



Automated bioinformatics for microbiology labs.

Analysis Name	Long Read Analysis for Capstone
Sample Name	75312bbb_noBarcode
Sample Type	Generic
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, 19:21 UTC

General Statistics

Sample Name	Pathogenic	Abundance	N50 (Kbp)	Assembly Length (Kbp)	≥ 20X	Median
Bacilli		0.3%	35.8Kbp	38.8Kbp		
Bacillus spizizenii		13.8%	2 070.1Kbp	4 032.8Kbp	100.0%	23.0X
Cellular organisms		0.0%	6.0Kbp	8.9Kbp		
Cryptococcus		0.0%	12.8Kbp	49.7Kbp		
Cryptococcus neoformans	Always	0.1%	4.9Kbp	120.1Kbp		0.0X
Enterobacteriaceae		0.4%	119.1Kbp	119.1Kbp		
Enterococcus faecalis		13.0%	2 830.7Kbp	2 830.7Kbp	93.0%	31.0X
Escherichia coli		11.3%	722.4Kbp	4 753.0Kbp		16.0X
Haloferax		0.0%	12.8Kbp	12.8Kbp		
Homo		0.0%	6.0Kbp	6.0Kbp		
Limosilactobacillus fermentum		8.7%	1 131.4Kbp	1 905.1Kbp	88.0%	27.0X
Listeria monocytogenes		12.0%	2 488.6Kbp	2 976.8Kbp	96.0%	27.0X
Opisthokonta		0.0%	16.7Kbp	22.9Kbp		
Pseudomonas aeruginosa		12.3%	734.1Kbp	6 855.0Kbp	1.0%	12.0X

Sample Name	Pathogenic	Abundance	N50 (Kbp)	Assembly Length (Kbp)	≥ 20X	Median
Saccharomyces		0.3%	12.8Kbp	591.2Kbp		
Saccharomyces cerevisiae		0.1%	11.0Kbp	226.5Kbp		0.0X
Salmonella enterica		12.0%	1 637.6Kbp	4 792.9Kbp	1.0%	17.0X
Staphylococcus aureus		12.9%	2 713.4Kbp	2 713.4Kbp	98.0%	32.0X

Plasmid Detection

Cluster IDs reflect unique taxonomic identifiers for plasmids 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". 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 also 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

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

Confidence explanation:

- Very high confidence reflects a 100% identity match across 100% of the reference gene sequence.
- High confidence reflects a 100% identity match across less than 100% of the reference gene sequence.
- Moderate confidence reflects less than 100% identity match across less than 100% of the reference gene sequence.

Enterococcus faecalis

Antimicrobial	Class	Genotypic Predictor of Resistance	Confidence	Genotypic Determinant
Gentamicin	Aminoglycoside	Not Detected		
Chloramphenicol	Amphenicol	Not Detected		
Fosfomycin	Fosfomycin	Not Detected		
Teicoplanin	Glycopeptide	Not Detected		
Vancomycin	Glycopeptide	Not Detected		
Erythromycin	Macrolide	Not Detected		
Linezolid	Oxazolidinone	Not Detected		
Ciprofloxacin	Quinolone	Not Detected		
Tetracycline	Tetracycline	Not Detected		
Tigecycline	Tetracycline	Not Detected		

Staphylococcus aureus

Antimicrobial	Class	Genotypic Predictor of Resistance	Confidence	Genotypic Determinant
Penicillin	Beta-Lactam	Present	High	blaZ
Cefoxitin	Beta-Lactam	Not Detected		
Ceftaroline	Beta-Lactam	Not Detected		
Gentamicin	Aminoglycoside	Not Detected		
Chloramphenicol	Amphenicol	Not Detected		
Sulfamethoxazole	Folate Pathway Antagonist	Not Detected		
Trimethoprim	Folate Pathway Antagonist	Not Detected		
Teicoplanin	Glycopeptide	Not Detected		
Vancomycin	Glycopeptide	Not Detected		
Clindamycin	Lincosamide	Not Detected		
Azithromycin	Macrolide	Not Detected		
Erythromycin	Macrolide	Not Detected		
Linezolid	Oxazolidinone	Not Detected		
Ciprofloxacin	Quinolone	Not Detected		
Levofloxacin	Quinolone	Not Detected		
Rifampicin	Rifamycin	Not Detected		
Quinupristin dalfopristin	Streptogramin A	Not Detected		
Doxycycline	Tetracycline	Not Detected		
Minocycline	Tetracycline	Not Detected		
Tetracycline	Tetracycline	Not Detected		

