BUGSEQ

Automated bioinformatics for microbiology labs.

Analysis Name	Long Read Analysis for Capstone
Run ID	43431b14-7ba9-4031-a077-b79803550bd4
BugSeq Pipeline Version	Latest (2023-03-25)
Metagenomic Database	BugSeq Default
Contact E-mail	support@bugseq.com

Report generated on 2023-03-25, 19:22 UTC

General Statistics

Sample Name	% Host	Median Read Length	Median Read Phred Score	% Limosilactobacillus fermentum	% Top 5 Species	% Unclassified	% Bacillus spizizenii	% Top 5 Species	% Unclassified	N50 (Mbp)	Assembly Length (Mbp)	K Reads After Filtering	% PF
75312bbb_noBarcode	0.5%	2205bp	33	14.6%	65.4%	0.1%	13.8%	64.0%	2.9%	1.6Mbp	32.1Mbp	206.3	100.0%

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".

Sample Name	AB726	AB461	AA747
75312bbb_noBarcode	Present	Present	Present

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	blaOXA-486	blaPAO	blaZ	crpP	fosX	mph(K)
75312bbb_noBarcode	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.

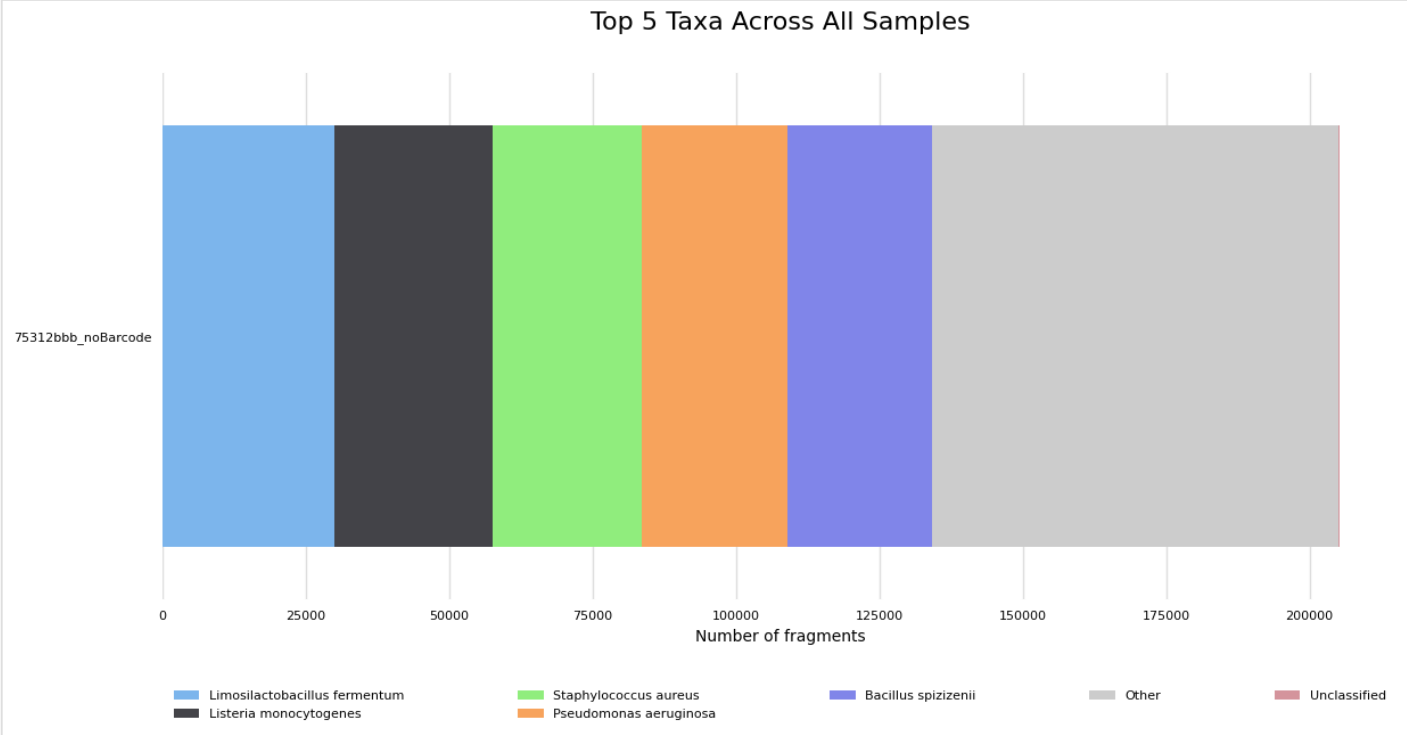
Data is too large to include in PDF report. Please check interactive HTML report or raw results files.

