

Guidelines for Genetic Sample Collection of Small Mustelids

Author: Andrin C. Dürst, University of Bern, Switzerland

ORCID iD: <https://orcid.org/0009-0004-8878-8994>

DOI: [dx.doi.org/10.17504/protocols.io.eq2ly4wmp1x9/v1](https://doi.org/10.17504/protocols.io.eq2ly4wmp1x9/v1)

Version: 1.2 (05.03.2026)



Disclaimer: This document is a working guideline and is provided for informational purposes only. The author does not guarantee the accuracy, completeness, or appropriateness of the methods described for any specific context. Use of this guideline is at the user's own risk. The author accepts no responsibility or liability for any outcomes, errors, or consequences resulting from the use or misuse of this document. Users are solely responsible for ensuring compliance with applicable laws, institutional guidelines, and safety or ethical standards.

Abstract

These guidelines provide standardized recommendations for the collection, preservation, and documentation of genetic samples from small mustelids, including stoats (*Mustela erminea*), weasels (*M. nivalis*), and polecats (*M. putorius*). They cover tissues, scat, and hair samples, with practical instructions for handling, storage, labelling, and metadata recording, while emphasizing legal and ethical considerations.

By applying these guidelines, researchers and conservation practitioners can generate high-quality and comparable genetic datasets across institutions and regions, enabling collaborative analyses of population structure, connectivity, and conservation status. This first published version establishes a common framework designed to support reproducible and interoperable research on small mustelids.

Introduction

The collection and analysis of genetic material from wildlife species have become essential tools in conservation biology, population genetics, and ecological research. For small mustelids—such as stoats (*Mustela erminea*), weasels (*Mustela nivalis*), and polecats (*Mustela putorius*)—genetic sampling enables researchers to study population structure, gene flow, hybridization, historical demography, and evolutionary processes. Despite their ecological importance and conservation concern in some regions, small mustelids remain understudied compared to other carnivores, partly due to their elusive behaviour, small size, and low detectability in the field.

To address this gap, researchers from across institutions and countries agreed to jointly develop standardized guidelines to facilitate collaborative research and ensure consistency in data collection. The idea for this document originated at the International Small Mustelid Meeting 2025 in Groningen, where it was recognized that harmonized protocols are essential for

generating high-quality, comparable datasets from multiple sources. The meeting also led to the creation of the European Weasel Gang (<https://europeanweaselgang.eu/>), an informal network of researchers working on small mustelids across Europe. The network serves as a platform for communication and collaboration among projects and can help facilitate coordinated sampling efforts and the harmonization of methodologies. It does not function as a centralized repository or storage facility for genetic samples.

These guidelines aim to assist biologists, conservation practitioners, curators, and other stakeholders in the proper collection, handling, preservation, and documentation of genetic samples from small mustelids. By providing general recommendations—adaptable to local contexts and capacities—this document encourages the sharing and synthesis of data across national and institutional boundaries. It also addresses the practical and ethical considerations of collecting samples from both opportunistic and standardized sources.

While the primary focus is on tissues, scats, and hair samples, the guidelines also acknowledge the possibility of using swabs and blood samples, which are beyond the scope of this particular document. A complementary, method-specific protocol for carcass collection is already available, and we plan to develop similar protocols for other methods as follow-up resources.

1. Purpose and scope

This guideline serves to provide a shared foundation for researchers and institutions collecting genetic material from small mustelids. It is intended as a **general framework**—not a detailed protocol—meant to ensure that independently collected samples follow common principles that facilitate data comparability.

Objectives:

- To guide the collection, preservation, and documentation of genetic samples from *Mustela erminea*, *M. nivalis*, and *M. putorius*.
- To promote the use of standardized metadata structures, enabling future collaborative analyses.

These guidelines are applicable to both **opportunistic** (e.g., roadkill, cat kills, museum collections) and **targeted** (e.g., live trapping) sample collection efforts. They are also designed to be globally adaptable, allowing for variation in local context.

