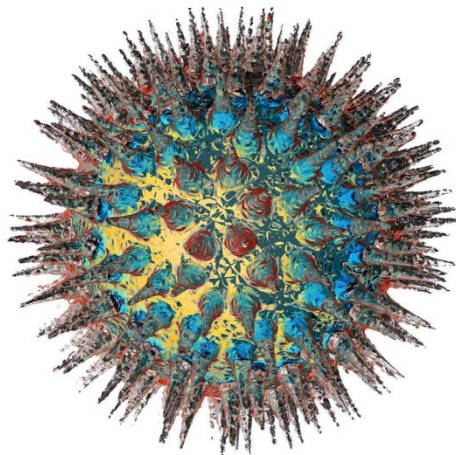


# Technical Issues with CMV Viral Load Testing and Standards



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# Viral Load Testing- Common Methods

1. DNA Extraction
2. Real-Time PCR Amplification and Detection

# Extraction

# Extraction (DNA Purification)

- \* Variety of Methods

1. Lysis of Cell Membranes

2. Removal of Proteins

- \* Chiatropic agent and a protease enzyme

3. Binding of DNA to Solid Support

- \* Spin Columns with Silica coated on to a membrane

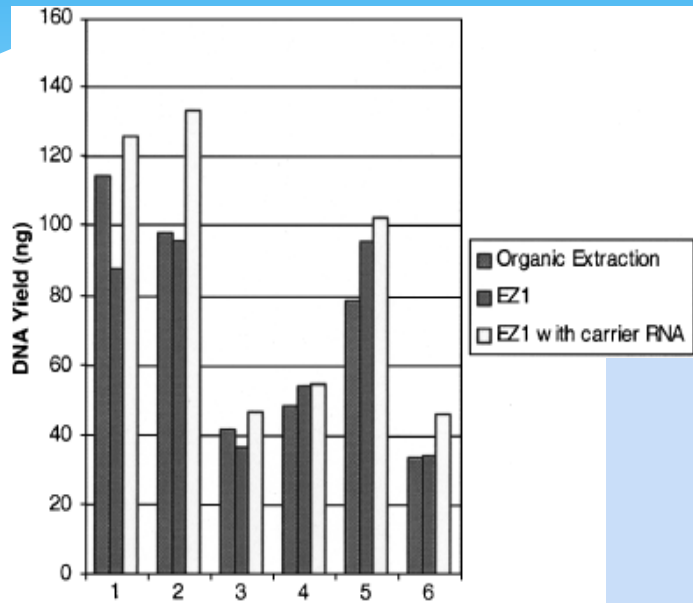
- \* Magnetic Beads coated with Silica – Automated Methods with instrumentation (6-96 samples)

4. Washing and Elution

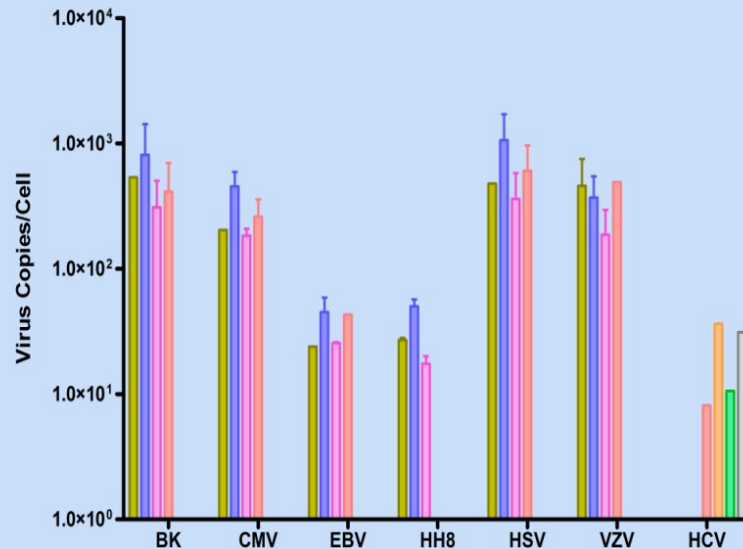
# Extraction Evaluation?

- \* Yield?
- \* Cross-Contamination?
- \* Linearity?
  - \* In Virology testing usually can only be assessed by PCR measurements
  - \* Some methods combine both Extraction and PCR so can only assess at the end of both methods.
- \* For large DNA viruses not a major variable in testing if utilizing commercial extraction equipment/reagents

# Measurement of Actual Viral Yield



Kishore, et al. *J. Forensic Sci.*  
51:1156, 2006



Poster, Atienza, A. et al. CVS 2005

# Extraction – Sample Type

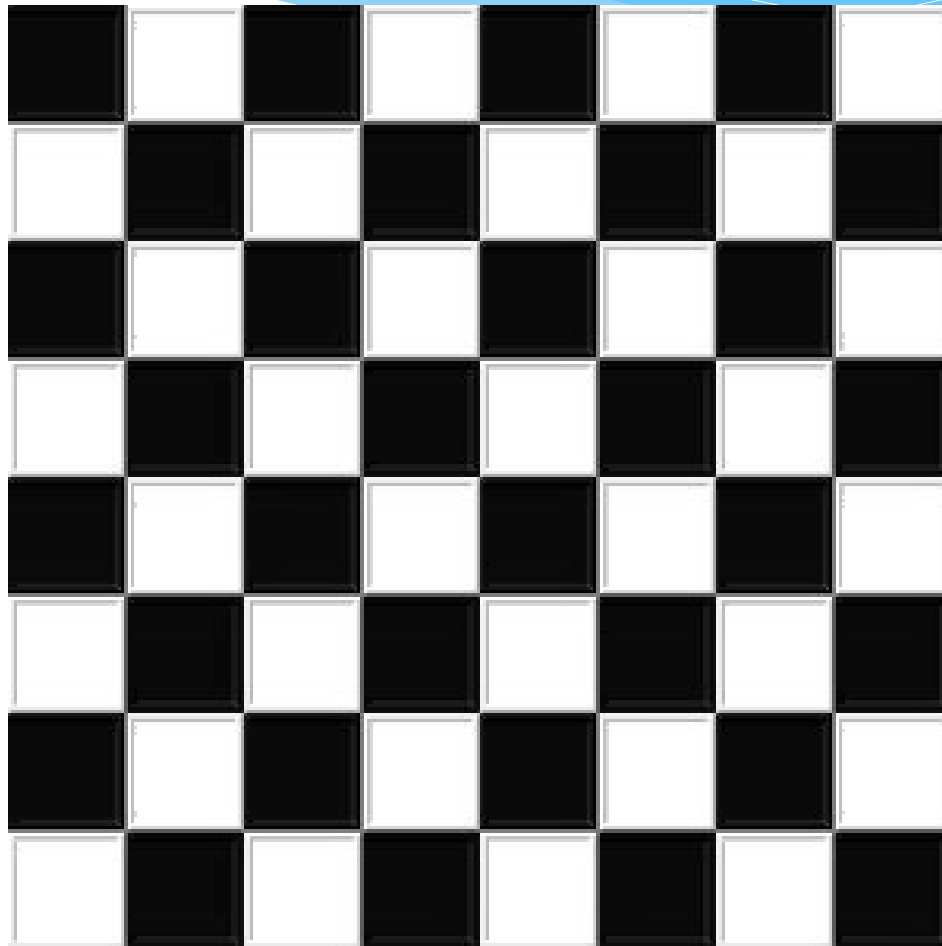
- \* Plasma – (EDTA)
- \* Whole Blood
- \* CSF
- \* Dried Blood Spots
- \* Urine

# “Checkerboard” Extractions

(Instrument Function)

High Pos

Negative



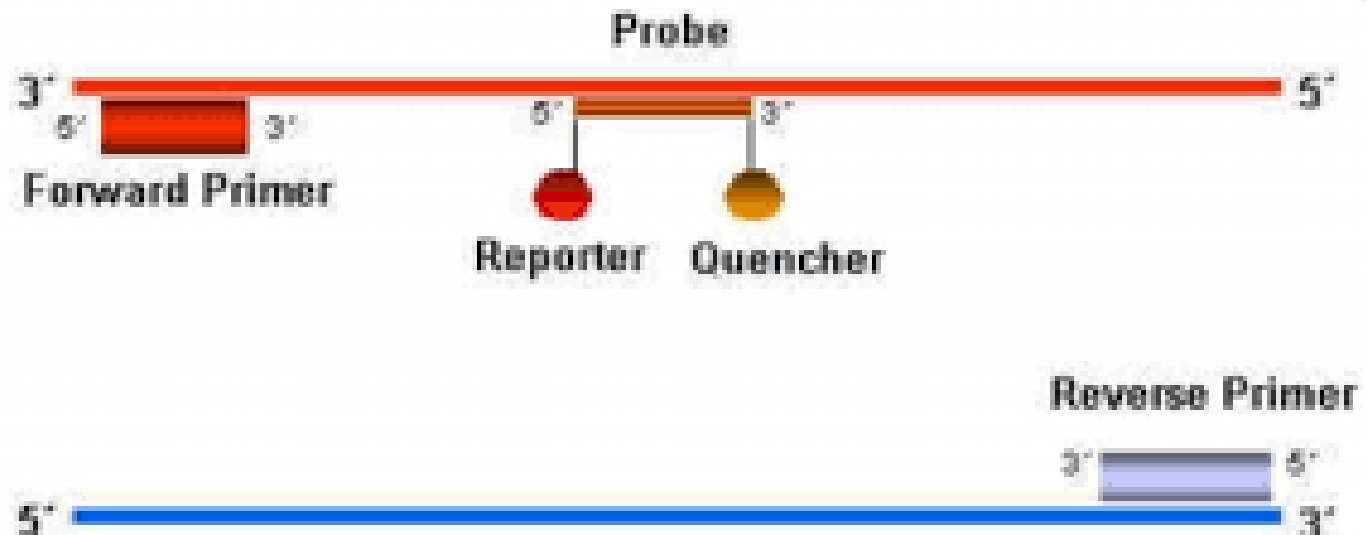


# Technical Aspects - PCR Method

Tools Needed ?

