



**GHENT
UNIVERSITY**

PROSPECTS FOR DIGITAL PCR IN ABSOLUTE QUANTIFICATION OF DNA

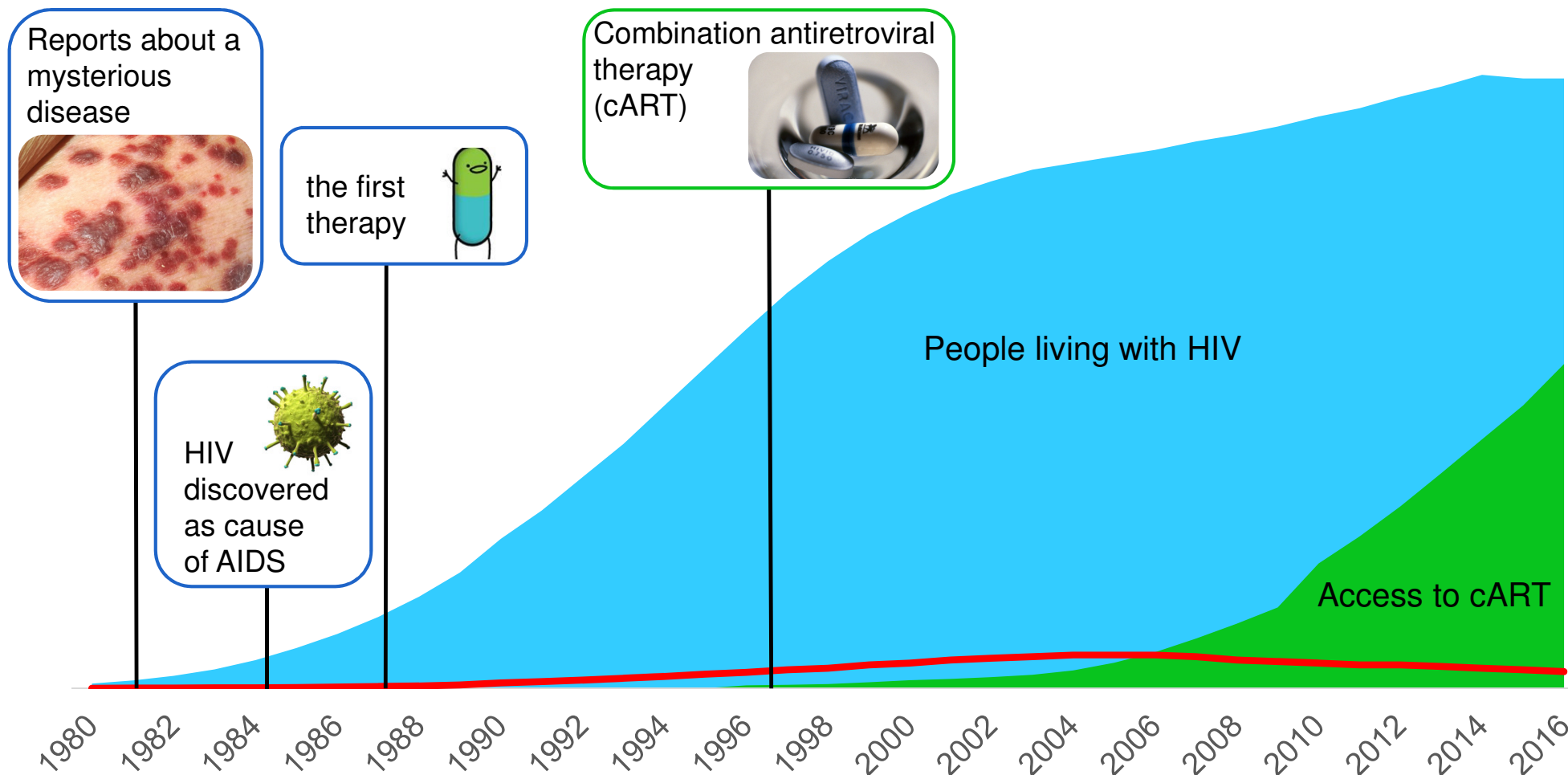
LESSONS LEARNED FROM HIV CURE AND FOLLOW-UP