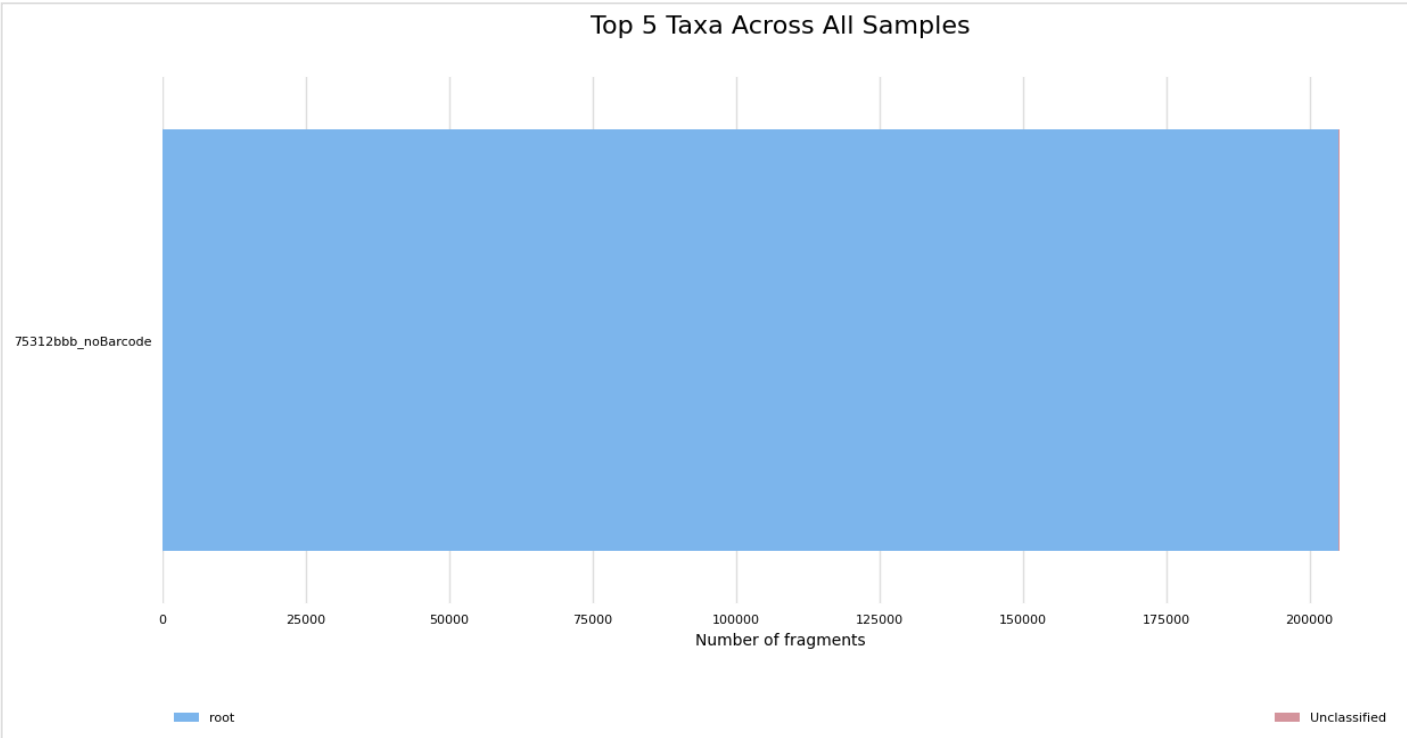
Metagenomic Classification from Reads

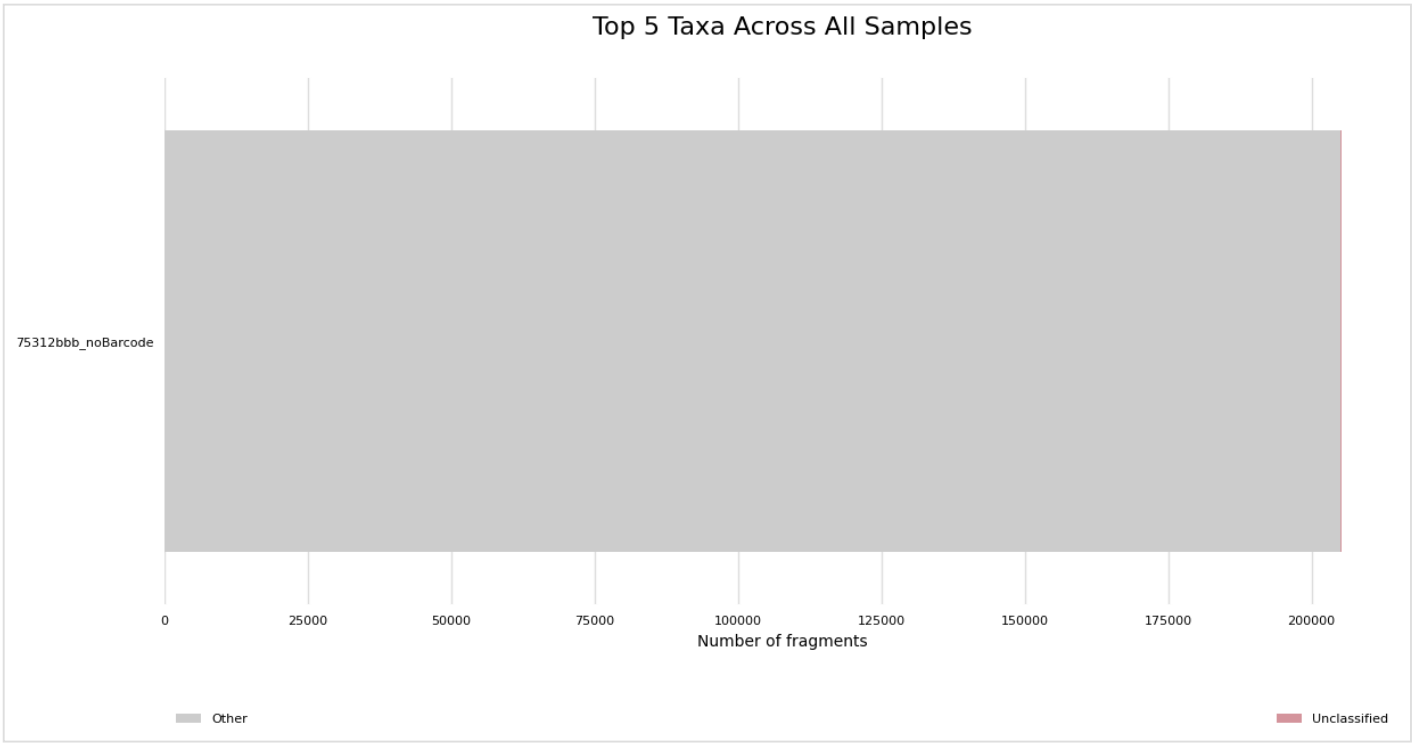
Metagenomic Classification from Reads as reported below is performed with platform specific, leading accuracy metagenomic classifiers. *DOI: 10.1186/s12859-021-04089-5.*

Top taxa

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





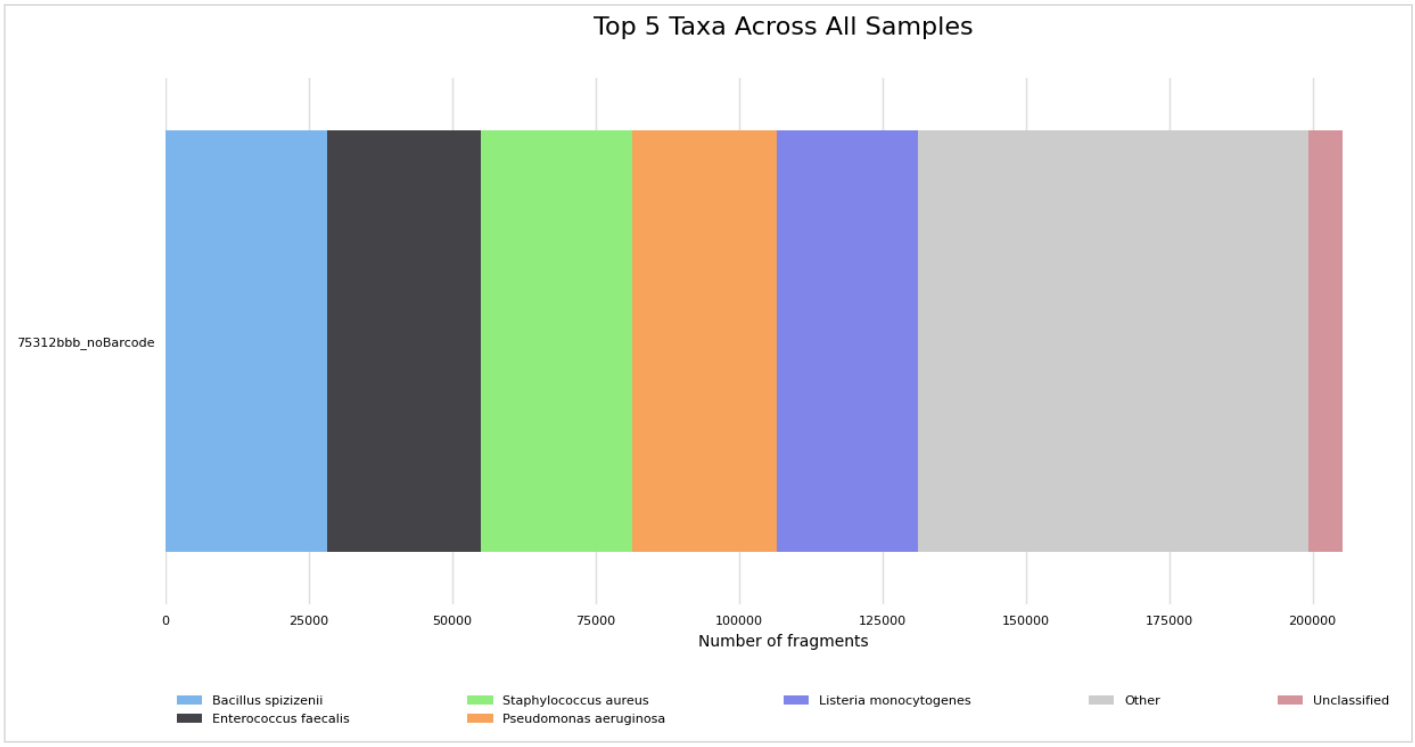

Top 5 Taxa Across All Samples
75312bbb_noBarcode
0
25000
50000
75000
100000
125000
150000
175000
200000
Number of fragments
Other
Unclassified

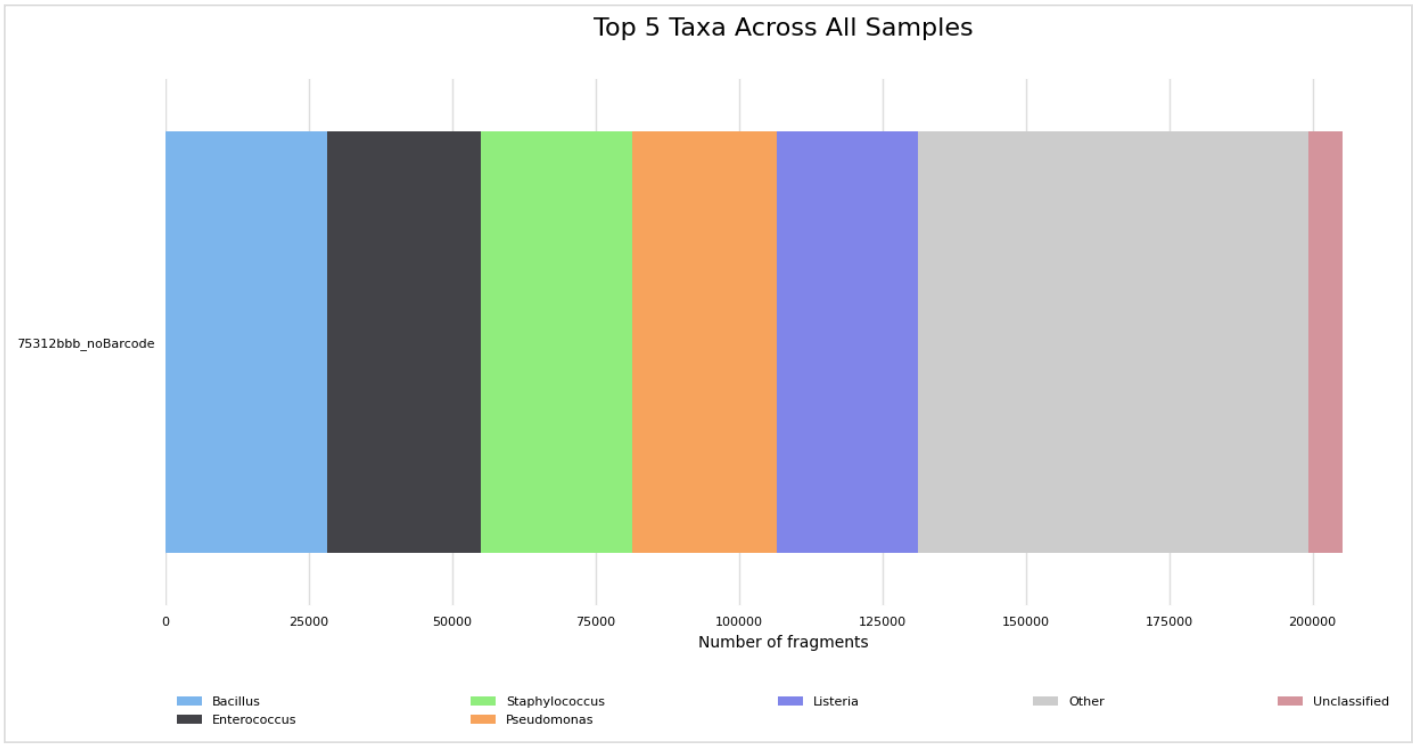
Metagenomic Classification from Assembly