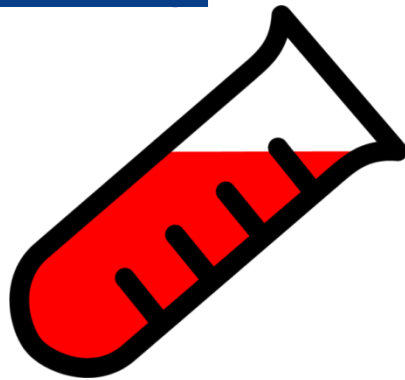


# Real-Time PCR



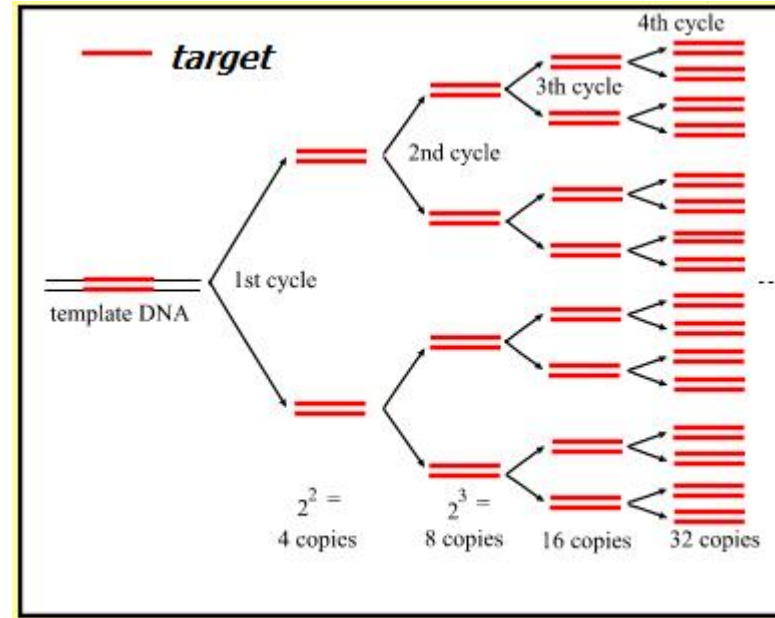
# PCR Reaction

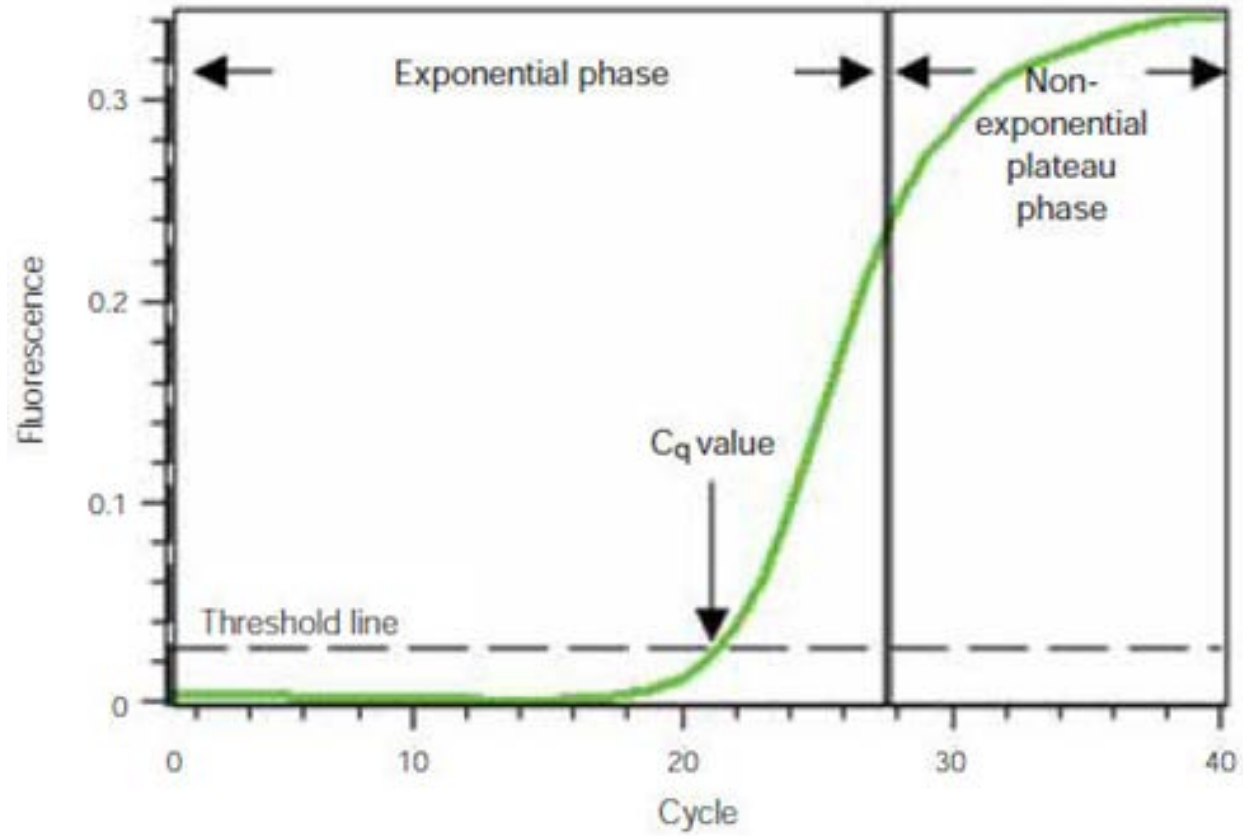
## \* Chemistry



- \* DNA Polymerase
- \* Buffers and Cations
- \* Primers and Probes
- \* dNTPs
- \* “Enhancing Agents”