Pseudomonas aeruginosa

Antimicrobial	Class	Genotypic Predictor of Resistance	Confidence	Genotypic Determinant
Aztreonam	Beta-Lactam	Present	High	blaPAO
Ceftazidime	Beta-Lactam	Present	High	blaPAO
Piperacillin	Beta-Lactam	Present	High	blaOXA-486; blaPAO
Piperacillin tazobactam	Beta-Lactam	Present	High	blaOXA-486; blaPAO
Ticarcillin clavulanic acid	Beta-Lactam	Present	High	blaOXA-486; blaPAO
Unknown beta-lactam	Beta-Lactam	Present	High	blaOXA-486
Cefepime	Beta-Lactam	Not Detected		
Ceftazidime avibactam	Beta-Lactam	Not Detected		
Imipenem	Beta-Lactam	Not Detected		
Meropenem	Beta-Lactam	Not Detected		
Ciprofloxacin	Quinolone	Present	High	crpP
Levofloxacin	Quinolone	Not Detected		
Amikacin	Aminoglycoside	Not Detected		
Gentamicin	Aminoglycoside	Not Detected		
Tobramycin	Aminoglycoside	Not Detected		
Colistin	Polymyxin	Not Detected		

Salmonella enterica

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

Enterobacteriaceae

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

Limosilactobacillus fermentum

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

Listeria monocytogenes

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

Bacilli

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

Escherichia coli

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

Bacillus spizizenii

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Multilocus Sequence Typing

Schemes available on PubMLST.

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Salmonella Serotyping

Further detail on Salmonella serovar prediction is available here: https://github.com/phac-nml/sistr_cmd.

Genome Name	Subspecies	Serovar	QC Status	QC Comment
Salmonella enterica	S. enterica subsp. enterica	Choleraesuis	Pass	

Assembly Statistics

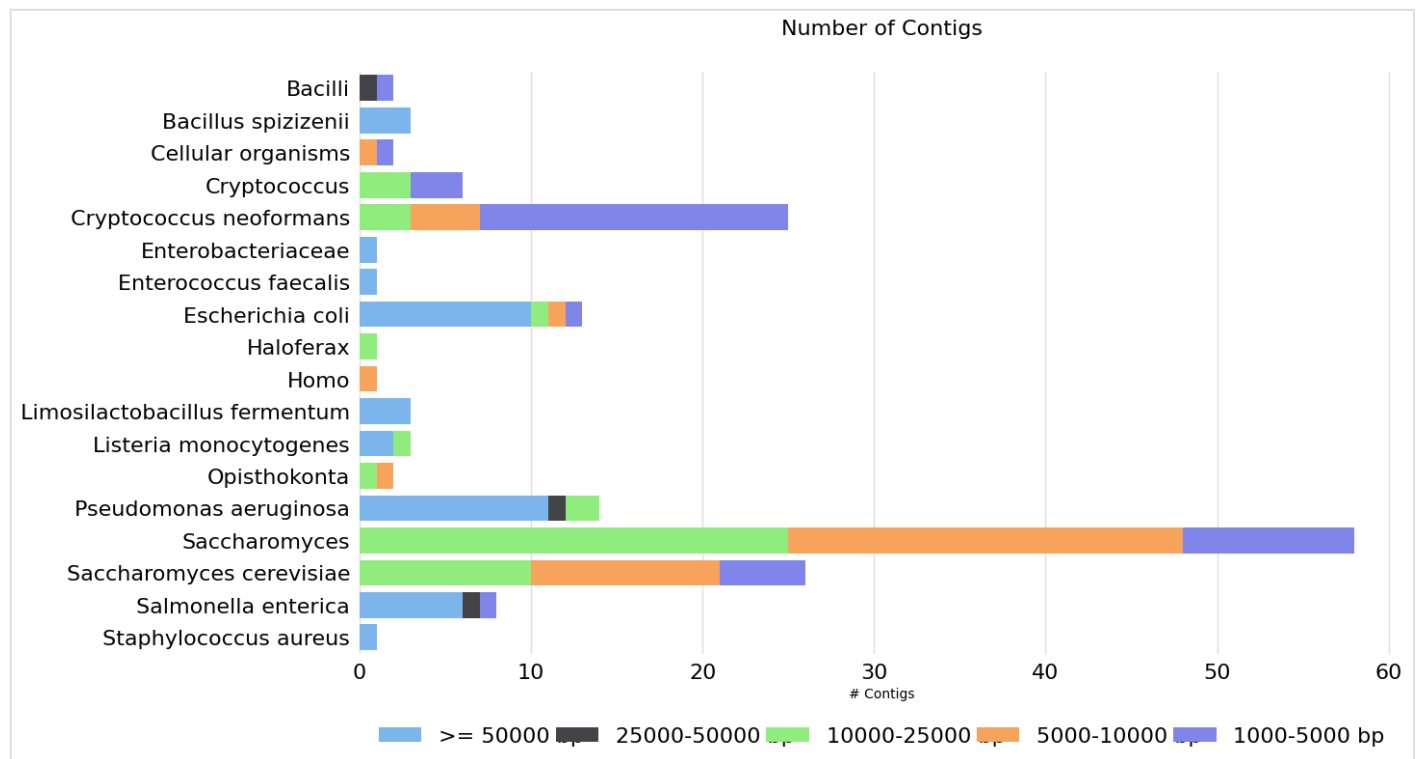
Assembly Statistics reports the length, contiguity and and quality of assemblies. *DOI: 10.1093/bioinformatics/btt086.*

