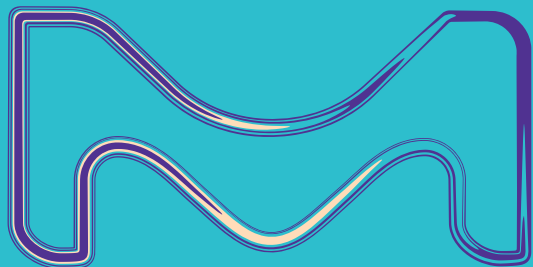


The life science business of Merck KGaA, Darmstadt, Germany operates as MilliporeSigma in the U.S. and Canada.

sigma-Aldrich®

platform

Microbiome



Millipore
Sigma

Sigma-Aldrich® Metagenome Web Platform for Microbiome Data Analysis

1

Easy upload and management of sequencing projects

2

Species-level taxonomic classification of 16s-seq data is best-in-class.

3

One-click quality control processing of fastq files along with quality reports.

4

Statistical and graphical analysis of microbiome communities

why use our
platform?



File Upload and Management

Sample Management

[+ New Project](#)

Search by Name Show 20

| Project Name | Size | Samples | |
|--------------|---------|---------|--|
| Project1 | 1.8 GB | 18 | |
| atcceven | 22.5 MB | 1 | |

1 to 2 of 2

« < 1 > »

Samples Files Meta-Data

[Add File\(s\)](#) Search by Name Perform QC Show 20

| Sample | Layout | Type | Submitted | Size | QC Status | Actions |
|---------------------------------|--------|--------------|-------------|----------|-----------|---------|
| <input type="checkbox"/> 967309 | PAIRED | Amplicon-seq | 14-Apr-2020 | 113.3 MB | | |
| <input type="checkbox"/> 967310 | PAIRED | Amplicon-seq | 14-Apr-2020 | 110.6 MB | | |
| <input type="checkbox"/> 967311 | PAIRED | Amplicon-seq | 14-Apr-2020 | 109.3 MB | | |
| <input type="checkbox"/> 967312 | PAIRED | Amplicon-seq | 14-Apr-2020 | 92.9 MB | | |
| <input type="checkbox"/> 967313 | PAIRED | Amplicon-seq | 14-Apr-2020 | 88.9 MB | | |
| <input type="checkbox"/> 967314 | PAIRED | Amplicon-seq | 14-Apr-2020 | 105.4 MB | | |
| <input type="checkbox"/> 967315 | PAIRED | Amplicon-seq | 14-Apr-2020 | 106 MB | | |
| <input type="checkbox"/> 967316 | PAIRED | Amplicon-seq | 14-Apr-2020 | 155.7 MB | | |
| <input type="checkbox"/> 967317 | PAIRED | Amplicon-seq | 14-Apr-2020 | 101.7 MB | | |
| <input type="checkbox"/> 967318 | PAIRED | Amplicon-seq | 14-Apr-2020 | 91.1 MB | | |
| <input type="checkbox"/> 967319 | PAIRED | Amplicon-seq | 14-Apr-2020 | 102.4 MB | | |
| <input type="checkbox"/> 967320 | PAIRED | Amplicon-seq | 14-Apr-2020 | 85.8 MB | | |
| <input type="checkbox"/> 967321 | PAIRED | Amplicon-seq | 14-Apr-2020 | 88.5 MB | | |
| <input type="checkbox"/> 967322 | PAIRED | Amplicon-seq | 14-Apr-2020 | 106.4 MB | | |
| <input type="checkbox"/> 967323 | PAIRED | Amplicon-seq | 14-Apr-2020 | 96.2 MB | | |



Quality Control Reports

← Back 967309

Metadata **Pre-QC** Perform-QC Post-QC

Select sample file 967309_R1_L001.fastq.gz ▾

Basic Statistics

| | | |
|----------------------------------|-------------------------|-------------------------------|
| Filename | 967309_R1_L001.fastq.gz | Download Data |
| File Type | Conventional base calls | |
| Encoding | Sanger / Illumina 1.9 | |
| Total Sequence | 551614 | |
| Sequence Flagged As Poor Quality | 0 | |
| Sequence Length | 301 | |
| %GC | 53 | |

