Individual Report

QCMD 2024 Arthropod-Borne Viruses EQA Programme

Catalogue Code:	Ref Code:	Challenge:	Analysis Type:	Dataset:	Report UID:	Laboratory
QAM194206	ARBO24	S	Multiple Pathogen Qualitative	799585	2258/98603/7128	EE006

Panel Composition

Sample Code	Sample Content	Matrix	Sample Relationships[1]	Detected / Determined[2]		Not Detected / Not Determined[2]		Not Tested[2]	
				(%)	*(n)*	*(%)*	*(n)*	*(%)*	*(n)*
ARBO24S-01	Rift Valley Fever virus	Transport Medium	-	37.9	11	3.4	1	58.6	17
ARBO24S-02	Negative	Transport Medium	-	96.6	28	3.4	1	N/A	0
ARBO24S-03	Tick-borne encephalitis virus	Transport Medium	DS1_1	75.9	22	6.9	2	17.2	5
ARBO24S-04	Japanese encephalitits virus	Transport Medium	DS3_2	55.2	16	3.4	1	41.4	12
ARBO24S-05	Tick-borne encephalitis virus	Transport Medium	DS1_3	75.9	22	6.9	2	17.2	5
ARBO24S-06	Sandfly Fever Virus Toscana	Transport Medium	DS2_1	31	9	6.9	2	62.1	18
ARBO24S-07	Japanese encephalitits virus	Transport Medium	DS3_1	55.2	16	3.4	1	41.4	12
ARBO24S-08	Japanese encephalitits virus	Transport Medium	DS3_3	37.9	11	20.7	6	41.4	12
ARBO24S-09	Tick-borne encephalitis virus	Transport Medium	DS1_2	75.9	22	6.9	2	17.2	5
ARBO24S-10	Sandfly Fever Virus Toscana	Transport Medium	DS2_2	34.5	10	3.4	1	62.1	18

[1] **Sample Relationships:** Indicates the relationships of the samples within this challenge. The highest titre member of dilution series DS1 is indicated by DS1_1 and further members of the series as DS1_2, DS1_3 etc. in order of reducing titre. Additional dilution series are indicated by DS2 (e.g DS2_1, DS2_2 etc.), DS3 (e.g. DS3_1, DS3_2 etc.). If one duplicate pair is present this is indicated by 'D1'. Further duplicate pairs are indicated by 'D2', 'D3' etc.
[2] **Detected / Determined; Not Detected / Not Determined; Not Tested:** The percentage (%) of datasets reported by all participants in relation to the assigned status of the panel member i.e. 'positive' or 'negative' and the expected pathogen type as defined through pre-testing and the total number of datasets (n) for each panel member.
For further details please refer to the current participant manual.

EQA Assessment Group[1]	N/A (Refer to **My Workflow details** section below)

Your Summary Results (Core Samples)

Sample Code	**Expected Result[2]**		**Your Final Laboratory Reported Result[3]**			**Sample Status[7]**	**Detection Frequency[8]**	**Detection Score[9]**
	Qualitative	**Pathogen ID**	**Pathogen included in workflow(s)[4] Yes/No**	**Qualitative[5]**	**Reported Pathogen ID[6]**			
ARBO24S-02	Negative		N/A	Negative		Core	Negative	0
ARBO24S-03	Positive	Tickborne encephalitis virus	Yes	Positive	Tickborne encephalitis virus	Core	Detected	0
ARBO24S-04	Positive	Japanese encephalitis virus	No	Negative		Core	Detected	-
ARBO24S-05	Positive	Tickborne encephalitis virus	Yes	Positive	Tickborne encephalitis virus	Core	Detected	0
ARBO24S-06	Positive	Sandfly fever Toscana virus	No	Negative		Core	Detected	-
ARBO24S-07	Positive	Japanese encephalitis virus	No	Negative		Core	Detected	-
ARBO24S-09	Positive	Tickborne encephalitis virus	Yes	Positive	Tickborne encephalitis virus	Core	Detected	0
ARBO24S-10	Positive	Sandfly fever Toscana virus	No	Negative		Core	Detected	-

[1] **EQA Assessment Group:** To aid 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] **Expected Result:** positive / negative result and the specific pathogen present within each panel member.

[3] **Your Final Laboratory Reported Result:** the final reported result which may be based on one or more workflows used to test each panel member.

[4] **Pathogen included in workflow(s):** Yes / No answer to whether the expected pathogen was tested for.

[5] **Qualitative:** The final qualitative result you reported for each sample within this EQA challenge / distribution.

[6] **Reported Pathogen ID:** The final pathogen(s) identification you reported for each sample within this EQA challenge / distribution.

[7] **Sample Status:** 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.

[8] **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 by participants within the EQA challenge/distribution. Note that the detection frequency is assigned using only datasets submitted using workflows including the target pathogen.

[9] **Detection Score:** Your detection scores are based on the assigned detection frequency of each panel member, where 0 is "highly satisfactory" and 3 (three) is "highly unsatisfactory"

For further details please refer to the current participant manual.

Multiple Pathogen Programme - Qualitative Assessment of Results

Results are categorised based on the workflow used and the pathogen(s) targeted as shown in the table below.