Importantly, this is a living document. As methods and technologies evolve and collaborative projects progress, future revisions may refine or expand upon the practices outlined here.

2. Target species

These guidelines are developed specifically for the collection of genetic material from small mustelids of the genus *Mustela*. Focusing on the following three species:

- **Stoat** (*Mustela erminea*)
- **Weasel** (*Mustela nivalis*)
- **Polecat** (*Mustela putorius*)

While the emphasis is on European species, the recommendations are applicable globally.

3. Sample sources and collection contexts

Samples may be obtained from a wide range of situations. These guidelines cover material from both standardized monitoring efforts and opportunistic encounters. The goal is to ensure that even diverse and irregularly collected samples can be useful for genetic studies if handled and documented properly.

Sample sources include:

- **Carcasses:** Sourced from roadkill, cat kill, trapping programs, or found dead in the field. These are often the most accessible and common sources for tissue collection. (For a detailed protocol on how to collect, handle, and store small mustelid carcasses, see: Dürst 2025, DOI: [dx.doi.org/10.17504/protocols.io.3byl469pogo5/v1](https://doi.org/10.17504/protocols.io.3byl469pogo5/v1))
- **Tissue samples:** Can be taken from carcasses or sourced from institutions such as taxidermists, museum collections, or live-trapping studies.
- **Scats (faeces):** Often the only non-lethal sample type available. They contain host DNA (mainly from intestinal lining cells) and must be handled with care to prevent degradation or contamination. Can be found opportunistically, by species detection dogs or collected in animal care centres.
- **Hair (with follicles):** May be collected from animals found dead or during handling (e.g., from fur remains or during live trapping). Follicles must be present to ensure sufficient nuclear DNA for most genetic analyses.

Note:

- ***Oral and rectal swabs and blood samples** may also be used for genetic research, but they are not covered in detail within this guideline.*
- *The **collection method should be adapted to the context**, available equipment, and legal permissions.*
- *Samples from museum specimens or taxidermy may be valuable for temporal studies but may present preservation-related challenges.*

4. Legal and ethical considerations

Before collecting or handling samples from small mustelids, it is essential that all contributors fully comply with **legal requirements** and **ethical standards** applicable in the **country of origin** of each sample. These obligations may vary significantly between jurisdictions and depending on the species' conservation status, the type of material collected, or whether the animal is dead or alive.

Key responsibilities of contributors:

- **Permits and authorisations**
Contributors must ensure they hold valid **collection permits** and, where applicable, **export/import documentation** (e.g. for CITES-listed populations or cross-border collaborations). Permits may differ for live animal handling, carcass recovery, or sample export.

- **Ethical treatment of animals**

For any sample obtained from **live animals**, the welfare of the animal must be the highest priority. Appropriate ethical approvals from institutional or governmental animal care committees are required for all invasive or non-invasive live animal procedures.

- **Biosecurity and handler safety**

Safe and hygienic practices must be followed during sample collection and processing. This includes:

- Wearing **disposable gloves**.
- Using **clean, sterilized tools** for each animal or sample to avoid cross-contamination.
- Storing biological samples and waste in accordance with local health and safety regulations.

- **Verification of species identity**

The designated coordinator is responsible for **verifying the taxonomic identity** of each specimen, ideally to species level. When uncertainty exists, it must be **explicitly recorded** (e.g. *Mustela sp.* or *M. erminea?*). Supporting photos or field notes may help with retrospective identification.

- **Documentation of origin**

Each sample must be linked to clearly documented metadata (see Section 7) indicating where, when, and how it was collected, and by whom. Contributors must avoid accepting undocumented or illegally sourced samples into their collections.

- **Institutional responsibility**

In multi-person teams or citizen science collaborations, a designated coordinator takes responsibility for verifying legal compliance and ensuring data quality and sample storage. These individuals act as custodians and contact points for future data use or collaborations.