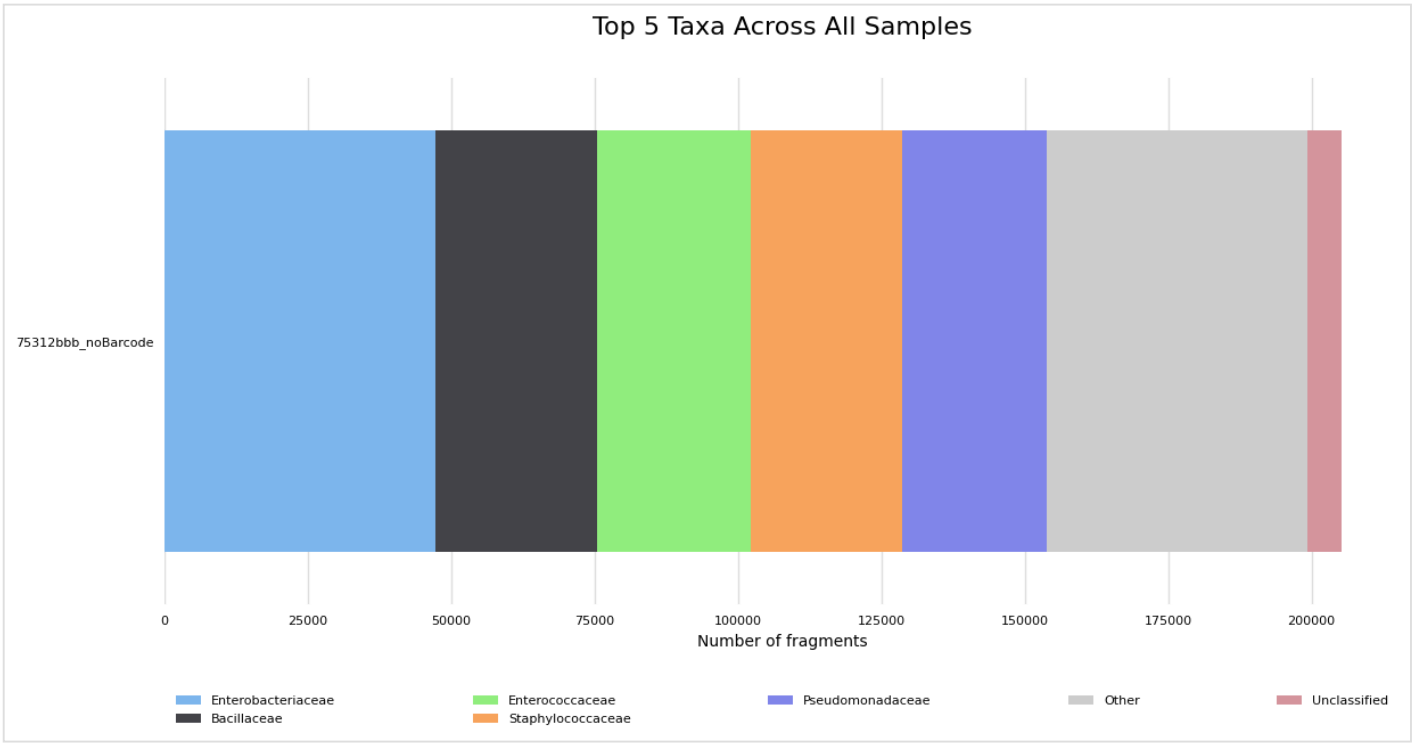
Metagenomic Classification from Assembly as reported below is performed with BugSplit. *DOI: 10.1038/s42003-022-03114-4.*

