BUGSEQ

Automated bioinformatics for microbiology labs.

Analysis Name	JJS Capstone Short Reads
Run ID	31374a14-6b15-4dc6-9d9d-7ae870d1b1a1
BugSeq Pipeline Version	Latest (2023-04-26)
Metagenomic Database	BugSeq Default
Contact E-mail	support@bugseq.com

Report generated on 2023-04-26, 21:36 UTC

General Statistics

Sample Name	% Host	% Limosilactobacillus fermentum	% Top 5 Species	% Unclassified	% Escherichia coli	% Top 5 Species	% Unclassified	N50 (Kbp)	Assembly Length (Mbp)	K Reads After Filtering	% PF
R8-ZymoMCS	0.1%	4.3%	8.5%	50.3%	16.3%	66.7%	0.7%	36.9Kbp	59.8Mbp	229 007.1	99.9%

Plasmid Detection

Column names reflect unique cluster IDs for detected plasmids. These IDs are like taxonomic identifiers and are stable across time. Cluster IDs are generated separately from bacterial host identification and therefore may be used to track plasmid spread across species. Novel plasmids not found in the BugSeq database are labelled "Novel_-like".

Data is too large to include in PDF report. Please check interactive HTML report or raw results files.

Plasmid Overview

If a detected replicon cannot be assigned to a known incompatibility group, it is assigned to a replicon cluster ("rep_cluster_*"). These replicon cluster types remain stable over time.

Data is too large to include in PDF report. Please check interactive HTML report or raw results files.

Detection of Genotypic Markers Predicting Antimicrobial Resistance

Genotypic Resistance Markers

Sample Name	aac(6')-Iaa	blaOXA-486	blaPAO	blaZ	crpP	fosX
R8-ZymoMCS	Present	Present	Present	Present	Present	Present

Genotypic Resistance Markers Stratified by Antimicrobial and Organism

Note: Genotype does not necessarily predict phenotypic antimicrobial resistance. Laboratory and clinical correlation are required.

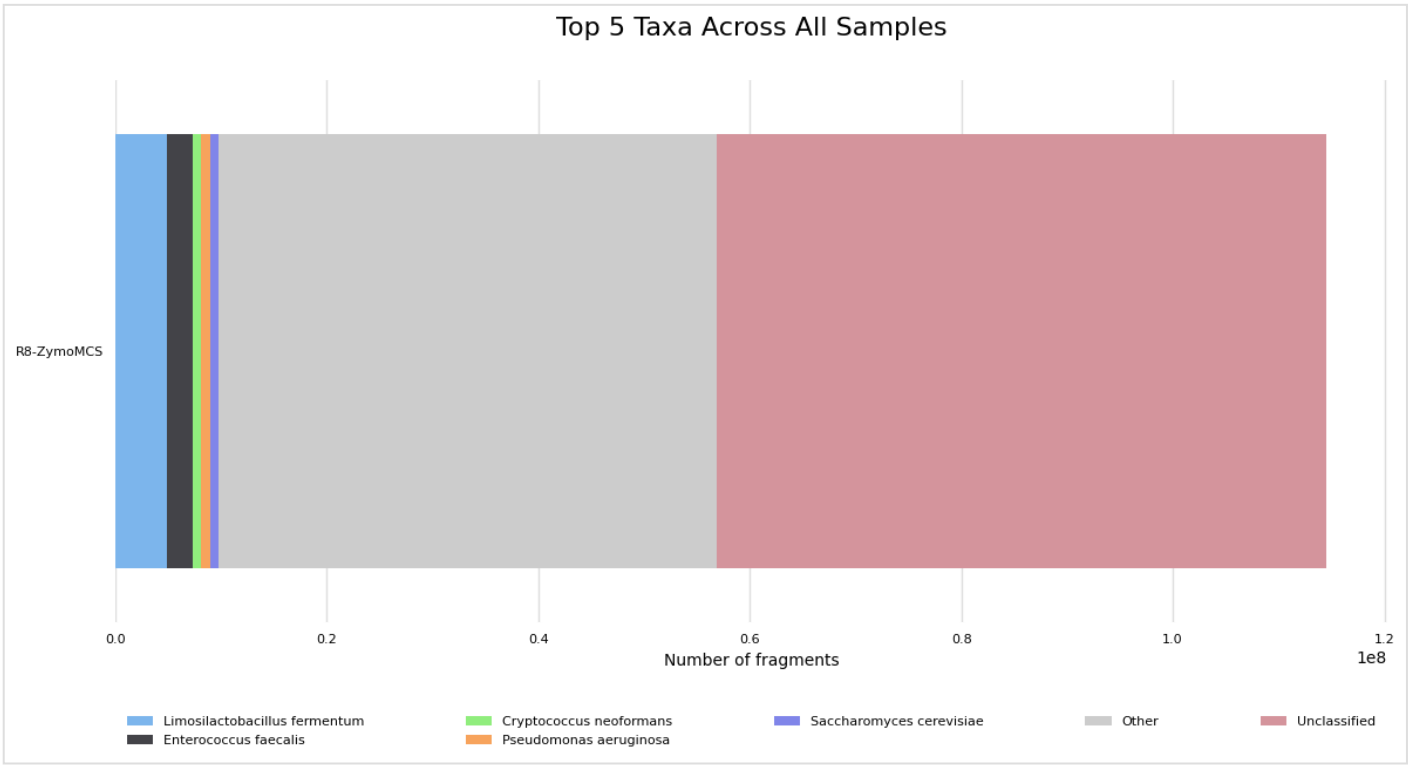
Data is too large to include in PDF report. Please check interactive HTML report or raw results files.

