

SPECIFIC TECHNICAL SPECIFICATIONS

**HIGH-THROUGHPUT DNA SEQUENCING SERVICES FOR THE MEDITERRANEAN FOREST ECOLOGY RESEARCH UNIT
(URFM) OF THE INRAE PACA CENTRE**

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Article 1: Purpose of the Contract and Presentation of the Purchase and Its Context

The **National Research Institute for Agriculture, Food, and the Environment (INRAE)** is a public research institution bringing together a workforce of **12,000 people**, with over **200 research, service, and experimental units** located across **18 centers** in France. INRAE ranks among the world's leading institutions in **agricultural and food sciences, plant and animal sciences**. Its research aims to develop solutions for **multi-performance agriculture, high-quality food, and sustainable management of resources and ecosystems**.

The **Mediterranean Forest Ecology Research Unit (URFM)** is a multidisciplinary unit based in Avignon at the **INRAE Provence-Alpes-Côte d'Azur center**. Its overarching scientific goal is to **understand and model the biological, physical, and anthropogenic processes** involved in the **functioning, evolution, and dynamics of Mediterranean forests**, as well as their disturbances.

Within this unit, the **Population Biology and Evolution (BioPopEvol) team** is involved in the **PangénomeBEECH project** (jointly funded by **DFG (Germany)** and **ANR (France)**), which aims to **analyze the pangenome of the European beech (*Fagus sylvatica*)** to elucidate the role of **structural genetic variation in local adaptation and phenotypic differentiation** across diverse environments.

As part of this project, the BioPopEvol team intends to commission **high-throughput sequencing of total DNA** extracted from **2,200 beech samples** sourced from French and German common gardens.

Article 2: Phasing and Batching

The service will be divided into **two independent phases**:

- **Phase 1:** Sequencing of **1,500 individuals**. This will commence upon receipt of the DNA samples by the sequencing platform. The data must be made available immediately after completion of sequencing for this first batch.
- **Phase 2:** Sequencing of the **remaining 700 samples**, to be initiated **six months after Phase 1**.

Article 3: Technical Specifications for Supplies or Services

The service consists of **whole-genome sequencing** of beech DNA samples using an **Illumina Paired-End 150 bp platform** (or equivalent).

The service includes the following steps:

- **Quality control of received DNA preparations:** Assessment of concentration using **fluorometric methods**.
- In the event of issues (e.g., **degraded samples, presence of inhibitors**), the provider commits to collaborating to find a solution (e.g., **resending certain samples if necessary**).
- **Preparation of sequencing libraries** for **Illumina short-read sequencing** (or equivalent) from the DNA samples.

- **Illumina (or equivalent) Paired-End sequencing** with short fragments (**2 × 150 bp**), targeting a minimum output of **66 million read pairs per sample (≈ 20 Gb)**.
- **Delivery of data in FASTQ format.**
- **Quality control of the generated data.**
- At each stage of the process (quality control, library preparation, sequencing, demultiplexing), the provider commits to **informal exchanges (e.g., via email)** with the research team to assess any necessary adjustments.
- At the end of the service, a **technical report** detailing the various stages of the process will be provided for each sample. The candidate must include a **report template** in their offer.
- The provider must supply a **download link** for the sequencing data and keep this link active for **at least 6 months after the project's completion** (the exact duration must be specified in the offer).

The **maximum number of samples to be sequenced** is **2,200**, distributed as follows: **1,500 in July 2026** and **700 in December 2026**. The samples to be processed are grouped into **2 batches**. Each batch corresponds to a set of samples prepared simultaneously internally by the BioPopEvol team.

The BioPopEvol team will handle the **shipment of samples on dry ice in 96-well plates**, according to the provider's preference. The candidate must specify in their offer the **address to which the samples should be sent**.

During transport between the laboratory (**84000 Avignon, France**) and the service execution location, **opening the package is strictly prohibited** to prevent any manipulation of the samples that could degrade the DNA or result in sample loss. Due to these risks, **re-routing of samples is prohibited**.

Candidates must include the following information in their offer by completing the "**Cadre de Réponse Technique**" (CRT) section of the tender documents :

- The service provider **must agree to process DNA samples** meeting at least the **following quality criteria**:
 - **260/280 purity ratio ≥ 1.6,**
 - **260/230 purity ratio ≥ 1.3,**
 - **≥ 200 ng of genomic DNA** at a concentration of **≥ 10 ng/μL.**
- The **library preparation kit** used.
- The **technology and type of sequencer** employed for sequencing.
- The **unit price** for sequencing one sample (**66 million read pairs**) for each step of the process, to be indicated per **BPU (Base Pair Unit)**.
- **Quality control criteria** for the generated data.
- **Turnaround time** between sample receipt and data availability.
- **Method of providing raw and demultiplexed data** (NAS, hard drive, FTP).
- **Duration of data retention** by the provider after completion of the service.
- **Duration of retention of biological samples** after completion of the service.
- **Measures implemented to ensure data confidentiality.**
- **Address** to which samples should be sent.

- **Method for recycling plastic consumables** implemented under this contract.
- **Details of the provider's waste management policy** under this contract.

If the quality of one or more samples is insufficient during the service, the contractor will **systematically request approval** from the BioPopEvol team before proceeding with the service for the entire batch of samples.

Article 4: Acceptance Criteria for Sequencing Results

For each sample:

- **At least 85% of bases** must achieve a **QScore of 30 or higher**.
- If the **sequencing data quantity per individual is less than 20 Gb**, the result will **not be accepted**, and the contractor must **re-sequence at their own expense** (unless the sample was of poor quality and/or insufficient quantity).
- If the **data quantity exceeds 20 Gb**, no additional cost will be borne by the BioPopEvol team.
- Payment will be made **after the delivery of data for each batch** and following **final validation by the research team**.
- If the sequencing process for a sample is interrupted (see **Article 3**), the provider will only invoice for the **successfully completed steps**.

Article 5: Additional Requirements

In the event of **contamination attributable to the contractor**, observed by the BioPopEvol team following analysis of the sequencing results provided by the contractor, the **sample will be re-sequenced at the contractor's expense**.

The requester will be informed if a sample is re-sequenced at the contractor's initiative. The provider must retain **residual DNA extracts for at least three months** after the results are made available to allow for repetition of all or part of the analytical process in case of issues. If the candidate can offer a longer retention period, they must specify this in their offer.