Guidelines for Completion of the Sample Submission Form

Once you have returned a signed copy of the quote and a PO please fill in a submission form and email it to your project manager at least two days before you deliver or ship your samples.

⚠️ To ensure the safety of your samples, please do not send them to us prior to receiving notification by email from your project manager that they have been logged into our LIMS system.

A copy of the latest sample submission form can be found on our website http://www.well.ox.ac.uk/ogc/documents

To ensure there are no delays in initiating your project, please confirm that all the requested information is provided on the submission excel form.

Required information: sample Name, reference genome, sample concentration (except for the occasional sample where quantification is impossible), volume, and pooling (if applicable). Please extend the table as appropriate and ensure that there are no duplicate sample names.

Please provide a container ID eg Plate #1, 2 ... your name and the quote number, which should then be written on the plate. The layout of the plate should maintain the order shown for the Sample/Well Location with no gaps in between (Example: 10 samples should go in wells A1-H1 and A2-B2).

In ‘Pooling’ please specify multiplex groupings by mp1 for all samples in the first multiplex, mp2 etc.

In ‘additional comments’ please note if you want your samples returned and if there is a priority order (1, 2, 3 etc) within the project, we will try to accommodate this where possible. Also for ChIP-Seq, please note the fold-enrichment between the ChIP and the control samples (as determined by qPCR). If this is not possible, please state that this is unknown.

Please select your reference genome of choice from the dropdown list, see tab 2 ‘reference genomes’ column A (column B provides a further description). If it is not in our current list, please enter "other" and provide a link to the reference genome that you wish to use.
Appendix 1

WTCHG High Throughput Sequencing Sample Submission Form

1. Forms should be filled in and returned by email for electronic sample submission.
2. Please order the samples as appropriate.
3. Ensure that all sample numbers are unique.
4. For each submission, please provide a container ID and maintain the order shown for the row ID and column ID with no gaps in between. Container Name and File Location are not necessary for tube submissions.
5. In passing, please exactly match samples by row 1 for all samples in the first row, and so forth. Note in ‘additional comments’ if you exceed your samples returned.
6. For CHIP-seq, where it has been possible to determine the fold change between CHIP and controls by IPCL, please add these fold changes in ‘additional comments’. If this has not been possible, please state that this is unknown.
7. Reference genome for human genome or human exome sequencing and recommend selecting hg19/hg38.
8. Reference genome. For human RNA sequencing, we recommend selecting GRCh37/GRCh38-hg19/hg38.
9. Reference genome. If your reference genome of choice is not on the dropdown list, please select it, please enter ‘other’ and provide a link to the reference genome that you wish to use. There is a transcription list on the other sheet.

These references, must be referred to by the user. & go to our n by name. Please discuss this with your project manager if you unsure which is most suitable for your project.

<table>
<thead>
<tr>
<th>Control Name</th>
<th>Sample Type</th>
<th>Sample Code</th>
<th>Sample Notes</th>
<th>Status</th>
<th>Source</th>
<th>Sample ID</th>
<th>Sample ID</th>
<th>Sample ID</th>
<th>Sample ID</th>
<th>Sample ID</th>
<th>Sample ID</th>
</tr>
</thead>
<tbody>
<tr>
<td>A1</td>
<td>E3</td>
<td>C1</td>
<td>D1</td>
<td>E1</td>
<td>F1</td>
<td>G1</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>B1</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>