	Laboratory Reported Results						Result Category		Sample Weighting			
Expected Qualitative Result	Positive	Negative	Not Determined	Expected pathogen(s) included in workflow(s)		Expected pathogen(s) not included in workflow(s)						
				Expected pathogen(s) detected	Expected pathogen(s) not detected				Frequently Detected (>95% positive)	Detected (Between 65 and 95% positive)	Infrequently Detected (Less than 65% positive)	Negative
Positive	✓			✓			Expected Pathogen Reported	Detected / Determined	0	0	0	N/A
Negative		✓					No pathogen reported	Detected / Determined	N/A	N/A	N/A	0
Negative	✓						False Positive	False Positive	3	3	3	N/A
Positive	✓					✓	Reported Pathogen(s) not as expected	False Positive	3	3	3	N/A
Positive	✓				✓		Reported Pathogen(s) not as expected	False Positive	3	3	3	N/A
Positive or Negative			✓				Result reported as not determined	Not Determined	3	2	1	N/A
Positive		✓			✓		No pathogen reported	False Negative	3	2	1	N/A
Positive		✓				✓	Expected pathogen not tested for	Not Tested	Not Scored	Not Scored	Not Scored	N/A

My Workflow Details:

Name	Tick-borne encephalitis virus (v2)
Description	
Targets	V tickborne encephalitis virus
Assays	*Extraction* - Thermo Scientific™ - Thermo Scientific™ KingFisher™ Flex Purification System ● Commercial ○ Kit Manufacturer: *Applied Biosystems* ○ Kit Type: *MagMAX Viral/Pathogen II Nucleic Acid Isolation* *Amplification* - Bio-Rad - CFX96 Touch Real-Time PCR Detection System ● Multiplex ● Commercial ○ Kit Manufacturer: *Certest* ○ Kit Type: *VIASURE Tick Borne Diseases Real Time PCR Detection* ○ Kit Version: *VS-TBD112LE*

Used to test samples:	ARBO24S-01, ARBO24S-02, ARBO24S-03, ARBO24S-04, ARBO24S-05, ARBO24S-06, ARBO24S-07, ARBO24S-08, ARBO24S-09, ARBO24S-10

Your Summary Results (Educational Samples)

Sample Code	Expected Result[2]		Your Final Laboratory Reported Result[3]			Sample Status[7]	Detection Frequency[8]	Detection Score[9]
	Qualitative	Pathogen ID	Pathogen included in workflow(s)[4] Yes/No	Qualitative[5]	Reported Pathogen ID[6]			
ARBO24S-01	Positive	Rift Valley fever virus	No	Negative		Educational	Detected	-
ARBO24S-08	Positive	Japanese encephalitis virus	No	Negative		Educational	Detected	-

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For further details please refer to the current participant manual.

Further Programme Details

Number of Participants	31
Number of Countries	17
Number of Respondents	26
Number of Datasets Submitted	29

EQA Programme Aims

The Arthropod-borne virus EQA focuses on the molecular detection and determination of different arthropod-borne viruses (including viruses from Flavi-, Toga-, Bunya-, and/or Reoviridae families).

Feedback and Enquiries

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

Any enquiries should be submitted through the ‘Contact Us’ form that you can find in the ‘Help’ section of your QCMD (ITEMS) Participant Profile Area.

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

Individual Panel Member Analysis (Core Samples)

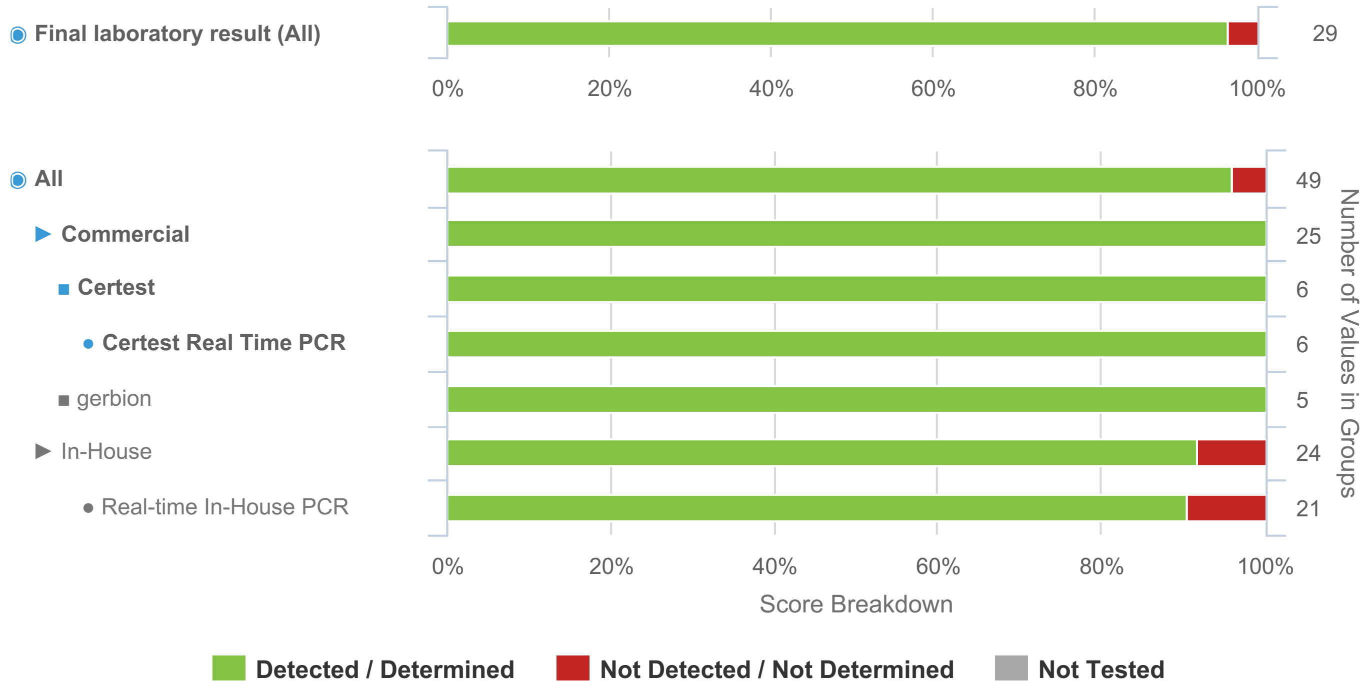
Qualitative analysis for each panel member is provided in relation to your EQA assessment group. EQA assessment groups are established using the molecular workflow information reported by all participants within this EQA challenge / distribution.

