Individual Report	QCMD 2022 Neisseria gonorrhoeae DNA EQA Programme

Catalogue Code:	Ref Code:	Challenge:	Analysis Type:	Dataset:	Report UID:	Laboratory
QAB034126	NgDNA22	C1	Qualitative	532357	2677/532357/4407	CZ023

Intended Results / Panel Composition

Sample Code	Sample Content	Matrix	Sample Relationships [1]	Detection Frequency [2]	Sample Status [3]	Percentage Correct (All) [4]	
						(%)	*(n)*
NgDNA22C1-01	N. gonorrhoeae	Urine	DS1_1	Frequently Detected	CORE	100.0	50
NgDNA22C1-02	N. gonorrhoeae	Simulated swab	-	Frequently Detected	CORE	100.0	50
NgDNA22C1-03	Negative	Urine	-	Negative	CORE	100.0	50
NgDNA22C1-04	N. gonorrhoeae	Urine	DS1_2	Frequently Detected	CORE	100.0	50
NgDNA22C1-05	N. gonorrhoeae + C. trachomatis (LGV)	Urine	-	Detected	CORE	90.0	50

[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] **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] **Percentage Correct (All):** Percentage of datasets (%) reporting the correct qualitative result and the total number of datasets (n) reported for each panel member.
For further details please refer to the current participant manual.

Your Summary Results

EQA Assessment Group [1]	GeneProof Real Time PCR kit
Core Panel Detection (Qualitative) Score [2]	0

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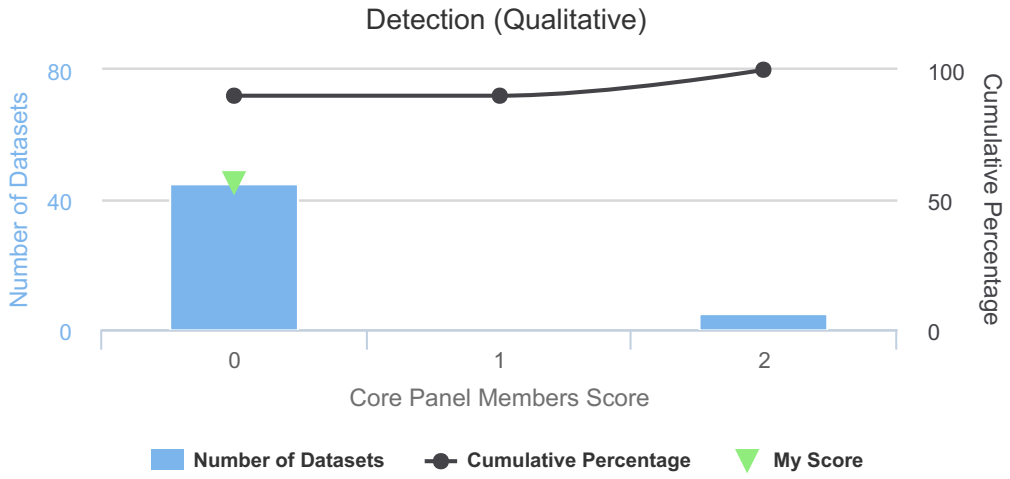
Core Panel Members Results

Sample Code	Qualitative Results			Your Quantitative Data (for information only) [3]		
	Percentage Correct (All) [4]	Your Result [5]	Detection Score [6]	Reported Value	Unitage	Cycle Threshold
NgDNA22C1-01	100.0	Positive	0		N/A	26.19
NgDNA22C1-02	100.0	Positive	0		N/A	22.32
NgDNA22C1-03	100.0	Negative	0		N/A	-
NgDNA22C1-04	100.0	Positive	0		N/A	32.11
NgDNA22C1-05	90.0	Positive	0		N/A	34.49

[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] **Quantitative Data (for information only):** This is the quantitative value, unitage and cycle threshold you provided when you submitted your results. For qualitative programmes this information is not used as part of your formal EQA assessment.
[4] **Percentage Correct (All):** Percentage of datasets (%) reporting the correct qualitative results for each panel member.
[5] **Your Result:** The qualitative result you reported for each sample within this EQA challenge / distribution.
[6] **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.

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".

For further details please refer to the current participant manual.