Detailed Quality Control Report

- Per Base Sequence Quality** ⚠
- Per Tile Sequence Quality ✓
- Per Sequence Quality Scores ✓
- Per Base Sequence Content ✗
- Per Sequence GC Content ✗
- Per Base N Content ✓

Per Base Sequence Quality

Quality scores across all bases (Sanger / Illumina 1.9 encoding)

The plot displays quality scores across all bases (Sanger / Illumina 1.9 encoding). The y-axis ranges from 28 to 38. The plot shows a blue line representing the mean quality score, which starts at approximately 34, rises to a peak of about 38, and then gradually declines towards the end of the sequence. Vertical bars represent the distribution of quality scores for each base, with green bars for higher quality and yellow bars for lower quality. A red dashed line is visible at the top of the plot, around 38.5.



Taxonomic Classification

Multiple Reference Databases Available

Metagenome Classification

Search by Name Show 20

| Project ID | Size | Samples |
|------------|---------|---------|
| Project1 | 1.8 GB | 18 |
| atcseven | 22.5 MB | 1 |

1 to 2 of 2

Select Sample Name Select Reference Classify Search by Name Show 20

| Samples | Reference Dataset | Submitted | Status | Action |
|---------------------------------|--------------------------|-------------------|--------|--------|
| <input type="checkbox"/> 967310 | Merck_Bacteria-16S_V3-V4 | 15-Apr-2020 20:11 | ✓ | Result |
| <input type="checkbox"/> 967309 | Merck_Bacteria-16S_V3-V4 | 15-Apr-2020 20:11 | ✓ | Result |
| <input type="checkbox"/> 967311 | Merck_Bacteria-16S_V3-V4 | 15-Apr-2020 20:10 | ✓ | Result |
| <input type="checkbox"/> 967312 | Merck_Bacteria-16S_V3-V4 | 15-Apr-2020 20:09 | ✓ | Result |
| <input type="checkbox"/> 967313 | Merck_Bacteria-16S_V3-V4 | 15-Apr-2020 20:07 | ✓ | Result |
| <input type="checkbox"/> 967316 | Merck_Bacteria-16S_V3-V4 | 15-Apr-2020 20:06 | ✓ | Result |
| <input type="checkbox"/> 967315 | Merck_Bacteria-16S_V3-V4 | 15-Apr-2020 20:06 | ✓ | Result |
| <input type="checkbox"/> 967314 | Merck_Bacteria-16S_V3-V4 | 15-Apr-2020 20:06 | ✓ | Result |
| <input type="checkbox"/> 967317 | Merck_Bacteria-16S_V3-V4 | 15-Apr-2020 20:03 | ✓ | Result |
| <input type="checkbox"/> 967319 | Merck_Bacteria-16S_V3-V4 | 15-Apr-2020 20:02 | ✓ | Result |
| <input type="checkbox"/> 967318 | Merck_Bacteria-16S_V3-V4 | 15-Apr-2020 20:02 | ✓ | Result |
| <input type="checkbox"/> 967321 | Merck_Bacteria-16S_V3-V4 | 15-Apr-2020 19:59 | ✓ | Result |
| <input type="checkbox"/> 967322 | Merck_Bacteria-16S_V3-V4 | 15-Apr-2020 19:59 | ✓ | Result |
| <input type="checkbox"/> 967324 | Merck_Bacteria-16S_V3-V4 | 15-Apr-2020 19:58 | ✓ | Result |
| <input type="checkbox"/> 967320 | Merck_Bacteria-16S_V3-V4 | 15-Apr-2020 19:58 | ✓ | Result |
| <input type="checkbox"/> 967325 | Merck_Bacteria-16S_V3-V4 | 15-Apr-2020 19:55 | ✓ | Result |