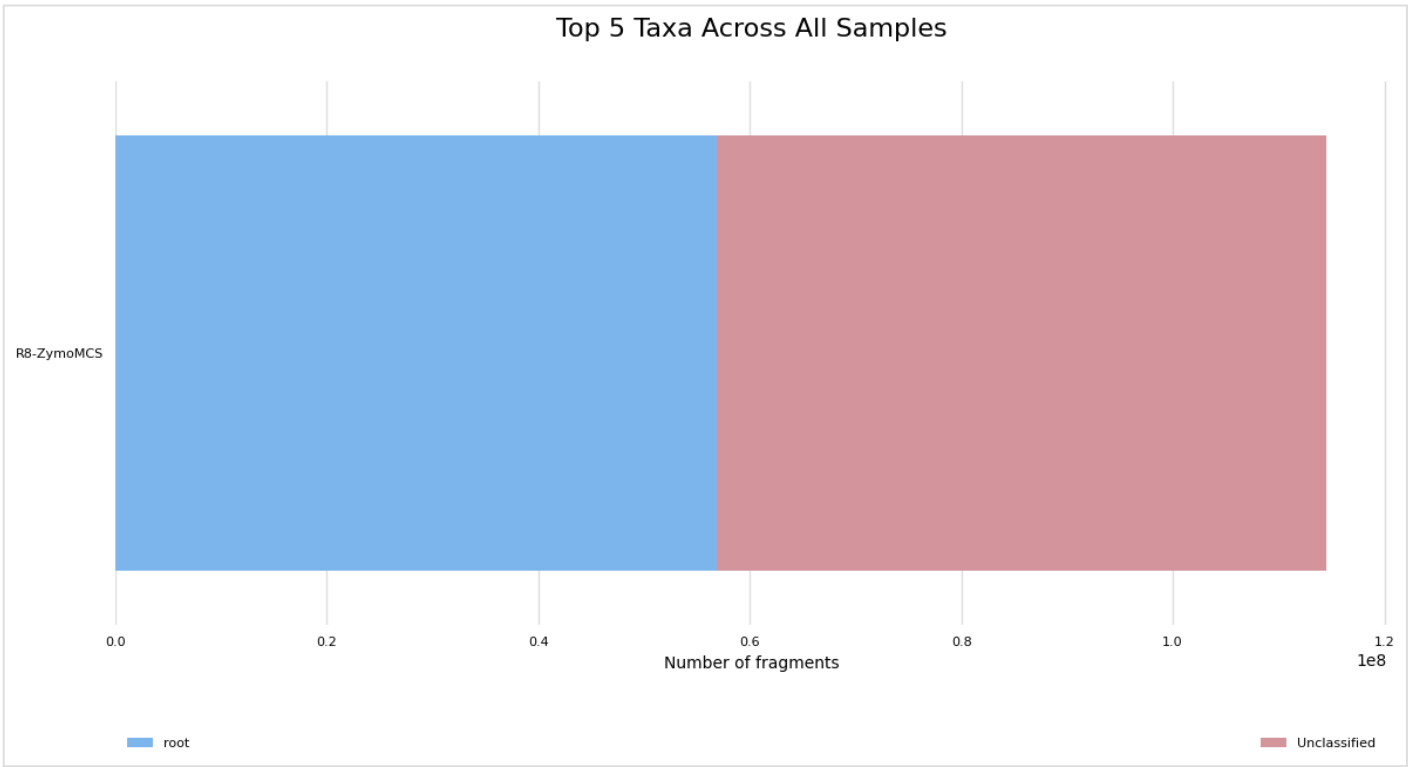
Metagenomic Classification from Reads

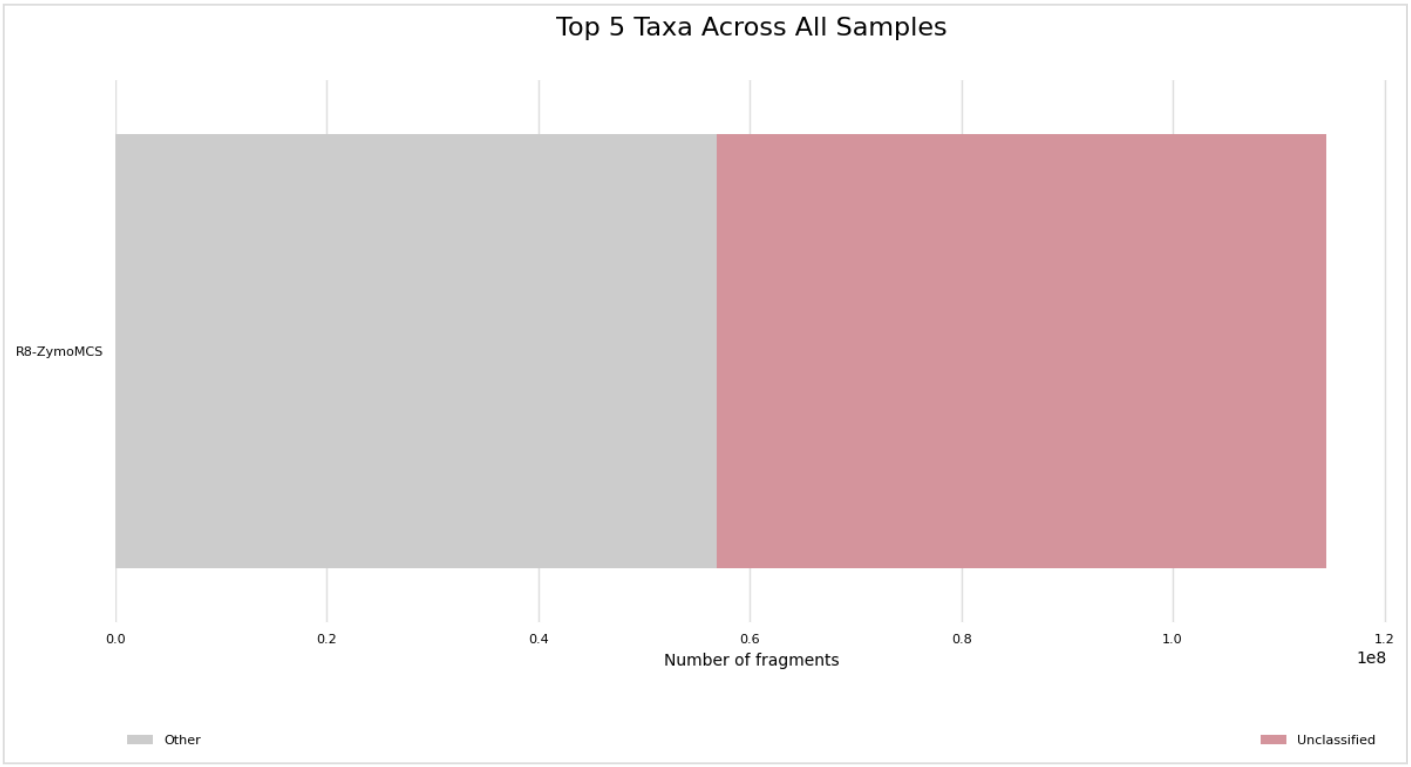
Metagenomic Classification from Reads as reported below is performed with platform specific, leading accuracy metagenomic classifiers. *DOI: 10.1186/s12859-021-04089-5.*

Top taxa

The number of reads falling into the top 5 taxa across different ranks.





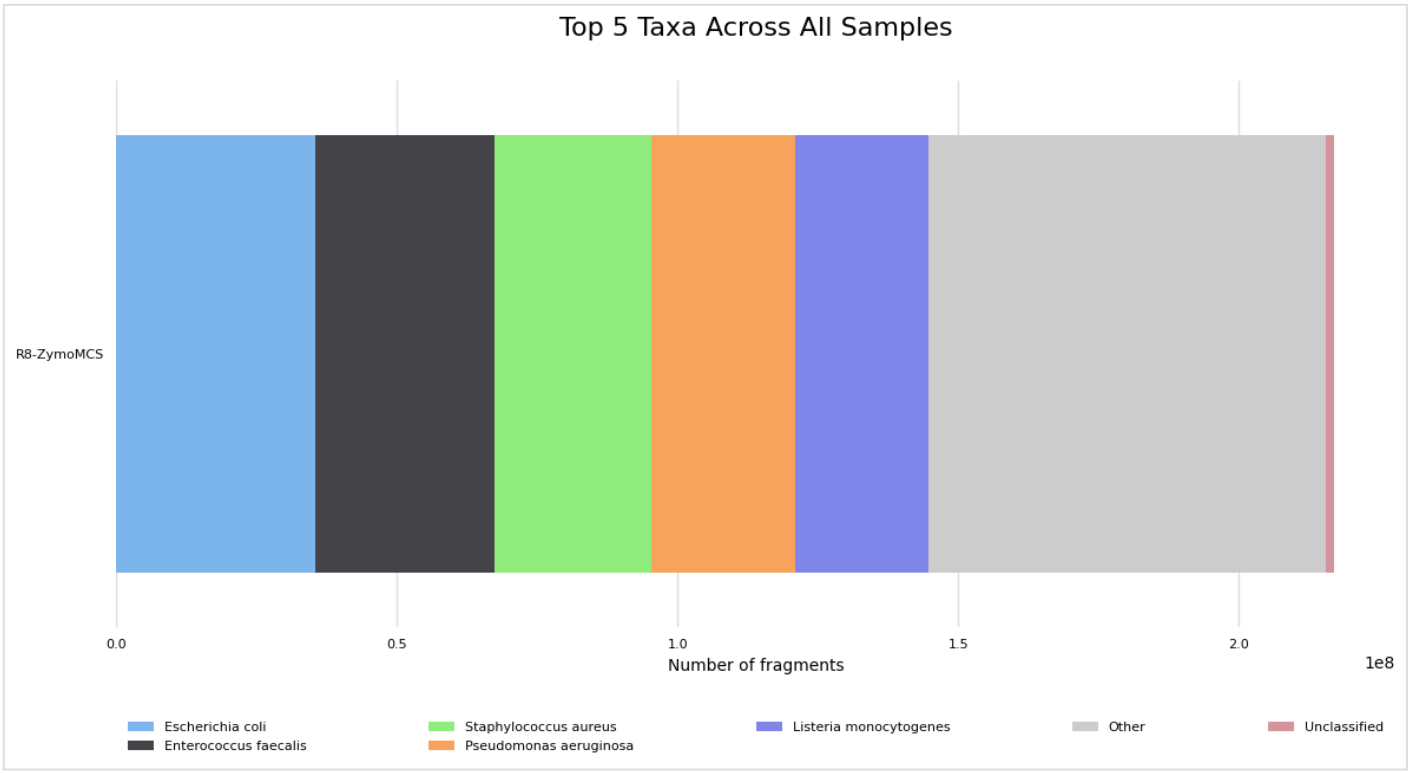

Top 5 Taxa Across All Samples
R8-ZymoMCS
0.0
0.2
0.4
0.6
0.8
1.0
1.2
1e8
Number of fragments
Other
Unclassified

