

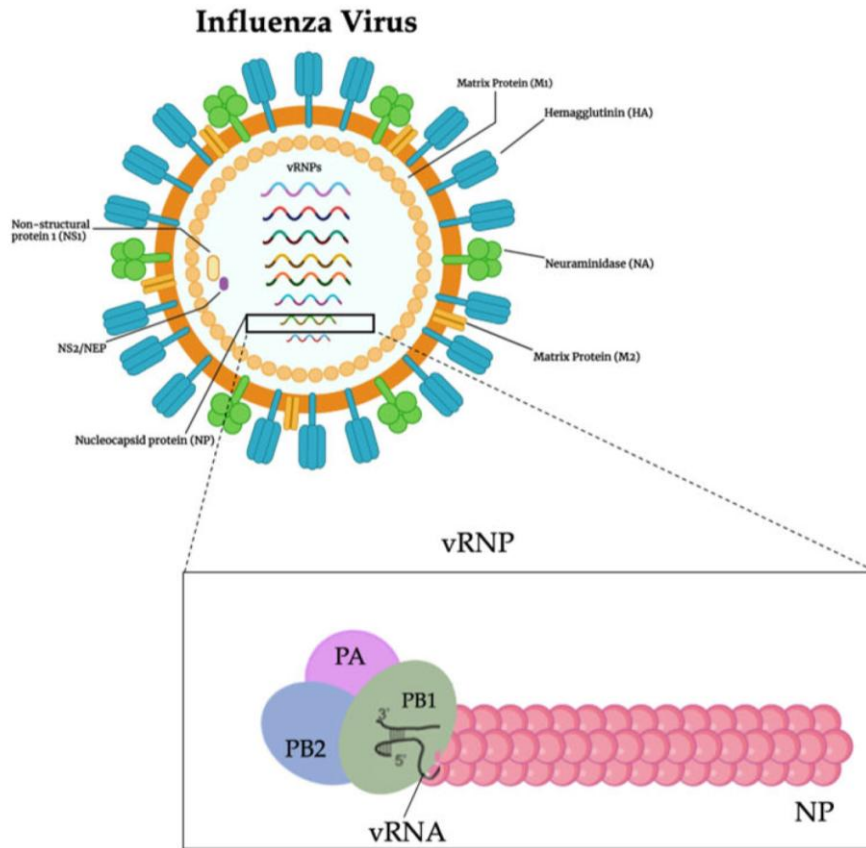


Application of Digital PCR for Sensitive Detection of Avian Influenza Viral RNA in Poultry Matrices with Low Viral Loads

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Background



(Imperia et al., 2023)

Avian influenza virus (AIV) is a highly contagious disease of poultry that causes significant economic losses and poses serious risks to animal and public health worldwide.

Sensitive and accurate diagnosis is critical for early detection, effective outbreak control, and surveillance.

Although real-time RT-PCR is the current standard for AIV diagnosis, it may have limited sensitivity in low viral load and complex poultry samples.

Digital PCR (dPCR) as a potential complementary/alternative method?

Objectives

```
graph TD; A[Objectives] --> B((1)); A --> C((2)); B --- D[To compare the analytical performance of dPCR with real-time RT-PCR for the detection and quantification of AIV genomes.]; C --- E[To evaluate the application of dPCR for sensitive and precise detection of AIV in diverse poultry sample matrices, particularly those with low viral loads.];
```

1

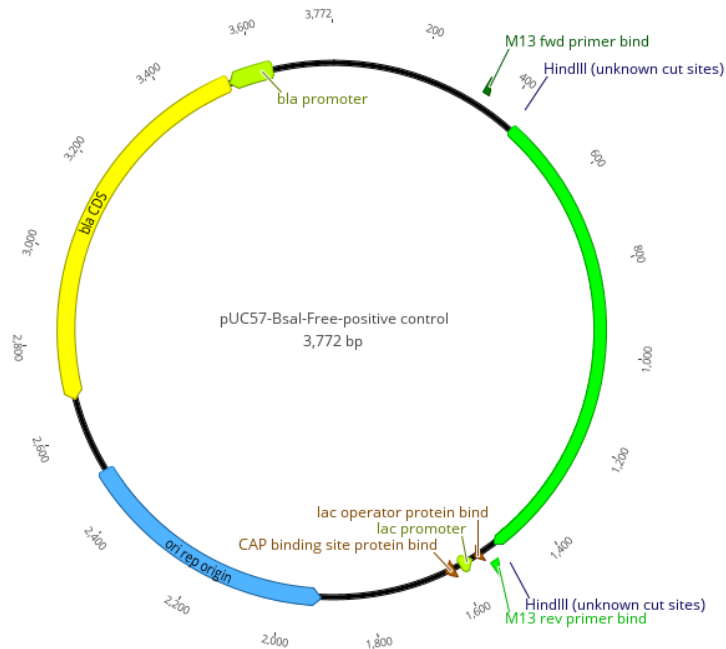
To compare the analytical performance of dPCR with real-time RT-PCR for the detection and quantification of AIV genomes.

2

To evaluate the application of dPCR for sensitive and precise detection of AIV in diverse poultry sample matrices, particularly those with low viral loads.

Materials and methods

A synthetic plasmid containing the **matrix (M)** gene of AIV was used as the reference material for analytical evaluation.



Consensus
Identity
1. pUC57-Bsal-Free-positive_control
2. 1.FluA(LC208490)

BioEdit Sequence Alignment Editor - [C:\Users\Acer\Desktop\1.fasta]

File Edit Sequence Alignment View Accessory Application RNA Options Window Help



Courier New 11 B

11 total sequences

Mode: Edit

Overwrite

Selection: 0

Position:

Sequence Mask: None

Numbering Mask: None

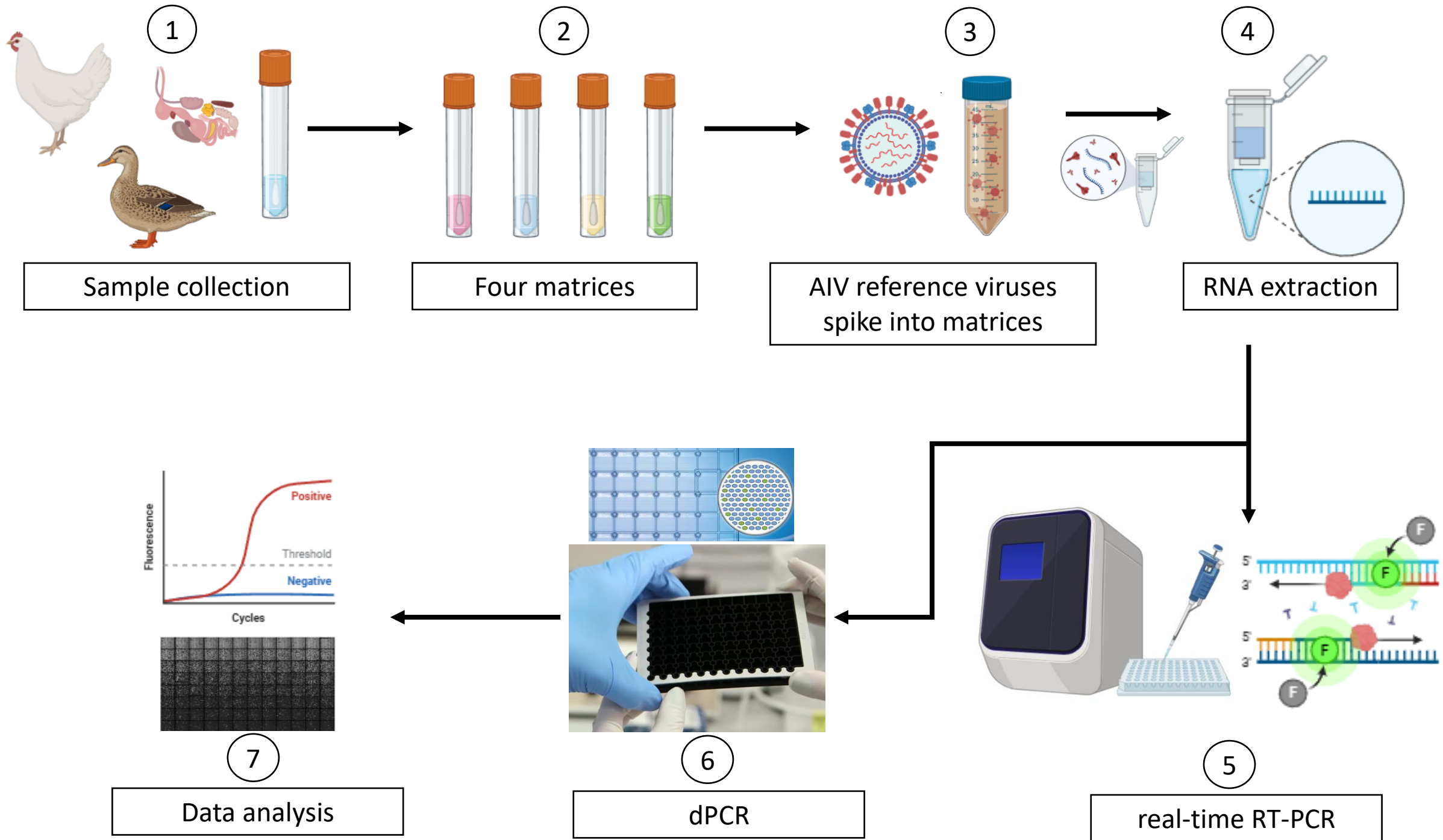
Start ruler at: 1

Scroll speed slow fast

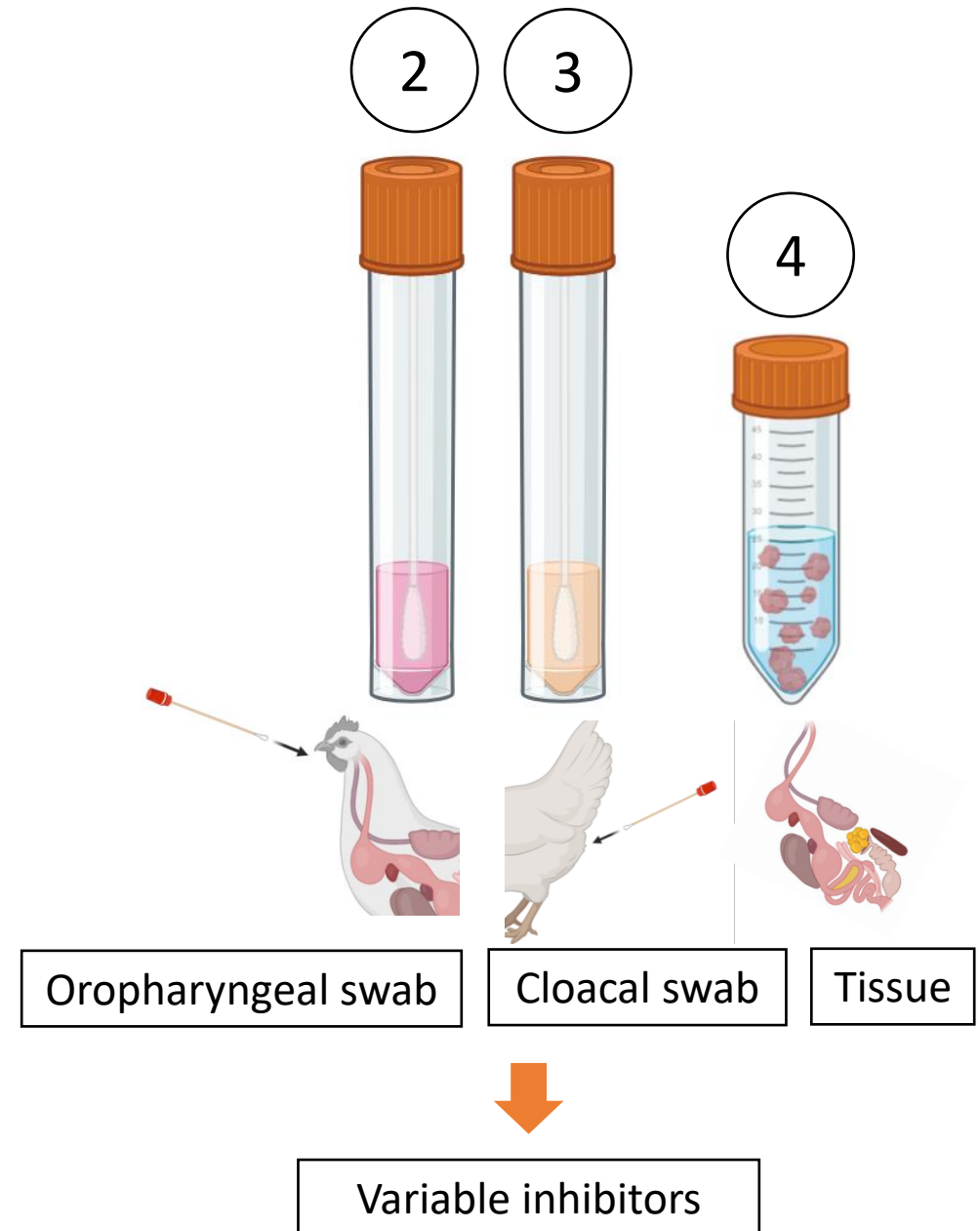
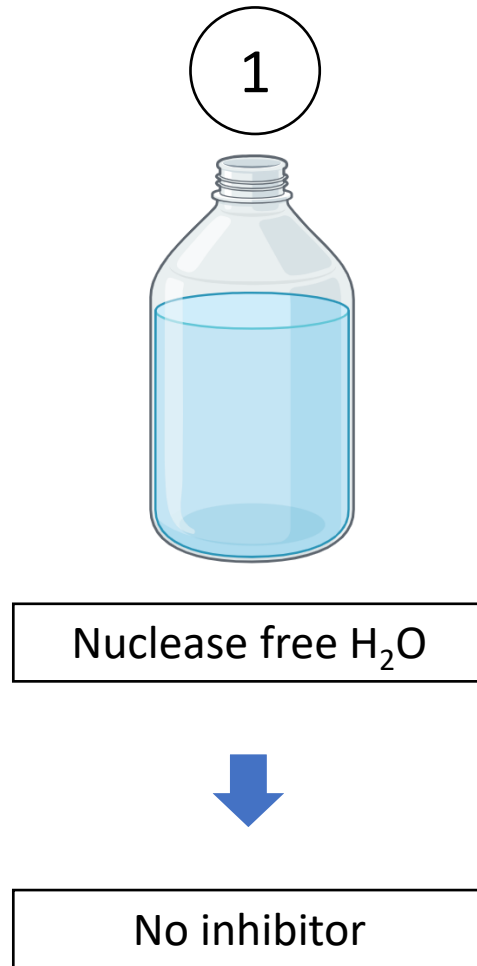
430 440 450 460 470 480 490 500 510 520 530 540 550

pUC57-Positi GCAAGCTTAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATTCATCAGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAGGATGTTTTTGCAATGGCTCCTCGGZ

1.FluA (LC208) -----AGATGAGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTCTATCATTCATCAGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAGGATGTTTTTGCA-----



Four matrices





Nuclease free H₂O



Quantification
range



LOD



Repeatability



Specificity

Three matrices



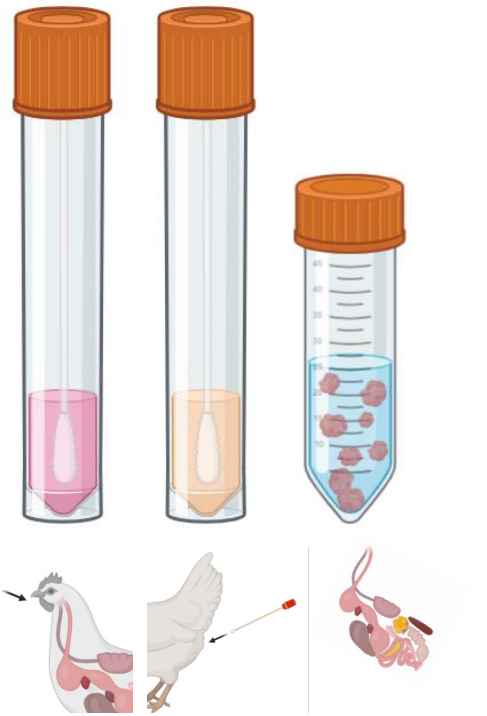
Viral loads



Correlation

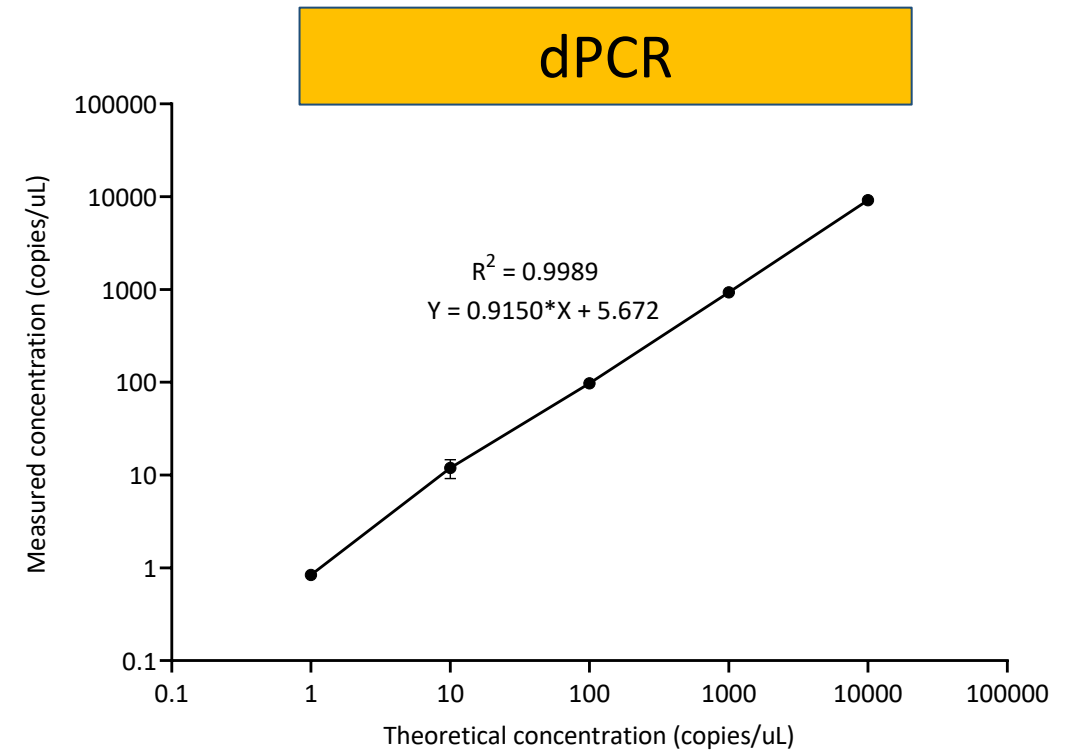
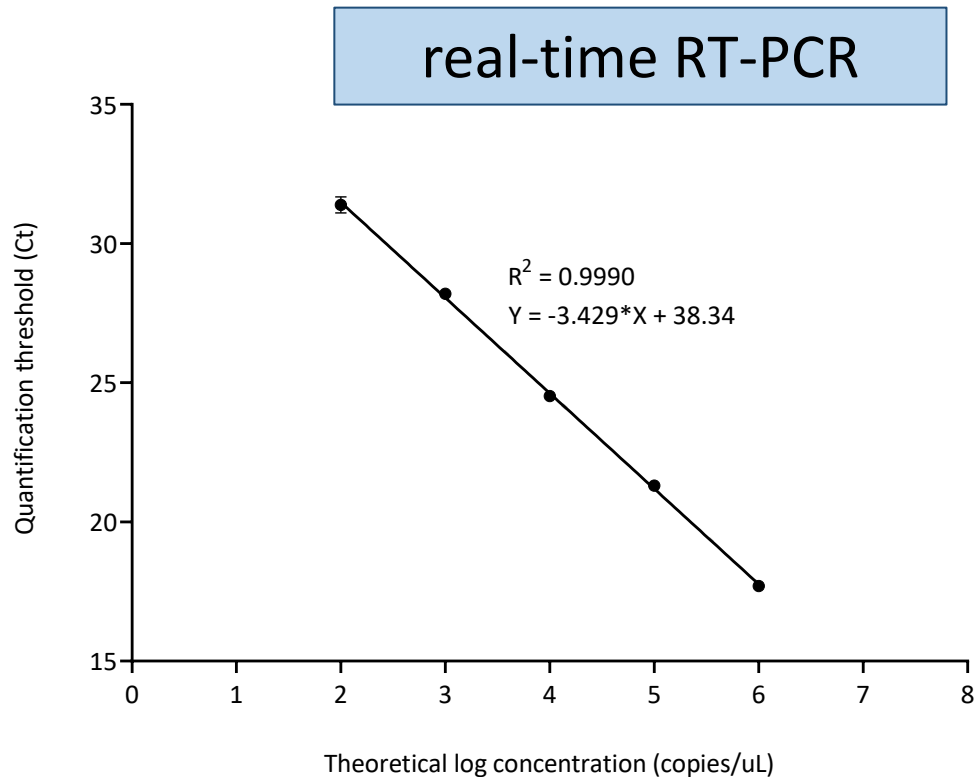
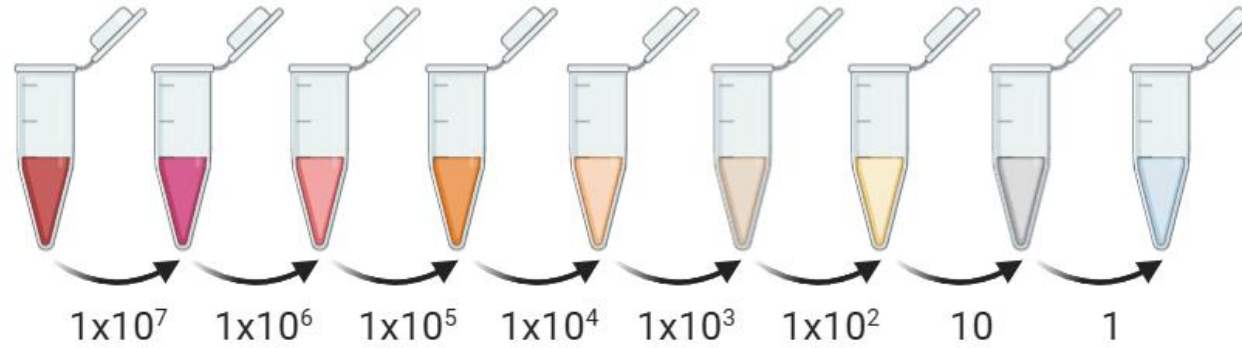