Search reference db...
Merck_Bacteria-16S_V3-V4
Refseq_16S_V3-V4
SILVA_16S_V3-V4
Greengenes_16S_V3-V4



Single Sample Classification Report

Back 967310

Sequence Alignment Summary Rank Based Summary Classification Summary

Unclassified Sequences : 1184(0.32%) Classified Sequences : 374010(99.68%)

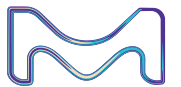
Abundance Bar Chart Pie Chart Collapsible Tree Cake Chart

Any Kingdom Phylum Class Order Family Genus Species

Search by Name

Show 20

| Tax Id | % of fragment | Clade Count | taxon Count | Rank | Kingdom | Phylum | Class | Order | Family | Genus | Species |
|--------|---------------|-------------|-------------|------|----------|---------------------|---------------------|-------------------|--------------------|----------------|--------------------------|
| 1311 | 9.6 | 36006 | 36006 | S | Bacteria | Firmicutes | Bacilli | Lactobacillales | Streptococcaceae | Streptococcus | Streptococcus agalactiae |
| 1309 | 9.57 | 35901 | 35901 | S | Bacteria | Firmicutes | Bacilli | Lactobacillales | Streptococcaceae | Streptococcus | Streptococcus mutans |
| 1351 | 8.55 | 32071 | 32071 | S | Bacteria | Firmicutes | Bacilli | Lactobacillales | Enterococcaceae | Enterococcus | Enterococcus faecalis |
| 470 | 7.8 | 29264 | 29264 | S | Bacteria | Proteobacteria | Gammaproteobacteria | Pseudomonadales | Moraxellaceae | Acinetobacter | Acinetobacter baumannii |
| 1299 | 7.66 | 28729 | 0 | S | Bacteria | Deinococcus-Thermus | Deinococci | Deinococcales | Deinococcaceae | Deinococcus | Deinococcus radiodurans |
| 562 | 7.41 | 27787 | 27787 | S | Bacteria | Proteobacteria | Gammaproteobacteria | Enterobacteriales | Enterobacteriaceae | Escherichia | Escherichia coli |
| 1280 | 5.01 | 18781 | 15707 | S | Bacteria | Firmicutes | Bacilli | Bacillales | Staphylococcaceae | Staphylococcus | Staphylococcus aureus |
| 287 | 4.63 | 17353 | 17353 | S | Bacteria | Proteobacteria | Gammaproteobacteria | Pseudomonadales | Pseudomonadaceae | Pseudomonas | Pseudomonas aeruginosa |
| 821 | 2.78 | 10428 | 0 | S | Bacteria | Bacteroidetes | Bacteroidia | Bacteroidales | Bacteroidaceae | Bacteroides | Bacteroides vulgatus |
| 487 | 2.66 | 9969 | 9969 | S | Bacteria | Proteobacteria | Betaproteobacteria | Neisseriales | Neisseriaceae | Neisseria | Neisseria meningitidis |
| 1063 | 2.39 | 8977 | 8977 | S | Bacteria | Proteobacteria | Alphaproteobacteria | Rhodobacterales | Rhodobacteraceae | Rhodobacter | Rhodobacter |