Assembly Statistics

Sample Name	N50 (Kbp)	L50	Largest contig (Kbp)	Length (Kbp)	Genome Fraction
Bacilli	35.8Kbp	1.0	35.8Kbp	38.8Kbp	
Bacillus spizizenii	2 070.1Kbp	1.0	2 070.1Kbp	4 032.8Kbp	99.6%
Cellular organisms	6.0Kbp	1.0	6.0Kbp	8.9Kbp	
Cryptococcus	12.8Kbp	2.0	14.8Kbp	49.7Kbp	
Cryptococcus neoformans	4.9Kbp	8.0	11.3Kbp	120.1Kbp	0.5%
Enterobacteriaceae	119.1Kbp	1.0	119.1Kbp	119.1Kbp	
Enterococcus faecalis	2 830.7Kbp	1.0	2 830.7Kbp	2 830.7Kbp	89.6%
Escherichia coli	722.4Kbp	2.0	2 100.8Kbp	4 753.0Kbp	74.7%
Haloferax	12.8Kbp	1.0	12.8Kbp	12.8Kbp	
Homo	6.0Kbp	1.0	6.0Kbp	6.0Kbp	
Limosilactobacillus fermentum	1 131.4Kbp	1.0	1 131.4Kbp	1 905.1Kbp	85.3%
Listeria monocytogenes	2 488.6Kbp	1.0	2 488.6Kbp	2 976.8Kbp	92.1%
Opisthokonta	16.7Kbp	1.0	16.7Kbp	22.9Kbp	
Pseudomonas aeruginosa	734.1Kbp	4.0	1 372.3Kbp	6 855.0Kbp	96.4%
Saccharomyces	12.8Kbp	18.0	24.4Kbp	591.2Kbp	
Saccharomyces cerevisiae	11.0Kbp	8.0	21.8Kbp	226.5Kbp	1.8%
Salmonella enterica	1 637.6Kbp	2.0	1 799.5Kbp	4 792.9Kbp	91.5%
Staphylococcus aureus	2 713.4Kbp	1.0	2 713.4Kbp	2 713.4Kbp	91.4%