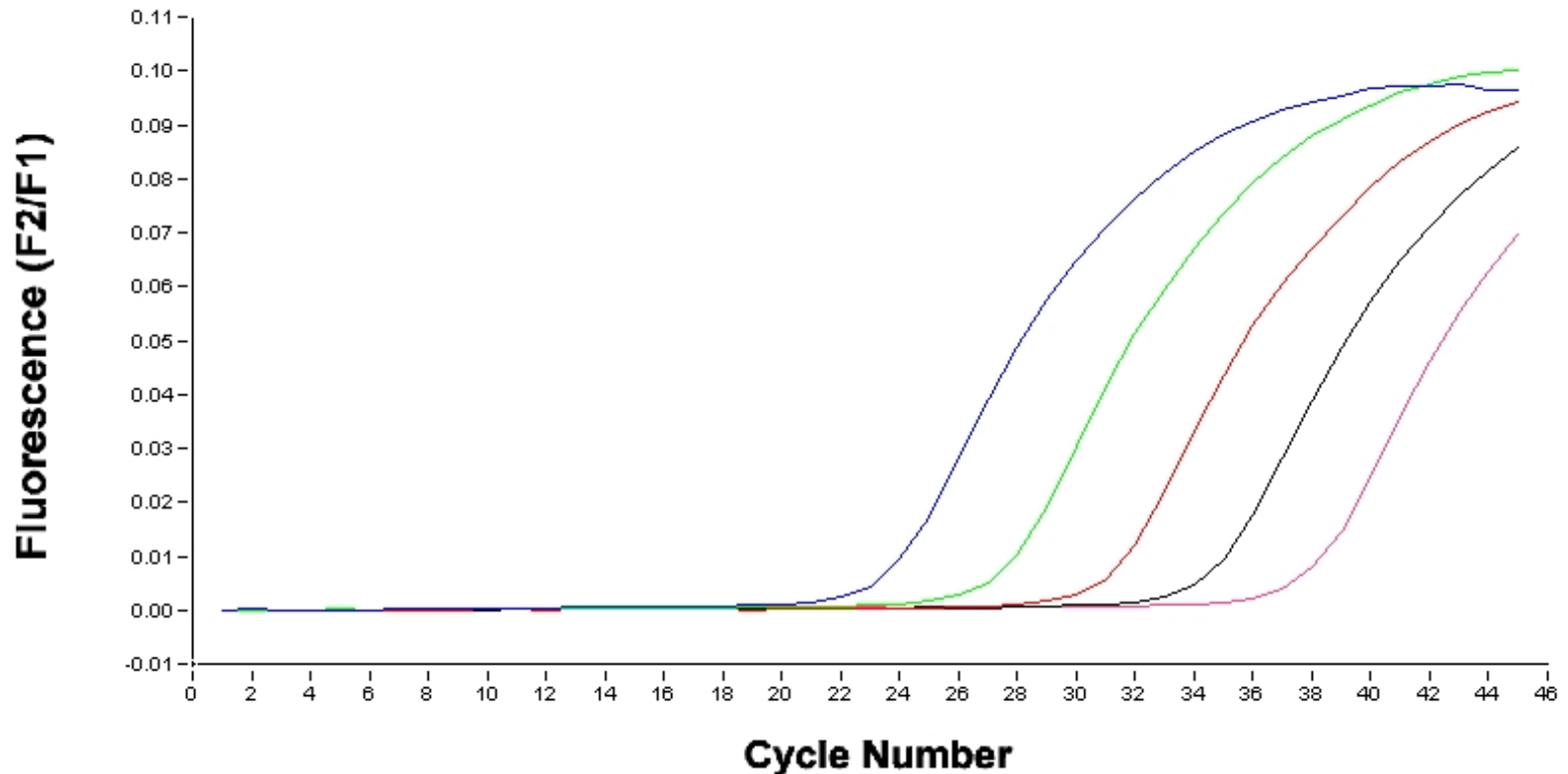
## \* Multiple Replication Cycles





# Maximize the Assay Efficiency

- \* Variety of master mixes available
- \* Adjust mix components, conditions, add “enhancers”, etc.



# Slope Calculation



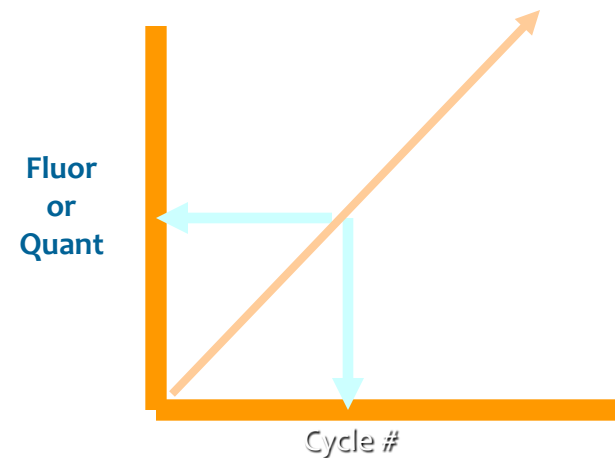
Std Curve  
(Serial  
dilutions)

**Do a Linear Regression – Ct vs Quantity**  
**Calculate the Slope of the Line**  
**-- most Real-Time instruments do this for you.**

# Efficiency Calculations

- \* Units – Perfect Efficiency

- \* Start with 1 copy
- \* End of 1<sup>st</sup> cycle    copy = 2
- \* End of 2<sup>nd</sup> cycle    copy = 4
- \* End of 3<sup>rd</sup> cycle    copy = 8
- \* End of 4<sup>th</sup> cycle    copy = 16



10 fold increase = 3.32 Cycles

# Statistical Measures of Assay Efficiency

- \* Slope of line

- \* Perfect is 3.32

Range = 3.12 – 3.52

- \* Efficiency

- \* Perfect is 100%

- \*  $E = -1 + 10^{(-1/\text{slope})}$

Range = 90-110%

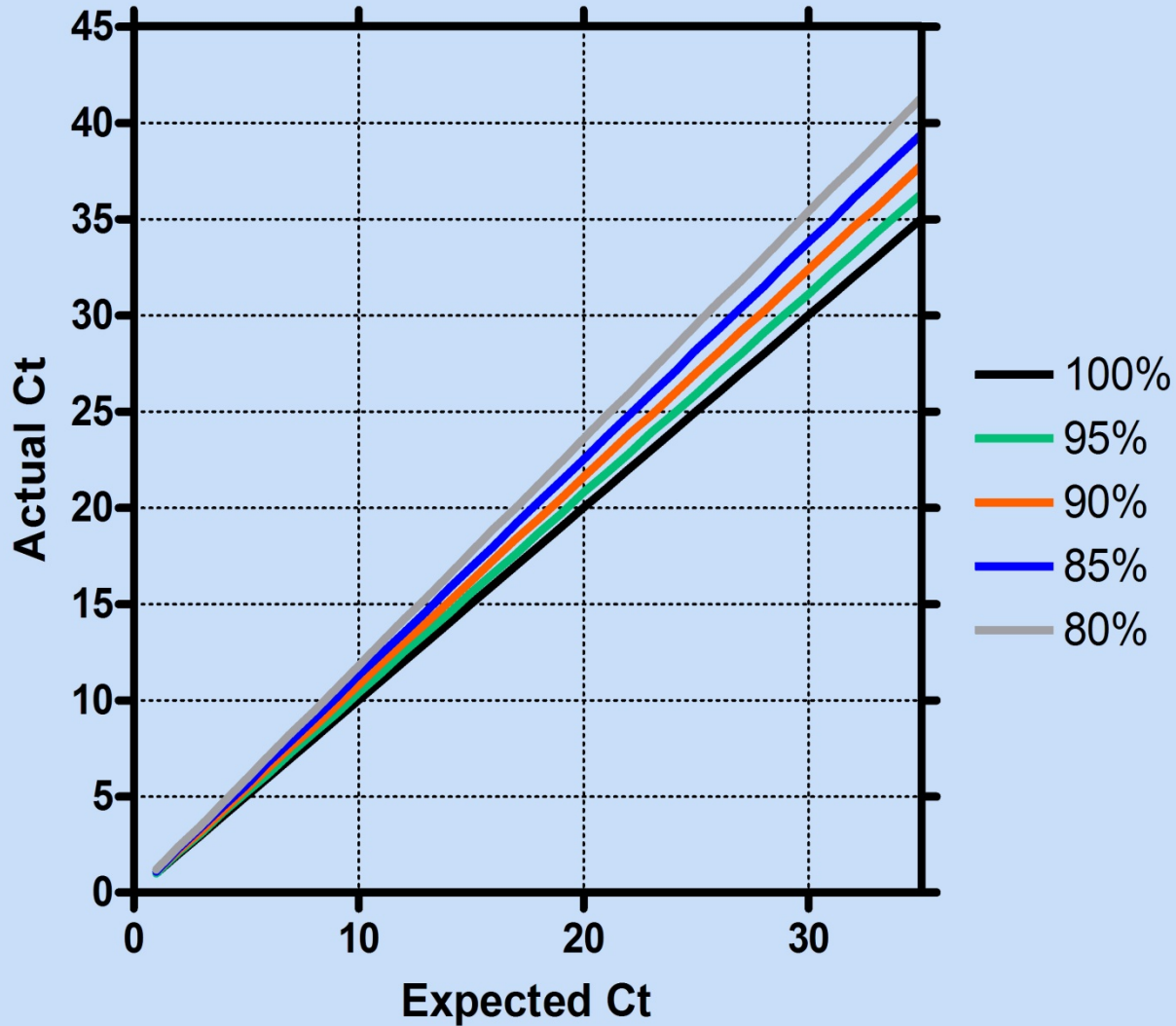
- \* Exponential Amplification

- \* Perfect is 2.0

- \*  $E = 10^{(-1/\text{slope})}$

Range = 1.81-2.02





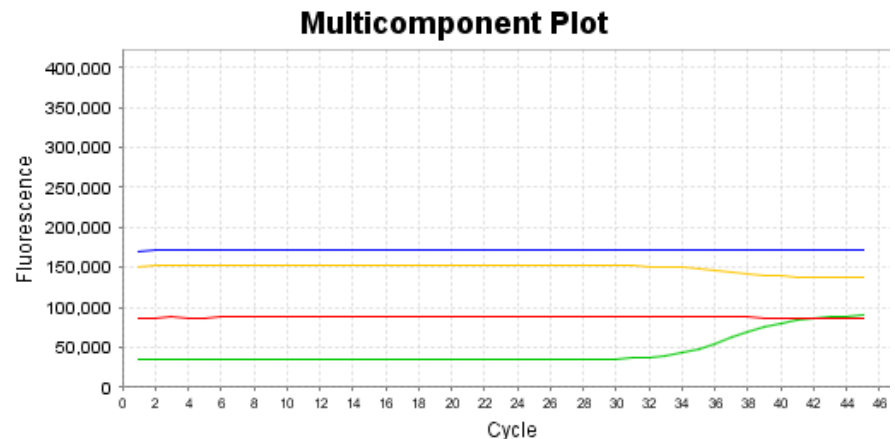
Authors – a 5% difference in efficiency results in a 2 fold difference in product quantity after 26 cycles.

