

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:

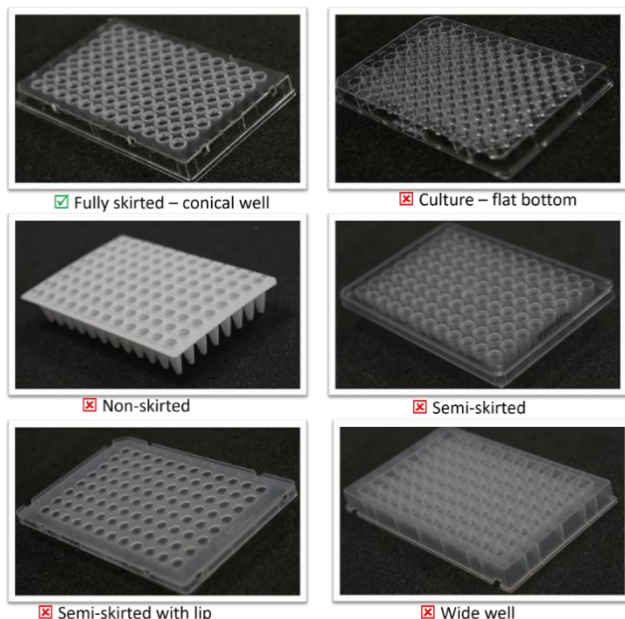
- are submitted in nuclease-free water, TE buffer or low-TE buffer. Other sample buffers have not been tested. If buffer exchange is required, this will incur additional costs.
- have been stored at 4°C (short term) or -20/-80°C (long term) and have not undergone multiple freeze-thaw cycles, which can 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 Mg^{2+}) 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)	$\geq 10 \mu l$
	Qubit	N/A (unlikely to be known in advance)	$\geq 10 \mu l$
	Fragment analyzer	1 ng/ μl for genomic DNA 2 ng/ μl for fragmented DNA	$\geq 10 \mu l$
RNA	Nanodrop	N/A (unlikely to be known in advance)	$\geq 10 \mu l$
	Qubit	N/A (unlikely to be known in advance)	$\geq 10 \mu l$
	Fragment analyzer	5 ng/ μl	$\geq 10 \mu l$
	Bioanalyzer	5 ng/ μl	$\geq 10 \mu l$

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.