My Workflow Details

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

Name	Neisseria gonorrhoeae-croBEE (v2)
Description	
Targets	B Neisseria gonorrhoeae

Assays	*Extraction* - GeneProof - croBEE NA16 Nucleic Acid Extraction System
	• Commercial
	  ◦ Kit Manufacturer: *GeneProof*
	  ◦ Kit Type: *croBEE 201A Nucleic Acid Extraction Kit*
	Amplification - GeneProof - croBEE Real-Time PCR System
	• Commercial
	  ◦ Kit Manufacturer: *GeneProof*
	  ◦ Kit Type: *GeneProof Neisseria gonorrhoeae PCR Kit*
	  ◦ Kit Version: *ISEX*

Further Programme Details

Number of Participants	35
Number of Countries	12
Number of Respondents	35
Number of Datasets Submitted	50
Qualitative Results Returned	50 (100.0%)

EQA Programme Aims

To assess proficiency of laboratories in the detection of *Neisseria gonorrhoeae* using molecular technologies.

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.

Additional Core Samples Information

The following section has been categorised as shown below:

Core ► Qualitative

Individual Panel Member Analysis (Qualitative)

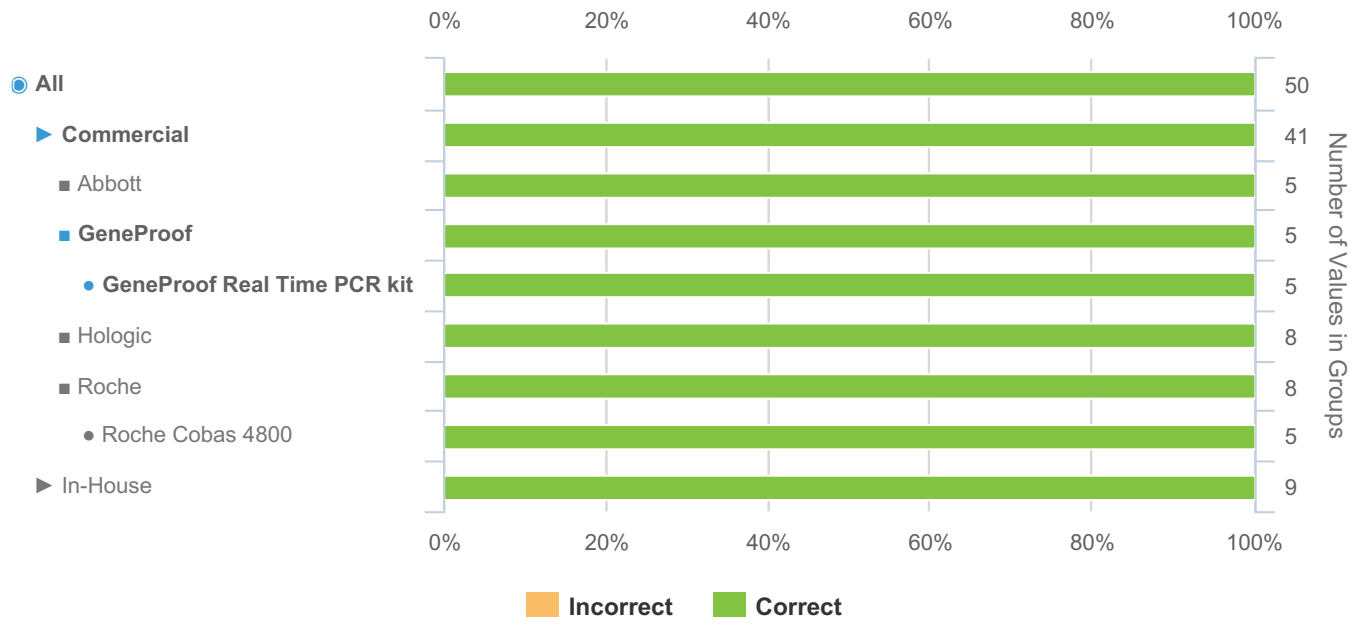
Qualitative analysis for each panel member is provided in relation to your EQA assessment group. EQA assessment groups are established using the molecular workflow information reported by all participants within this EQA challenge / distribution. The principal level of assessment is at the individual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

NgDNA22C1-01 - Qualitative Results Breakdown

Sample Code	Sample Content	Matrix	Sample Relationships	Detection Frequency	Sample Status	Percentage Correct (All)	
						(%)	*(n)*
NgDNA22C1-01	N. gonorrhoeae	Urine	DS1_1	Frequently Detected	CORE	100.0	50

