

Sample Submission

Library Type	Material	Amount Required	Concentration
gDNA	DNA	5-10 µg	min 500 ng /µl
mRNAseq	Total RNA / mRNA	5-10 µg / equivalent	min 500 ng/µl
ChIPseq	IP	10 ng	min 0,3 ng/µl
Mate Pair	DNA	10 µg	Min 500 ng/µl
User Prepared Library	Finished Library	5-10 µl	min 2 ng /µl

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 ran 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, (max volume 16 µl).
- RNA samples will undergo mRNA selection by means of poly A selection with oligo d(T) coated magnetic beads (standard Illumina protocol). If other protocols are wishes (eg RiboMinus by Invitrogen), this for the time being is the responsibility of the user.
- DNA samples need to be submitted with a gel image showing that they are intact, and free from RNA contamination. This is extremely important for samples submitted for Mate Pair library production.
- Samples submitted for ChIPseq or MeDIPseq need to have the bulk their fragments in the 200 bp range, due to size selection. A supporting gel image of the Input material is required on submission.
- User submitted libraries need to have a supporting BioAnalyzer trace where the fragment size can be determined clearly.

-- If samples fail to meet incoming quality checks they will be rejected with a given reason --

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.