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 for all workflows used by participants on each of the panel members within this EQA challenge / distribution is provided below. Note: participants may use multiple workflows for each sample.

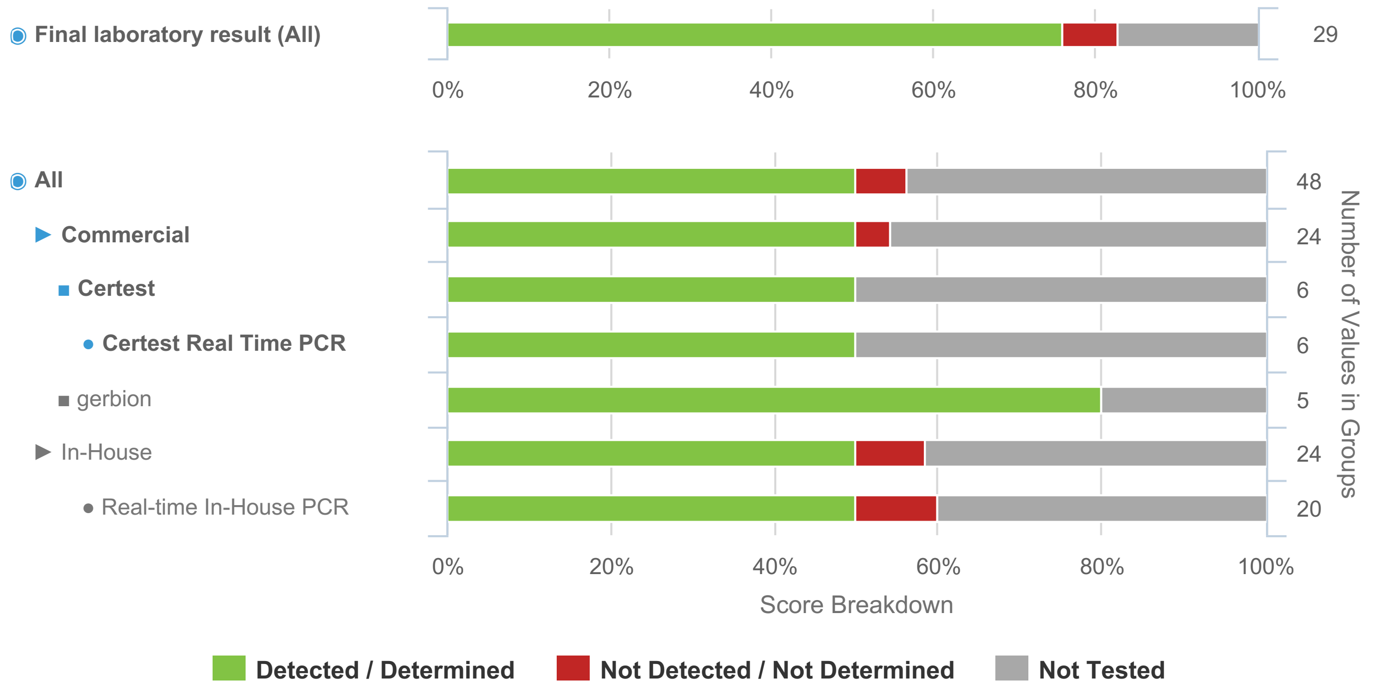
The final laboratory result indicates the final reported result which may be based on one or more workflows used to test each panel member.

Sample Code	Sample Content	Matrix	Sample Relationships	Expected targets	Detected / Determined		Not Detected / Not Determined		Not Tested	
					(%)	*(n)*	*(%)*	*(n)*	*(%)*	*(n)*
ARBO24S-02	Negative	Transport Medium	-		96.6	28	3.4	1	N/A	0



Groups below n=5: Altona Diagnostics (n=1), Altona Diagnostics - Altona Diagnostics RealStar (n=1), Clonit (n=1), Clonit - Clonit quanty kit (n=1), Geno Sen's (n=1), Geno Sen's - Geno Sen's Real Time Kit (n=1), Mikrogen (n=2), Mikrogen - Mikrogen alphaCube (n=2), Oxford Nanopore Technologies (n=2), Oxford Nanopore Technologies - Oxford Nanopore GridION (n=1), Oxford Nanopore Technologies - Oxford Nanopore MinION (n=1), Progenie Molecular (n=3), Progenie Molecular - Progenie Molecular RealCycler (n=3), Seegene (n=1), Seegene - Seegene Novaplex (n=1), Vitassay (n=2), Vitassay - Vitassay Real-Time PCR (n=2), bioPerfectus (n=1), bioPerfectus - bioPerfectus Real Time PCR (n=1), In-House - Conventional In-House PCR (n=1), In-House - Conventional Sequencing Analysis (n=2)
Groups Rolled Up: gerbion - gerbion virella (n=5)

Sample Code	**Sample Content**	**Matrix**	**Sample Relationships**	**Expected targets**	**Detected / Determined**		**Not Detected / Not Determined**		**Not Tested**	
					(%)	***(n)***	***(%)***	***(n)***	***(%)***	***(n)***
ARBO24S-03	Tick-borne encephalitis virus	Transport Medium	DS1_1	Tickborne encephalitis virus	75.9	22	6.9	2	17.2	5



