BUGSEQ

Automated bioinformatics for microbiology labs.

Analysis Name	JJS Capstone Short Reads
Sample Name	R8-ZymoMCS
Sample Type	Generic
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, 21:35 UTC

General Statistics

Sample Name	Pathogenic	Abundance	N50 (Kbp)	Assembly Length (Kbp)	≥ 20X	≥ 50X	Median
Bacilli		0.2%	2.9Kbp	5.0Kbp			
Bacillus		2.0%	59.7Kbp	623.1Kbp			
Bacillus spizizenii		8.0%	263.1Kbp	2 633.3Kbp	65.0%	65.0%	310.0X
Bacteria		0.2%	106.8Kbp	141.0Kbp			
Cryptococcus		0.3%	2.2Kbp	1 139.9Kbp			
Cryptococcus neoformans	Always	0.8%	3.6Kbp	8 220.6Kbp			0.0X
Dikarya		0.1%	21.2Kbp	26.1Kbp			
Enterobacteri aceae		0.4%	55.1Kbp	108.1Kbp			
Enterococcus faecalis		14.8%	128.4Kbp	3 477.3Kbp	91.0%	91.0%	437.0X
Escherichia coli		16.3%	69.1Kbp	6 121.6Kbp	75.0%	75.0%	288.0X
Limosilactob acillus fermentum		9.4%	37.3Kbp	1 800.5Kbp	85.0%	85.0%	479.0X
Listeria monocytogen es		11.0%	256.9Kbp	2 841.1Kbp	74.0%	74.0%	425.0X
Pseudomona s aeruginosa		11.8%	161.4Kbp	6 599.5Kbp	95.0%	95.0%	189.0X

Sample Name	Pathogenic	Abundance	N50 (Kbp)	Assembly Length (Kbp)	≥ 20X	≥ 50X	Median
Root		0.6%	7.0Kbp	306.5Kbp			
Saccharomyces		1.5%	26.5Kbp	8 993.5Kbp			
Saccharomyces cerevisiae		0.3%	22.4Kbp	2 326.3Kbp	1.0%		0.0X
Salmonella enterica		8.8%	106.5Kbp	3 246.3Kbp	58.0%	58.0%	275.0X
Staphylococcus aureus		12.9%	76.9Kbp	2 939.4Kbp	96.0%	96.0%	500.0X

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.

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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		

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		

Escherichia coli

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Enterobacteriaceae

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Bacilli

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.

Bacillus spizizenii

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

Bacillus

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

Salmonella enterica

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

Bacteria

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.

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.

