


<b>Individual Report</b>		<b>QCMD 2018 Human Immunodeficiency Virus RNA EQA Programme</b>			 <small>Quality Control for Molecular Diagnostics</small>		
<b>Catalogue Code:</b> QAV994108	<b>Ref Code:</b> HIVRNA18	<b>Challenge:</b> C1	<b>Analysis Type:</b> Qualitative and Quantitative	<b>Dataset:</b>	<b>Report UID:</b>	<b>Laboratory</b>	

### Intended Results / Panel Composition

Sample Code	Sample Content	Matrix	Sample Relationships [1]	Detection Frequency [2]	Sample Status [3]	Consensus (Copies/ml) [4]		Range [5]
						(Log <sub>10</sub> )	(n)	
HIVRNA18C1-01	HIV-1 Type C	Plasma		Frequently Detected	CORE	2.382	214	1.643 - 3.401
HIVRNA18C1-02	HIV-1 Type B	Plasma		Frequently Detected	CORE	3.727	218	3.179 - 5.911
HIVRNA18C1-03	HIV Negative Plasma	Plasma		Negative	CORE	N/A	N/A	N/A
HIVRNA18C1-04	HIV-1 Type AG	Plasma		Frequently Detected	CORE	2.915	221	1.875 - 5.504

[1] **Sample Relationships:** Indicates the relationships of the samples within this challenge. Dilution series are indicated by 'DS1' with each panel member in the dilution series represented by a number in order of titre, where DS1\_1 represents the highest titre within that dilution series. Further dilution series are indicated by 'DS2' 'DS3' etc. If one duplicate pair is present this is indicated by 'D1'. Further duplicate pairs are indicated by 'D2', 'D3' etc.

[2] **Detection Frequency:** To aid qualitative analysis each panel member is assigned a frequency of detection. This is based on the peer group consensus of all qualitative results returned from participants within the EQA challenge / distribution.

[3] **Sample Status:** EQA samples are defined as "CORE" or "EDUCATIONAL". Core proficiency samples are reviewed by the QCMD Scientific Expert(s). This is on the basis of scientific information, clinical relevance, current literature and, where appropriate, professional clinical guidelines. Participating laboratories are expected to report core proficiency samples correctly within the EQA challenge / distribution.

[4] **Consensus (Copies/ml):** Mean consensus (Log<sub>10</sub>) calculated from data returned by participants with outliers removed and number of quantitative results (n) returned for each panel member.

[5] **Range:** Maximum and minimum quantitative value (Copies/ml) reported by participants within this challenge without outliers removed.

*For further details please refer to the current participant manual.*

### Your Summary Results

<b>Units</b>	Copies/ml
<b>EQA Assessment Group [1]</b>	Abbott Real Time PCR
<b>Core Panel Detection (Qualitative) Score [2]</b>	N/A
<b>Core Panel Estimation (Quantitative) Score [3]</b>	0

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**Core Panel Members Results**

Sample Code	Unitage	EQA Assessment Group Consensus [4]	SD [5]	Quantitative Result		Qualitative Result		
				Your Result [6]	Estimation Score [7]	Percentage Correct (All) [8]	Your Result [9]	Detection Score [10]
HIVRNA18C1-01	Copies/ml	2.115	0.197	2.037	0	-	-	-
HIVRNA18C1-02	Copies/ml	3.660	0.160	3.623	0	-	-	-
HIVRNA18C1-03	Copies/ml	N/A	-	LOD/NR	N/A	-	-	-
HIVRNA18C1-04	Copies/ml	3.124	0.172	3.063	0	-	-	-

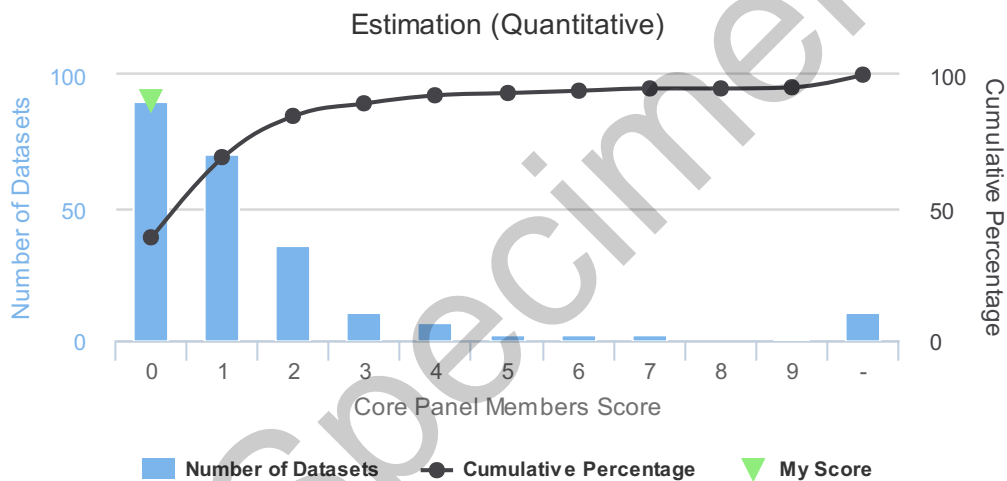
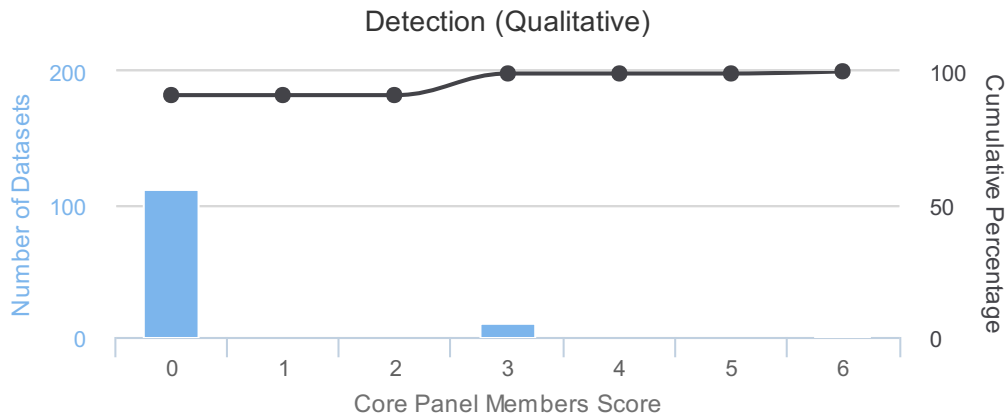
All quantitative values above expressed in Log<sub>10</sub> Copies/ml.

