Parent Class	Field	Ontology Identifier	Definition	Guidance	Examples	Deprecated Label	Deprecated ID	Version Tracking Label	ID	Description/Guidance
	Colour Code Legend									
	field name in yellow = required									
	field name in purple = recommended									
	field name in white = optional									
						IMPORTANT: Only labels and/or IDs will be deprecated, always with replacement version provided. If a term changes in its meaning, a new term will be created.				
Database Identifiers		**GENEPIO:0001122**								
	specimen collector sample ID	GENEPIO:0001123	The user-defined name for the sample.	Store the collector sample ID. If this number is considered identifiable information, provide an alternative ID. Be sure to store the key that maps between the original and alternative IDs for traceability and follow up if necessary. Every collector sample ID from a single submitter must be unique. It can have any format, but we suggest that you make it concise, unique and consistent within your lab.	prov_mpox_1234			1.0.0	1.0.0	1.0.0
	case ID	GENEPIO:0100281	The identifier used to specify an epidemiologically detected case of disease.	Provide the case identifer. The case ID greatly facilitates linkage between laboratory and epidemiological data. The case ID may be considered identifiable information. Consult the data steward before sharing.	ABCD1234			1.0.0	1.0.0	1.0.0
	bioproject accession	GENEPIO:0001136	The INSDC accession number of the BioProject(s) to which the BioSample belongs.	Required if submission is linked to a BioProject. BioProjects are an organizing tool that links together raw sequence data, assemblies, and their associated metadata. A valid BioProject accession has prefix PRJN, PRJE or PRJD, e.g., PRJNA12345 and is created once at the beginning of a new sequencing project. Your laboratory can have one or many BioProjects.	PRJNA12345			1.0.0	1.0.0	1.0.0
	biosample accession	GENEPIO:0001139	The identifier assigned to a BioSample in INSDC archives.	Store the accession returned from the BioSample submission. NCBI BioSamples will have the prefix SAMN, while ENA BioSamples will have the prefix SAMEA.	SAMN14180202			1.0.0	1.0.0	1.0.0
	SRA accession	GENEPIO:0001142	The Sequence Read Archive (SRA) identifier linking raw read data, methodological metadata and quality control metrics submitted to the INSDC.	Store the accession assigned to the submitted "run". NCBI-SRA accessions start with SRR.	SRR11177792			1.0.0	1.0.0	1.0.0
	GenBank accession	GENEPIO:0001145	The GenBank identifier assigned to the sequence in the INSDC archives.	Store the accession returned from a GenBank submission (viral genome assembly).	MN908947.3			1.0.0	1.0.0	1.0.0
	GISAID virus name	GENEPIO:0100282	Identifier of the specific isolate.	Provide the GISAID EpiPox virus name, which should be written in the format "hMpxV/Canada/2 digit provincial ISO code-xxxxx/year". If the province code cannot be shared for privacy reasons, put "UN" for "Unknown".	hMpxV/Canada/UN-NML-12345/2022			1.0.0	1.0.0	1.0.0
	GISAID accession	GENEPIO:0001147	The GISAID accession number assigned to the sequence.	Store the accession returned from the GISAID submission.	EPI_ISL_436489			1.0.0	1.0.0	1.0.0
Sample collection and processing		**GENEPIO:0001150**								
	sample collected by	GENEPIO:0001153	The name of the agency that collected the original sample.	The name of the sample collector should be written out in full, (with minor exceptions) and be consistent across multple submissions e.g. Public Health Agency of Canada, Public Health Ontario, BC Centre for Disease Control. The sample collector specified is at the discretion of the data provider (i.e. may be hospital, provincial public health lab, or other).	BC Centre for Disease Control			1.0.0	1.0.0	1.0.0
	sample collector contact email	GENEPIO:0001156	The email address of the contact responsible for follow-up regarding the sample.	The email address can represent a specific individual or lab e.g. johnnyblogs@lab.ca, or RespLab@lab.ca	RespLab@lab.ca			1.0.0	1.0.0	1.0.0