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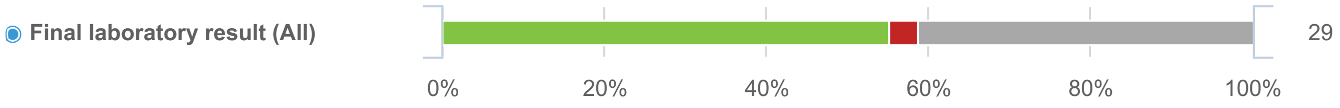
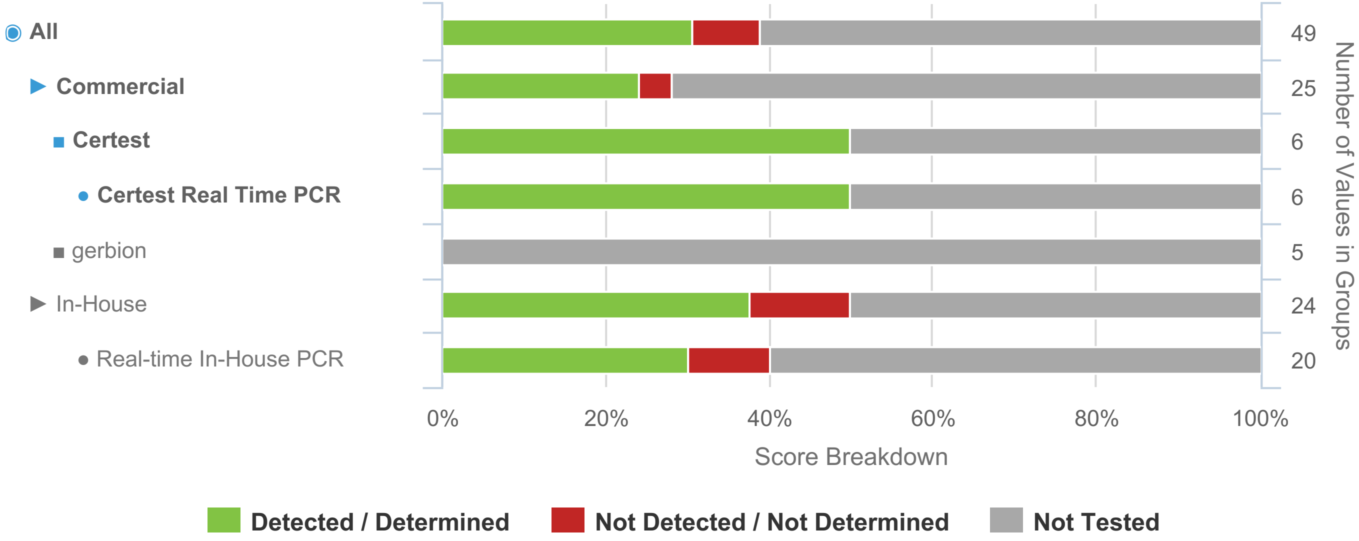
Groups Rolled Up: gerbion - gerbion virella (n=5)

Sample Code	**Sample Content**	**Matrix**	**Sample Relationships**	**Expected targets**	**Detected / Determined**		**Not Detected / Not Determined**		**Not Tested**	
					(%)	***(n)***	***(%)***	***(n)***	***(%)***	***(n)***
ARBO24S-04	Japanese encephalitits virus	Transport Medium	DS3_2	Japanese encephalitis virus	55.2	16	3.4	1	41.4	12





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Groups Rolled Up: gerbion - gerbion virella (n=5)

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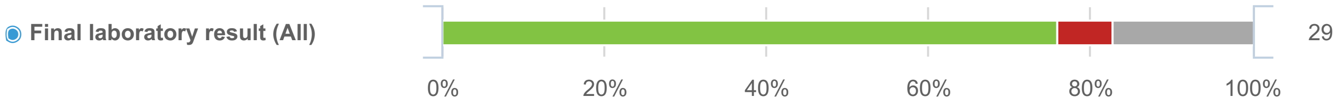
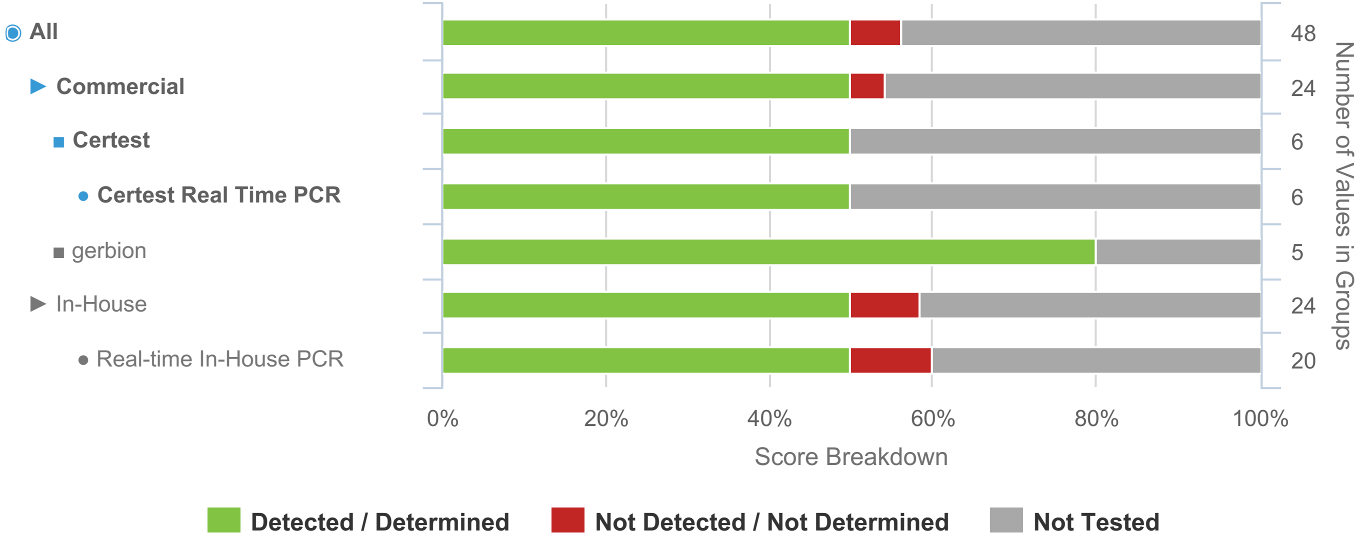
Catalogue Code:	Ref Code:	Challenge:	Analysis Type:	Dataset:	Report UID:	Laboratory
QAM194206	ARBO24	S	Multiple Pathogen Qualitative	799585	2258/98603/7128	EE006