5. Tissue Samples

Tissue samples represent one of the most valuable sources of high-quality DNA for population genetic and genomic studies. These are typically obtained from carcasses, live-trapped individuals (if permitted) or taxidermy mounts.

5.1 Recommended tissue types

When possible, **multiple tissue types** should be collected to increase the range of potential downstream applications (e.g. genomics, diet studies, toxicology). Priority for dead animals should be given as follows:

- **Heart muscle** – small, compact, and yields high-quality DNA (priority #1)
- **Liver** – important for toxicology (priority #2)
- **Hind limb muscle or tongue** (often easily accessible muscle), or **back muscle** (can be accessed through the ventral cavity, often less decomposed) (priority #3)

If the carcass is to be preserved for taxidermy, more discreet tissue options (e.g. tongue) may be taken without affecting the visual integrity of the specimen.

Contributors are encouraged to collect **as many different tissues as possible**, including additional organs (e.g. spleen, kidney, stomach) if available and if the infrastructure allows it. These may prove useful for other research purposes (e.g. parasite studies, food analysis), even if not used for genetics.

Sampling is also possible with live animals:

- **Ear tissue** – suitable as least invasive option for live-trapped animals (invasive sampling may require specific permits)

5.2 Sampling procedure

- Use clean, sterilized tools (scissors, scalpel, forceps).
- Dissect tissue as soon as possible after discovery to minimize degradation.
- Cut small pieces (e.g. minimum of 0.5–1 cm³, see note below) and immediately preserve.
- Avoid excessive tissue mass in a single container, which can slow down preservation.

Minimum sample size:

For genetic analyses, the tissue sample should be at least the size of a grain of rice (approximately 20–30 mg), although larger is preferred to allow for replicate testing or future analyses. Where possible, collect multiple small pieces rather than a single large chunk to improve preservation and reduce degradation risk (see Fig. 1).

If samples come from a carcass in poor condition (e.g. partially decomposed), note this in the metadata and prioritize less-exposed internal tissue. Especially when the carcass was not collected and only a tissue sample was taken directly in the field.



Figure 1: Example of tissue samples preserved in ethanol for genetic analysis.

5.3 Preservation and storage

- **Ethanol AND freezing** (preferred):
The combination of preserving tissue frozen in ethanol is the ideal case. See details below for each method.

- **Freezing:**

If facilities allow, samples should be **frozen immediately** at **−20°C or colder**. For long-term storage (e.g. months to years), **−80°C** is ideal.

- **Ethanol preservation:**

If freezing is not possible (e.g. fieldwork), tissue samples can be stored in **95–100% ethanol** (non-denatured). Ensure:

- A sufficient tissue-to-ethanol ratio (at least 1:5 by volume).
- Containers are tightly sealed and clearly labelled (e.g. screw cap microcentrifuge tubes).
- (Changing ethanol after 24 hours is only necessary for large tissue samples. For small pieces, this step is not required.)

- **Labelling:**

Each sample tube should be labelled with a unique ID (see Section 8), written with ethanol-proof ink or with pencil. Alternatively, preprinted labels with ethanol-proof ink are advised as they ensure correct labelling with predetermined labels. (See section 8.6 for best labelling practices.)

6. Hair Samples

Hair samples can provide a viable, non-lethal alternative or complement to tissue collection, especially when tissue is unavailable (e.g. from museum specimens, live trapping, or hair traps). When properly collected and stored, hair samples can yield usable nuclear and mitochondrial DNA from the **hair follicles** (roots).

6.1 Sampling procedure

- Use clean **forceps** to remove hair from the animal's body. Hair samples can be collected, for example, from the tail base. Do not collect whiskers from live animals.
- Always aim to extract **a tuft of hair with follicles** (roots) attached, e.g. 10 individual hairs.
- Instead of removing one large bundle, remove **multiple small tufts** to minimize trauma to the skin (especially in small-bodied animals).
- Wear gloves and use a clean surface to avoid contamination between individuals.