	sample collector contact address	GENEPIO:0001158	The mailing address of the agency submitting the sample.	The mailing address should be in the format: Street number and name, City, Province/Territory, Postal Code, Country	655 Lab St, Vancouver, British Columbia, V5N 2A2, Canada			1.0.0	1.0.0	1.0.0
	sequenced by	GENEPIO:0100416	The name of the agency that generated the sequence.	The name of the agency should be written out in full, (with minor exceptions) and be consistent across multiple submissions. If submitting specimens rather than sequencing data, please put the "National Microbiology Laboratory (NML)".	Public Health Ontario (PHO)			1.0.0	1.0.0	1.0.0
	sequenced by contact email	GENEPIO:0100422	The email address of the contact responsible for follow-up regarding the sequence.	The email address can represent a specific individual or lab e.g. johnnyblogs@lab.ca, or RespLab@lab.ca	RespLab@lab.ca			1.0.0	1.0.0	1.0.0
	sequenced by contact address	GENEPIO:0100423	The mailing address of the agency submitting the sequence.	The mailing address should be in the format: Street number and name, City, Province/Territory, Postal Code, Country	123 Sunnybrooke St, Toronto, Ontario, M4P 1L6, Canada			1.0.0	1.0.0	1.0.0
	sequence submitted by	GENEPIO:0001159	The name of the agency that submitted the sequence to a database.	The name of the agency should be written out in full, (with minor exceptions) and be consistent across multiple submissions. If submitting specimens rather than sequencing data, please put the "National Microbiology Laboratory (NML)".	Public Health Ontario (PHO)			1.0.0	1.0.0	1.0.0
	sequence submitter contact email	GENEPIO:0001165	The email address of the agency responsible for submission of the sequence.	The email address can represent a specific individual or lab e.g. johnnyblogs@lab.ca, or RespLab@lab.ca	RespLab@lab.ca			1.0.0	1.0.0	1.0.0
	sequence submitter contact address	GENEPIO:0001167	The mailing address of the agency responsible for submission of the sequence.	The mailing address should be in the format: Street number and name, City, Province/Territory, Postal Code, Country	123 Sunnybrooke St, Toronto, Ontario, M4P 1L6, Canada			1.0.0	1.0.0	1.0.0
	sample collection date	GENEPIO:0001174	The date on which the sample was collected.	Sample collection date is critical for surveillance and many types of analyses. Required granularity includes year, month and day. If this date is considered identifiable information, it is acceptable to add "jitter" by adding or subtracting a calendar day (acceptable by GISAID). Alternatively, "received date" may be used as a substitute. The date should be provided in ISO 8601 standard format "YYYY-MM-DD".	43906			1.0.0	1.0.0	1.0.0
	sample received date	GENEPIO:0001179	The date on which the sample was received.	ISO 8601 standard "YYYY-MM-DD".	43910			1.0.0	1.0.0	1.0.0
	geo_loc_name (country)	GENEPIO:0001181	The country where the sample was collected.	Provide the country name from the controlled vocabulary provided.	Canada			1.0.0	1.0.0	1.0.0
	geo_loc_name (state/province/territory)	GENEPIO:0001185	The state/province/territory where the sample was collected.	Provide the province/territory name from the controlled vocabulary provided.	Saskatchewan			1.0.0	1.0.0	1.0.0

Parent Class	Field	Ontology Identifier	Definition	Guidance	Examples	Deprecated Label	Deprecated ID	Version Tracking		
	geo_loc latitude	GENEPIO:0100309	The latitude coordinates of the geographical location of sample collection.	Provide latitude coordinates if available. Do not use the centre of the city/region/province/state/country or the location of your agency as a proxy, as this implicates a real location and is misleading. Specify as degrees latitude in format "d[d.dddd] N|S".	38.98 N			1.0.0	1.0.0	1.0.0
	geo_loc longitude	GENEPIO:0100310	The longitude coordinates of the geographical location of sample collection.	Provide longitude coordinates if available. Do not use the centre of the city/region/province/state/country or the location of your agency as a proxy, as this implicates a real location and is misleading. Specify as degrees longitude in format "d[dd.dddd] W|E".	77.11 W			1.0.0	1.0.0	1.0.0
