

Intended Result	Your Report	Your Score
Specimen 8103 Median concentration 2.87 log copies/mL	3.08 log copies/mL	
Specimen 8104 Median concentration 2.86 log copies/mL	2.98 log copies/mL	
Average of the median differences in conc. between specimens 8103 and 8104 is 0.02 log copies/mL	Difference in conc. is 0.10 log copies/mL	2

Cumulative score information

Total number of specimens sent to you for **UK NEQAS for HIV1 RNA quantification** over the last 3 distributions is 6
For these distributions specimen numbers 7714 7916 8103 have been analysed and scored.

Number of reports analysed 3
Number of specimens reported as not examined (not scored) 0
Number of specimens received too late for analysis (not scored) 0
Number of specimens for which no result was returned (not scored) (figure displayed is based upon the result for the first specimen) 0
Your cumulative score for these specimens was 6 out of a possible total of 6

The mean score calculated from the reports returned by **UK** laboratories was 5.72 (with a standard error of 1.12)

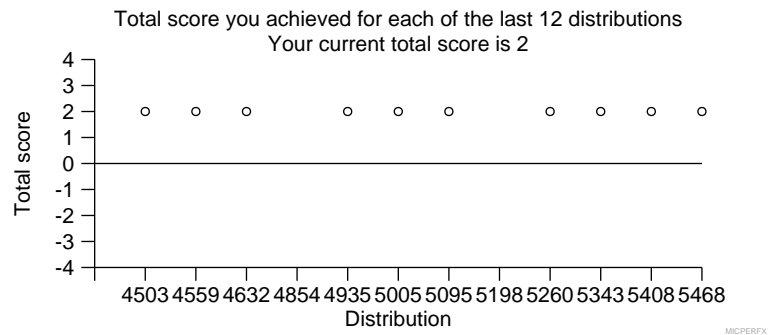
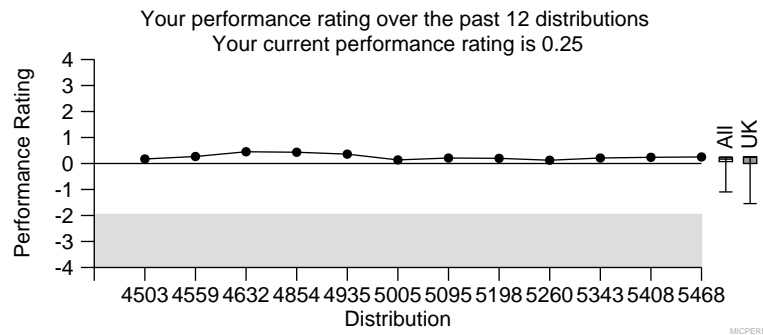
Performance rating

Your performance rating for **UK NEQAS for HIV1 RNA quantification** (i.e. the number of standard errors by which your cumulative score lies above or below the mean) for **UK** laboratories is 0.25.

A performance rating of more than 1.96 standard errors below the mean indicates possible poor performance.

Please note your performance rating may alter if other participants' results are amended.

No score penalty is incurred for non return of reports. However non return of results may be used as a measure of poor performance.



Comments:

A total of 189 sets of specimens were distributed for testing with 176 participants responding within the specified period.

The overall performance for this distribution was excellent with 96.5% of participants reporting results within 0.30 log copies/mL of the average of the median difference in concentration from all received results.

Outlying results:

Four participants reported a result >0.3 to 0.5 log copies/mL of the average of the median difference in concentration. Methods used: Nuclisens Easy-Q v2 n=1; Cepheid GeneXpert n=1; Hologic Aptima n=1; Roche cobas 6800/8800 n=1. One participant submitted an incorrect result for one specimen (Cepheid GeneXpert) and one participant submitted incorrect results for both specimens (method not specified).

Please see comments page 3 for general comments

In the specimen results tables on page 2, a maximum of 12 kits results are displayed: these include the most commonly used methods and the method(s) used in your laboratory. The figures in the specimen results tables and those in the difference table may differ:

- (1) due to the exclusion of kits not providing valid quantitative results for both specimens resulting in a lower number of data sets or
- (2) due to participants using more than one kit or providing two sets of results resulting in higher numbers of data sets in the individual specimen results tables.