Data shows at 35 cycles – 6.3 cycles or about 2 logs difference between 100% and 80% efficiency

# 2<sup>nd</sup> Check on PCR Assay Performance

## \* “Internal Control”

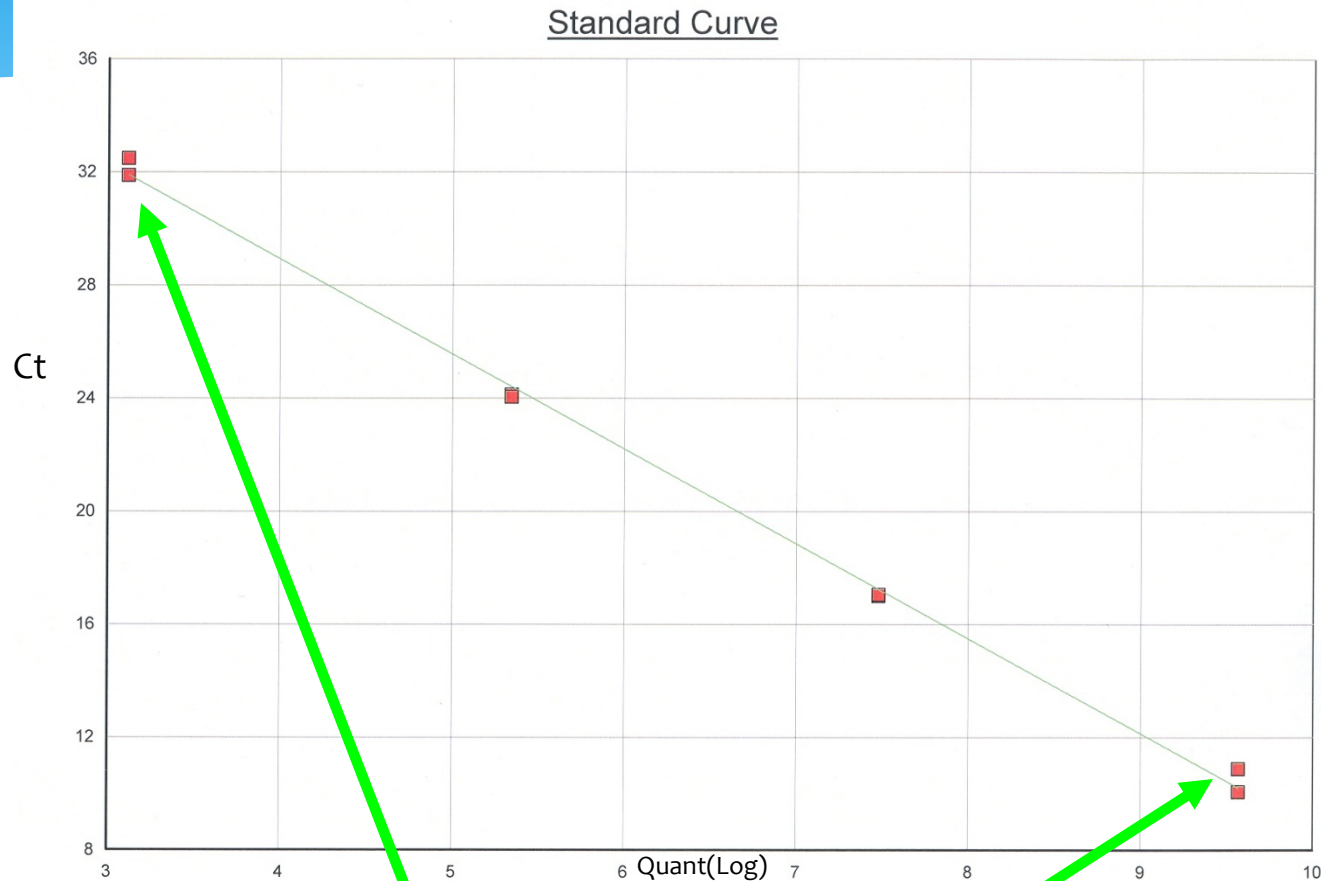
- \* Another unrelated piece of DNA added to the amplification mix
  - \* Often added into the sample before extraction
  - \* Material goes through the entire process
  - \* Master mix contains primer/probes necessary to amplify
  - \* Usually kept at a lower concentration



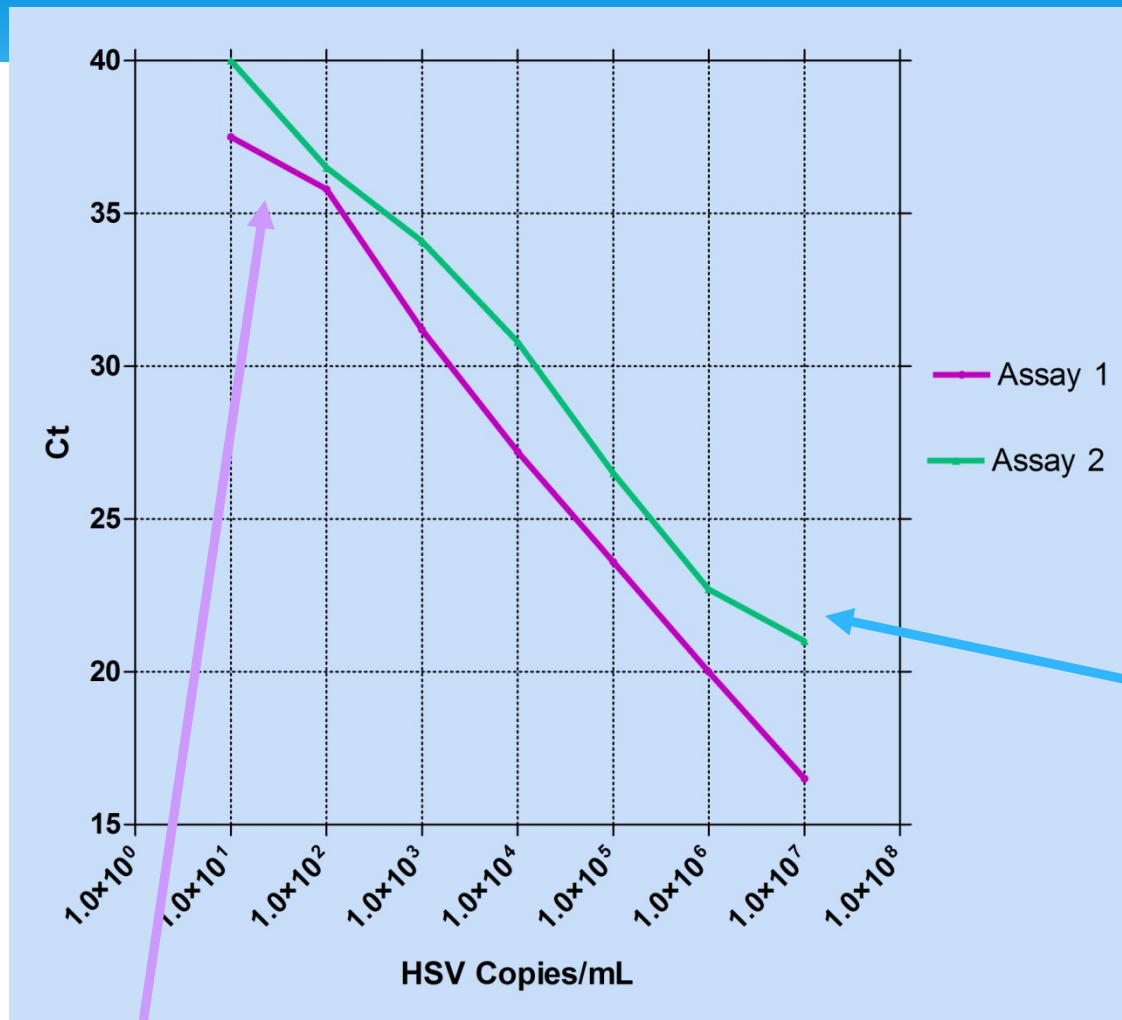
# Assay Linearity

Extraction  
PCR Assay

# Linearity of the Assay



**At High & Low Viral Quants –  
Enough primer, probe ?  
Extraction Efficiency**



Non-linear  
at the bottom

Non-linear at  
the top

Usual to have 6-7 logs measuring range

# Assay Sensitivity

# Assay Sensitivity – Extraction + PCR

- \* **Linearity + Probability**

- \* May detect 1 virus in well
- \* Can you get the virus into the well?