	organism	GENEPIO:0001191	Taxonomic name of the organism.	Use "Mpox virus". This value is provided in the template. Note: the Mpox virus was formerly referred to as the "Monkeypox virus" but the international nomenclature has changed (2022).	Mpox virus			1.0.0	1.0.0	1.0.0
	isolate	GENEPIO:0001644	Identifier of the specific isolate.	This identifier should be an unique, indexed, alpha-numeric ID within your laboratory. If submitted to the INSDC, the "isolate" name is propagated throughtout different databases. As such, structure the "isolate" name to be ICTV/INSDC compliant in the following format: "MpxV/host/country/sampleID/date".	MpxV/human/USA/CA-CDPH-001/2020			1.0.0	1.0.0	1.0.0
	purpose of sampling	GENEPIO:0001198	The reason that the sample was collected.	As all samples are taken for diagnostic purposes, "Diagnostic Testing" should be chosen from the picklist at this time. The reason why a sample was originally collected may differ from the reason why it was selected for sequencing, which should be indicated in the "purpose of sequencing" field.	Diagnostic testing			1.0.0	1.0.0	1.0.0
	purpose of sampling details	GENEPIO:0001200	The description of why the sample was collected, providing specific details.	Provide an expanded description of why the sample was collected using free text. The description may include the importance of the sample for a particular public health investigation/surveillance activity/research question. If details are not available, provide a null value.	Symptomology and history suggested Monkeypox diagnosis.			1.0.0	1.0.0	1.0.0
	anatomical material	GENEPIO:0001211	A substance obtained from an anatomical part of an organism e.g. tissue, blood.	Provide a descriptor if an anatomical material was sampled. Use the picklist provided in the template. If a desired term is missing from the picklist, contact emma_griffiths@sfu.ca. If not applicable, do not leave blank. Choose a null value.	Lesion (Pustule)			1.0.0	1.0.0	1.0.0
	anatomical part	GENEPIO:0001214	An anatomical part of an organism e.g. oropharynx.	Provide a descriptor if an anatomical part was sampled. Use the picklist provided in the template. If a desired term is missing from the picklist, contact emma_griffiths@sfu.ca. If not applicable, do not leave blank. Choose a null value.	Genital area			1.0.0	1.0.0	1.0.0
	body product	GENEPIO:0001216	A substance excreted/secreted from an organism e.g. feces, urine, sweat.	Provide a descriptor if a body product was sampled. Use the picklist provided in the template. If a desired term is missing from the picklist, contact emma_griffiths@sfu.ca. If not applicable, do not leave blank. Choose a null value.	Pus			1.0.0	1.0.0	1.0.0
	environmental material	GENEPIO:0001223	A substance obtained from the natural or man-made environment e.g. soil, water, sewage.	Provide a descriptor if an environmental material was sampled. Use the picklist provided in the template. If a desired term is missing from the picklist, contact emma_griffiths@sfu.ca. If not applicable, do not leave blank. Choose a null value.	Bed linen			1.0.0	1.0.0	1.0.0
	collection device	GENEPIO:0001234	The instrument or container used to collect the sample e.g. swab.	Provide a descriptor if a device was used for sampling. Use the picklist provided in the template. If a desired term is missing from the picklist, contact emma_griffiths@sfu.ca. If not applicable, do not leave blank. Choose a null value.	Swab			1.0.0	1.0.0	1.0.0
	collection method	GENEPIO:0001241	The process used to collect the sample e.g. phlebotamy, necropsy.	Provide a descriptor if a collection method was used for sampling. Use the picklist provided in the template. If a desired term is missing from the picklist, contact emma_griffiths@sfu.ca. If not applicable, do not leave blank. Choose a null value.	Biopsy			1.0.0	1.0.0	1.0.0
	specimen processing	GENEPIO:0001253	Any processing applied to the sample during or after receiving the sample.	Critical for interpreting data. Select all the applicable processes from the pick list. If virus was passaged, include information in "lab host", "passage number", and "passage method" fields. If none of the processes in the pick list apply, put "not applicable".	Specimens pooled			1.0.0	1.0.0	1.0.0
