UNIVERSITY OF LIVERPOOL

Centre for Genomic Research

# Submission of samples for quality control services

The CGR cannot guarantee good results from samples that do not meet the requirements set out in this document.

## Maximising sample quality

To maximise quality, we recommend that your nucleic acid samples:

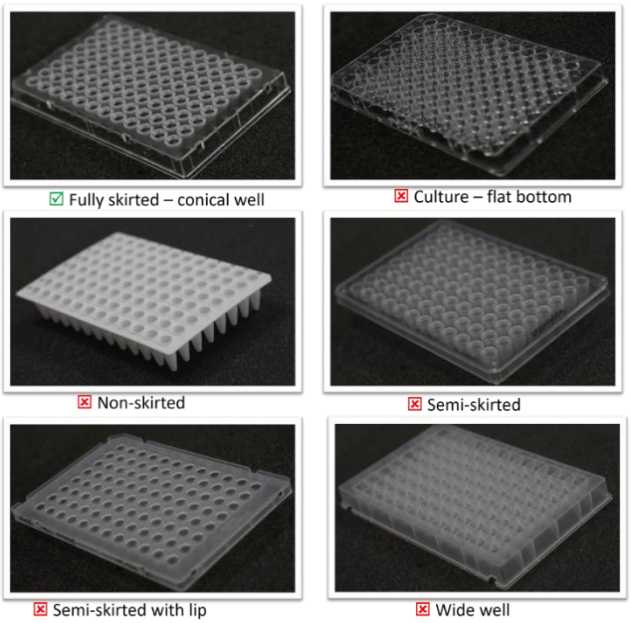
- are submitted in nuclease-free water, TE buffer or low-TE buffer. Other sample buffers have not been tested. If buffer exchange is required, this will incur additional costs.
- have been stored at 4°C (short term) or -20/-80°C (long term) and have not undergone multiple freeze-thaw cycles, which can affect quality.
- have not been exposed to high temperatures or extremes of pH.
- have a 260:280 and a 260:230 ratio of ≥ 1.8.
- do not contain insoluble material.
- are free from contamination, including contamination with other nucleic acids.
- have not been exposed to intercalating fluorescent dyes or ultraviolet radiation.
- do not contain denaturants (such as guanidinium salts or phenol), divalent metal cations (such as Mg2+) or detergents (such as SDS or Triton-X100).
- do not contain ethanol.

## Sample submission requirements

The concentrations required will depend on the type of platform being used and material being assessed. The table below outlines the input requirements for each application.

| Material | Platform | Concentration | Volume per sample |
|---|---|---|---|
| DNA | Nanodrop | N/A (unlikely to be known in advance) | ≥10 µl |
| | Qubit | N/A (unlikely to be known in advance) | ≥10 µl |
| | Fragment analyzer | 1 ng/µl for genomic DNA<br>2 ng/µl for fragmented DNA | ≥10 µl |
| RNA | Nanodrop | N/A (unlikely to be known in advance) | ≥10 µl |
| | Qubit | N/A (unlikely to be known in advance) | ≥10 µl |
| | Fragment analyzer | 5 ng/µl | ≥10 µl |
| | Bioanalyzer | 5 ng/µl | ≥10 µl |

If you are unable to meet the requirements set out in this document, please contact us at CGR_Lab@liverpool.ac.uk and we will be happy to offer further advice. Please note that we cannot QC samples with concentrations below 0.5 ng/µl or a total nucleic acid quantity of below 5 ng. We will charge for any work carried out on such samples.




For projects that involve ≥24 samples, we require samples to be submitted in a 96-well, fully-skirted plate. Please arrange your samples down the plate in a column-wise fashion, leaving 2 empty wells per plate so that we can add internal controls, as shown in the diagram below.

Sample position is very important for our workflows. If the submitted samples are not arranged as in the diagram below, you will be charged an additional £50 per plate to cover the cost of re-ordering the samples. It may also take longer for us to complete your project.

| | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| A | Sample 1 | Sample 9 | Sample 17 | Sample 25 | Sample 33 | Sample 41 | Sample 49 | Sample 57 | Sample 65 | Sample 73 | Sample 81 | Sample 89 |
| B | Sample 2 | Sample 10 | Sample 18 | Sample 26 | Sample 34 | Sample 42 | Sample 50 | Sample 58 | Sample 66 | Sample 74 | Sample 82 | Sample 90 |
| C | Sample 3 | Sample 11 | Sample 19 | Sample 27 | Sample 35 | Sample 43 | Sample 51 | Sample 59 | Sample 67 | Sample 75 | Sample 83 | Sample 91 |
| D | Sample 4 | Sample 12 | Sample 20 | Sample 28 | Sample 36 | Sample 44 | Sample 52 | Sample 60 | Sample 68 | Sample 76 | Sample 84 | Sample 92 |
| E | Sample 5 | Sample 13 | Sample 21 | Sample 29 | Sample 37 | Sample 45 | Sample 53 | Sample 61 | Sample 69 | Sample 77 | Sample 85 | Sample 93 |
| F | Sample 6 | Sample 14 | Sample 22 | Sample 30 | Sample 38 | Sample 46 | Sample 54 | Sample 62 | Sample 70 | Sample 78 | Sample 86 | Sample 94 |
| G | Sample 7 | Sample 15 | Sample 23 | Sample 31 | Sample 39 | Sample 47 | Sample 55 | Sample 63 | Sample 71 | Sample 79 | Sample 87 | Empty |
| H | Sample 8 | Sample 16 | Sample 24 | Sample 32 | Sample 40 | Sample 48 | Sample 56 | Sample 64 | Sample 72 | Sample 80 | Sample 88 | Empty |

Please pay careful attention to the sealing of 96-well plates prior to shipping: unfortunately, we do occasionally receive poorly sealed plates in which samples have leaked from their wells, leading to cross contamination.

For projects involving <24 samples, submission in a 96-well plate is still recommended but we will also accept tubes. We require that samples submitted in tubes are clearly labelled in numerical order for ease of sample identification. Please underline any numbers that could be misread upside-down (e.g. 6/9, 16/91).

If you have any further questions, please contact us at CGR_Lab@liverpool.ac.uk .