

Metadata category	Metadata	Requirement	Description	Syntax	Example value	Specificity to UVIGs
General genome metadata	source of UVIGs	Mandatory	Type of dataset from which the UVIG was obtained	[ metagenome (not viral targeted)   viral fraction metagenome (virome)   sequence-targeted metagenome   metatranscriptome (not viral targeted)   viral fraction RNA metagenome (RNA virome)   sequence-targeted RNA metagenome   microbial single amplified genome (SAG)   viral single amplified genome (vSAG)   isolate microbial genome   other ]	viral fraction metagenome (virome)	New and specific to UVIGs
	assembly software	Mandatory	Tool(s) used for assembly and/or binning, including version number and parameters	{software};{version};{parameters}	metaSPAdes; 3.11.0; kmer set 21,33,55,77,99,121, default parameters otherwise	Identical MIMAG / MISAG
	viral identification software	Mandatory	Tool(s) used for the identification of UVIG as a viral genome, software or protocol name including version number, parameters, and cutoffs used (see Table S2)	{software};{version};{parameters}	VirSorter; 1.0.4; Virome database, category 2	New and specific to UVIGs
	predicted genome type	Mandatory	Type of genome predicted for the UVIG	[ DNA   dsDNA   ssDNA   RNA   dsRNA   ssRNA   ssRNA (+)   ssRNA (-)   mixed   uncharacterized ]	dsDNA	New and specific to UVIGs
	predicted genome structure detection type	Mandatory	Expected structure of the viral genome	[ segmented   non-segmented   undetermined ]	non-segmented	New and specific to UVIGs
			Type of UVIG detection	[ independent sequence (UVIG)   provirus (UpVIG) ]	independent sequence (UVIG)	New and specific to UVIGs
Genome quality	assembly quality	Mandatory	The assembly quality categories, specific for virus genomes, are based on sets of criteria as follows. <b>Finished:</b> Single, validated, contiguous sequence per replicon without gaps or ambiguities, with extensive manual review and editing to annotate putative gene functions and transcriptional units. <b>High-quality draft genome:</b> One or multiple fragments, totalling ≥ 90% of the expected genome or replicon sequence or predicted complete. <b>Genome fragment(s):</b> One or multiple fragments, totalling < 90% of the expected genome or replicon sequence, or for which no genome size could be estimated. Total number of contigs composing the UVIG	[ Finished genome   High-quality draft genome   Genome fragment(s) ]	High-quality draft genome	Comparable to and adapted from MIMAG / MISAG
	number of contigs	Mandatory		{number}	1	Identical MIMAG / MISAG
	completeness score	Conditional (required for finished genomes and high-quality draft genomes, optional for other categories)	Estimated completeness of the UVIG	{quality};{percentage}	high;92%	Comparable to and adapted from MIMAG / MISAG
	completeness approach	Conditional (required if a completeness estimation is provided)	Approach used to estimate the UVIG completeness, including reference genome or group used, and contig feature suggesting a complete genome	{text}	UVIG length compared to the average length of reference genomes from the P22virus genus (NCBI RefSeq v83)	Comparable to and adapted from MIMAG / MISAG
Genome annotation	feature prediction	Conditional (required if genome annotation is provided)	Method used to predict UVIGs features such as ORFs, integration site, etc.	{software};{version};{parameters}	Prodigal; 2.6.3; default parameters	Comparable to and adapted from MIMAG / MISAG
	reference database(s)	Conditional (required if a viral-specific ORF annotation is provided)	List of database(s) used for ORF annotation, along with version number and reference to website or publication	{database};{version};{reference}	pVOGS; 5; <a href="http://dmk-brain.ecn.uiova.edu/pVOGS/">http://dmk-brain.ecn.uiova.edu/pVOGS/</a> Grazziotin et al. 2017 doi:10.1093/nar/gkx975	Comparable to and adapted from MIMAG / MISAG
	similarity search method	Conditional (required if a viral reference database is provided)	Tool used to compare ORFs with database, along with version and cutoffs used	{software};{version};{parameters}	HMMER3; 3.1b2; hmmssearch, cutoff of 50 on score	Comparable to and adapted from MIMAG / MISAG
	taxonomic classification	Conditional (required if a taxonomic classification is provided)	Method used for taxonomic classification, along with reference database used, classification rank, and thresholds used to classify new genomes	{text}	e.g. vContact VContact2 (references from NCBI RefSeq v83, genus rank classification, default parameters)	Comparable to and adapted from MIMAG / MISAG
	vOTU classification approach	Conditional (required if a vOTU classification is provided)	Note that results from standard 95% ANI / 85% AF clustering should be provided alongside vOTUS defined from another set of thresholds, even if the latter are the ones primarily used during the analysis.	{ANI cutoff};{AF cutoff};{clustering method}	95% ANI;85% AF; greedy incremental clustering	New and specific to UVIGs
	vOTU sequence comparison approach	Conditional (required if a vOTU classification is provided)	Tool and thresholds used to compare sequences when computing "species-level" vOTUS.	{software};{version};{parameters}	blastn; 2.6.0+; e-value cutoff: 0.001	New and specific to UVIGs
	vOTU database	Conditional (required if a vOTU classification is provided)	Reference database (i.e. sequences not generated as part of the current study) used to cluster new genomes in "species-level" vOTUS, if any	{database};{version}	NCBI Viral RefSeq; 83	New and specific to UVIGs
	host prediction approach	Conditional (required if a predicted host is provided)	Tool or approach used for host prediction	[ provirus   host sequence similarity   CRISPR spacer match   kmer similarity   co-occurrence   combination   other ]	CRISPR spacer match	New and specific to UVIGs
	host prediction estimated accuracy	Conditional (required if a host prediction is provided, except for proviruses)	For each tool or approach used for host prediction, estimated false discovery rates should be included, either computed de novo or from the literature (see Table S4)	{text}	CRISPR spacer match: 0 or 1 mismatches, estimated 8% FDR at the host genus rank (Edwards et al. 2016 doi:10.1093/femsre/fuv048)	New and specific to UVIGs
viral SAG metadata	sorting technology	Conditional (required for UVIG obtained from vSAGs)	Method used to sort/isolate cells or particles of interest	[ flow cytometric cell sorting   microfluidics   laser-tweezing   optical manipulation   micromanipulation   other ]	flow cytometry cell sorting	Comparable to and adapted from MIMAG / MISAG
	single cell or viral particle lysis approach	Conditional (required for UVIG obtained from vSAGs)	Method used to free DNA from interior of the cell(s) or particle(s)	[ chemical   enzymatic   physical   combination ]	chemical	Comparable to and adapted from MIMAG / MISAG
	single cell or viral particle lysis kit protocol	Optional	Name of the kit or standard protocol used for cell(s) or particle(s) lysis	{text}	MagMAX™ Viral RNA Isolation Kit	Comparable to and adapted from MIMAG / MISAG
	WGA amplification approach	Conditional (required for UVIG obtained from vSAGs)	Method used to amplify genomic DNA in preparation for sequencing	[ pcr based   mda based   none ]	mda based	Identical MIMAG / MISAG
WGA amplification kit	Optional	Kit used to amplify genomic DNA in preparation for sequencing	{text}	REPLI-g Mini Kit	Identical MIMAG / MISAG	
viral MAG metadata	size fraction selected	Conditional (required for UVIG assembled from metagenomes)	Filtering pore size used in sample preparation	{float};{float} {unit}	0-0.22 µm	New and specific to UVIGs
	virus enrichment approach	Conditional (required for UVIG assembled from metagenomes)	List of approaches used to enrich the sample for viruses, if any	[ filtration   ultrafiltration   centrifugation   ultracentrifugation   PEG Precipitation   FeCl Precipitation   CsCl density gradient   DNase   RNase   targeted sequence capture   other   none ]	filtration + FeCl Precipitation + ultracentrifugation + DNase	New and specific to UVIGs
	nucleic acid extraction	Conditional (required for UVIG assembled from metagenomes)	A link to a literature reference, electronic resource or a standard operating procedure (SOP), that describes the material separation to recover the nucleic acid fraction from a sample	{PMID}   {DOI}   {URL}	10.1111/j.1462-2920.2012.02836.x	Identical MIMAG / MISAG
	WGA amplification approach	Conditional (required for UVIG assembled from metagenomes)	Description of the approach used for whole genome amplification, if any	[ pcr based   mda based   none ]	none	Identical MIMAG / MISAG
	binning parameters	Conditional (required if genome bin(s) were defined)	The parameters that have been applied during the extraction of genomes from metagenomic datasets	[ homology search   kmer   coverage   codon usage   combination ]	kmer and coverage	Identical MIMAG / MISAG
	binning software	Conditional (required if genome bin(s) were defined)	Tool(s) used for the extraction of genomes from metagenomic datasets	[ metabat   maxbin   concoct   groupm   esom   metawatt   combination   other ]	metabat	Identical MIMAG / MISAG
	reassemble post binning	Conditional (required if genome bin(s) were defined)	Has an assembly been performed on a genome bin extracted from a metagenomic assembly?	[ yes   no ]	yes	Identical MIMAG / MISAG
	MAG coverage software	Optional	Tool(s) used to determine the genome coverage if coverage is used as a binning parameter in the extraction of genomes from metagenomic datasets	[ bwa   bbmap   bowtie   other ]	bowtie	Identical MIMAG / MISAG

Metadata category	Metadata	Requirement	Description	Syntax	Example value	Specificity to UVIGs	UVIGs in this study
General genome metadata	source of UVIGs	Mandatory	Type of dataset from which the UVIG was obtained	[ metagenome (not viral targeted)   viral fraction metagenome (virome)   sequence-targeted metagenome   metatranscriptome (not viral targeted)   viral fraction RNA metagenome (RNA virome)   sequence-targeted RNA metagenome   microbial single amplified genome (SAG)   viral single amplified genome (vSAG)   isolate microbial genome   other ]	viral fraction metagenome (virome)	New and specific to UVIGs	viral fraction metagenome (virome)
	assembly software	Mandatory	Tool(s) used for assembly and/or binning, including version number and parameters	{software};{version};{parameters}	metaSPAdes; 3.11.0; kmer set 21,33,55,77,99,121, default parameters otherwise	Identical MIMAG / MISAG	Flye; v.2.9, --meta
	viral identification software	Mandatory	Tool(s) used for the identification of UVIG as a viral genome, software or protocol name including version number, parameters, and cutoffs used (see Table S2)	{software};{version};{parameters}	VirSorter; 1.0.4; Virome database, category 2	New and specific to UVIGs	VirSorter2; 2.2.3; --min-score 0.5, --min-length 4000; CheckV; 0.7.0, viral genes > 0 or viral genes = 0 & host genes = 0 or VirSorter2 score = 0.95 or hallmark genes > 2.