Bland-Altman



LOD : limit of detection

Results



Both methods showed strong linearity across 10-fold serial dilutions ($R^2 > 0.99$).

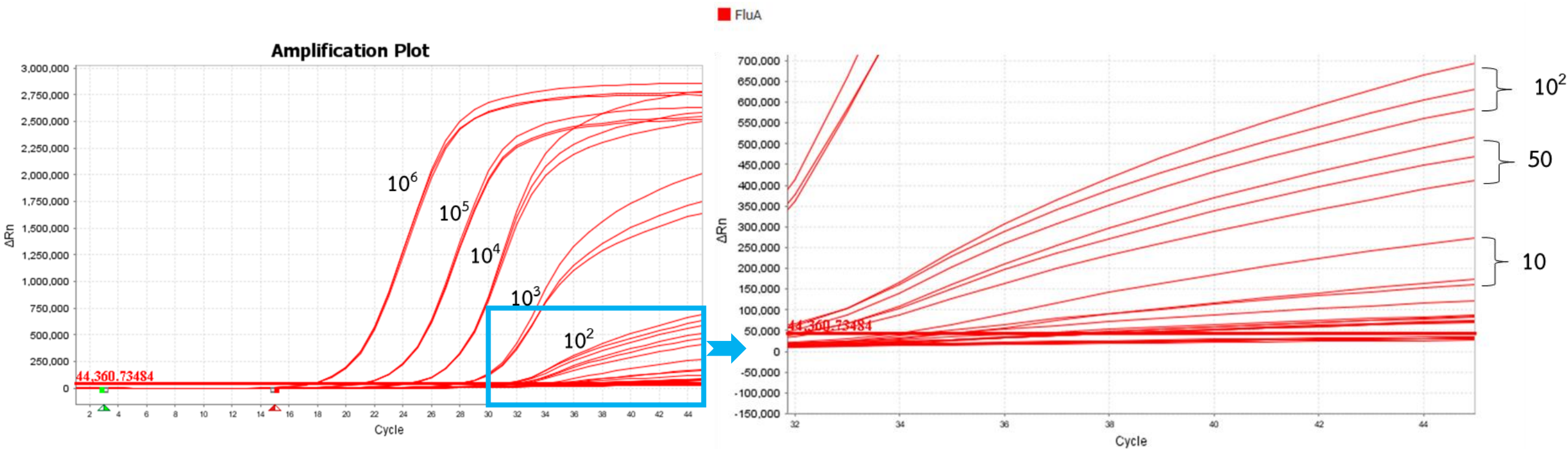
Quantification range

Theoretical concentration (copies/μL)	real-time RT-PCR (ct)				dPCR (copies/μL)			
	1	2	3	Average	1	2	3	Average
10 ⁶	17.74	17.67	17.67	17.69	ADR	ADR	ADR	ADR
10 ⁵	21.32	21.32	21.27	21.30	ADR	ADR	ADR	ADR
10 ⁴	24.53	24.44	24.59	24.52	8,776.8	9,366.2	9,322.4	9,155.14
10 ³	28.16	28.24	28.20	28.20	946.80	923.90	920.40	930.37
10 ²	31.11	31.68	31.38	31.39	95.80	101.90	93.78	97.16
50	31.98	32.41	32.15	32.18	50.39	46.67	52.91	49.99
10	38.20	34.52	35.19	35.97	11.92	14.62	9.15	11.89
5	37.56	37.37	36.57	37.17	4.21	3.64	7.40	5.08
2.5	38.41	37.96	UND	38.19	4.17	2.66	1.80	2.87
1	UND	UND	UND	UND	0.81	0.86	0.84	0.84

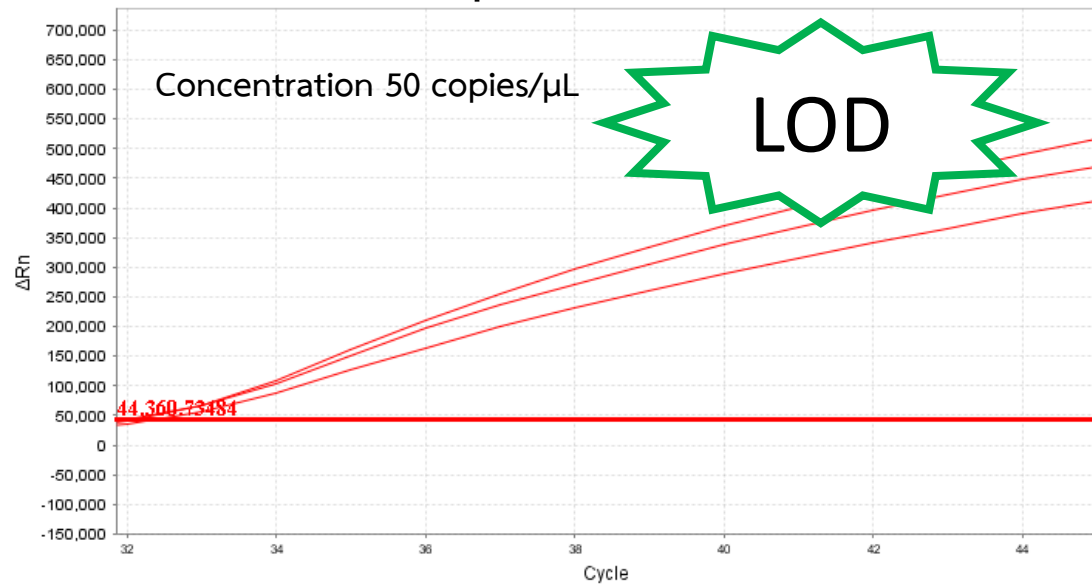
*UND = Under detected

*ADR = Above dynamic range (saturated)