Ward De Spiegelare,
5th qPCR & Digital PCR congress

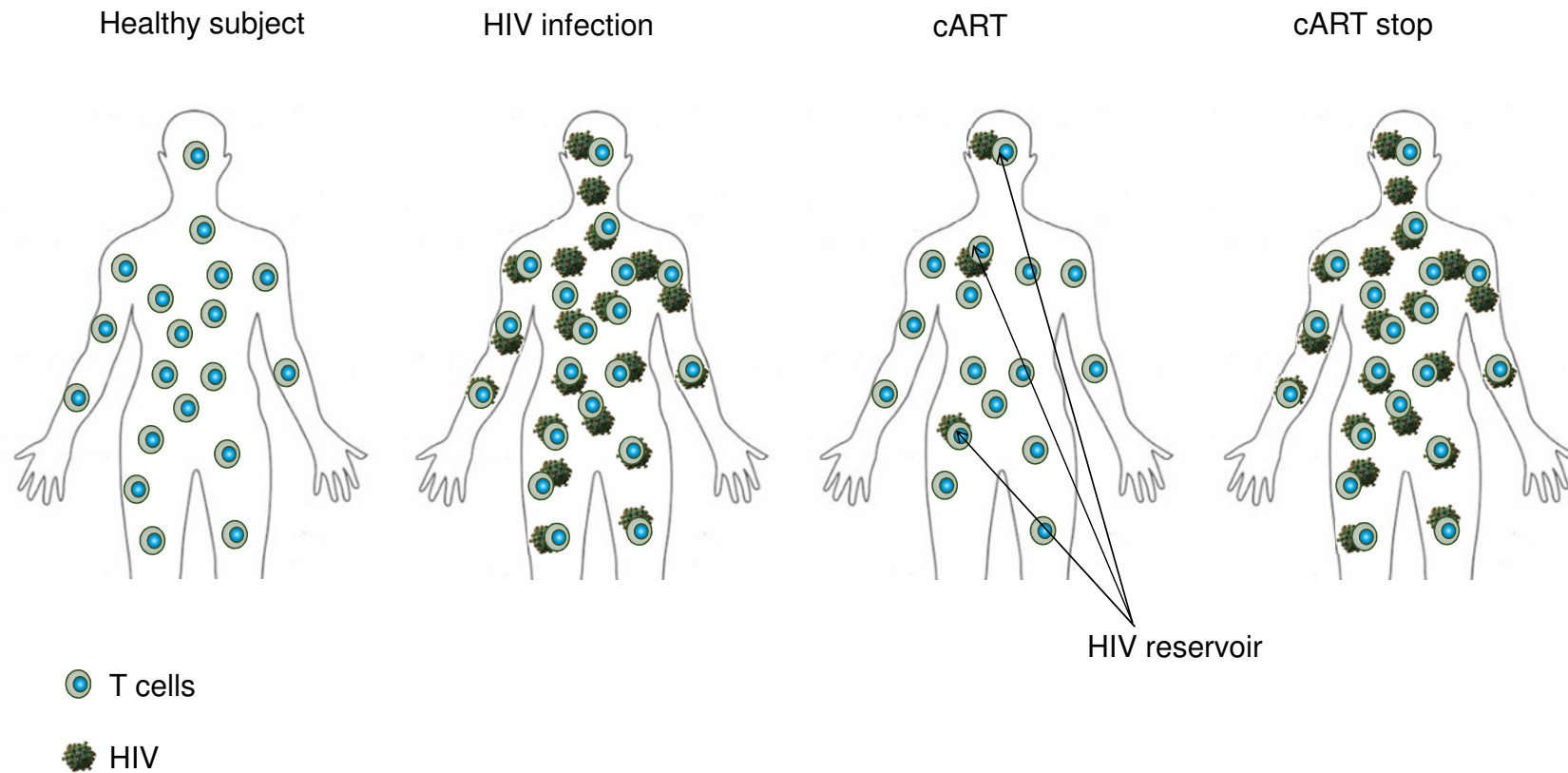


HIV Cure Research Center

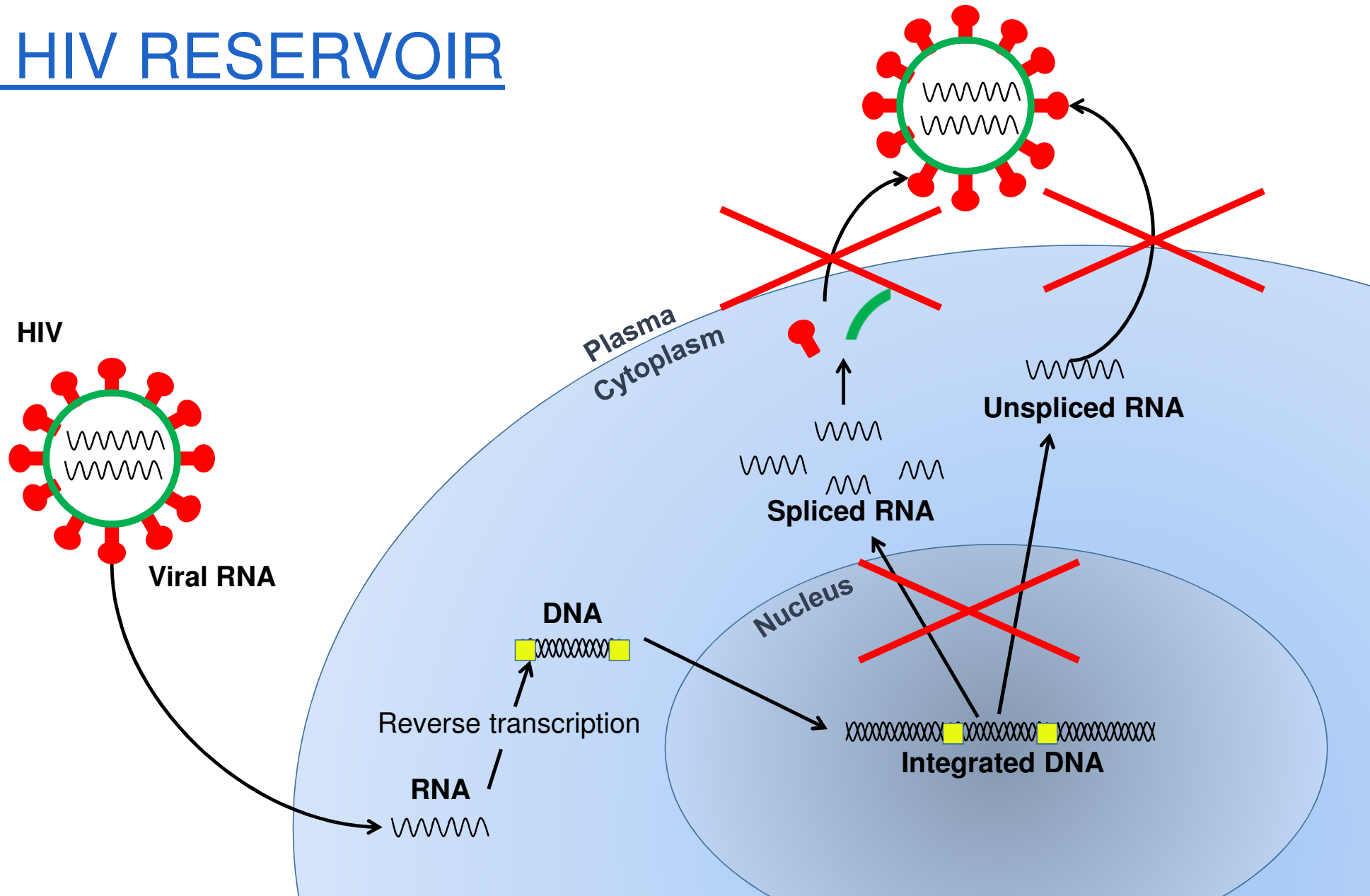
THE HIV/AIDS PANDEMIC



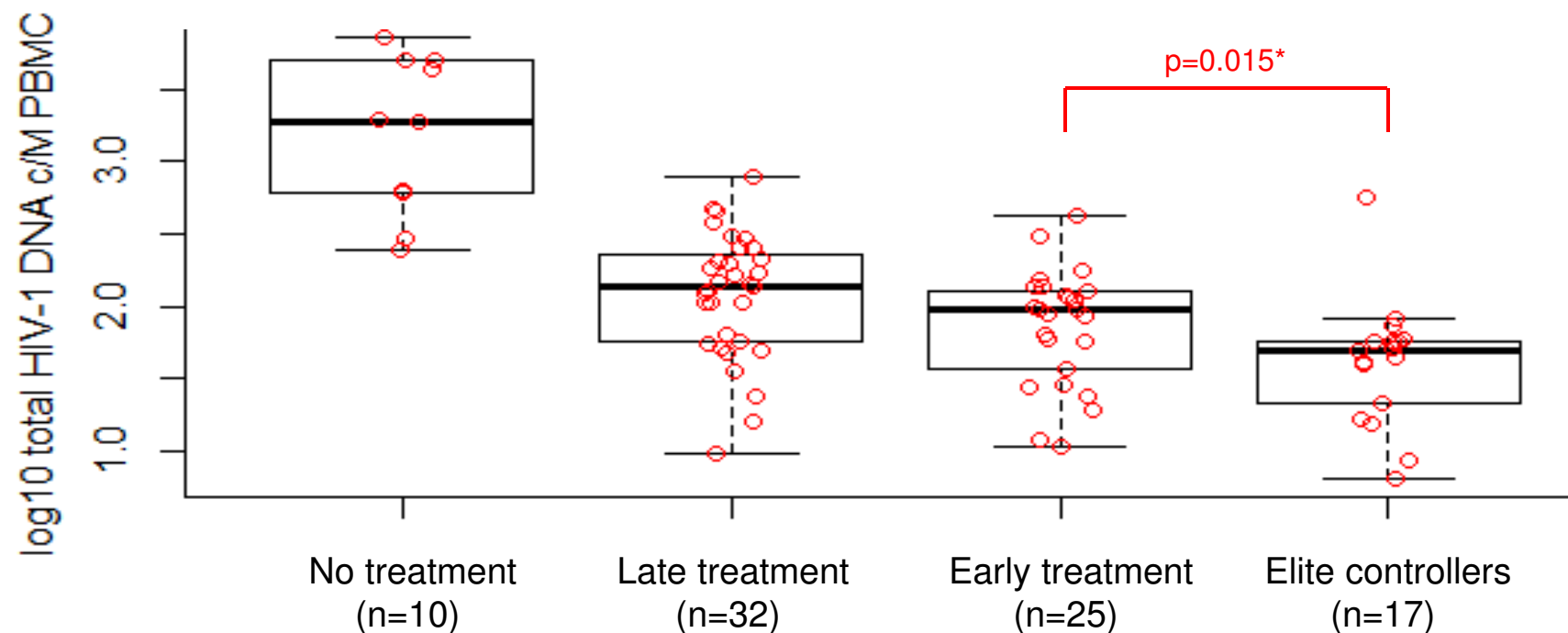
HIV TREATABLE, BUT INCURABLE



THE HIV RESERVOIR



HOW BIG IS THE HIV RESERVOIR



DPCR IS MORE PRECISE THAN QPCR

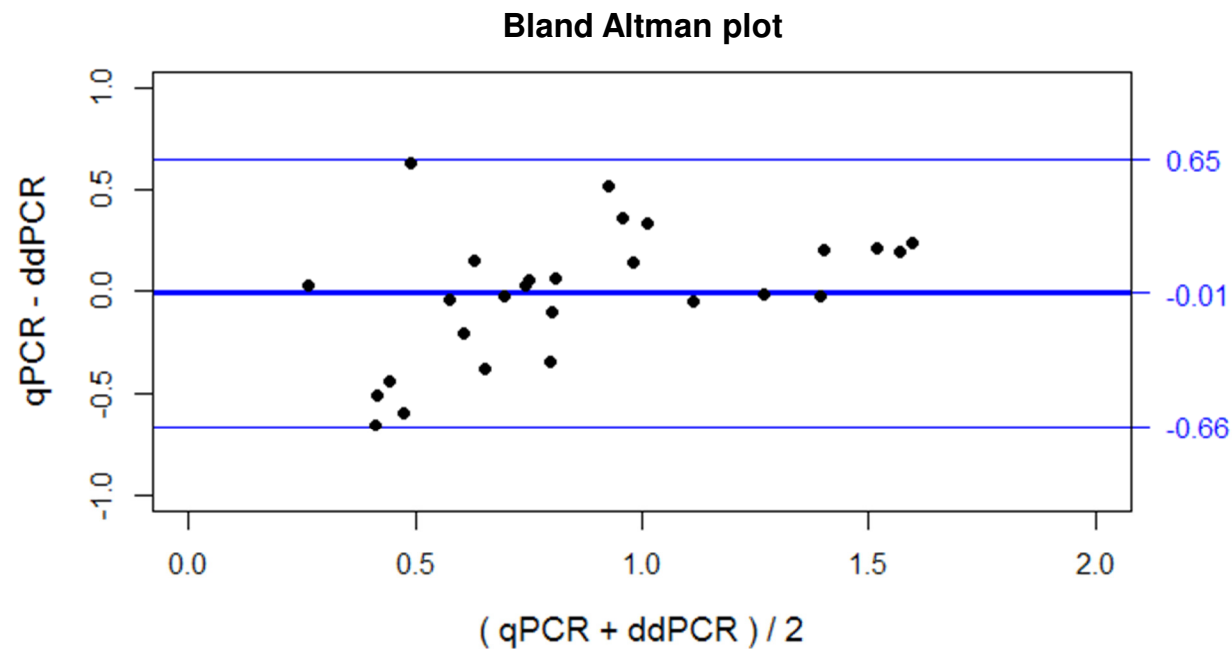
Comparison of ddPCR versus seminested qPCR for HIV DNA quantification