- \* **Example –**

- \* Start with 200 uL serum
- \* Elute purified DNA into 100 uL buffer
  - \* [2 fold concentration – if assume 100% yield]
- \* Use 10 uL in the PCR assay

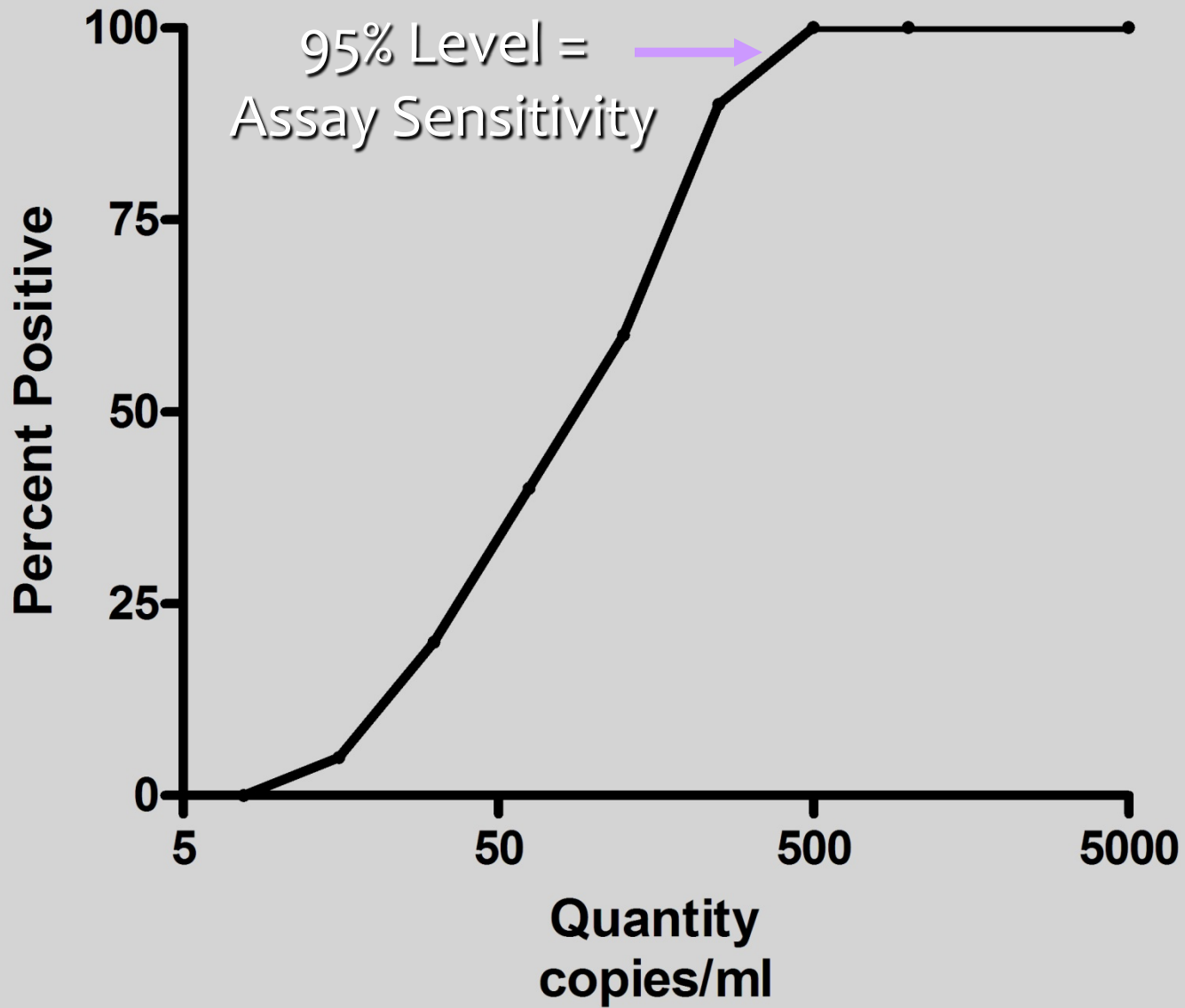


**Start with 25,000 c/ml virus**

- Or 5,000 copies (start)
- After elution have 5,000 c/100 ul
- 500 copies into the PCR assay

**Start with 250 c/ml virus**

- Or 50 copies (start)
- After elution have 50 c/100 ul
- 5 copies into the PCR well



Serial two-fold dilutions – at least 6 replicates



# Example – Assay Sensitivity Determined Utilizing a Probit Statistical Analysis

Dilutions	# Run	Quant c/mL	Pt 1 # Pos	Quant c/mL	Pt 2 # Pos
Neat	6	1,799	6	1,011	6
1:2	6	961	6	437	6
1:4	6	727	6	197	6
1:8	6	309	6	148	6
1:16	6	120	6	72	4
1:32	6	109	6	60	4
1:64	6	32	5	46	4

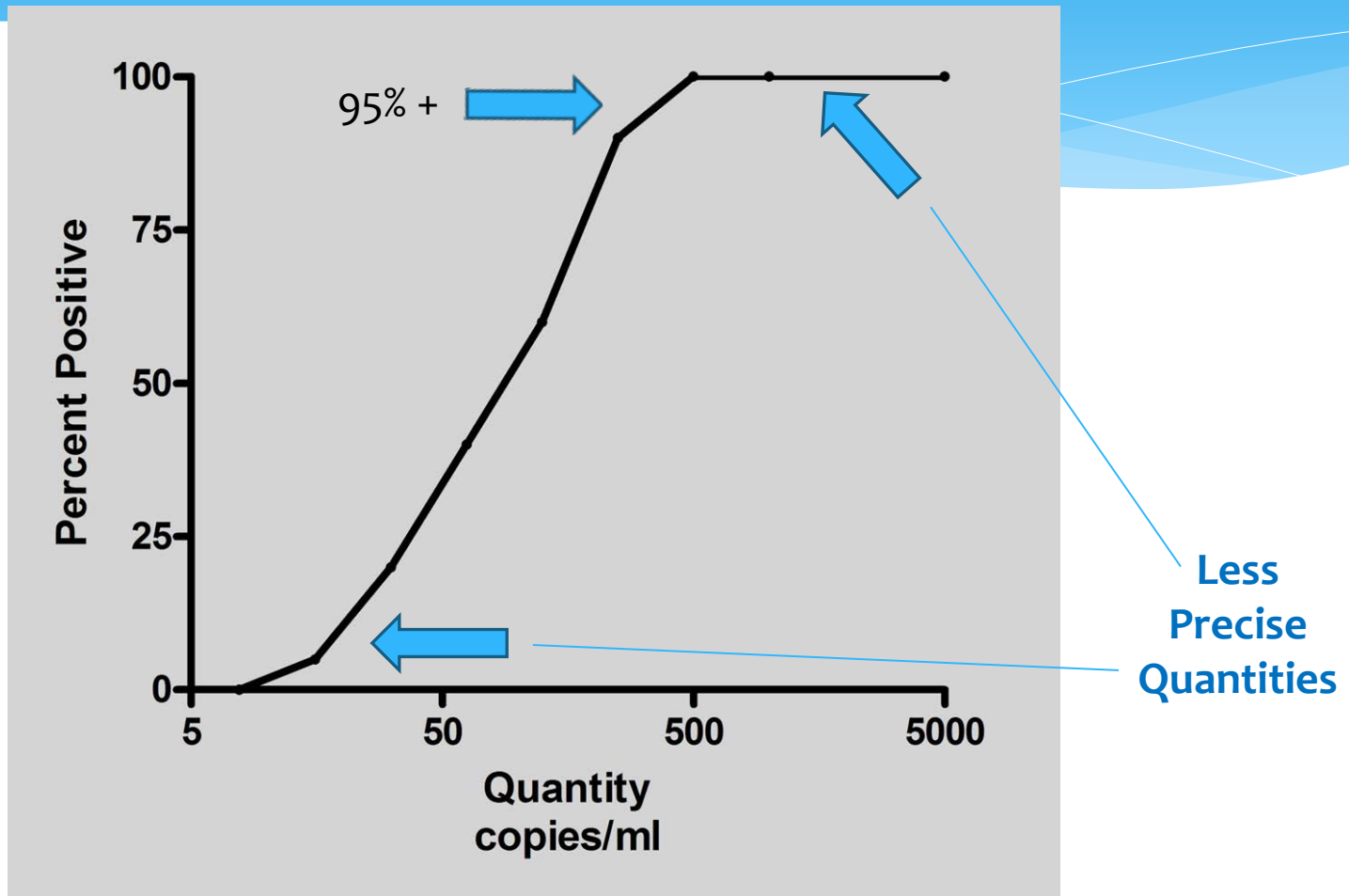
95% Level about 100 and 140 in these 2 samples