	specimen processing details	GENEPIO:0100311	Detailed information regarding the processing applied to a sample during or after receiving the sample.	Provide a free text description of any processing details applied to a sample.	5 swabs from different body sites were pooled and further prepared as a single sample during library prep.			1.0.0	1.0.0	1.0.0
Host Information		**GENEPIO:0001268**								
	host (common name)	GENEPIO:0001386	The commonly used name of the host.	Common name or scientific name are required if there was a host. Both can be provided, if known. Use terms from the pick lists in the template. Common name e.g. human.	Human			1.0.0	1.0.0	1.0.0
	host (scientific name)	GENEPIO:0001387	The taxonomic, or scientific name of the host.	Common name or scientific name are required if there was a host. Both can be provided, if known. Use terms from the pick lists in the template. Scientific name e.g. Homo sapiens, If the sample was environmental, put "not applicable	Homo sapiens			1.0.0	1.0.0	1.0.0
	host health state	GENEPIO:0001388	Health status of the host at the time of sample collection.	If known, select a value from the pick list.	Asymptomatic			1.0.0	1.0.0	1.0.0
	host health status details	GENEPIO:0001389	Further details pertaining to the health or disease status of the host at time of collection.	If known, select a descriptor from the pick list provided in the template.	Hospitalized			1.0.0	1.0.0	1.0.0
	host health outcome	GENEPIO:0001389	Further details pertaining to the health or disease status of the host at time of collection.	If known, select a descriptor from the pick list provided in the template.	Hospitalized			1.0.0	1.0.0	1.0.0
	host disease	GENEPIO:0001391	The name of the disease experienced by the host.	Select "Mpox" from the pick list provided in the template. Note: the Mpox disease was formerly referred to as "Monkeypox" but the international nomenclature has changed (2022).	Mpox			1.0.0	1.0.0	1.0.0
	host subject ID	GENEPIO:0001398	A unique identifier by which each host can be referred to.	This identifier can be used to link samples from the same individual. Caution: consult the data steward before sharing as this value may be considered identifiable information.	12345B-222			1.0.0	1.0.0	1.0.0
	host age	GENEPIO:0001392	Age of host at the time of sampling.	If known, provide age. Age-binning is also acceptable.	79			1.0.0	1.0.0	1.0.0

Parent Class	Field	Ontology Identifier	Definition	Guidance	Examples	Deprecated Label	Deprecated ID	Version Tracking		
	host age unit	GENEPIO:0001393	The units used to measure the host's age.	If known, provide the age units used to measure the host's age from the pick list.	year			1.0.0	1.0.0	1.0.0
	host age bin	GENEPIO:0001394	The age category of the host at the time of sampling.	Age bins in 10 year intervals have been provided. If a host's age cannot be specified due to proovacy concerns, an age bin can be used as an alternative.	50 - 59			1.0.0	1.0.0	1.0.0
	host gender	GENEPIO:0001395	The gender of the host at the time of sample collection.	If known, select a value from the pick list.	Male			1.0.0	1.0.0	1.0.0
	host residence geo_loc name (country)	GENEPIO:0001396	The country of residence of the host.	Select the country name from pick list provided in the template.	Canada			1.0.0	1.0.0	1.0.0
	symptom onset date	GENEPIO:0001399	The date on which the symptoms began or were first noted.	If known, provide the symptom onset date in ISO 8601 standard format "YYYY-MM-DD".	44706			1.0.0	1.0.0	1.0.0
	signs and symptoms	GENEPIO:0001400	A perceived change in function or sensation, (loss, disturbance or appearance) indicative of a disease, reported by a patient.	Select all of the symptoms experienced by the host from the pick list.	Lesion (Pustule), Swollen Lymph Nodes, Myalgia (muscle pain)			1.0.0	1.0.0	1.0.0
	pre-existing conditions and risk factors	GENEPIO:0001401	Patient pre-existing conditions and risk factors. Pre-existing condition: A medical condition that existed prior to the current infection. Risk Factor: A variable associated with an increased risk of disease or infection.	Select all of the pre-existing conditions and risk factors experienced by the host from the pick list. If the desired term is missing, contact the curation team.				1.0.0	1.0.0	1.0.0