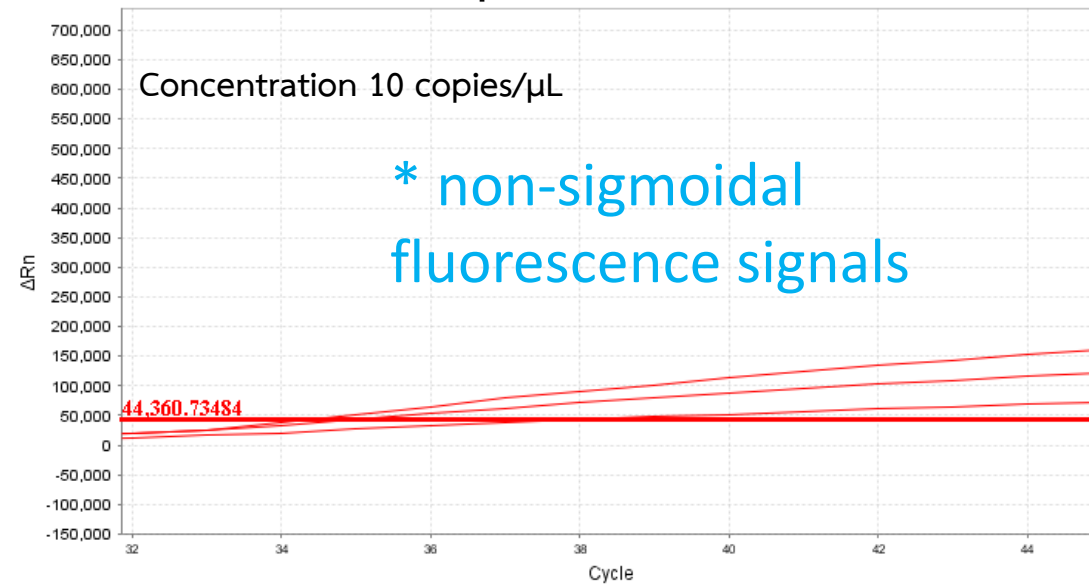
real time RT-PCR



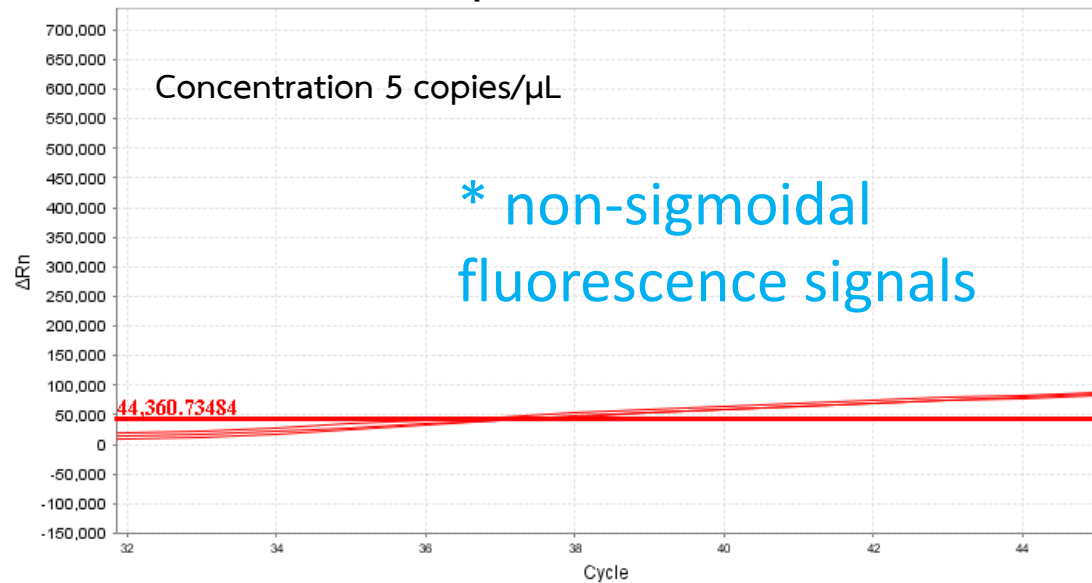
Amplification Plot



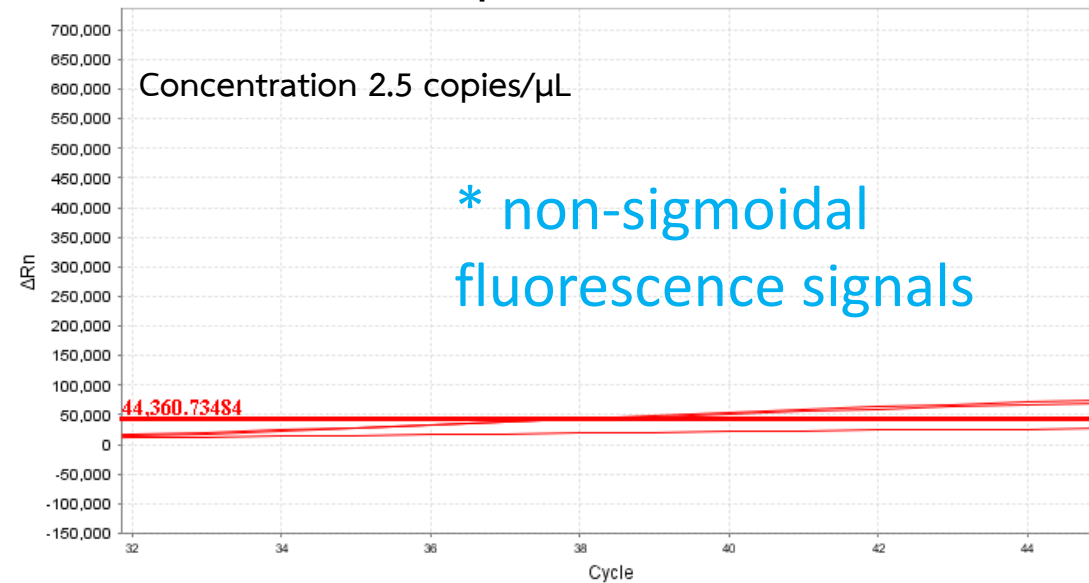
Amplification Plot



Amplification Plot



Amplification Plot



Quantification range

Theoretical concentration (copies/ μ L)	Real-time RT-PCR (ct)				Digital PCR (copies/ μ L)			
	1	2	3	Average	1	2	3	Average
10^6	17.74	17.67	17.67	17.69	ADR	ADR	ADR	ADR
10^5	21.32	21.32	21.27	21.30	ADR	ADR	ADR	ADR
10^4	24.53	24.44	24.59	24.52	8,776.8	9,366.2	9,322.4	9,155.14
10^3	28.16	28.24	28.20	28.20	946.80	923.90	920.40	930.37
10^2	31.11	31.68	31.38	31.39	95.80	101.90	93.78	97.16
50	31.98	32.41	32.15	32.18	50.39	46.67	52.91	49.99
10	38.20	34.52	35.19	35.97	11.92	14.62	9.15	11.89
5	37.56	37.37	36.57	37.17	4.21	3.64	7.40	5.08
2.5	38.41	37.96	UND	38.19	4.17	2.66	1.80	2.87
1	UND	UND	UND	UND	0.81	0.86	0.84	0.84

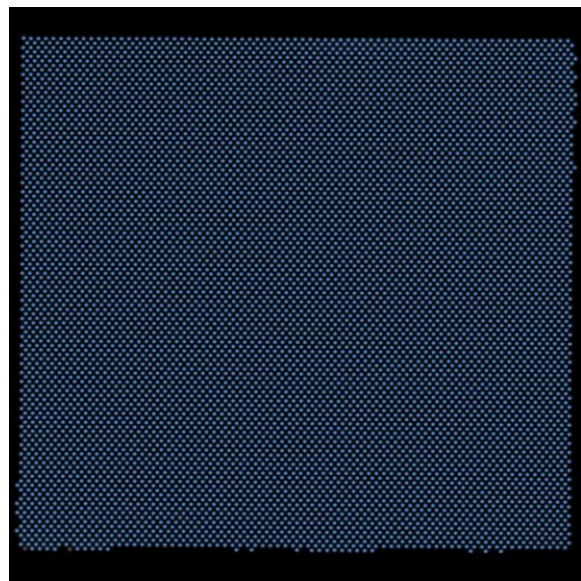
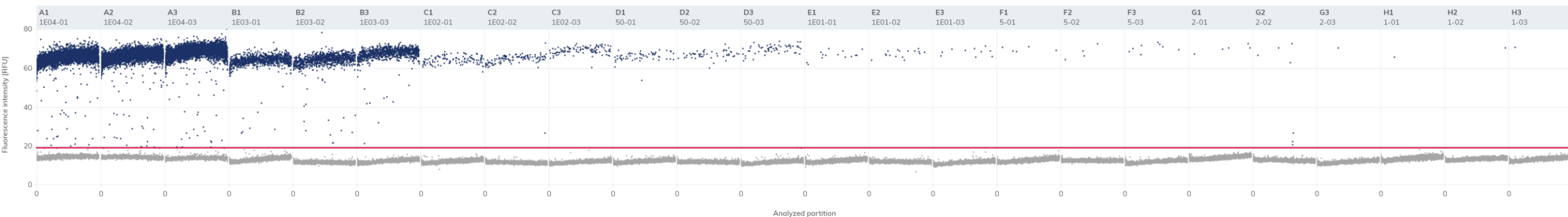
*UND = Under detected

*ADR = Above dynamic range (saturated)

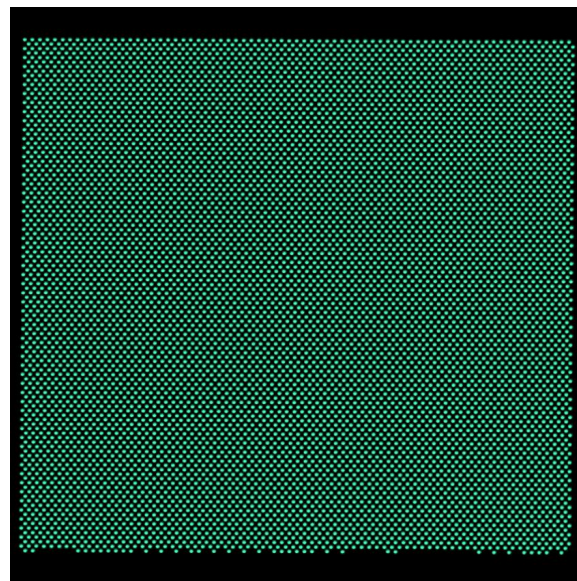
AIV (24 wells)

● Green

dPCR



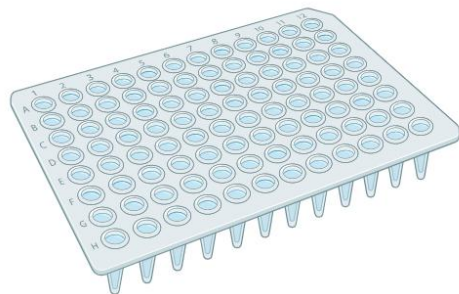
Valid partitions



Positive partitions

Theoretical concentration (copies/ μ L)	Valid	Positive	Negative
10^7	8,265	8,265	0
10^6	8,276	8,276	0
10^5	8,253	8,253	0
10^4	8,277	6,102	2,175
10^3	8,241	1,064	7,177
10^2	8,279	114	8,165
50	8,253	53	8,202
10	8,282	14	8,268
5	8,276	5	8,271
2.5	8,264	3	8,261
1	8,256	1	8,255

*saturated



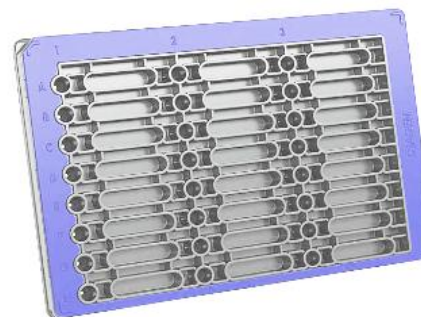
real-time RT-PCR



Quantification range
 $50 - \geq 10^6$ (copies/ μ L)



LOD
 50 (copies/ μ L)



dPCR



Quantification range
 $\leq 1 - 10^4$ (copies/ μ L)



LOD
 ≤ 1 (copies/ μ L)