- [1] **EQA Assessment Group:** To aid data analysis, participant results are grouped according to the molecular amplification/detection method specified within their molecular workflow for this challenge / distribution. For further details refer to the *Additional Information: Individual Panel Member Analysis* section of this report.
- [2] **Core Panel Detection (Qualitative) Score:** An overall core panel detection score provided per challenge / distribution.
- [3] **Core Panel Estimation (Quantitative) Score:** An overall core panel estimation score provided per challenge / distribution.
- [4] **EQA Assessment Group Consensus:** The mean value for all results within your EQA assessment group.
- [5] **SD:** The standard deviation for results from your EQA assessment group.
- [6] **Your Quantitative Result:** The quantitative result you returned for each sample within this EQA challenge. LOD/NR (limit of detection or not reported).
- [7] **Estimation Score:** Your estimation (quantitative) scores are calculated based on your variation from the consensus for your EQA assessment group. With 0 (zero) scored if the quantitative value you reported is within one standard deviation (SD) from your EQA assessment group consensus, 1 (one) if your quantitative value is between one and two SDs, 2 (two) if your quantitative value is within two and three SDs and 3 (three) if your quantitative value is more than three SDs from the mean of your EQA assessment group.
- [8] **Percentage Correct (All):** Percentage of datasets reporting the correct qualitative results for each panel members.
- [9] **Your Qualitative Result:** The qualitative result you reported for each sample within this EQA challenge / distribution.
- [10] **Detection Score:** Your detection (qualitative) scores are based on the assigned detection frequency of each panel members, where 0 (zero) is "highly satisfactory" and 3 (three) is "highly unsatisfactory". Scores are provided for individual panel members.

**For further details please refer to the current participant manual.**


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### Core Panel Member Score Breakdown



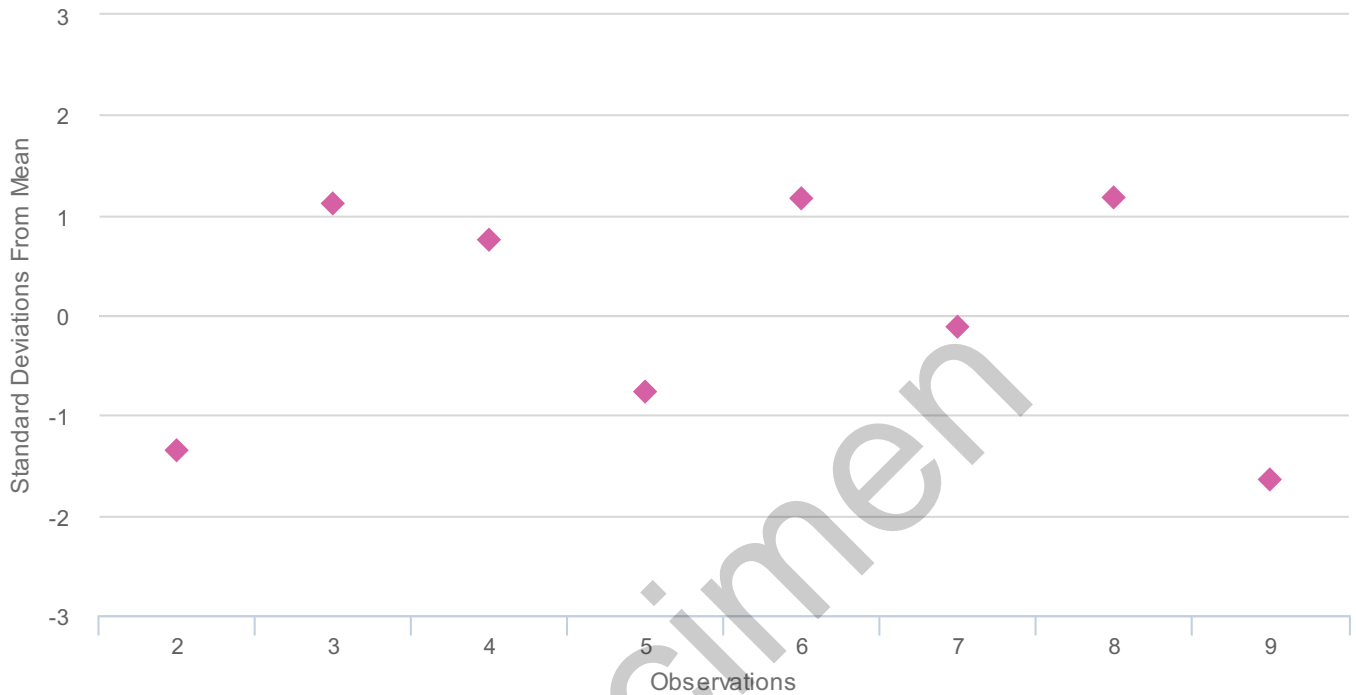
**Core Panel Member Score Breakdown - Detection:** This figure gives you a breakdown of the qualitative detection scores for all qualitative datasets returned within this EQA challenge / distribution independent of the EQA assessment group. Panel detection scores are generated from only those panel members that are defined as "CORE".

**Core Panel Member Score Breakdown - Estimation:** This figure gives you a breakdown of the quantitative estimation scores for all quantitative datasets returned within this EQA challenge / distribution independent of the EQA assessment group. Panel estimation scores are based on positive core panel members only. Those datasets that did not return quantitative values for all core samples are represented by '-'.  
**For further details please refer to the current participant manual.**

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## Duplicate Sample Performance Over Time

### HIV-1 Type B



#### Observation Details


2: HIVRNA15C3-02 - HIVRNA15C1-04: Your Variation -0.193 (Copies/ml): Overall Mean Variation 0.096: Overall SD 0.214.  
 3: HIVRNA16C1-02 - HIVRNA15C3-02: Your Variation 0.091 (Copies/ml): Overall Mean Variation -0.217: Overall SD 0.276.  
 4: HIVRNA16C1-04 - HIVRNA16C1-02: Your Variation 0.065 (Copies/ml): Overall Mean Variation -0.003: Overall SD 0.090.  
 5: HIVRNA16C3-04 - HIVRNA16C1-04: Your Variation -0.154 (Copies/ml): Overall Mean Variation 0.025: Overall SD 0.234.  
 6: HIVRNA17C1-02 - HIVRNA16C3-04: Your Variation 0.352 (Copies/ml): Overall Mean Variation 0.024: Overall SD 0.281.  
 7: HIVRNA17C1-04 - HIVRNA17C1-02: Your Variation -0.016 (Copies/ml): Overall Mean Variation -0.006: Overall SD 0.088.  
 8: HIVRNA17C3-04 - HIVRNA17C1-04: Your Variation 0.173 (Copies/ml): Overall Mean Variation -0.036: Overall SD 0.178.  
 9: HIVRNA18C1-02 - HIVRNA17C3-04: Your Variation -0.394 (Copies/ml): Overall Mean Variation -0.023: Overall SD 0.226.