Coefficient of Variation (CV) between triplicates

	n	replicates	CV ddPCR	CV qPCR	Fold difference
Standard curve	7	3	14%	43%	3
Patient samples	17	3	8%	29%	3.5

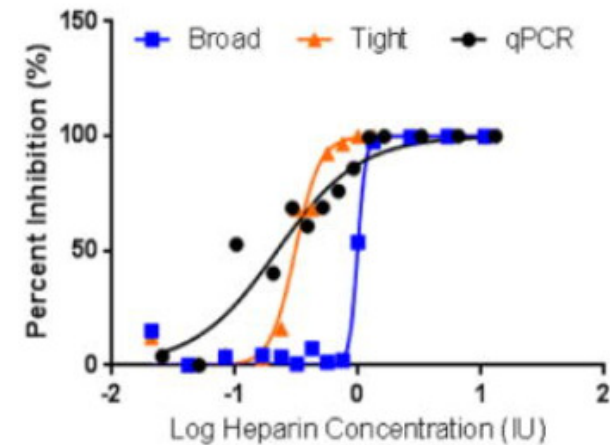
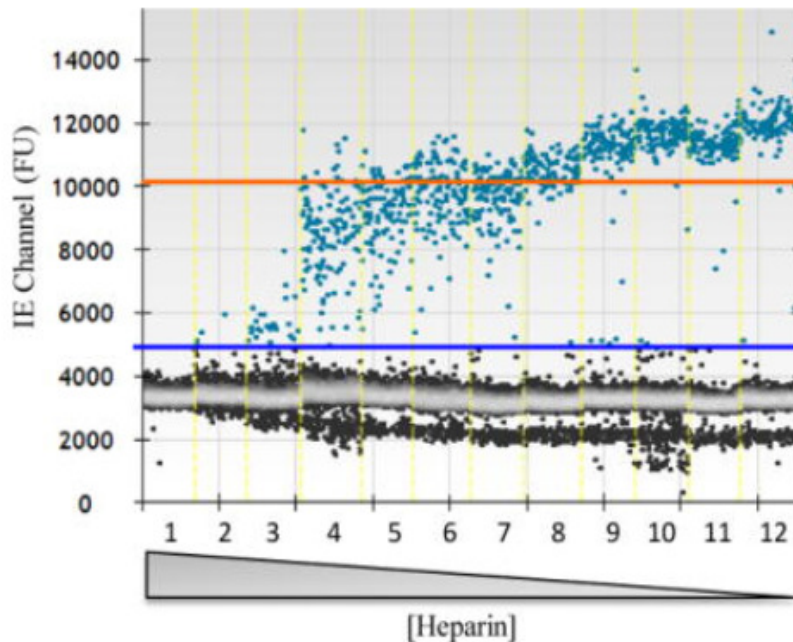
ACCURACY

No significant bias compared to qPCR on HIV DNA measurement



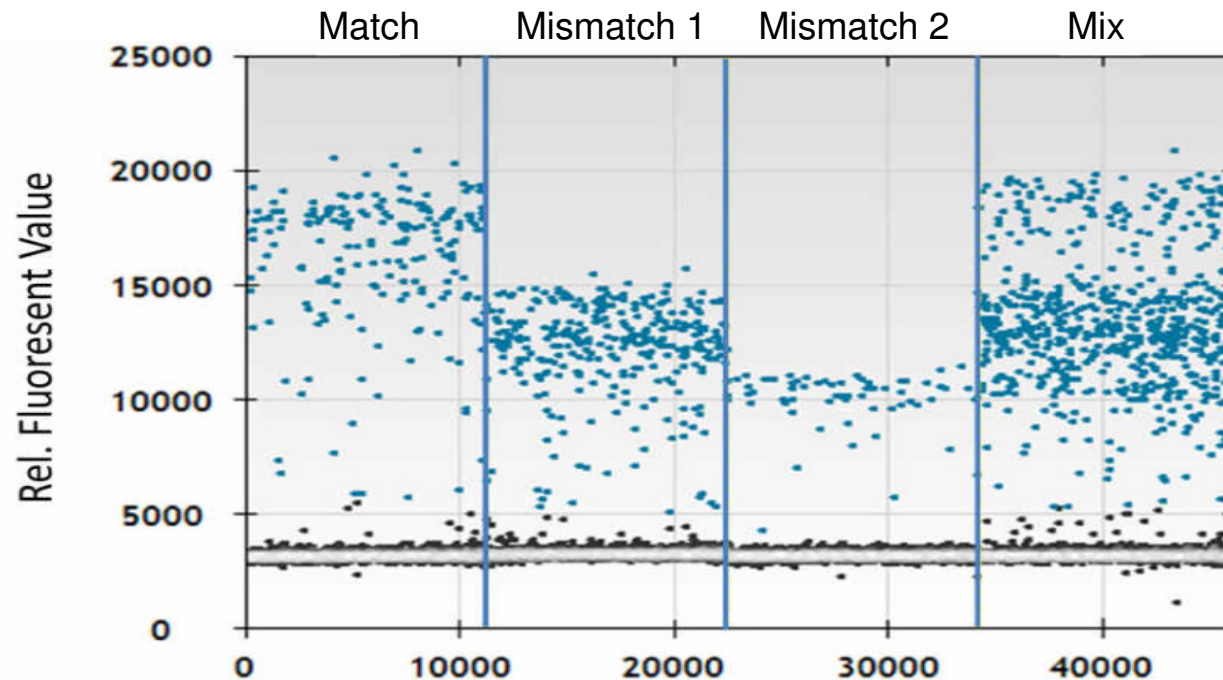
DPCR AND INHIBITION

dPCR outperforms qPCR comparing inhibitory substances
(SDS, EDTA and Heparin)