Multi-Sample Comparative Analysis

| Read Stats | Abundance | Stacked Bar Chart | Heat Map | Alpha Diversity | Beta Diversity | | | |
|-------------|-------------|-------------------|----------------|-----------------|----------------|----------------------|------------------------|---------|
| Show Graph | | | | | | Search by Name | Download | Show 40 |
| Sample Name | Total Input | QC Passed | Unjoined Pairs | Chimeric | Total Passed | Classified Sequences | Unclassified Sequences | |
| 2_S2_L001 | 105130 | 95151 | 6432 | 6093 | 82626 | 82616 | 10 | |
| 3_S3_L001 | 75380 | 69288 | 5006 | 4817 | 59465 | 59460 | 5 | |
| 4_S4_L001 | 115940 | 106686 | 9525 | 4915 | 92246 | 92244 | 2 | |
| 5_S5_L001 | 98590 | 92257 | 5433 | 6023 | 80801 | 80796 | 5 | |
| 6_S6_L001 | 89154 | 83552 | 4781 | 3935 | 74836 | 74830 | 6 | |
| 7_S7_L001 | 100962 | 91753 | 6226 | 5089 | 80438 | 80436 | 2 | |
| 8_S8_L001 | 93143 | 84349 | 5970 | 4259 | 74120 | 74118 | 2 | |
| 9_S9_L001 | 112408 | 104756 | 6213 | 6205 | 92338 | 92325 | 13 | |
| 17_S17_L001 | 81783 | 75674 | 4536 | 5514 | 65624 | 65622 | 2 | |
| 16_S16_L001 | 1676 | 1345 | 289 | 70 | 986 | 986 | NA | |
| 20_S20_L001 | 141897 | 130082 | 7951 | 6763 | 115368 | 115359 | 9 | |
| 18_S18_L001 | 94797 | 88675 | 5259 | 6528 | 76888 | 76884 | 4 | |
| 21_S21_L001 | 97334 | 90809 | 5408 | 6163 | 79238 | 79238 | NA | |
| 22_S22_L001 | 80040 | 73840 | 4806 | 4132 | 64902 | 64900 | 2 | |
| 23_S23_L001 | 93973 | 87531 | 6030 | 5385 | 76116 | 76116 | NA | |
| 24_S24_L001 | 119894 | 109161 | 7989 | 5731 | 95441 | 95436 | 5 | |
| 25_S25_L001 | 90001 | 81458 | 5691 | 5992 | 69775 | 69762 | 13 | |
| 26_S26_L001 | 96520 | 87370 | 5575 | 5298 | 76497 | 76492 | 5 | |



Taxonomic Profile Summary

Download

SVG (bars) SVG (legend) CSV

Taxonomic Level

Level 2

Color Palette

schemeSet1

Sort Samples By

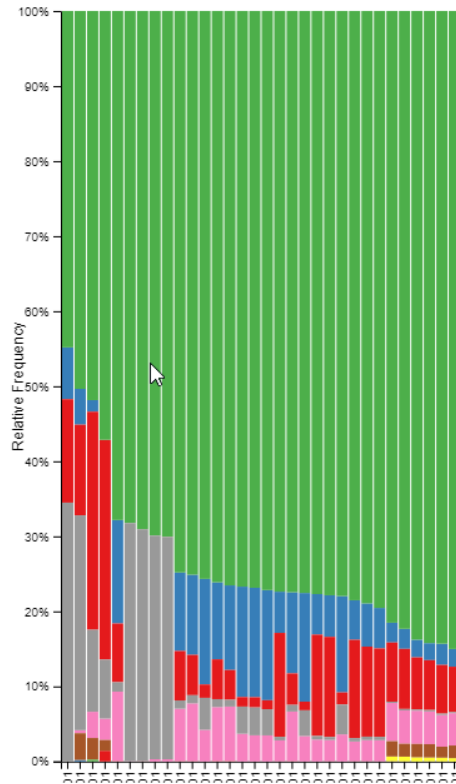
d__Bacteria;p__Firmicutes

Ascending

Bar Width



30_S30_L001 | d__Bacteria;p__Firmicutes | 69.908%



- d__Bacteria;p__Firmicutes
- d__Bacteria;p__Actinobacteria
- d__Bacteria;p__Bacteroidetes
- d__Bacteria;p__Proteobacteria
- d__Bacteria;__
- d__Bacteria;p__Verrucomicrobia
- d__Archaea;p__Euryarchaeota
- d__Bacteria;p__Candidatus_Saccharibacteria
- d__Eukaryota;__
- d__Eukaryota;p__Nematoda
- d__Bacteria;p__Cyanobacteria
- d__Bacteria;p__Armatimonadetes