Important: *Cut or shed hairs typically lack roots and therefore yield insufficient or no DNA.*

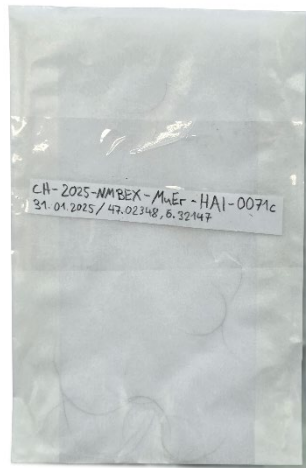


Figure 2: Example of hair samples stored in a paper bag.

6.2 Preservation and storage

Hair samples may be stored using one of the following methods, chosen according to context (field conditions, storage duration, transport constraints):

- **Silica gel drying** (preferred field option)
 - Place hairs into an **acid-free and breathable bag or envelope** (e.g. paper or filter bag, see Fig. 2)
 - Add **silica gel** (desiccant) outside the paper envelope inside an **airtight container**.
 - Store in a **cool, dry, and dark location**, away from UV radiation, moisture, and heat.
- **Ethanol Preservation**
 - Place hairs into **95–100% ethanol** in clearly labelled tubes or vials.
 - Ensure that the container is tightly sealed to prevent ethanol evaporation.
 - Can be combined with freezing.
- **Freezing**
 - Store samples in clean, labelled containers and place in a freezer at **–20°C or colder**.
 - Suitable for storage for months to years.
 - Not suitable for repeated freezing and thawing.

7. Scat samples

Scat (faeces) samples are a valuable, non-invasive source of genetic material and can provide insights into population genetics, diet, and species presence. However, scat-derived DNA is often degraded or contaminated, and therefore requires careful handling, preservation, and metadata documentation.

7.1 Sampling procedure

- **Always collect the entire scat** whenever possible. Small mustelid scats are typically small, and collecting the full sample maximizes the chance of obtaining sufficient DNA (and allows for additional studies such as food analysis).

- If multiple scats are present, **do not pool them** — they may originate from different individuals.
- Use clean forceps, tweezers, or gloves to handle scat. Avoid direct contact for health and contamination reasons. Even though smell can be used as a distinguishing feature for species identification, this should be avoided due to the potential presence of volatile pathogens.
- Place the sample into a clean, labelled container (e.g. screw-cap tubes).
- Record the physical state of the scat at the time of collection:
 - *Fresh, dry, old, desiccated, washed out, etc.*



Important: Most host DNA is found on the outer surface of the scat. If it is not possible to collect the entire sample, then as much of the surface as possible should be collected.



Figure 3: Example of a scat sample stored in a tube and preserved by freezing.

7.2 Preservation and storage

Scat samples may be stored using one of the following methods, chosen according to context (field conditions, storage duration, transport constraints):

- **Silica gel drying** (preferred field option)
 - Place scat into an **acid-free and breathable bag or envelope** (e.g. paper or filter bag) or **on sterile wadding** (e.g. polyester). Or without an additional layer directly into the container (see next step).
 - Place this into an **airtight container** with a minimum **5:1 weight ratio** of silica gel to scat. (If scat were directly placed on silica gel, move the scat to a new container when arriving in the laboratory.)
 - Ensure silica is dry and replace if saturated (colour indicator can help).
 - Store in a **cool, dry, and dark location**, avoiding UV light, moisture, and heat.
- **Freezing**
 - Place the scat into a leak-proof container (e.g. screw-cap tubes, see Fig. 3).
 - Freeze at **-20°C or colder** as soon as possible. Use a cooling box for fieldwork.
 - **Avoid repeated freeze-thaw cycles**
- **Ethanol** (95–100%, not recommended as first choice)
 - Use leak-proof tubes filled with ethanol and fully submerge the scat.
 - The DNA is preserved, but the faecal material falls apart.

