

Sample Submission

Deep Sequencing Core Facility

June 28, 2024

Library Type	Material	Amount Required	Concentration	Quality
gDNA	DNA	1 µg	min 100 ng /µL	260/280
mRNAseq	Total RNA / mRNA	1 µg (total RNA)	min 50 ng /µL	RIN ≥ 7
ChIPseq	IP	10 ng	1 ng /µL	Fragments 200 – 500 bp
miRNA/smRNA	Total RNA	1 µg	100 ng /µL	RIN ≥ 7
Amplicon	PCR	20 ng	1 ng /µL	Fragments 200 – 500 bp
User Prepared Library	Finished Library	5-10 µL	min 2 ng/µL	Fragments smaller than 700 bp (defined peak)

1 Important Points on Submission

- All samples should be registered in iLabs before bringing them to the facility (hmls.corefacilities.org)
- Each sample should be submitted in a 1.5 ml low bind tube (eg Eppendorf)
- Please e-mail the facility to organise a drop-off time for your samples
- DNA samples need to be submitted with a gel image showing that they are intact and free from RNA contamination
- RNA samples need to be DNase treated to remove gDNA
- User submitted libraries need to have a supporting BioAnalyzer trace where the fragment size can be determined clearly

2 Quality Control

- All samples submitted for library preparation will be measured using the Qubit fluorometer from Invitrogen to accurately determine its concentration
- RNA samples will additionally be run on the Agilent BioAnalyzer (when Total RNA is provided), and where appropriate only samples with a RIN higher than 7 will be accepted
- RNA samples submitted as mRNA need to have supporting BioAnalyzer trace, and the mRNA submitted should be from an equivalent quantity of Total RNA noted above
- ChIP samples will be run on the Agilent Bioanalyzer to determine their size range
- Where necessary, gDNA samples will be run on the Tape Station to determine their integrity
- If samples fail to meet incoming quality checks they will be rejected with a given reason

3 Important Notes

1. The Deep Sequencing Unit reserves the right to terminate sample preparation at any stage if it is thought the material/sample is in some way compromised. The user will always be informed as to any problems relating to their sample and possible solutions where applicable.
2. The unit does not have the ability to store samples or their respective libraries indefinitely. It is up to the user to collect any remaining sample material, or their respective libraries after the sequencing data has been released, or in the case of rejection/failure after notification is given. Storage will be a maximum of two months.
3. Only data that is deemed of suitable quality by the unit based on their internal control will be released.
4. The Deep Sequencing Unit has limited data storage capabilities. All sequencing data will be deleted two months after release date.
5. Data is provided in FASTQ format only.
6. NGS consists of to parts, library preparation and sequencing. Each part has their own price depending on preparation type and sequencing mode, these will be billed accordingly.