Number of Contigs

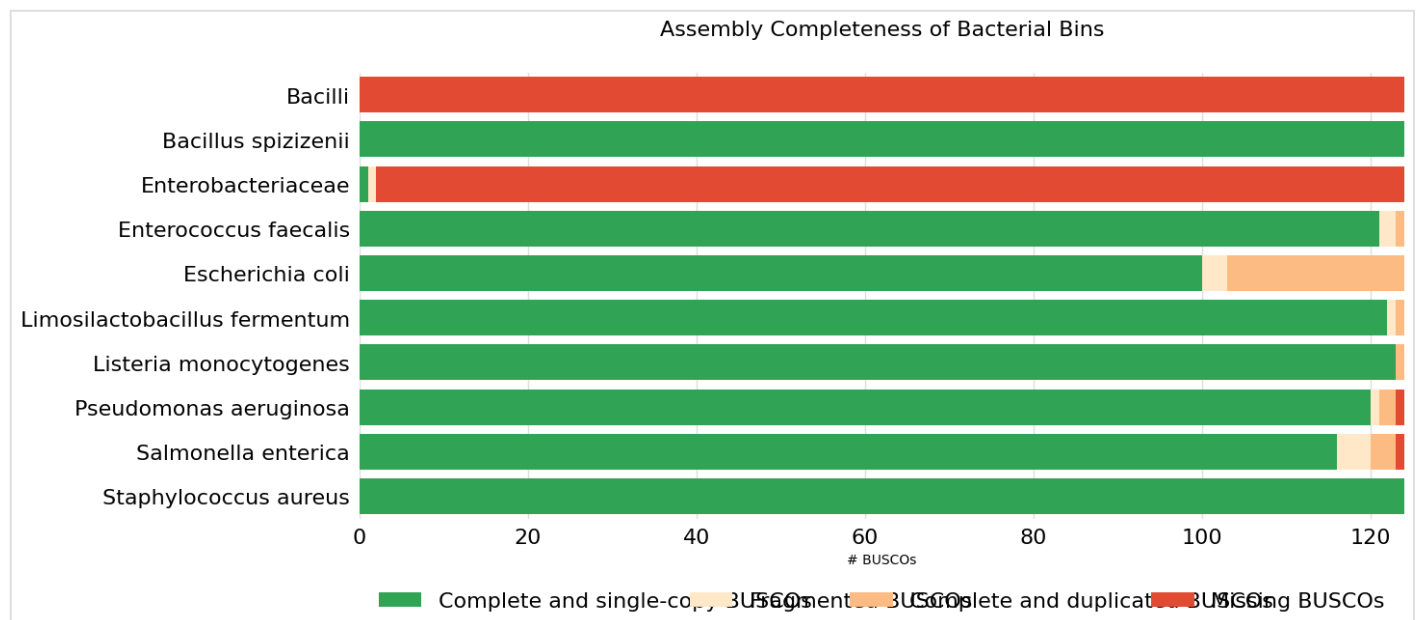
This plot shows the number of contigs found for each assembly, broken down by length.



Assembly Completeness

Assembly Completeness is assessed using universal single-copy orthologs. DOI: [10.1093/bioinformatics/btv351](https://doi.org/10.1093/bioinformatics/btv351).