QCMD monitors your laboratory's performance over time based on the reported quantitative variation between duplicate panel members within the EQA challenge and, where appropriate, across EQA challenges.

The mean variation and standard deviation are calculated from the quantitative variation reported by each participant between duplicate panel members in the same unit of measurement once outliers have been removed. (See 'Observation Details')



Previous and current observations are plotted on the chart as the number of standard deviations your variation was from the mean variation for all participants who submitted corresponding results in the same unitage.

Any reported variation greater than  $\pm 3$  SD will not be shown on the graph, but your variation value will be provided **in red** in the *Observation Details*. When "N/A" is displayed for an observation, either no valid quantitative results were provided or there was a change in reported unitage.

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## My Workflow Details

The details of the workflow used to submit your results for this challenge.

<b>Name</b>	HIVRNA (v3)
<b>Description</b>	
<b>Targets</b>	<b>V</b> human immunodeficiency virus
<b>Assays</b>	<ul style="list-style-type: none"> <li> <i>Extraction - Abbott - Abbott m2000sp</i> <ul style="list-style-type: none"> <li>• Commercial <ul style="list-style-type: none"> <li>◦ Kit Manufacturer: <i>Abbott</i></li> <li>◦ Kit Type: <i>Abbott m2000sp</i></li> </ul> </li> </ul> </li> <li> <i>Amplification - Abbott - Abbott m2000rt</i> <ul style="list-style-type: none"> <li>• Commercial <ul style="list-style-type: none"> <li>◦ Kit Manufacturer: <i>Abbott</i></li> <li>◦ Kit Type: <i>Abbott RealTime HIV-1</i></li> <li>◦ Kit Version: <i>Not Applicable</i></li> </ul> </li> </ul> </li> </ul>

## Further Programme Details

Number of Participants	259
Number of Countries	35
Number of Respondents	237
Number of Datasets Submitted	269
Quantitative Results Returned (All)	232 (86.2%)
- Quantitative Results Returned (IU/ml)	11 (4.7%)
- Quantitative Results Returned (Copies/ml)	221 (95.3%)
Qualitative Results Returned	123 (45.7%)


## EQA Programme Aims

To assess the proficiency of laboratories in detection and quantitation of human immunodeficiency virus (HIV) RNA.  
To assess the proficiency of laboratories in detection and quantitation in different HIV genotypes.

## Feedback and Enquiries

Participants are encouraged to read the QCMD Participants' Manual, which can be downloaded from the QCMD website.

Any queries about this report should be addressed to the QCMD Neutral Office ([neutraloffice@qcmd.org](mailto:neutraloffice@qcmd.org)).

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<b>Catalogue Code:</b> QAV994108	<b>Ref Code:</b> HIVRNA18	<b>Challenge:</b> C1	<b>Analysis Type:</b> Qualitative and Quantitative	<b>Dataset:</b>	<b>Report</b>	<b>Laboratory</b>

Panel member analysis is separated into CORE samples followed by EDUCATIONAL samples.

### Additional Core Samples Information

The following section has been categorised as shown below:

Core ► Quantitative ► Copies/ml, IU/ml ► Qualitative

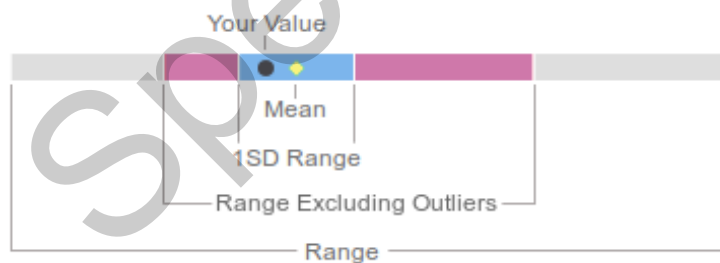
### Individual Panel Member Analysis (Quantitative)

Quantitative analysis for each panel member is provided in relation to your EQA assessment group. EQA assessment groups are established using the molecular workflow information reported by all participants within this EQA challenge / distribution. The principal level of assessment is at the individual method level which is defined based on your reported “amplification/detection method” and other laboratories using the same or similar amplification/detection methods.

To allow meaningful assessment at the individual method level the EQA assessment group must consist of 5 or more datasets. If there are not sufficient datasets at the individual method level then your results will be included within a higher EQA assessment group based on whether it is a commercial or in house technology/method. The highest level assessment grouping is all reported results using the same unit of measurement (i.e. Copies/ml or IU/ml).

The results below provide a breakdown of participant reported values on each of the panel members within this EQA challenge / distribution. Your result for each panel member is indicated by “your value”. You can compare your value to the “mean” within your EQA assessment group and the overall consensus for each sample within this EQA challenge / distribution.

