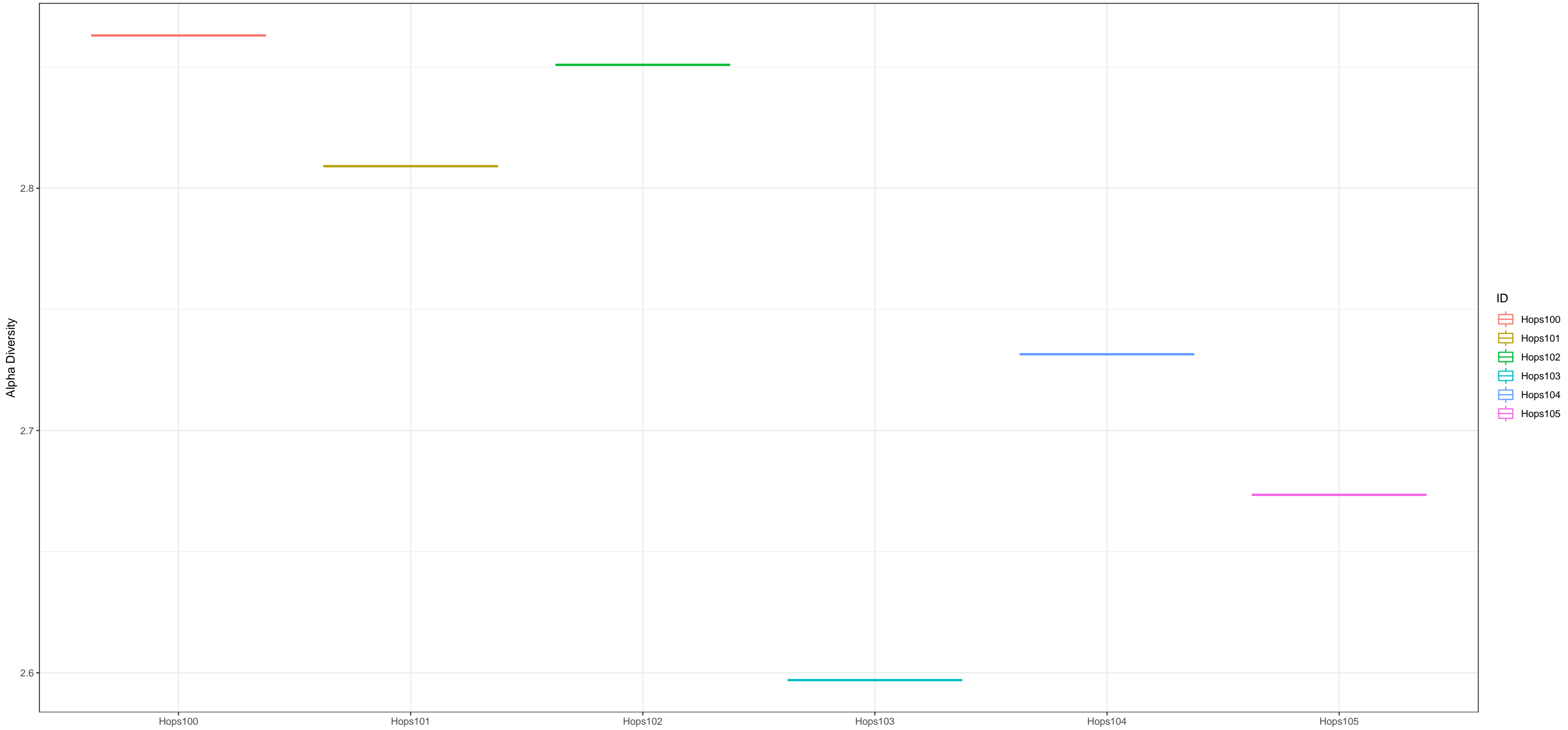
Metagenomics Analysis

Alpha Rarefaction Curve



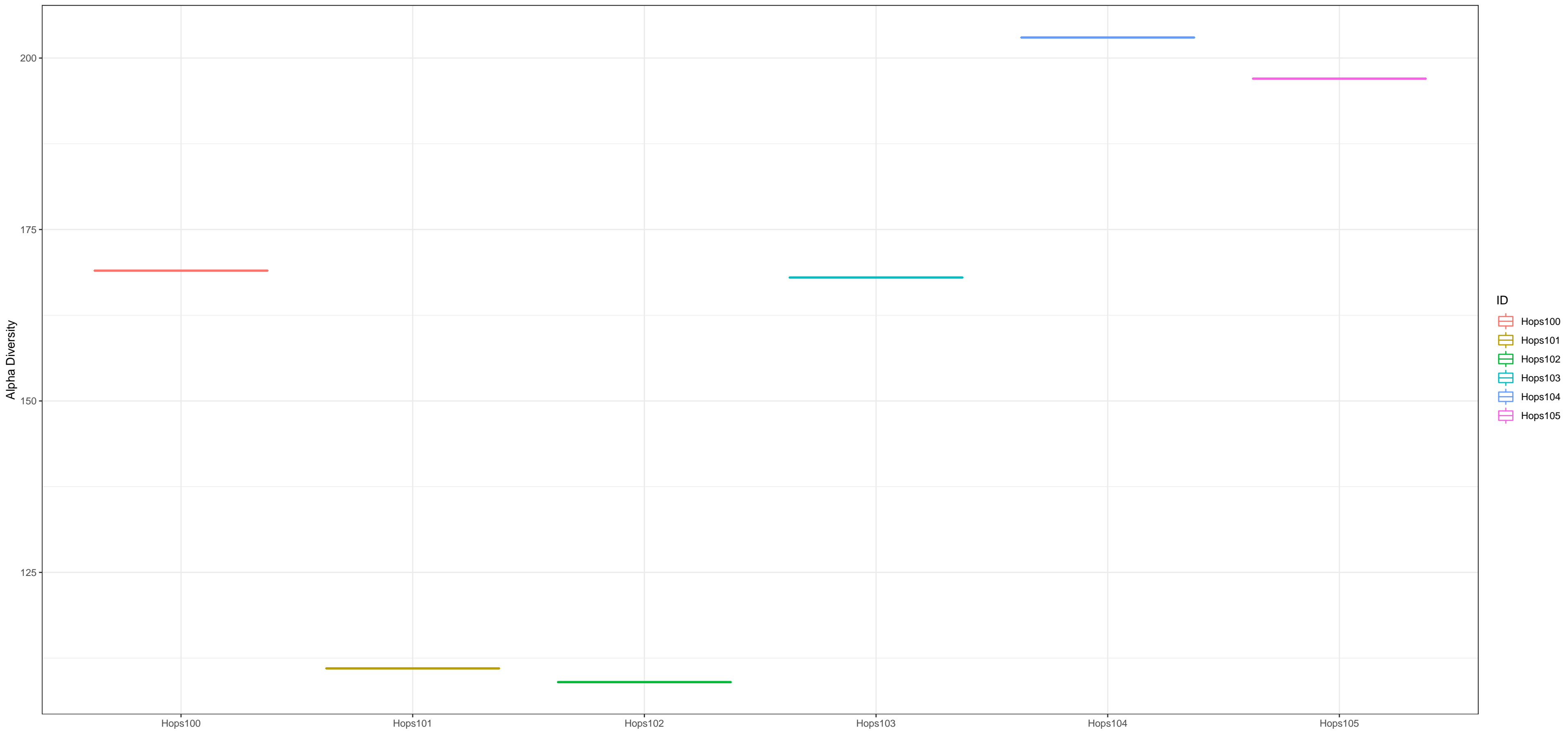