8. Sample identification and labelling system

A consistent and well-structured sample identification (ID) system is essential for collaborative genetic studies, ensuring that samples can be traced, shared, and interpreted across institutions and borders. These guidelines propose a standardized, yet flexible, format to assign unique identifiers to all genetic samples collected under this framework.

8.1 General principles

- **Each sample must have a unique identifier** clearly and permanently attached to the sample container and recorded in the metadata spreadsheet.
- The **same individual animal** can provide multiple types of samples (e.g. tissue, scat, hair). These samples must share a **base ID** and be differentiated using suffixes or sub-codes.
- The labelling system must be used **consistently across all collaborators and institutions** to avoid duplication and confusion. The coordinator oversees assigning IDs and avoiding duplicates.

8.2 Sample identification system

To maintain consistency across all collections and enable easy tracking and data sharing, use a **standardized unique ID format**:

[CountryCode]-[Year]-[InstitutionCode]-[TaxonCode]-[SampleType]-[SampleNumber][LetterSuffix]

Component	Description	Format / Rules
CountryCode	Country of sample collection	2-letter ISO 3166-1 alpha-2 code
Year	Year of collection	4 digits
InstitutionCode	Code for the collecting or managing institution	Exactly 5 uppercase letters (complete with X(s) if necessary)
TaxonCode	Code for species or taxon, based on Latin name	4 letters: 2 from genus + 2 from species (first letters uppercase)
SampleType	Type of material collected	3 uppercase letters
SampleNumber	Unique identifier for the sample (=individual)	Exactly 4 digits (with leading zeros if necessary)
LetterSuffix	Optional letter to indicate sub-samples from the same individual	1 lowercase letter starting from a

Example: SE-2025-NRMXX-MuEr-SCT-0034b

This represents:

- SE = Sweden (ISO 3166-1 alpha-2 country code)
- 2025 = Year of collection
- NRMXX = Institution code (e.g. Swedish Museum of Natural History, completed with Xs)
- MuEr = Taxon code (e.g. *Mustela erminea*)
- SCT = Sample type (e.g. scat)
- 0034 = Sample number 0034
- b = Subsample “b” of individual 34 (e.g. second scat from the same individual)

8.3 Taxon code

Standardized codes for taxon codes include (non-exhaustive list):

Common name	Scientific name	Taxon code
Stoat	<i>Mustela erminea</i>	MuEr
Least weasel	<i>Mustela nivalis</i>	MuNi
European polecat	<i>Mustela putorius</i>	MuPu
Long-tailed weasel	<i>Mustela frenata</i>	MuFr
European mink	<i>Mustela lutreola</i>	MuLu
American mink	<i>Neogale vison</i>	NeVi
Pine marten	<i>Martes martes</i>	MaMa
Stone marten	<i>Martes foina</i>	MaFo
Red fox	<i>Vulpes vulpes</i>	VuVu
Eurasian badger	<i>Meles meles</i>	MeMe
Unspecified Mustela	<i>Mustela sp.</i>	MuSp

8.4 Sample Type Abbreviations

Standardized codes for common sample types include:

Code	Sample type
CAR	Carcass (whole)
TIS	Tissue sample
SCT	Scat (faeces)
HAI	Hair
SWB	Swab (oral/rectal)
BLO	Blood

Note: Even though other sample types are not covered in this guideline, the ID structure is designed to accommodate additional types for completeness.

8.5 Suffixes for Sub-Samples

When multiple samples of same or different types are taken from a single individual, append a **letter suffix** (a, b, c, etc.) to indicate that they are subsamples from the same source.

Example:

- DE-2025-UNDRF-CAR-002a = Carcass from individual 002
- DE-2025-UNDRF-TIS-002b = Heart sample from the same individual
- DE-2025-UNDRF-SCT-002c = Scat sample from the same individual
- DE-2025-UNDRF-SCT-002d = Second scat sample from the same individual

8.6 Labelling best practices

- **Labels must be water- and ethanol-resistant** and legible under field and laboratory conditions.
- Use permanent ink (ethanol resistant), pencil or printed labels (preferably thermally printed).