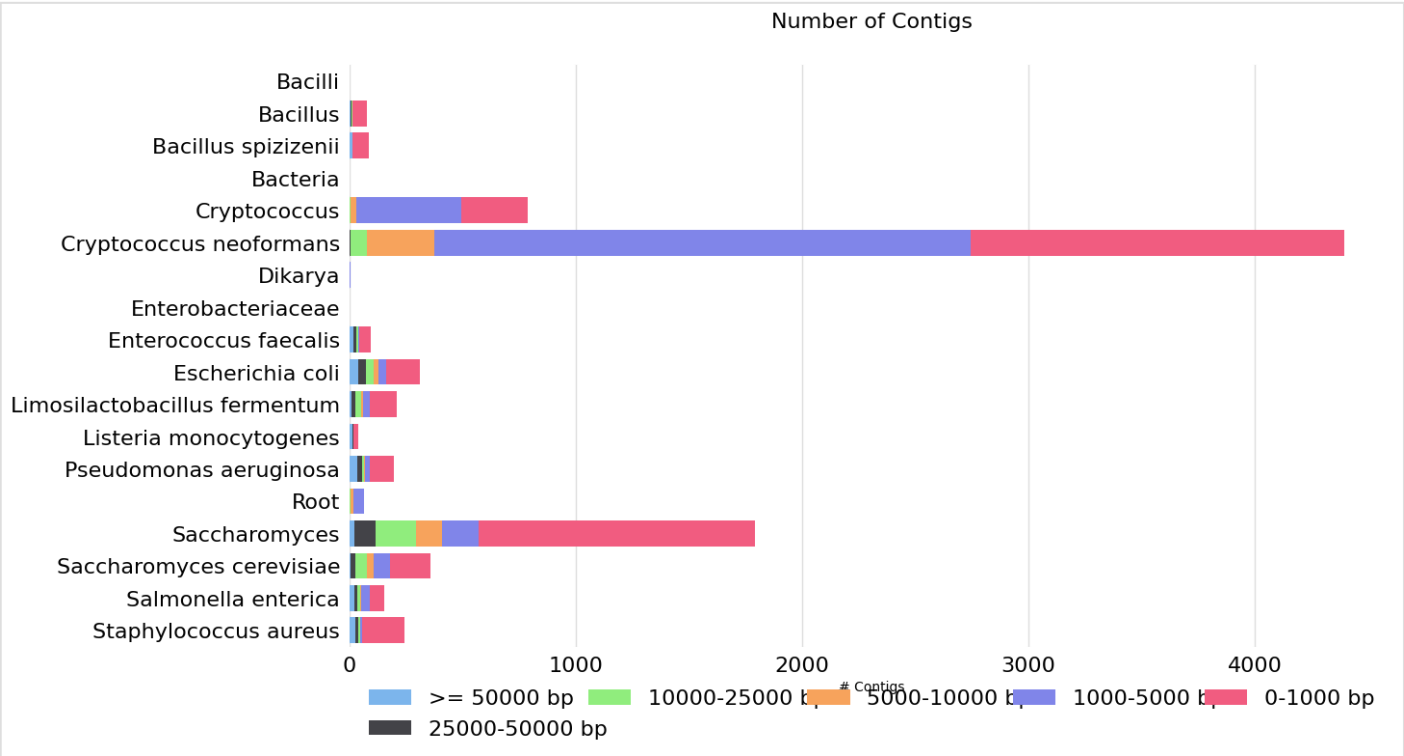| Genome Name	Subspecies	Serovar	QC Status	QC Comment
Salmonella enterica	S. enterica subsp. enterica	-:-:-	**Fail**	Large number of cgMLST330 loci missing (n=112 > 30) | Wzx/Wzy genes missing. Cannot determine O-antigen group/serogroup. Cannot accurately predict serovar from antigen genes. | H1 antigen gene (fliC) missing. Cannot determine H1 antigen. Cannot accurately predict serovar from antigen genes. | Input genome size (3246321 bp) not within expected range of 4000000-6000000 (bp) for Salmonella | Only matched 186 cgMLST330 loci. Minimum threshold for confident serovar prediction from cgMLST is 297.

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	2.9Kbp	1.0	2.9Kbp	5.0Kbp	
Bacillus	59.7Kbp	3.0	149.6Kbp	623.1Kbp	
Bacillus spizizenii	263.1Kbp	4.0	530.9Kbp	2 633.3Kbp	65.0%
Bacteria	106.8Kbp	1.0	106.8Kbp	141.0Kbp	
Cryptococcus	2.2Kbp	137.0	20.8Kbp	1 139.9Kbp	
Cryptococcus neoformans	3.6Kbp	607.0	31.9Kbp	8 220.6Kbp	37.5%
Dikarya	21.2Kbp	1.0	21.2Kbp	26.1Kbp	
Enterobacteriaceae	55.1Kbp	1.0	55.1Kbp	108.1Kbp	
Enterococcus faecalis	128.4Kbp	7.0	537.6Kbp	3 477.3Kbp	88.7%
Escherichia coli	69.1Kbp	25.0	304.2Kbp	6 121.6Kbp	69.6%
Limosilactobacillus fermentum	37.3Kbp	15.0	103.2Kbp	1 800.5Kbp	83.2%
Listeria monocytogenes	256.9Kbp	4.0	632.0Kbp	2 841.1Kbp	70.3%
Pseudomonas aeruginosa	161.4Kbp	11.0	847.6Kbp	6 599.5Kbp	94.0%
Root	7.0Kbp	11.0	30.8Kbp	306.5Kbp	
Saccharomyces	26.5Kbp	108.0	118.7Kbp	8 993.5Kbp	
Saccharomyces cerevisiae	22.4Kbp	28.0	86.5Kbp	2 326.3Kbp	18.8%
Salmonella enterica	106.5Kbp	11.0	244.9Kbp	3 246.3Kbp	56.7%
Staphylococcus aureus	76.9Kbp	14.0	175.9Kbp	2 939.4Kbp	90.3%