Alpha Diversity Analysis

A measurement of microbial richness and evenness using Shannons Diversity Index

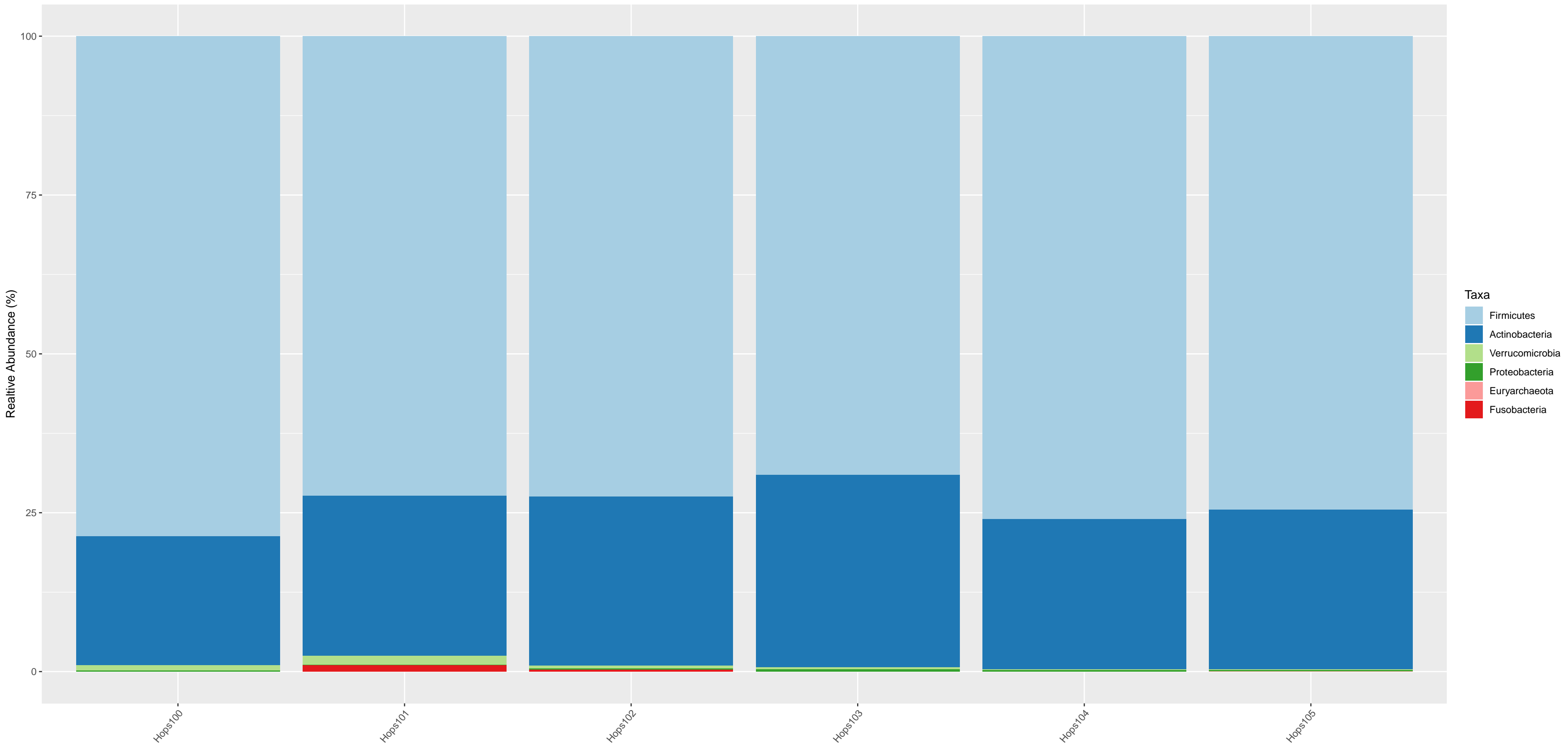


Alpha Diversity Analysis

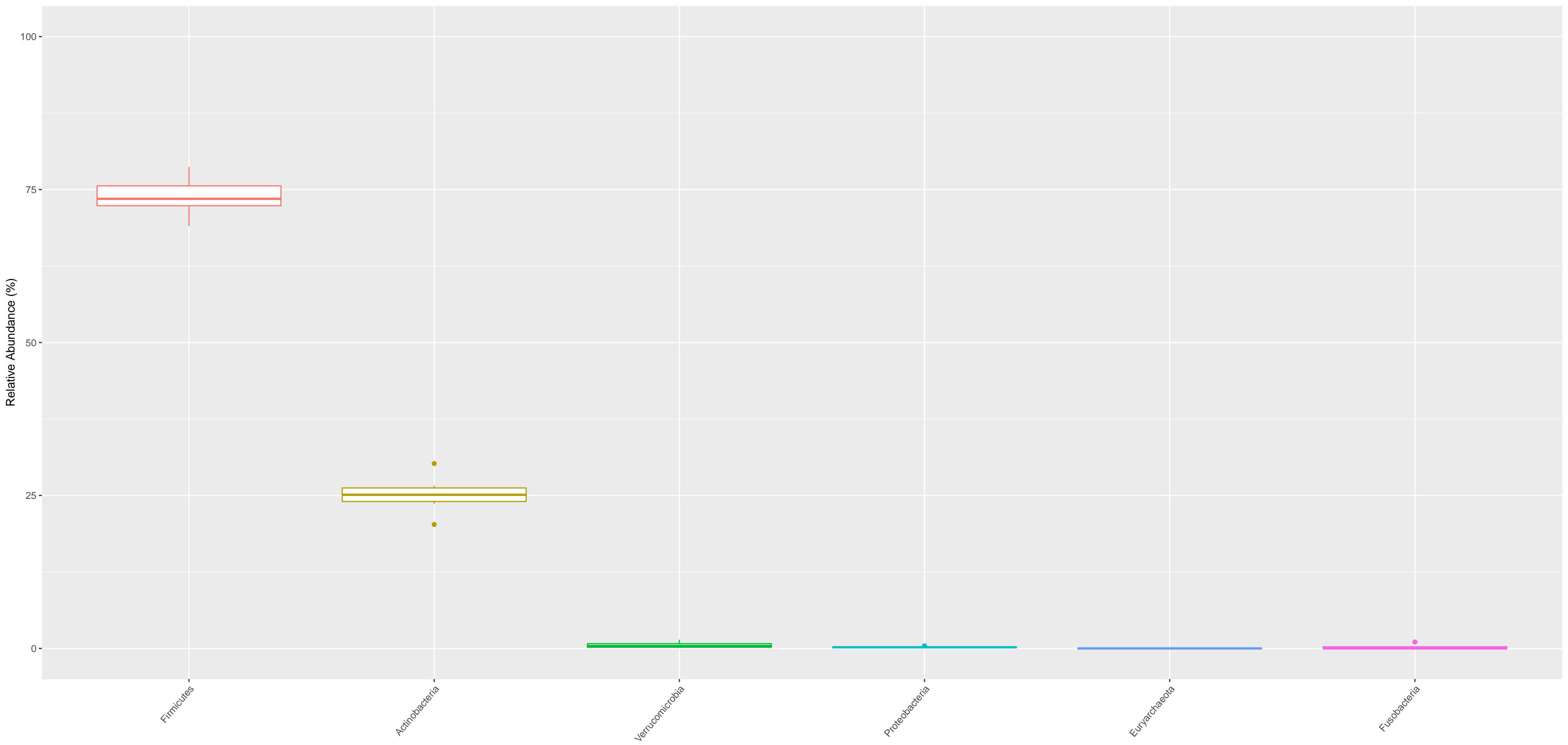
A measurement of microbial richness