Sample Code	Sample Content	Matrix	Sample Relationships	Expected targets	Detected / Determined		Not Detected / Not Determined		Not Tested	
					(%)	*(n)*	*(%)*	*(n)*	*(%)*	*(n)*
ARBO24S-05	Tick-borne encephalitis virus	Transport Medium	DS1_3	Tickborne encephalitis virus	75.9	22	6.9	2	17.2	5





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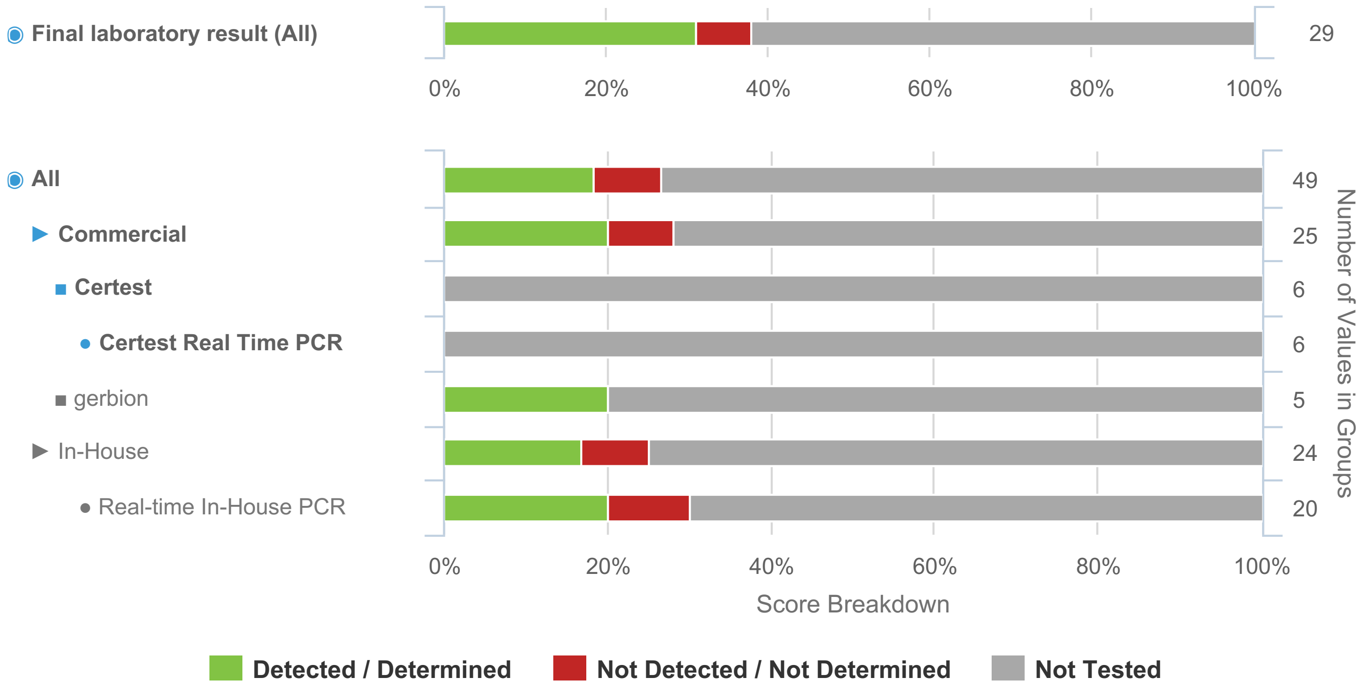
Groups Rolled Up: gerbion - gerbion virella (n=5)

Sample Code	Sample Content	Matrix	Sample Relationships	Expected targets	Detected / Determined		Not Detected / Not Determined		Not Tested	
					(%)	*(n)*	*(%)*	*(n)*	*(%)*	*(n)*
ARBO24S-06	Sandfly Fever Virus Toscana	Transport Medium	DS2_1	Sandfly fever Toscana virus	31	9	6.9	2	62.1	18



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Groups Rolled Up: gerbion - gerbion virella (n=5)

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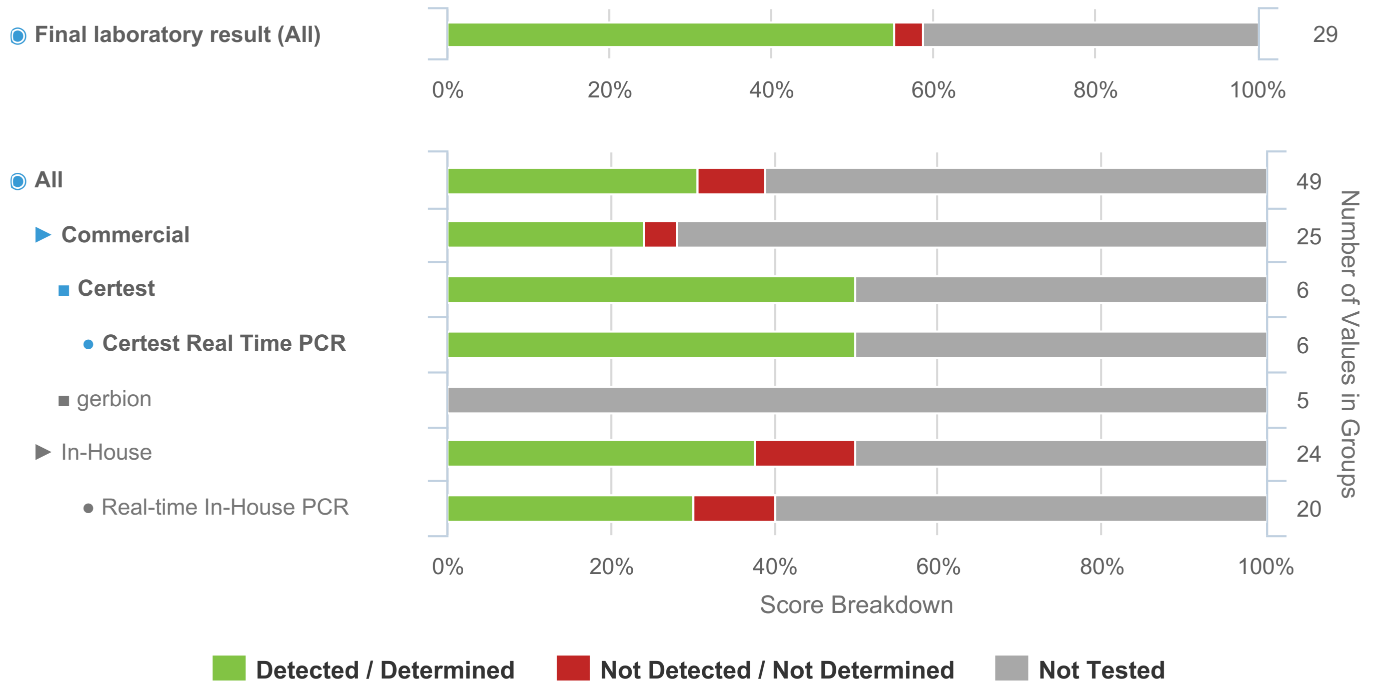
QAM194206	ARBO24	S	Multiple Pathogen Qualitative	799585	2258/98603/7128	EE006

