

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		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_mpo_x_1234			1.0.0	1.0.0	1.0.0
	Related specimen primary ID	GENEPIO:0001128	The user-defined name for the sample.	Store the primary ID of the related specimen previously submitted to the repository.	SR20-12345			1.0.0	1.0.0	1.0.0
	case ID	GENEPIO:0100281	The primary ID of a related specimen previously submitted to the repository.	Store the case identifier. 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 identifier used to specify an epidemiologically detected case of disease.	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 INSDC accession number of the BioProject(s) to which the BioSample belongs.	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 identifier assigned to a BioSample in INSDC archives.	The Sequence Read Archive (SRA) identifier linking raw read data, methodological metadata and quality control metrics submitted to the INSDC.	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 assigned to the submitted "run". NCBI-SRA accessions start with SRR.	MN908947.3			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 a GenBank submission (viral genome assembly).	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 multiple 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 collection date precision	GENEPIO:0001177	The precision to which the "sample collection date" was provided.	Provide the precision of granularity to the "day", "month", or "year" for the date provided in the "sample collection date" field. The "sample collection date" will be truncated to the precision specified upon export; "day" for "YYYY-MM-DD", "month" for "YYYY-MM", or "year" for "YYYY".	year			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

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	organism	GENEPIO:0001191		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).						
			Taxonomic name of the organism.		Mpox virus			1.0.0	1.0.0	1.0.0
	isolate	GENEPIO:0001195		Provide the GISAID EpiPox virus name, which should be written in the format "hMpoxV/Canada/2 digit provincial ISO code-xxxx/year". If the province code cannot be shared for privacy reasons, put "UN" for "Unknown".	hMpoxV/Canada/UN-NML-12345/2022			1.0.0	1.0.0	1.0.0
	purpose of sampling	GENEPIO:0001198		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		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
	NML submitted specimen type	GENEPIO:0001204		This information is required for upload through the CNPHI LaSER system. Select the specimen type from the pick list provided. If sequence data is being submitted rather than a specimen for testing, select "Not Applicable".	Nucleic Acid			1.0.0	1.0.0	1.0.0
	Related specimen relationship type	GENEPIO:0001209		Provide the tag that describes how the previous sample is related to the current sample being submitted from the pick list provided, so that the samples can be linked and tracked in the system.	Previously Submitted			1.0.0	1.0.0	1.0.0
	anatomical material	GENEPIO:0001211		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		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		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
	collection device	GENEPIO:0001234		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		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		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.	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										
	host (common name)	GENEPIO:0001268		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		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.	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.	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.	Hospitalized			1.0.0	1.0.0	1.0.0
	host disease	GENEPIO:0001391		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 age	GENEPIO:0001392		Age of host at the time of sampling.	79			1.0.0	1.0.0	1.0.0
	host age unit	GENEPIO:0001393		If known, provide age. Age-binning is also acceptable.	year			1.0.0	1.0.0	1.0.0
	host age bin	GENEPIO:0001394		The units used to measure the host's age.	50 - 59			1.0.0	1.0.0	1.0.0
	host gender	GENEPIO:0001395		Age bins in 10 year intervals have been provided. If a host's age cannot be specified due to privacy concerns, an age bin can be used as an alternative.	Male			1.0.0	1.0.0	1.0.0
	host residence geo_loc name (country)	GENEPIO:0001396		If known, select a value from the pick list.	Canada			1.0.0	1.0.0	1.0.0
	host residence geo_loc name (state/province/territory)	GENEPIO:0001397		Select the country name from pick list provided in the template.	Quebec			1.0.0	1.0.0	1.0.0
	symptom onset date	GENEPIO:0001399		Select the province/territory name from pick list provided in the template.				1.0.0	1.0.0	1.0.0
				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

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	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								
	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 received 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								
	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			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.	Select the province name from the pick list provided in the template.				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.	Canada			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			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			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			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			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								
	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			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			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
Sequencing								
		GENEPIO:0001441						