Viral load categories (copies/ μ L)



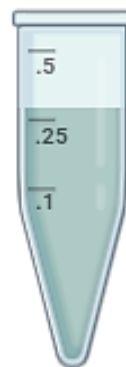
10^4

High



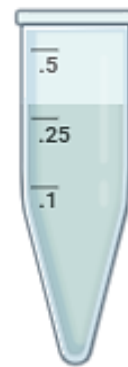
10^3

Intermediate



100

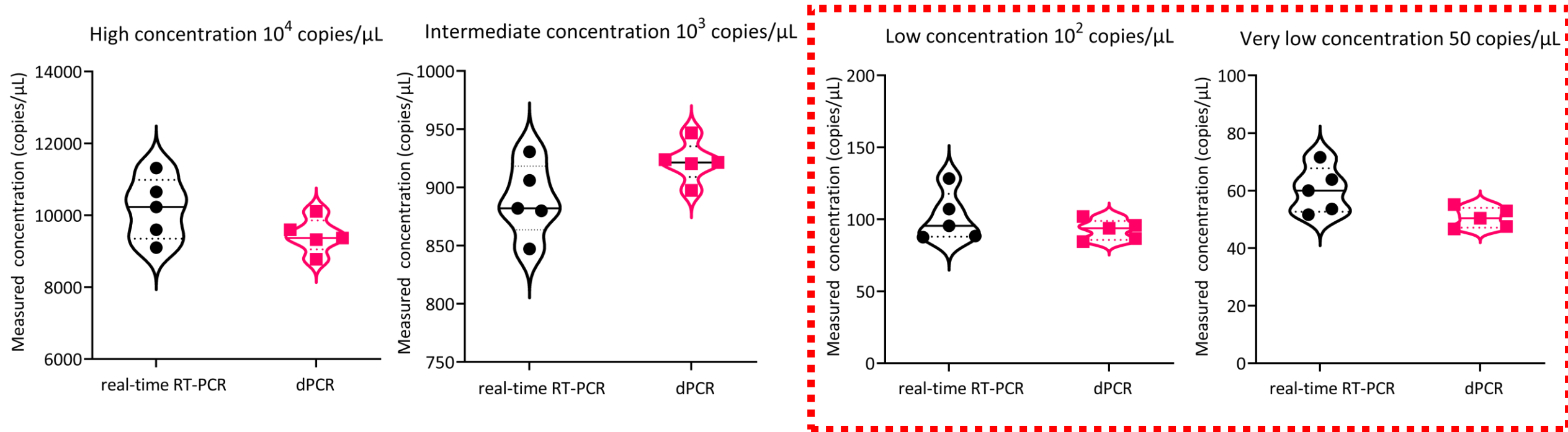
Low



50

Very low

Assay repeatability; intra-assay precision



Comparison of the repeatability is represented in a violin plot and it shows median values and the 25% and 75% interquartile ranges.

dPCR demonstrated improved precision at low and very low viral loads

Assay specificity

Inclusivity test

cross-reactivity panel

no contamination

almost perfect agreement

Agents	real-time RT-PCR			dPCR		
	1	2	3	1	2	3
HPAI H5N1 strain A/guinea fowl/Nigeria/KN-GF-14-16C_23VIR1455-1/2022	Pos	Pos	Pos	Pos	Pos	Pos
HPAI H5N5 strain A/European herring gull/Norway/2023-07-2935_23VIR9749-12/2023	Pos	Pos	Pos	Pos	Pos	Pos
HPAI H7N6 strain A/chicken/South Africa/SA2310_23VIR11588-2/2023	Pos	Pos	Pos	Pos	Pos	Pos
LP AI H7N3 strain A/chicken/Netherlands/23025569-021_24VIR4103-4/2023	Pos	Pos	Pos	Pos	Pos	Pos
LP AI H9N2 strain A/chicken/Niger/13-23_23VIR3551-49/2023	Pos	Pos	Pos	Pos	Pos	Pos
AAvV-1/chicken/Macedonia/1400-1_20VIR1984-5/2020 virulent strain	Neg	Neg	Neg	Neg	Neg	Neg
AOAV-1/Gallus gallus/Belgium/8744/2022 avirulent strain	Neg	Neg	Neg	Neg	Neg	Neg
IBV	Neg	Neg	Neg	Neg	Neg	Neg
<i>E. coli</i>	Neg	Neg	Neg	Neg	Neg	Neg
negative extraction control (NEC)	Neg	Neg	Neg	Neg	Neg	Neg
no template control (NTC)	Neg	Neg	Neg	Neg	Neg	Neg
Concordance					100	
Cohen's Kappa					1.0	