# Precision and Accuracy

Sensitivity of the Assay  
Serial Measurements

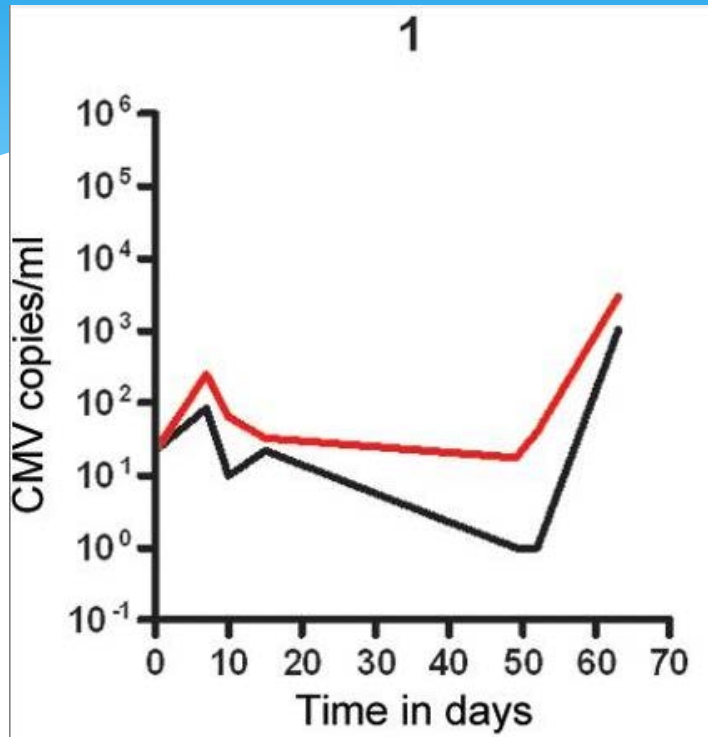


# Assay Imprecision

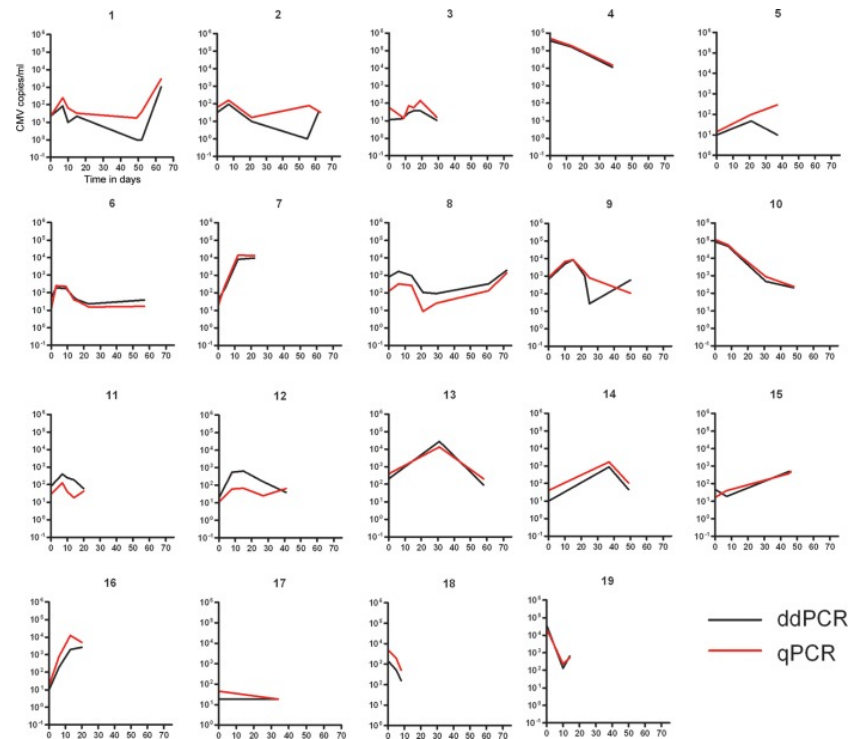


Limit of Detection vs Limit of Quantification

# Reproducibility – 19 Patients CMV qPCR vs ddPCR



No difference between Methods  
and Clinical Response Time  
(flair detection no earlier)



# CMV Specific Information

Standards & Commutability

Primers & Probes

# Available CMV Standardization Materials

- \* 1<sup>st</sup> WHO International Standard for Human CMV
  - \* NIBSC 09/162
  - \*  $5.0 \times 10^6$  IU/mL
  - \* Needs Extraction
  
- \* NIST Standard – SRM 2366a CMV DNA (Towne $\Delta$ 147 BAC)
  - \*  $1.8 \times 10^6$  Copies/mL
  - \* Purified DNA material (PCR control only)
  
- \* Secondary Reference Materials
  - \* Quantitative Panels – 3 commercial sources
    - \* Needs Extraction
  - \* Purified, Quantified Virus
    - \* DNA material (PCR control only)
  
- \* **Limited quantity so can't be used for routine testing**

# Routine Use of Standard Curves

- \* Frequency

1. Instrument Software – Stored Standard Curve

- \* Calibrate 1 time, then use for the duration of that lot of mix
- \* Current CLIA/CAP guidelines require “Calibration Verification” checks at least every 6 months

2. If not, then run a standard curve with every run

- \* Plasmid Clone Preparations
  - \* Either amplicon or larger area of sequence

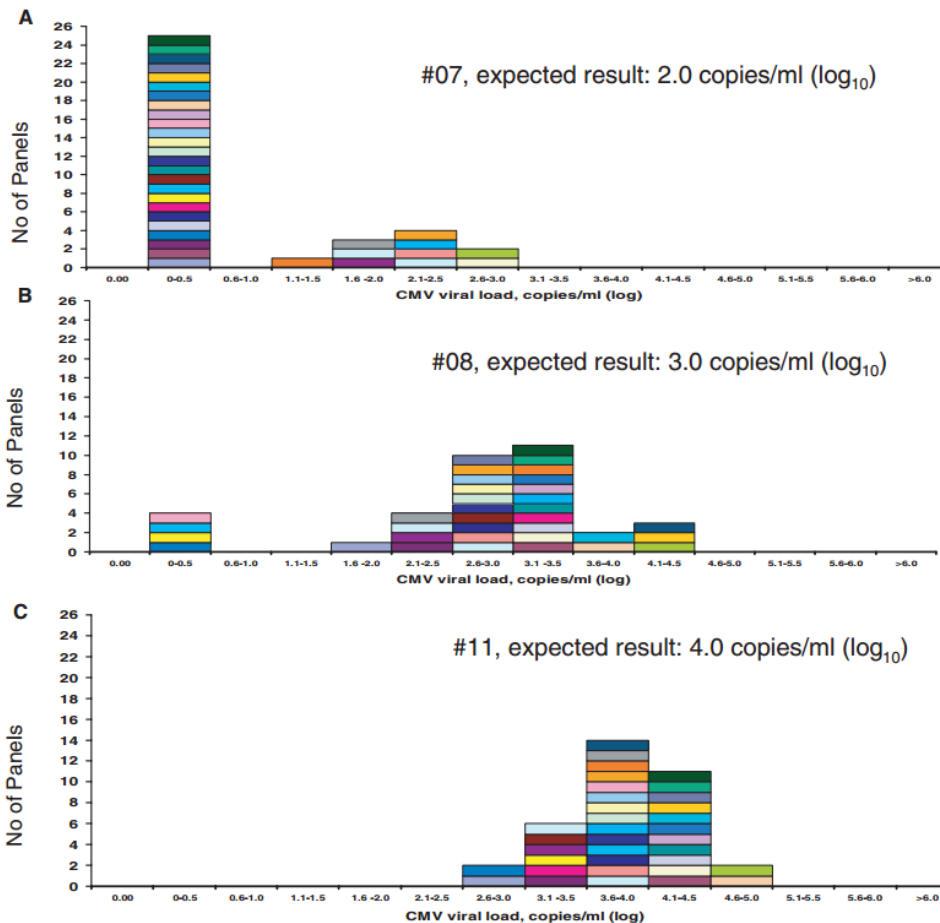
# Standards Purpose

1. Assign the “correct value” to your standard materials
2. Assure that the value doesn't change over time within a single lab
3. Assure that the same values are obtained across methods and across multiple labs



# Pre-WHO Standard Between-Lab Comparison -33 labs

Pang, et al 2009

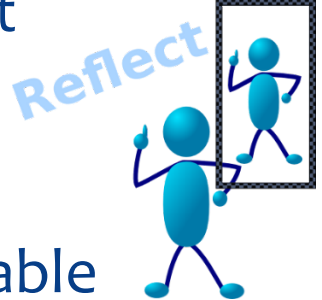


**Wide variation of results, both above and below a commonly used Clinical Cutoff of 1,000 Copies/mL**

Post WHO Release ??