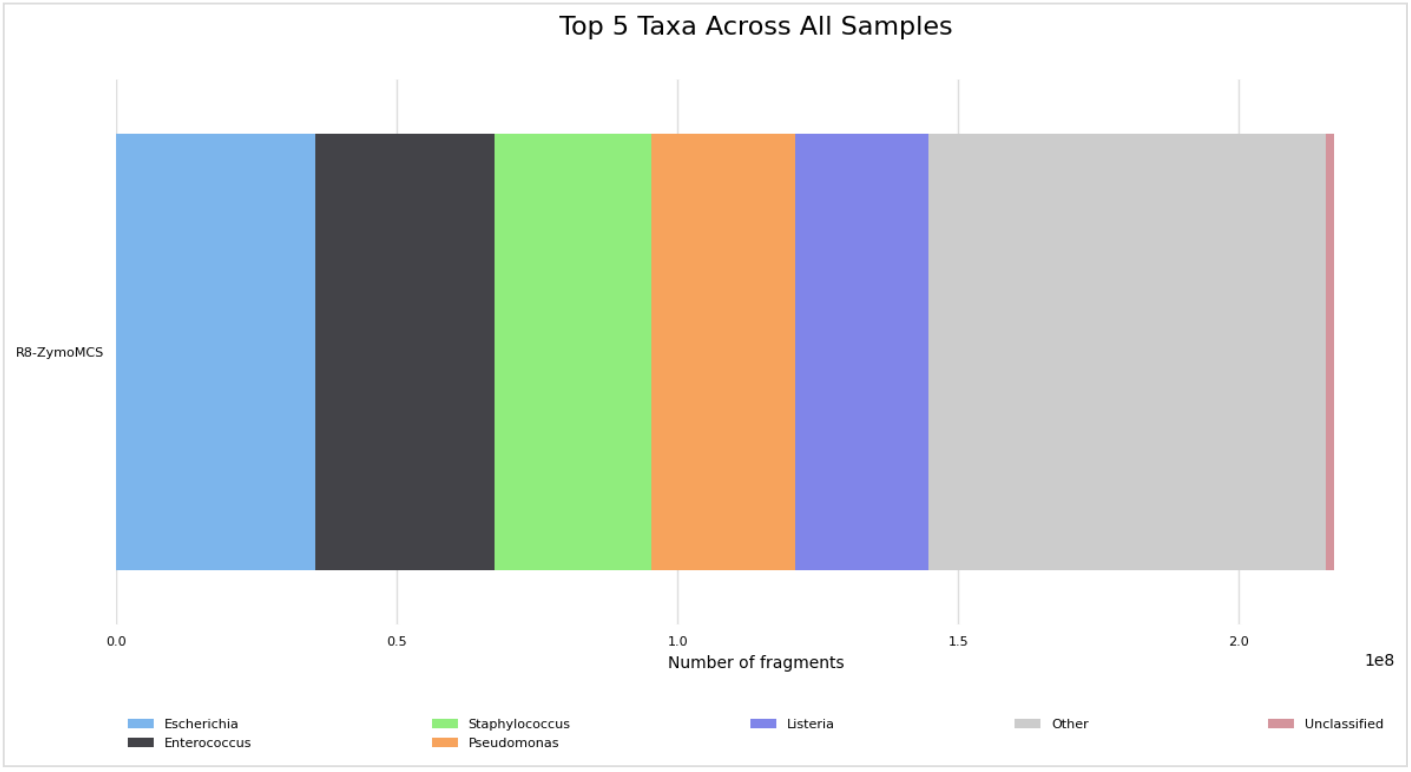
Metagenomic Classification from Assembly

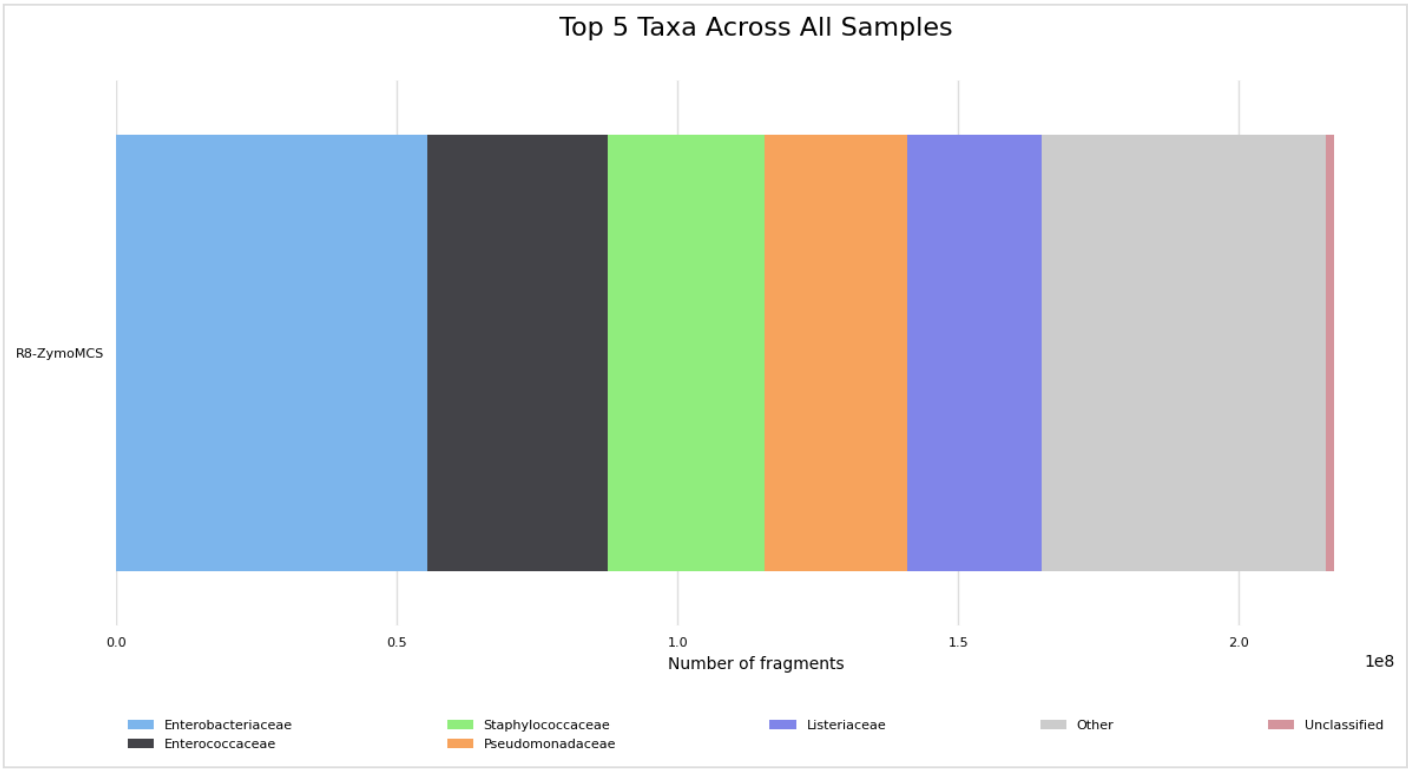
Metagenomic Classification from Assembly as reported below is performed with BugSplit. *DOI: 10.1038/s42003-022-03114-4.*