Nuclease free H₂O



Quantification
range



LOD



Repeatability



Specificity

Results

Three matrices



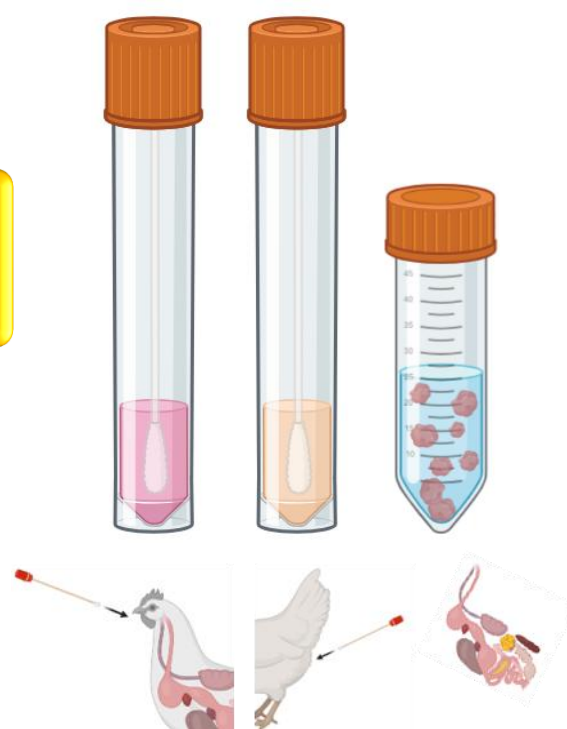
Viral loads



Correlation

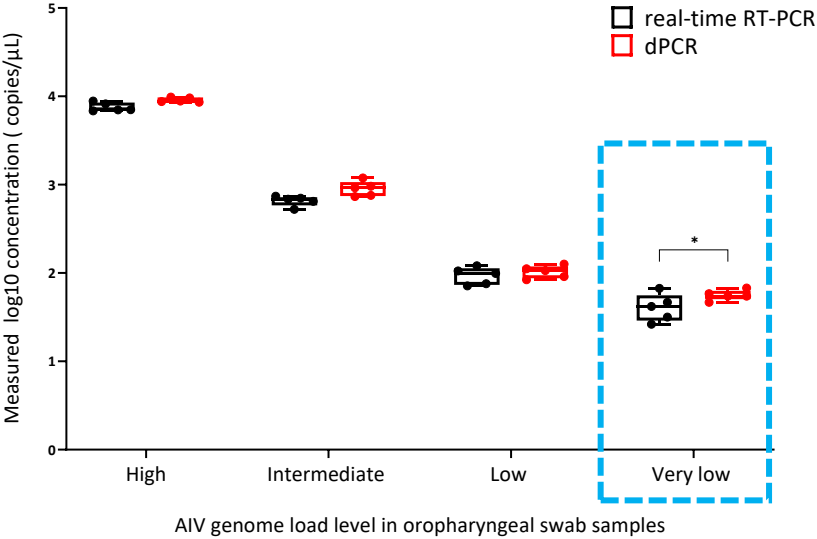


Bland-Altman

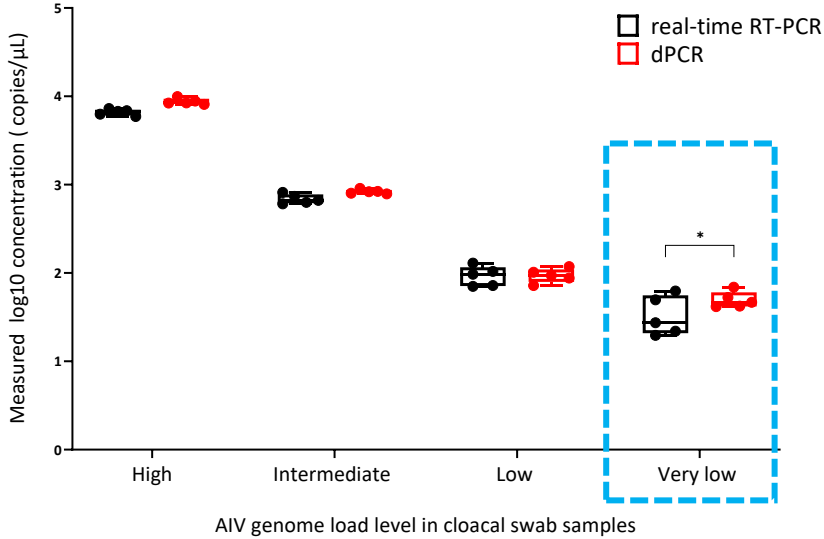


Viral load in matrices

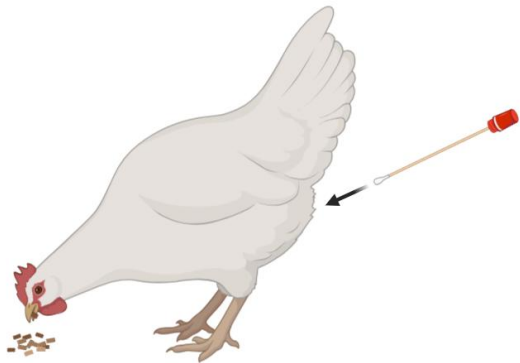
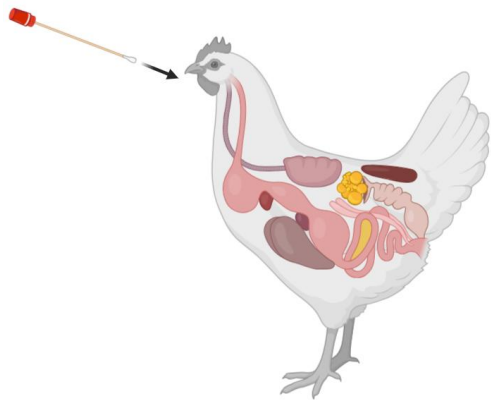
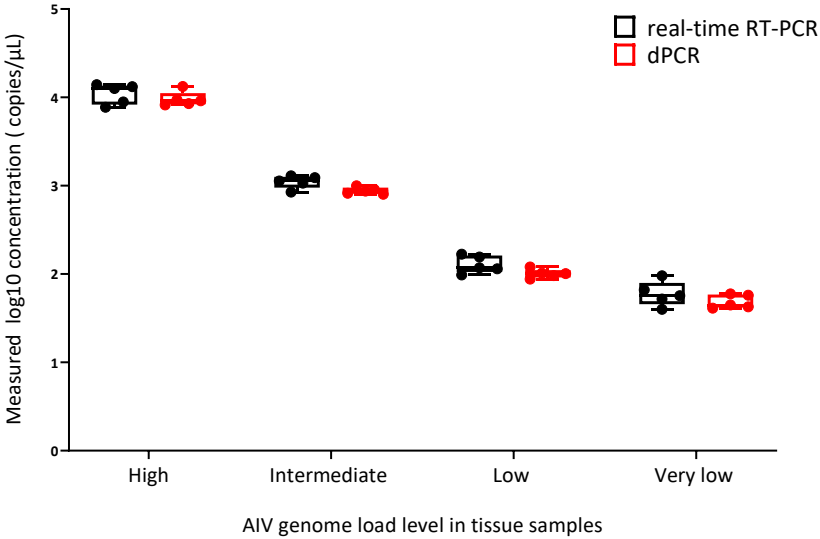
Oropharyngeal swab



Cloacal swab



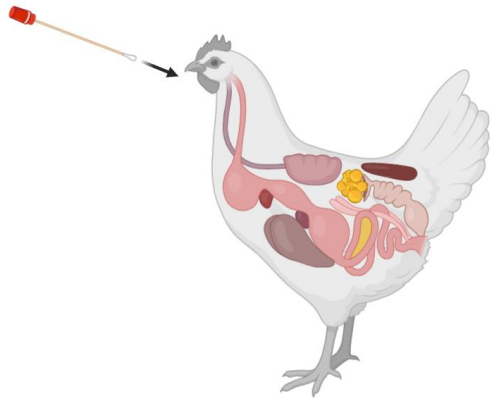
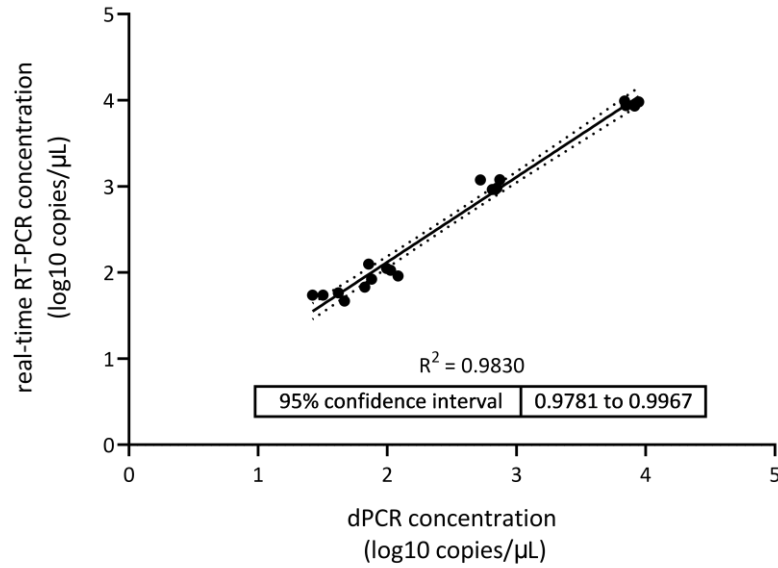
Tissue



Correlation analysis in matrices

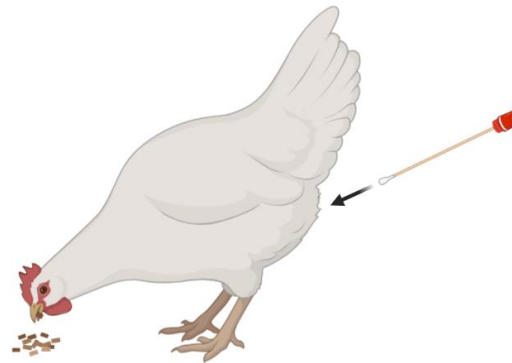
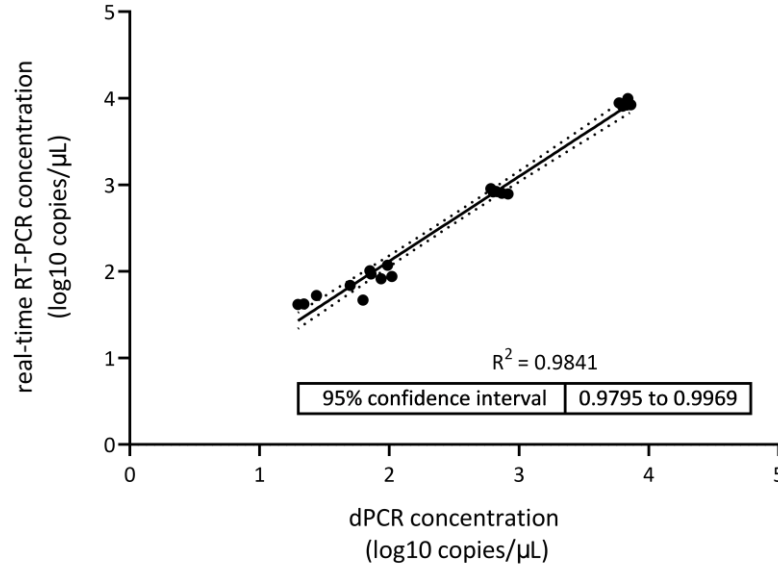
Oropharyngeal swab

Correlation of oropharyngeal swab



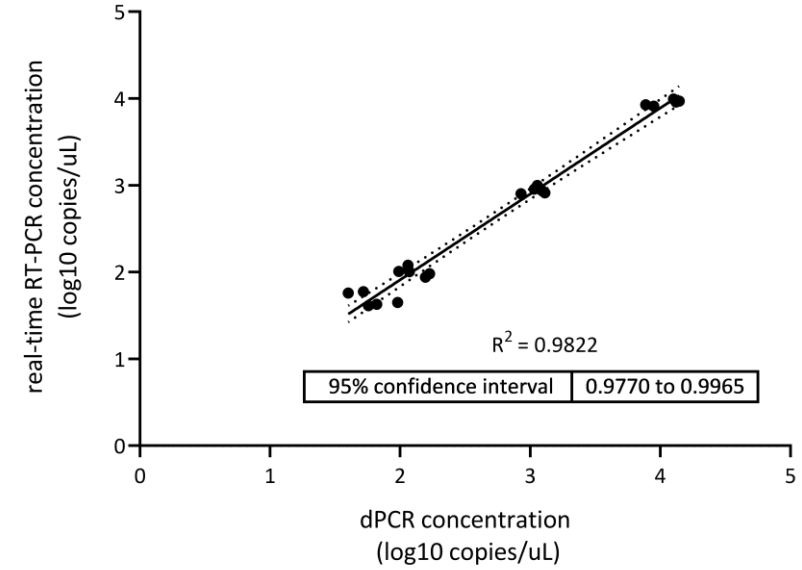
Cloacal swab

Correlation of cloacal swab



Tissue

Correlation of tissue sample



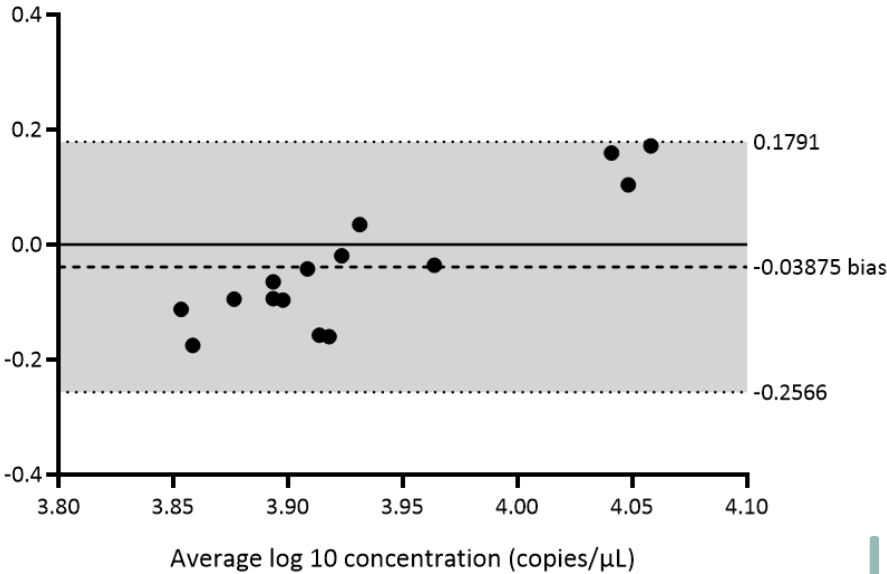
Bland–Altman analysis



10⁴

High

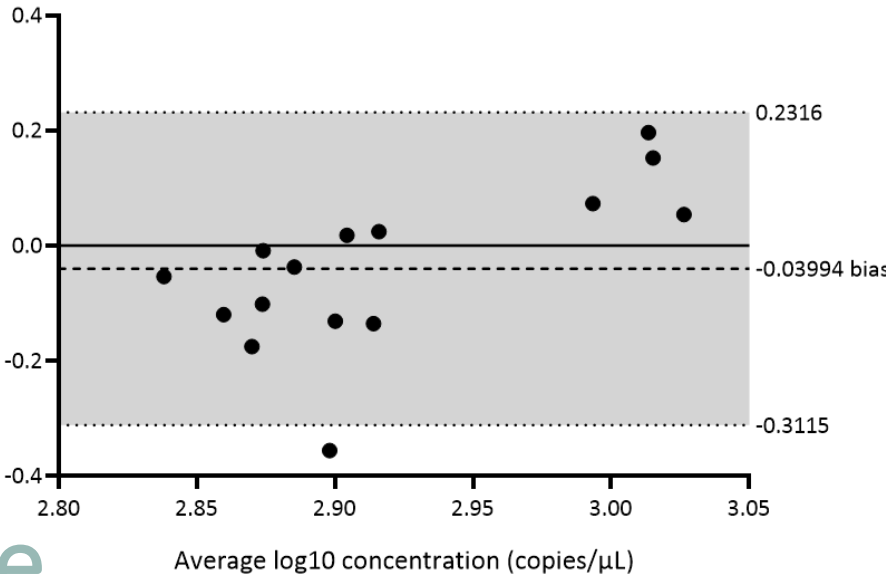
Difference in copy number
(log10 real-time RT-PCR - log10 dPCR)



