How to fill in the sample submission form

Group

Name of your PI

Grant code

For internal projects, it makes recharges easier if we know the grant code.

Description

Put anything we might need to know about your project!

GM and Biosafety risk assessment number

We are asking for this to ensure that your project has fulfilled all the correct paperwork requirements prior to us working with your samples.

Have you got low input material?

You might not have quantified your material, then just put unsure. If you have less than 100ng of total RNA per sample we might have to consider the low input protocols. If you submit ChIP DNA, anything under 3ng qualifies as low input.

Depletion of RNA

We offer either PolyA selection or ribosomal depletion for standard RNA protocols. PolyA is cheaper and will make libraries from anything with a PolyA tail. rRNA depletion is more costly, and RNA species such as long noncoding RNAs remain in your libraries.

ERCC spike-ins required

http://tools.thermofisher.com/content/sfs/manuals/cms_086340.pdf

Will you require sequencing through us?

We can submit your samples to the CIGC sequencing core for sequencing. Alternatively, you can receive the pooled libraries back from us should you prefer to sequence them elsewhere.

Cost Code for sequencing

If you sequence through the CRUK Genomics Core (our default), then we will need you to have set up an account with them in advance, which will deliver a specific cost code. Without this, we cannot submit your samples into the CRUK LIMS system.

Run type for sequencing

The NovaseqX has 3 flowcell types (1.5B; 10B; 25B). All Novaseq runs are paired end, and the read length can be 2x50, 2x100, or 2x150.

How many lanes on the Novaseq

Work out how many reads per sample/cell you require. Then see below the approximate output of the different flowcell lanes in million reads. The Novaseq flowcells have 8 lanes (or 2 lanes for 1.5B). The Genomics core at CRUK will queue submissions until they reach a full lane. This may occasionally result in a small wait time.

lane type	up to mio reads per lane
SLX_NovaSeqX_1.5B	750
SLX_NovaSeqX_10B	1250
SLX_NovaSeqX_25B	3100

If you are submitting human samples, have you got ethical consent?

We are asking for this to ensure that your project has fulfilled all the correct paperwork requirements prior to us working with your samples.

How was the sample quantified

We will do a QC with Qubit and tapestation where possible. If you have already quantified your sample, please provide your data as a reference point.

What containment level is required

For single cell samples and fresh frozen tissue, we need to know in advance whether containment level 2 is required for sample processing!