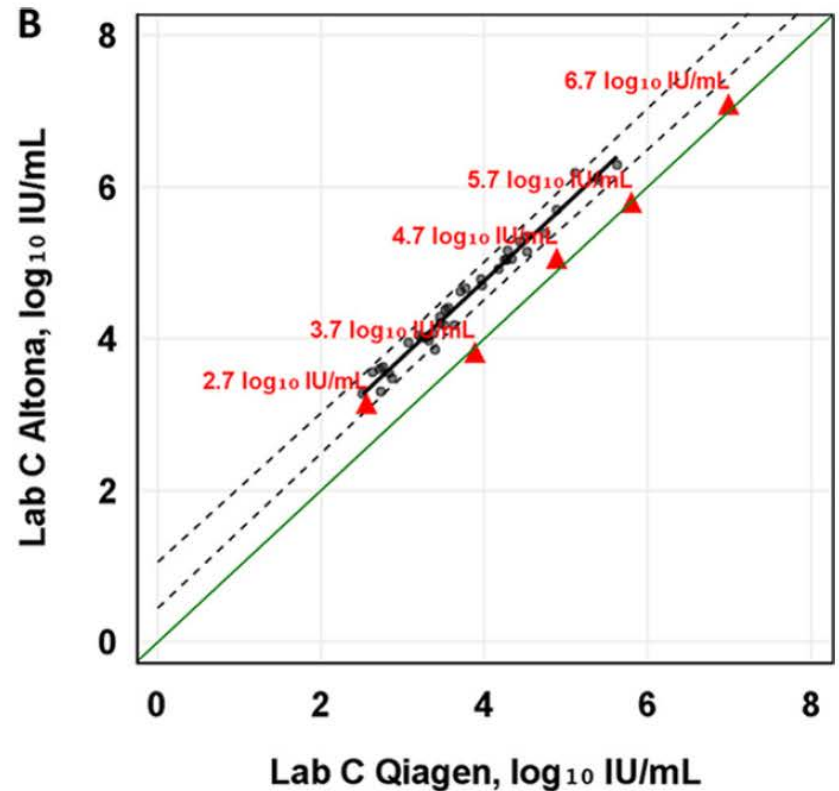
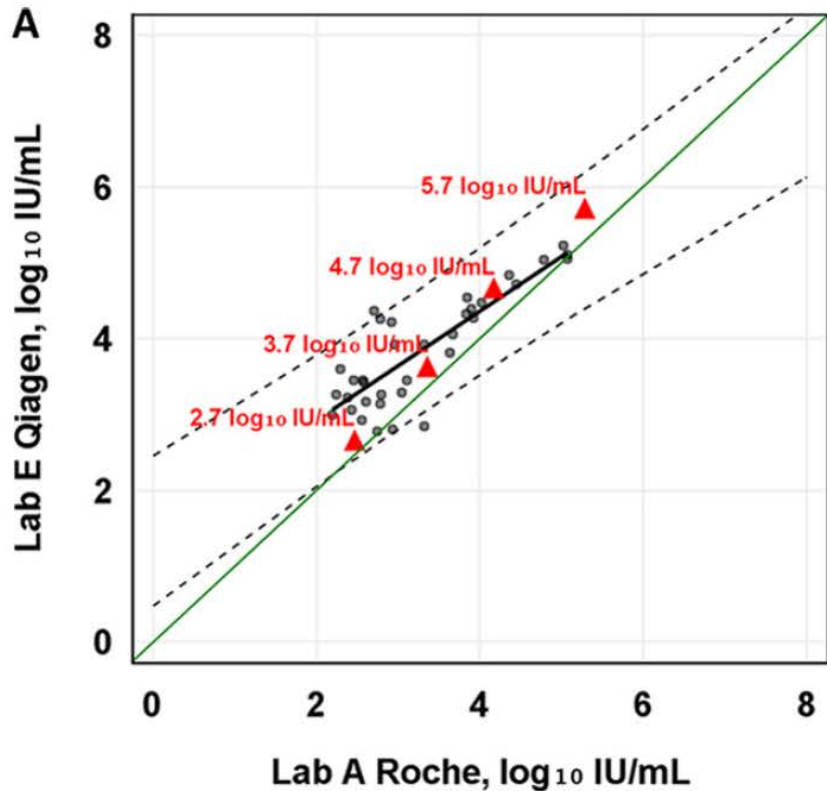
# “Commutability”

1. A RM would be considered commutable when a measurement procedure produces the same result for a RM as it does for an authentic patient sample that contained the same analyte concentration.
2. Measurement procedures calibrated with commutable RMs will produce results for clinical samples that are equivalent among all procedures, i.e. the results are traceable to the reference system and there is no calibration bias among the measurement procedures.



# Commutability Evaluation Data

Hayden, 2015 (40 positive samples, 6 labs/methods)



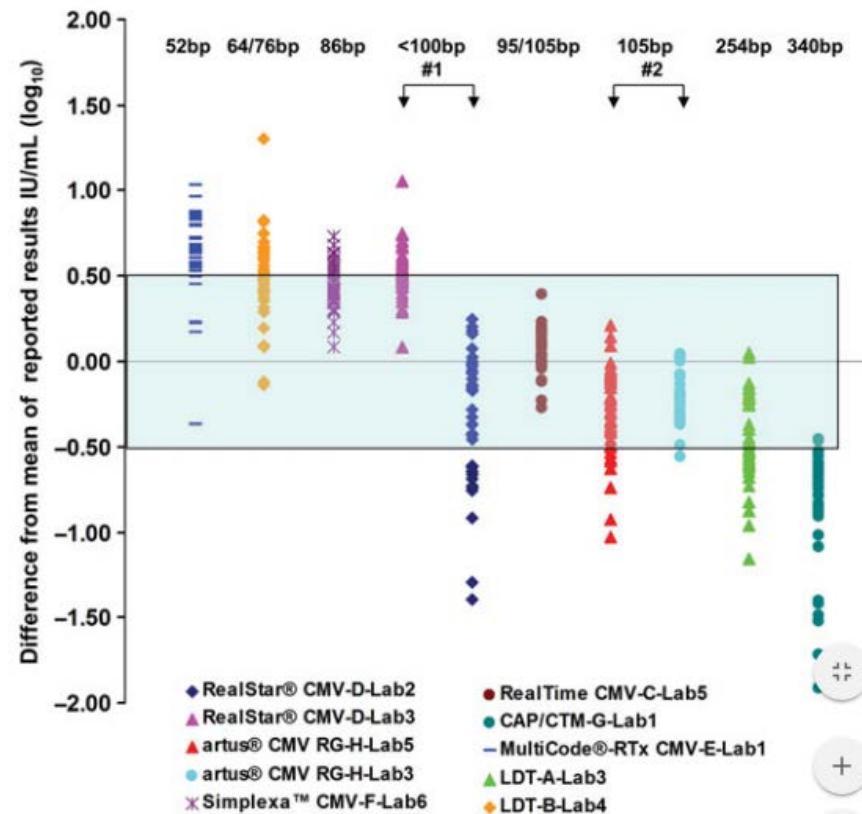
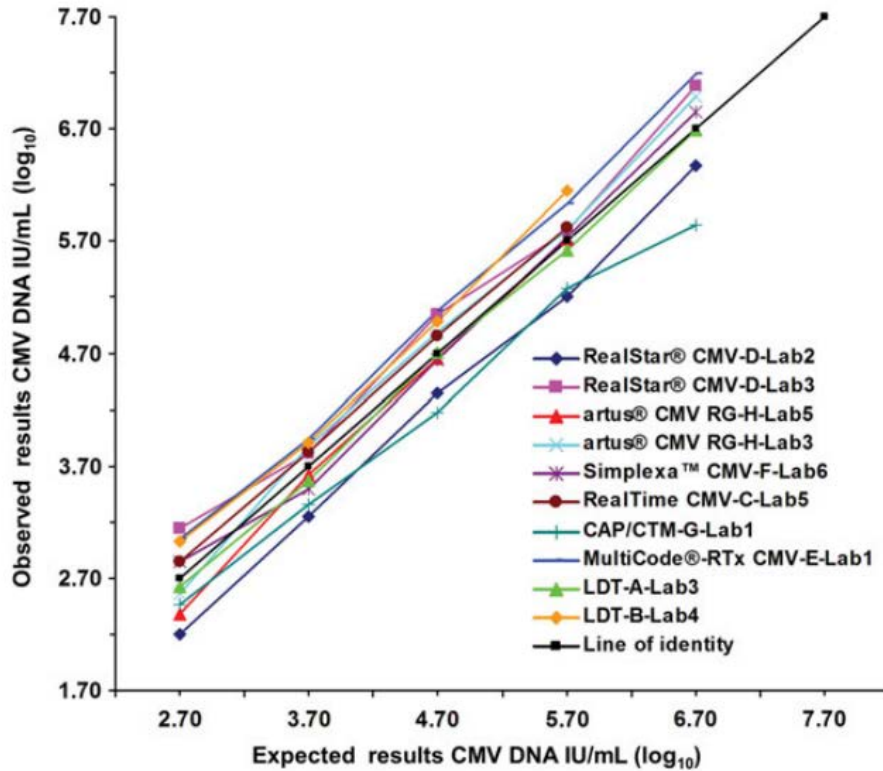
# Cross Lab & Method Commutability