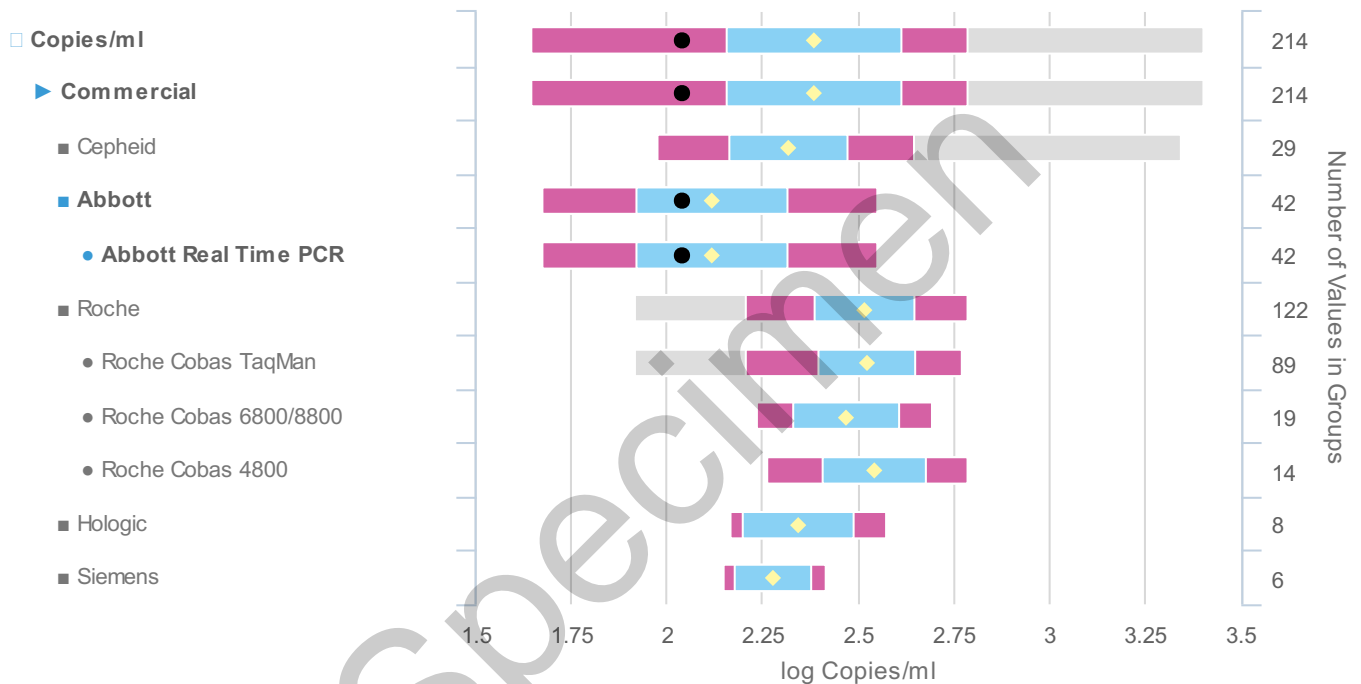
#### Key



<b>Catalogue Code:</b> QAV994108	<b>Ref Code:</b> HIVRNA18	<b>Challenge:</b> C1	<b>Analysis Type:</b> Qualitative and Quantitative	<b>Dataset:</b>	<b>Report UID:</b>	<b>Laboratory</b>
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**HIVRNA18C1-01 - Quantitative Results Breakdown (Copies/ml)**

Sample Code	Sample Content	Matrix	Sample Relationships	Detection Frequency	Sample Status	Consensus (Copies/ml)		Range
						(Log <sub>10</sub> )	(n)	
HIVRNA18C1-01	HIV-1 Type C	Plasma		Frequently Detected	CORE	2.382	214	1.643 - 3.401



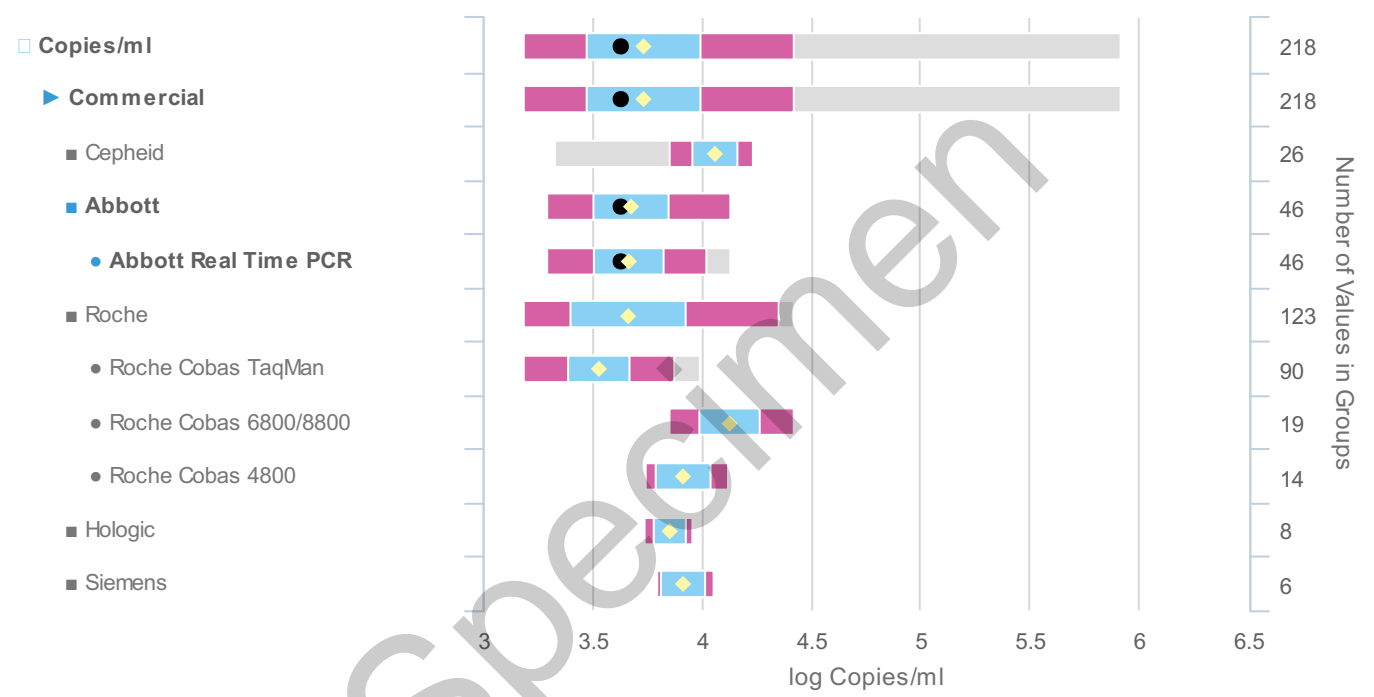
**Groups below n=5:** bioMerieux (n=3), bioMerieux - NucliSENS EasyQ (n=3), Biocentric (n=1), Biocentric - Biocentric Generic (n=1), QIAGEN (n=3), QIAGEN - QIAGEN Artus Real Time (n=2), QIAGEN - Qiagen Artus Real Time (n=1)

**Groups Rolled Up:** Cepheid - Cepheid Xpert kit (n=29), Hologic - Hologic Aptima (n=8), Siemens - Siemens Versant (n=6)

<b>Catalogue Code:</b> QAV994108	<b>Ref Code:</b> HIVRNA18	<b>Challenge:</b> C1	<b>Analysis Type:</b> Qualitative and Quantitative	<b>Dataset:</b>	<b>Report UID:</b>	<b>Laboratory</b>
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**HIVRNA18C1-02 - Quantitative Results Breakdown (Copies/ml)**

