

16S Metagenomics Sequencing Data Report

Prepared for Dr Xxxxx Xxxxx

MM/DD/YYYY



16S Metagenomics Sequencing Data Report

Client Name	Dr Xxxxx Xxxxx
Norgen Order Number	NG001
Number of Samples to Process	10 Samples
Sample Type	Stool (collected in Norgen's Stool Collection and Transport Tubes)
Sequencing Service Provided	16S Metagenomics
Sequencing Platform	Illumina MiSeq
Sequencing Platform Reagent	MiSeq Reagent Kit v3
Product Used for Library Preparation	Norgen's 16S Metagenomic Workflow with Illumina Nextara XT Index Kit

Date and Time of Release of Report: MM/DD/YYYY	
Report Prepared by: Dr. NGS Technologist	Date: MM/DD/YYYY
Report Approved by: Dr. Service Director	Date: MM/DD/YYYY
16S Metagenomics Data Analysis Workflow Used	
Illumina 16S Metagenomics Pipeline (v1.0.1) (Weblink: https://basespace.illumina.com/apps/593593/16S-Metagenomics?preferredversion)	

Structure of Files Provided

I. "Raw Reads" Folder

-Contains compressed original FASTQ file of each sample

II. "16S Metagenomics Analysis" Folder

(a) "Aggregate Summary" sub-Folder

- Contains Aggregate/Combined Data Summary and Analysis of all samples

(b) "Individual Sample Summary" sub-Folder

- Contains folder of Data Summary and Analysis of each individual samples

Sample Index

Sample	Index 2	Index 1
1	S507	N701
2	S507	N702
3	S507	N703
4	S507	N704
5	S507	N705
6	S507	N706
7	S507	N707
8	S507	N708
9	S507	N709
10	S507	N710

Sample Information

Sample	Number Reads PF	% Reads Classified to Genus
1	1160096	83.96%
2	2078912	78.41%
3	1183805	78.95%
4	911710	80.76%
5	1522781	82.95%
6	1239753	86.33%
7	1281630	78.33%
8	1548018	71.69%
9	1046534	77.80%
10	1563290	85.70%

Species Diversity Results

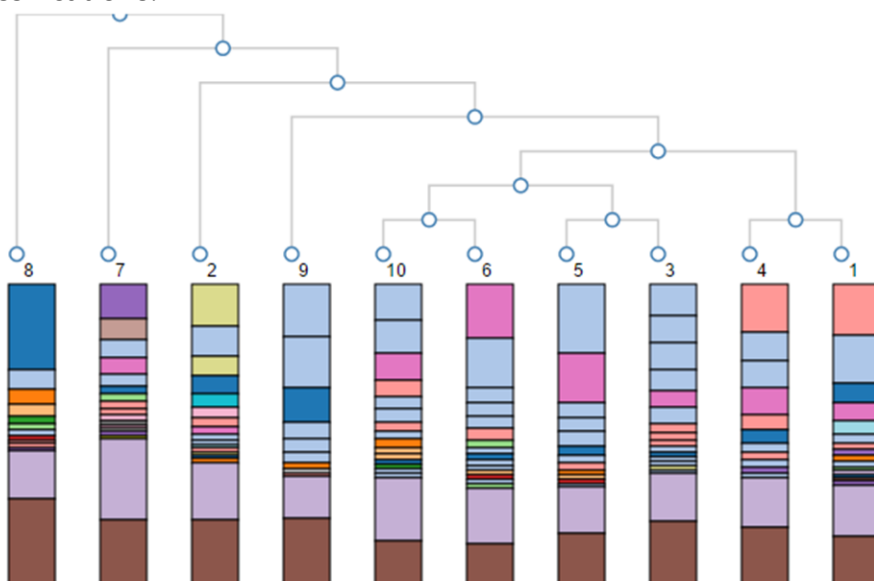
Shannon Species Diversity measures the entropy of Species-level classifications in the sample.

See http://en.wikipedia.org/wiki/Species_diversity for more information.

Sample ID	Shannon Species Diversity	Number of Species Identified
1	2.111	648
2	2.137	835
3	2.366	579
4	1.738	592
5	1.902	602
6	2.211	564
7	2.605	777
8	1.964	680
9	2.225	576
10	2.249	664

Hierarchical Clustering Dendrogram

This dendrogram shows a hierarchical clustering of samples based on genus-level classifications.



Principal Coordinate Analysis (PCoA)

This scatterplot shows a Principal Coordinate Analysis (PCoA) of the normalized relative abundance of all samples at the genus-level classifications.