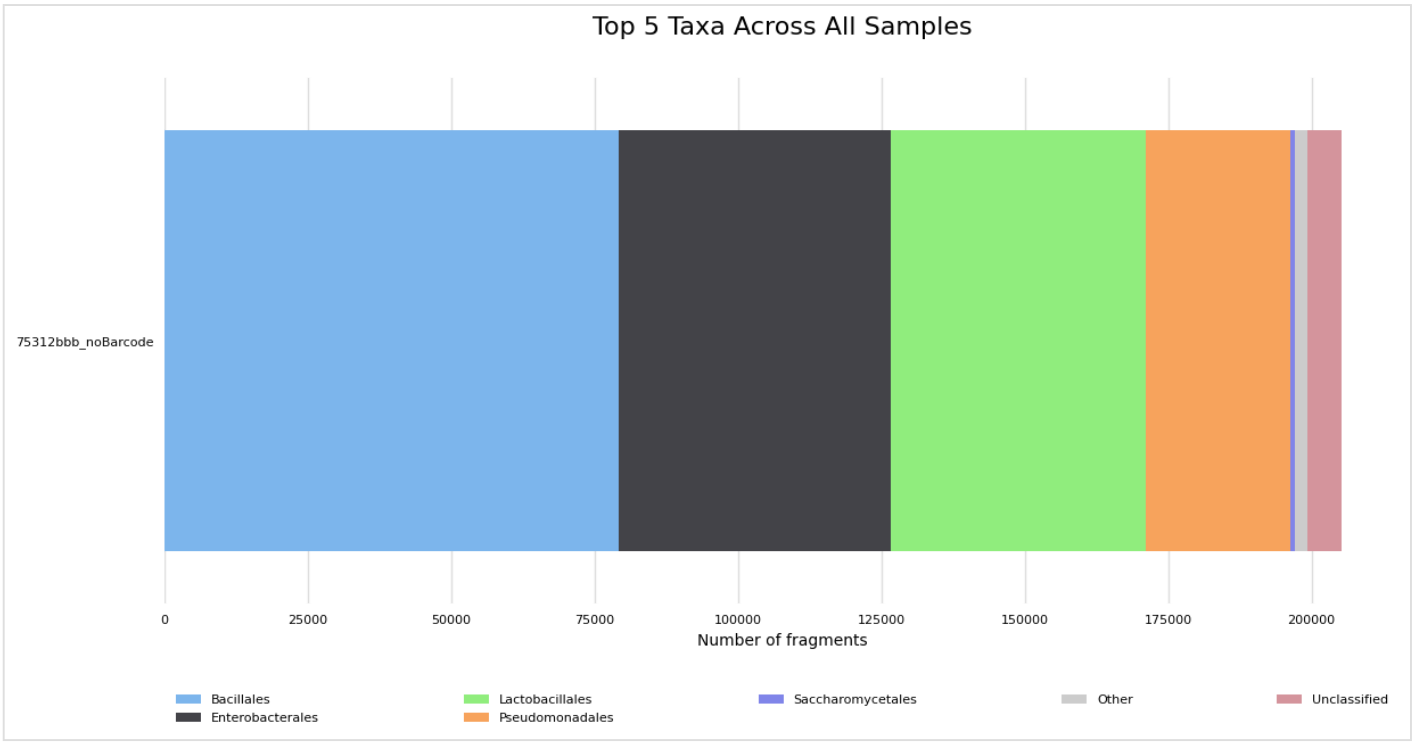
Top taxa

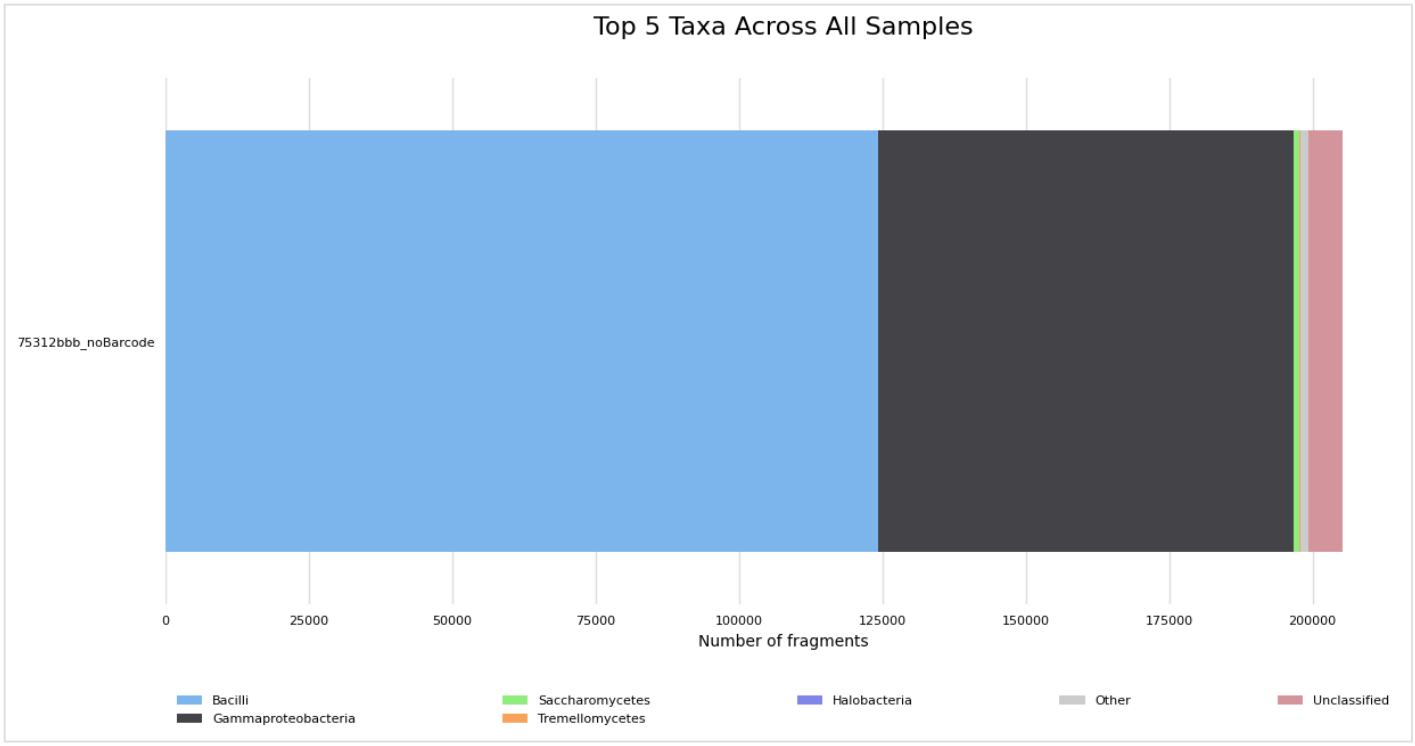
The number of reads falling into the top 5 taxa across different ranks.