	predicted genome type	Mandatory	Type of genome predicted for the UVIG	[ DNA   dsDNA   ssDNA   RNA   dsRNA   ssRNA   ssRNA (+)   ssRNA (-)   mixed   uncharacterized ]	dsDNA	New and specific to UVIGs	dsDNA
	predicted genome structure detection type	Mandatory	Expected structure of the viral genome	[ segmented   non-segmented   undetermined ]	non-segmented	New and specific to UVIGs	undetermined
		Mandatory	Type of UVIG detection	[ independent sequence (UVIG)   provirus (UpVIG) ]	independent sequence (UVIG)	New and specific to UVIGs	Independent sequence (UVIG)
Genome quality	assembly quality	Mandatory	The assembly quality categories, specific for virus genomes, are based on sets of criteria as follows. <b>Finished:</b> Single, validated, contiguous sequence per replicon without gaps or ambiguities, with extensive manual review and editing to annotate putative gene functions and transcriptional units. <b>High-quality draft genome:</b> One or multiple fragments, totaling ≥ 90% of the expected genome or replicon sequence or predicted complete. <b>Genome fragment(s):</b> One or multiple fragments, totaling < 90% of the expected genome or replicon sequence, or for which no genome size could be estimated. Total number of contigs composing the UVIG	[ Finished genome   High-quality draft genome   Genome fragment(s) ]	High-quality draft genome	Comparable to and adapted from MIMAG / MISAG	reported in next sheet
	number of contigs	Mandatory	Estimated completeness of the UVIG	{number}	1	Identical MIMAG / MISAG	1
	completeness score	Conditional (required for finished genomes and high-quality draft genomes, optional for other categories)	Approach used to estimate the UVIG completeness, including reference genome or group used, and contig feature suggesting a complete genome	{quality};{percentage}	high:92%	Comparable to and adapted from MIMAG / MISAG	reported in next sheet
	completeness approach	Conditional (required if a completeness estimation is provided)	Method used to predict UVIGs features such as ORFs, integration site, etc.	{text}	UVIG length compared to the average length of reference genomes from the P22virus genus (NCBI RefSeq v83)	Comparable to and adapted from MIMAG / MISAG	reported in next sheet
Genome annotation	feature prediction	Conditional (required if genome annotation is provided)	Method used to predict UVIGs features such as ORFs, integration site, etc.	{software};{version};{parameters}	Prodigal; 2.6.3, default parameters	Comparable to and adapted from MIMAG / MISAG	Prodigal; 2.6.3; default parameters
	reference database(s)	Conditional (required if a virus-specific ORF annotation is provided)	List of database(s) used for ORF annotation, along with version number and reference to website or publication	{database};{version};{reference}	pVOGs; 5; <a href="http://dmk-brain.ecn.uio.no/pVOGs/">http://dmk-brain.ecn.uio.no/pVOGs/</a>   Graziotin et al. 2017 doi:10.1093/nar/gkx975	Comparable to and adapted from MIMAG / MISAG	
	similarity search method	Conditional (required if a viral reference database is provided)	Tool used to compare ORFs with database, along with version and cutoffs used	{software};{version};{parameters}	HMMER3; 3.102; hmmersearch, cutoff of 50 on score	Comparable to and adapted from MIMAG / MISAG	
	taxonomic classification	Conditional (required if a taxonomic classification is provided)	Method used for taxonomic classification, along with reference database used, classification rank, and thresholds used to classify new genomes	{text}	e.g. vContact vContact2 (references from NCBI RefSeq v83, genus rank classification, default parameters)	Comparable to and adapted from MIMAG / MISAG	vContact2 (References from NCBI RefSeq v201 and list of Crass-like phages <a href="https://doi.org/10.1038/s41467-021-21350-w">https://doi.org/10.1038/s41467-021-21350-w</a> , family rank classification, default parameters), HMM profile similarities (ViPhOGs database (29/06/2021), family rank classification, significant hits = sequence eval <= 0.001 and domain eval <= 0.1, >=20% of ORFs with significant hits and >=60% of those hits assigned to the same taxon)
	VOTU classification approach	Conditional (required if a VOTU classification is provided)	Cutoffs and approach used when clustering new UVIGs in "species-level" VOTUs. Note that results from standard 95% ANI / 85% AF clustering should be provided alongside VOTUS defined from another set of thresholds, even if the latter are the ones primarily used during the analysis.	{ANI cutoff};{AF cutoff};{clustering method}	95% ANI, 85% AF; greedy incremental clustering	New and specific to UVIGs	
	VOTU sequence comparison approach	Conditional (required if a VOTU classification is provided)	Tool and thresholds used to compare sequences when computing "species-level" VOTUs.	{software};{version};{parameters}	blastn; 2.6.0+; e-value cutoff: 0.001	New and specific to UVIGs	vContact2; 0.9.19; default parameters. Hmmer; 3.3.2; sequence eval <= 0.001 & domain eval <= 0.1
	VOTU database	Conditional (required if a VOTU classification is provided)	Reference database (i.e. sequences not generated as part of the current study) used to cluster new genomes in "species-level" VOTUs, if any	{database};{version}	NCBI Viral RefSeq; 83	New and specific to UVIGs	NCBI Prokaryotic RefSeq; 201 ViPhOGs; (29/06/2021)
	host prediction approach	Conditional (required if a predicted host is provided)	Tool or approach used for host prediction	[ provirus   host sequence similarity   CRISPR spacer match   kmer similarity   co-occurrence   combination   other ]	CRISPR spacer match	New and specific to UVIGs	VirHostMatcher-Net; 1.0
	host prediction estimated accuracy	Conditional (required if a host prediction is provided, except for proviruses)	For each tool or approach used for host prediction, estimated false discovery rates should be included, either computed de novo or from the literature (see Table S4)	{text}	CRISPR spacer match: 0 or 1 mismatches, estimated 8% FDR at the host genus rank (Edwards et al. 2016 doi:10.1093/femsre/fuv048)	New and specific to UVIGs	VirHostMatcher-Net; Estimated 10% FDR at the host phylum level; <a href="https://doi.org/10.1093/nargab/lqaa044">https://doi.org/10.1093/nargab/lqaa044</a>
	Viral SAG metadata	sorting technology	Conditional (required for UVIG obtained from vSAGs)	Method used to sort/isolate cells or particles of interest	[ flow cytometric cell sorting   microfluidics   laser-tweezing   optical manipulation   micromanipulation   other ]	flow cytometry cell sorting	Comparable to and adapted from MIMAG / MISAG
single cell or viral particle lysis approach		Conditional (required for UVIG obtained from vSAGs)	Method used to free DNA from interior of the cell(s) or particle(s)	[ chemical   enzymatic   physical   combination ]	chemical	Comparable to and adapted from MIMAG / MISAG	
single cell or viral particle lysis kit protocol		Optional	Name of the kit or standard protocol used for cell(s) or particle(s) lysis	{text}	MagMAX™ Viral RNA Isolation Kit	Comparable to and adapted from MIMAG / MISAG	
WGA amplification approach		Conditional (required for UVIG obtained from vSAGs)	Method used to amplify genomic DNA in preparation for sequencing	[ pcr based   mda based   none ]	mda based	Identical MIMAG / MISAG	
WGA amplification kit	Optional	Kit used to amplify genomic DNA in preparation for sequencing	{text}	REPLI-g Mini Kit	Identical MIMAG / MISAG		
viral MAG metadata	size fraction selected	Conditional (required for UVIG assembled from metagenomes)	Filtering pore size used in sample preparation	{float};{float} {unit}	0-0.22 µm	New and specific to UVIGs	None
	virus enrichment approach	Conditional (required for UVIG assembled from metagenomes)	List of approaches used to enrich the sample for viruses, if any	[ filtration   ultrafiltration   centrifugation   ultracentrifugation   PEG Precipitation   FeCl Precipitation   CsCl density gradient   DNase   RNase   targeted sequence capture   other   none ]	filtration + FeCl Precipitation + ultracentrifugation + DNase	New and specific to UVIGs	centrifugation + PEG precipitation + chloroform + DNase
	nucleic acid extraction	Conditional (required for UVIG assembled from metagenomes)	A link to a literature reference, electronic resource or a standard operating procedure (SOP), that describes the material separation to recover the nucleic acid fraction from a sample	{PMID}   {DOI}   {URL}	10.1111/j.1462-2920.2012.02836.x	Identical MIMAG / MISAG	
	WGA amplification approach	Conditional (required for UVIG assembled from metagenomes)	Description of the approach used for whole genome amplification, if any	[ pcr based   mda based   none ]	none	Identical MIMAG / MISAG	
	binning parameters	Conditional (required if genome bin(s) were defined)	The parameters that have been applied during the extraction of genomes from metagenomic datasets	[ homology search   kmer   coverage   codon usage   combination ]	kmer and coverage	Identical MIMAG / MISAG	
	binning software	Conditional (required if genome bin(s) were defined)	Tool(s) used for the extraction of genomes from metagenomic datasets	[ metabat   maxbin   concoct   groupm   esom   metawatt   combination   other ]	metabat	Identical MIMAG / MISAG	
	reassembly post binning	Conditional (required if genome bin(s) were defined)	Has an assembly been performed on a genome bin extracted from a metagenomic assembly?	[ yes   no ]	yes	Identical MIMAG / MISAG	
	MAG coverage software	Optional	Tool(s) used to determine the genome coverage if coverage is used as a binning parameter in the extraction of genomes from metagenomic datasets	[ bwa   bmap   bowtie   other ]	bowtie	Identical MIMAG / MISAG	

UViG	VirSorter2 score	Predicted genome type	Provirus	Completeness quality	Completeness (%)	Assembly quality	Completeness approach	Family	Host phylum	Host species
TM39_BL_k141_1394	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	ITR (high-confidence)		Bacillota	<i>Ruminococcus bromii</i>
TM39_BL_k141_164480	0.993	dsDNAphage	No	High-quality	91.16	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Intestinibacter bartlettii</i>
TM37_BL_k141_30158	1	dsDNAphage	No	High-quality	98.05	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Dorea formicigenerans</i>
TM37_BL_k141_41808	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Anaerostipes hadrus</i>
TM36_BL_k141_130482	1	dsDNAphage	No	High-quality	98.25	High-quality draft genome	AAI-based (high-confidence)		Bacteroidota	<i>Prevotella copri</i>
TM35_BL_k141_126246	0.98	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Roseburia intestinalis</i>
TM35_BL_k141_219044	0.98	dsDNAphage	No	High-quality	99.48	High-quality draft genome	AAI-based (high-confidence)			
TM35_BL_k141_222994	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TM35_BL_k141_38646	0.98	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TM35_BL_k141_50710	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacillota	<i>Coprococcus eutactus</i>
TM35_BL_k141_211301	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacillota	<i>Tyzzzeria nexilis</i>
TM33_BL_k141_83767	1	dsDNAphage	No	High-quality	91.05	High-quality draft genome	AAI-based (medium-confidence)		Bacillota	<i>Megamonas hypermegale</i>
TM33_BL_k141_91201	0.98	dsDNAphage	No	High-quality	99.83	High-quality draft genome	AAI-based (medium-confidence)	Podoviridae		
TM32_BL_k141_14519	1	dsDNAphage	No	High-quality	97	High-quality draft genome	AAI-based (high-confidence)	Microviridae		
TM30_BL_k141_11430	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Blautia obeum</i>
TM30_BL_k141_65637	0.993	dsDNAphage	No	High-quality	94.31	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Butyrivibrio crossotus</i>
TM30_BL_k141_133743	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Actinomycetota	<i>Bifidobacterium adolescentis</i>
TM30_BL_k141_244284	1	dsDNAphage	No	High-quality	99.04	High-quality draft genome	AAI-based (high-confidence)			
TM30_BL_k141_106705	1	dsDNAphage	No	High-quality	98.21	High-quality draft genome	AAI-based (high-confidence)	Siphoviridae	Bacteroidota	<i>Bacteroides massiliensis</i>
TM28_BL_k141_98145	0.98	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TM28_BL_k141_234234	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TM28_BL_k141_234449	0.987	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TM27_BL_k141_2158	1	dsDNAphage	No	High-quality	99.8	High-quality draft genome	AAI-based (high-confidence)	Siphoviridae		
TM27_BL_k141_114298	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TM27_BL_k141_36806	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)	Siphoviridae	Bacteroidota	<i>Bacteroides xylanisolvens</i>
TM27_BL_k141_55186	1	dsDNAphage	No	High-quality	97.55	High-quality draft genome	AAI-based (high-confidence)			
TM27_BL_k141_95823	0.987	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacteroidota	<i>Prevotella melaninogenica</i>