Sample Code	Sample Content	Matrix	Sample Relationships	Detection Frequency	Sample Status	Consensus (Copies/ml)		Range
						(Log <sub>10</sub> )	(n)	
HIVRNA18C1-02	HIV-1 Type B	Plasma		Frequently Detected	CORE	3.727	218	3.179 - 5.911



**Groups below n=5:** bioMerieux (n=3), bioMerieux - NucliSENS EasyQ (n=3), Biocentric (n=1), Biocentric - Biocentric Generic (n=1), QIAGEN (n=4), QIAGEN - QIAGEN Artus Real Time (n=3), QIAGEN - Qiagen Artus Real Time (n=1), RTA Laboratories (n=1), RTA Laboratories - RTA Laboratories Real Time (n=1)

**Groups Rolled Up:** Cepheid - Cepheid Xpert kit (n=26), Hologic - Hologic Aptima (n=8), Siemens - Siemens Versant (n=6)



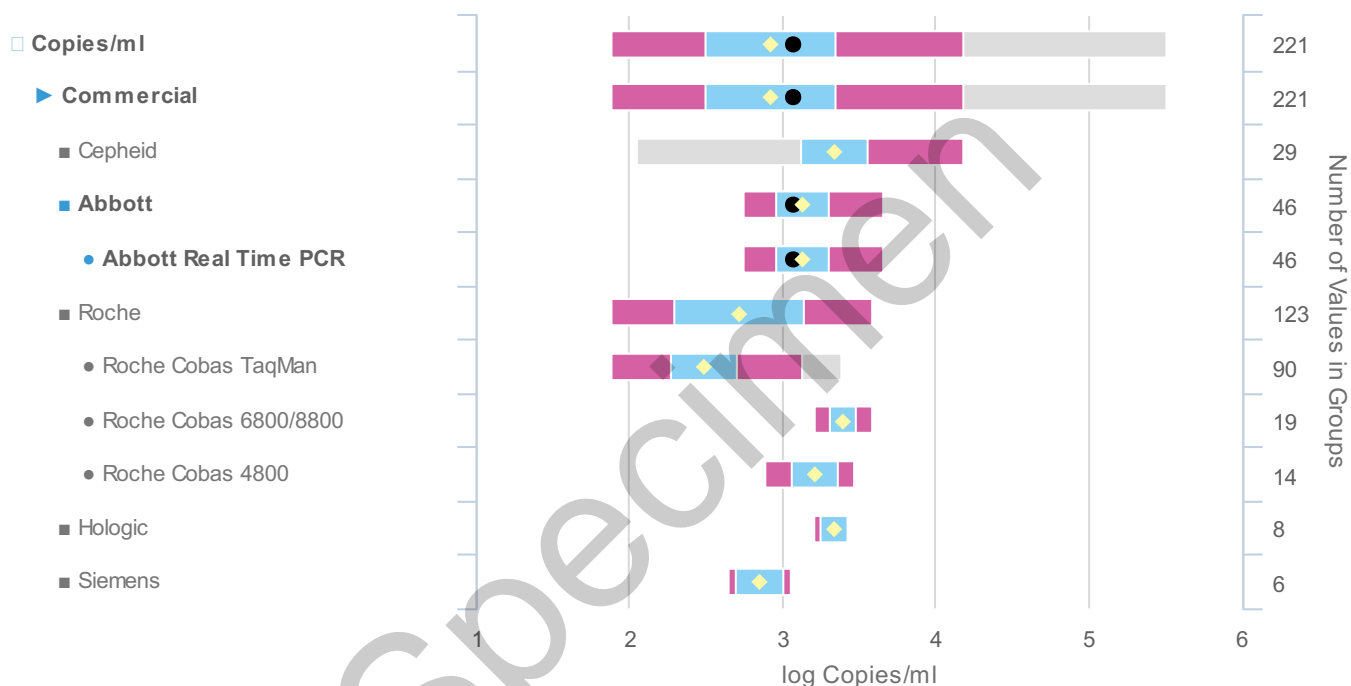
**Individual Report**      **QCMD 2018 Human Immunodeficiency Virus RNA EQA Programme**



<b>Catalogue Code:</b> QAV994108	<b>Ref Code:</b> HIVRNA18	<b>Challenge:</b> C1	<b>Analysis Type:</b> Qualitative and Quantitative	<b>Dataset:</b>	<b>Report UID:</b>	<b>Laboratory</b>
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**HIVRNA18C1-04 - Quantitative Results Breakdown (Copies/ml)**

Sample Code	Sample Content	Matrix	Sample Relationships	Detection Frequency	Sample Status	Consensus (Copies/ml)		Range
						(Log <sub>10</sub> )	(n)	
HIVRNA18C1-04	HIV-1 Type AG	Plasma		Frequently Detected	CORE	2.915	221	1.875 - 5.504



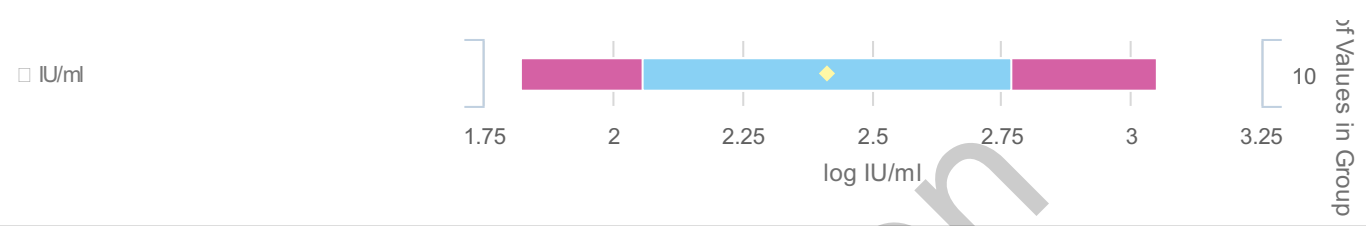
**Groups below n=5:** bioMerieux (n=3), bioMerieux - NucliSENS EasyQ (n=3), Biocentric (n=1), Biocentric - Biocentric Generic (n=1), QIAGEN (n=4), QIAGEN - QIAGEN Artus Real Time (n=3), QIAGEN - Qiagen Artus Real Time (n=1), RTA Laboratories (n=1), RTA Laboratories - RTA Laboratories Real Time (n=1)

**Groups Rolled Up:** Cepheid - Cepheid Xpert kit (n=29), Hologic - Hologic Aptima (n=8), Siemens - Siemens Versant (n=6)