Number of Contigs

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

Number of Contigs

Legend: >= 50000 bp, 10000-25000 bp, 5000-10000 bp, 1000-5000 bp, 0-1000 bp, 25000-50000 bp

Assembly Completeness

Assembly Completeness is assessed using universal single-copy orthologs. *DOI: 10.1093/bioinformatics/btv351.*

Lineage: bacteria_odb10

Assembly Completeness of Bacterial Bins

Legend: Complete and single-copy BUSCOs, Fragmented BUSCOs, Complete and duplicated BUSCOs, Missing BUSCOs
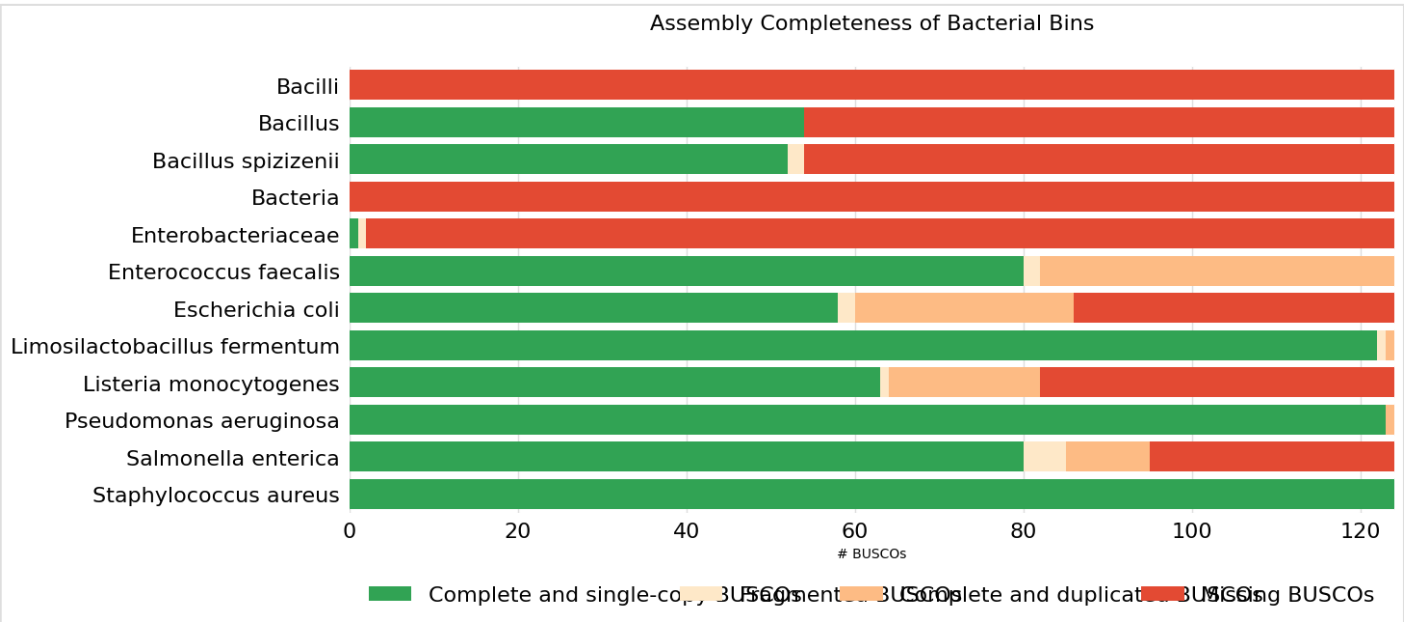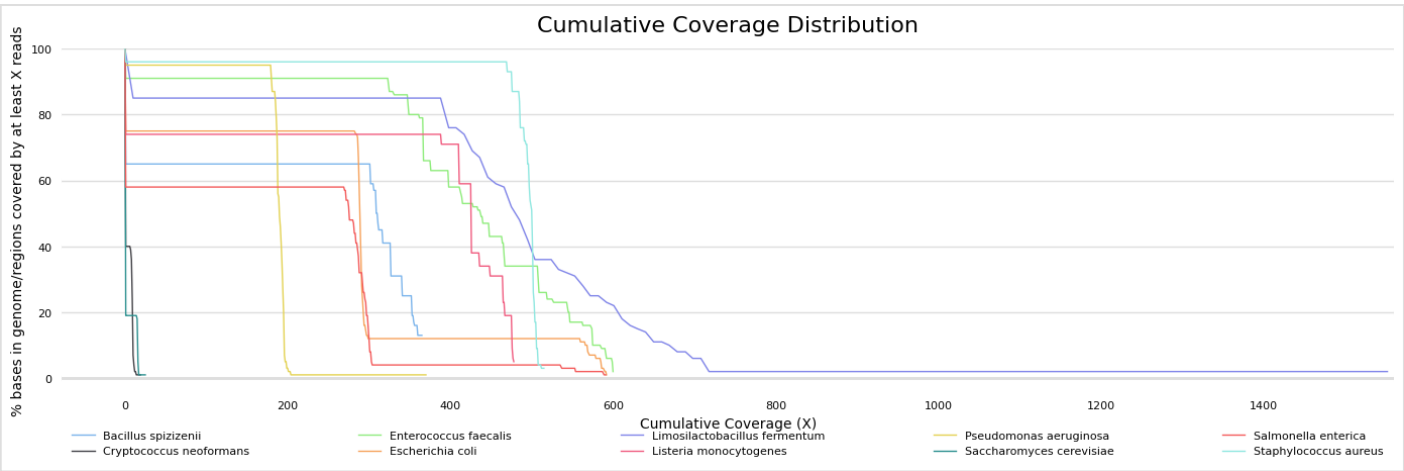
Depth of Sequencing