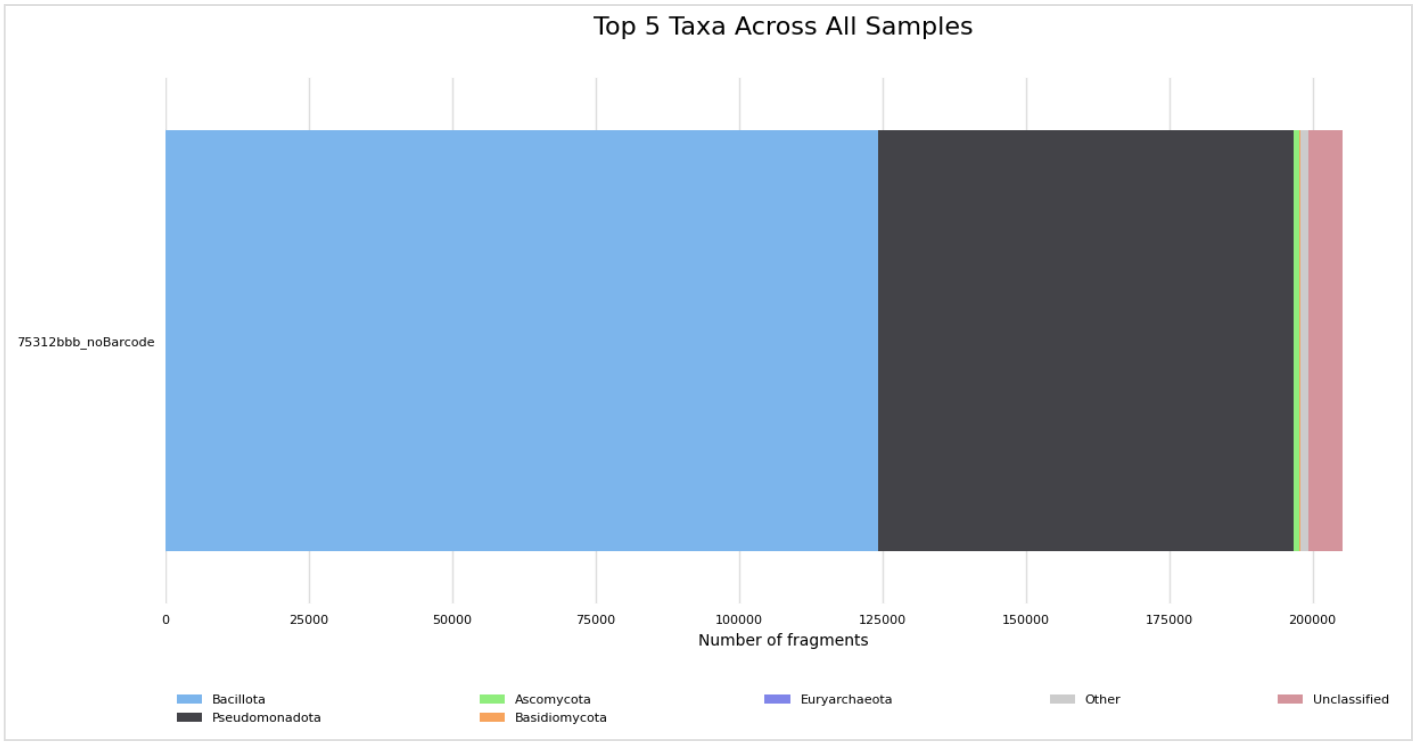


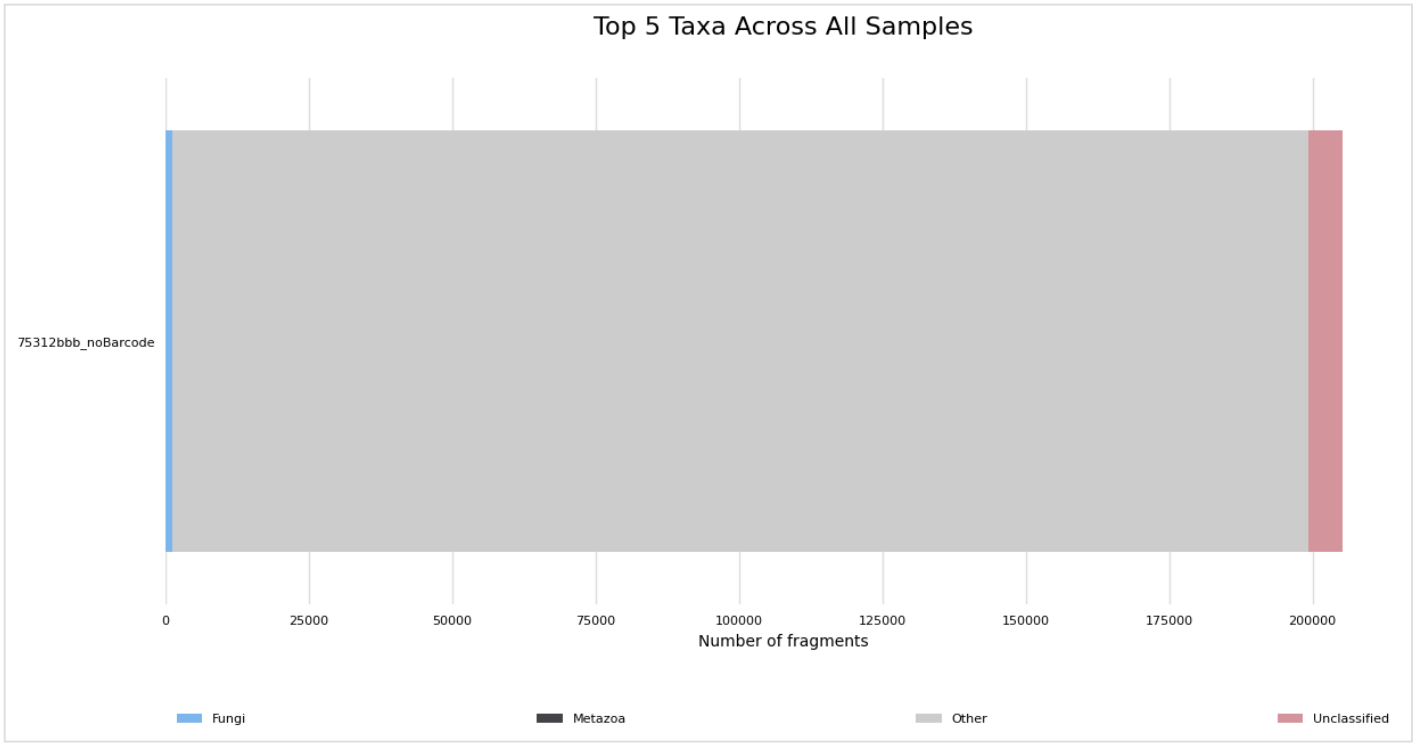


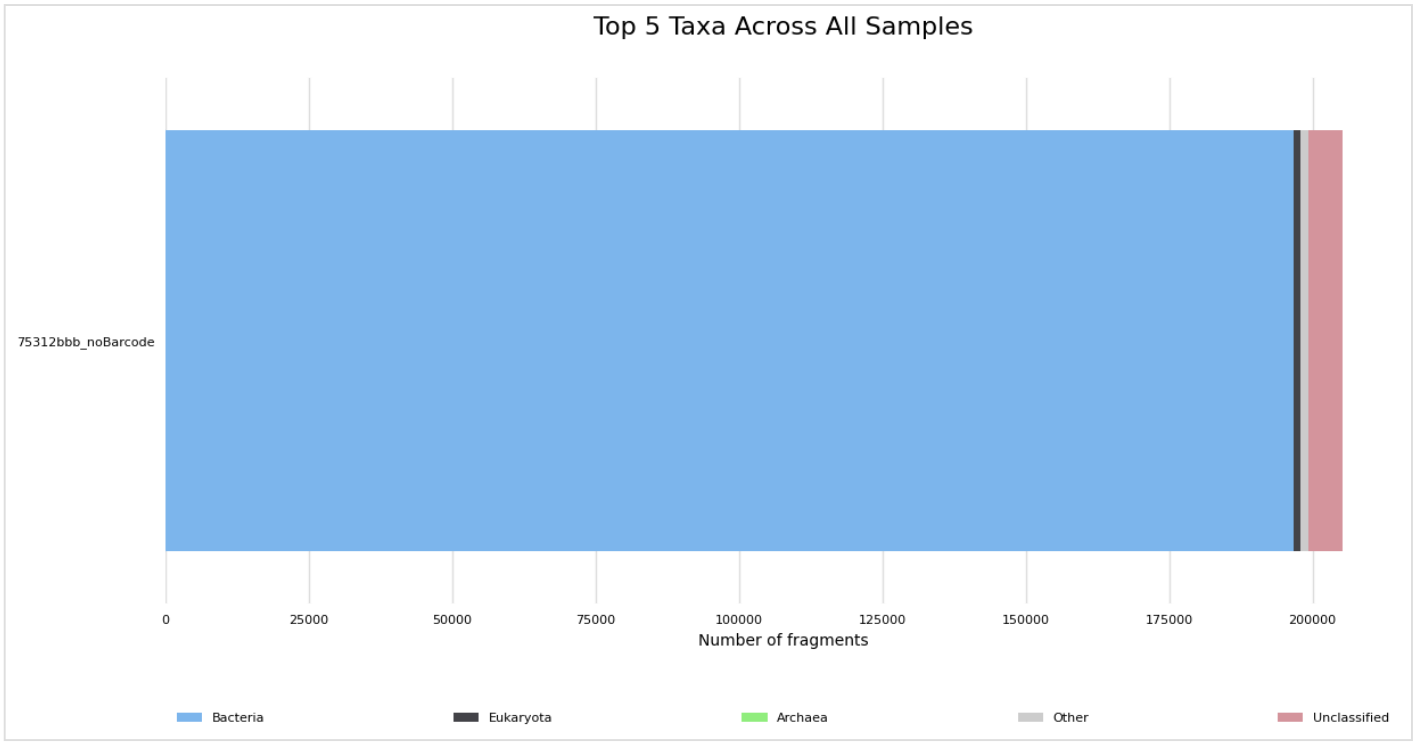

Top 5 Taxa Across All Samples
75312bbb_noBarcode
0
25000
50000
75000
100000
125000
150000
175000
200000
Number of fragments
Enterobacteriaceae
Bacillaceae
Enterococcaceae
Staphylococcaceae
Pseudomonadaceae
Other
Unclassified

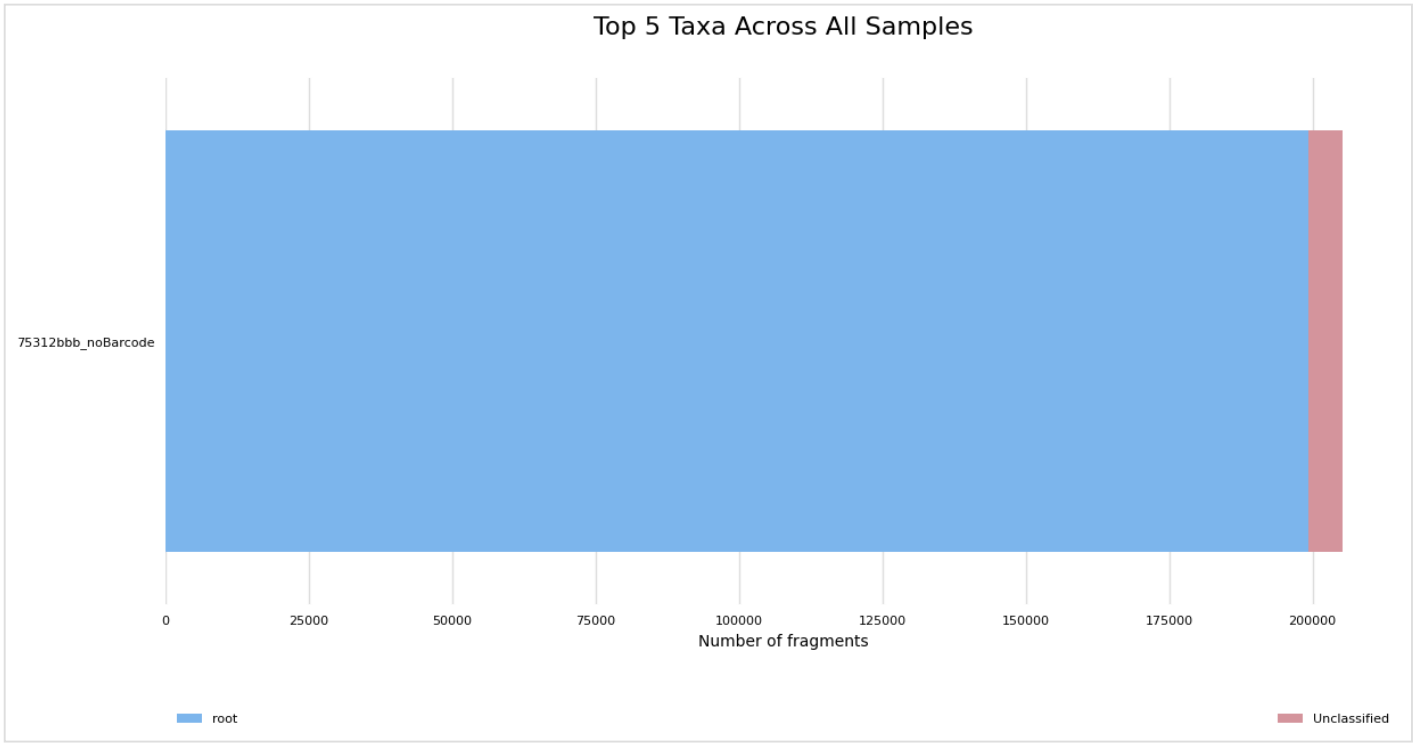

Top 5 Taxa Across All Samples
75312bbb_noBarcode
0
25000
50000
75000
100000
125000
150000
175000
200000
Number of fragments
Bacillales
Enterobacterales
Lactobacillales
Pseudomonadales
Saccharomycetales
Other
Unclassified