Catalogue Code: QAV994108	Ref Code: HIVRNA18	Challenge: C1	Analysis Type: Qualitative and Quantitative	Dataset:	Report UID:	Laboratory
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**HIVRNA18C1-01 - Quantitative Results Breakdown (IU/ml)**

Sample Code	Sample Content	Matrix	Sample Relationships	Detection Frequency	Sample Status	Consensus (IU/ml)		Range
						(Log <sub>10</sub> )	(n)	
HIVRNA18C1-01	HIV-1 Type C	Plasma		Frequently Detected	CORE	2.411	10	1.820 - 3.048

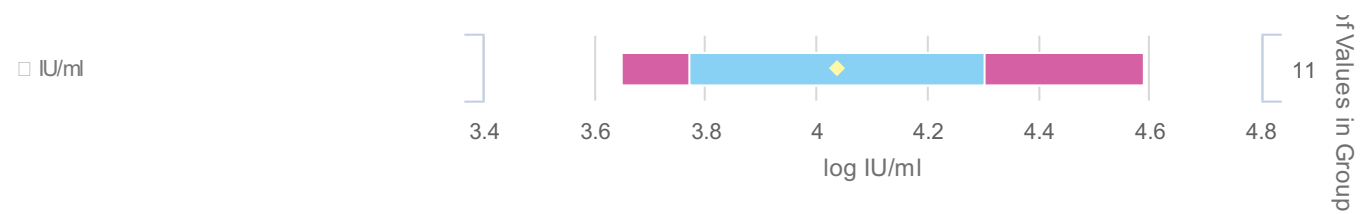


**Groups below n=5:** Abbott (n=4), Abbott - Abbott Real Time PCR (n=4), Sansure Biotech (n=1), Sansure Biotech - Sansure Real Time PCR (n=1), Anatolia Geneworks (n=1), Anatolia Geneworks - Anatolia Geneworks Bosphore (n=1), Hologic (n=1), Hologic - Hologic Aptima (n=1), QIAGEN (n=3), QIAGEN - QIAGEN Artus Real Time (n=3)

**Groups Rolled Up:** Commercial (n=10)

**HIVRNA18C1-02 - Quantitative Results Breakdown (IU/ml)**

Sample Code	Sample Content	Matrix	Sample Relationships	Detection Frequency	Sample Status	Consensus (IU/ml)		Range
						(Log <sub>10</sub> )	(n)	
HIVRNA18C1-02	HIV-1 Type B	Plasma		Frequently Detected	CORE	4.035	11	3.647 - 4.588



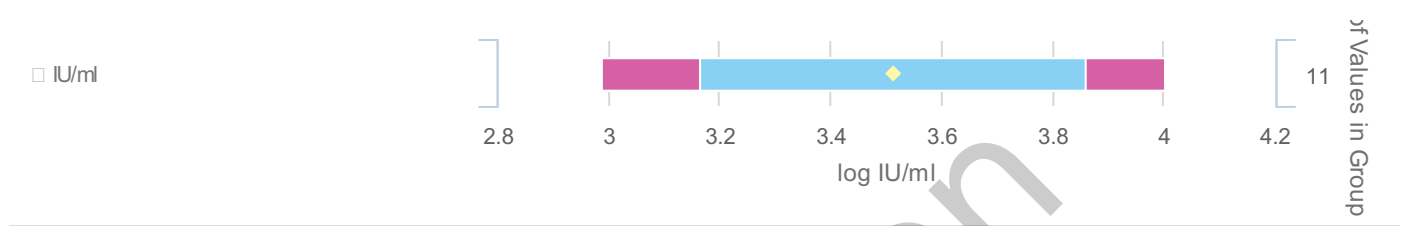
**Groups below n=5:** Abbott (n=4), Abbott - Abbott Real Time PCR (n=4), Iontek (n=1), Iontek - Iontek Fluorion (n=1), Sansure Biotech (n=1), Sansure Biotech - Sansure Real Time PCR (n=1), Anatolia Geneworks (n=1), Anatolia Geneworks - Anatolia Geneworks Bosphore (n=1), Hologic (n=1), Hologic - Hologic Aptima (n=1), QIAGEN (n=3), QIAGEN - QIAGEN Artus Real Time (n=3)

**Groups Rolled Up:** Commercial (n=11)

Catalogue Code: QAV994108	Ref Code: HIVRNA18	Challenge: C1	Analysis Type: Qualitative and Quantitative	Dataset:	Report UID:	Laboratory
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**HIVRNA18C1-04 - Quantitative Results Breakdown (IU/ml)**

Sample Code	Sample Content	Matrix	Sample Relationships	Detection Frequency	Sample Status	Consensus (IU/ml)		Range
						(Log <sub>10</sub> )	(n)	
HIVRNA18C1-04	HIV-1 Type AG	Plasma		Frequently Detected	CORE	3.511	11	2.986 - 4.001



**Groups below n=5:** Abbott (n=4), Abbott - Abbott Real Time PCR (n=4), Iontek (n=1), Iontek - Iontek Fluorion (n=1), Sansure Biotech (n=1), Sansure Biotech - Sansure Real Time PCR (n=1), Anatolia Geneworks (n=1), Anatolia Geneworks - Anatolia Geneworks Bosphore (n=1), Hologic (n=1), Hologic - Hologic Aptima (n=1), QIAGEN (n=3), QIAGEN - QIAGEN Artus Real Time (n=3)

**Groups Rolled Up:** Commercial (n=11)

**Individual Panel Member Analysis (Qualitative)**

Qualitative analysis for each panel member is provided in relation to your EQA assessment group. EQA assessment groups are established using the molecular workflow information reported by all participants within this EQA challenge / distribution. The principal level of assessment is at the individual method level which is defined based on your reported “amplification/detection method” and other laboratories using the same or similar amplification/detection methods.