	complications	GENEPIO:0001402	Patient medical complications that are believed to have occurred as a result of host disease.	Select all of the complications experienced by the host from the pick list. If the desired term is missing, contact the curation team.	Delayed wound healing (lesion healing)			1.0.0	1.0.0	1.0.0
	antiviral therapy	GENEPIO:0100580	Treatment of viral infections with agents that prevent viral replication in infected cells without impairing the host cell function.	Provide details of all current antiviral treatment during the current Monkeypox infection period. Consult with the data steward prior to sharing this information.	Tecovirimat used to treat current Monkeypox infection; AZT administered for concurrent HIV infection			1.0.0	1.0.0	1.0.0
Host vaccination information		**GENEPIO:0001403**								
	host vaccination status	GENEPIO:0001404	The vaccination status of the host (fully vaccinated, partially vaccinated, or not vaccinated).	Select the vaccination status of the host from the pick list.	Not Vaccinated			1.0.0	1.0.0	1.0.0
	number of vaccine doses received	GENEPIO:0001406	The number of doses of the vaccine recived by the host.	Record how many doses of the vaccine the host has received.	1			1.0.0	1.0.0	1.0.0
	vaccination dose 1 vaccine name	GENEPIO:0100313	The name of the vaccine administered as the first dose of a vaccine regimen.	Provide the name and the corresponding manufacturer of the Smallpox vaccine administered as the first dose.	IMVAMUNE (Bavarian Nordic)			1.0.0	1.0.0	1.0.0
	vaccination dose 1 vaccination date	GENEPIO:0100314	The date the first dose of a vaccine was administered.	Provide the date the first dose of Smallpox vaccine was administered. The date should be provided in ISO 8601 standard format "YYYY-MM-DD".	44713			1.0.0	1.0.0	1.0.0
	vaccination history	GENEPIO:0100321	A description of the vaccines received and the administration dates of a series of vaccinations against a specific disease or a set of diseases.	Free text description of the dates and vaccines administered against a particular disease/set of diseases. It is also acceptable to concatenate the individual dose information (vaccine name, vaccination date) separated by semicolons.	IMVAMUNE (Bavarian Nordic); 2022-06-01			1.0.0	1.0.0	1.0.0
Host exposure information		**GENEPIO:0001409**								
	location of exposure geo_loc name (country)	GENEPIO:0001410	The country where the host was likely exposed to the causative agent of the illness.	Select the country name from the pick list provided in the template.	Canada [GAZ:00002560]			1.0.0	1.0.0	1.0.0
	destination of most recent travel (city)	GENEPIO:0001411	The name of the city that was the destination of most recent travel.	Provide the name of the city that the host travelled to. Use this look-up service to identify the standardized term: https://www.ebi.ac.uk/ols/ontologies/gaz	New York City			1.0.0	1.0.0	1.0.0
	destination of most recent travel (state/province/territory)	GENEPIO:0001412	The name of the state/province/territory that was the destination of most recent travel.	Provide the name of the state/province/territory that the host travelled to. Use this look-up service to identify the standardized term: https://www.ebi.ac.uk/ols/ontologies/gaz	California			1.0.0	1.0.0	1.0.0
	destination of most recent travel (country)	GENEPIO:0001413	The name of the country that was the destination of most recent travel.	Select the country name from the pick list provided in the template.	United Kingdom [GAZ:00002637]			1.0.0	1.0.0	1.0.0
	most recent travel departure date	GENEPIO:0001414	The date of a person's most recent departure from their primary residence (at that time) on a journey to one or more other locations.	Provide the travel departure date.	2020-03-16			1.0.0	1.0.0	1.0.0
	most recent travel return date	GENEPIO:0001415	The date of a person's most recent return to some residence from a journey originating at that residence.	Provide the travel return date.	2020-04-26			1.0.0	1.0.0	1.0.0
