

# Sample Requirements & Submission Guidelines

NGS Core Facility – University of Bonn

## 1. Input Requirements

### Overview of Input Material and Plate Requirements

The table below summarises the required input material, concentration range, quality metrics, and minimum volumes for each application offered by the NGS Core Facility.

| Application                               | Starting Material       | LibPrep Input Amount               | Concentration                   | Quality Req.    | Plate Type                | Min. Volume   |
|-------------------------------------------|-------------------------|------------------------------------|---------------------------------|-----------------|---------------------------|---------------|
| RNA-Seq (mRNA)                            | Total RNA               | 50 ng<br>100 ng<br>200 ng          | 5 -100 ng/ $\mu$ L <sup>1</sup> | RIN $\geq$ 7    | Full-skirted <sup>2</sup> | 25 $\mu$ L    |
| RNA-Seq (POLARIS depletion)               | Total RNA               | 50 ng<br>100 ng<br>200 ng          | 5 -100 ng/ $\mu$ L <sup>1</sup> | RIN $\geq$ 7    | Full-skirted <sup>2</sup> | 25 $\mu$ L    |
| RNA-Seq (POLARIS depletion)               | FFPE RNA                | 10 ng<br>50 ng<br>100 ng<br>200 ng | 5-100 ng/ $\mu$ L <sup>1</sup>  | DV200 > 35%     | Full-skirted <sup>2</sup> | 25 $\mu$ L    |
| RNA Ultra Low                             | Total RNA               | 1 ng<br>5 ng<br>10 ng              | 1-10 ng/ $\mu$ L <sup>1</sup>   | RIN $\geq$ 7    | Full-skirted <sup>2</sup> | 25 $\mu$ L    |
| miRNA (Revvity)                           | Total RNA/<br>small RNA | 10-500 ng                          | 5-100 ng/ $\mu$ L <sup>1</sup>  | RIN > 7         | Full-skirted <sup>2</sup> | 20 $\mu$ L    |
| WGS (DNA)                                 | gDNA                    | 500 ng                             | >50ng/ $\mu$ L <sup>1</sup>     | DIN > 7         | Full-skirted <sup>2</sup> | 25 $\mu$ L    |
| WES (DNA)                                 | gDNA                    | 50 ng                              | >10 ng/ $\mu$ L <sup>1</sup>    | DIN > 7         | Full-skirted <sup>2</sup> | 20 $\mu$ L    |
| Panel-based Targeted Enrichment           | gDNA                    | 50 ng                              | >10 ng/ $\mu$ L <sup>1</sup>    | DIN > 7         | Full-skirted <sup>2</sup> | 20 $\mu$ L    |
| Amplicon / Microbiome                     | gDNA                    | 50 ng                              | 5–50 ng/ $\mu$ L <sup>1</sup>   | —               | Full-skirted <sup>2</sup> | 30 $\mu$ L    |
| Pre-made libraries                        | Final Library           | Per sequencer                      | —                               | —               | Full-skirted <sup>2</sup> | Per sequencer |
| 5mC Methylation Sequencing (EMSeq, TAPS+) | gDNA                    | 50 ng<br>100 ng<br>200 ng          | >20 ng/ $\mu$ L <sup>1</sup>    | DIN > 7         | Full-skirted <sup>2</sup> | 25 $\mu$ L    |
| Protein profiling                         | Serum/Plasma/biofluids  | —                                  | —                               | —               | Full-skirted <sup>2</sup> | 50 $\mu$ l    |
| scRNA-Seq (10x Chromium / BD Rhapsody)    | Cell suspension         | Per protocol                       | 700–1200 cells/ $\mu$ L         | Viability > 80% | On-site delivery          | Per protocol  |

1: If multiple samples are sent, they must be at comparable concentrations (e.g.,  $\pm$  10 ng/ $\mu$ l or  $\pm$  20%).

2: If samples are sent in plates, arrange samples column-wise on plate in same order as on sample sheet (no empty wells). Only full-skirted conical transparent PCR plates can be accepted.

## 2. Project Sheets

Please request the appropriate project sheet via e-mail ([NGS-Core@uni-bonn.de](mailto:NGS-Core@uni-bonn.de)). The completed form must be sent electronically to [NGS-Core@uni-bonn.de](mailto:NGS-Core@uni-bonn.de) before submitting your samples. Sample submissions are only accepted under a valid project ID that will be provided by the NGS Core project management team after completion and receipt of all necessary documents.

## 3. General Sample Preparation and Shipping Instructions

Please follow the instructions below carefully to ensure your samples arrive in optimal condition and can be processed immediately. For input requirements and sample layout, please refer to Table 1 and the corresponding project sheet, respectively.

### Tubes or Plates

- For any project with 8 or more samples, we expect submission in fully-skirted, conical, clear well 96-well PCR plates.
- For projects with <8 samples, samples can be submitted in 1.5 ml Eppendorf tubes.
- When pipetting, please ensure the correct orientation (A1→H1; A2→H2; etc.) and layout indicated in the project sheet. Do not leave any wells empty in between samples. Do not add water or buffer to unused wells. The plate must be sealed with a suitable adhesive foil. Do not use aluminium seals or heat sealing.
- **Important note:** Please do not use Parafilm.

### Labelling

- Please ensure that all plates or tubes are clearly labelled with the IDs listed in the corresponding project sheet.

### Packaging & Sample Delivery

- Samples can be submitted in person at the NGS Core Facility laboratory (building 76, 3<sup>rd</sup> floor) Monday to Thursday between 1:00 PM and 2:00 PM. We recommend to schedule shipment of samples for the beginning of a week. Please note that no sample submissions are accepted on public holidays.
- We recommend delivering or shipping samples frozen and on (dry) ice.
- If dry ice is used, please place samples in a separate bag or box to avoid direct contact with dry ice.
- When shipping your samples, please include a printed copy of page 1 of the project sheet in the package, clearly indicating the project ID, sample type (DNA, RNA, or other), total sample count, and the shipper's name.
- Whenever possible, submit all samples at a uniform volume and concentration range (e.g., 20-40 ng/μl or 50-100 ng/μl).

## 4. Technical Descriptions & Policies

### Quality Control

Quality control measurements (TapeStation and Qubit/Quant-iT) will be performed for every sample. If the amount, concentration, and/or quality of the starting material do not meet the requirements for further processing, we will contact you to discuss how to proceed.

For libraries prepared from starting material that has not successfully passed our initial QC, all output specifications and guarantees are void. If you decide to proceed with the project despite failed QC, this will be done at your own risk and all services performed will be invoiced as specified.

## Sample Submission

Most of our processes are highly automated. It is therefore important that samples are submitted in the required sample format. If samples are sent in a non-compliant way, we reserve the right to extend the turnaround time due to necessary manual adjustments (e.g., transfer to correct sample tubes or plates) and to invoice additional personnel costs.

## Material and Data Storage

We will keep your starting material as well as the final library material for a maximum time period of **4 weeks** and sequencing data generated for the project for a maximum time period of **6 months** after sequencing data have been uploaded. If required, you can place a re-order within this time frame. After 4 weeks, all project materials will be disposed. After 6 months, all data will be deleted.

If you wish to collect residual sample material, please pick it up at the NGS Core Facility within 4 weeks after receipt of the data download link.

## 5. Contact & Support

For questions regarding sample submission, shipping, or any of the services listed above, please contact us:

### NGS Core Facility Bonn

University of Bonn

E-mail: [NGS-Core@uni-bonn.de](mailto:NGS-Core@uni-bonn.de)

Website: <https://www.medfak.uni-bonn.de/en/research/infrastructure/ngs>