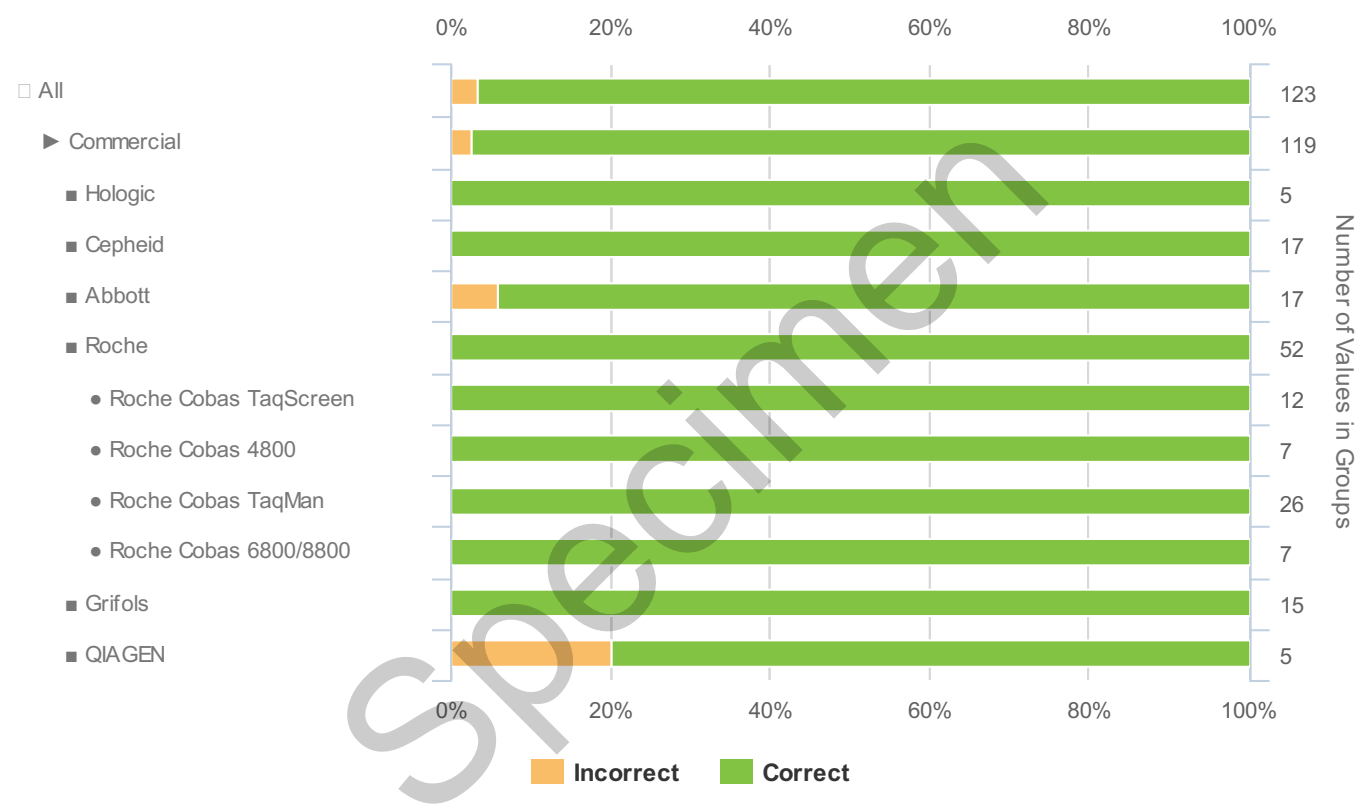
To allow meaningful assessment at the individual method level the EQA assessment group must consist of 5 or more datasets. If there are not sufficient datasets at the individual method level then your results will be included within a higher EQA assessment group based on whether it is a commercial or in house technology/method. The highest level assessment grouping is “All” participant reported qualitative results.

A breakdown of qualitative results reported by participants on each of the panel members within this EQA challenge / distribution is provided below. You can compare your results to those within your EQA assessment group and those obtained within other EQA assessment groups or to the overall consensus for each sample within this EQA challenge / distribution.

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**HIVRNA18C1-01 - Qualitative Results Breakdown**

Sample Code	Sample Content	Matrix	Sample Relationships	Detection Frequency	Sample Status	Percentage Correct All	
						(%)	(n)
HIVRNA18C1-01	HIV-1 Type C	Plasma		Frequently Detected	CORE	96.7	



**Groups below n=5:** InterLabService (n=1), InterLabService - InterLabService AmpliSens (n=1), Iontek (n=1), Iontek - Iontek Fluorion (n=1), Sansure Biotech (n=1), Sansure Biotech - Sansure Real Time PCR (n=1), bioMerieux (n=2), bioMerieux - NucliSENS EasyQ (n=2), Biocentric (n=1), Biocentric - Biocentric Generic (n=1), Siemens (n=2), Siemens - Siemens Versant (n=2), In-House (n=4), In-House - Real-time In-House PCR (n=4)

**Groups Rolled Up:** Hologic - Hologic Aptima (n=5), Cepheid - Cepheid Xpert kit (n=17), Abbott - Abbott Real Time PCR (n=17), Grifols - Grifols Procleix Ultrio (n=15), QIAGEN - QIAGEN Artus Real Time (n=5)

<b>Individual Report</b>		<b>QCMD 2018 Human Immunodeficiency Virus RNA EQA Programme</b>			 Quality Control for Molecular Diagnostics		
<b>Catalogue Code:</b> QAV994108	<b>Ref Code:</b> HIVRNA18	<b>Challenge:</b> C1	<b>Analysis Type:</b> Qualitative and Quantitative	<b>Dataset:</b>	<b>Report UID:</b>	<b>Laboratory</b>	


**HIVRNA18C1-02 - Qualitative Results Breakdown**

Sample Code	Sample Content	Matrix	Sample Relationships	Detection Frequency	Sample Status	Percentage Correct All	
						(%)	(n)
HIVRNA18C1-02	HIV-1 Type B	Plasma		Frequently Detected	CORE	97.6	



**Groups below n=5:** InterLabService (n=1), InterLabService - InterLabService AmpliSens (n=1), Iontek (n=1), Iontek - Iontek Fluorion (n=1), Sansure Biotech (n=1), Sansure Biotech - Sansure Real Time PCR (n=1), bioMerieux (n=2), bioMerieux - NucliSENS EasyQ (n=2), Biocentric (n=1), Biocentric - Biocentric Generic (n=1), Siemens (n=2), Siemens - Siemens Versant (n=2), In-House (n=4), In-House - Real-time In-House PCR (n=4)

**Groups Rolled Up:** Hologic - Hologic Aptima (n=5), Cepheid - Cepheid Xpert kit (n=17), Abbott - Abbott Real Time PCR (n=17), Grifols - Grifols Procleix Ultrio (n=15), QIAGEN - QIAGEN Artus Real Time (n=5)

<b>Individual Report</b>		<b>QCMD 2018 Human Immunodeficiency Virus RNA EQA Programme</b>			 Quality Control for Molecular Diagnostics		
<b>Catalogue Code:</b> QAV994108	<b>Ref Code:</b> HIVRNA18	<b>Challenge:</b> C1	<b>Analysis Type:</b> Qualitative and Quantitative	<b>Dataset:</b>	<b>Report UID:</b>	<b>Laboratory</b>	

