When submitting samples, please follow these simple guidelines:

1) Bulk samples

Always make sure you have got the best possible quality of your RNA or DNA - to get good libraries, you need good starting material!

As part of our service, we will do a QC wherever possible, so don't worry if you have not got access to Qubit or tapestation.

1a) RNA samples

RNA can be extracted using any commercially available RNA extraction kit. For any RNA library prep, we require clean, high-quality RNA in RNase free water. RNA can be extracted using any commercially available RNA extraction kit. It is necessary to include a DNAse treatment to eliminate any DNA background signal in your data We will quantify and run samples on bioanalyzer/tapestation to check quality.

Please make the labelling easy and understandable!

We have different RNA protocols, which are aimed at different input amounts. In general, we would like to have as much RNA as you can isolate in the lowest possible volume. The type of protocol we choose for your samples will depend on the outcome of your sample's QC. However, we are constrained by the input amounts of the different protocol:

Samples with total RNA amounts of 50ng to 1000ng can be processed with the standard kit (stranded), and can be either depleted of ribosomal RNA, or selected for PolyA. (PolyA is often chosen when transcript counting and cost limitation are what is required. Ribosomal depletion allows for non-coding RNA to be present and has less 3' bias, but is more costly.) For these two methods we require the samples to be in volumes of 10ul (rRNA depletion) or up to 50ul (PolyA).

Low input samples from 250pg to 10ng will be processed with a low input kit (stranded), which has proprietary ribosomal depletion built into the protocol. The required input volume for this is 8ul, the sample you supply will need to be in no more than 12ul volume. This kit will also be used for degraded samples.

We also have a single cell kit available for very low input/single cell samples (below 500pg). This is non-stranded, and requires good quality RNA.

ERCC spike-ins are also an option, if you need them. Due to the requirement of matching the amount of spike-ins to the amount of input RNA, the spike-ins will be increasingly more error-prone, the lower the input amount of RNA.

1b) DNA samples

Genomic DNA should be free of RNA, and you should check the integrity and size before submitting. If samples have been exposed to phenol or other organic solvents, they should be run through a cleanup column prior to submission to avoid contaminants that may inhibit the activities of enzymes used in subsequent steps. Please make the labelling easy and understandable!

2) Single cell samples

Please arrange a booking with us in advance. We take samples from 9 to 4 every day, and we need 1.5h per booking.

If your experiment is not already submitted in our online submission form, please can you do this, so we have all necessary information there. (https://genomics-sci.atlassian.net/servicedesk/customer/portal/1) It makes sense to submit here for all the samples that will be sequenced together. I understand that this is hard to predict, but we can communicate via this portal to organise things in more detail.

We are on the ground floor, in the single cell room just behind reception. If you don't have access, there is a doorbell that you can ring.

Please email us 30 min before you are handing over your samples, so that we can defrost the reagents in time. If you become aware that your timings may be off, please let us know as soon as possible so we can fit you around other bookings, if necessary.

We will receive your cells, which you will have accurately counted and resuspended in the required volume (we will supply submission guidelines specific top the protocol you use). We do not perform cell counting or a viability check in our lab, so we rely on you to be confident about the quality and quantity of the cells you give us. As speed is critical in 10x Genomics experiments we load cells into the chip immediately after receiving them from you.

We will process your samples and keep you updated about their progress.

3) Spatial transcriptomics samples

Tissue sectioning, fixation, staining, and imaging are typically performed at the Histology core facility or by the research groups themselves. If you are planning to perform any of these steps yourself, contact us both in advance since there are strict guidelines for the spatial transcriptomics workflow.

3a) Visium HD FFPE
Needs to be made

3b) Visium HD 3'
Needs to be made

3c) Xenium
needs to be made

4) Logging your project into the system

We require each project to be submitted into the online submission system:

https://genomics-sci.atlassian.net/servicedesk/customer/portal/1

Please create your own account for this system, none of your university affiliations are registered.

We will require information about you, your group, assurance that you have the correct GM and biosafety assessment, your grant code, and of course details about your project. Please see our submission help file for specific questions about these points!

Once submitted, we can arrange a handover for your samples.