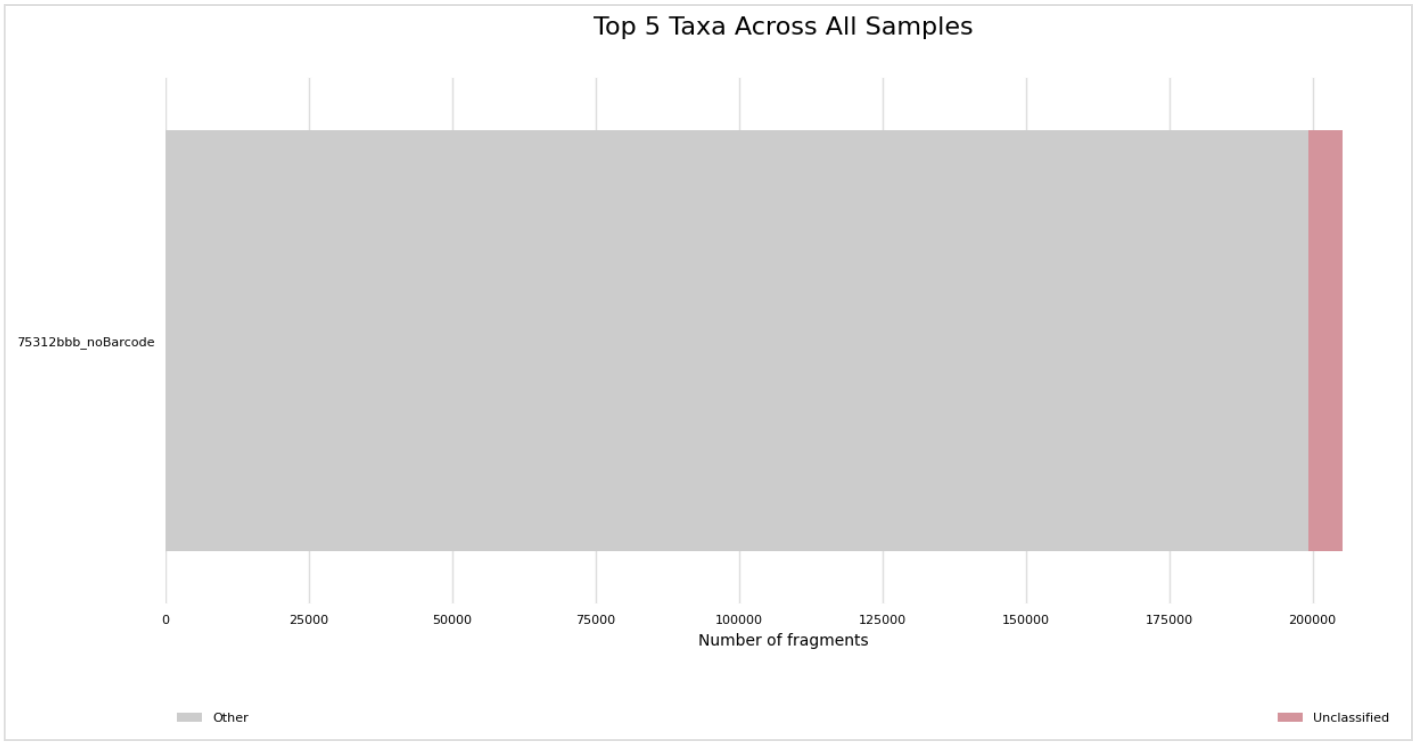

Top 5 Taxa Across All Samples
75312bbb_noBarcode
0
25000
50000
75000
100000
125000
150000
175000
200000
Number of fragments
Bacilli
Gammaproteobacteria
Saccharomycetes
Tremellomycetes
Halobacteria
Other
Unclassified


Top 5 Taxa Across All Samples
75312bbb_noBarcode
0
25000
50000
75000
100000
125000
150000
175000
200000
Number of fragments
Bacillota
Pseudomonadota
Ascomycota
Basidiomycota
Euryarchaeota
Other
Unclassified


Top 5 Taxa Across All Samples
75312bbb_noBarcode
0
25000
50000
75000
100000
125000
150000
175000
200000
Number of fragments
Fungi
Metazoa
Other
Unclassified


Top 5 Taxa Across All Samples
75312bbb_noBarcode
0
25000
50000
75000
100000
125000
150000
175000
200000
Number of fragments
Bacteria
Eukaryota
Archaea
Other
Unclassified


Top 5 Taxa Across All Samples
75312bbb_noBarcode
0
25000
50000
75000
100000
125000
150000
175000
200000
Number of fragments
root
Unclassified


Top 5 Taxa Across All Samples
75312bbb_noBarcode
0
25000
50000
75000
100000
125000
150000
175000
200000
Number of fragments
Other
Unclassified

Assembly Statistics

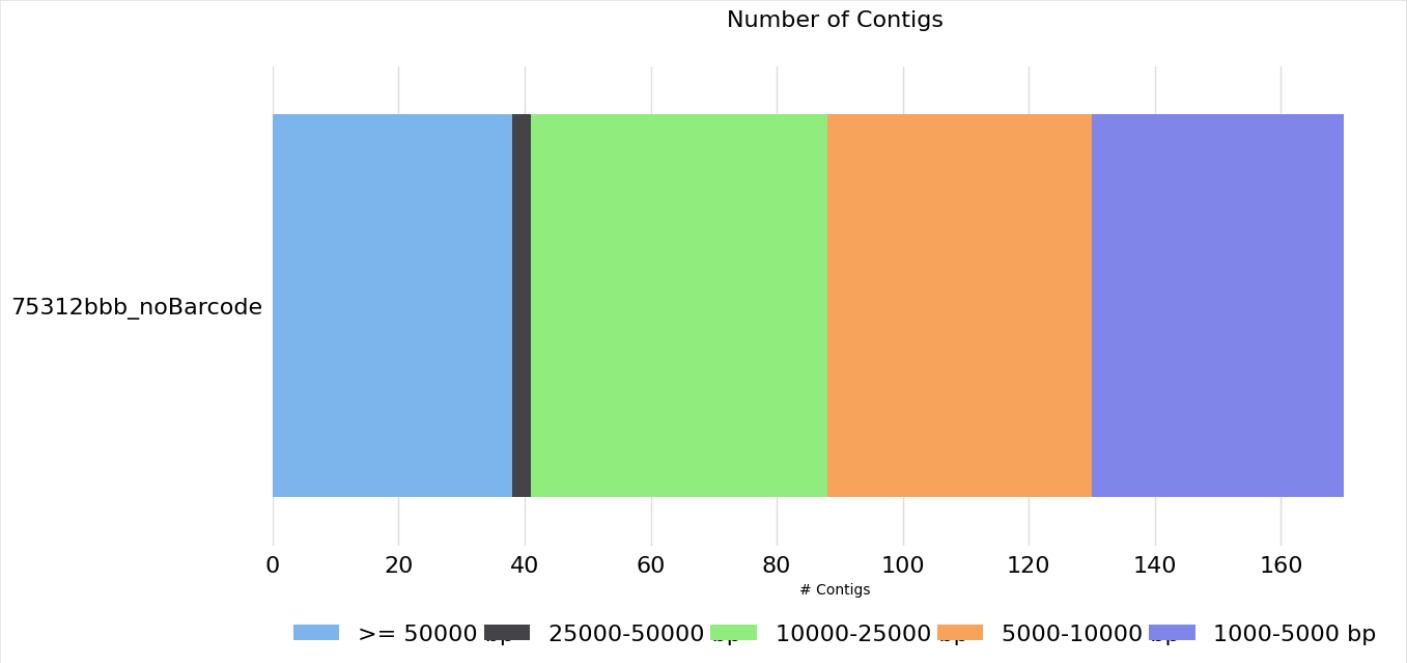
Assembly Statistics reports the length, contiguity and and quality of assemblies. *DOI: 10.1093/bioinformatics/btt086.*

Assembly Statistics

Sample Name	N50 (Mbp)	L50	Largest contig (Mbp)	Length (Mbp)
75312bbb_noBarcode	1.6Mbp	8.0	2.8Mbp	32.1Mbp