Sample Code	**Sample Content**	**Matrix**	**Sample Relationships**	**Expected targets**	**Detected / Determined**		**Not Detected / Not Determined**		**Not Tested**	
					(%)	***(n)***	***(%)***	***(n)***	***(%)***	***(n)***
ARBO24S-07	Japanese encephalitits virus	Transport Medium	DS3_1	Japanese encephalitis virus	55.2	16	3.4	1	41.4	12



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Groups Rolled Up: gerbion - gerbion virella (n=5)

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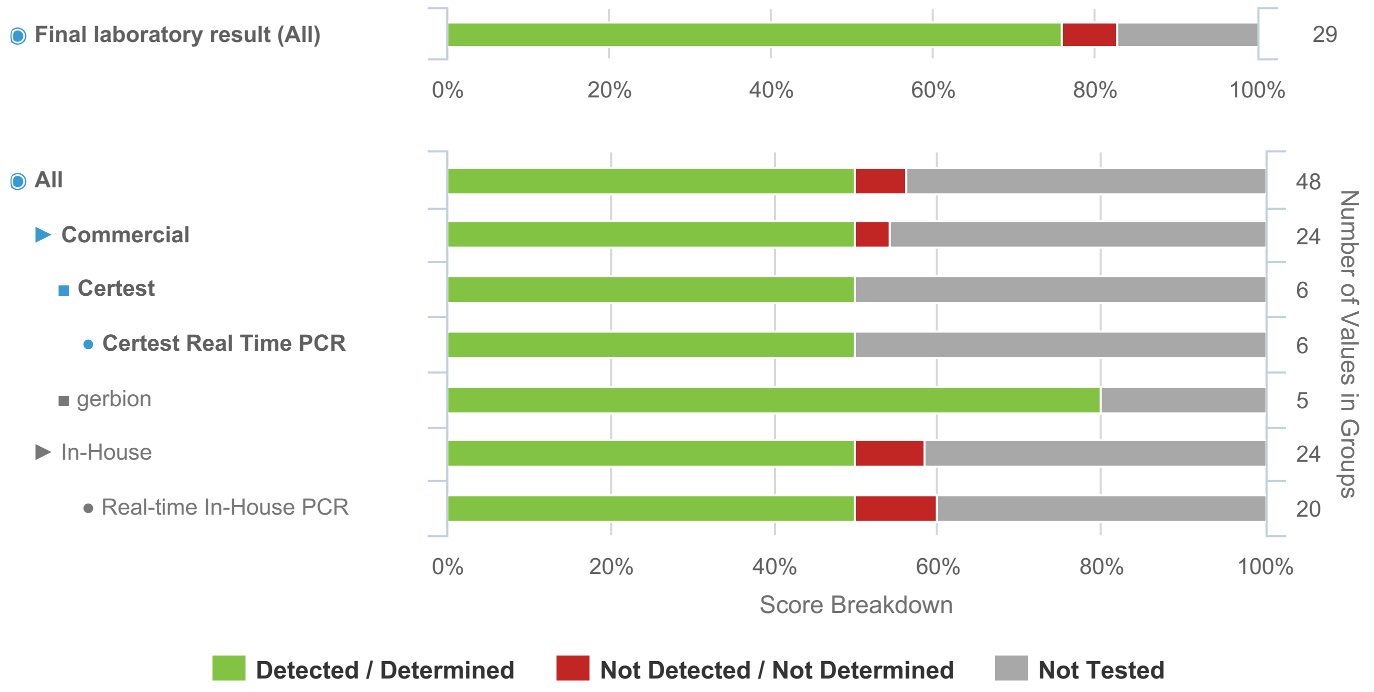
					(%)	*(n)*	*(%)*	*(n)*	*(%)*	*(n)*
ARBO24S-09	Tick-borne encephalitis virus	Transport Medium	DS1_2	Tickborne encephalitis virus	75.9	22	6.9	2	17.2	5