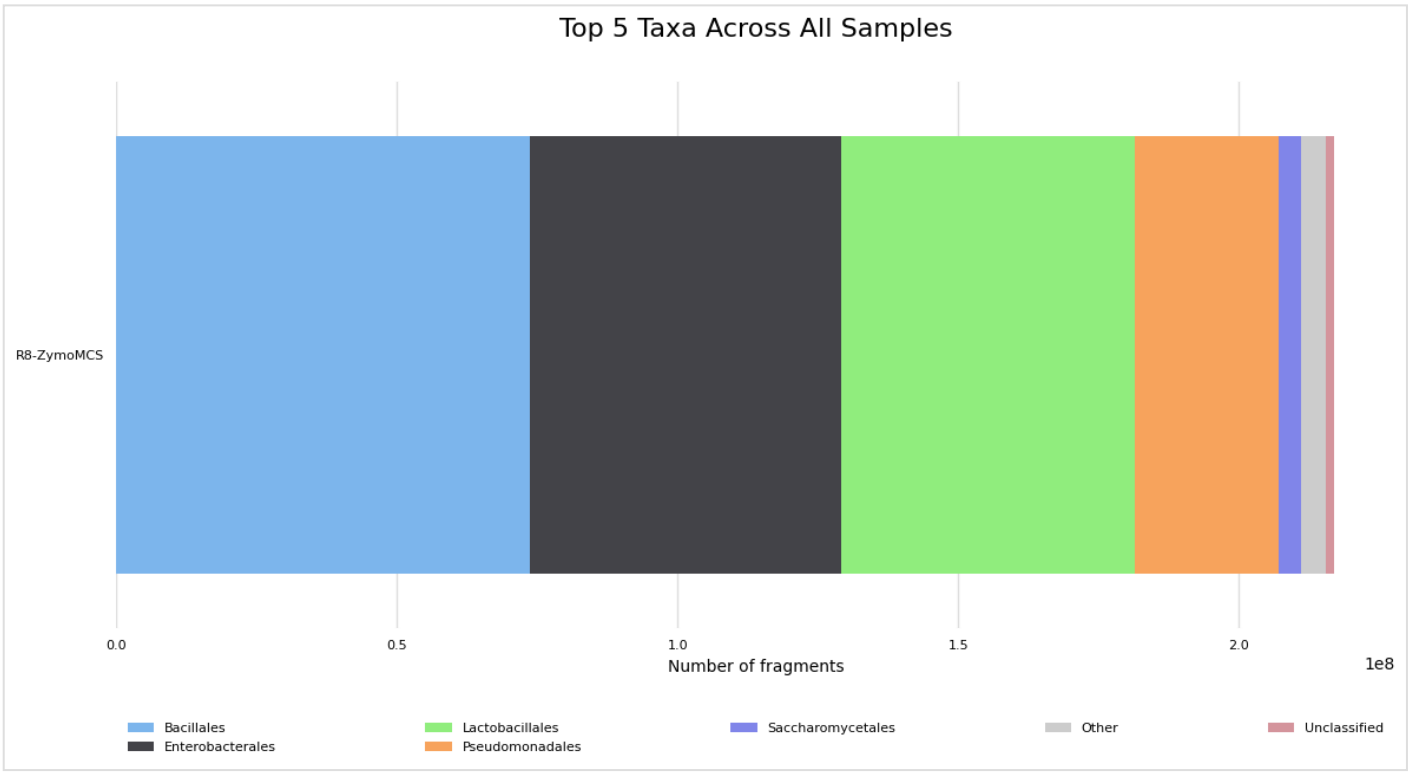
Top taxa

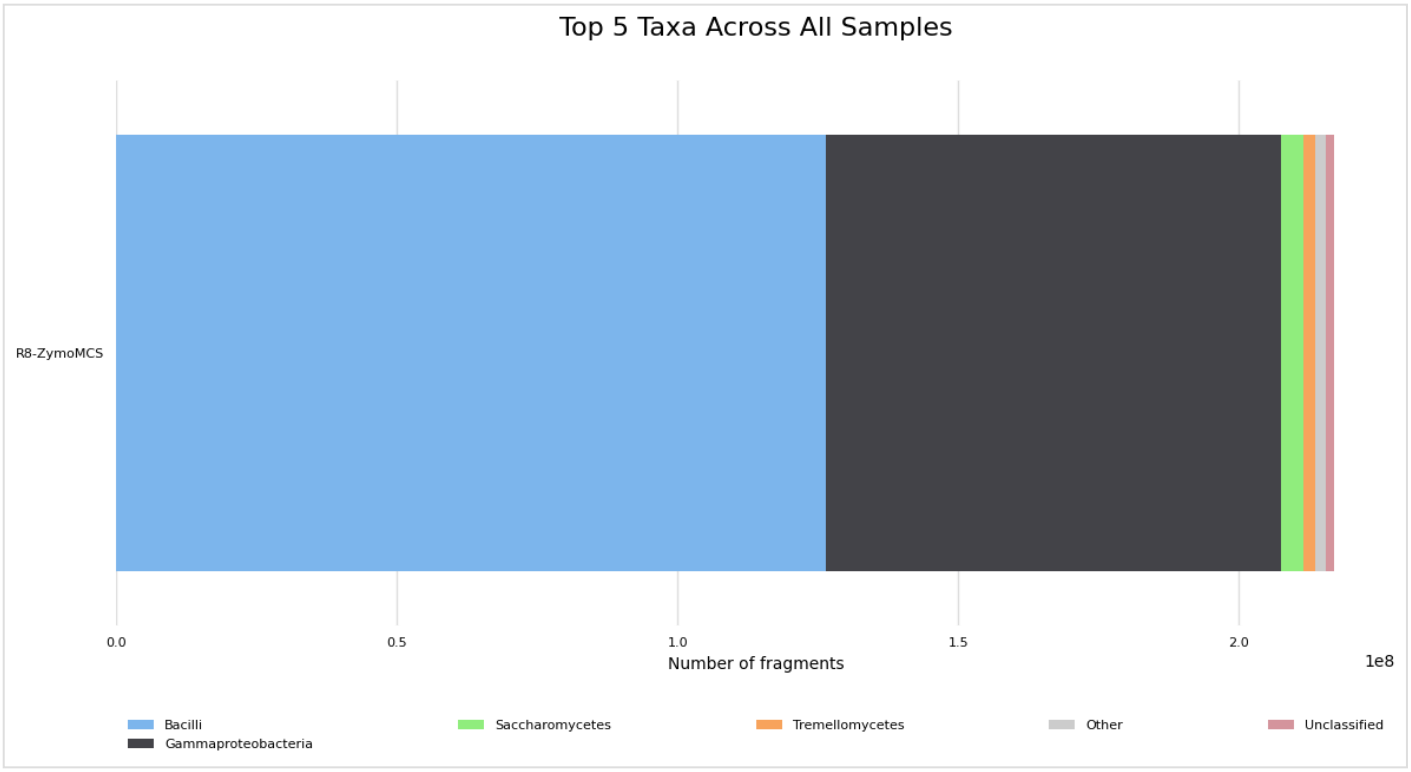
The number of reads falling into the top 5 taxa across different ranks.