Turn around time: The time taken to report your results was 0-days. This information is provided for your own use and does not form part of your performance assessment.

Acknowledgements: We thank colleagues from UKHSA Bristol and UKHSA Manchester for their kind assistance with pre-distribution tests.

Enquiries: Pre-distribution test results are available should you experience a technical failure and wish to discuss the results. Written enquiries about this distribution should be addressed to Dr Sanjiv Rughooputh at organiser@ukneqasmicro.org.uk.

For repeat specimens in case of an EQA failure, please request using the web form at <https://ukneqasmicro.org.uk/participant-info/order-repeat-specimens/>.

UK NEQAS for Microbiology Scientific day: Friday 24 November 2023. Follow link for details: <https://ukneqasmicro.org.uk/annualscientificmeeting/>

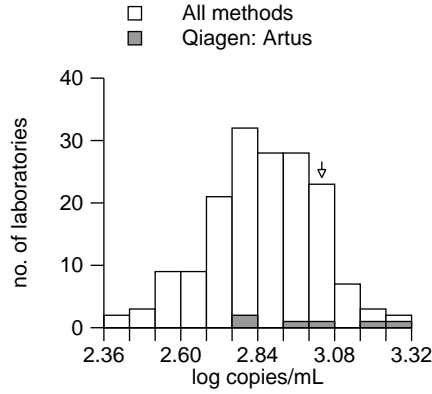
Report authorised by: Dr Sanjiv Rughooputh, Scheme Organiser.



Two specimens of freeze dried plasma were dispatched with a request for the quantification of HIV-1 RNA. Both specimens were derived from a single HIV-1 (subtype B) RNA positive plasma donation diluted 1:190 in negative human plasma and freeze-dried.

Specimen : 8103

	n (UK)	range	median	5%-95%
All methods	207 (68)	1.72-3.31	2.87	2.53-3.11
Abbott Real-Time	8 (2)	2.70-3.03	2.87	2.71-3.02
Abbott: Alinity	6 (1)	2.72-3.07	2.92	2.75-3.06
Abbott: Alinity m	20 (7)	2.74-3.13	2.96	2.79-3.13
Cepheid: GeneXpert	27 (11)	2.45-2.98	2.84	2.59-2.95
Cobas 6800/8800	46 (13)	2.33-3.08	2.75	2.53-3.00
Cobas Amplip TaqMan v2	7	2.89-3.25	3.07	2.93-3.20
Hologic: Aptima	15 (7)	2.59-3.15	2.94	2.59-3.12
Other	10 (3)	2.71-3.19	2.79	2.73-3.12
Qiagen: Artus	7 (5)	2.17-3.31	2.94	2.35-3.28
Roche: Cobas 4800	21 (3)	2.38-3.12	2.89	2.67-3.11
Roche: Cobas 5800	5 (1)	2.72-3.22	2.95	2.73-3.17
Unspecified	5 (1)	2.81-3.07	2.92	2.83-3.05