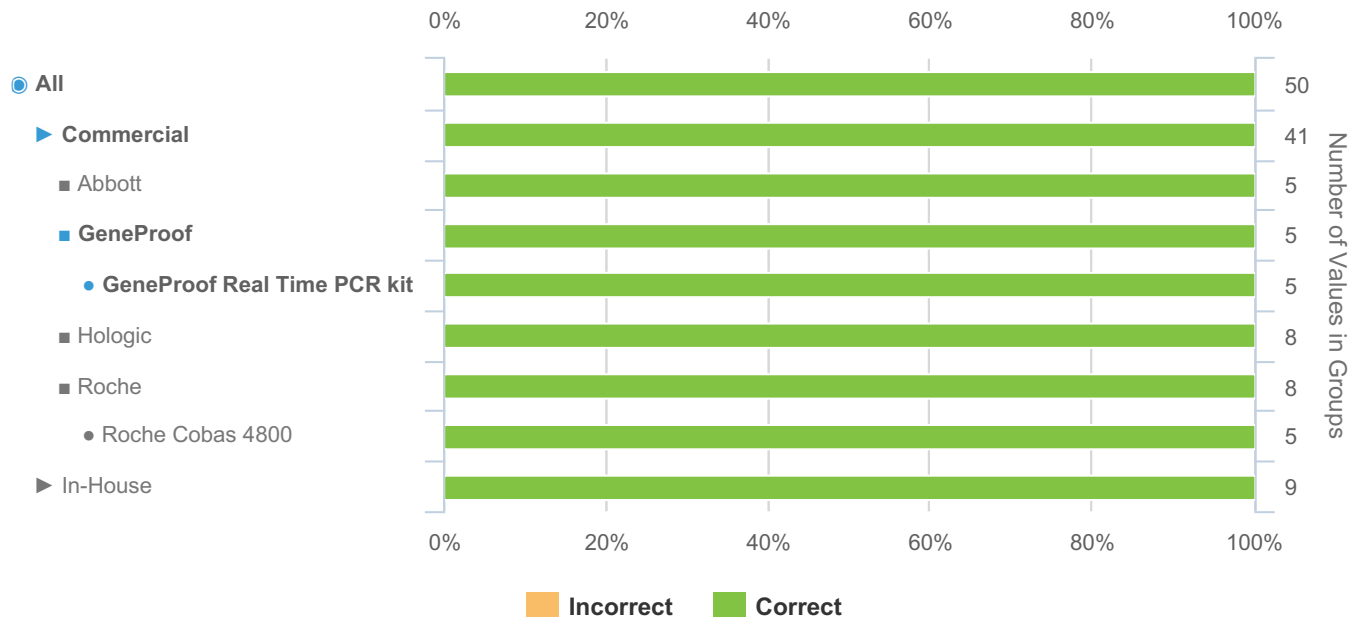


Groups below n=5: AB Analitica (n=4), AB Analitica - AB Analitica REALQUALITY RQ (n=4), Abbott - Abbott Alinity M (n=1), Abbott - Abbott RealTime m2000 (n=4), AusDiagnostics (n=1), AusDiagnostics - AusDiagnostics TademPlex (n=1), BD Molecular Diagnostics (n=2), BD Molecular Diagnostics - BD MAX (n=1), BD Molecular Diagnostics - BD ProbeTec (n=1), Goffin Molecular Technologies (n=1), Goffin Molecular Technologies - Goffin Presto (n=1), QIAGEN (n=3), QIAGEN - QIAGEN Artus Real Time (n=3), Randox (n=1), Randox - Randox Multiplex Array (n=1), Roche - Roche Cobas 6800/8800 (n=3), Seegene (n=3), Seegene - Seegene Allplex (n=2), Seegene - Seegene Anyplex (n=1)

Groups Rolled Up: Hologic - Hologic Aptima (n=8), In-House - Real-time In-House PCR (n=9)

NgDNA22C1-02 - Qualitative Results Breakdown

Sample Code	Sample Content	Matrix	Sample Relationships	Detection Frequency	Sample Status	Percentage Correct (All)	
						(%)	*(n)*
NgDNA22C1-02	N. gonorrhoeae	Simulated swab	-	Frequently Detected	CORE	100.0	50