10³

Intermediate

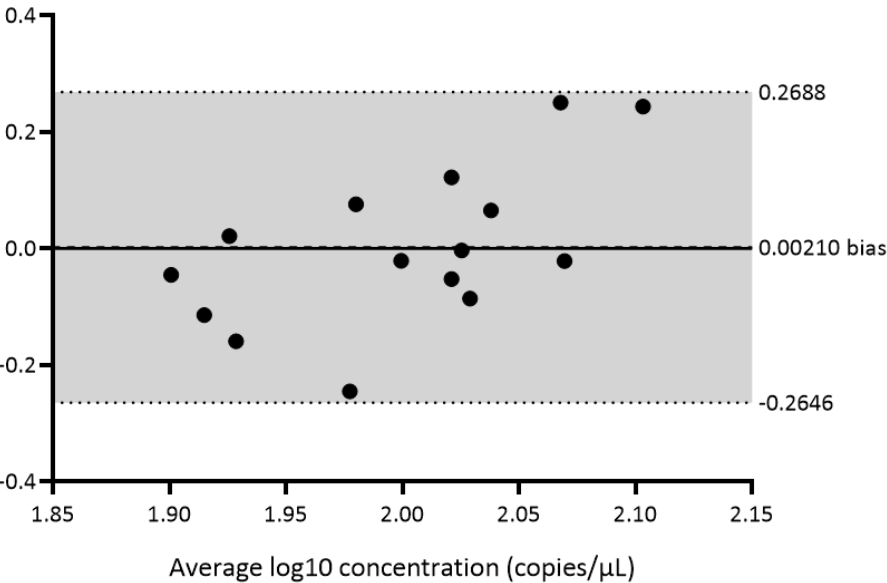
Difference in copy number
(log10 real-time RT-PCR - log10 dPCR)



10²

Low

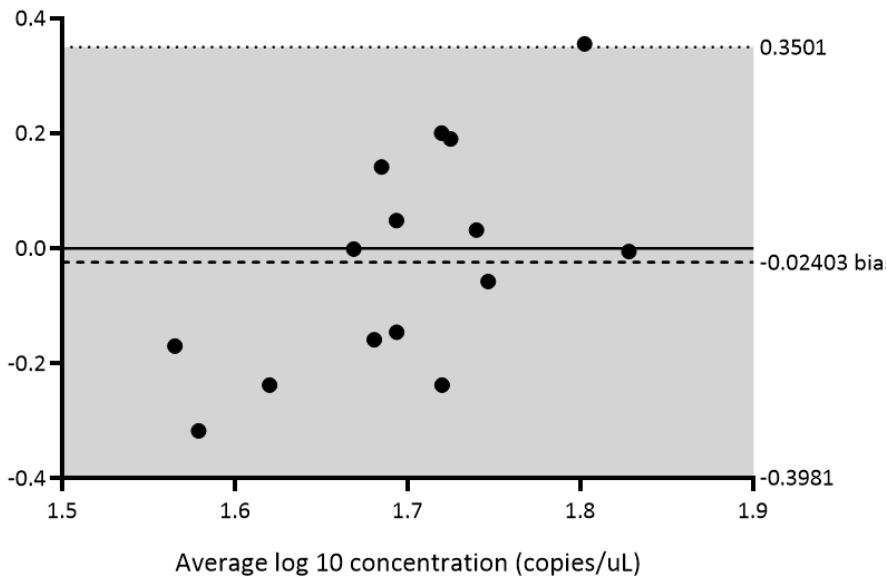
Difference in copy number
(log10 real-time RT-PCR - log10 dPCR)



50

Very low

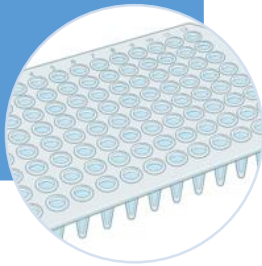
Difference in copy number
(log10 real-time RT-PCR - log10 dPCR)



Discussions and conclusion

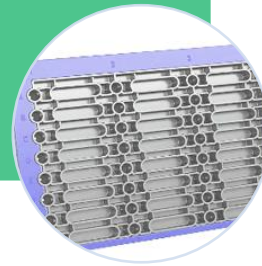
- real-time RT-PCR exhibited a wider quantification range, while dPCR was limited at high target concentrations because of partition saturation. dPCR showed higher sensitivity.

1



- dPCR performed better in swab samples, likely because it is more tolerant of PCR inhibitors, while both methods showed similar performance in tissue samples.

2



- Both methods showed excellent agreement and produced comparable results within the validated quantification range.

3



Critiques and future directions

1

This study focused on influenza A genome detection only and did not evaluate subtype identification by dPCR.

2

Development of subtype-specific or multiplex dPCR assays for HA and NA genes (e.g., H5 and H7) is needed.

3

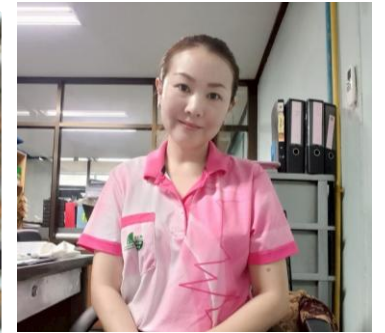
Future studies should validate these assays using diverse field samples to strengthen AIV surveillance and preparedness.

Acknowledgements



I would like to express my sincere gratitude to my **Director** for continuous support and encouragement throughout this study.

I would also like to thank my **co-authors** for their valuable guidance and contributions.



The Virology Laboratory for their technical assistance, collaboration, and support.

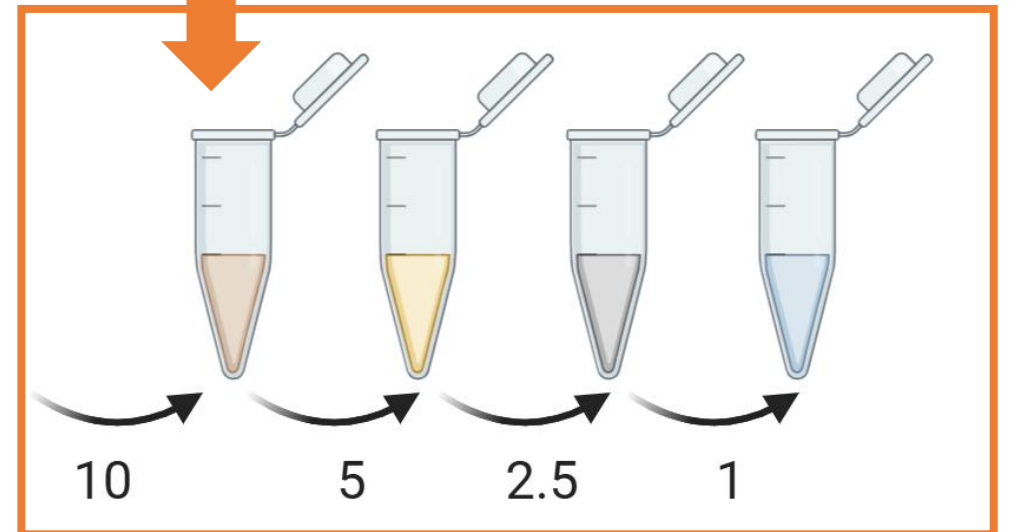
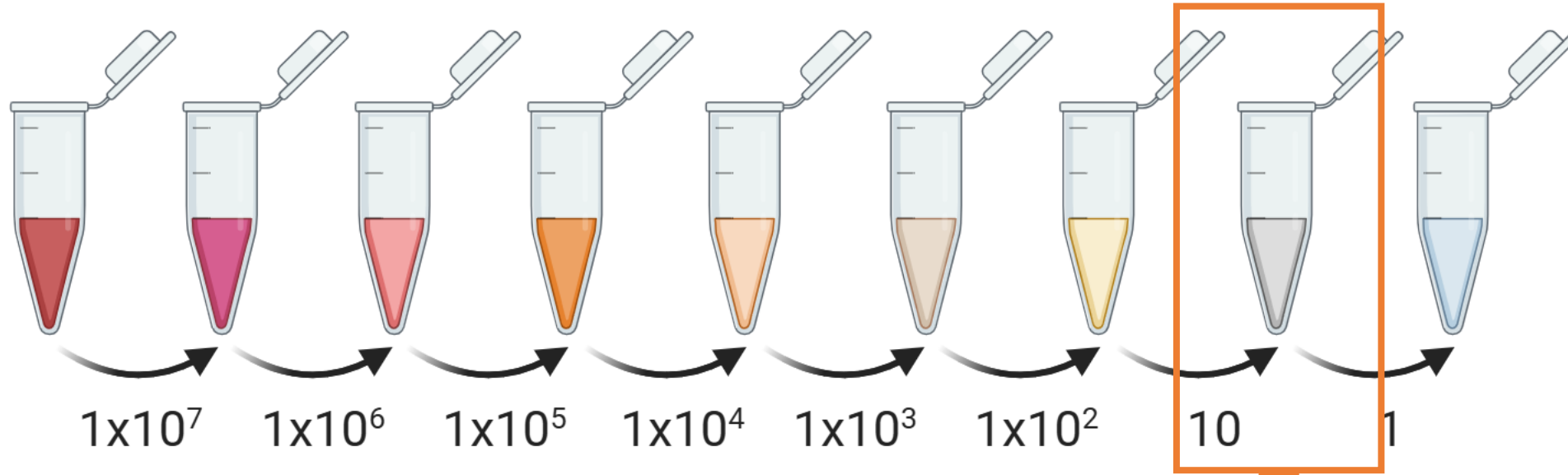