View samples at different ranks of the taxonomic hierarchy

Sort and rename samples by experimental metadata factors



Alpha Diversity Statistical Tests

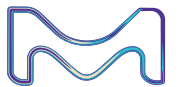
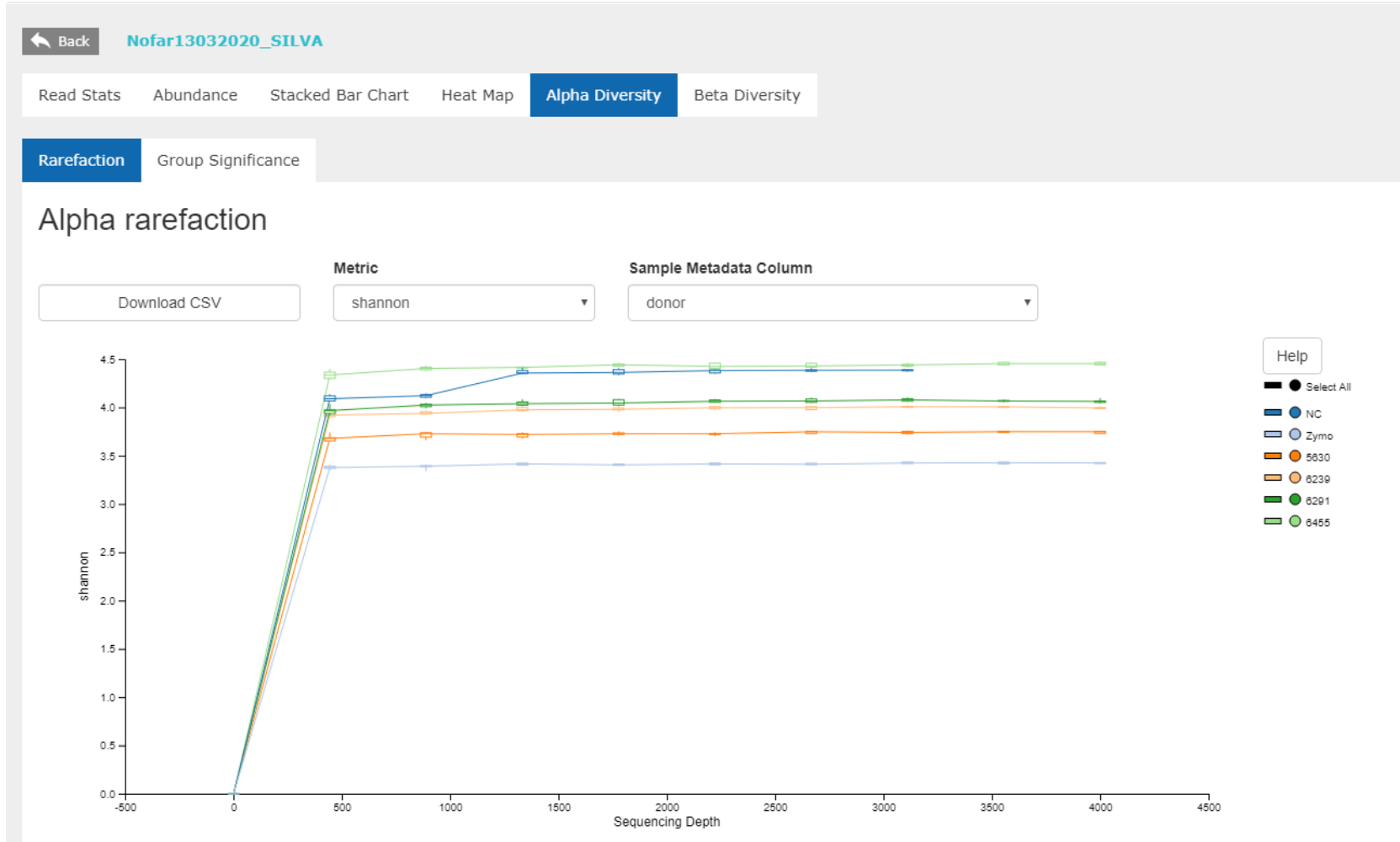