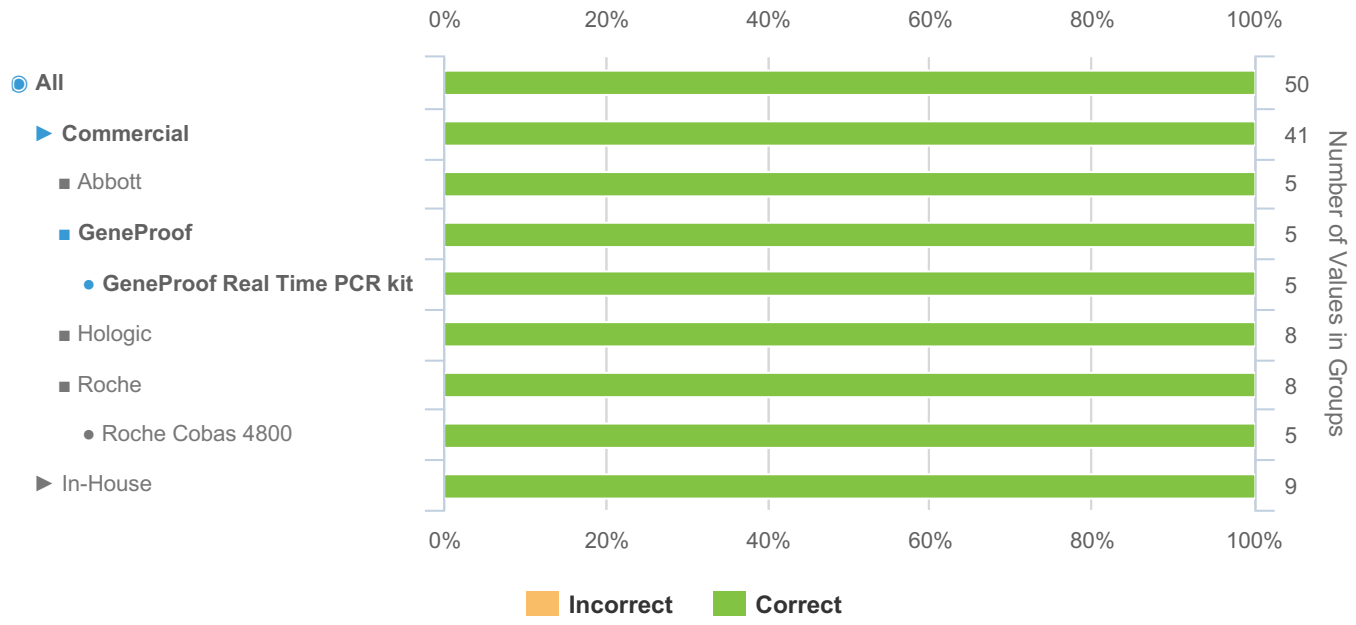


Groups below n=5: AB Analitica (n=4), AB Analitica - AB Analitica REALQUALITY RQ (n=4), Abbott - Abbott Alinity M (n=1), Abbott - Abbott RealTime m2000 (n=4), AusDiagnostics (n=1), AusDiagnostics - AusDiagnostics TademPlex (n=1), BD Molecular Diagnostics (n=2), BD Molecular Diagnostics - BD MAX (n=1), BD Molecular Diagnostics - BD ProbeTec (n=1), Goffin Molecular Technologies (n=1), Goffin Molecular Technologies - Goffin Presto (n=1), QIAGEN (n=3), QIAGEN - QIAGEN Artus Real Time (n=3), Randox (n=1), Randox - Randox Multiplex Array (n=1), Roche - Roche Cobas 6800/8800 (n=3), Seegene (n=3), Seegene - Seegene Allplex (n=2), Seegene - Seegene Anyplex (n=1)

Groups Rolled Up: Hologic - Hologic Aptima (n=8), In-House - Real-time In-House PCR (n=9)

NgDNA22C1-03 - Qualitative Results Breakdown

Sample Code	Sample Content	Matrix	Sample Relationships	Detection Frequency	Sample Status	Percentage Correct (All)	
						(%)	*(n)*
NgDNA22C1-03	Negative	Urine	-	Negative	CORE	100.0	50