- Printed labels are preferred over handwritten tags.
- Ensure that the sample ID in the label matches exactly with the ID in the metadata file.
- Labels should be placed **inside and outside** the sample container when possible (e.g. labelled tubes or zip lock bags containing a tag inside written with pencil, Fig. 1).



Figure 4: Examples of screw-cap tubes with a label outside (left) and inside (right).



Important: Mislabelling or duplicate IDs are major sources of error in multi-site projects. Extra care should be taken by the coordinator to double-check all codes during and after fieldwork.

9. Metadata

To ensure that all collected data are FAIR (Findable, Accessible, Interoperable, and Reusable), we aim to record metadata following the **Darwin Core (DwC)** standard (<https://dwc.tdwg.org>), with extensions or complementary formats such as the **Global Genome Biodiversity Network (GGBN)** standard (<https://www.ggbn.org>) where appropriate. This approach facilitates data sharing, integration, and long-term usability.

All relevant information is recorded systematically. A complete list of metadata fields, including definitions and standardized terms, is provided in **Appendix A**.

A template metadata table is available from the authors and will be shared upon request among collaborators.

9.1 Metadata management

Each lab or contributor should maintain their metadata in an Excel file (or compatible format) based on the standardized structure proposed in these guidelines. This should be:

- **Consistently formatted** to ensure interoperability across datasets.
- **Backed up regularly**, both locally and in institutional storage (where possible).
- In **English**, use standard terminology and abbreviations provided in this document.

Although no centralized database is yet established, a metadata template may be provided by the authors in the future. Contributors should be prepared to convert or export their metadata into this shared format when available.

10. Sample handling and custody

Proper handling, documentation, and storage of genetic samples are critical to ensuring their long-term usability and scientific value. These guidelines outline general responsibilities and best practices for the custody of samples following collection, with an emphasis on decentralized collaboration.

10.1 Responsibilities of contributors

Each contributor (individual, institution, or research group) is responsible for:

- **Ensuring secure, contamination-free storage** of the samples under their custody.
- **Maintaining accurate and up-to-date metadata**, with direct correspondence to labelled samples.
- **Verifying species identity**, at least to the genus level. If species identity cannot be confirmed with certainty, this uncertainty must be recorded in the metadata.
- **Compliance with legal and ethical requirements**, including documentation of collection permits, ethical approvals, and any restrictions on sample use or transfer.

If a sample was provided by a third party (e.g. museum staff, hunters, taxidermists), the coordinator is responsible for checking and confirming the sample's identity and details.

10.2 Sample storage and safety

Samples must be stored under suitable conditions based on sample type and preservation method. Contributors should ensure:

- **Stable storage conditions** are maintained.
- Samples are **protected from cross-contamination**, especially for low-DNA-content materials like scat or hair.
- Each sample container is **securely closed**, clearly labelled, and physically robust enough for long-term storage or transport.

10.3 Sample custody and access

At this stage of the initiative:

- Samples remain under the **custody of the collecting institution or individual**.
- There is **no central storage or repository** currently designated. Collaborators are expected to retain their samples locally unless specific agreements are made.
- **Access to samples for future collaborative research** should be based on mutual agreements and aligned with any national or institutional policies on data/material sharing.

Contributors are encouraged to consider the long-term availability of the samples they collect, including whether adequate storage facilities and institutional support are in place.

11. Optional additions

This section outlines additional recommendations and tools that can enhance sample quality, documentation, and future usability, particularly for field teams and decentralized collaborators. While not strictly required, these practices are strongly encouraged to improve data consistency and facilitate integration across studies.

11.1 Field datasheets

A standardized **field datasheet** (paper or digital) can significantly improve the quality and completeness of sample metadata. Such a sheet can be pre-formatted to include all the necessary metadata.