TM27_BL_k141_173843	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacillota	<i>Roseburia intestinalis</i>
TM25_BL_k141_5792	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacillota	<i>Blautia obeum</i>
TM24_BL_k141_56009	0.947	dsDNAphage	No	High-quality	97.48	High-quality draft genome	AAI-based (medium-confidence)		Bacillota	<i>Flavonifractor plautii</i>
TM24_BL_k141_59765	1	dsDNAphage	No	High-quality	92.89	High-quality draft genome	AAI-based (high-confidence)			
TM24_BL_k141_154851	1	dsDNAphage	No	High-quality	98.02	High-quality draft genome	AAI-based (high-confidence)			
TM24_BL_k141_218959	1	dsDNAphage	No	High-quality	92.39	High-quality draft genome	AAI-based (medium-confidence)		Bacteroidota	<i>Bacteroides caccae</i>
TM24_BL_k141_39037	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TM24_BL_k141_226208	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacillota	<i>Staphylococcus aureus</i>
TM24_BL_k141_226284	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TM23_BL_k141_5519	1	dsDNAphage	No	High-quality	91.91	High-quality draft genome	AAI-based (high-confidence)	Microviridae		
TM23_BL_k141_8924	1	dsDNAphage	No	High-quality	99.38	High-quality draft genome	AAI-based (high-confidence)	Microviridae		
TM23_BL_k141_91299	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)	Microviridae		
TM23_BL_k141_127508	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)	Microviridae		
TM22_BL_k141_99182	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (medium-confidence)			
TM21_BL_k141_11158	0.987	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TM20_BL_k141_42446	0.987	dsDNAphage	No	High-quality	99.56	High-quality draft genome	AAI-based (high-confidence)			
TM20_BL_k141_158691	1	dsDNAphage	No	High-quality	96.27	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Staphylococcus aureus</i>
TM20_BL_k141_220161	0.993	dsDNAphage	No	High-quality	98.05	High-quality draft genome	AAI-based (high-confidence)			
TM19_BL_k141_26001	0.993	dsDNAphage	No	High-quality	90.62	High-quality draft genome	AAI-based (high-confidence)			
TM19_BL_k141_96262	0.993	dsDNAphage	No	High-quality	98.04	High-quality draft genome	AAI-based (high-confidence)	Microviridae		
TM19_BL_k141_102104	0.993	ssDNA	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	Microviridae		
TM19_BL_k141_154505	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacillota	<i>Megamonas funiformis</i>
TM17_BL_k141_86957	0.993	dsDNAphage	No	High-quality	92.54	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Megamonas hypermegale</i>
TM17_BL_k141_102184	0.98	dsDNAphage	No	High-quality	92.32	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Faecalibacterium prausnitzii</i>
TM17_BL_k141_271	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacillota	<i>Megamonas funiformis</i>
TM17_BL_k141_22008	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TM16_BL_k141_38398	1	dsDNAphage	No	High-quality	99.14	High-quality draft genome	AAI-based (high-confidence)	Myoviridae		
TM16_BL_k141_67074	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Staphylococcus aureus</i>
TM16_BL_k141_147977	1	dsDNAphage	No	High-quality	99.23	High-quality draft genome	AAI-based (high-confidence)	Microviridae		
TM16_BL_k141_184790	0.9	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TM16_BL_k141_200956	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TM16_BL_k141_224760	0.987	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TM15_BL_k141_13658	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacteroidota	<i>Parabacteroides merdae</i>
TM15_BL_k141_112441	0.987	dsDNAphage	No	High-quality	91.92	High-quality draft genome	AAI-based (high-confidence)			
TM15_BL_k141_159356	1	dsDNAphage	No	High-quality	96.33	High-quality draft genome	AAI-based (medium-confidence)			
TM15_BL_k141_18088	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacillota	<i>Blautia obeum</i>
TM15_BL_k141_121071	0.933	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TM14_BL_k141_9153	1	dsDNAphage	No	Complete	100	High-quality draft genome	ITR (high-confidence)	Podoviridae	Bacillota	<i>Lactobacillus plantarum</i>
TM14_BL_k141_13499	1	dsDNAphage	No	Complete	100	High-quality draft genome	ITR (high-confidence)	Podoviridae		
TM14_BL_k141_106576	1	dsDNAphage	No	High-quality	99.99	High-quality draft genome	AAI-based (medium-confidence)		Bacillota	<i>Lactobacillus ruminis</i>
TM14_BL_k141_145828	1	dsDNAphage	No	High-quality	91.03	High-quality draft genome	AAI-based (high-confidence)			
TM14_BL_k141_146503	1	dsDNAphage	No	High-quality	99.3	High-quality draft genome	AAI-based (high-confidence)	Podoviridae		
TM14_BL_k141_18641	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TM14_BL_k141_34805	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacillota	<i>Blautia obeum</i>
TM14_BL_k141_59230	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacillota	<i>Blautia obeum</i>
TM14_BL_k141_91088	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TM14_BL_k141_127016	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TM14_BL_k141_174143	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacillota	<i>Staphylococcus aureus</i>
TM13_BL_k141_5783	1	dsDNAphage	No	High-quality	99.5	High-quality draft genome	AAI-based (high-confidence)			
TM13_BL_k141_42765	1	dsDNAphage	No	High-quality	96.85	High-quality draft genome	AAI-based (medium-confidence)			
TM13_BL_k141_166935	0.98	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)	Microviridae	Bacteroidota	<i>Prevotella bivia</i>
TM11_BL_k141_898	0.92	ssDNA	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Ruminococcus bromii</i>
TM11_BL_k141_10988	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	Microviridae		
TM11_BL_k141_72415	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)	Siphoviridae	Bacillota	<i>Staphylococcus aureus</i>
TM11_BL_k141_113598	0.987	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)	Podoviridae		
TM10_BL_k141_15129	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)	Siphoviridae	Bacteroidota	<i>Bacteroides caccae</i>

UViG	VirSorter2 score	Predicted genome type	Provirus	Completeness quality	Completeness (%)	Assembly quality	Completeness approach	Family	Host phylum	Host species
TM10_BL_k141_57373	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacillota	<i>Staphylococcus aureus</i>
TM10_BL_k141_75400	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)	Microviridae		
TM09_BL_k141_8686	1	dsDNAphage	No	High-quality	93.79	High-quality draft genome	AAI-based (high-confidence)			
TM09_BL_k141_67591	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)	Podoviridae		
TM09_BL_k141_92076	0.98	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacillota	<i>Blautia obeum</i>
TM08_BL_k141_90468	0.993	dsDNAphage	No	High-quality	95.01	High-quality draft genome	AAI-based (medium-confidence)			
TM08_BL_k141_806	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacillota	<i>Roseburia intestinalis</i>
TM07_BL_k141_174835	0.973	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (medium-confidence)			
TM07_BL_k141_177779	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TM07_BL_k141_194286	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)	Microviridae		
TM07_BL_k141_194303	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)	Microviridae		
TM06_BL_k141_167295	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (medium-confidence)			
TM06_BL_k141_189536	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)	Siphoviridae	Bacteroidota	<i>Bacteroides fragilis</i>
TM05_BL_k141_42705	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TM05_BL_k141_80740	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	Microviridae		
TM05_BL_k141_95302	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TM05_BL_k141_107025	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Butyrivibrio crossotus</i>
TM05_BL_k141_128586	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (medium-confidence)		Bacillota	<i>Streptococcus pneumoniae</i>
TM05_BL_k141_156053	1	dsDNAphage	No	High-quality	99.4	High-quality draft genome	AAI-based (high-confidence)			
TM05_BL_k141_211466	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (medium-confidence)			
TM05_BL_k141_112731	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (medium-confidence)			
TM05_BL_k141_122283	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TM05_BL_k141_191987	0.993	ssDNA	No	Complete	100	High-quality draft genome	DTR (high-confidence)	Microviridae	Bacteroidota	<i>Prevotella disiens</i>
TM05_BL_k141_226998	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TM05_BL_k141_227004	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TM04_BL_k141_126443	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Actinomycetota	<i>Bifidobacterium longum</i>
TM04_BL_k141_127596	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TM04_BL_k141_166734	0.987	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TM03_BL_k141_39109	1	dsDNAphage	No	High-quality	98.5	High-quality draft genome	AAI-based (high-confidence)			
TM03_BL_k141_116489	0.94	ssDNA	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TM03_BL_k141_107969	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacillota	<i>Blautia obeum</i>
TM01_BL_k141_70138	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Flavonifractor plautii</i>
TF51_BL_k141_32081	1	dsDNAphage	No	High-quality	96.09	High-quality draft genome	AAI-based (high-confidence)	Siphoviridae	Bacillota	<i>Streptococcus anginosus</i>
TF50_BL_k141_127135	0.987	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF50_BL_k141_118405	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacillota	<i>Phascolarctobacterium succinatutens</i>
TF50_BL_k141_158079	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacillota	<i>Staphylococcus aureus</i>
TF50_BL_k141_158103	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)	Microviridae		
TF49_BL_k141_704	0.993	dsDNAphage	No	High-quality	99.91	High-quality draft genome	AAI-based (high-confidence)	Myoviridae	Bacillota	<i>Staphylococcus aureus</i>
TF49_BL_k141_9149	0.913	ssDNA	No	High-quality	98.62	High-quality draft genome	HMM-based (lower-bound)			
TF49_BL_k141_147319	0.987	dsDNAphage	No	Complete	100	High-quality draft genome	ITR (high-confidence)			
TF49_BL_k141_163529	0.987	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (medium-confidence)		Bacillota	<i>Faecalibacterium prausnitzii</i>
TF49_BL_k141_198424	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TF48_BL_k141_16267	1	dsDNAphage	No	High-quality	93.92	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Intestinibacter bartlettii</i>
TF48_BL_k141_65679	0.993	dsDNAphage	No	High-quality	95.11	High-quality draft genome	AAI-based (high-confidence)	Microviridae		
TF48_BL_k141_13497	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)	Microviridae		
TF48_BL_k141_76186	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)	Microviridae		
TF48_BL_k141_146489	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacillota	<i>Faecalibacterium prausnitzii</i>
TF47_BL_k141_15608	1	ssDNA	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	Microviridae	Bacteroidota	<i>Prevotella disiens</i>
TF47_BL_k141_100985	0.98	dsDNAphage	No	High-quality	98.73	High-quality draft genome	AAI-based (high-confidence)		Bacteroidota	<i>Prevotella disiens</i>
TF47_BL_k141_13475	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)	Microviridae	Bacillota	<i>Coprococcus comes</i>
TF47_BL_k141_64390	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacillota	<i>Staphylococcus aureus</i>
TF47_BL_k141_163863	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TF47_BL_k141_180785	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)	Microviridae		
TF46_BL_k141_17880	1	dsDNAphage	No	High-quality	95.89	High-quality draft genome	AAI-based (high-confidence)	Microviridae		
TF46_BL_k141_110724	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TF45_BL_k141_47053	0.987	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	Microviridae		
TF45_BL_k141_138304	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)	Microviridae		
TF44_BL_k141_38987	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (medium-confidence)			
TF44_BL_k141_39390	1	dsDNAphage	No	High-quality	96.16	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Clostridioides difficile</i>
TF44_BL_k141_2963	0.987	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)	Microviridae	Bacteroidota	<i>Prevotella disiens</i>
TF43_BL_k141_154294	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)	Siphoviridae		
TF43_BL_k141_157878	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacillota	<i>Clostridioides difficile</i>
TF42_BL_k141_62593	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	Microviridae		
TF42_BL_k141_109215	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	ITR (high-confidence)			