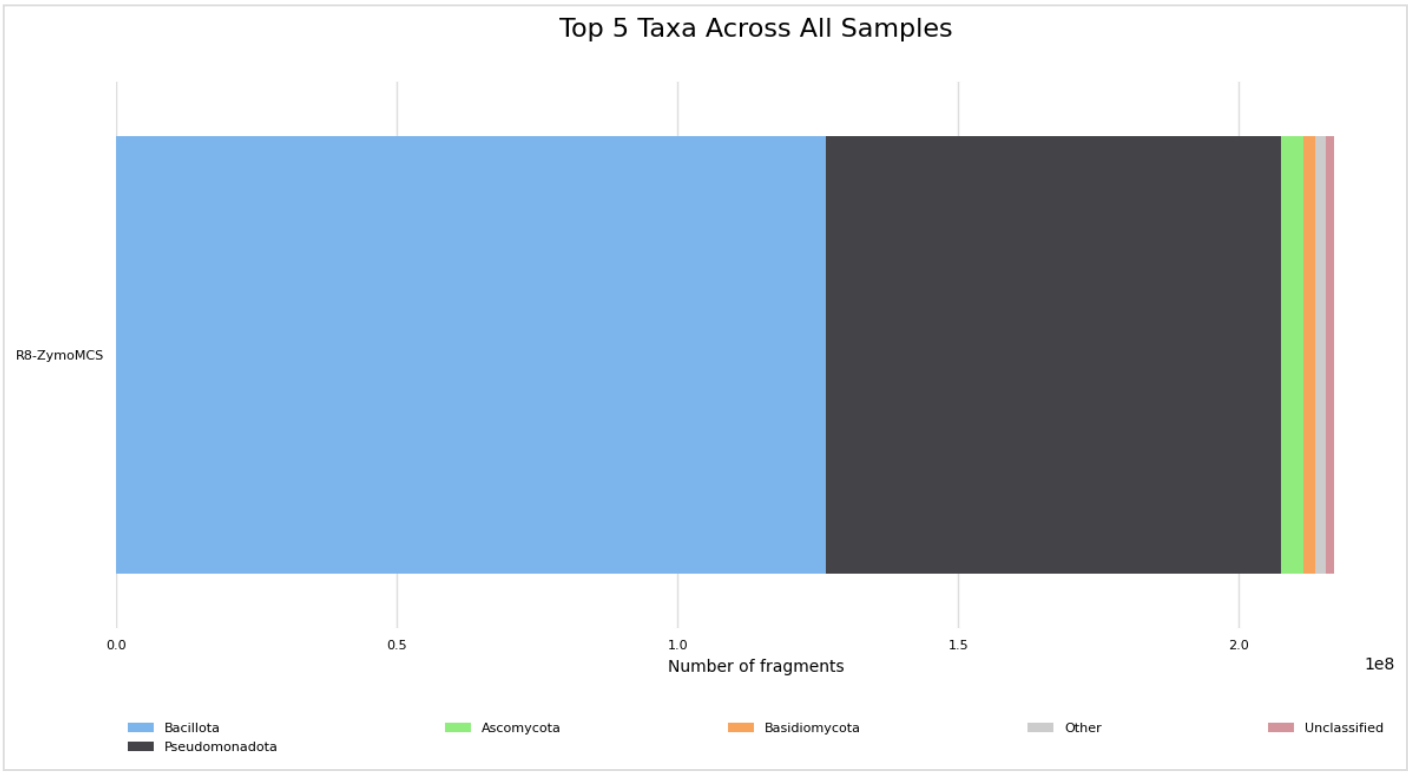


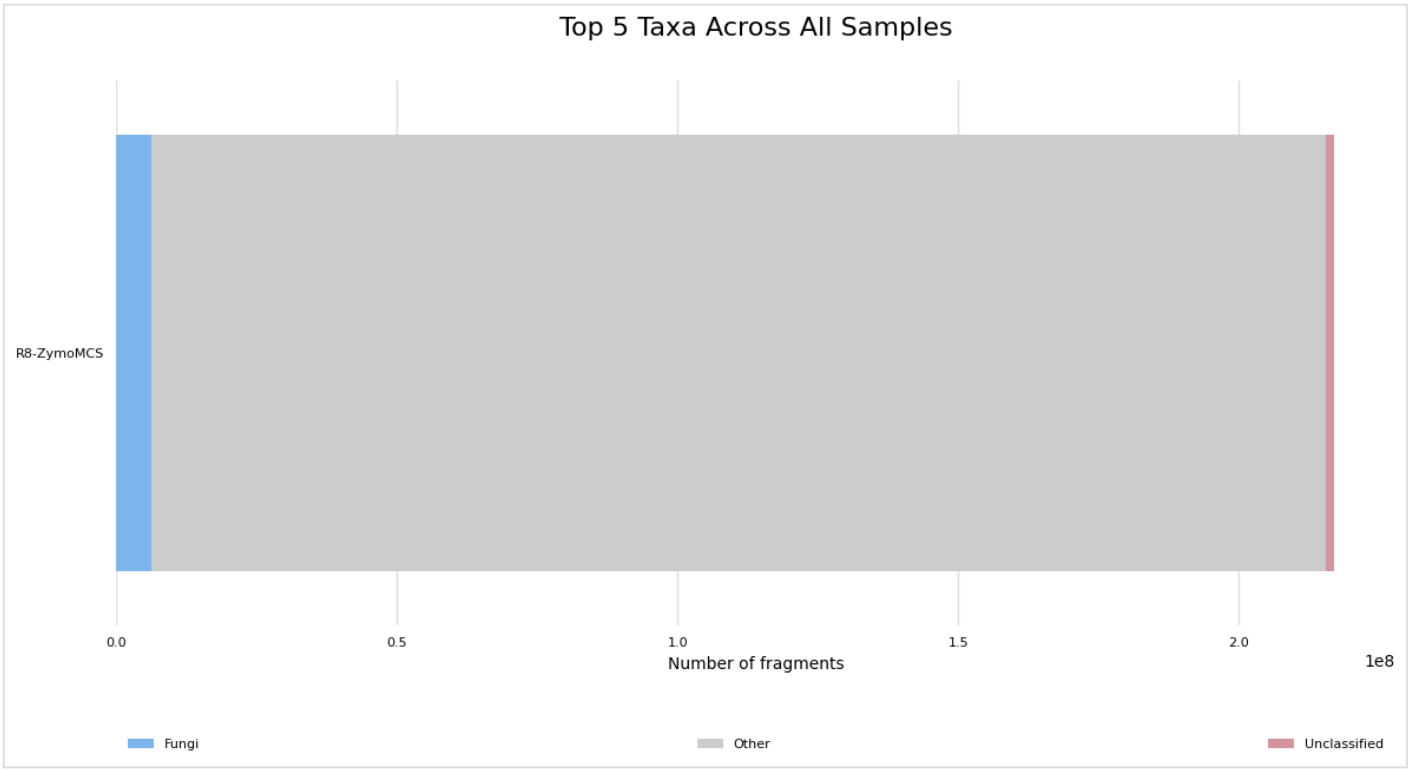


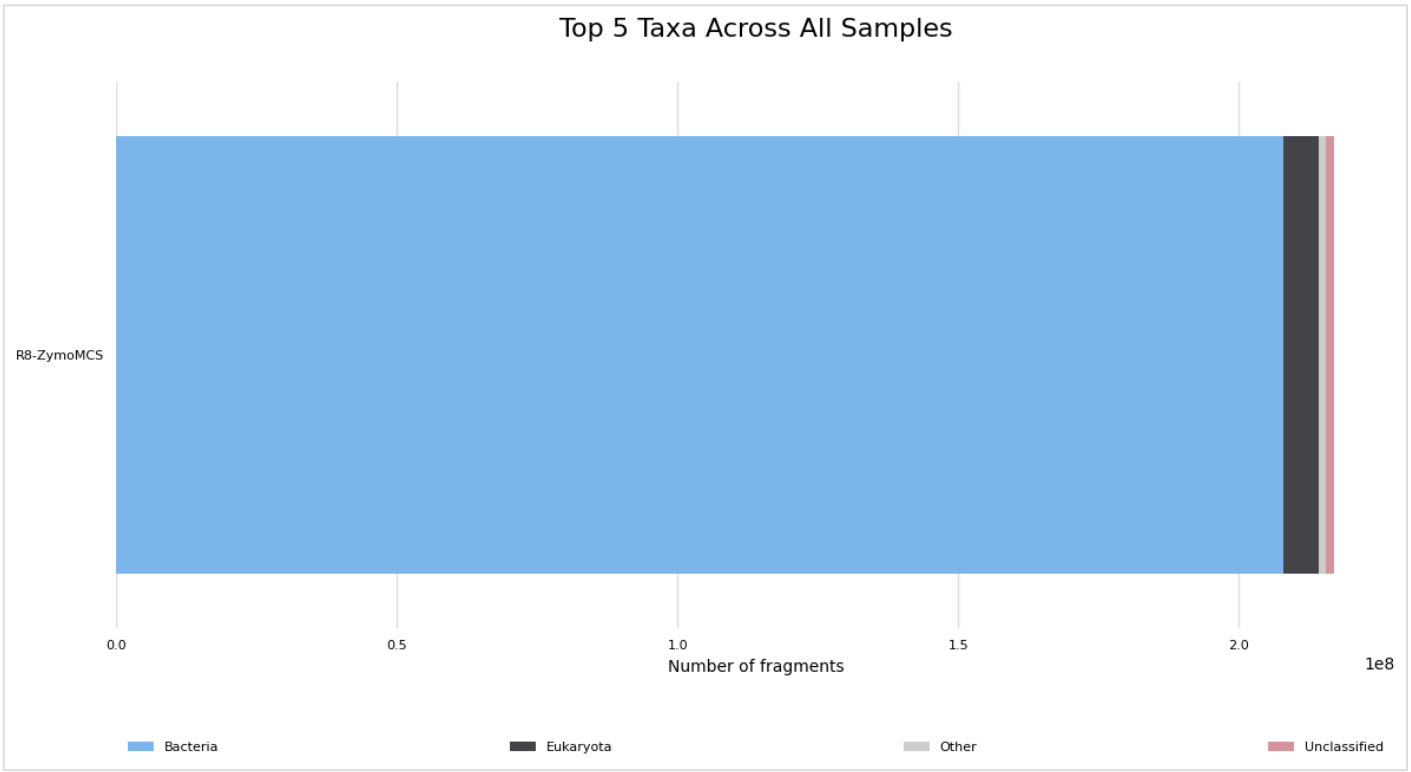

Top 5 Taxa Across All Samples
R8-ZymoMCS
0.0
0.5
1.0
1.5
2.0
Number of fragments
1e8
Enterobacteriaceae
Enterococcaceae
Staphylococcaceae
Pseudomonadaceae
Listeriaceae
Other
Unclassified