and evenness based on observed OTUs



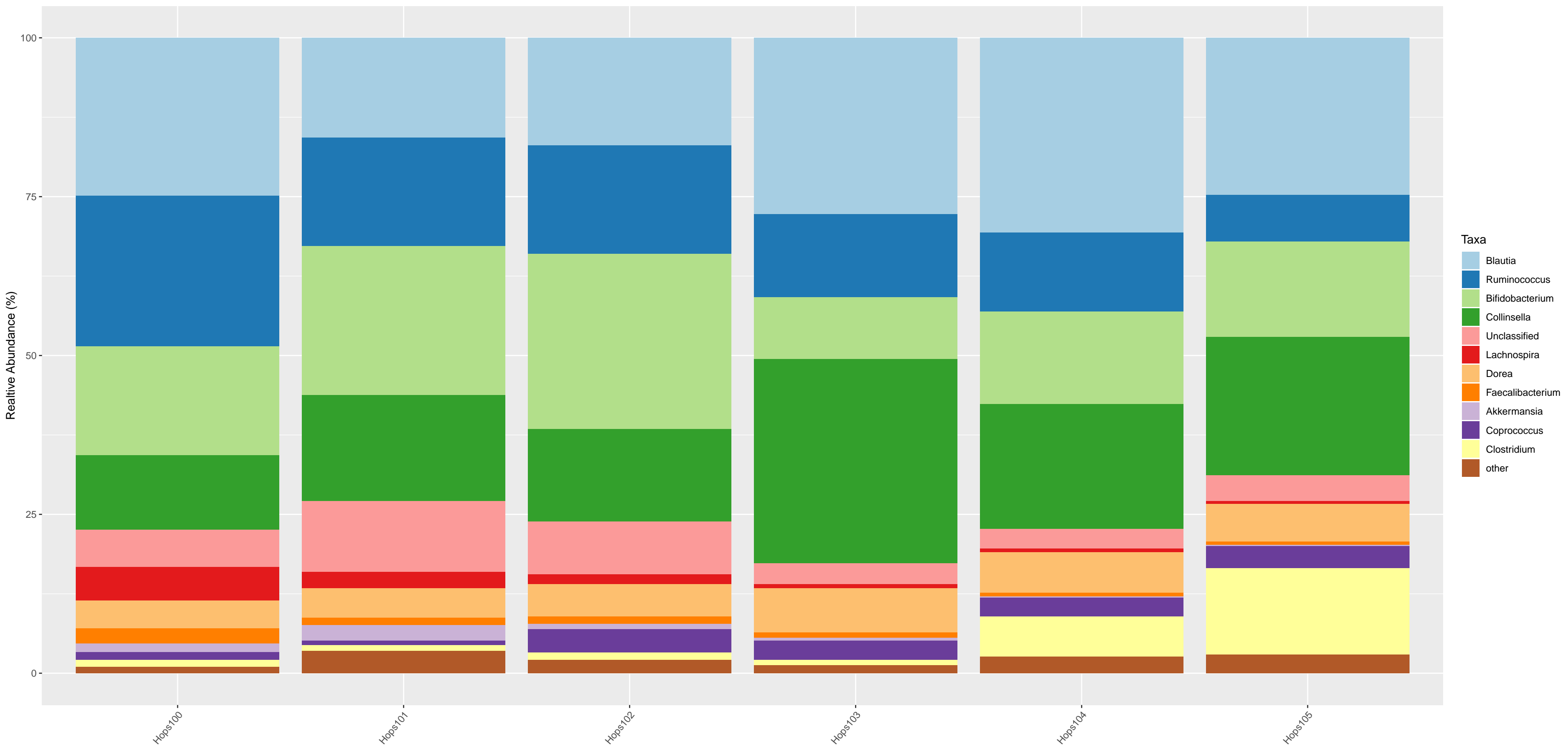
Relative abundance per sample: Phylum Level