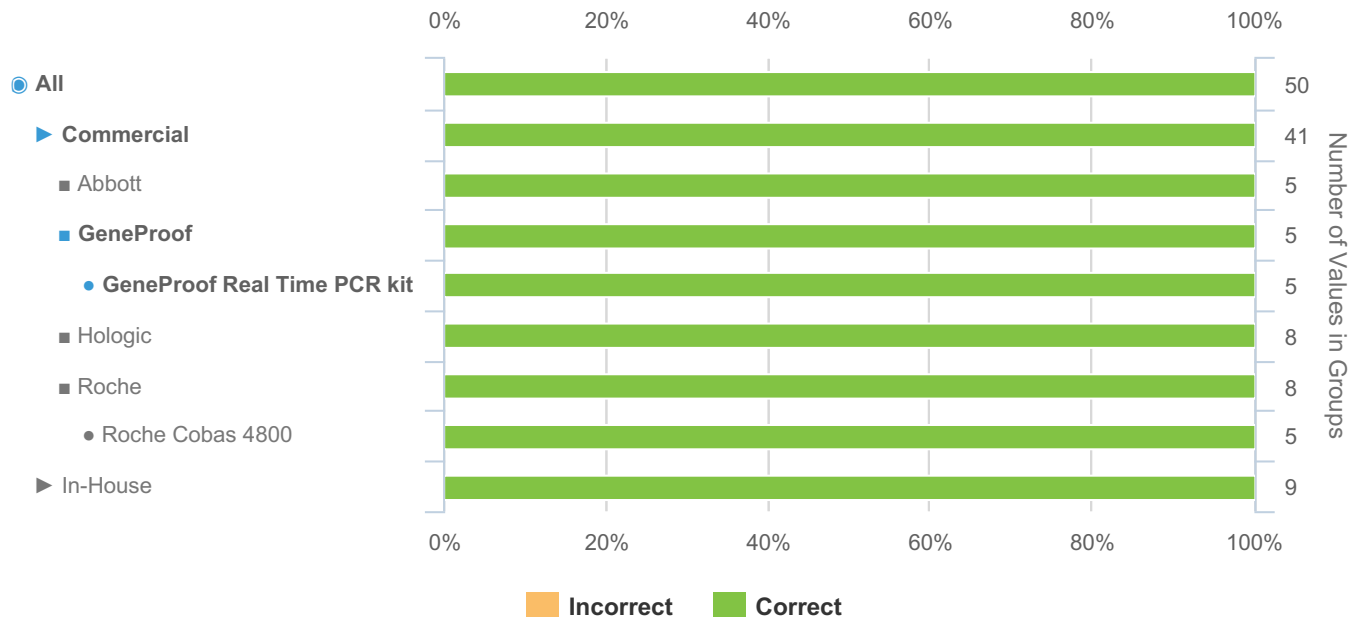


Groups below n=5: AB Analitica (n=4), AB Analitica - AB Analitica REALQUALITY RQ (n=4), Abbott - Abbott Alinity M (n=1), Abbott - Abbott RealTime m2000 (n=4), AusDiagnostics (n=1), AusDiagnostics - AusDiagnostics TademPlex (n=1), BD Molecular Diagnostics (n=2), BD Molecular Diagnostics - BD MAX (n=1), BD Molecular Diagnostics - BD ProbeTec (n=1), Goffin Molecular Technologies (n=1), Goffin Molecular Technologies - Goffin Presto (n=1), QIAGEN (n=3), QIAGEN - QIAGEN Artus Real Time (n=3), Randox (n=1), Randox - Randox Multiplex Array (n=1), Roche - Roche Cobas 6800/8800 (n=3), Seegene (n=3), Seegene - Seegene Allplex (n=2), Seegene - Seegene Anyplex (n=1)

Groups Rolled Up: Hologic - Hologic Aptima (n=8), In-House - Real-time In-House PCR (n=9)

NgDNA22C1-04 - Qualitative Results Breakdown

Sample Code	Sample Content	Matrix	Sample Relationships	Detection Frequency	Sample Status	Percentage Correct (All)	
						(%)	*(n)*
NgDNA22C1-04	N. gonorrhoeae	Urine	DS1_2	Frequently Detected	CORE	100.0	50