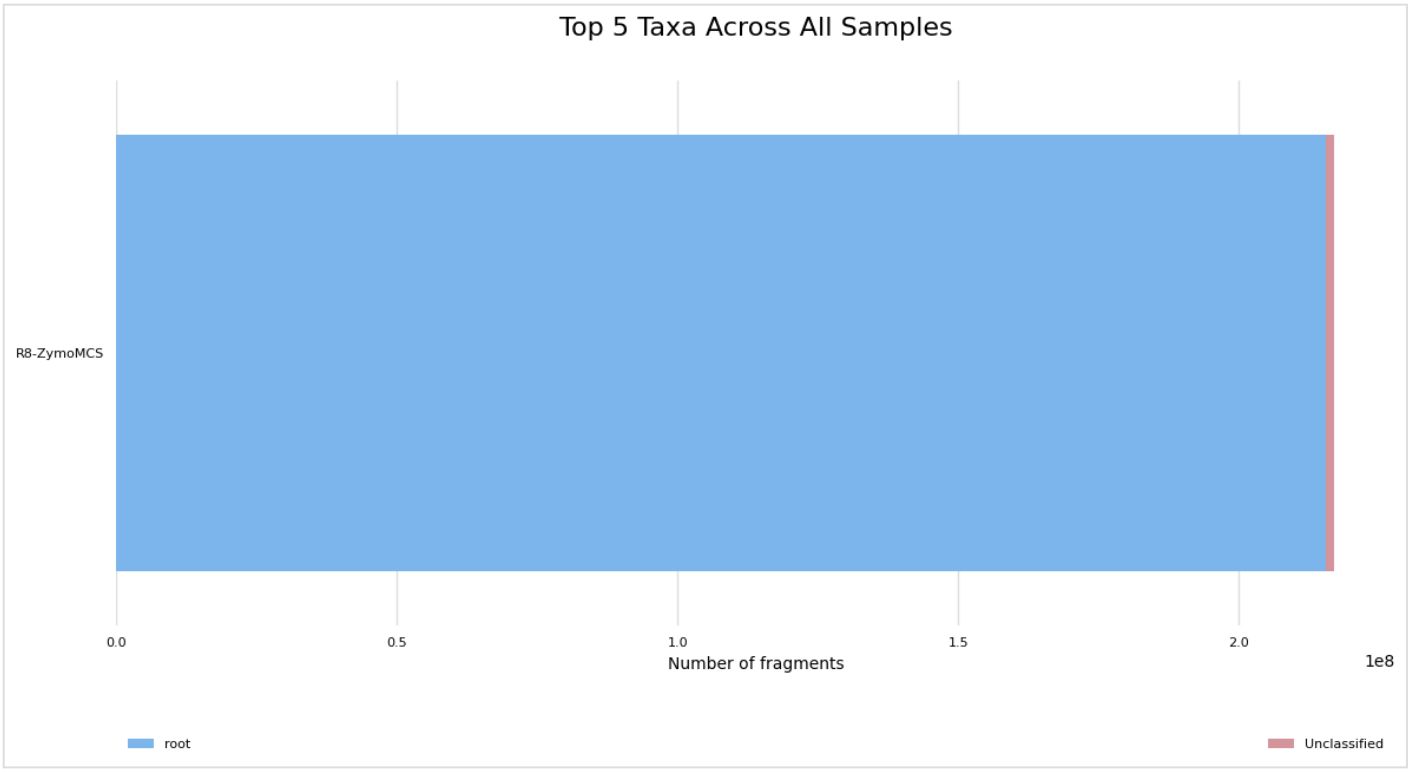

Top 5 Taxa Across All Samples
R8-ZymoMCS
0.0
0.5
1.0
1.5
2.0
Number of fragments
1e8
Bacillales
Enterobacterales
Lactobacillales
Pseudomonadales
Saccharomycetales
Other
Unclassified

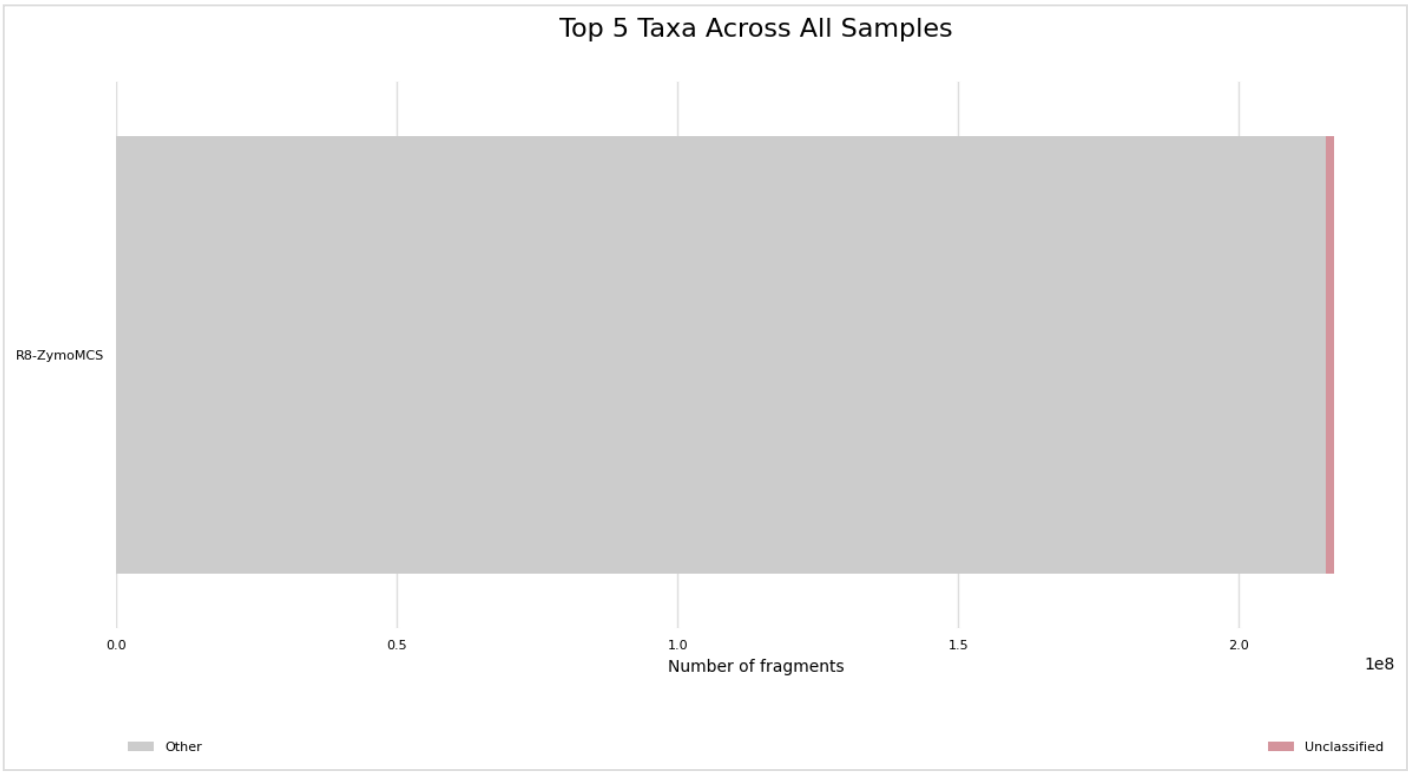

Top 5 Taxa Across All Samples
R8-ZymoMCS
0.0
0.5
1.0
1.5
2.0
Number of fragments
1e8
Bacilli
Gammaproteobacteria
Saccharomycetes
Tremellomycetes
Other
Unclassified


Top 5 Taxa Across All Samples
R8-ZymoMCS
0.0
0.5
1.0
1.5
2.0
Number of fragments
1e8
Bacillota
Pseudomonadota
Ascomycota
Basidiomycota
Other
Unclassified


Top 5 Taxa Across All Samples
R8-ZymoMCS
0.0
0.5
1.0
1.5
2.0
Number of fragments
1e8
Fungi
Other
Unclassified


Top 5 Taxa Across All Samples
R8-ZymoMCS
0.0
0.5
1.0
1.5
2.0
Number of fragments
1e8
Bacteria
Eukaryota
Other
Unclassified


Top 5 Taxa Across All Samples
R8-ZymoMCS
0.0
0.5
1.0
1.5
2.0
Number of fragments
1e8
root
Unclassified


Top 5 Taxa Across All Samples
R8-ZymoMCS
0.0
0.5
1.0
1.5
2.0
Number of fragments
1e8
Other
Unclassified