Lineage: bacteria_odb10

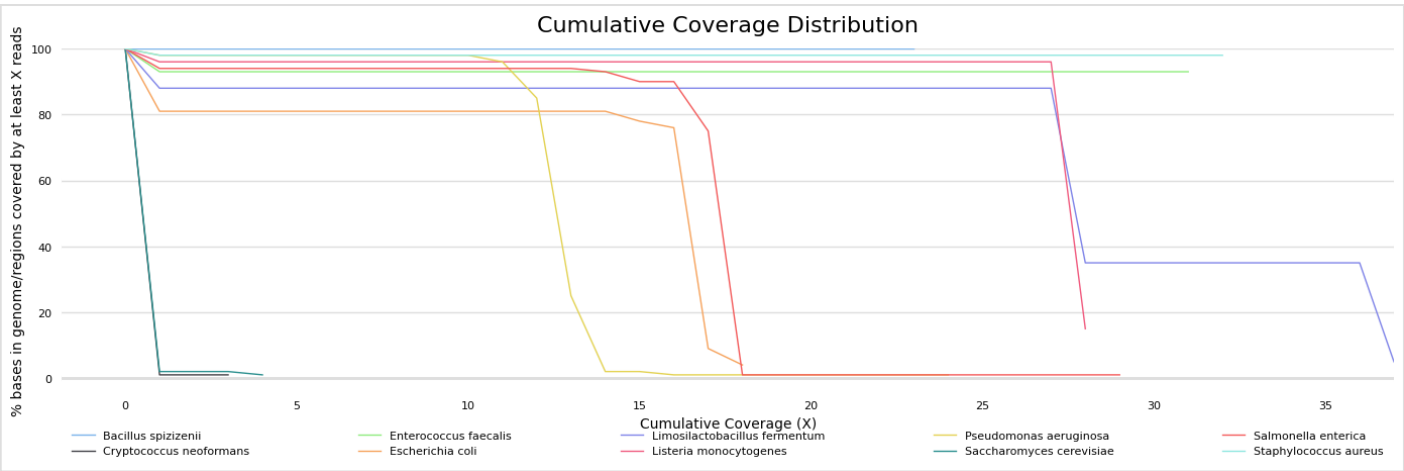


Depth of Sequencing

Depth of Sequencing is calculated relative to the reference genome of each species. Reference genomes are designated by NCBI. DOI: 10.1093/bioinformatics/btx699.

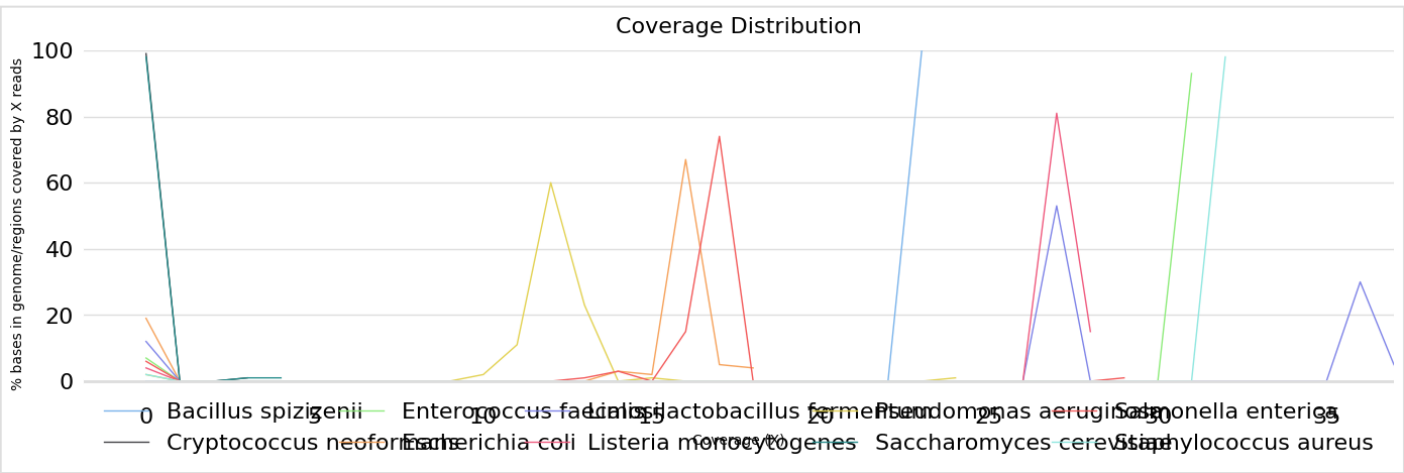
Cumulative coverage distribution

Proportion of bases in the reference genome with, at least, a given depth of coverage



Coverage distribution

Proportion of bases in the reference genome with a given depth of coverage



Coverage Per Reference Sequence

Y-axis: Average Coverage (0 to 30). X-axis: Region (NZ_CP004016.1 to 95.1).

Legend:

- Bacillus spizizenii
- Cryptococcus neoformans
- Enterococcus faecalis
- Escherichia coli
- Limosilactobacillus fermentum
- Listeria monocytogenes
- Pseudomonas aeruginosa
- Saccharomyces cerevisiae
- Salmonella enterica
- Staphylococcus aureus