Supports multiple
Alpha Rarefaction metrics

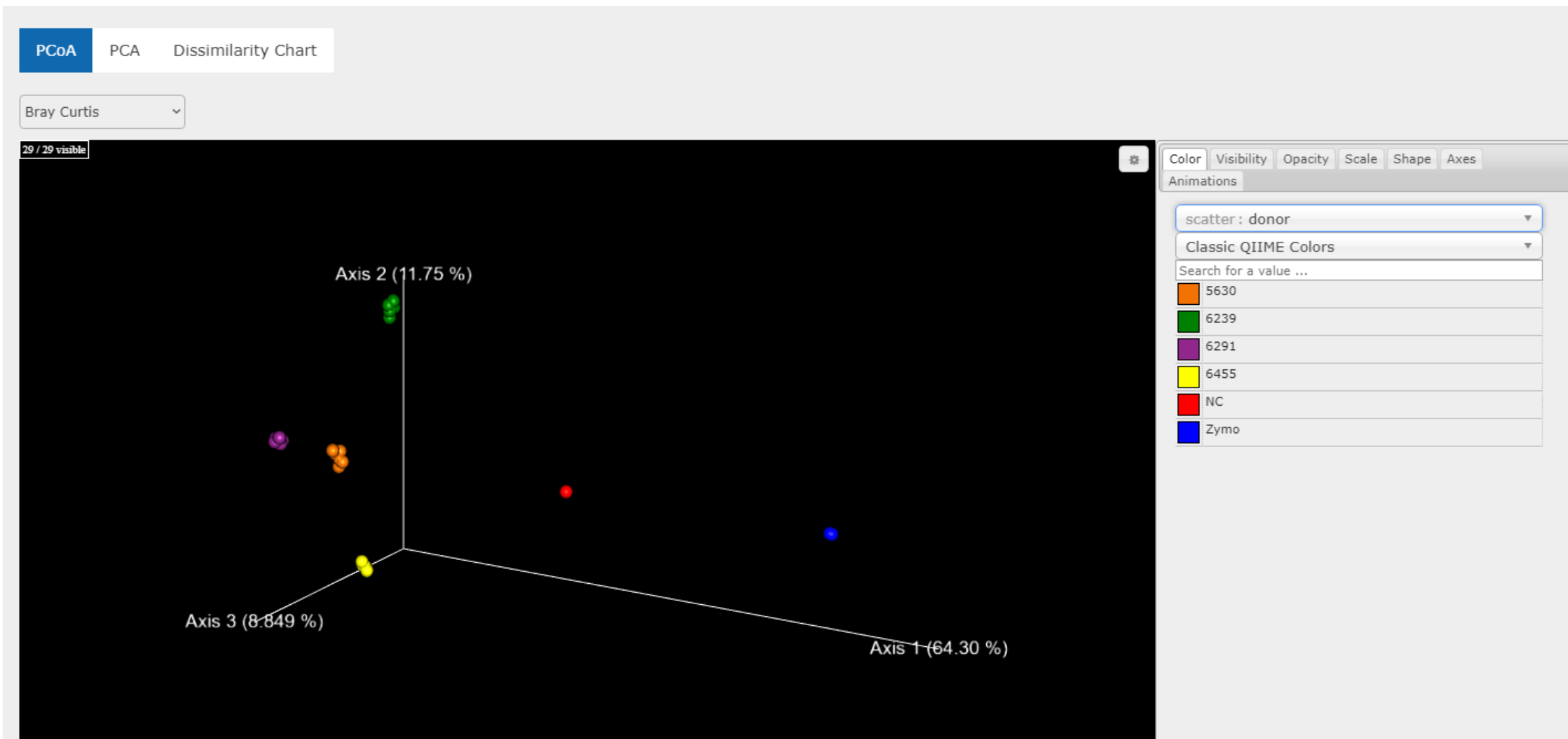
Kruskall-Wallis one-way analysis
of variance for differences
between sample groups



Alpha Rarefaction Curves



Beta Diversity PCoA



Michal Daniely

Graziella Amarainghe

Andrew Schriefer

MicrobiomeServices@milliporesigma.com