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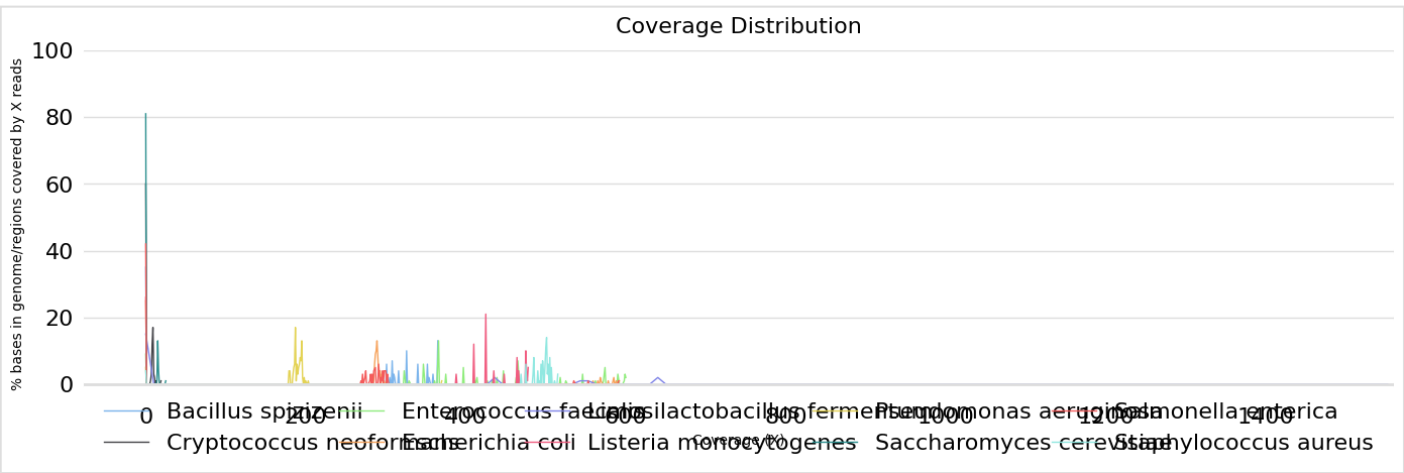
Cumulative coverage distribution

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

Average coverage per contig

Average coverage per contig or chromosome

Coverage Per Reference Sequence