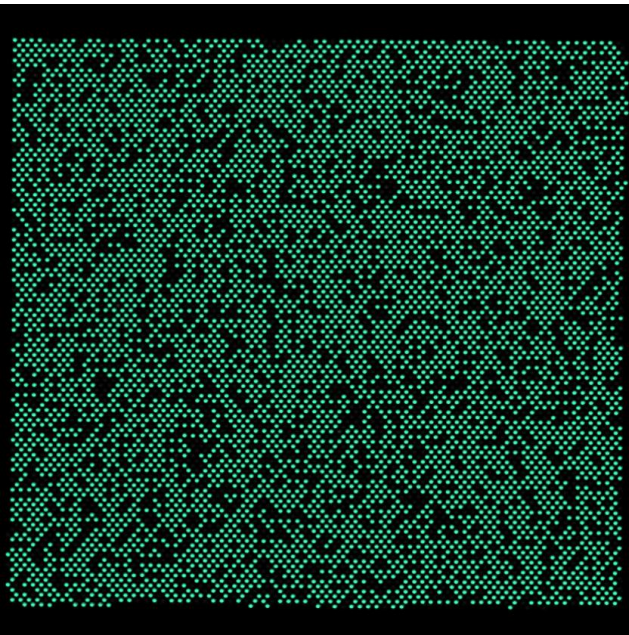
Thank you for your attention

Additional data

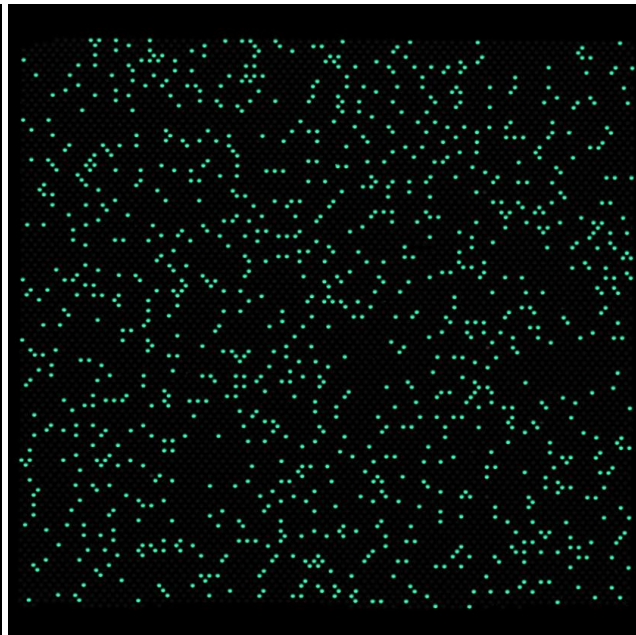
10-fold serial dilutions & 2-fold serial dilutions



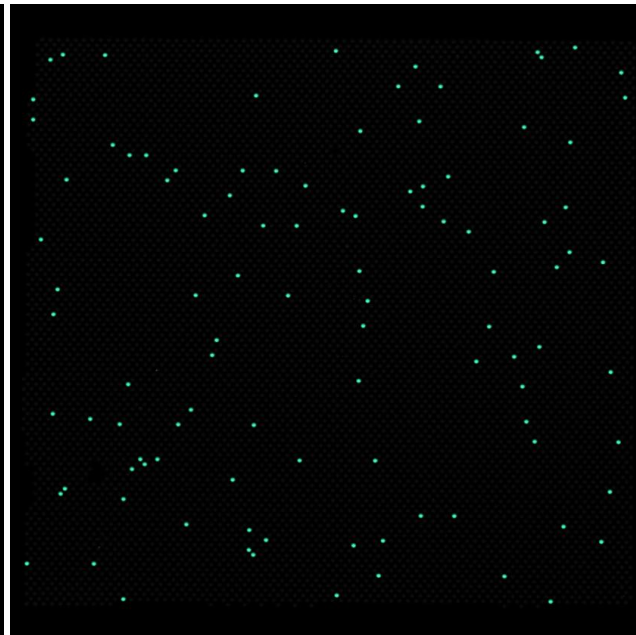
10^4 copies/ μL



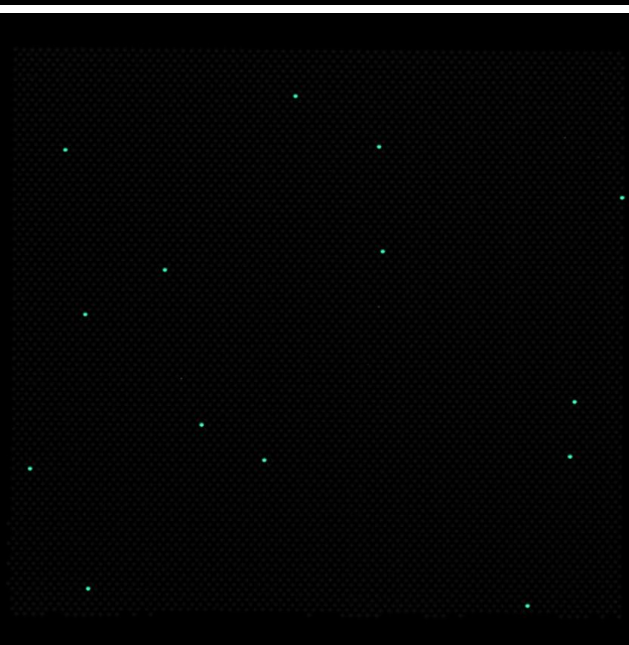
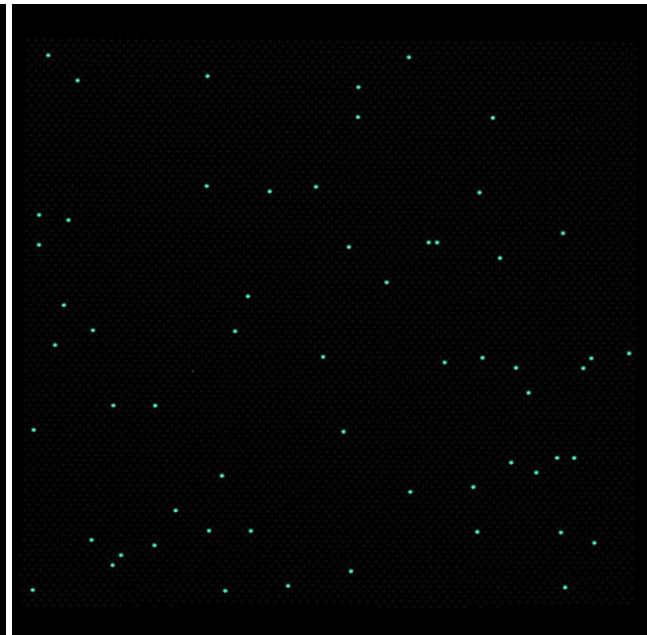
10^3 copies/ μL



10^2 copies/ μL



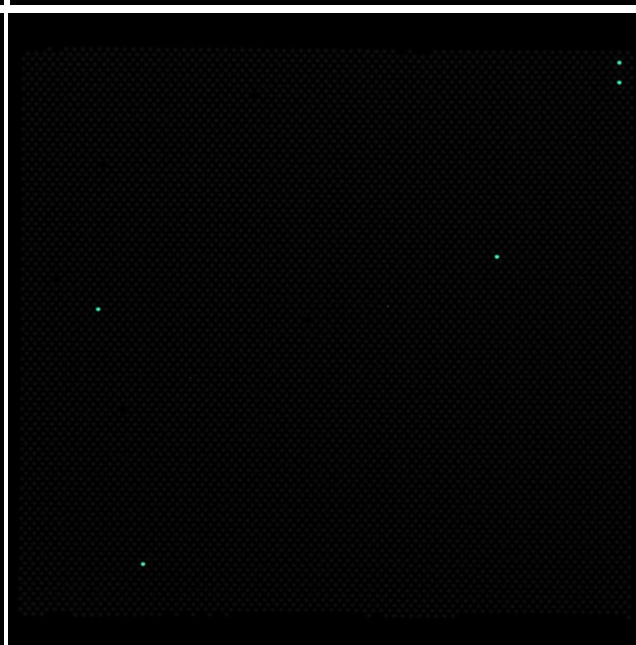
50 copies/ μL



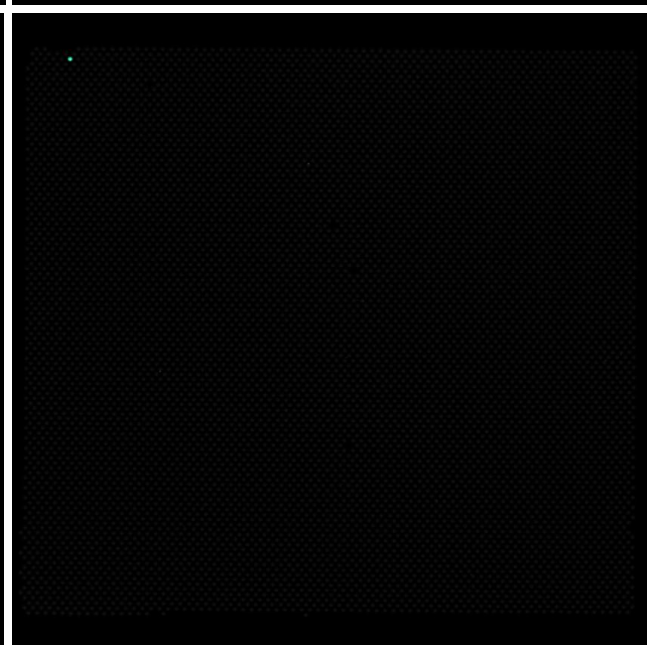
10 copies/ μL



5 copies/ μL



2.5 copies/ μL



1 copies/ μL

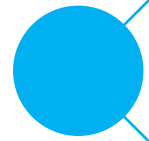
Conclusion



dPCR provides highly sensitive and precise detection with absolute quantification of AIV genomes.



dPCR provides greater sensitivity and precision than real-time RT-PCR in very low viral load samples.



dPCR can serve as a valuable complementary tool to real-time RT-PCR for early diagnosis and surveillance.