Number of Contigs

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

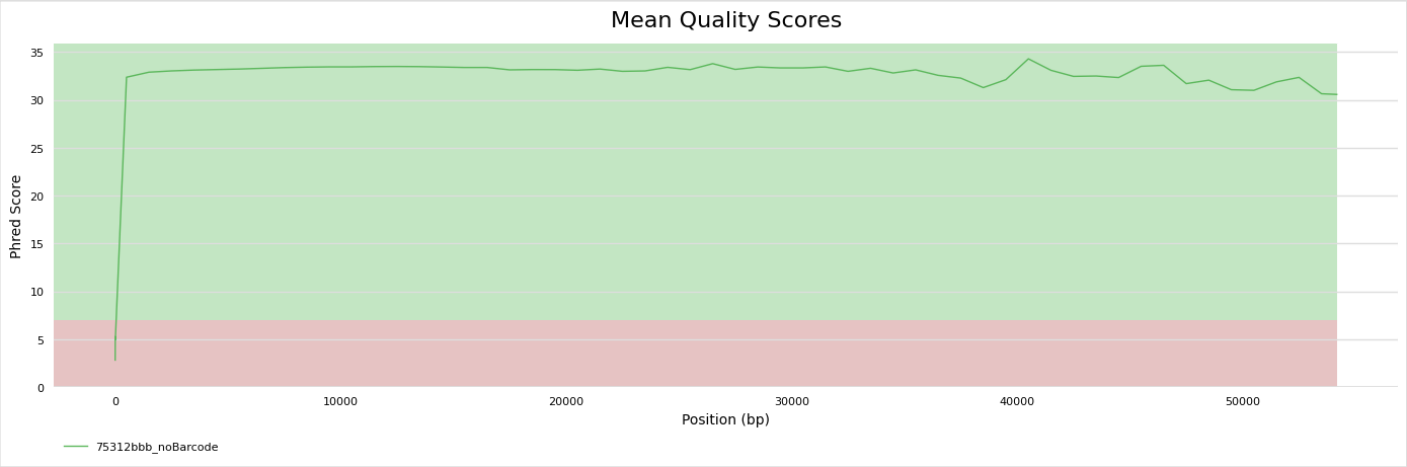


Read Quality Control

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

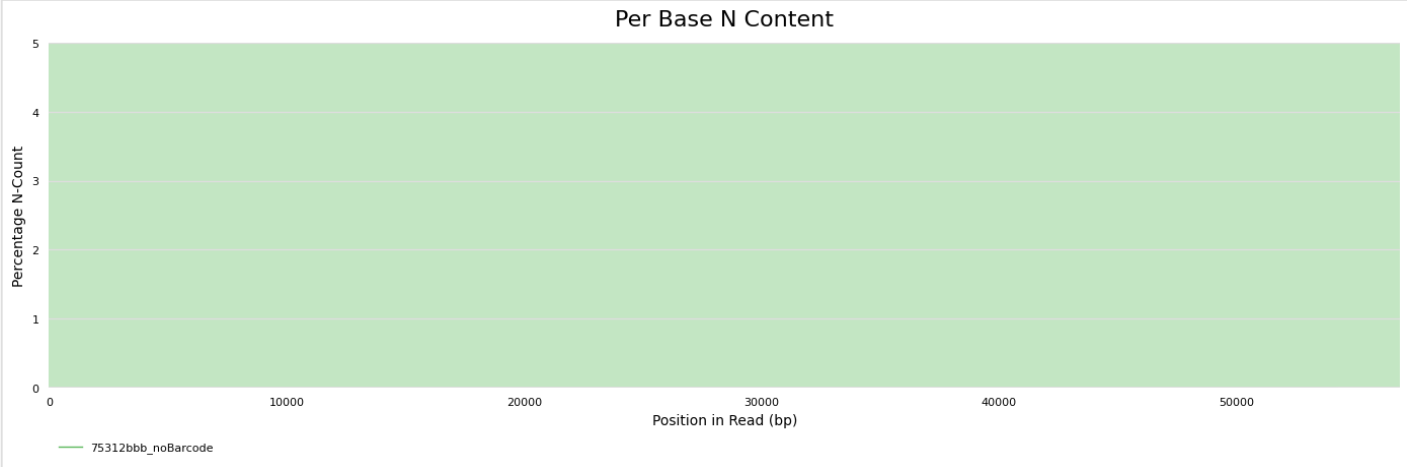
Sequence Quality Histograms

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



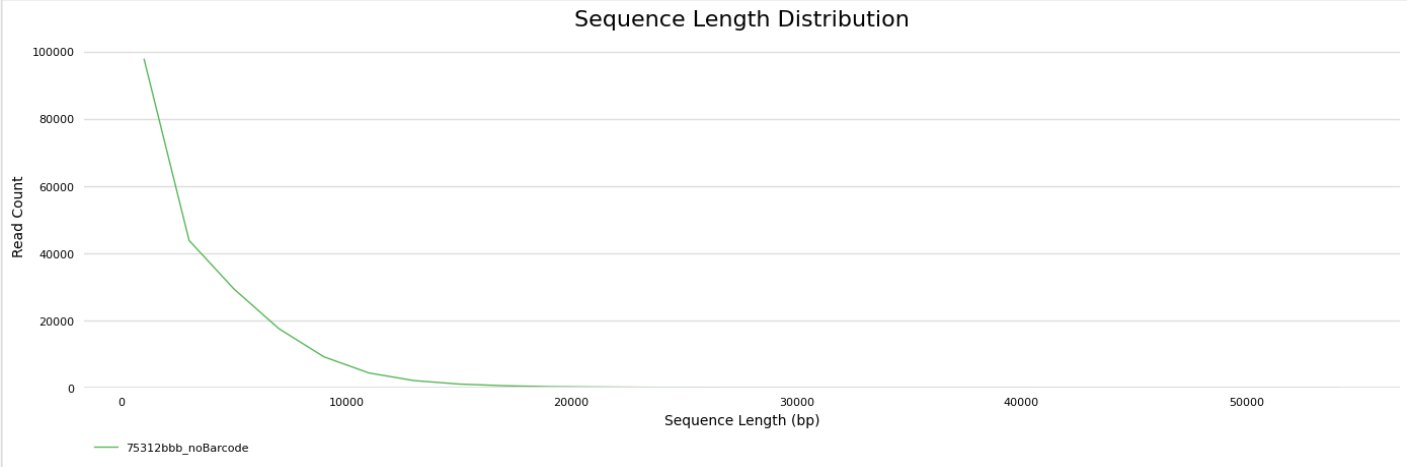
Per Base N Content

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.

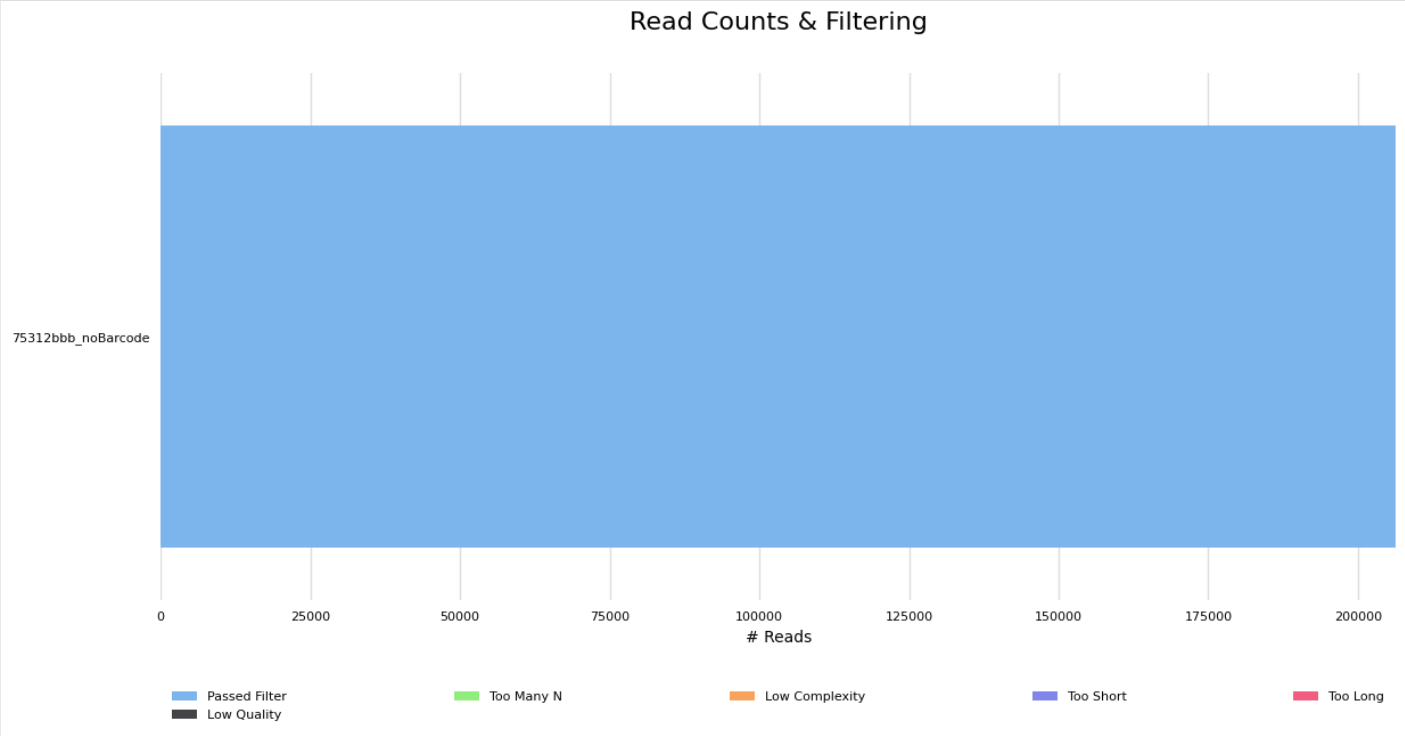
No samples found with any adapter contamination > 0.1%

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.