Assembly Statistics

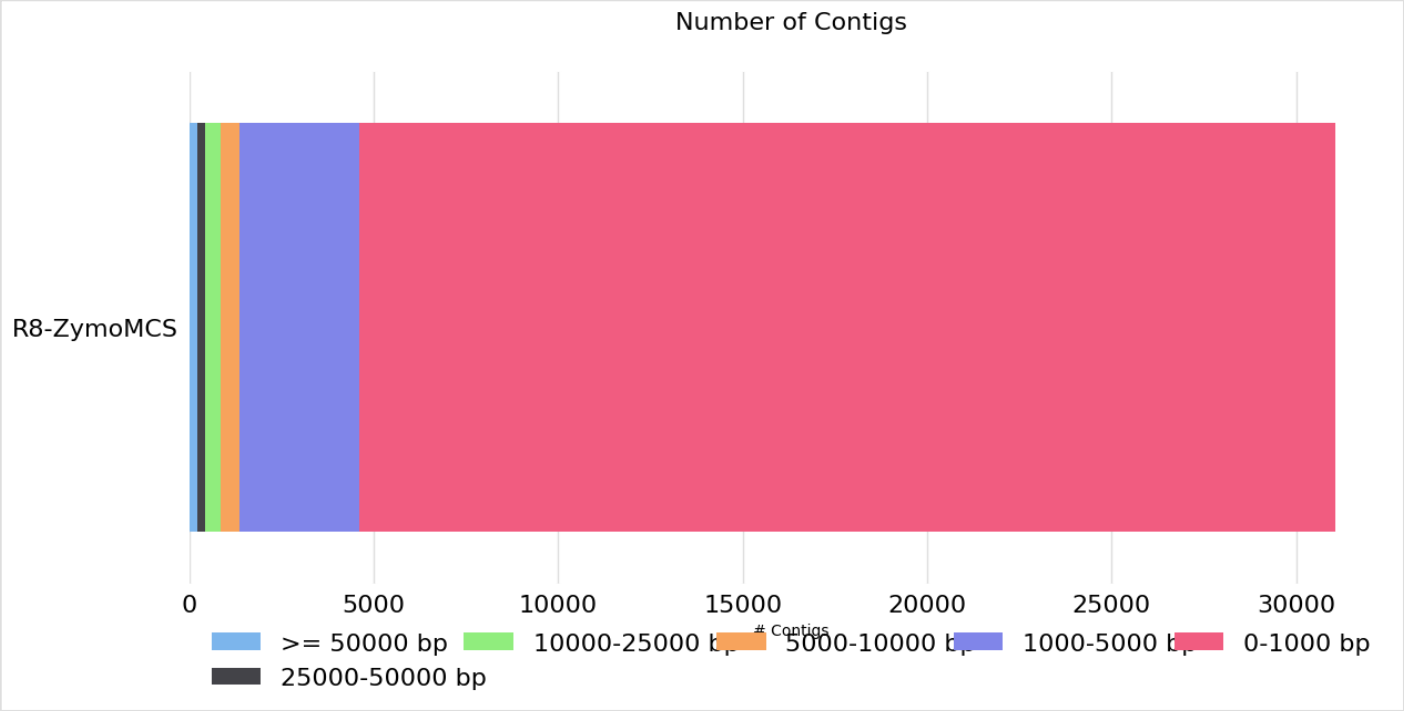
Assembly Statistics reports the length, contiguity and and quality of assemblies. *DOI: 10.1093/bioinformatics/btt086.*

Assembly Statistics

Sample Name	N50 (Kbp)	L50	Largest contig (Kbp)	Length (Mbp)
R8-ZymoMCS	36.9Kbp	310.0	847.6Kbp	59.8Mbp

Number of Contigs

This plot shows the number of contigs found for each assembly, broken down by length.

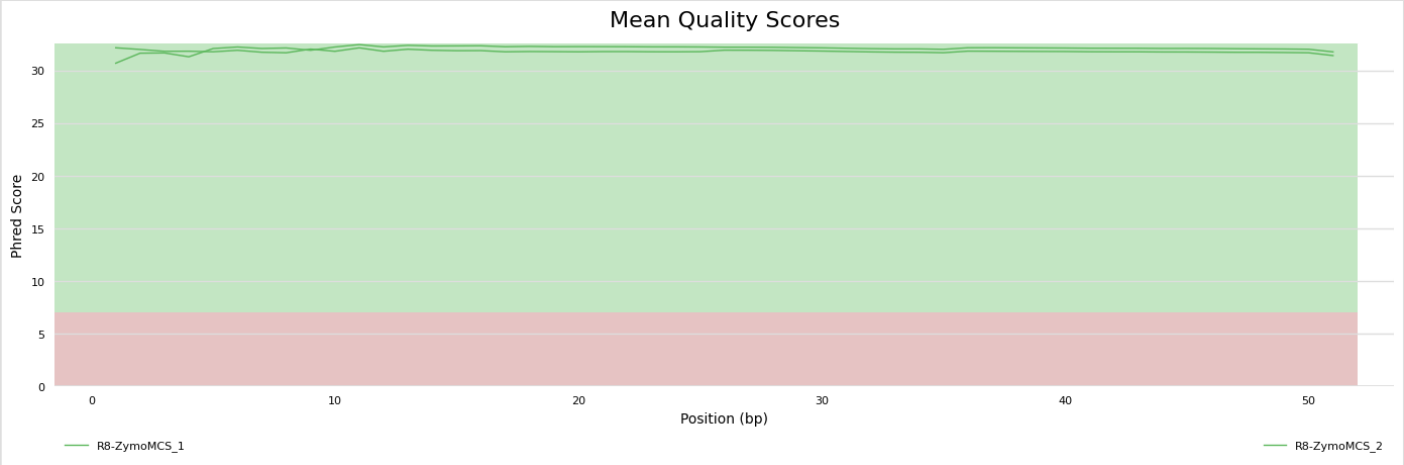


Read Quality Control

Read Quality Control assesses the quality of input reads before any processing. BugSeq automatically trims and filters reads before downstream analysis.

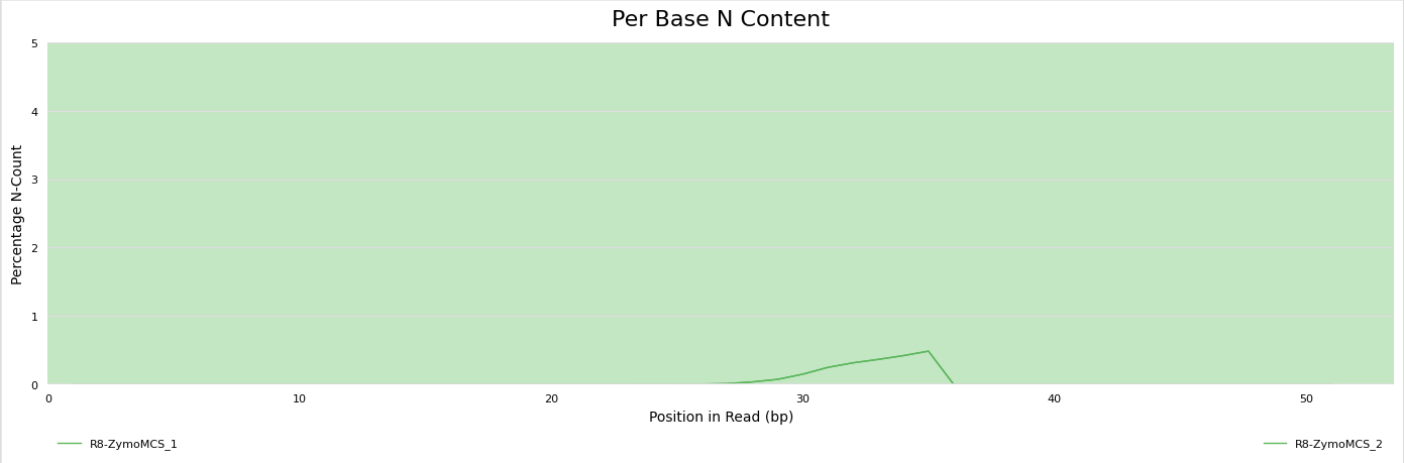
Sequence Quality Histograms

The mean quality value across each base position in the read.



