

# Details about 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](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.

### Run type for sequencing

The HiSeq4000 has either paired end 150bp (PE150) or single end 50bp (SE50) run types. If you require any different you might have to fill all 8 lanes of a flowcell.

The Novaseq has 4 flowcell types (SP, S1, S2, S4). All Novaseq runs are paired end, and the read length can be 2x50, 2x100, or 2x150.

### How many lanes on the HiSeq 4000 or Novaseq

Work out how many reads per sample you require. Then see below the approximate output of the different flowcell lanes in million reads. The Novaseq flowcells have 2 lanes (or 4 lanes for S4); if you chose only one we will need to partner you up with another user. This may result in a small wait time.

flow cell	million reads per lane
HiSeq4000	350
NovaSeq6000_SP	350
NovaSeq6000_S1	800
NovaSeq6000_S2	2050
NovaSeq6000_S4	2500

### 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.