**HIVRNA18C1-03 - Qualitative Results Breakdown**

Sample Code	Sample Content	Matrix	Sample Relationships	Detection Frequency	Sample Status	Percentage Correct All	
						(%)	(n)
HIVRNA18C1-03	HIV Negative Plasma	Plasma		Negative	CORE	96.7	



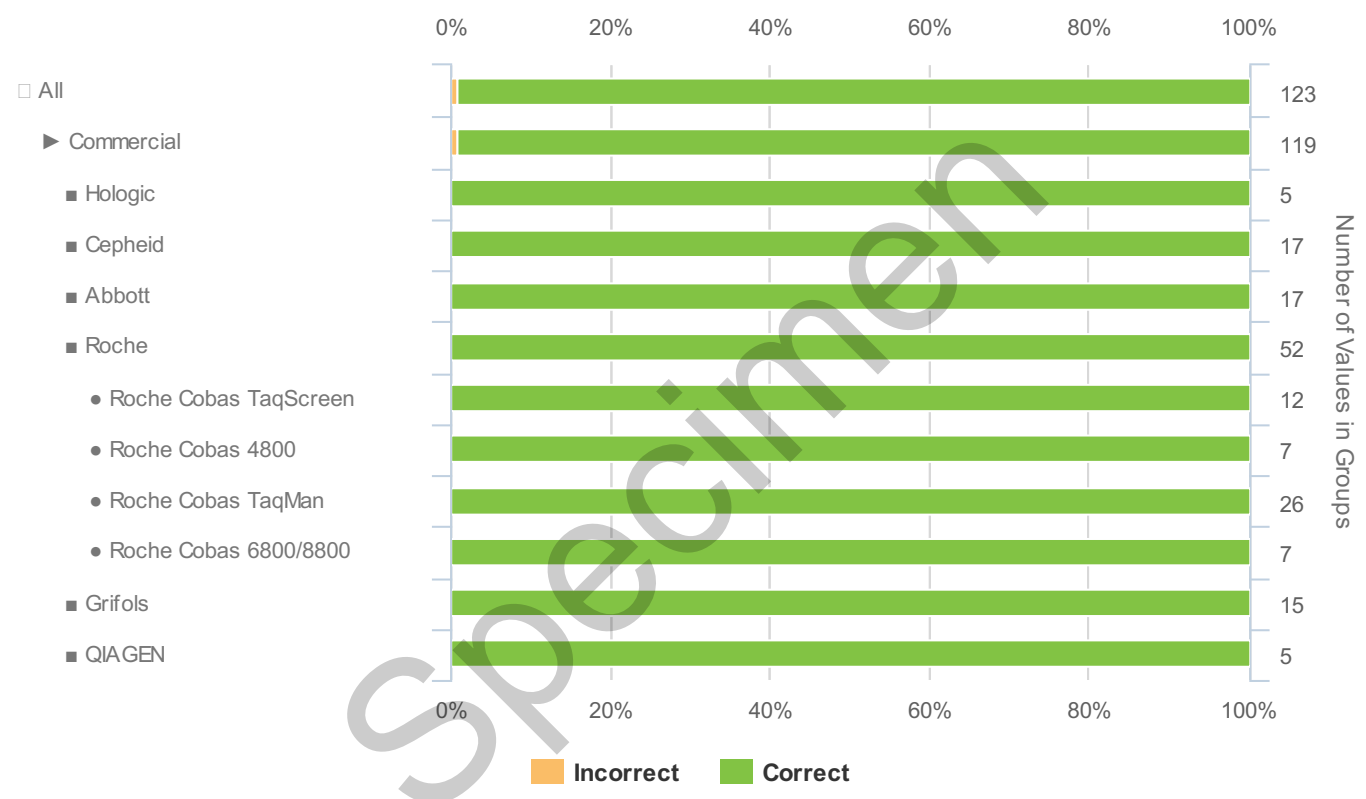
**Groups below n=5:** InterLabService (n=1), InterLabService - InterLabService AmpliSens (n=1), Iontek (n=1), Iontek - Iontek Fluorion (n=1), Sansure Biotech (n=1), Sansure Biotech - Sansure Real Time PCR (n=1), bioMerieux (n=2), bioMerieux - NucliSENS EasyQ (n=2), Biocentric (n=1), Biocentric - Biocentric Generic (n=1), Siemens (n=2), Siemens - Siemens Versant (n=2), In-House (n=4), In-House - Real-time In-House PCR (n=4)

**Groups Rolled Up:** Hologic - Hologic Aptima (n=5), Cepheid - Cepheid Xpert kit (n=17), Abbott - Abbott Real Time PCR (n=17), Grifols - Grifols Procleix Ultrio (n=15), QIAGEN - QIAGEN Artus Real Time (n=5)

Catalogue Code: QAV994108	Ref Code: HIVRNA18	Challenge: C1	Analysis Type: Qualitative and Quantitative	Dataset:	Report UID:	Laboratory
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**HIVRNA18C1-04 - Qualitative Results Breakdown**

Sample Code	Sample Content	Matrix	Sample Relationships	Detection Frequency	Sample Status	Percentage Correct All	
						(%)	(n)
HIVRNA18C1-04	HIV-1 Type AG	Plasma		Frequently Detected	CORE	99.2	



**Groups below n=5:** InterLabService (n=1), InterLabService - InterLabService AmpliSens (n=1), Iontek (n=1), Iontek - Iontek Fluorion (n=1), Sansure Biotech (n=1), Sansure Biotech - Sansure Real Time PCR (n=1), bioMerieux (n=2), bioMerieux - NucliSENS EasyQ (n=2), Biocentric (n=1), Biocentric - Biocentric Generic (n=1), Siemens (n=2), Siemens - Siemens Versant (n=2), In-House (n=4), In-House - Real-time In-House PCR (n=4)

**Groups Rolled Up:** Hologic - Hologic Aptima (n=5), Cepheid - Cepheid Xpert kit (n=17), Abbott - Abbott Real Time PCR (n=17), Grifols - Grifols Procleix Ultrio (n=15), QIAGEN - QIAGEN Artus Real Time (n=5)

<b>Individual Report</b>	<b>QCMD 2018 Human Immunodeficiency Virus RNA EQA Programme</b>					
<b>Catalogue Code:</b> QAV994108	<b>Ref Code:</b> HIVRNA18	<b>Challenge:</b> C1	<b>Analysis Type:</b> Qualitative and Quantitative	<b>Dataset:</b>	<b>Report UID:</b>	<b>Laboratory</b>

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