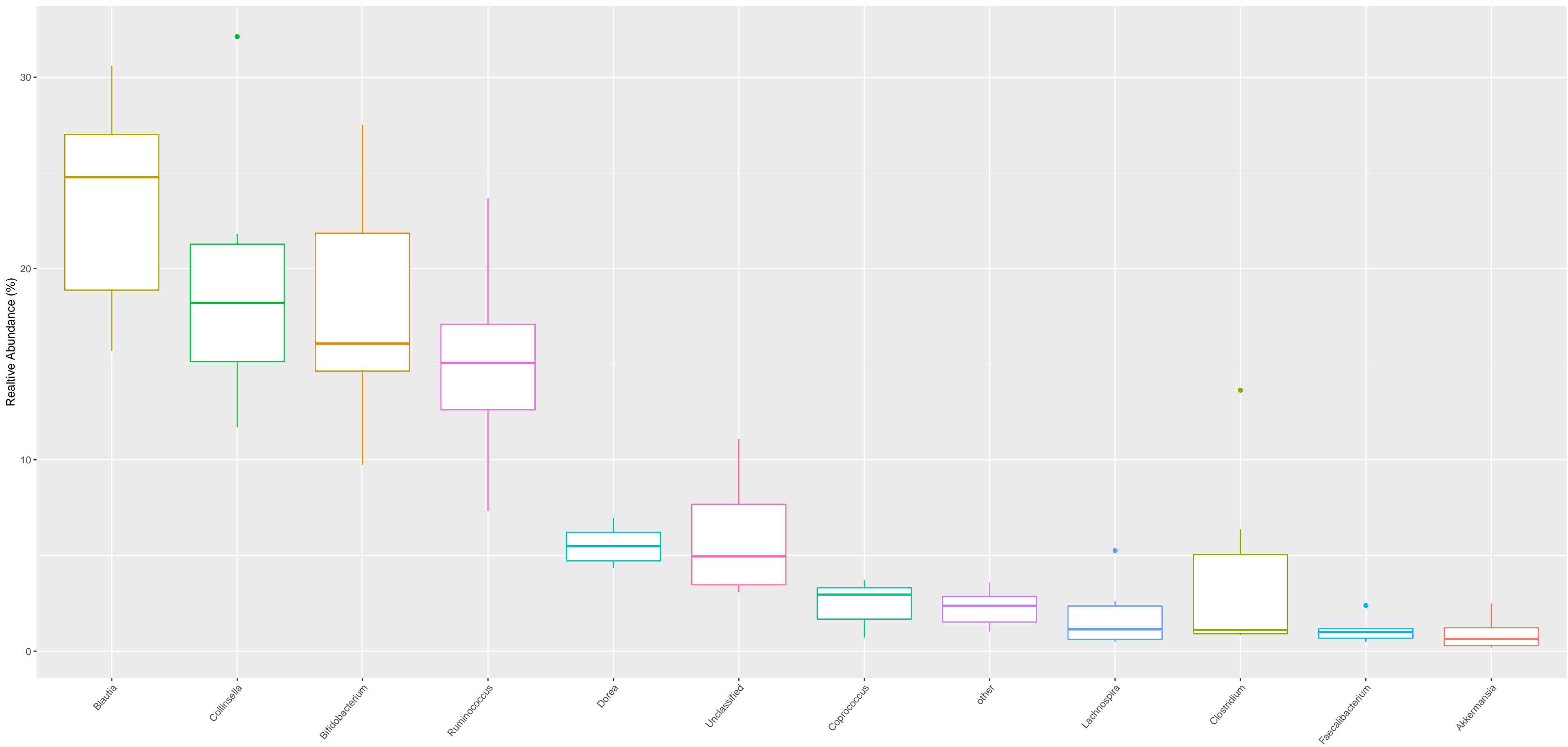
Relative abundance of libraries: Phylum Level