Digital versions can be tailored for mobile use in field apps or tablets, with dropdowns or validation fields to reduce data entry errors (e.g. QField or Epicollect5).

A template datasheet will be made available by the authors or shared upon request among collaborators.

11.2 Supplementary sample types

Although this guideline focuses on tissue, hair, and scat samples, several other sample types may be useful for future studies:

- **Swabs** (oral, rectal, skin) — Can be useful for microbiome or low-yield DNA applications. It could be air-dried and stored dry in sterile tubes.
- **Blood** — Collection should only be performed under appropriate permits and with veterinary oversight. Storage methods include ethanol or specialized buffers (e.g. EDTA) and freezing.

Note: Detailed protocols for swabs and blood collection are not included here but may be added in future supplementary documents.

11.3 Photographic records and measurements

Photographs and measurements can provide valuable supplementary metadata, particularly when specimens are decomposed, rare, in unusual condition or with morphological anomalies (e.g. weasel with black tail tip). Contributors are encouraged to:

Photograph:

- The whole animal and the sampling site.
- The head with throat patch
- Dentures
- Label photo files with the **corresponding Sample ID** and metadata reference.

Measurements:

- Circumference of head and neck (cm)
- Body and tail length (cm)
- Hind foot (cm)
- Weight (grams)

Acknowledgements

The idea for developing these guidelines originated during the European Small Mustelid Meeting held in Groningen, the Netherlands. I am grateful to the participants of the meeting for the stimulating discussions and valuable feedback that shaped the development of the standardized sampling protocol. In particular, I would like to thank Stephen P. Carter, Marco Granata, Tim R. Hofmeester, Jeroen Mos, Pieter J. Otte, Salvador Salvador, Vasco Valdez, and Karol Zub for their constructive input and exchange of ideas.

Appendix A

Table A.1: Metadata Fields, Definitions, and Standards

If possible, entries should be recorded according to Darwin Core (DwC) or Global Genome Biodiversity Network (GGBN) standard.

Entry	Implemented in DwC (or GGBN)	Definition (DwC if applicable)	Term URL (DwC or GGBN)
materialSampleID	x	A unique identifier for a MaterialSample entity.	https://dwc.tdwg.org/terms/#materialSampleID
sampleNumber		A unique numeric identifier assigned to each individual genetic sample within the study. Used to differentiate samples collected from the same individual or multiple individuals. Must be consistent across all records.	
subsampleID		An optional identifier appended to the primary sampleNumber to denote subsamples or multiple sample types collected from the same individual. Represented by a lowercase letter suffix (e.g., a, b, c) in alphabetic order.	
eventDate	x	The date-time or interval during which an Event occurred.	https://dwc.tdwg.org/terms/#eventDate
country	x	The name of the country or major administrative unit in which the Location occurs.	https://dwc.tdwg.org/terms/#country
decimalLatitude	x	Geographic latitude in decimal degrees, using the spatial reference system given in geodeticDatum. [WGS84 format preferred]	https://dwc.tdwg.org/terms/#decimalLatitude
decimalLongitude	x	Geographic longitude in decimal degrees, using the spatial reference system given in	https://dwc.tdwg.org/terms/#decimalLongitude

		geodeticDatum. [WGS84 format preferred]	
coordinateUncertaintyInMeters	x	The horizontal distance (in meters) from the given decimalLatitude and decimalLongitude describing the smallest circle containing the whole of the Location.	https://dwc.tdwg.org/terms/#coordinateUncertaintyInMeters
geodeticDatum	x	The ellipsoid, geodetic datum, or spatial reference system (SRS) upon which the geographic coordinates are based.	https://dwc.tdwg.org/terms/#geodeticDatum
locationID	x	An identifier for the set of location information (data associated with dcterms:Location).	https://dwc.tdwg.org/terms/#locationID
scientificName	x	The full scientific name, with authorship and date information if known.	https://dwc.tdwg.org/terms/#scientificName
taxonCode		A standardized, unique alphanumeric code representing a species or taxonomic unit. The code is derived from the Latin scientific name by combining the first two letters of the genus name and the first two letters of the species name, with the first letter of each part capitalized (e.g., <i>Mustela erminea</i> → MuEr).	
identificationCertainty		A qualitative or quantitative assessment of confidence in the taxonomic identification of the specimen or sample. Indicates whether the identification is confirmed, probable, tentative, or uncertain. (see list)	
causeOfDeath		A description or coded term indicating the suspected or confirmed cause of death of the sampled individual (e.g., natural predation, roadkill, disease).	
causeOfDeathCertainty		A statement or rating indicating the degree of certainty associated with the recorded cause of death, distinguishing between confirmed and assumed causes. (see list)	