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Sample Code	Sample Content	Matrix	Sample Relationships	Expected targets	Detected / Determined		Not Detected / Not Determined		Not Tested	
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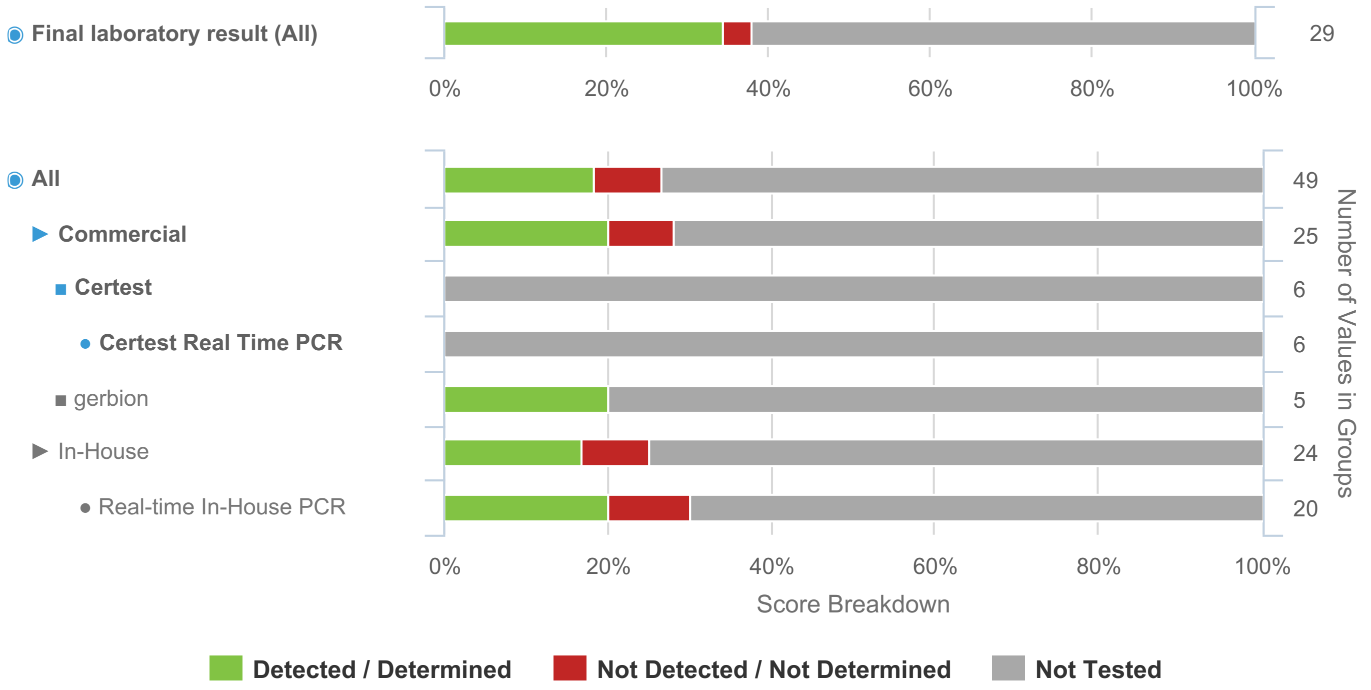
ARBO24S-10	Sandfly Fever Virus Toscana	Transport Medium	DS2_2	Sandfly fever Toscana virus	34.5	10	3.4	1	62.1	18