Relative abundance per sample: Genus Level

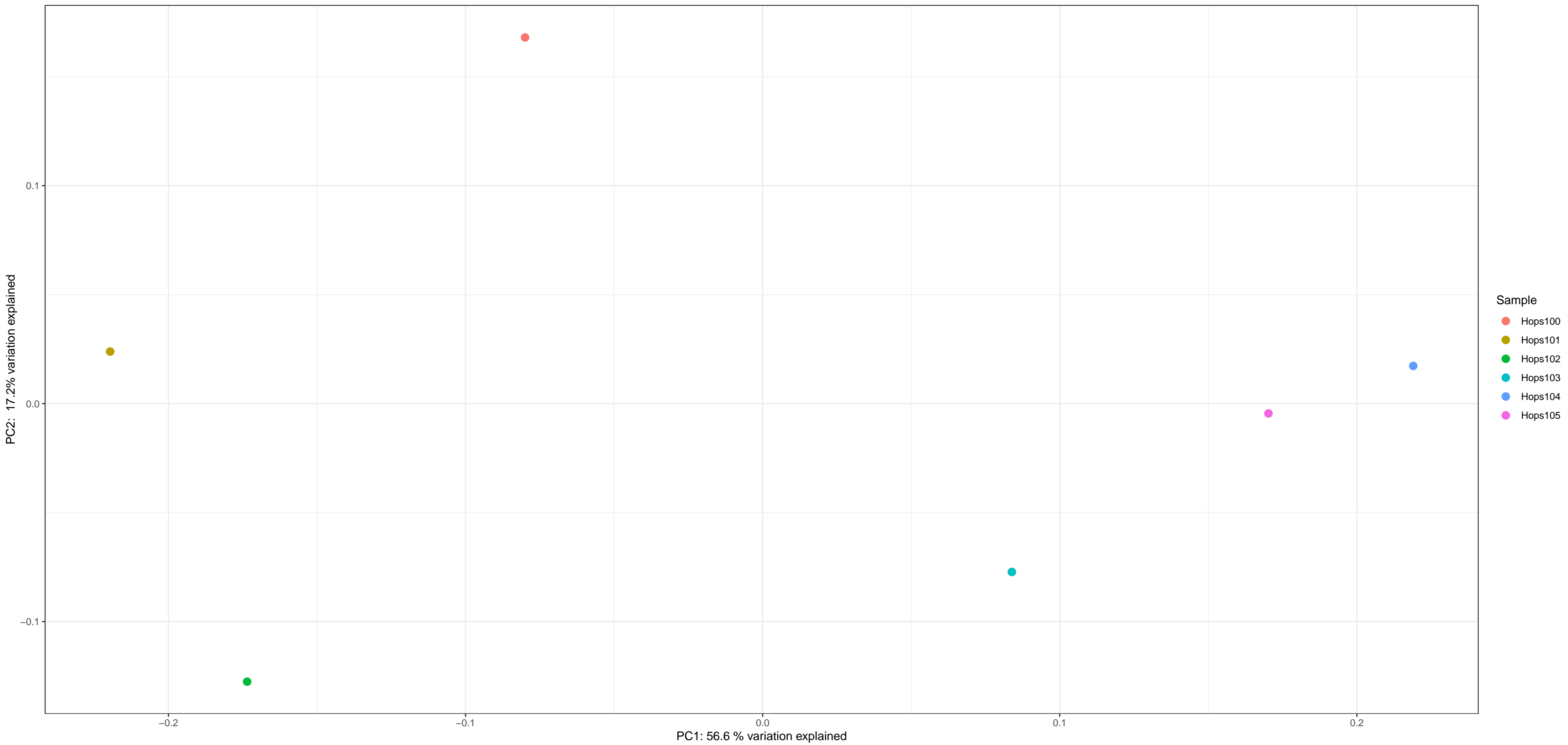


Relative abundance of libraries: Genus Level



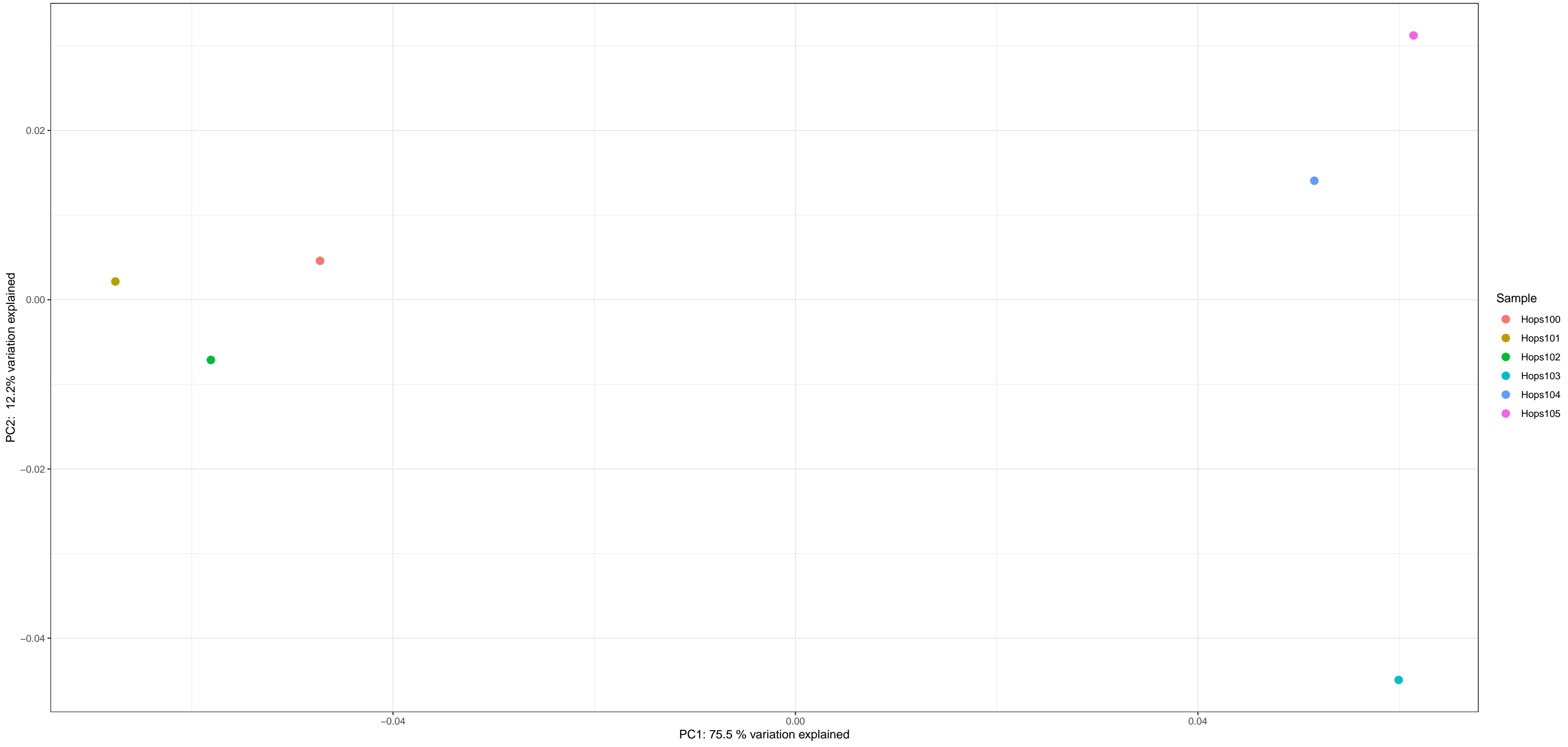
Beta Diversity Analysis

In-between sample difference – Unweighted UniFrac

