Sample Requirements Reference

DNA, RNA, and raw biological samples for sequencing services

Please read these guidelines carefully before submitting samples. For questions or specific requirements, contact us — we are happy to help you plan your submission.

Quick Reference

Minimum requirements at a glance:

Sample Type	Min. Amount	Min. Volume	Buffer / Notes
Genomic DNA (standard)	60 ng	50 µL	Water, EB, or TE buffer (pH 8.0)
Genomic DNA (PCR-free library prep)	300–800 ng	50 µL	Water, EB, or TE buffer (pH 8.0)
Total RNA — Human mRNA-seq	60 ng/µL	50 µL	RIN ≥7 recommended; aliquot 6 µL for QC
Total RNA — Microbial mRNA-seq	110 ng/µL	50 µL	RIN ≥7 recommended; aliquot 6 µL for QC
Raw Samples (fecal, swabs, tissue, blood)	Contact us	Contact us	Sterile containers; arrange delivery in advance

Genomic DNA Samples

Submit extracted genomic DNA meeting the following specifications:

- **Minimum amount:** 60 ng in a volume of 50 µL.
- **Recommended buffer:** Water, EB buffer, or TE buffer (pH 8.0).
- **PCR-free library preparation:** Requires 300–800 ng in 50 µL.

Total RNA Samples

Submit extracted total RNA according to the sequencing application:

Human mRNA sequencing

- Submit total RNA at 60 ng/µL concentration in a minimum volume of 50 µL.

Microbial mRNA sequencing

- Submit total RNA at 110 ng/µL concentration in a minimum volume of 50 µL.

General RNA quality requirements

- **RIN value:** A RIN ≥7 is recommended. Samples with a lower RIN risk failure during library preparation and sequencing.
- **Aliquot for QC:** Please aliquot a minimum of 6 µL of extracted RNA for our internal quality control upon sample reception. This minimises freeze-thaw cycles and improves library prep success.

Raw Biological Samples

Raw samples (fecal, swabs, tissue, blood, etc.) are accepted for extraction and sequencing. Please contact us before sending to discuss details and arrange delivery.

Collection and storage

- Collect samples in sterile containers.
- **Storage:** Samples may be stored frozen (–80°C) or in a stabilisation buffer (e.g. DNA/RNA Shield or RNAlater). Please indicate clearly which buffer was used.

Swab samples

- Use sterile synthetic swabs (Dacron or Nylon). **Do not use cotton or wooden-shaft swabs** as they absorb the buffer.
- If needed, break or cut the swab shaft to fit the sample collection tube.

Labelling

- Each sample tube must carry a unique ID matching the submission form.
- Use barcodes where possible — avoid hand-written labels.

> Important: The sender is responsible for ensuring that all samples carry valid ethical approval for their intended use.

Plate Layout and Sample Sheet

All DNA and RNA samples must be submitted in 96-well plates with the following requirements:

Plate preparation

- Use a leak-proof, strong, adhesive PCR foil seal to prevent evaporation and cross-contamination.
- Arrange samples in column order: A1, B1 … H1, then A2 … H2, and so on.
- Leave column 12 and wells G11 and H11 empty — reserved for internal quality control.

Sample sheet

- Fill in and submit the AmbioGen sample sheet template.
- Ensure the plate layout matches the submitted sample sheet exactly.
- **Field naming:** project_id, plate_id, and sample_id may only contain letters, numbers, underscores, or dashes. No other symbols.
- **Sample type:** Select from the dropdown list, or enter the sample type directly if the correct option is not available.
- **Sequencing coverage:** Specify using fold notation (e.g. 30X, 100X) for whole genome sequencing. Contact us if you are unsure.
- Use the comments column for any additional information or special requirements.

Contact Us

For questions about sample requirements, sequencing options, or special handling, please reach out before submitting. We are happy to review your samples and discuss the best approach for your project.