	travel history	GENEPIO:0001416	Travel history in last six months.	Specify the countries (and more granular locations if known, separated by a comma) travelled in the last six months; can include multiple travels. Separate multiple travel events with a semi-colon. List most recent travel first.	Canada, Vancouver; USA, Seattle; Italy, Milan			1.0.0	1.0.0	1.0.0
	exposure event	GENEPIO:0001417	Event leading to exposure.	Select an exposure event from the pick list provided in the template. If the desired term is missing, contact the DataHarmonizer curation team.	Party [PCO:0000035]			1.0.0	1.0.0	1.0.0
	exposure contact level	GENEPIO:0001418	The exposure transmission contact type.	Select exposure contact level from the pick-list.	Contact with infected individual [GENEPIO:0100357]			1.0.0	1.0.0	1.0.0
	host role	GENEPIO:0001419	The role of the host in relation to the exposure setting.	Select the host's personal role(s) from the pick list provided in the template. If the desired term is missing, contact the DataHarmonizer curation team.	Acquaintance of case [GENEPIO:0100266]			1.0.0	1.0.0	1.0.0
	exposure setting	GENEPIO:0001428	The setting leading to exposure.	Select the host exposure setting(s) from the pick list provided in the template. If a desired term is missing, contact the DataHarmonizer curation team.	Healthcare Setting [GENEPIO:0100201]			1.0.0	1.0.0	1.0.0
	exposure details	GENEPIO:0001431	Additional host exposure information.	Free text description of the exposure.	Large party, many contacts			1.0.0	1.0.0	1.0.0
Host reinfection information		**GENEPIO:0001434**								
	prior Mpox infection	GENEPIO:0100532	The absence or presence of a prior Mpox infection.	If known, provide information about whether the individual had a previous Mpox infection. Select a value from the pick list.	Prior infection [GENEPIO:0100037]			1.0.0	1.0.0	1.0.0
	prior Mpox infection date	GENEPIO:0100533	The date of diagnosis of the prior Mpox infection.	Provide the date that the most recent prior infection was diagnosed. Provide the prior Mpox infection date in ISO 8601 standard format "YYYY-MM-DD".	2022-06-20			1.0.0	1.0.0	1.0.0
	prior Mpox antiviral treatment	GENEPIO:0100534	The absence or presence of antiviral treatment for a prior Mpox infection.	If known, provide information about whether the individual had a previous Mpox antiviral treatment. Select a value from the pick list.	Prior antiviral treatment [GENEPIO:0100037]			1.0.0	1.0.0	1.0.0
	prior antiviral treatment during prior Mpox infection	GENEPIO:0100535	Antiviral treatment for any infection during the prior Mpox infection period.	Provide a description of any antiviral treatment administered for viral infections (not including Mpox treatment) during the prior Mpox infection period. This field is meant to capture concurrent treatment information.	AZT was administered for HIV infection during the prior Mpox infection.			1.0.0	1.0.0	1.0.0

Parent Class	Field	Ontology Identifier	Definition	Guidance	Examples	Deprecated Label	Deprecated ID	Version Tracking		
Sequencing		**GENEPIO:0001441**								
	purpose of sequencing	*GENEPIO:0001445*	The reason that the sample was sequenced.	The reason why a sample was originally collected may differ from the reason why it was selected for sequencing. The reason a sample was sequenced may provide information about potential biases in sequencing strategy. Provide the purpose of sequencing from the picklist in the template. The reason for sample collection should be indicated in the "purpose of sampling" field.	Baseline surveillance (random sampling) [GENEPIO:0100005]			1.0.0	1.0.0	1.0.0
	purpose of sequencing details	*GENEPIO:0001446*	The description of why the sample was sequenced providing specific details.	Provide an expanded description of why the sample was sequenced using free text. The description may include the importance of the sequences for a particular public health investigation/surveillance activity/research question. Suggested standardized descriptions include: Screened due to travel history, Screened due to close contact with infected individual.	Outbreak in MSM community			1.0.0	1.0.0	1.0.0