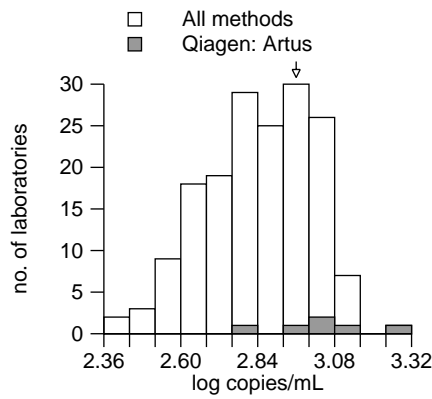
Your result :
3.08 log copies/mL

Method median concentration :
2.94 log copies/mL

Median concentration :
2.87 log copies/mL

Specimen : 8104

	n (UK)	range	median	5%-95%
All methods	208 (68)	1.81-3.27	2.86	2.56-3.09
Abbott Real-Time	8 (2)	2.66-3.16	2.90	2.67-3.11
Abbott: Alinity	6 (1)	2.63-3.10	2.93	2.68-3.08
Abbott: Alinity m	20 (7)	2.72-3.14	2.98	2.80-3.12
Cepheid: GeneXpert	28 (11)	2.65-2.97	2.82	2.67-2.95
Cobas 6800/8800	46 (13)	2.40-3.06	2.72	2.53-3.02
Cobas Amplip TaqMan v2	7	2.76-3.12	2.98	2.80-3.10
Hologic: Aptima	15 (7)	2.63-3.12	2.93	2.72-3.09
Other	10 (3)	2.66-3.03	2.82	2.67-3.03
Qiagen: Artus	7 (5)	2.24-3.27	3.02	2.40-3.22
Roche: Cobas 4800	20 (3)	2.56-3.08	2.86	2.64-3.06
Roche: Cobas 5800	5 (1)	2.57-3.01	2.77	2.60-2.97
Unspecified	5 (1)	2.68-3.06	2.78	2.68-3.05



Your result :
2.98 log copies/mL

Method median concentration :
3.02 log copies/mL

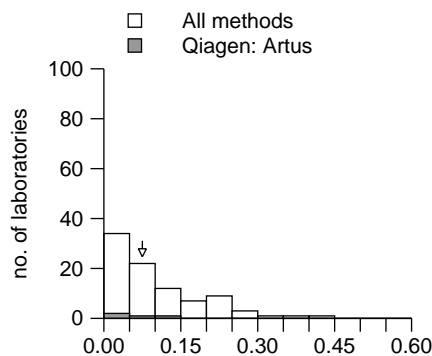
Median concentration :
2.86 log copies/mL

Intended result : -0.28 to 0.32 log copies/mL

(average median of the reported differences in concentration between specimen 8103 and 8104 +/- 0.3 log copies/mL, with an uncertainty of 0.013)

Difference in concentration between specimen 8103 and 8104 expressed in log copies/mL :

	n (UK)	range	av. median	5%-95%
All methods	171 (55)	-0.40-0.43	0.02	-0.22-0.23
Abbott Real-Time	8 (2)	-0.14-0.12	-0.01	-0.11-0.09
Abbott: Alinity	6 (1)	-0.06-0.10	-0.00	-0.06-0.09
Abbott: Alinity m	19 (7)	-0.16-0.23	-0.04	-0.14-0.16
Cepheid: GeneXpert	25 (11)	-0.32-0.21	0.01	-0.24-0.16
Cobas 6800/8800	42 (11)	-0.24-0.43	-0.01	-0.23-0.21
Cobas Amplip TaqMan v2	6	-0.04-0.31	0.06	-0.04-0.27
Hologic: Aptima	13 (7)	-0.23-0.40	-0.02	-0.19-0.24
NeuMoDx 96	4	-0.19--0.08	-0.10	-0.17--0.08
Other	6 (3)	-0.08-0.15	0.05	-0.07-0.13
Qiagen: Artus	7 (5)	-0.25-0.13	0.03	-0.22-0.12
Roche: Cobas 4800	20 (3)	-0.26-0.29	0.05	-0.21-0.29
Roche: Cobas 5800	5 (1)	-0.01-0.21	0.18	0.02-0.21



Your result :
Difference in conc. is 0.10 log copies/mL

Your score : 2

Overall results	UK	All	Score
Median			
+/- 0.3 log	54	167	2
+/- >0.3 to 0.5 log	1	4	1
+/- >0.5 to 0.75 log	0	0	0
+/- >0.75 log	0	0	-1
Partial result	0	1	1
Two incorrect	0	1	-2
Total	55	173	
%Correct	98.2	96.5	



Comments on distribution 5468

The overall performance in this distribution was excellent with 96.5% of participants reporting within +/- 0.3 Log difference and scoring a maximum of 2. This is a slight decline of 0.1% on previous distribution 5408, where the overall performance 96.5%

One hundred and eighty nine sets of specimens were dispatched with 176 participants returning results. This represents a return rate of 93.1%, a decline of 2.6 % to the previous distribution, where the return rate was 95.7%.

Participants who did not obtain the intended results are requested to investigate and report the plausible root cause by completing an incident review form (IRF) online within 30 days of this report being published. Non return of results without a valid reason is considered as poor performance and should also be reported in a similar manner. IRFs are taken into considerations when poor performance analysis is carried out for the National Quality Assurance Advisory Panel (NQAAP). IRFs can be completed on the following link: <https://ukneqasmicro.org.uk/incident-review-form>

End of report