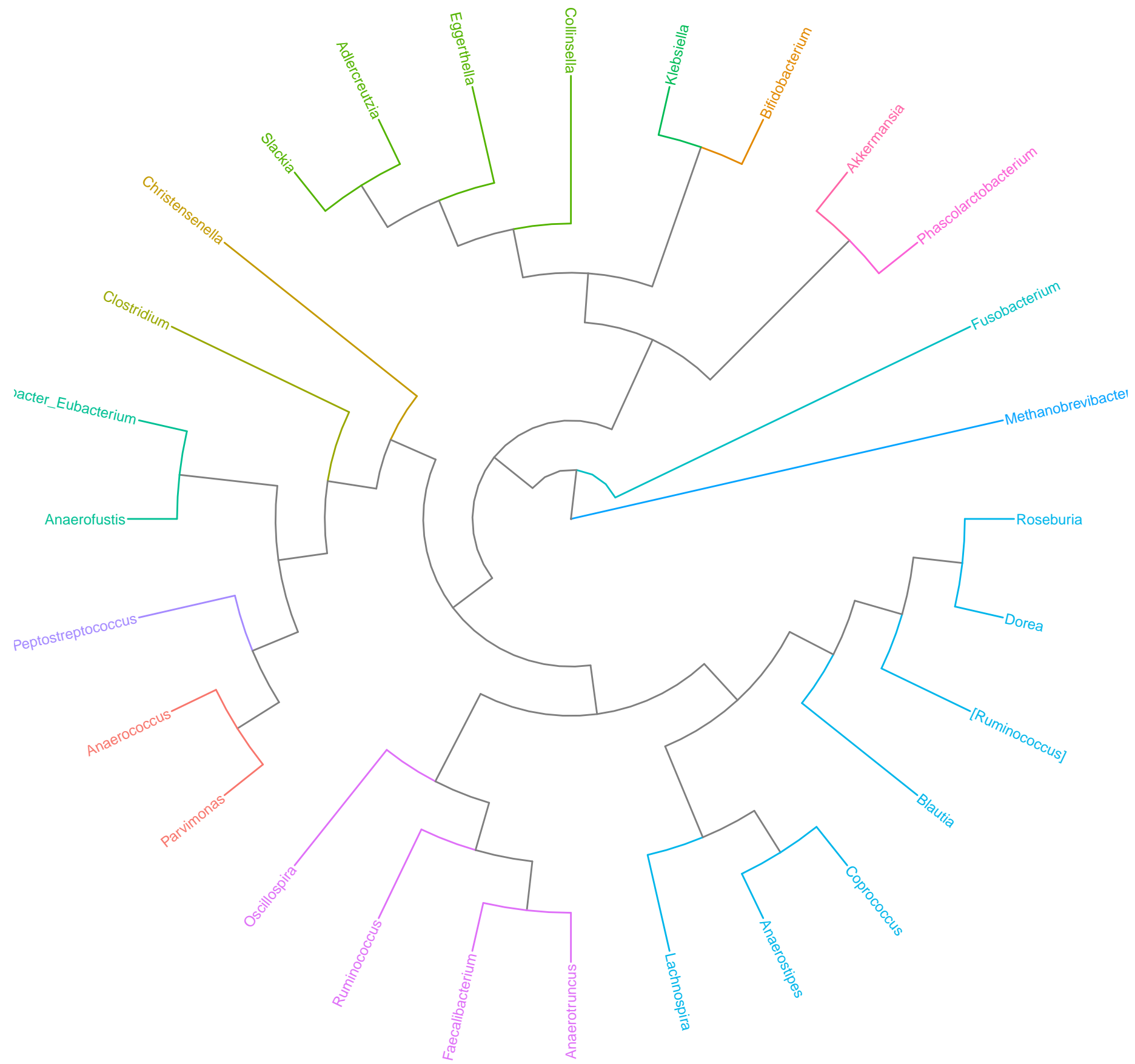


Beta Diversity Analysis

In-between sample difference – Weighted UniFrac



Phylogenetic tree at the Genus level



Help and Technical Support

For any questions or additional help regarding this report, please contact our Technical Support Team between the hours of 9:00 AM and 5:30 PM (Eastern Standard Time) at (905) 227-8848 or Toll Free at 1-866-667-4362. Technical support can also be obtained through email at techsupport@norgenbiotek.com.