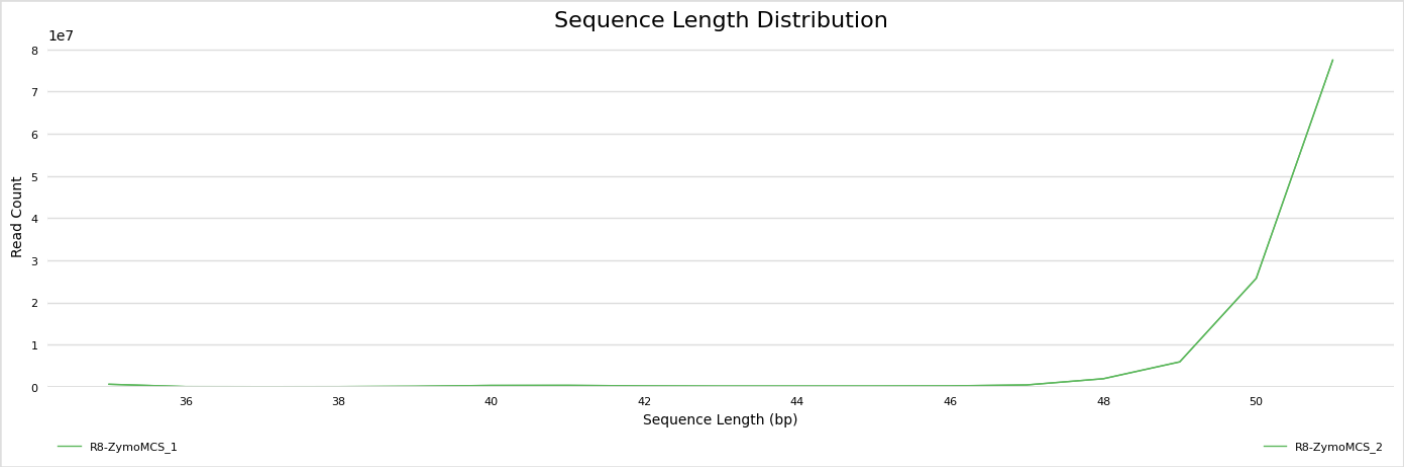
Per Base N Content

The percentage of base calls at each position for which an `N` was called.



Sequence Length Distribution

The distribution of fragment sizes (read lengths) found. See the FastQC help



Adapter Content

The cumulative percentage count of the proportion of your library which has seen each of the adapter sequences at each position.

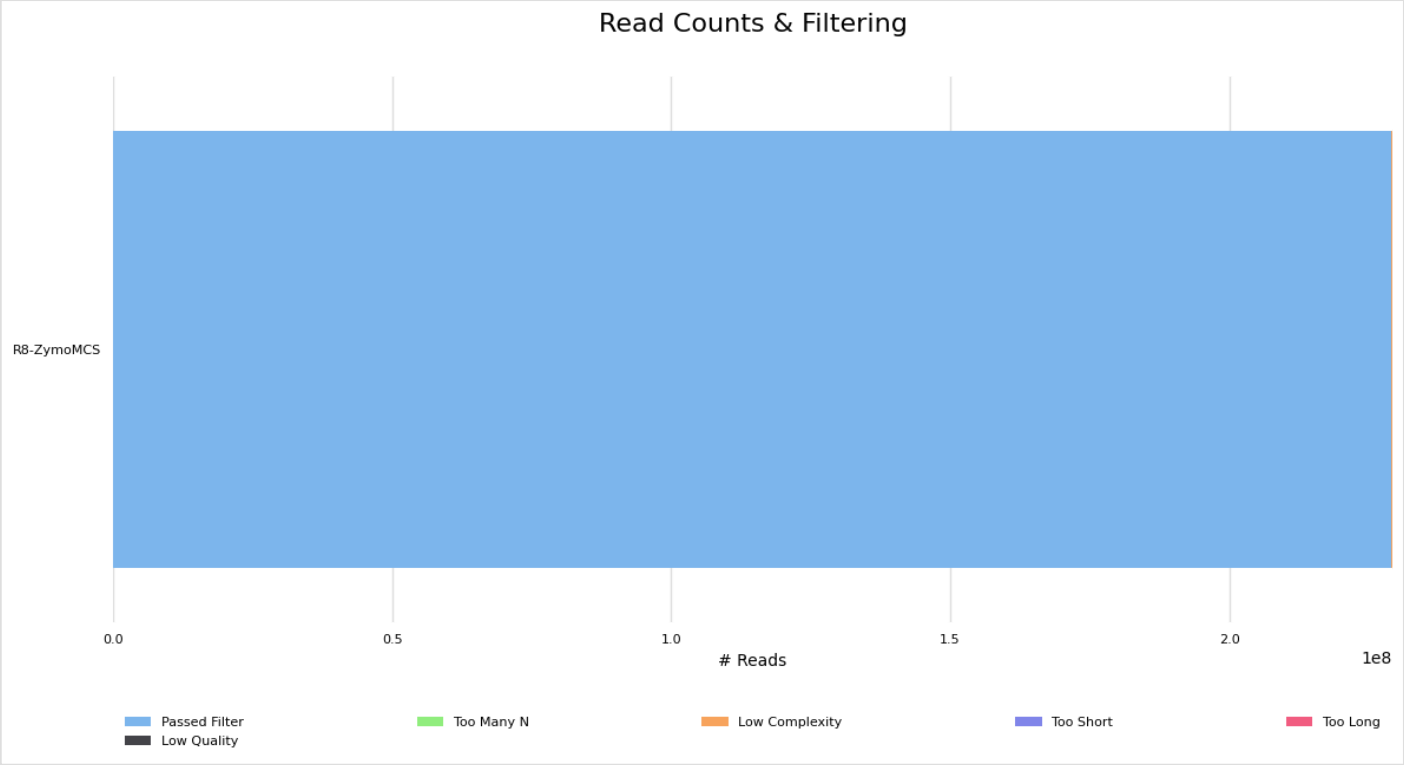
No samples found with any adapter contamination > 0.1%

Read Preprocessing

Read Preprocessing trims, filters and corrects reads before further processing. Thresholds for trimming and filtering are based on sequencing platform and experiment type. *DOI: 10.1093/bioinformatics/bty560.*

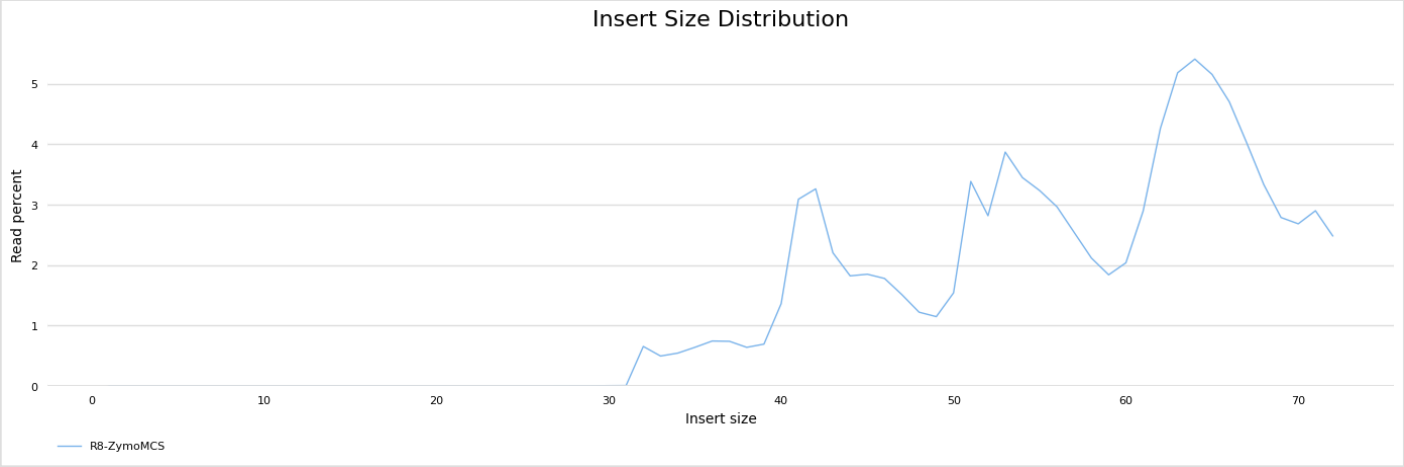
Filtered Reads

Filtering statistics of sampled reads.



Insert Sizes

Insert size estimation of sampled reads.



Per Sequence Quality Scores

The number of reads with median quality scores. Shows if a subset of reads has poor quality.