Long-reads DNA Sequencing
Sample preparation and Shipping Guidelines

Contents

SERVICE CONDITIONS

Please read carefully!

The samples must meet the quality and quantity criteria and the shipping conditions, as indicated in the "Sample Requirements" and "Shipping" sections below. In case such specifications are not available the Customer shall enquire before sending any material. If storing and shipping conditions or sample specifications do not meet the required standards, IGA Technology Services may ask for an additional processing fee and the standard turnaround time might be delayed. Please note that the experimental setup and processing will be based on the information reported in the Sample Spreadsheet (**see Documents/Guidelines section in https://igatechnology.com/)**. The first checkpoint of the workflow will be performed on the provided DNA. In the case of inconsistencies between values declared in the Sample Spreadsheet and observed measurements, the customer will be notified, and library preparation will be performed at the customer's request and full service will be charged. IGA Technology Services will not be responsible for any lack of results or inadequate quality and quantity of sequencing data.

If some samples within a batch fail the library preparation step or has poor sequencing yield, while others succeed, the failure is deemed to be caused by sample properties, *i.e.* a presence of impurities of contaminants in template DNA, and IGA Technology Services is not obliged to repeat the experiment. A second round of preparation will be carried out to recover them at the customer's request. Minor changes to the protocol might be applied to overcome the issues that hinder library preparation and/or sequencing. After the second round of preparation, samples with low yields can be loaded on the sequencer at the customer's request and full service will be charged, otherwise, only the library preparation will be charged for such samples.

Extra processing fees

Extra processing fee can be applied in the following cases:

- Extra purification of DNA
- In-process QC

Please enquire for more information.

Contacts

All requests for information about the service must only be sent via email (long-read@igatechnology.com) and will be dealt with within a maximum of two working days from receipt.

In case problems arise during the sample processing, the Customer will be contacted directly to agree on possible solutions. Notifications will be sent to the contact person indicated in the Sample Spreadsheet at the sample reception and delivery.

For sample return and data storage and delivery refer to general Terms and Conditions.

SAMPLE REQUIREMENTS

Pseudonymization.

Please refer to general Terms and Conditions.

If human samples are provided in the form of tissue or body fluid, please fill out the* Human samples clearance *form* *and return a signed copy.

DNA extraction

IGA Tech offers nucleic acid extraction services from plants, soil, and stool. We can set up a dedicated extraction workflow for your specific substrate. Please enquire.

DNA specifications for standard libraries

- Diluent: water or 10mM Tris-HCl pH 8.5
- Concentration: >20ng/uL (by fluorimetry)

Keep in mind that absorbance-based methods (*e.g.,* Nanodrop) might largely **overestimate** the DNA quantity. The A260:A280 and A260:A230 ratios for DNA samples should be > 1.8. The use of DNA with lower ratios may result in low amplification yield.

- Minimum volume: 100uL

DNA specifications for ultralong libraries

- Extraction should be performed with methods adequate to obtain high molecular weight DNA, such as Qiagen® Genomic Tips or NEB Monarch HMW DNA Extraction
- Diluent: water or 10mM Tris-HCl pH 8.5
- Concentration: >100ng/uL (by fluorimetry)
- Minimum volume: 300uL

DNA specifications for pooled libraries

- Diluent: water or 10mM Tris-HCl pH 8.5
- Concentration: >40ng/uL or >100ng/uL (if using ≤4 barcodes) (by fluorimetry)
- Minimum volume: 20uL

Obligatory! Indicate in the Sample sheet of the Sample Spreadsheet:

- Putative genome size for WGS experiments

Amplicon specifications

- Diluent: water or 10mM Tris-HCl pH 8.5

- Concentration range:>20 fmol/uL (>13ng/uL per 1 kb amplicon) per sample to be barcoded (by fluorimetry)
- Minimum volume: 25uL

Obligatory! Indicate in the Sample sheet of the Sample Spreadsheet:

- Expected amplicon length for amplicon sequencing experiments

Library specification

In case the Customer is sending libraries or library pools for direct sequencing, please follow the Custom libraries Illumina or Custom libraries Element Bioscience sample preparation guidelines and shipping.

SHIPPING

For batches of <=24 samples, 1.5 mL or 2 mL tubes can be accepted. They must be sealed with parafilm. The tubes must have on the vial top, a clear and permanent sign (or a thin label) with a **progressive number** corresponding to information specified in the Sample Spreadsheet.
For batches of >24 samples, samples are only accepted in 96-well plate, sealed with adhesive/heat-sealed aluminum foil or multiwell strip caps. Each plate must be labeled with a plate identifier indicated on the Sample Spreadsheet.

IMPORTANT!!! 0,5 mL and 0.2 mL tubes as well as strips are not accepted!

For more details, please follow "Shipping and Packaging Guidelines" PDF file available at https://igatechnology.com/igatech/documents/

It is **MANDATORY to send us the compiled Sample Spreadsheet**, both with the shipped parcel and via e-mail. To properly track and safeguard your samples, send us the Tracking Number via e-mail (see Contacts).

Shipping Address:

IGA Technology Services srl
via Jacopo Linussio 51
33100 Udine Z.I.U.
Italy