

Important Information for Sampling

For collection

- Carefully read this sampling protocol.
- Complete the data sheet in .xlsx format (feuille_de_données) :
 - Always write the nine (9) digits of the sheep's digital ID in the "ATQ_sheep" column (or tatou if none);
 - Indicate the sheep's breed in the "Breed" column;
 - Indicate the sheep's sex in the "Sex" column;
 - If the sheep has a particular condition (e.g., cramping, color, horn, etc.), mention it in the "Comment" column.
 - If a sample collection fails, discard the tube and leave the corresponding line blank in the data file.
- The tube number (ATQ_tube) and box number (Box) are found on the sample box:



- Only sample purebred sheep registered in GenOvis for cofinancing category.
- Sample tubes (both new and used) must be stored at room temperature and kept out of direct sunlight.
- Sheep must be restrained before sampling to prevent injuries or improper sampling.

For returning samples

- Submit a sample return request using the form available on the SEMRPQ website (<https://www.sempq.net/genomique-ovine/procedure-et-formulaire/>). Once the form has been received, a return label and the scheduled collection date will be sent to you by email.
- Once the samples are received, the university team will inform SEMRPQ of the number of samples received and send them for genotyping.
- Genotyping fees apply to all submitted samples. If genomic results cannot be obtained due to insufficient DNA or tissue absence, a \$2 discount will be applied.
- Once the genotyping results are available, SEMRPQ will send you an invoice, payable upon receipt.
- After payment is received and genomic analyses are completed, results will be sent to you by the project team.

For any questions, feel free to contact us!

sempq@sempq.com
william.poisson.1@ulaval.ca

Required Equipment:

- Allflex pliers (blue).
- Sample tubes.
- Data sheet (feuille_de_données) in Excel format.

*****Note: The data sheet must be returned in digital format (.XLSX) via email after sampling.**

Procedure

A. Loading a sample tube in the pliers

1

1. Remove an unused sample tube from the box (following data sheet tube order). The tube should be in one piece; if not, reassemble it (blade with white base, red intermediate piece, and tube)

2

2. Ensure the retention ring on the pliers is open (black piece at the bottom; if closed, turn it) and insert the sample tube as illustrated

3

3. Once the tube is inserted, turn the retention ring to the closed position.

4

4. Align the tube with the piston (if not aligned) and squeeze the pliers until the piston is flush with the white base of the blade (yellow arrow on the image).

5

5. Release the pliers, ensuring the white base and blade move with the piston. If not, reapply pressure.

6

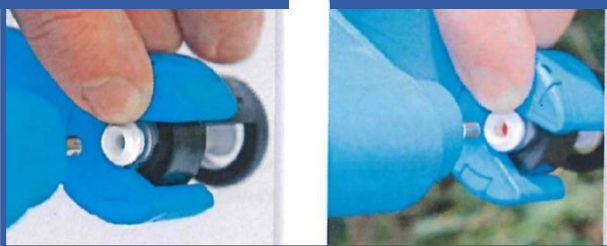
6. Remove the red intermediate piece by holding both tabs and **keep** it for later tube storage.

Warning: The blade is VERY sharp.

B. Sampling process

Unused

Used



1. Verify that the inserted tube is unused.

→ **Used** tubes are marked with a **red dot** on top and **green marble** **INSIDE** the tube (not on top).

2



2. Slide the sheep's ear into the pliers, avoiding the edges (<1cm), large veins, and cartilage folds.

Important: Restrain the animal to prevent injuries.

B. Sampling process



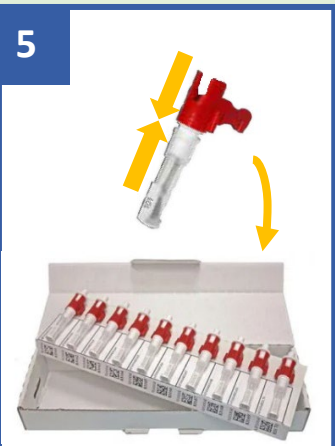
3. Firmly and quickly squeeze the pliers, then release.

Important: Follow the animal's movements to avoid tears.



4. Turn the retention ring and remove the tube.

Important: Ensure the sample is present in the tube. If not, discard the tube, mark the missed sample on the data sheet, and retry with a new tube.



5. Replace the previously removed red intermediate piece on the tube, then store it in its designated slot (according to ATQ_tube number) in the box.



6. Remove the blade by separating the pliers and discard it.



7. Complete the corresponding tube row in the data sheet (**Excel format**):

- **ATQ_sheep** column: 9-digit ATQ (numeric ID) of the animal (tatou ID if none).
- **Breed column**: Breed code
- **Sex column**: Sex (M or F).
- **Anomaly column**: 1 if the animal has been classified as abnormal, else nothing.
- **Comment column**: Add any notes (e.g., different phenotype, parentage, etc.).

Final Notes:

- The **full ID of the animal must be recorded correctly** (9 digits for digital (ATQ) ID or full tatou ID) in the appropriate row, or the sample will not be processed.
- Report any discrepancies in data file to ensure accurate results.

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semrpq@semrpq.net

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