TF41_BL_k141_26780	0.987	dsDNAphage	No	High-quality	91.41	High-quality draft genome	AAI-based (medium-confidence)			
TF41_BL_k141_31025	0.993	dsDNAphage	No	High-quality	93.63	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Ruminococcus bromii</i>
TF41_BL_k141_47565	0.973	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (medium-confidence)			
TF41_BL_k141_50668	1	dsDNAphage	No	High-quality	95.41	High-quality draft genome	AAI-based (high-confidence)			
TF41_BL_k141_83801	0.987	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Blautia obeum</i>
TF41_BL_k141_88124	1	dsDNAphage	No	Complete	100	High-quality draft genome	ITR (high-confidence)	Podoviridae		
TF41_BL_k141_135989	1	ssDNA	No	High-quality	99.23	High-quality draft genome	AAI-based (high-confidence)	Microviridae		
TF41_BL_k141_111562	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)	Siphoviridae	Actinomycetota	<i>Bifidobacterium adolescentis</i>
TF41_BL_k141_149250	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TF41_BL_k141_181721	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacillota	<i>Roseburia inulinivorans</i>
TF40_BL_k141_53225	0.973	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Ruminococcus bromii</i>
TF40_BL_k141_109655	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacillota	<i>Blautia obeum</i>
TF39_BL_k141_6810	0.987	dsDNAphage	No	High-quality	92.29	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Ruminococcus bromii</i>
TF39_BL_k141_182662	0.987	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacillota	<i>Faecalibacterium prausnitzii</i>
TF38_BL_k141_14896	1	dsDNAphage	No	High-quality	92.97	High-quality draft genome	AAI-based (high-confidence)	Microviridae		
TF37_BL_k141_157812	1	dsDNAphage	No	High-quality	94.24	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Staphylococcus epidermidis</i>
TF37_BL_k141_163928	1	dsDNAphage	No	High-quality	95.55	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Blautia obeum</i>
TF37_BL_k141_15963	0.987	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacillota	<i>Blautia obeum</i>
TF37_BL_k141_166384	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)	Siphoviridae	Bacteroidota	<i>Bacteroides caccae</i>

UViG	VirSorter2 score	Predicted genome type	Provirus	Completeness quality	Completeness (%)	Assembly quality	Completeness approach	Family	Host phylum	Host species
TF35_BL_k141_33687	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF34_BL_k141_20175	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF34_BL_k141_116470	1	dsDNAphage	No	High-quality	99.91	High-quality draft genome	AAI-based (high-confidence)		Bacteroidota	<i>Bacteroides xylanisolvens</i>
TF34_BL_k141_122109	0.993	dsDNAphage	No	High-quality	96.99	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Faecalibacterium prausnitzii</i>
TF34_BL_k141_6602	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacillota	<i>Butyrivibrio crossotus</i>
TF34_BL_k141_58925	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacillota	<i>Ruminococcus lactaris</i>
TF33_BL_k141_57142	1	dsDNAphage	No	High-quality	90.66	High-quality draft genome	AAI-based (high-confidence)	Podoviridae	Bacteroidota	<i>Prevotella melaninogenica</i>
TF33_BL_k141_60141	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	Myoviridae	Pseudomonota	<i>Escherichia coli</i>
TF33_BL_k141_129900	0.973	dsDNAphage	No	High-quality	94.13	High-quality draft genome	AAI-based (high-confidence)			
TF33_BL_k141_164065	0.98	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	Siphoviridae	Pseudomonota	<i>Escherichia coli</i>
TF33_BL_k141_175106	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (medium-confidence)			
TF33_BL_k141_39184	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TF33_BL_k141_43709	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (medium-confidence)			
TF33_BL_k141_155278	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacteroidota	<i>Prevotella amnii</i>
TF32_BL_k141_7610	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	Siphoviridae		
TF32_BL_k141_54419	1	dsDNAphage	No	High-quality	93.66	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Staphylococcus aureus</i>
TF31_BL_k141_41691	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Actinomycetota	<i>Bifidobacterium longum</i>
TF30_BL_k141_145842	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Ruminococcus bromii</i>
TF30_BL_k141_67260	0.987	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacillota	<i>Faecalibacterium prausnitzii</i>
TF30_BL_k141_71792	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)	Podoviridae	Bacteroidota	<i>Prevotella melaninogenica</i>
TF29_BL_k141_12258	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF28_BL_k141_137	1	dsDNAphage	No	High-quality	96.34	High-quality draft genome	AAI-based (high-confidence)		Bacteroidota	<i>Prevotella copri</i>
TF28_BL_k141_84913	0.987	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Actinomycetota	<i>Bifidobacterium longum</i>
TF28_BL_k141_87572	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacteroidota	<i>Prevotella copri</i>
TF27_BL_k141_24768	0.98	dsDNAphage	No	High-quality	98.68	High-quality draft genome	AAI-based (high-confidence)		Bacteroidota	<i>Prevotella copri</i>
TF27_BL_k141_24951	0.987	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacillota	<i>Blautia obeum</i>
TF27_BL_k141_97127	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Dorea longicatena</i>
TF27_BL_k141_127685	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Tyzzrella nexilis</i>
TF27_BL_k141_145456	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TF26_BL_k141_43273	0.74	dsDNAphage	No	High-quality	100	High-quality draft genome	HMM-based (lower-bound)			
TF26_BL_k141_101968	1	dsDNAphage	No	High-quality	98.01	High-quality draft genome	AAI-based (high-confidence)			
TF26_BL_k141_159994	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacteroidota	<i>Prevotella stercorea</i>
TF25_BL_k141_2711	1	dsDNAphage	No	High-quality	96.22	High-quality draft genome	AAI-based (high-confidence)	Microviridae		
TF25_BL_k141_91908	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	Microviridae		
TF25_BL_k141_117557	0.98	dsDNAphage	No	High-quality	92.29	High-quality draft genome	AAI-based (high-confidence)			
TF25_BL_k141_12814	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacillota	<i>Blautia obeum</i>
TF25_BL_k141_90639	0.987	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TF25_BL_k141_143955	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TF24_BL_k141_77233	0.967	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Actinomycetota	<i>Bifidobacterium bifidum</i>
TF24_BL_k141_128850	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TF23_BL_k141_62365	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacteroidota	<i>Prevotella disiens</i>
TF23_BL_k141_92706	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TF23_BL_k141_92707	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)	Microviridae		
TF22_BL_k141_42604	0.993	dsDNAphage	No	High-quality	93.21	High-quality draft genome	AAI-based (high-confidence)			
TF22_BL_k141_85607	1	dsDNAphage	No	High-quality	92.19	High-quality draft genome	AAI-based (medium-confidence)			
TF22_BL_k141_119577	1	dsDNAphage	No	High-quality	90.93	High-quality draft genome	AAI-based (medium-confidence)			
TF22_BL_k141_162553	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Staphylococcus aureus</i>
TF20_BL_k141_103023	1	dsDNAphage	No	High-quality	97.22	High-quality draft genome	AAI-based (medium-confidence)			
TF20_BL_k141_144470	0.987	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TF20_BL_k141_157662	1	dsDNAphage	No	High-quality	91.55	High-quality draft genome	AAI-based (high-confidence)			
TF20_BL_k141_3999	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)	Microviridae		
TF20_BL_k141_79752	0.98	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TF20_BL_k141_193097	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TF20_BL_k141_197090	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacteroidota	<i>Prevotella copri</i>
TF19_BL_k141_40941	0.993	dsDNAphage	No	High-quality	98.09	High-quality draft genome	AAI-based (high-confidence)			
TF19_BL_k141_195246	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacteroidota	<i>Bacteroides xylanisolvens</i>
TF19_BL_k141_202732	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacillota	<i>Faecalibacterium prausnitzii</i>
TF19_BL_k141_202808	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TF18_BL_k141_96694	0.987	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF18_BL_k141_170467	1	dsDNAphage	No	High-quality	98.98	High-quality draft genome	AAI-based (high-confidence)	Siphoviridae	Bacteroidota	<i>Bacteroides caccae</i>
TF18_BL_k141_171432	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacillota	<i>Butyrivibrio crossotus</i>
TF17_BL_k141_70197	1	dsDNAphage	No	High-quality	97.69	High-quality draft genome	AAI-based (high-confidence)	Myoviridae	Bacillota	<i>Coprococcus comes</i>
TF17_BL_k141_133972	0.993	dsDNAphage	No	High-quality	96.29	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Tyzzrella nexilis</i>
TF17_BL_k141_20504	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TF15_BL_k141_40241	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	Microviridae		
TF15_BL_k141_117091	0.98	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TF15_BL_k141_120713	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacillota	<i>Blautia obeum</i>
TF14_BL_k141_198259	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TF14_BL_k141_215283	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TF14_BL_k141_215417	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TF13_BL_k141_121504	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	Myoviridae		
TF13_BL_k141_143964	0.687	dsDNAphage	No	High-quality	91.12	High-quality draft genome	AAI-based (high-confidence)			
TF12_BL_k141_1209	0.993	dsDNAphage	No	High-quality	93.39	High-quality draft genome	AAI-based (medium-confidence)		Bacillota	<i>Roseburia intestinalis</i>
TF12_BL_k141_10077	0.98	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF12_BL_k141_89792	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF12_BL_k141_163785	0.987	dsDNAphage	No	High-quality	98.01	High-quality draft genome	AAI-based (medium-confidence)			
TF12_BL_k141_83531	0.667	dsDNAphage	No	High-quality	99.31	High-quality draft genome	AAI-based (high-confidence)			
TF12_BL_k141_228078	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacillota	<i>Roseburia inulinivorans</i>
TF12_BL_k141_228226	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacillota	<i>Roseburia inulinivorans</i>
TF11_BL_k141_25374	1	dsDNAphage	No	High-quality	99.19	High-quality draft genome	AAI-based (high-confidence)		Bacteroidota	<i>Prevotella disiens</i>
TF10_BL_k141_173990	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TF09_BL_k141_41779	0.94	ssDNA	No	High-quality	100	High-quality draft genome	AAI-based (medium-confidence)			
TF08_BL_k141_73109	1	dsDNAphage	No	High-quality	93.32	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Staphylococcus epidermidis</i>

UViG	VirSorter2 score	Predicted genome type	Provirus	Completeness quality	Completeness (%)	Assembly quality	Completeness approach	Family	Host phylum	Host species
TF08_BL_k141_106168	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (medium-confidence)			
TF08_BL_k141_107198	0.993	dsDNAphage	No	High-quality	99.5	High-quality draft genome	AAI-based (high-confidence)	Microviridae		
TF08_BL_k141_129009	1	dsDNAphage	No	High-quality	97.7	High-quality draft genome	AAI-based (high-confidence)		Bacillota	Holdemanelia bififormis
TF07_BL_k141_58583	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TF07_BL_k141_132584	0.967	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TF06_BL_k141_20226	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (medium-confidence)		Bacillota	Ruminococcus bromii
TF06_BL_k141_37971	1	dsDNAphage	No	High-quality	94.25	High-quality draft genome	AAI-based (high-confidence)		Bacillota	Staphylococcus aureus
TF06_BL_k141_87120	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	Microviridae		
TF06_BL_k141_174128	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacillota	Tyzzereella nexilis
TF05_BL_k141_23701	0.993	dsDNAphage	No	High-quality	91.88	High-quality draft genome	AAI-based (high-confidence)	Podoviridae		
TF05_BL_k141_72410	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacillota	Phascolarctobacterium succinatutens
TF04_BL_k141_10907	0.973	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF04_BL_k141_17372	1	dsDNAphage	No	High-quality	90.96	High-quality draft genome	AAI-based (high-confidence)		Bacillota	Butyrivibrio crossotus
TF04_BL_k141_49760	1	dsDNAphage	No	High-quality	93.47	High-quality draft genome	AAI-based (high-confidence)	Microviridae		
TF04_BL_k141_78349	1	dsDNAphage	No	High-quality	99.34	High-quality draft genome	AAI-based (high-confidence)			