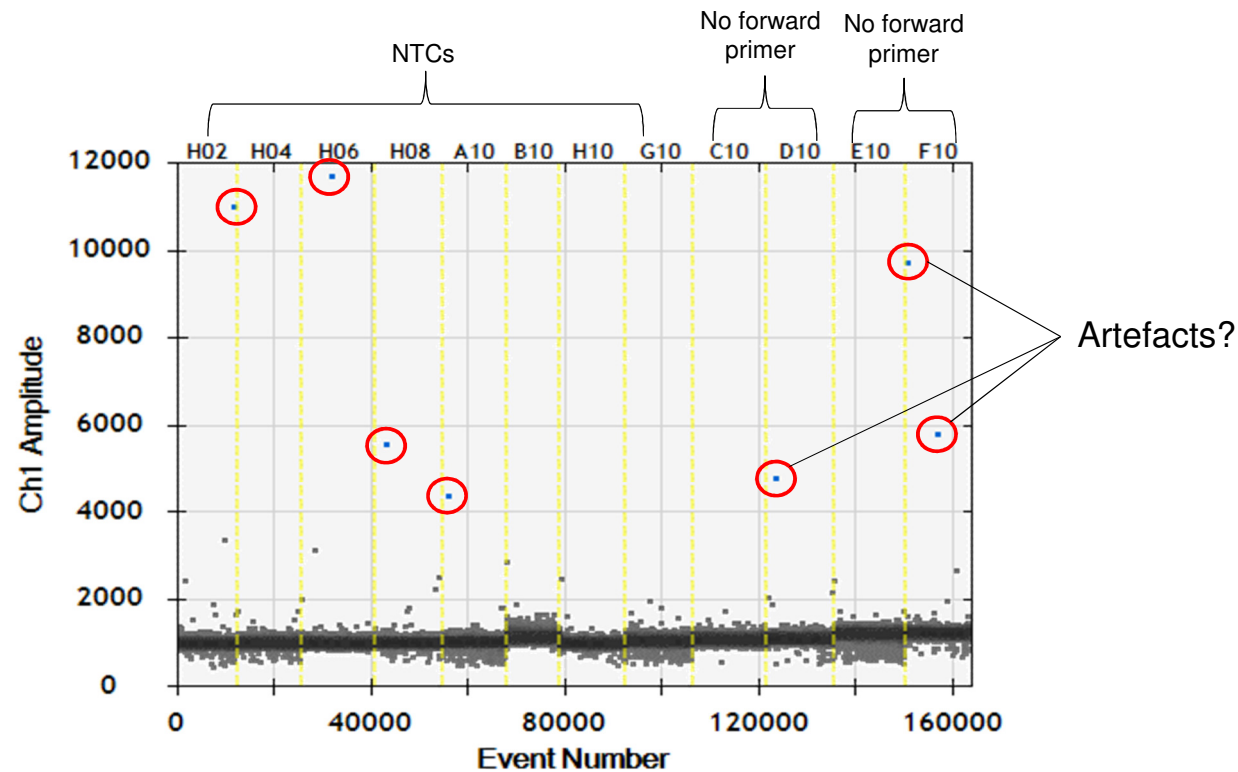
DPCR AND INHIBITION: MISMATCHES

Probe mismatches



Lower fluorescence would harm qPCR but less harm to ddPCR

SENSITIVITY: FALSE POSITIVES IN DDPCR



DPCR PERFORMANCE

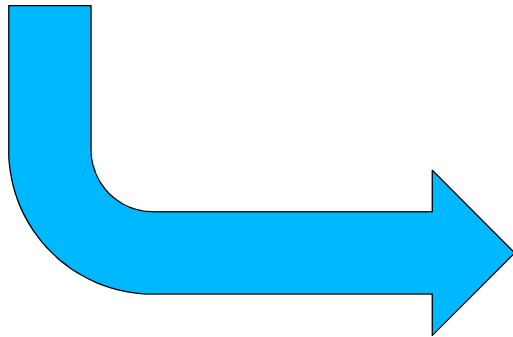
-Better accuracy and precision



-Less refractory to inhibition



-More sensitive?

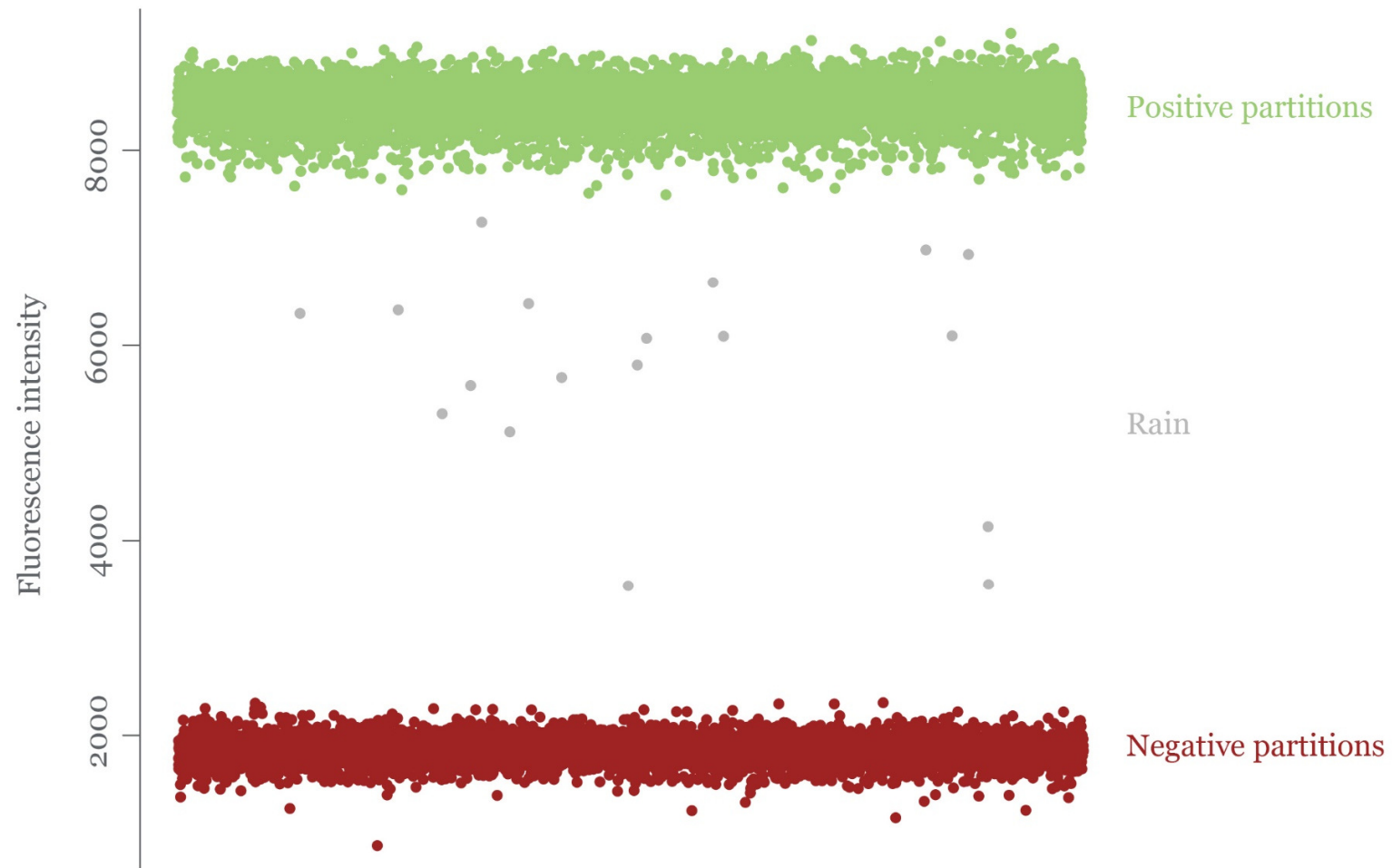


When to use dPCR or qPCR depends on the question:

Template present? → go for standar PCR or nested

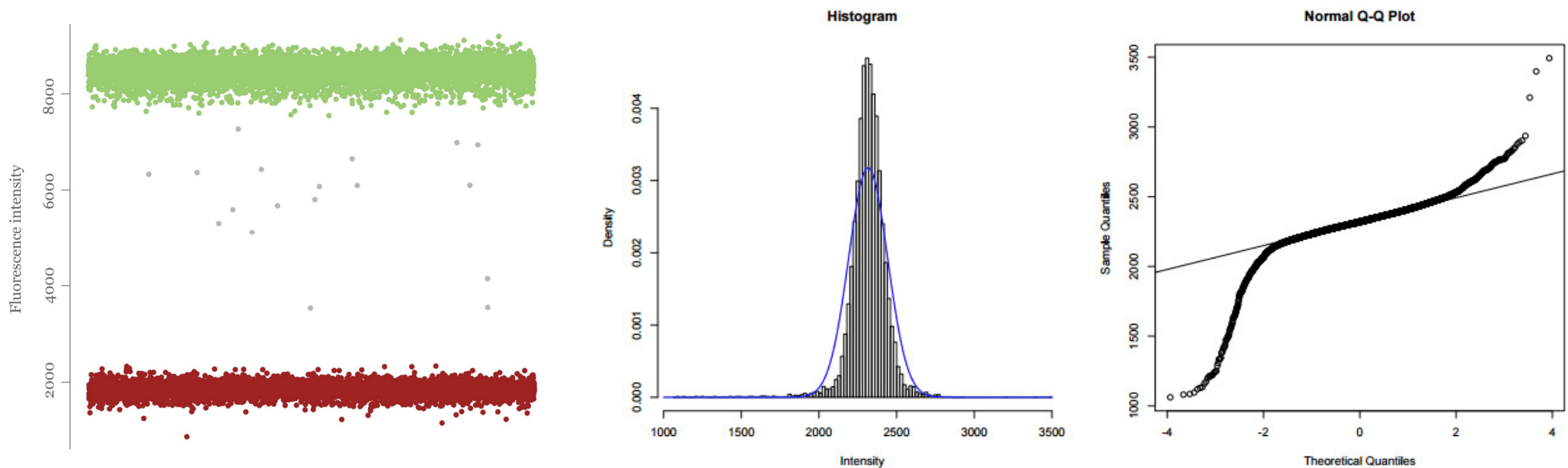
How much? → go for digital PCR

SETTING A TRESHOLD FOR DIGITAL PCR

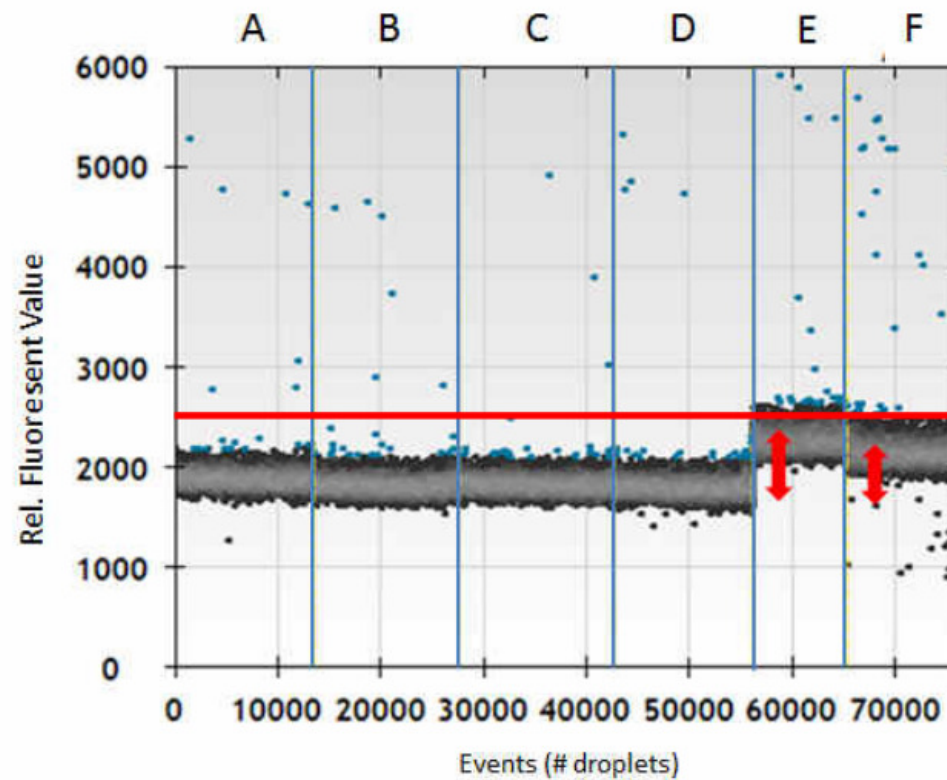


DATA DRIVEN METHODS:HARD TRESHOLDING

Do not use parametric distributions!



BACKGROUND SHIFT



DDPCRQUANT

ddpcRquant

Input Data

Choose Input Data

Upload ddpcrfiles

Upload CSV Files

Browse... No file selected

Choose BioRad QX system (demodata = qx100)

qx200

Start Analysis Reset Analysis

Data Input

Overview Assays

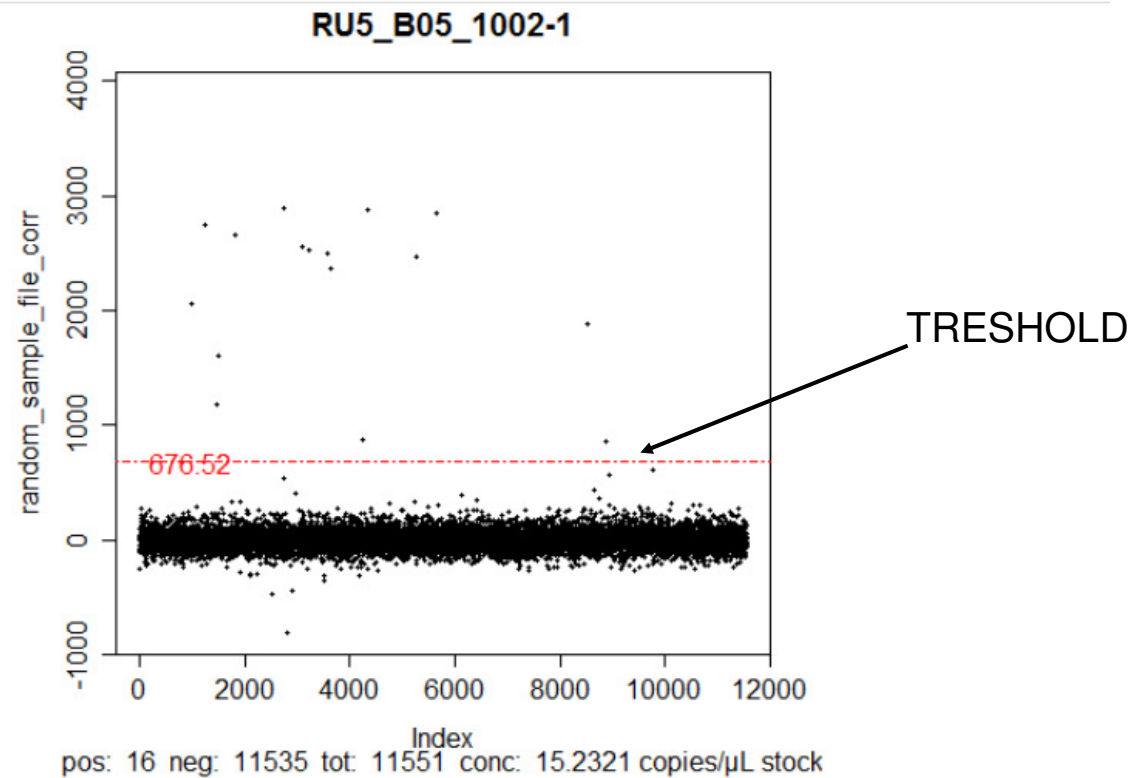
NTC Threshold Analysis

Sample Analysis

Summary

Replicate Analysis

How To Use



SOFT TRESHOLDING (MODELLING THE RAIN)

Model-Based Classification for Digital PCR: Your Umbrella for Rain

Bart K. M. Jacobs,^{*,†,§} Els Goetghebeur,[†] Jo Vandesompele,^{‡,§} Ariane De Ganck,[¶] Nele Nijs,[¶] Anneleen Beckers,[¶] Nina Papazova,^{||} Nancy H. Roosens,^{||} and Lieven Clement^{*,†,§}

[†]Department of Applied Mathematics, Computer Science and Statistics, Ghent University, Ghent, Belgium

[‡]Center for Medical Genetics Ghent (CMGG), Ghent University, Ghent, Belgium

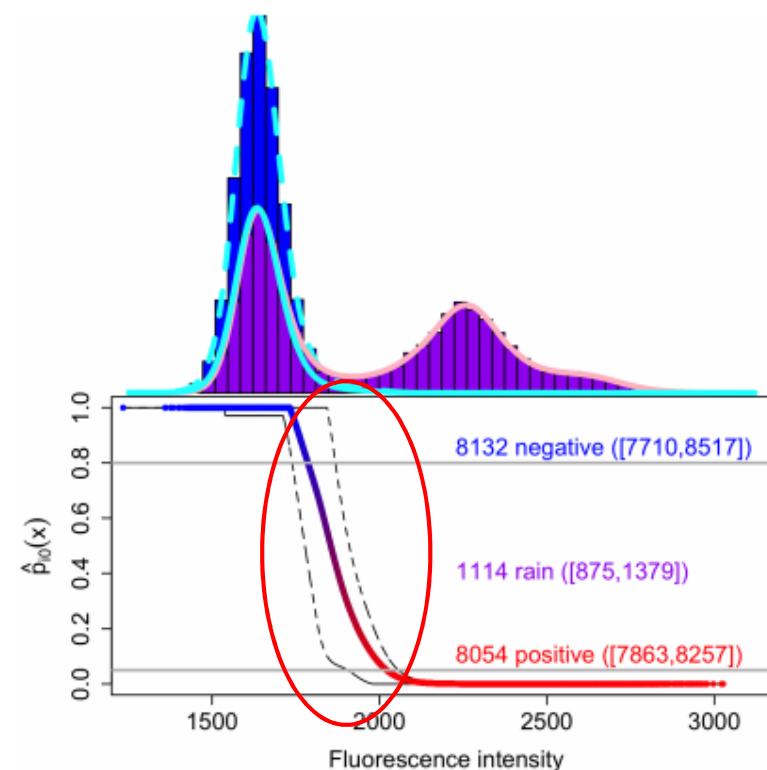
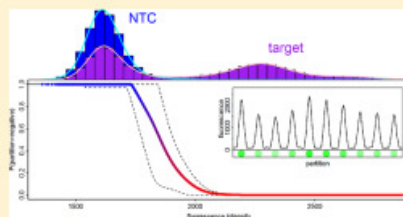
[¶]Biogazelle, Zwijnaarde, Belgium

[§]Bioinformatics Institute Ghent From Nucleotides to Networks (Big N2N), Ghent University, Ghent, Belgium

^{||}Scientific Institute of Public Health (WIV-ISP), Brussels, Belgium

Supporting Information

ABSTRACT: Standard data analysis pipelines for digital PCR estimate the concentration of a target nucleic acid by digitizing the end-point fluorescence of the parallel micro-PCR reactions, using an automated hard threshold. While it is known that misclassification has a major impact on the concentration estimate and substantially reduces accuracy, the uncertainty of this classification is typically ignored. We introduce a model-based clustering method to estimate the probability that the target is present (absent) in a partition conditional on its observed fluorescence and the distributional shape in no-template control samples. This methodology acknowledges the inherent uncertainty of the classification and provides a natural measure of



MEASURING THE HIV RESERVOIR

1) HIV cure research

- Monitoring efficacy of experimental treatment

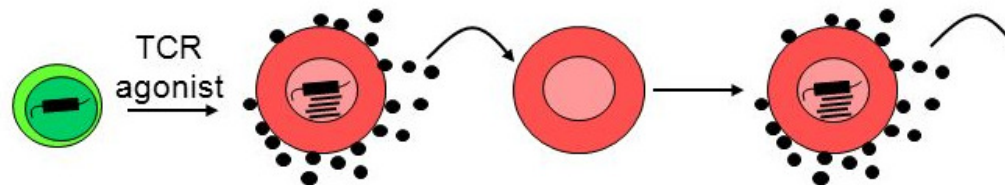
Question: does the DNA reservoir correlate with the replication competent reservoir?