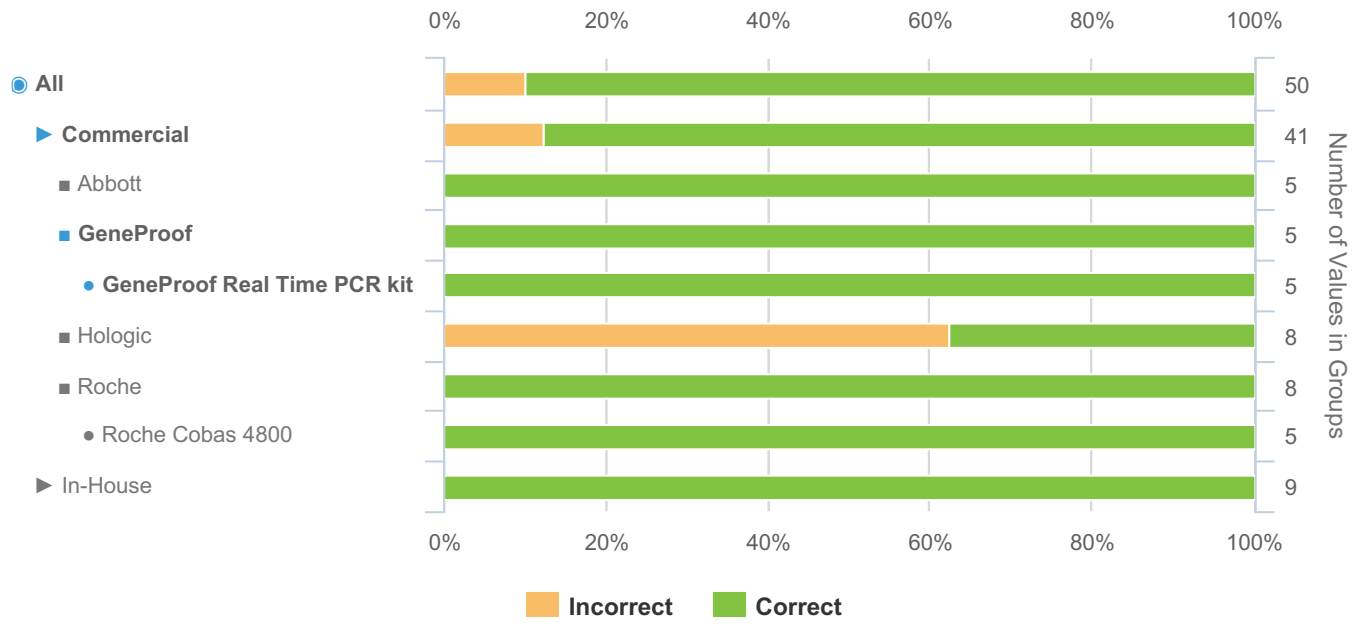


Groups below n=5: AB Analitica (n=4), AB Analitica - AB Analitica REALQUALITY RQ (n=4), Abbott - Abbott Alinity M (n=1), Abbott - Abbott RealTime m2000 (n=4), AusDiagnostics (n=1), AusDiagnostics - AusDiagnostics TademPlex (n=1), BD Molecular Diagnostics (n=2), BD Molecular Diagnostics - BD MAX (n=1), BD Molecular Diagnostics - BD ProbeTec (n=1), Goffin Molecular Technologies (n=1), Goffin Molecular Technologies - Goffin Presto (n=1), QIAGEN (n=3), QIAGEN - QIAGEN Artus Real Time (n=3), Randox (n=1), Randox - Randox Multiplex Array (n=1), Roche - Roche Cobas 6800/8800 (n=3), Seegene (n=3), Seegene - Seegene Allplex (n=2), Seegene - Seegene Anyplex (n=1)

Groups Rolled Up: Hologic - Hologic Aptima (n=8), In-House - Real-time In-House PCR (n=9)

NgDNA22C1-05 - Qualitative Results Breakdown

Sample Code	Sample Content	Matrix	Sample Relationships	Detection Frequency	Sample Status	Percentage Correct (All)	
						(%)	*(n)*
NgDNA22C1-05	N. gonorrhoeae + C. trachomatis (LGV)	Urine	-	Detected	CORE	90.0	50



Groups below n=5: AB Analitica (n=4), AB Analitica - AB Analitica REALQUALITY RQ (n=4), Abbott - Abbott Alinity M (n=1), Abbott - Abbott RealTime m2000 (n=4), AusDiagnostics (n=1), AusDiagnostics - AusDiagnostics TademPlex (n=1), BD Molecular Diagnostics (n=2), BD Molecular Diagnostics - BD MAX (n=1), BD Molecular Diagnostics - BD ProbeTec (n=1), Goffin Molecular Technologies (n=1), Goffin Molecular Technologies - Goffin Presto (n=1), QIAGEN (n=3), QIAGEN - QIAGEN Artus Real Time (n=3), Randox (n=1), Randox - Randox Multiplex Array (n=1), Roche - Roche Cobas 6800/8800 (n=3), Seegene (n=3), Seegene - Seegene Allplex (n=2), Seegene - Seegene Anyplex (n=1)

Groups Rolled Up: Hologic - Hologic Aptima (n=8), In-House - Real-time In-House PCR (n=9)