TF04_BL_k141_120155	0.987	dsDNAphage	No	High-quality	92.6	High-quality draft genome	AAI-based (high-confidence)			
TF04_BL_k141_130514	1	dsDNAphage	No	High-quality	95.99	High-quality draft genome	AAI-based (high-confidence)	Podoviridae		
TF04_BL_k141_39365	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TF04_BL_k141_52388	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TF04_BL_k141_59896	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF04_BL_k141_169754	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)	Bacillota		Tyzzereella nexilis
TF04_BL_k141_169960	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)	Bacillota		Staphylococcus aureus
TF04_BL_k141_170090	0.987	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)	Microviridae		
TF03_BL_k141_15633	0.993	dsDNAphage	No	High-quality	93.94	High-quality draft genome	AAI-based (medium-confidence)	Myoviridae	Bacillota	Roseburia inulinivorans
TF03_BL_k141_88338	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacteroidota	Prevotella amnii
TF03_BL_k141_183968	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TF02_BL_k141_154309	0.993	dsDNAphage	No	High-quality	98.47	High-quality draft genome	AAI-based (medium-confidence)		Bacillota	Staphylococcus aureus
TF02_BL_k141_182005	0.987	dsDNAphage	No	High-quality	90.44	High-quality draft genome	AAI-based (high-confidence)		Bacteroidota	Bacteroides vulgatus
TF02_BL_k141_204357	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacillota	Staphylococcus epidermidis
TF01_BL_k141_26495	0.987	dsDNAphage	No	High-quality	94.77	High-quality draft genome	AAI-based (high-confidence)	Siphoviridae		
TF01_BL_k141_18041	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TF01_BL_k141_84458	0.987	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacillota	Anaerostipes caccae
TM24_BL_k141_226221	0.827	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (medium-confidence)			
TM16_BL_k141_129376	0.6	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (medium-confidence)			
TM06_BL_k141_63358	0.933	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TF39_BL_k141_77209	0.667	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF02_BL_k141_249967	1	dsDNAphage	Yes	Complete	100	High-quality draft genome	DTR (medium-confidence)			
TF10_BL_k141_167042	1	dsDNAphage	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF12_BL_k141_32608	0.993	dsDNAphage	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	Bacillota		Ruminococcus bromii
TF12_BL_k141_149545	1	dsDNAphage	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	Bacillota		Coprococcus comes
TF13_BL_k141_164829	0.98	dsDNAphage	Yes	High-quality	99.21	High-quality draft genome	AAI-based (high-confidence)	Actinomycetota		Bifidobacterium adolescentis
TF14_BL_k141_145060	1	dsDNAphage	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	Myoviridae	Pseudomonota	Escherichia coli
TF15_BL_k141_39114	1	dsDNAphage	Yes	High-quality	98.09	High-quality draft genome	AAI-based (medium-confidence)			
TF16_BL_k141_82309	0.98	dsDNAphage	Yes	High-quality	97.3	High-quality draft genome	AAI-based (high-confidence)		Bacillota	Ruminococcus lactaris
TF25_BL_k141_88272	1	dsDNAphage	Yes	Complete	100	High-quality draft genome	Provirus (high-confidence)	Myoviridae	Bacillota	Catenibacterium mitsuokai
TF29_BL_k141_42158	0.993	dsDNAphage	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	Siphoviridae	Bacillota	Lactobacillus ruminis
TF29_BL_k141_53177	0.98	dsDNAphage	Yes	High-quality	100	High-quality draft genome	AAI-based (medium-confidence)		Bacillota	Lactobacillus ruminis
TF30_BL_k141_117602	0.993	dsDNAphage	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacillota	Clostridioides difficile
TF32_BL_k141_91180	0.993	dsDNAphage	Yes	High-quality	94.36	High-quality draft genome	AAI-based (medium-confidence)			
TF33_BL_k141_26384	0.973	dsDNAphage	Yes	High-quality	94.47	High-quality draft genome	AAI-based (high-confidence)	Myoviridae	Pseudomonota	Escherichia coli
TF33_BL_k141_136424	1	dsDNAphage	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF34_BL_k141_46996	0.993	dsDNAphage	Yes	High-quality	99.2	High-quality draft genome	AAI-based (high-confidence)			
TF35_BL_k141_30905	0.993	dsDNAphage	Yes	High-quality	94.82	High-quality draft genome	AAI-based (high-confidence)			
TF37_BL_k141_70116	0.987	dsDNAphage	Yes	High-quality	99.94	High-quality draft genome	AAI-based (high-confidence)			
TF37_BL_k141_71358	1	dsDNAphage	Yes	High-quality	96.03	High-quality draft genome	AAI-based (high-confidence)			
TF37_BL_k141_76854	0.993	dsDNAphage	Yes	High-quality	98.98	High-quality draft genome	AAI-based (high-confidence)		Bacillota	Faecalibacterium prausnitzii
TF37_BL_k141_134872	1	dsDNAphage	Yes	High-quality	97.74	High-quality draft genome	AAI-based (high-confidence)		Bacillota	Anaerostipes hadrus
TF41_BL_k141_48942	0.993	dsDNAphage	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF44_BL_k141_13693	0.993	dsDNAphage	Yes	High-quality	91.78	High-quality draft genome	AAI-based (high-confidence)		Pseudomonota	Klebsiella pneumoniae
TF46_BL_k141_38989	0.993	dsDNAphage	Yes	Complete	100	High-quality draft genome	Provirus (medium-confidence)			
TF47_BL_k141_41904	0.98	dsDNAphage	Yes	Complete	100	High-quality draft genome	Provirus (high-confidence)	Myoviridae		
TF48_BL_k141_133798	0.987	dsDNAphage	Yes	High-quality	98.33	High-quality draft genome	AAI-based (high-confidence)		Bacillota	Staphylococcus epidermidis
TF51_BL_k141_83967	0.987	dsDNAphage	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Actinomycetota	Bifidobacterium pseudocatenulatum
TM03_BL_k141_187643	0.993	dsDNAphage	Yes	High-quality	90.11	High-quality draft genome	AAI-based (high-confidence)			
TM05_BL_k141_2835	0.993	dsDNAphage	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TM05_BL_k141_97981	1	dsDNAphage	Yes	High-quality	90.01	High-quality draft genome	AAI-based (high-confidence)		Bacillota	Faecalibacterium prausnitzii
TM05_BL_k141_123633	1	dsDNAphage	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	Myoviridae	Bacillota	Faecalibacterium prausnitzii
TM05_BL_k141_141877	0.973	dsDNAphage	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TM05_BL_k141_198673	0.987	dsDNAphage	Yes	High-quality	99.04	High-quality draft genome	AAI-based (high-confidence)			
TM12_BL_k141_14288	0.98	dsDNAphage	Yes	High-quality	92.25	High-quality draft genome	AAI-based (high-confidence)			
TM12_BL_k141_60911	1	dsDNAphage	Yes	High-quality	94.51	High-quality draft genome	AAI-based (high-confidence)		Bacillota	Dorea formicigenerans
TM14_BL_k141_71288	0.973	dsDNAphage	Yes	High-quality	96.09	High-quality draft genome	AAI-based (high-confidence)	Siphoviridae		
TM20_BL_k141_177337	1	dsDNAphage	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	Siphoviridae	Bacillota	Streptococcus pyogenes
TM23_BL_k141_34704	1	dsDNAphage	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	Microviridae		
TM32_BL_k141_103800	0.98	dsDNAphage	Yes	High-quality	100	High-quality draft genome	AAI-based (medium-confidence)	Myoviridae		
TM35_BL_k141_52471	1	dsDNAphage	Yes	High-quality	97.07	High-quality draft genome	AAI-based (high-confidence)		Bacillota	Anaerobutyricum hallii
TM35_BL_k141_169923	1	dsDNAphage	Yes	High-quality	100	High-quality draft genome	AAI-based (medium-confidence)		Bacillota	Anaerobutyricum hallii
TM35_BL_k141_228064	0.993	dsDNAphage	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TM39_BL_k141_105211	1	dsDNAphage	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TM39_BL_k141_39466	0.993	dsDNAphage	No	High-quality	94.67	High-quality draft genome	AAI-based (high-confidence)			
TM39_BL_k141_174763	0.987	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TM37_BL_k141_3065	1	dsDNAphage	No	High-quality	92.6	High-quality draft genome	AAI-based (high-confidence)		Bacillota	Coprococcus comes
TM37_BL_k141_37236	0.973	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			

UViG	VirSorter2 score	Predicted genome type	Provirus	Completeness quality	Completeness (%)	Assembly quality	Completeness approach	Family	Host phylum	Host species
TM37_BL_k141_114302	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	<i>Myoviridae</i>	<i>Bacillota</i>	<i>Roseburia inulinivorans</i>
TM37_BL_k141_120569	0.98	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TM36_BL_k141_9530	1	dsDNAphage	No	High-quality	97.03	High-quality draft genome	AAI-based (high-confidence)			
TM36_BL_k141_23034	0.98	dsDNAphage	No	High-quality	98.54	High-quality draft genome	AAI-based (high-confidence)	<i>Myoviridae</i>	<i>Bacillota</i>	<i>Faecalibacterium prausnitzii</i>
TM36_BL_k141_68517	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		<i>Bacillota</i>	<i>Ruminococcus lactaris</i>
TM36_BL_k141_176999	0.987	dsDNAphage	No	High-quality	95.13	High-quality draft genome	AAI-based (high-confidence)			
TM35_BL_k141_15263	0.993	dsDNAphage	No	High-quality	99.24	High-quality draft genome	AAI-based (high-confidence)		<i>Bacillota</i>	<i>Coprococcus comes</i>
TM35_BL_k141_37764	1	dsDNAphage	No	High-quality	99.87	High-quality draft genome	AAI-based (high-confidence)		<i>Bacillota</i>	<i>Butyrivibrio crossotus</i>
TM35_BL_k141_232929	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		<i>Bacillota</i>	<i>Streptococcus pyogenes</i>
TM35_BL_k141_45190	0.96	ssDNA	No	High-quality	100	High-quality draft genome	HMM-based (lower-bound)			
TM34_BL_k141_155966	1	dsDNAphage	No	High-quality	98.96	High-quality draft genome	AAI-based (high-confidence)			
TM32_BL_k141_106105	0.993	dsDNAphage	No	High-quality	94.72	High-quality draft genome	AAI-based (high-confidence)		<i>Actinomycetota</i>	<i>Bifidobacterium adolescentis</i>
TM32_BL_k141_12693	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		<i>Bacillota</i>	<i>Butyrivibrio crossotus</i>
TM30_BL_k141_206919	0.64	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TM29_BL_k141_185016	1	dsDNAphage	No	High-quality	91.23	High-quality draft genome	AAI-based (high-confidence)		<i>Bacillota</i>	<i>Faecalibacterium prausnitzii</i>
TM29_BL_k141_193829	0.953	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TM28_BL_k141_237776	1	dsDNAphage	No	High-quality	99.36	High-quality draft genome	AAI-based (high-confidence)		<i>Actinomycetota</i>	<i>Bifidobacterium longum</i>
TM28_BL_k141_144142	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)	<i>Siphoviridae</i>	<i>Bacillota</i>	<i>Faecalibacterium prausnitzii</i>
TM27_BL_k141_46134	1	dsDNAphage	No	High-quality	90.69	High-quality draft genome	AAI-based (high-confidence)		<i>Bacillota</i>	<i>Faecalibacterium prausnitzii</i>
TM27_BL_k141_150840	1	dsDNAphage	No	High-quality	99.17	High-quality draft genome	AAI-based (high-confidence)		<i>Bacillota</i>	<i>Faecalibacterium prausnitzii</i>
TM27_BL_k141_174045	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		<i>Bacillota</i>	<i>Faecalibacterium prausnitzii</i>
TM24_BL_k141_25888	0.993	dsDNAphage	No	High-quality	96.3	High-quality draft genome	AAI-based (high-confidence)			
TM24_BL_k141_81302	1	dsDNAphage	No	High-quality	92.17	High-quality draft genome	AAI-based (high-confidence)			
TM24_BL_k141_98109	0.92	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (medium-confidence)			
TM24_BL_k141_98473	1	dsDNAphage	No	High-quality	94.99	High-quality draft genome	AAI-based (high-confidence)		<i>Bacteroidota</i>	<i>Parabacteroides distasonis</i>
TM24_BL_k141_167944	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TM24_BL_k141_170823	1	dsDNAphage	No	High-quality	96.99	High-quality draft genome	AAI-based (high-confidence)		<i>Bacillota</i>	<i>Ruminococcus bromii</i>
TM24_BL_k141_27249	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		<i>Bacillota</i>	<i>Faecalibacterium prausnitzii</i>
TM24_BL_k141_57943	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TM23_BL_k141_6899	0.987	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (medium-confidence)			
TM23_BL_k141_47369	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		<i>Bacillota</i>	<i>Roseburia intestinalis</i>
TM23_BL_k141_48430	1	dsDNAphage	No	High-quality	97.2	High-quality draft genome	AAI-based (high-confidence)			
TM23_BL_k141_57832	0.9	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TM23_BL_k141_77532	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	<i>Myoviridae</i>		
TM23_BL_k141_12147	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		<i>Bacteroidota</i>	<i>Bacteroides ovatus</i>
TM23_BL_k141_127515	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		<i>Actinomycetota</i>	<i>Bifidobacterium bifidum</i>
TM22_BL_k141_109820	0.913	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TM22_BL_k141_81824	1	ssDNA	No	High-quality	94.51	High-quality draft genome	AAI-based (medium-confidence)			
TM21_BL_k141_59897	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	<i>Myoviridae</i>		
TM20_BL_k141_37334	0.987	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		<i>Bacillota</i>	<i>Faecalibacterium prausnitzii</i>