2) Current clinical follow-up

- Stratifying high risk vs low risk
- Regimen change to monotherapy

DDPCR IN HIV CURE STUDIES?

- 1) Validation of HIV DNA as a relevant marker for the HIV reservoir
Comparison with an *ex vivo* viral outgrowth assay



- 2) Analysis of HIV DNA levels in cure studies

Clinical Infectious Diseases

MAJOR ARTICLE

 **IDSA**
Infectious Diseases Society of America

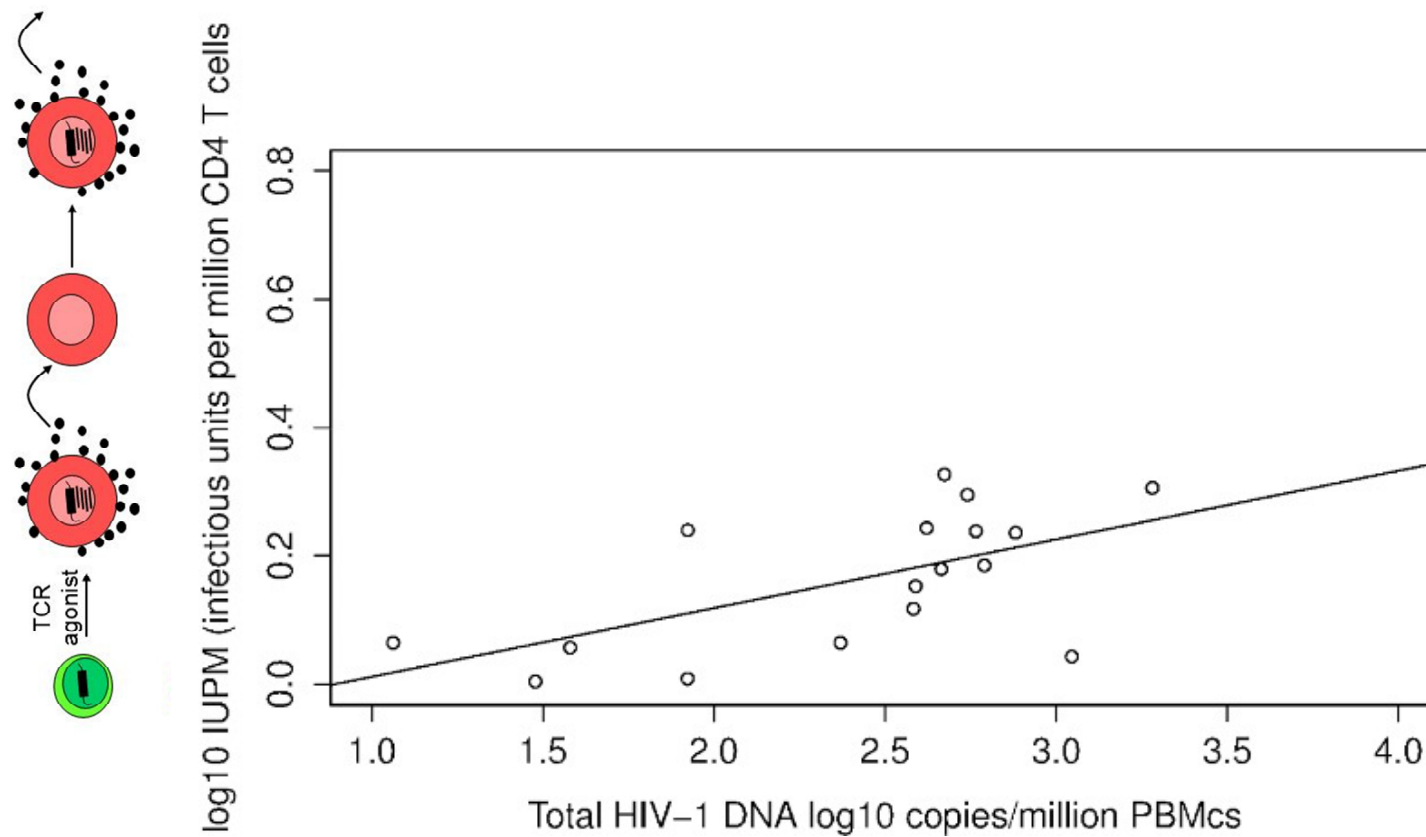
hivma
hiv medicine association

 OXFORD

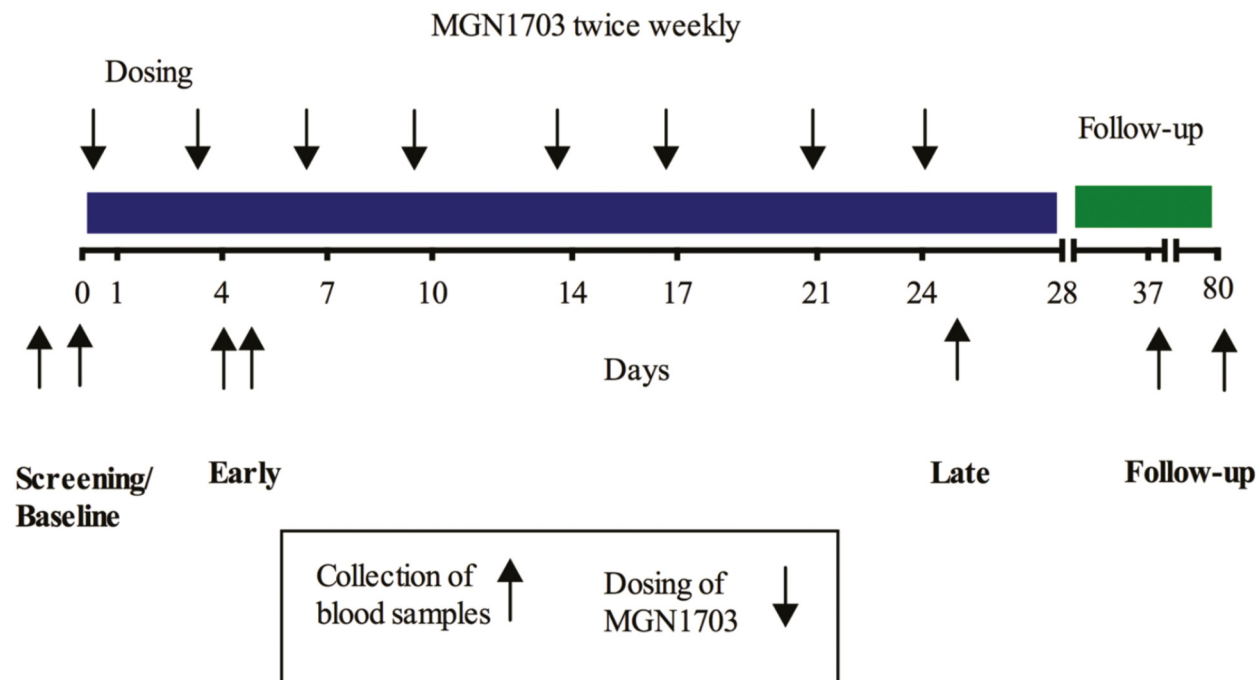
Short-Course Toll-Like Receptor 9 Agonist Treatment Impacts Innate Immunity and Plasma Viremia in Individuals With Human Immunodeficiency Virus Infection

Line Vibholm,^{1,2,a} Mariane H. Schleimann,^{1,2,a} Jesper F. Højen,^{1,2} Thomas Benfield,³ Rasmus Offersen,^{1,2} Katrine Rasmussen,¹ Rikke Olesen,¹ Anders Dige,^{2,4} Jørgen Agnholt,^{2,4} Judith Grau,⁵ Maria Buzon,⁵ Burghardt Wittig,⁶ Mathias Lichterfeld,⁷ Andreas Munk Petersen,^{8,9} Xutao Deng,^{10,11} Mohamed Abdel-Mohsen,^{10,11,12} Satish K. Pillai,^{10,11} Sofia Rutezart,¹³ Wim Trunçon,¹³ Ward De Spiegelaere,^{13,14} Lieve Vandekerckhove,¹³