	sequencing date	*GENEPIO:0001447*	The date the sample was sequenced.	ISO 8601 standard "YYYY-MM-DD".	2020-06-22			1.0.0	1.0.0	1.0.0
	library ID	*GENEPIO:0001448*	The user-specified identifier for the library prepared for sequencing.	The library name should be unique, and can be an autogenerated ID from your LIMS, or modification of the isolate ID.	XYZ_123345			1.0.0	1.0.0	1.0.0
	amplicon size	*GENEPIO:0001449*	The length of the amplicon generated by PCR amplification.	Provide the amplicon size, including the units.	300bp			1.0.0	1.0.0	1.0.0
	library preparation kit	*GENEPIO:0001450*	The name of the DNA library preparation kit used to generate the library being sequenced.	Provide the name of the library preparation kit used.	Nextera XT			1.0.0	1.0.0	1.0.0
	sequencing instrument	*GENEPIO:0001452*	The model of the sequencing instrument used.	Select a sequencing instrument from the picklist provided in the template.	Oxford Nanopore MinION [GENEPIO:0100142]			1.0.0	1.0.0	1.0.0
	sequencing protocol	*GENEPIO:0001454*	The protocol used to generate the sequence.	Provide a free text description of the methods and materials used to generate the sequence. Suggested text, fill in information where indicated.: "Viral sequencing was performed following a metagenomic shotgun sequencing approach. Sequencing was performed using a **<fill in>** sequencing instrument. Libraries were prepared using **<fill in>** library kit. "	Viral sequencing was performed following a metagenomic shotgun sequencing approach. Libraries were created using Illumina DNA Prep kits, and sequence data was produced using Miseq Micro v2 (500 cycles) sequencing kits.			1.0.0	1.0.0	1.0.0
	sequencing kit number	*GENEPIO:0001455*	The manufacturer's kit number.	Alphanumeric value.	AB456XYZ789			1.0.0	1.0.0	1.0.0
	amplicon pcr primer scheme	*GENEPIO:0001456*	The specifications of the primers (primer sequences, binding positions, fragment size generated etc) used to generate the amplicons to be sequenced.	Provide the name and version of the primer scheme used to generate the amplicons for sequencing.	MPXV Sunrise 3.1			1.0.0	1.0.0	1.0.0
Bioinformatics and QC metrics		**GENEPIO:0001457**								
	raw sequence data processing method	*GENEPIO:0001458*	The names of the software and version number used for raw data processing such as removing barcodes, adapter trimming, filtering etc.	Provide the software name followed by the version e.g. Trimmomatic v. 0.38, Porechop v. 0.2.3	Porechop 0.2.3					
	dehosting method	*GENEPIO:0001459*	The method used to remove host reads from the pathogen sequence.	Provide the name and version number of the software used to remove host reads.	Nanostripper					
	consensus sequence name	*GENEPIO:0001460*	The name of the consensus sequence.	Provide the name and version number of the consensus sequence.	mpxvassembly3					
	consensus sequence filename	*GENEPIO:0001461*	The name of the consensus sequence file.	Provide the name and version number of the consensus sequence FASTA file.	mpxvassembly.fasta					
	consensus sequence filepath	*GENEPIO:0001462*	The filepath of the consensus sequence file.	Provide the filepath of the consensus sequence FASTA file.	/User/Documents/ViralLab/Data/mpxvassembly.fasta					
	consensus sequence software name	*GENEPIO:0001463*	The name of software used to generate the consensus sequence.	Provide the name of the software used to generate the consensus sequence.	iVar					
	consensus sequence software version	*GENEPIO:0001469*	The version of the software used to generate the consensus sequence.	Provide the version of the software used to generate the consensus sequence.	1.3					
	breadth of coverage value	*GENEPIO:0001472*	The percentage of the reference genome covered by the sequenced data, to a prescribed depth.	Provide value as a percent.	95%					
	depth of coverage value	*GENEPIO:0001474*	The average number of reads representing a given nucleotide in the reconstructed sequence.	Provide value as a fold of coverage.	400x					
	depth of coverage threshold	*GENEPIO:0001475*	The threshold used as a cut-off for the depth of coverage.	Provide the threshold fold coverage.	100x					