institutionCode	x	The name (or acronym) in use by the institution having custody of the object(s) or information referred to in the record.	https://dwc.tdwg.org/terms/#institutionCode
recordedBy	x	A list of names of people, groups, or organizations responsible for recording the original Occurrence.	https://dwc.tdwg.org/terms/#recordedBy
recordedByContact		Contact information (e.g., email, phone) for the person or team responsible for recording or collecting the sample, enabling follow-up communication if needed.	
coordinator		The name or identifier of the project coordinator responsible for overseeing sample collection, metadata consistency, and data management across participating institutions.	
coordinatorContact		Contact details (e.g., email address) of the project coordinator for coordination, troubleshooting, and communication purposes.	
habitat	x	A category or description of the habitat in which the Event occurred.	https://dwc.tdwg.org/terms/#habitat
locationRemarks	x	Comments or notes about the Location.	https://dwc.tdwg.org/terms/#locationRemarks
materialSampleType	x	The nature of the material sample; preferably from a controlled vocabulary.	https://dwc.tdwg.org/terms/#materialSampleType
preservationMethod	x	GGBN: Method used to preserve the material sample (e.g., ethanol 95%, frozen -80°C), from GGBN preservation vocabulary.	https://wiki.ggbn.org/ggbn/Ggbn:preservationType
sampleCondition		A qualitative description of the physical condition of the sample at the time of collection or processing, including notes on degradation, contamination, or any abnormalities affecting sample quality.	

measurementType_bodyLength	x	The linear distance from the tip of the snout to the base of the tail (excluding the tail).	https://dwc.tdwg.org/terms/#measurementType
measurementValue_bodyLength	x	Value of bodyLength (in mm)	https://dwc.tdwg.org/terms/#measurementValue
measurementUnit_bodyLength	x	Millimeters (mm)	https://dwc.tdwg.org/terms/#measurementUnit
measurementType_tailLength	x	The linear distance from the base of the tail to its tip (not including the hair at the tip).	https://dwc.tdwg.org/terms/#measurementType
measurementValue_tailLength	x	Value of tailLength (in mm)	https://dwc.tdwg.org/terms/#measurementValue
measurementUnit_tailLength	x	Millimeters (mm)	https://dwc.tdwg.org/terms/#measurementUnit
measurementType_bodyMass	x	The total mass (weight) of the animal measured using a precision scale.	https://dwc.tdwg.org/terms/#measurementType
measurementValue_bodyMass	x	Value of bodyMass (in g)	https://dwc.tdwg.org/terms/#measurementValue
measurementUnit_bodyMass	x	Grams (g)	https://dwc.tdwg.org/terms/#measurementUnit
sex	x	The sex of the biological individual(s) represented in the Occurrence.	https://dwc.tdwg.org/terms/#sex
furColour		Descriptive information about the coloration or pattern of the fur observed on the sampled individual, useful for phenotypic variation and identification. (see list)	
comments		Additional comments and remarks.	https://dwc.tdwg.org/terms/#dynamicProperties
associatedMedia	x	A list of identifiers (publication, global unique identifier, URI) of media associated with the Occurrence.	https://dwc.tdwg.org/terms/#associatedMedia