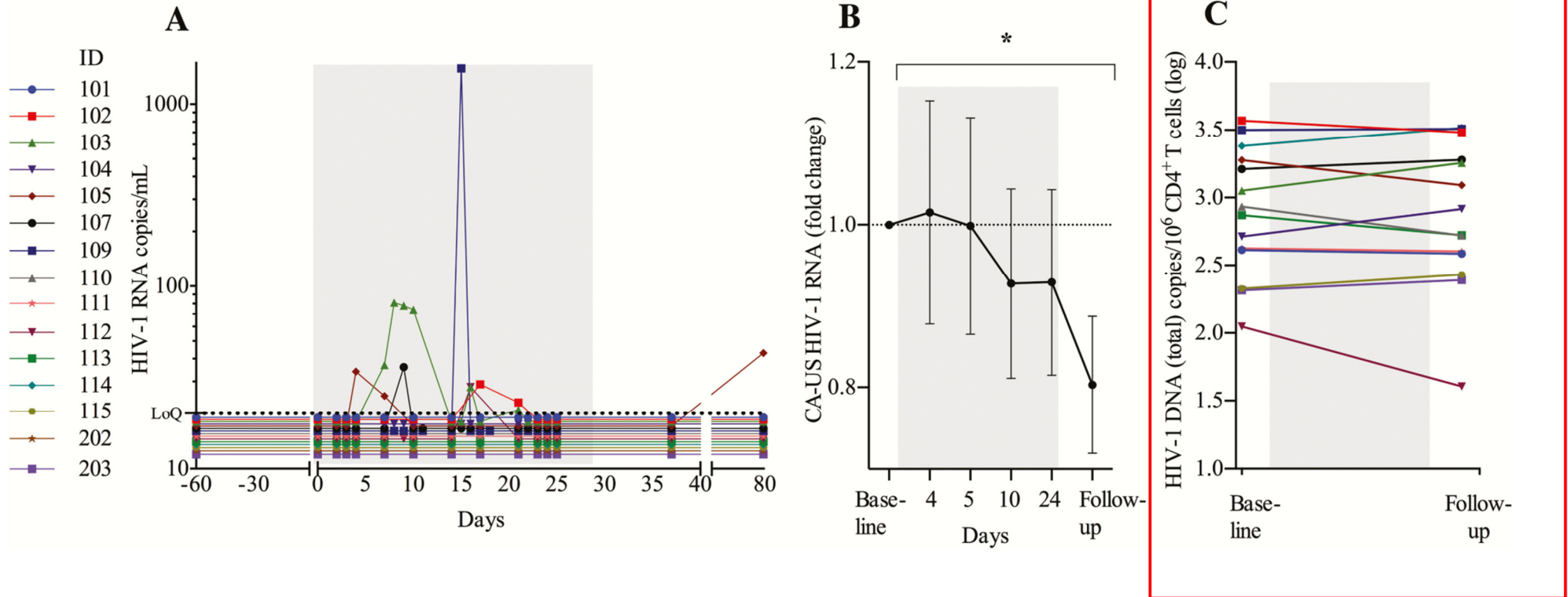
TOTAL HIV DNA CORRELATES WITH VIRAL OUTGROWTH



SHORT-COURSE TOLL-LIKE RECEPTOR 9 AGONIST TREATMENT

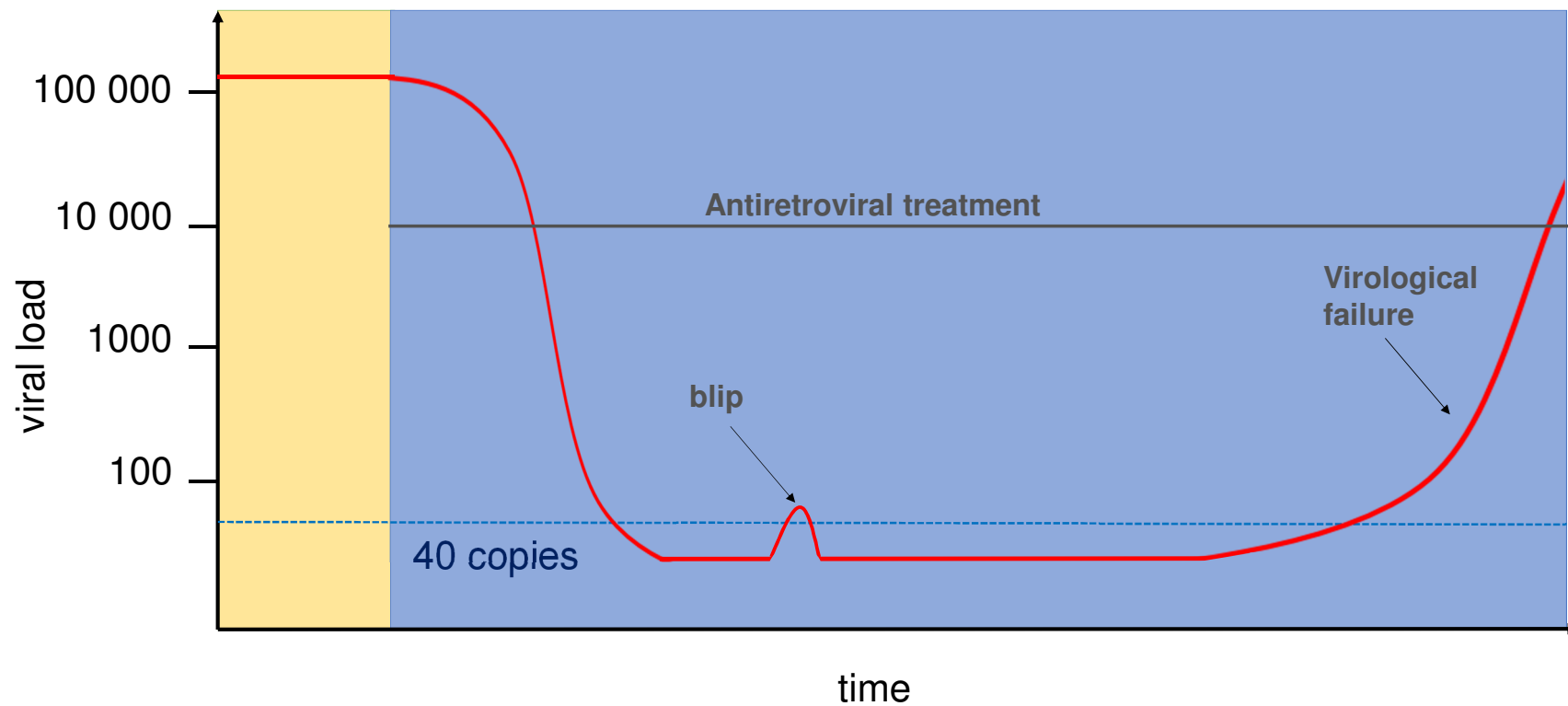


SHORT-COURSE TOLL-LIKE RECEPTOR 9 AGONIST TREATMENT



IN FOLLOW-UP

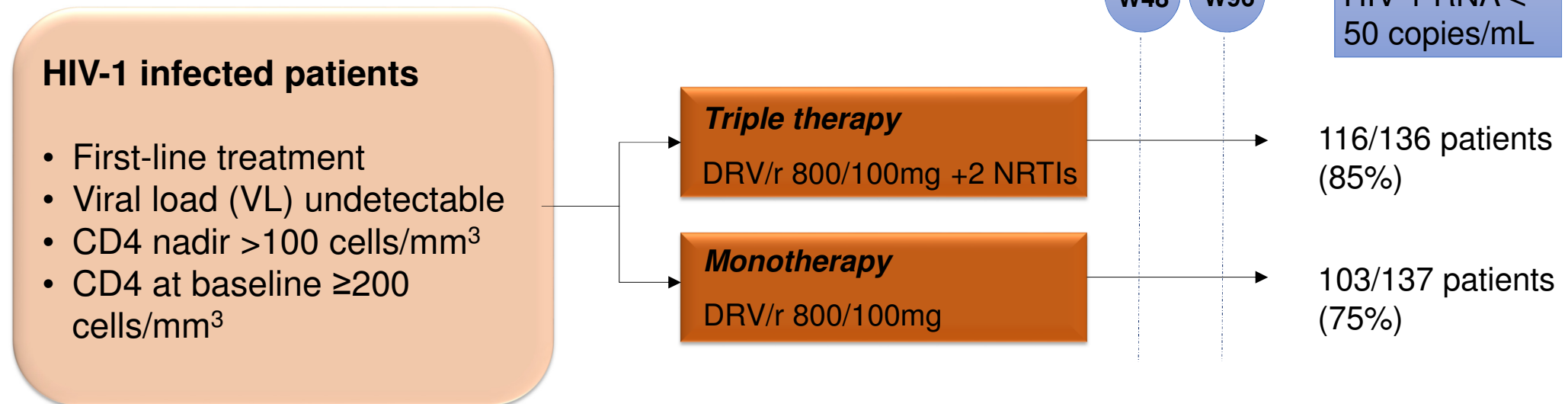
– Patient stratification



triple therapy → monotherapy?