TM20_BL_k141_82676	0.987	dsDNAphage	No	High-quality	90.79	High-quality draft genome	AAI-based (high-confidence)			
TM20_BL_k141_152324	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		<i>Bacillota</i>	<i>Faecalibacterium prausnitzii</i>
TM20_BL_k141_168269	1	dsDNAphage	No	High-quality	94.13	High-quality draft genome	AAI-based (high-confidence)		<i>Bacteroidota</i>	<i>Bacteroides dorei</i>
TM19_BL_k141_44432	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (medium-confidence)		<i>Bacillota</i>	<i>Faecalibacterium prausnitzii</i>
TM19_BL_k141_64230	1	dsDNAphage	No	High-quality	94.1	High-quality draft genome	AAI-based (high-confidence)		<i>Bacillota</i>	<i>Faecalibacterium prausnitzii</i>
TM19_BL_k141_96364	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		<i>Bacillota</i>	<i>Faecalibacterium prausnitzii</i>
TM18_BL_k141_21724	0.987	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (medium-confidence)		<i>Bacillota</i>	<i>Ruminococcus bromii</i>
TM18_BL_k141_23206	1	dsDNAphage	No	High-quality	91.45	High-quality draft genome	AAI-based (high-confidence)		<i>Bacteroidota</i>	<i>Bacteroides uniformis</i>
TM18_BL_k141_52293	0.993	dsDNAphage	No	High-quality	92.07	High-quality draft genome	AAI-based (high-confidence)			
TM18_BL_k141_69432	1	dsDNAphage	No	High-quality	98.7	High-quality draft genome	AAI-based (high-confidence)		<i>Bacillota</i>	<i>Faecalibacterium prausnitzii</i>
TM18_BL_k141_81350	0.987	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		<i>Bacillota</i>	<i>Blautia obeum</i>
TM17_BL_k141_83176	0.973	dsDNAphage	No	High-quality	95.29	High-quality draft genome	AAI-based (high-confidence)		<i>Bacillota</i>	<i>Faecalibacterium prausnitzii</i>
TM16_BL_k141_93934	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	<i>Myoviridae</i>		
TM16_BL_k141_122284	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		<i>Bacillota</i>	<i>Ruminococcus bromii</i>
TM16_BL_k141_93535	0.933	ssDNA	No	High-quality	100	High-quality draft genome	HMM-based (lower-bound)			
TM15_BL_k141_7777	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		<i>Bacillota</i>	<i>Blautia obeum</i>
TM15_BL_k141_65363	0.873	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TM15_BL_k141_157103	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		<i>Bacillota</i>	<i>Coprococcus comes</i>
TM15_BL_k141_71595	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TM14_BL_k141_50481	0.953	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (medium-confidence)			
TM14_BL_k141_68753	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		<i>Actinomycetota</i>	<i>Bifidobacterium bifidum</i>
TM14_BL_k141_46199	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TM14_BL_k141_174462	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		<i>Bacteroidota</i>	<i>Bacteroides vulgatus</i>
TM13_BL_k141_26623	0.987	dsDNAphage	No	High-quality	90.51	High-quality draft genome	AAI-based (high-confidence)			
TM13_BL_k141_49864	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TM13_BL_k141_156548	1	dsDNAphage	No	High-quality	99.45	High-quality draft genome	AAI-based (high-confidence)		<i>Bacillota</i>	<i>Faecalibacterium prausnitzii</i>
TM13_BL_k141_92789	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		<i>Bacillota</i>	<i>Staphylococcus aureus</i>
TM13_BL_k141_167044	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TM12_BL_k141_3928	0.767	ssDNA	No	High-quality	100	High-quality draft genome	HMM-based (lower-bound)			
TM12_BL_k141_5680	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (medium-confidence)		<i>Bacteroidota</i>	<i>Bacteroides ovatus</i>
TM12_BL_k141_17267	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		<i>Bacillota</i>	<i>Roseburia intestinalis</i>
TM12_BL_k141_27026	0.66	dsDNAphage	No	High-quality	100	High-quality draft genome	HMM-based (lower-bound)			
TM12_BL_k141_28054	0.98	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	<i>Myoviridae</i>		
TM12_BL_k141_37626	0.993	dsDNAphage	No	High-quality	99.21	High-quality draft genome	AAI-based (high-confidence)		<i>Bacillota</i>	<i>Roseburia inulinivorans</i>
TM12_BL_k141_119623	0.993	dsDNAphage	No	High-quality	90.8	High-quality draft genome	AAI-based (high-confidence)		<i>Bacillota</i>	<i>Faecalibacterium prausnitzii</i>
TM12_BL_k141_89394	0.98	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		<i>Bacillota</i>	<i>Faecalibacterium prausnitzii</i>
TM11_BL_k141_36729	1	dsDNAphage	No	High-quality	92.21	High-quality draft genome	AAI-based (high-confidence)			
TM11_BL_k141_76349	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		<i>Bacillota</i>	<i>Coprococcus comes</i>
TM11_BL_k141_8067	0.987	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		<i>Bacillota</i>	<i>Faecalibacterium prausnitzii</i>
TM11_BL_k141_72848	0.987	ssDNA	No	High-quality	100	High-quality draft genome	HMM-based (lower-bound)			
TM10_BL_k141_2577	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	<i>Myoviridae</i>		
TM10_BL_k141_11520	0.987	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	<i>Myoviridae</i>		
TM10_BL_k141_35499	0.993	dsDNAphage	No	High-quality	98.3	High-quality draft genome	AAI-based (high-confidence)		<i>Bacteroidota</i>	<i>Bacteroides caccae</i>

UViG	VirSorter2 score	Predicted genome type	Provirus	Completeness quality	Completeness (%)	Assembly quality	Completeness approach	Family	Host phylum	Host species
TM10_BL_k141_50059	0.973	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacillota	<i>Blautia hanseni</i>
TM09_BL_k141_3239	0.98	dsDNAphage	No	High-quality	93.34	High-quality draft genome	AAI-based (high-confidence)		Actinomycetota	<i>Bifidobacterium longum</i>
TM09_BL_k141_22035	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacillota	<i>Staphylococcus aureus</i>
TM09_BL_k141_53663	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TM09_BL_k141_91984	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (medium-confidence)		Bacillota	<i>Flavonifractor plautii</i>
TM08_BL_k141_71112	0.993	dsDNAphage	No	High-quality	99.67	High-quality draft genome	AAI-based (high-confidence)			
TM07_BL_k141_121955	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacteroidota	<i>Bacteroides xylanisolvens</i>
TM07_BL_k141_161272	0.993	dsDNAphage	No	High-quality	93.85	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Roseburia intestinalis</i>
TM07_BL_k141_35364	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)	Myoviridae		
TM06_BL_k141_126282	1	dsDNAphage	No	High-quality	99.08	High-quality draft genome	AAI-based (medium-confidence)		Bacteroidota	<i>Bacteroides uniformis</i>
TM05_BL_k141_137060	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)	Myoviridae		
TM04_BL_k141_39229	0.987	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (medium-confidence)			
TM04_BL_k141_70982	0.76	dsDNAphage	No	High-quality	100	High-quality draft genome	HMM-based (lower-bound)			
TM04_BL_k141_78047	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Coprococcus comes</i>
TM04_BL_k141_162564	1	dsDNAphage	No	High-quality	99.25	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Blautia obeum</i>
TM04_BL_k141_165097	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TM03_BL_k141_3571	0.98	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Tyzzereella nexitis</i>
TM03_BL_k141_43251	1	dsDNAphage	No	High-quality	95.35	High-quality draft genome	AAI-based (high-confidence)			
TM03_BL_k141_65793	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Actinomycetota	<i>Bifidobacterium longum</i>
TM03_BL_k141_68743	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Faecalibacterium prausnitzii</i>
TM03_BL_k141_76794	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TM03_BL_k141_142594	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacteroidota	<i>Parabacteroides distasonis</i>
TM02_BL_k141_4545	0.993	dsDNAphage	No	High-quality	96.13	High-quality draft genome	AAI-based (high-confidence)			
TM02_BL_k141_49248	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TM02_BL_k141_113543	0.98	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Coprococcus comes</i>
TM02_BL_k141_135590	0.993	dsDNAphage	No	High-quality	91.53	High-quality draft genome	AAI-based (medium-confidence)	Myoviridae		
TM02_BL_k141_109066	0.94	ssDNA	No	High-quality	100	High-quality draft genome	HMM-based (lower-bound)			
TM01_BL_k141_12466	0.993	dsDNAphage	No	High-quality	91.77	High-quality draft genome	AAI-based (medium-confidence)		Bacillota	<i>Flavonifractor plautii</i>
TM01_BL_k141_65202	0.987	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Coprococcus eutactus</i>
TM01_BL_k141_73834	1	dsDNAphage	No	High-quality	90.37	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Ruminococcus bromii</i>
TF51_BL_k141_4182	0.993	dsDNAphage	No	High-quality	98.98	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Roseburia inulinivorans</i>
TF51_BL_k141_27449	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Roseburia inulinivorans</i>
TF51_BL_k141_62319	0.973	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	Actinomycetota		<i>Bifidobacterium longum</i>
TF51_BL_k141_109485	0.993	dsDNAphage	No	High-quality	94.87	High-quality draft genome	AAI-based (high-confidence)	Bacillota		<i>Streptococcus anginosus</i>
TF51_BL_k141_134084	1	dsDNAphage	No	High-quality	97.34	High-quality draft genome	AAI-based (high-confidence)	Myoviridae		
TF50_BL_k141_9558	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Faecalibacterium prausnitzii</i>
TF50_BL_k141_139850	0.98	dsDNAphage	No	High-quality	92.4	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Coprococcus catus</i>
TF50_BL_k141_2982	0.98	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TF50_BL_k141_157761	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)	Podoviridae	Bacillota	<i>Staphylococcus aureus</i>
TF49_BL_k141_20012	0.993	dsDNAphage	No	High-quality	91.1	High-quality draft genome	AAI-based (high-confidence)			
TF49_BL_k141_92403	1	dsDNAphage	No	High-quality	92.96	High-quality draft genome	AAI-based (high-confidence)		Bacteroidota	<i>Bacteroides vulgatus</i>
TF49_BL_k141_131668	0.993	dsDNAphage	No	High-quality	92.56	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Faecalibacterium prausnitzii</i>
TF49_BL_k141_188979	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (medium-confidence)	Myoviridae		
TF49_BL_k141_199430	0.993	dsDNAphage	No	High-quality	97.34	High-quality draft genome	AAI-based (high-confidence)	Myoviridae		
TF49_BL_k141_200460	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacillota	<i>Staphylococcus aureus</i>
TF48_BL_k141_94050	0.987	dsDNAphage	No	High-quality	90.81	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Faecalibacterium prausnitzii</i>
TF48_BL_k141_117610	1	dsDNAphage	No	High-quality	93.89	High-quality draft genome	AAI-based (high-confidence)		Bacteroidota	<i>Parabacteroides johnsonii</i>
TF48_BL_k141_152754	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacteroidota	<i>Parabacteroides distasonis</i>
TF48_BL_k141_50957	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TF48_BL_k141_193477	0.893	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF47_BL_k141_24894	0.993	dsDNAphage	No	High-quality	93.73	High-quality draft genome	AAI-based (high-confidence)		Bacteroidota	<i>Bacteroides caccae</i>
TF47_BL_k141_75960	0.553	dsDNAphage	No	High-quality	100	High-quality draft genome	HMM-based (lower-bound)			
TF47_BL_k141_114798	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF46_BL_k141_62207	1	dsDNAphage	No	High-quality	96.97	High-quality draft genome	AAI-based (high-confidence)	Myoviridae		
TF45_BL_k141_23009	0.953	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (medium-confidence)		Bacillota	<i>Tyzzereella nexitis</i>
TF44_BL_k141_11163	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Staphylococcus aureus</i>
TF43_BL_k141_26960	0.987	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacillota	<i>Roseburia intestinalis</i>
TF43_BL_k141_98600	0.98	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	Myoviridae		
TF43_BL_k141_145085	1	dsDNAphage	No	High-quality	97.39	High-quality draft genome	AAI-based (high-confidence)		Bacteroidota	<i>Prevotella bivia</i>
TF43_BL_k141_151454	0.767	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF43_BL_k141_156113	0.993	dsDNAphage	No	High-quality	99.81	High-quality draft genome	AAI-based (high-confidence)		Bacteroidota	<i>Bacteroides dorei</i>
TF43_BL_k141_157925	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TF42_BL_k141_3039	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacteroidota	<i>Bacteroides xylanisolvens</i>
TF42_BL_k141_8796	0.98	dsDNAphage	No	High-quality	99.55	High-quality draft genome	AAI-based (high-confidence)		Fusobacteria	<i>Fusobacterium necrophorum</i>
TF42_BL_k141_62032	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Roseburia intestinalis</i>