Flowcell Quality Control

Flowcell Quality Control assesses the performance of the flowcell for a specific sequencing run. Reads from all barcodes on the sequencing run are aggregated if possible. *DOI: 10.1093/bioinformatics/bty149.*

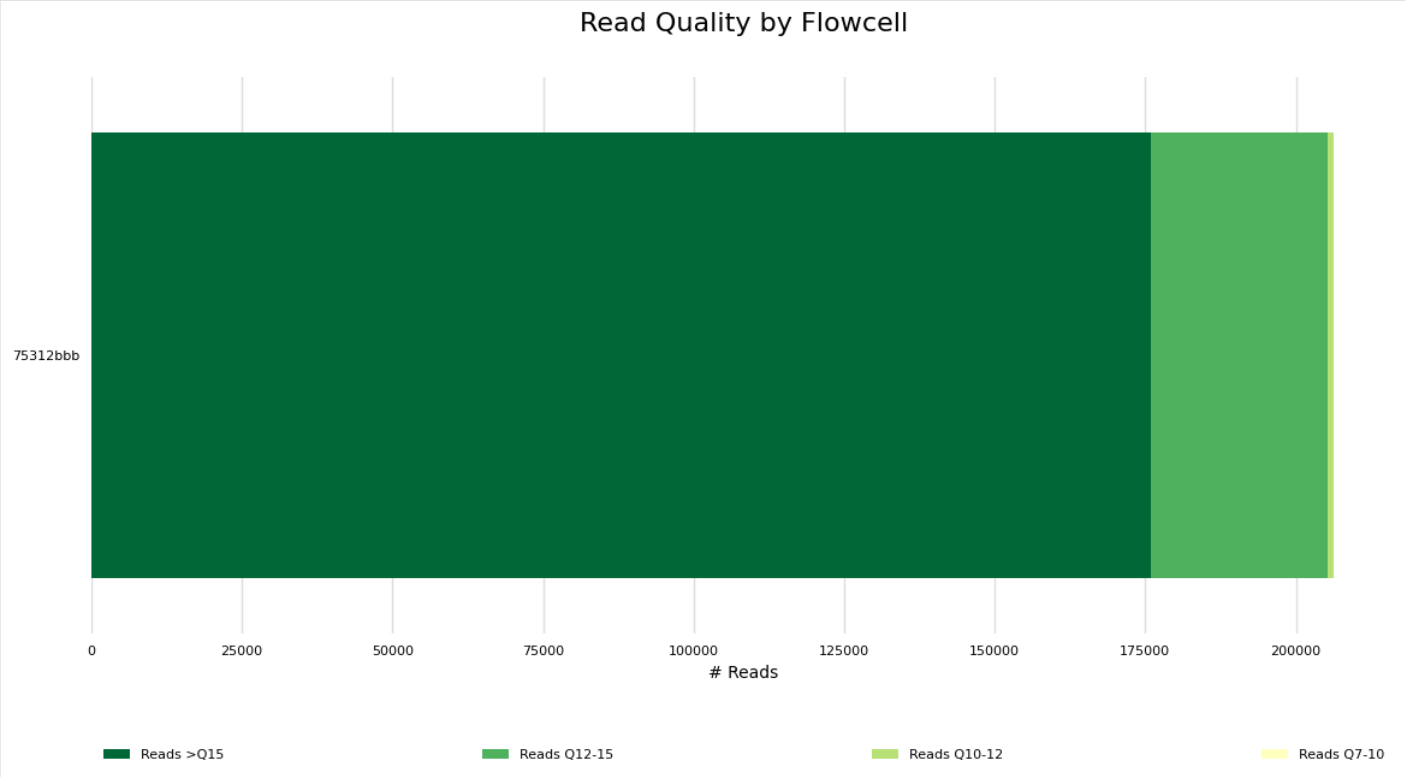
Seq summary stats

NanoStat statistics from albacore or guppy summary files.

Sample Name	Active channels	Median length	Read N50	# Reads (K)	Total Bases (Mb)
75312bbb	406	2 205 bp	5 692 bp	206.3	680.0

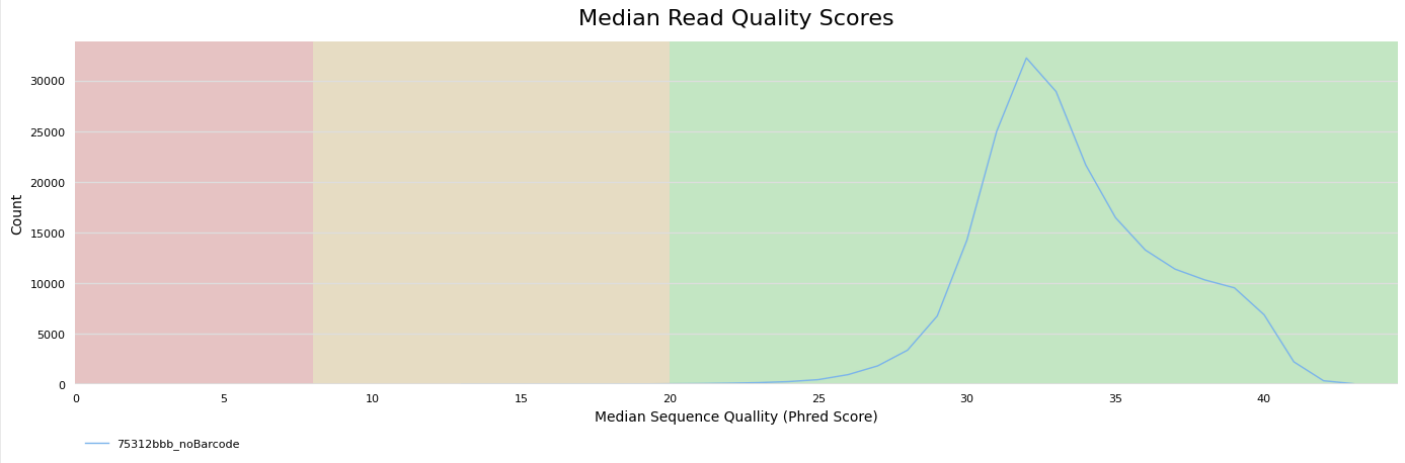
Reads by quality

Read counts categorised by read quality (phred score).

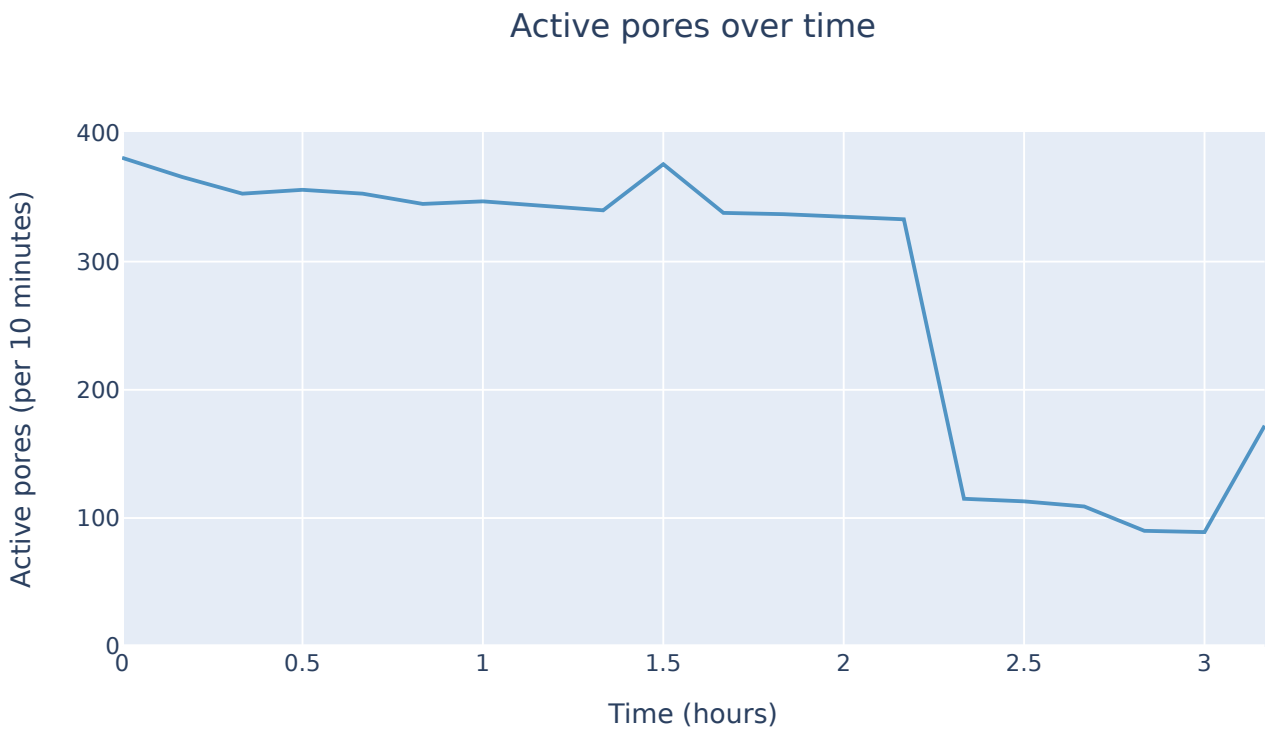


Per Sequence Quality Scores

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



Active Pores Over Time



Cumulative Yield Plot