MONOTHERAPY: PROTEA STUDY

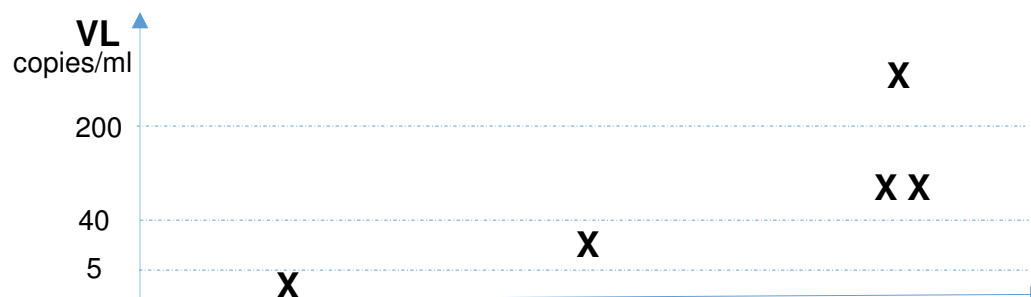
- Randomized clinical trial (NCT01448707)



- Switch to monotherapy shows lower efficacy but is safe
- **Can we predict this outcome upfront?**

PROTEA SUBSTUDY

Patient characteristics

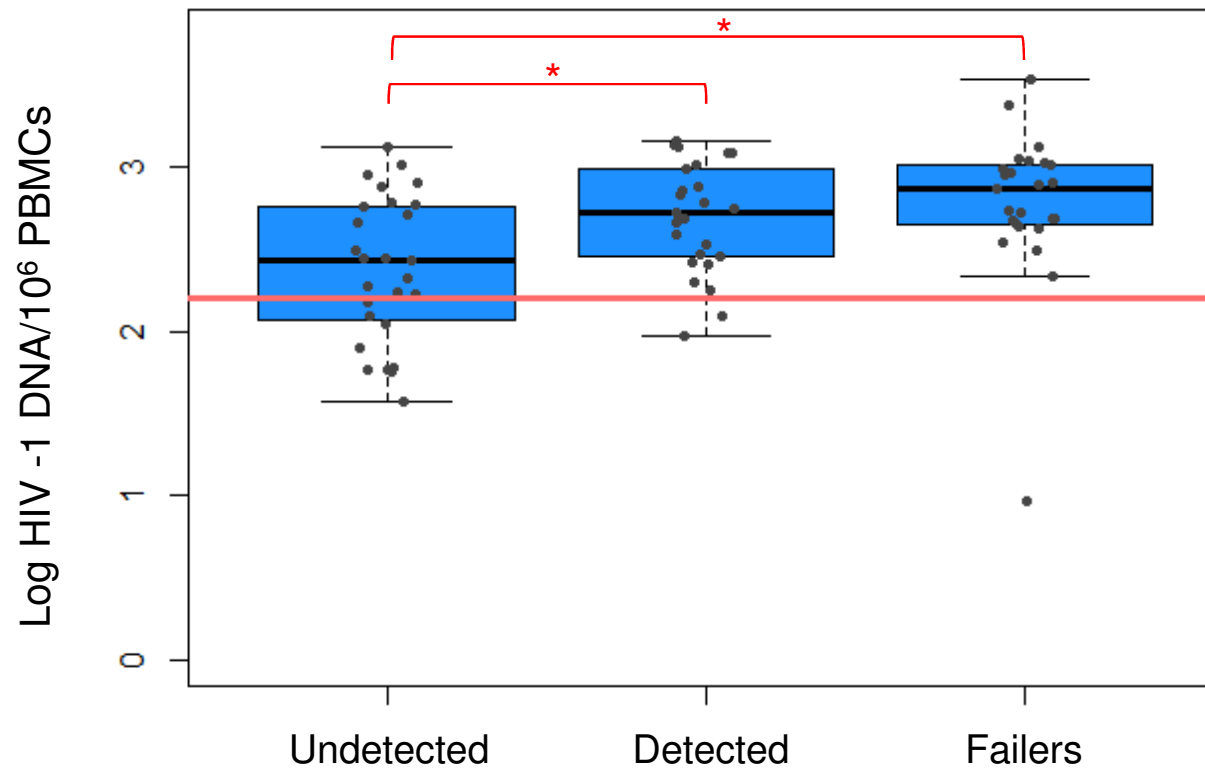


	Undetectable VL	Detected VL	Failers
N	27	25	25
Age, years, mean (SD)	45 (10.8)	42 (9.3)	48 (8.8)
Male sex, N (%)	21 (77.8)	20 (80)	20 (80)
CD4-nadir, cells/mm³	245 (204-309)	250 (190-357)	217 (169-311)
CD4 at baseline, cells/mm³	585 (399-644)	633 (522 - 796)	570 (447 - 765)
Time on cART, years	5.7 (3.3-9.45)	4.5 (2.8-7.4)	4.6 (2.4-8.3)

Data documented as median (Q1,Q3), unless stated otherwise.

TOTAL HIV-1 DNA

Level of total HIV-1 DNA in patients on DRV/r monotherapy

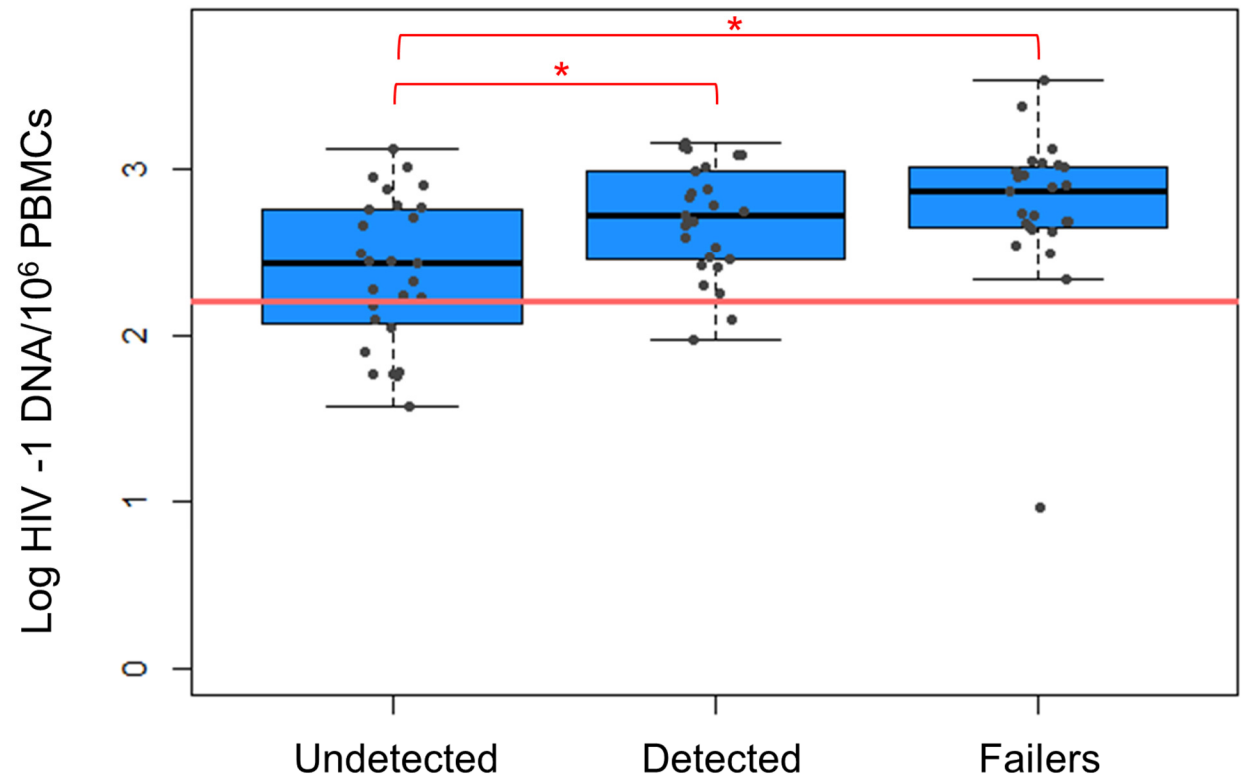


* : p<0,05

TOTAL HIV-1 DNA

Cut-off of **2.2 log** total HIV DNA/10⁶PBMCs.

DRV/r monotherapy:
66% of patients
success rate: 99%.



CONCLUSION

dPCR in HIV research

- Good performance for HIV DNA quantification
- Promising tool in current HIV follow-up
- Validation in HIV cure setting still required



HIV Cure Research Center



www.dPCR.ugent.be

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