TF42_BL_k141_71128	1	dsDNAphage	No	High-quality	99.81	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Coprococcus catus</i>
TF41_BL_k141_1239	0.98	dsDNAphage	No	High-quality	95.11	High-quality draft genome	AAI-based (high-confidence)			
TF41_BL_k141_54512	0.987	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF41_BL_k141_54892	1	dsDNAphage	No	High-quality	99.81	High-quality draft genome	AAI-based (high-confidence)	Myoviridae		
TF41_BL_k141_59395	1	dsDNAphage	No	High-quality	98.27	High-quality draft genome	AAI-based (high-confidence)	Myoviridae	Pseudomonota	<i>Escherichia coli</i>
TF41_BL_k141_87783	0.993	dsDNAphage	No	High-quality	98.9	High-quality draft genome	AAI-based (high-confidence)			
TF41_BL_k141_121839	0.72	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF41_BL_k141_176907	1	dsDNAphage	No	High-quality	91.07	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Filifactor alocis</i>
TF41_BL_k141_184976	0.967	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF41_BL_k141_183067	0.973	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TF40_BL_k141_2690	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF40_BL_k141_3744	0.987	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF40_BL_k141_63536	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF40_BL_k141_77591	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Ruminococcus lactaris</i>
TF40_BL_k141_90947	0.98	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Faecalibacterium prausnitzii</i>
TF40_BL_k141_100246	0.96	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF40_BL_k141_104397	0.927	dsDNAphage	No	High-quality	90.16	High-quality draft genome	AAI-based (high-confidence)			
TF40_BL_k141_83210	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacillota	<i>Roseburia intestinalis</i>



UViG	VirSorter2 score	Predicted genome type	Provirus	Completeness quality	Completeness (%)	Assembly quality	Completeness approach	Family	Host phylum	Host species
TF39_BL_k141_31829	0.773	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF39_BL_k141_58160	1	dsDNAphage	No	High-quality	99.57	High-quality draft genome	AAI-based (high-confidence)			
TF39_BL_k141_182776	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TF38_BL_k141_25887	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF38_BL_k141_43564	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF38_BL_k141_126039	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TF37_BL_k141_4890	0.947	dsDNAphage	No	High-quality	100	High-quality draft genome	HMM-based (lower-bound)			
TF37_BL_k141_33504	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF36_BL_k141_107271	0.967	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (medium-confidence)	Myoviridae	Bacillota	Roseburia inulinivorans
TF36_BL_k141_125732	1	dsDNAphage	No	High-quality	97.21	High-quality draft genome	AAI-based (medium-confidence)		Bacteroidota	Bacteroides fragilis
TF36_BL_k141_58164	0.887	ssDNA	No	High-quality	100	High-quality draft genome	HMM-based (lower-bound)			
TF36_BL_k141_70518	0.947	ssDNA	No	High-quality	100	High-quality draft genome	HMM-based (lower-bound)			
TF35_BL_k141_68394	1	dsDNAphage	No	High-quality	91.64	High-quality draft genome	AAI-based (high-confidence)		Bacillota	Blautia obeum
TF35_BL_k141_86399	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF34_BL_k141_20299	0.993	dsDNAphage	No	High-quality	98.84	High-quality draft genome	AAI-based (high-confidence)	Siphoviridae		
TF34_BL_k141_23649	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacillota	Coprococcus comes
TF34_BL_k141_27748	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF34_BL_k141_45326	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacteroidota	Parabacteroides distasonis
TF34_BL_k141_126948	0.987	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TF33_BL_k141_137790	1	dsDNAphage	No	High-quality	90.52	High-quality draft genome	AAI-based (high-confidence)		Bacteroidota	Bacteroides vulgatus
TF33_BL_k141_89761	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacillota	Faecalibacterium prausnitzii
TF33_BL_k141_109122	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TF32_BL_k141_5114	0.993	dsDNAphage	No	High-quality	99.53	High-quality draft genome	AAI-based (high-confidence)		Bacillota	Streptococcus constellatus
TF32_BL_k141_42758	0.947	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (medium-confidence)			
TF32_BL_k141_54858	0.967	dsDNAphage	No	High-quality	95.34	High-quality draft genome	AAI-based (high-confidence)		Bacillota	Faecalibacterium prausnitzii
TF32_BL_k141_72542	0.893	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF32_BL_k141_101121	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacillota	Coprococcus catus
TF32_BL_k141_103813	0.727	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (medium-confidence)			
TF32_BL_k141_105187	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacillota	Dorea longicatena
TF32_BL_k141_125530	1	dsDNAphage	No	High-quality	91.94	High-quality draft genome	AAI-based (high-confidence)		Bacillota	Faecalibacterium prausnitzii
TF32_BL_k141_131755	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF32_BL_k141_166984	0.893	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF32_BL_k141_103279	0.947	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF31_BL_k141_2337	0.967	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacillota	Faecalibacterium prausnitzii
TF31_BL_k141_94267	0.933	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF30_BL_k141_3585	0.98	dsDNAphage	No	High-quality	98.37	High-quality draft genome	AAI-based (high-confidence)			
TF30_BL_k141_6116	1	dsDNAphage	No	High-quality	97.94	High-quality draft genome	AAI-based (high-confidence)	Siphoviridae	Bacillota	Faecalibacterium prausnitzii
TF30_BL_k141_46259	1	dsDNAphage	No	High-quality	98.91	High-quality draft genome	AAI-based (high-confidence)		Bacillota	Dorea formicigenerans
TF30_BL_k141_7378	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacillota	Blautia hanseni
TF30_BL_k141_24082	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacillota	Staphylococcus aureus
TF30_BL_k141_115070	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TF30_BL_k141_151789	0.953	ssDNA	No	High-quality	100	High-quality draft genome	HMM-based (lower-bound)			
TF29_BL_k141_29916	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	Siphoviridae	Bacillota	Roseburia intestinalis
TF29_BL_k141_1434	0.973	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TF28_BL_k141_5465	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacillota	Dorea longicatena
TF28_BL_k141_54429	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	Myoviridae	Bacillota	Roseburia inulinivorans
TF28_BL_k141_47332	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Actinomycetota	Bifidobacterium longum
TF26_BL_k141_52625	0.993	dsDNAphage	No	High-quality	97.21	High-quality draft genome	AAI-based (high-confidence)			
TF26_BL_k141_88100	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TF25_BL_k141_15551	1	dsDNAphage	No	High-quality	98.31	High-quality draft genome	AAI-based (high-confidence)			
TF24_BL_k141_25900	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	Siphoviridae	Bacillota	Eubacterium ventriosum
TF24_BL_k141_71389	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	Myoviridae	Bacillota	Faecalibacterium prausnitzii
TF23_BL_k141_14031	1	dsDNAphage	No	High-quality	99.7	High-quality draft genome	AAI-based (high-confidence)			
TF23_BL_k141_43771	0.947	dsDNAphage	No	High-quality	100	High-quality draft genome	HMM-based (lower-bound)			
TF23_BL_k141_75286	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacillota	Faecalibacterium prausnitzii
TF22_BL_k141_22678	0.993	dsDNAphage	No	High-quality	95.69	High-quality draft genome	AAI-based (high-confidence)		Bacillota	Coprococcus comes
TF22_BL_k141_55058	1	dsDNAphage	No	High-quality	97.94	High-quality draft genome	AAI-based (high-confidence)		Bacteroidota	Bacteroides vulgatus
TF22_BL_k141_110462	1	dsDNAphage	No	High-quality	91.12	High-quality draft genome	AAI-based (medium-confidence)			
TF22_BL_k141_122122	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	Myoviridae		
TF22_BL_k141_162180	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacillota	Faecalibacterium prausnitzii
TF21_BL_k141_100170	1	dsDNAphage	No	High-quality	92.61	High-quality draft genome	AAI-based (high-confidence)		Bacteroidota	Bacteroides ovatus
TF20_BL_k141_53272	0.967	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF20_BL_k141_79461	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacillota	Faecalibacterium prausnitzii
TF20_BL_k141_146669	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF20_BL_k141_175365	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	Siphoviridae	Bacillota	Faecalibacterium prausnitzii
TF20_BL_k141_200746	0.933	dsDNAphage	No	High-quality	91.81	High-quality draft genome	AAI-based (high-confidence)			
TF20_BL_k141_203010	0.987	dsDNAphage	No	High-quality	97.66	High-quality draft genome	AAI-based (high-confidence)			
TF19_BL_k141_93493	0.52	dsDNAphage	No	High-quality	94.35	High-quality draft genome	AAI-based (high-confidence)			
TF19_BL_k141_128186	1	dsDNAphage	No	High-quality	92.21	High-quality draft genome	AAI-based (medium-confidence)		Bacteroidota	Bacteroides stercoris
TF19_BL_k141_202498	0.987	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		Bacillota	Ruminococcus bromii
TF19_BL_k141_127090	0.987	ssDNA	No	High-quality	100	High-quality draft genome	HMM-based (lower-bound)			
TF18_BL_k141_42110	0.62	dsDNAphage	No	High-quality	94.52	High-quality draft genome	AAI-based (high-confidence)			
TF18_BL_k141_46781	1	dsDNAphage	No	High-quality	99.37	High-quality draft genome	AAI-based (high-confidence)		Bacteroidota	Bacteroides caccae
TF18_BL_k141_127568	0.973	dsDNAphage	No	High-quality	99.3	High-quality draft genome	AAI-based (high-confidence)	Siphoviridae	Bacillota	Faecalibacterium prausnitzii
TF18_BL_k141_163513	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (medium-confidence)			
TF17_BL_k141_37790	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	Myoviridae		
TF17_BL_k141_47664	0.993	dsDNAphage	No	High-quality	94.5	High-quality draft genome	AAI-based (high-confidence)	Myoviridae	Bacillota	Roseburia inulinivorans
TF17_BL_k141_133605	0.993	dsDNAphage	No	High-quality	96.07	High-quality draft genome	AAI-based (high-confidence)		Bacillota	Ruminococcus bromii
TF17_BL_k141_75489	0.933	ssDNA	No	High-quality	100	High-quality draft genome	HMM-based (lower-bound)			
TF16_BL_k141_30264	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacillota	Coprococcus comes
TF16_BL_k141_70513	0.987	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	Myoviridae		
TF16_BL_k141_142243	0.987	dsDNAphage	No	High-quality	98.83	High-quality draft genome	AAI-based (high-confidence)			
TF15_BL_k141_8287	0.993	dsDNAphage	No	High-quality	97.79	High-quality draft genome	AAI-based (high-confidence)		Bacteroidota	Bacteroides caccae

UViG	VirSorter2 score	Predicted genome type	Provirus	Completeness quality	Completeness (%)	Assembly quality	Completeness approach	Family	Host phylum	Host species
TF15_BL_k141_14479	1	dsDNAphage	No	High-quality	93.57	High-quality draft genome	AAI-based (high-confidence)	<i>Myoviridae</i>		
TF15_BL_k141_95229	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	<i>Myoviridae</i>		
TF15_BL_k141_120586	0.98	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TF15_BL_k141_21499	0.98	dsDNAphage	No	High-quality	100	High-quality draft genome	HMM-based (lower-bound)		<i>Bacillota</i>	<i>Ruminococcus bromii</i>
TF14_BL_k141_133814	1	dsDNAphage	No	High-quality	90.57	High-quality draft genome	AAI-based (high-confidence)		<i>Actinomycetota</i>	<i>Bifidobacterium longum</i>
TF12_BL_k141_5526	1	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TF10_BL_k141_174044	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (medium-confidence)	<i>Siphoviridae</i>	<i>Bacillota</i>	<i>Lactobacillus salivarius</i>
TF09_BL_k141_9539	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		<i>Bacteroidota</i>	<i>Parabacteroides johnsonii</i>
TF09_BL_k141_12896	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF09_BL_k141_31304	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF09_BL_k141_183195	1	dsDNAphage	No	High-quality	91.78	High-quality draft genome	AAI-based (high-confidence)		<i>Bacillota</i>	<i>Ruminococcus bromii</i>
TF09_BL_k141_245662	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF09_BL_k141_261654	1	dsDNAphage	No	High-quality	95.98	High-quality draft genome	AAI-based (high-confidence)			
TF09_BL_k141_254407	0.987	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)	<i>Myoviridae</i>		
TF08_BL_k141_6144	0.993	dsDNAphage	No	High-quality	97.51	High-quality draft genome	AAI-based (high-confidence)		<i>Bacillota</i>	<i>Ruminococcus bromii</i>
TF08_BL_k141_10721	0.927	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF08_BL_k141_71550	0.993	dsDNAphage	No	High-quality	91.49	High-quality draft genome	AAI-based (high-confidence)			