	r1 fastq filename	*GENEPIO:0001476*	The user-specified filename of the r1 FASTQ file.	Provide the r1 FASTQ filename. This information aids in data management.	ABC123_S1_L001_R1_001.fastq.gz					
	r2 fastq filename	*GENEPIO:0001477*	The user-specified filename of the r2 FASTQ file.	Provide the r2 FASTQ filename. This information aids in data management.	ABC123_S1_L001_R2_001.fastq.gz					
	r1 fastq filepath	*GENEPIO:0001478*	The location of the r1 FASTQ file within a user's file system.	Provide the filepath for the r1 FASTQ file. This information aids in data management.	/User/Documents/ViralLab/Data/ABC123_S1_L001_R1_001.fastq.gz					
	r2 fastq filepath	*GENEPIO:0001479*	The location of the r2 FASTQ file within a user's file system.	Provide the filepath for the r2 FASTQ file. This information aids in data management.	/User/Documents/ViralLab/Data/ABC123_S1_L001_R2_001.fastq.gz					
	fast5 filename	*GENEPIO:0001480*	The user-specified filename of the FAST5 file.	Provide the FAST5 filename. This information aids in data management.	mpxv123seq.fast5					
	fast5 filepath	*GENEPIO:0001481*	The location of the FAST5 file within a user's file system.	Provide the filepath for the FAST5 file. This information aids in data management.	/User/Documents/RespLab/Data/mpxv123seq.fast5					
	number of base pairs sequenced	*GENEPIO:0001482*	The number of total base pairs generated by the sequencing process.	Provide a numerical value (no need to include units).	2639019					
	consensus genome length	*GENEPIO:0001483*	Size of the reconstructed genome described as the number of base pairs.	Provide a numerical value (no need to include units).	197063					
	reference genome accession	*GENEPIO:0001485*	A persistent, unique identifier of a genome database entry.	Provide the accession number of the reference genome.	NC_063383.1					
	bioinformatics protocol	*GENEPIO:0001489*	A description of the overall bioinformatics strategy used.	Further details regarding the methods used to process raw data, and/or generate assemblies, and/or generate consensus sequences can. This information can be provided in an SOP or protocol or pipeline/workflow. Provide the name and version number of the protocol, or a GitHub link to a pipeline or workflow.	https://github.com/phac-nml/monkeypox-nf					
Pathogen diagnostic testing		**GENEPIO:0001506**								
	gene name 1	*GENEPIO:0001507*	The name of the gene used in the diagnostic RT-PCR test.	Provide the full name of the gene used in the test. The gene symbol (short form of gene name) can also be provided. Standardized gene names and symbols can be found in the Gene Ontology using this look-up service: https://bit.ly/2Sq1Lbl	MPX (orf B6R)					
	diagnostic pcr Ct value 1	*GENEPIO:0001509*	The Ct value result from a diagnostic SARS-CoV-2 RT-PCR test.	Provide the CT value of the sample from the diagnostic RT-PCR test.	21					
	gene name 2	*GENEPIO:0001510*	The name of the gene used in the diagnostic RT-PCR test.	Provide the full name of another gene used in an RT-PCR test. The gene symbol (short form of gene name) can also be provided. Standardized gene names and symbols can be found in the Gene Ontology using this look-up service: https://bit.ly/2Sq1Lbl	OVP (orf 17L)					

Parent Class	Field	Ontology Identifier	Definition	Guidance	Examples	Deprecated Label	Deprecated ID	Version Tracking		
	diagnostic pcr Ct value 2	GENEPIO:0001512	The Ct value result from a diagnostic SARS-CoV-2 RT-PCR test.	Provide the CT value of the sample from the second diagnostic RT-PCR test.	36					
	gene name 3	GENEPIO:0001513	The name of the gene used in the diagnostic RT-PCR test.	Provide the full name of another gene used in an RT-PCR test. The gene symbol (short form of gene name) can also be provided. Standardized gene names and symbols can be found in the Gene Ontology using this look-up service: https://bit.ly/2Sq1Lbl	OPHA (orf B2R)					
	diagnostic pcr Ct value 3	GENEPIO:0001515	The Ct value result from a diagnostic SARS-CoV-2 RT-PCR test.	Provide the CT value of the sample from the second diagnostic RT-PCR test.	19					