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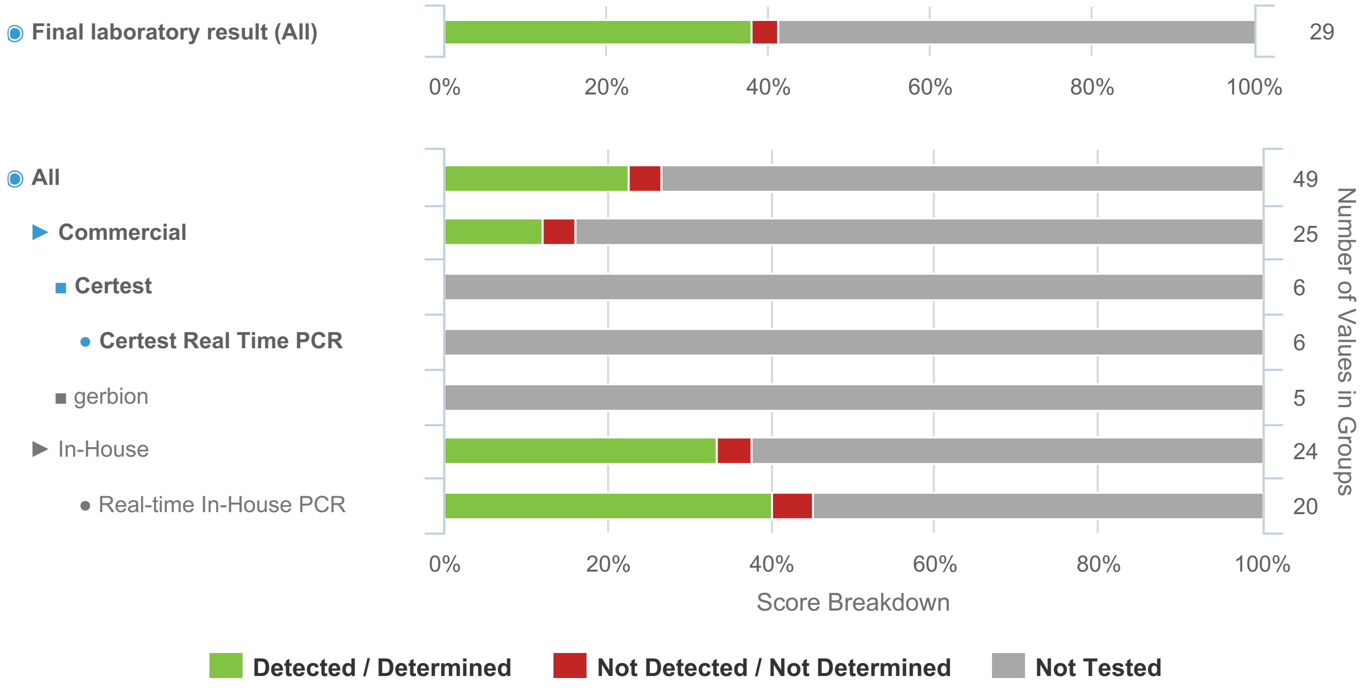
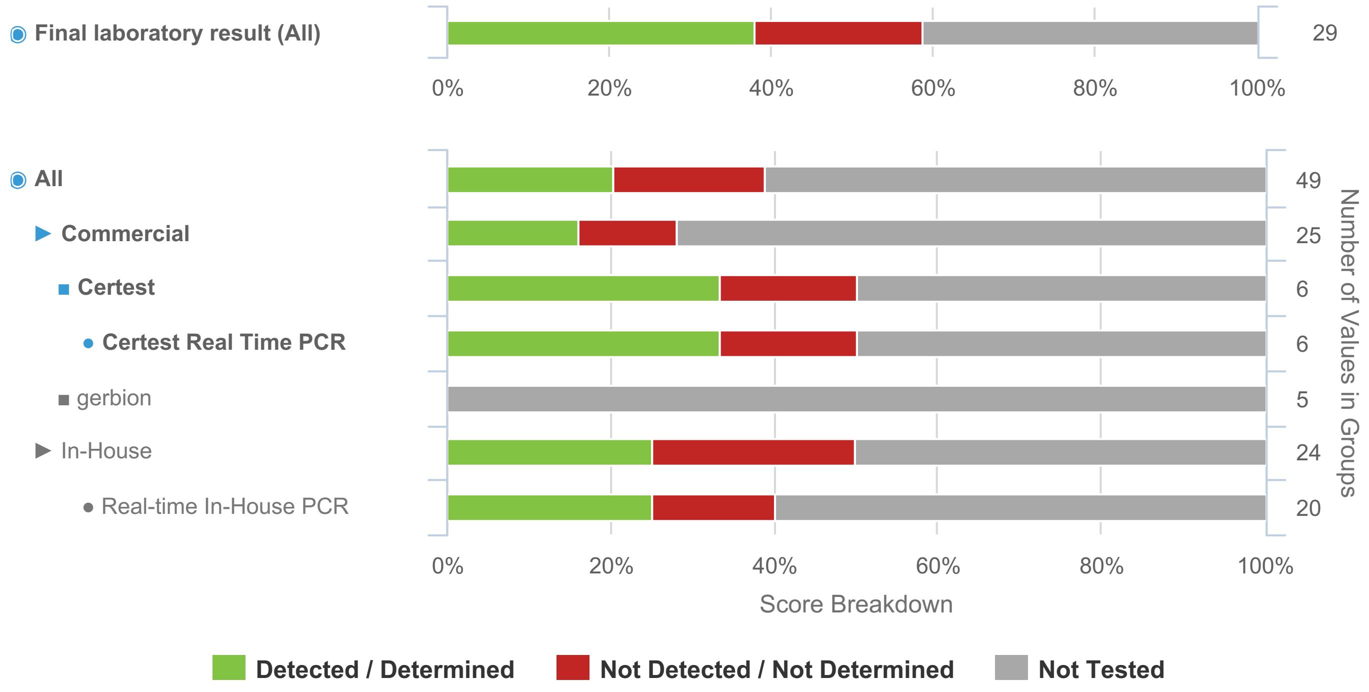
ARBO24S-01	Rift Valley Fever virus	Transport Medium	-	Rift Valley fever virus	37.9	11	3.4	1	58.6	17



Groups below n=5: Altona Diagnostics (n=1), Altona Diagnostics - Altona Diagnostics RealStar (n=1), Clonit (n=1), Clonit - Clonit quanty kit (n=1), Geno Sen's (n=1), Geno Sen's - Geno Sen's Real Time Kit (n=1), Mikrogen (n=2), Mikrogen - Mikrogen alphaCube (n=2), Oxford Nanopore Technologies (n=2), Oxford Nanopore Technologies - Oxford Nanopore GridION (n=1), Oxford Nanopore Technologies - Oxford Nanopore MinION (n=1), Progenie Molecular (n=3), Progenie Molecular - Progenie Molecular RealCycler (n=3), Seegene (n=1), Seegene - Seegene Novaplex (n=1), Vitassay (n=2), Vitassay - Vitassay Real-Time PCR (n=2), bioPerfectus (n=1), bioPerfectus - bioPerfectus Real Time PCR (n=1), In-House - Conventional In-House PCR (n=2), In-House - Conventional Sequencing Analysis (n=2)
Groups Rolled Up: gerbion - gerbion virella (n=5)

Sample Code	**Sample Content**	**Matrix**	**Sample Relationships**	**Expected targets**	**Detected / Determined**		**Not Detected / Not Determined**		**Not Tested**	
					(%)	***(n)***	***(%)***	***(n)***	***(%)***	***(n)***
ARBO24S-08	Japanese encephalitits virus	Transport Medium	DS3_3	Japanese encephalitis virus	37.9	11	20.7	6	41.4	12



Groups below n=5: Altona Diagnostics (n=1), Altona Diagnostics - Altona Diagnostics RealStar (n=1), Clonit (n=1), Clonit - Clonit quanty kit (n=1), Geno Sen's (n=1), Geno Sen's - Geno Sen's Real Time Kit (n=1), Mikrogen (n=2), Mikrogen - Mikrogen alphaCube (n=2), Oxford Nanopore Technologies (n=2), Oxford Nanopore Technologies - Oxford Nanopore GridION (n=1), Oxford Nanopore Technologies - Oxford Nanopore MinION (n=1), Progenie Molecular (n=3), Progenie Molecular - Progenie Molecular RealCycler (n=3), Seegene (n=1), Seegene - Seegene Novaplex (n=1), Vitassay (n=2), Vitassay - Vitassay Real-Time PCR (n=2), bioPerfectus (n=1), bioPerfectus - bioPerfectus Real Time PCR (n=1), In-House - Conventional In-House PCR (n=2), In-House - Conventional Sequencing Analysis (n=2)
Groups Rolled Up: gerbion - gerbion virella (n=5)