TF08_BL_k141_76711	1	dsDNAphage	No	High-quality	95.89	High-quality draft genome	AAI-based (high-confidence)	<i>Siphoviridae</i>	<i>Bacillota</i>	<i>Anaerobutyricum hallii</i>
TF08_BL_k141_80911	0.993	dsDNAphage	No	High-quality	95.67	High-quality draft genome	AAI-based (high-confidence)	<i>Siphoviridae</i>	<i>Bacillota</i>	<i>Faecalibacterium prausnitzii</i>
TF07_BL_k141_105679	0.987	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		<i>Bacteroidota</i>	<i>Bacteroides stercoris</i>
TF06_BL_k141_52433	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		<i>Bacillota</i>	<i>Butyrivibrio crossotus</i>
TF06_BL_k141_86981	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF06_BL_k141_127621	0.987	dsDNAphage	No	High-quality	96.36	High-quality draft genome	AAI-based (high-confidence)		<i>Bacillota</i>	<i>Dorea formicigenerans</i>
TF06_BL_k141_51221	1	dsDNAphage	No	High-quality	90.71	High-quality draft genome	AAI-based (high-confidence)		<i>Actinomycetota</i>	<i>Bifidobacterium longum</i>
TF05_BL_k141_93097	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		<i>Bacillota</i>	<i>Butyrivibrio crossotus</i>
TF05_BL_k141_94355	0.993	dsDNAphage	No	High-quality	97.42	High-quality draft genome	AAI-based (high-confidence)	<i>Siphoviridae</i>	<i>Bacillota</i>	<i>Dorea formicigenerans</i>
TF05_BL_k141_122470	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)		<i>Actinomycetota</i>	<i>Bifidobacterium adolescentis</i>
TF04_BL_k141_15741	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		<i>Bacillota</i>	<i>Faecalibacterium prausnitzii</i>
TF04_BL_k141_40649	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	<i>Myoviridae</i>		
TF04_BL_k141_69875	1	dsDNAphage	No	High-quality	93.42	High-quality draft genome	AAI-based (high-confidence)		<i>Bacillota</i>	<i>Ruminococcus bromii</i>
TF04_BL_k141_115524	0.993	dsDNAphage	No	High-quality	97.23	High-quality draft genome	AAI-based (high-confidence)			
TF04_BL_k141_117002	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		<i>Bacteroidota</i>	<i>Prevotella disiens</i>
TF04_BL_k141_144777	1	dsDNAphage	No	High-quality	94.39	High-quality draft genome	AAI-based (high-confidence)			
TF04_BL_k141_152263	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		<i>Bacillota</i>	<i>Blautia obeum</i>
TF03_BL_k141_17326	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF03_BL_k141_43153	0.993	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	<i>Myoviridae</i>	<i>Bacillota</i>	<i>Faecalibacterium prausnitzii</i>
TF03_BL_k141_95147	0.987	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF03_BL_k141_109671	0.58	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF03_BL_k141_186055	0.933	dsDNAphage	No	High-quality	99.12	High-quality draft genome	AAI-based (medium-confidence)			
TF02_BL_k141_2076	0.993	dsDNAphage	No	High-quality	97.61	High-quality draft genome	AAI-based (high-confidence)			
TF02_BL_k141_24343	0.98	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		<i>Bacillota</i>	<i>Faecalibacterium prausnitzii</i>
TF02_BL_k141_74151	0.993	dsDNAphage	No	High-quality	99.71	High-quality draft genome	AAI-based (high-confidence)		<i>Bacillota</i>	<i>Roseburia intestinalis</i>
TF02_BL_k141_90577	1	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF02_BL_k141_235973	1	dsDNAphage	No	High-quality	92.14	High-quality draft genome	AAI-based (high-confidence)			
TF02_BL_k141_252071	0.993	dsDNAphage	No	High-quality	98.67	High-quality draft genome	AAI-based (high-confidence)		<i>Bacillota</i>	<i>Faecalibacterium prausnitzii</i>
TF01_BL_k141_27375	0.987	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (medium-confidence)			
TF01_BL_k141_77709	0.953	dsDNAphage	No	High-quality	91.01	High-quality draft genome	AAI-based (high-confidence)		<i>Bacteroidota</i>	<i>Bacteroides vulgatus</i>
TF01_BL_k141_83586	0.993	dsDNAphage	No	High-quality	91.72	High-quality draft genome	AAI-based (high-confidence)		<i>Bacillota</i>	<i>Blautia obeum</i>
TF01_BL_k141_45634	0.993	dsDNAphage	No	Complete	100	High-quality draft genome	DTR (high-confidence)			
TF01_BL_k141_2359	0.973	ssDNA	No	High-quality	100	High-quality draft genome	HMM-based (lower-bound)			
TM16_BL_k141_23190	0.667	dsDNAphage	No	High-quality	100	High-quality draft genome	AAI-based (medium-confidence)			
TF02_BL_k141_64800	1	dsDNAphage	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF02_BL_k141_218601	0.993	dsDNAphage	Yes	High-quality	99.77	High-quality draft genome	AAI-based (high-confidence)			
TF03_BL_k141_13648	1	dsDNAphage	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		<i>Bacillota</i>	<i>Tyzzereella nexilis</i>
TF06_BL_k141_113913	0.987	dsDNAphage	Yes	High-quality	93.35	High-quality draft genome	AAI-based (high-confidence)			
TF08_BL_k141_47815	0.993	dsDNAphage	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF13_BL_k141_9193	0.993	dsDNAphage	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF13_BL_k141_83626	0.993	dsDNAphage	Yes	High-quality	96.76	High-quality draft genome	AAI-based (high-confidence)		<i>Bacillota</i>	<i>Ruminococcus bromii</i>
TF15_BL_k141_97860	1	dsDNAphage	Yes	High-quality	92.74	High-quality draft genome	AAI-based (high-confidence)			
TF15_BL_k141_119305	1	dsDNAphage	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF16_BL_k141_105814	0.647	dsDNAphage	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	<i>Microviridae</i>		
TF19_BL_k141_3399	0.993	dsDNAphage	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF21_BL_k141_91460	1	dsDNAphage	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		<i>Bacteroidota</i>	<i>Bacteroides xylanisolvens</i>
TF26_BL_k141_46478	0.98	dsDNAphage	Yes	High-quality	99.33	High-quality draft genome	AAI-based (high-confidence)			
TF27_BL_k141_44029	0.993	dsDNAphage	Yes	High-quality	91.76	High-quality draft genome	AAI-based (high-confidence)			
TF32_BL_k141_27999	1	dsDNAphage	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF32_BL_k141_39244	0.993	ssDNA	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF33_BL_k141_20531	0.92	dsDNAphage	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	<i>Microviridae</i>		
TF35_BL_k141_9170	0.993	dsDNAphage	Yes	High-quality	100	High-quality draft genome	AAI-based (medium-confidence)		<i>Bacillota</i>	<i>Faecalibacterium prausnitzii</i>
TF36_BL_k141_26183	0.98	dsDNAphage	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF37_BL_k141_91034	0.56	dsDNAphage	Yes	High-quality	100	High-quality draft genome	AAI-based (medium-confidence)			
TF37_BL_k141_107475	1	dsDNAphage	Yes	High-quality	98.49	High-quality draft genome	AAI-based (high-confidence)		<i>Bacillota</i>	<i>Blautia obeum</i>
TF39_BL_k141_10226	1	dsDNAphage	Yes	High-quality	95.63	High-quality draft genome	AAI-based (high-confidence)			
TF40_BL_k141_30040	0.987	dsDNAphage	Yes	High-quality	99.59	High-quality draft genome	AAI-based (high-confidence)		<i>Bacillota</i>	<i>Ruminococcus bromii</i>
TF40_BL_k141_64770	0.987	dsDNAphage	Yes	Complete	100	High-quality draft genome	Provirus (high-confidence)			
TF41_BL_k141_108183	0.993	dsDNAphage	Yes	Complete	100	High-quality draft genome	ITR (high-confidence)	<i>Myoviridae</i>	<i>Bacillota</i>	<i>Faecalibacterium prausnitzii</i>
TF42_BL_k141_103297	0.993	dsDNAphage	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF43_BL_k141_35049	0.987	dsDNAphage	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	<i>Siphoviridae</i>		
TF46_BL_k141_4714	1	dsDNAphage	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF46_BL_k141_25961	1	dsDNAphage	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		<i>Bacteroidota</i>	<i>Bacteroides clarus</i>
TF46_BL_k141_110370	0.993	dsDNAphage	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	<i>Myoviridae</i>	<i>Bacillota</i>	<i>Faecalibacterium prausnitzii</i>
TF46_BL_k141_118276	0.993	dsDNAphage	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF48_BL_k141_71125	0.98	dsDNAphage	Yes	High-quality	98.02	High-quality draft genome	AAI-based (high-confidence)		<i>Bacillota</i>	<i>Faecalibacterium prausnitzii</i>

UViG	VirSorter2 score	Predicted genome type	Provirus	Completeness quality	Completeness (%)	Assembly quality	Completeness approach	Family	Host phylum	Host species
TF49_BL_k141_80100	0.973	dsDNA	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TF51_BL_k141_4535	0.993	dsDNA	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacillota	Roseburia intestinalis
TF51_BL_k141_18208	1	dsDNA	Yes	High-quality	96.66	High-quality draft genome	AAI-based (high-confidence)		Bacillota	Coprococcus catus
TF51_BL_k141_107035	0.993	dsDNA	Yes	Complete	100	High-quality draft genome	Provirus (high-confidence)			
TM02_BL_k141_49023	0.88	ssDNA	Yes	High-quality	100	High-quality draft genome	HMM-based (lower-bound)			
TM04_BL_k141_51317	0.987	dsDNA	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			
TM06_BL_k141_106287	0.98	dsDNA	Yes	High-quality	91.55	High-quality draft genome	AAI-based (high-confidence)		Bacillota	Faecalibacterium prausnitzii
TM08_BL_k141_118205	0.98	dsDNA	Yes	High-quality	96.39	High-quality draft genome	AAI-based (high-confidence)			
TM08_BL_k141_129881	0.953	dsDNA	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	Microviridae		
TM09_BL_k141_80919	0.993	dsDNA	Yes	High-quality	98.51	High-quality draft genome	AAI-based (high-confidence)			
TM10_BL_k141_2265	0.987	dsDNA	Yes	High-quality	100	High-quality draft genome	AAI-based (medium-confidence)		Bacteroidota	Bacteroides xylanisolvens
TM12_BL_k141_68927	0.98	dsDNA	Yes	High-quality	94.16	High-quality draft genome	AAI-based (high-confidence)		Bacillota	Roseburia inulinivorans
TM13_BL_k141_15337	0.987	dsDNA	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacillota	Faecalibacterium prausnitzii
TM13_BL_k141_81986	1	dsDNA	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacillota	Faecalibacterium prausnitzii
TM13_BL_k141_123531	0.9	dsDNA	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	Microviridae		
TM18_BL_k141_68032	0.993	dsDNA	Yes	High-quality	98.88	High-quality draft genome	AAI-based (high-confidence)			
TM18_BL_k141_71605	0.993	dsDNA	Yes	High-quality	98	High-quality draft genome	AAI-based (high-confidence)			
TM19_BL_k141_13472	1	dsDNA	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	Myoviridae	Bacillota	Roseburia intestinalis
TM19_BL_k141_104926	1	dsDNA	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	Myoviridae		
TM25_BL_k141_22837	0.993	dsDNA	Yes	High-quality	93.14	High-quality draft genome	AAI-based (high-confidence)		Bacillota	Faecalibacterium prausnitzii
TM25_BL_k141_33361	0.993	dsDNA	Yes	High-quality	96.61	High-quality draft genome	AAI-based (high-confidence)		Bacillota	Tyzzereella nexilis
TM25_BL_k141_70406	0.98	dsDNA	Yes	Complete	100	High-quality draft genome	Provirus (medium-confidence)	Siphoviridae	Bacillota	Faecalibacterium prausnitzii
TM25_BL_k141_92966	0.98	dsDNA	Yes	High-quality	95.17	High-quality draft genome	AAI-based (high-confidence)			
TM25_BL_k141_127396	0.98	dsDNA	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacillota	Ruminococcus lactaris
TM27_BL_k141_67452	0.987	dsDNA	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	Siphoviridae	Bacillota	Faecalibacterium prausnitzii
TM28_BL_k141_40154	1	dsDNA	Yes	Complete	100	High-quality draft genome	Provirus (high-confidence)		Bacillota	Marvinbryantia formatexigens
TM28_BL_k141_111121	0.987	dsDNA	Yes	High-quality	91.46	High-quality draft genome	AAI-based (high-confidence)		Bacillota	Roseburia inulinivorans
TM32_BL_k141_9783	0.987	dsDNA	Yes	Complete	100	High-quality draft genome	Provirus (high-confidence)		Bacillota	Tyzzereella nexilis
TM33_BL_k141_14311	0.94	dsDNA	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Actinomycetota	Bifidobacterium bifidum
TM33_BL_k141_85036	1	dsDNA	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Actinomycetota	Bifidobacterium longum
TM34_BL_k141_39027	0.987	dsDNA	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)	Myoviridae	Bacillota	Roseburia inulinivorans
TM34_BL_k141_58974	1	dsDNA	Yes	Complete	100	High-quality draft genome	Provirus (high-confidence)	Siphoviridae		
TM34_BL_k141_120816	0.987	dsDNA	Yes	High-quality	91.25	High-quality draft genome	AAI-based (high-confidence)		Bacillota	Faecalibacterium prausnitzii
TM34_BL_k141_148153	1	dsDNA	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)		Bacillota	Faecalibacterium prausnitzii
TM35_BL_k141_63451	1	dsDNA	Yes	High-quality	90.48	High-quality draft genome	AAI-based (high-confidence)		Bacillota	Coprococcus comes
TM35_BL_k141_100928	0.993	dsDNA	Yes	High-quality	95.38	High-quality draft genome	AAI-based (high-confidence)	Myoviridae		
TM37_BL_k141_4258	0.987	dsDNA	Yes	High-quality	97.81	High-quality draft genome	AAI-based (high-confidence)		Bacillota	Tyzzereella nexilis
TM37_BL_k141_55499	1	dsDNA	Yes	High-quality	100	High-quality draft genome	AAI-based (high-confidence)			