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	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.	Select "Targeted surveillance (non-random sampling)" if the specimen fits any of the following criteria: Specimens attributed to individuals with no known intimate contacts to positive cases.Specimens attributed to youth/minors <18 yrs;.Specimens attributed to vulnerable persons living in transient shelters or congregate settings.Specimens attributed to individuals self-identifying as "female".For specimens with a recent international and/or domestic travel history, please select the most appropriate tag from the following three options: Domestic travel surveillance;International travel surveillance;Travel-associated surveillance.For specimens targeted for sequencing as part of an outbreak investigation, please select: Cluster/Outbreak investigation; In all other cases use: Baseline surveillance (random sampling).			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			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						1.0.0	1.0.0	1.0.0
	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			1.0.0	1.0.0	1.0.0
	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			1.0.0	1.0.0	1.0.0
	consensus sequence name	GENEPIO:0001460	The name of the consensus sequence.	Provide the name and version number of the consensus sequence.	mpxvassembly3			1.0.0	1.0.0	1.0.0
	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			1.0.0	1.0.0	1.0.0
	consensus sequence filepath	GENEPIO:0001462	The filepath of the consensus sequence file.	Provide the filepath of the consensus sequence FASTA file.	/User/Documents/Viral_Lab/Data/mpxvassembly.fasta			1.0.0	1.0.0	1.0.0
	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			1.0.0	1.0.0	1.0.0
	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			1.0.0	1.0.0	1.0.0
	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%			1.0.0	1.0.0	1.0.0
	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			1.0.0	1.0.0	1.0.0
	depth of coverage threshold	GENEPIO:0001475	The threshold used as a cut-off for the depth of coverage.	Provide the threshold fold coverage.	100x			1.0.0	1.0.0	1.0.0
	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			1.0.0	1.0.0	1.0.0
	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			1.0.0	1.0.0	1.0.0
	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			1.0.0	1.0.0	1.0.0
	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			1.0.0	1.0.0	1.0.0
	fast5 filename	GENEPIO:0001480	The user-specified filename of the FAST5 file.	Provide the FAST5 filename. This information aids in data management.	mpxv123seq.fast5			1.0.0	1.0.0	1.0.0
	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			1.0.0	1.0.0	1.0.0
	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			1.0.0	1.0.0	1.0.0
	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			1.0.0	1.0.0	1.0.0
	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			1.0.0	1.0.0	1.0.0
	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-crf			1.0.0	1.0.0	1.0.0
Pathogen diagnostic testing		GENEPIO:0001506								
	gene name 1	GENEPIO:0001507	The name of the gene used in the diagnostic RT-PCR test.	Select the name of the gene used for the diagnostic PCR from the standardized pick list.	MPX (orf B6R)			1.0.0	1.0.0	1.0.0

Parent Class	Field	Ontology Identifier	Definition	Guidance	Examples	Deprecated Label	Deprecated ID	Version Tracking		
	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		1.0.0	1.0.0	1.0.0
	gene name 2	GENEPIO:0001510	The name of the gene used in the diagnostic RT-PCR test.	Select the name of the gene used for the diagnostic PCR from the standardized pick list.	OVP (orf 17L)			1.0.0	1.0.0	1.0.0
	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		1.0.0	1.0.0	1.0.0
	gene name 3	GENEPIO:0001513	The name of the gene used in the diagnostic RT-PCR test.	Select the name of the gene used for the diagnostic PCR from the standardized pick list.	OPHA (orf B2R)			1.0.0	1.0.0	1.0.0
	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		1.0.0	1.0.0	1.0.0
	gene name 4	GENEPIO:0100576	The name of the gene used in the diagnostic RT-PCR test.	Select the name of the gene used for the diagnostic PCR from the standardized pick list.	G2R_G (TNFR)			1.0.0	1.0.0	1.0.0
	diagnostic pcr Ct value 4	GENEPIO:0100577	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.		27		1.0.0	1.0.0	1.0.0
	gene name 5	GENEPIO:0100578	The name of the gene used in the diagnostic RT-PCR test.	Select the name of the gene used for the diagnostic PCR from the standardized pick list.	RNase P			1.0.0	1.0.0	1.0.0
	diagnostic pcr Ct value 5	GENEPIO:0100579	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.		30		1.0.0	1.0.0	1.0.0