Hayden, RT et al JCM 2013

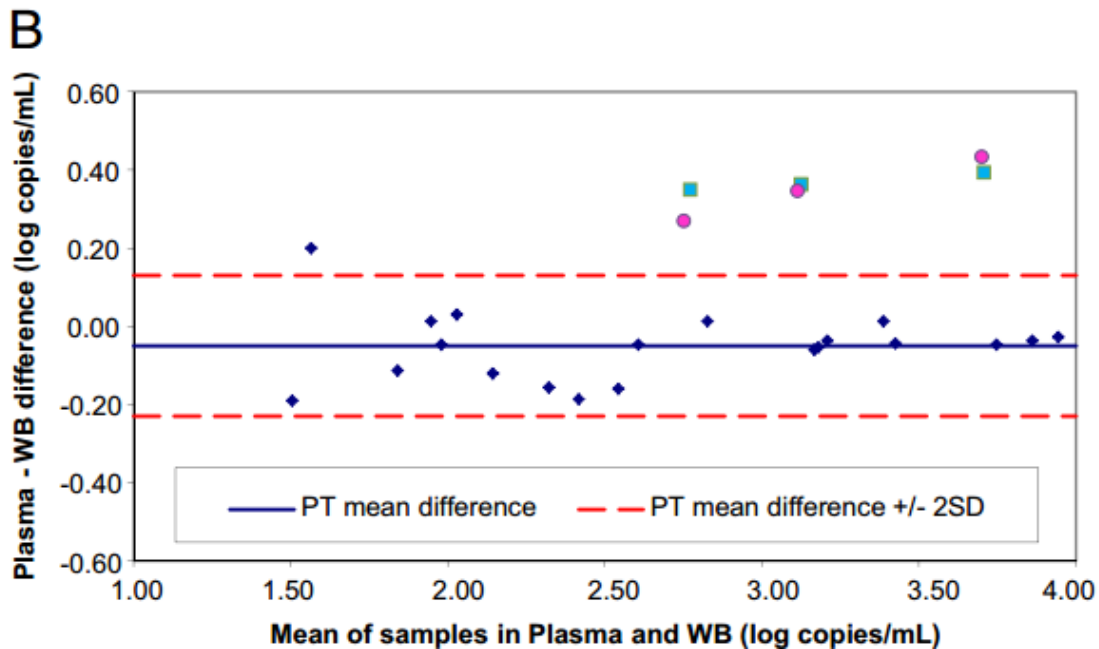
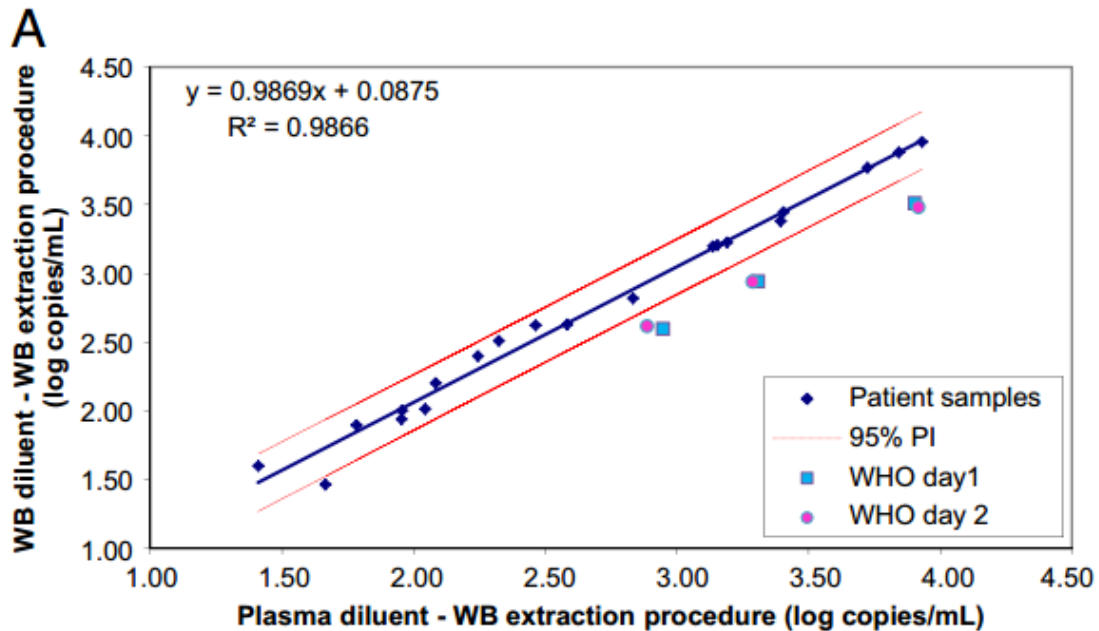
	Lab A Luminex	Lab A Roche	Lab B Altona	Lab C Altona	Lab C LDT	Lab C Qiagen	Lab D LDT	Lab E Abbott	Lab E Qiagen
Lab A Roche	3/4								
Lab B Altona	4/4	4/4							
Lab C Altona	4/4	3/5	4/4						
Lab C LDT	2/4	5/5	4/4	3/5					
Lab C Qiagen	0/4	4/5	4/4	1/5	4/5				
Lab D LDT	3/3	4/4	3/3	4/4	4/4	2/4			
Lab E Abbott	0/3	4/4	3/3	2/4	3/4	3/4	4/4		
Lab E Qiagen	2/3	4/4	3/3	3/4	4/4	4/4	4/4	4/4	
Lab F Focus	4/4	3/4	4/4	4/4	2/4	0/4	3/3	0/3	0/3

Commutable
 
 Marginally commutable
 
 Not commutable

# Preiksaitis, et al 2016



# Jones, et al 2016



**CMV WHO Standard  
lack of commutability  
in Whole Blood**

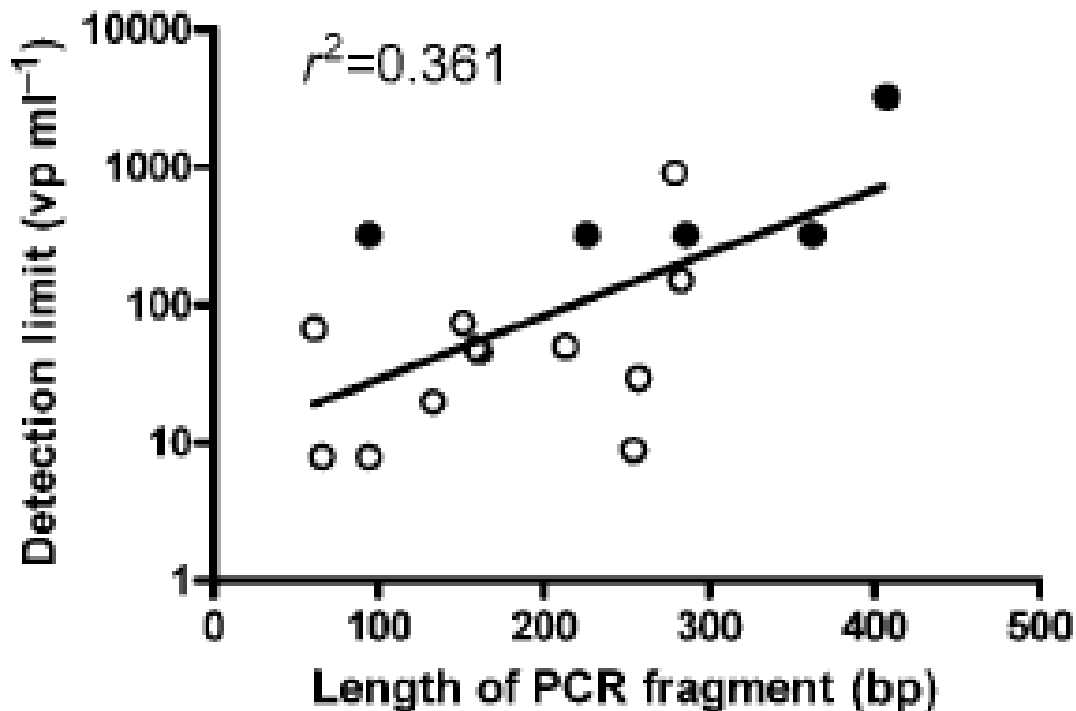
# Primer and Probe Design



# CMV Primer and Probe Design

- \* Habbal, W, Monem, F, and Gartner, BC. – 2009
- \* Identified 57 papers describing 82 primer pairs
- \* 17 Selected for further evaluation based on absence of mismatching with CMV sequences in GenBank.
- \* Evaluated all for their assay sensitivity
  - \* 5 immediately eliminated due to lack of sensitivity
  - \* Best sensitivity was seen with 3 primer sets in gB region
  - \* Also found.....

# Primer/Probe Design



Detection levels highest for the smallest primer sets

# Primer Selection and Standardization

Mannonen 2014

Comparison of Two CMV-PCR Tests

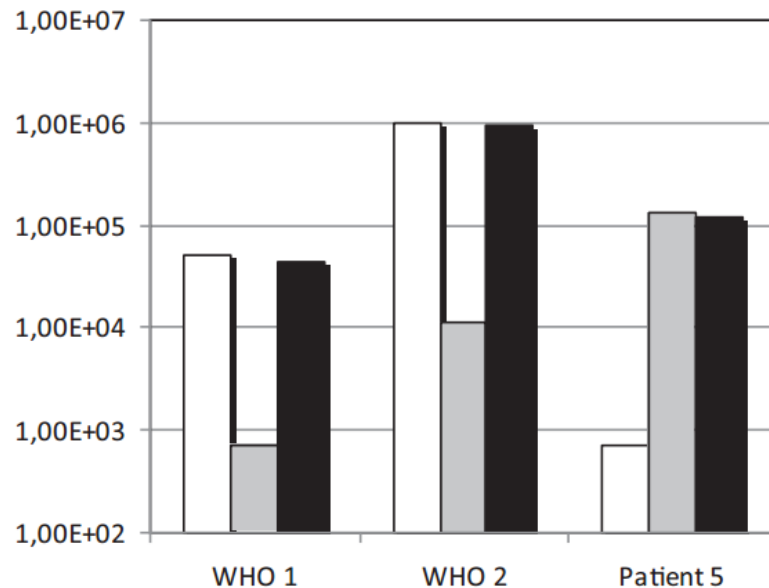


Fig. 4. Impact of the G to T mutation in the binding region of forward primer. PCR mixes containing 900mM of the normal forward primer (white bars), the G to T modified forward primer (gray bars) and a mix of both (450mM each; black bars) were used to amplify the patient sample (patient 5). Two dilutions of the CMV WHO standards amplified with the normal forward primers were used as quantification standards (WHO 1:  $1 \times 10^6$  IU/ml, WHO 2:  $5 \times 10^4$  IU/ml). The impact of the mutation on the quantification of the DNA extract from the patients and of the WHO standard is approximately 2-log.

**Forward Primer Mismatch resulted in a significant decrease in Amplification for the patient sample**

# Current FDA Approved CMV Quant Tests

- \* Roche Cobas Ampliprep/Cobas Taqman Assay
  - \* Solid Organ transplant monitoring – July 2012
  - \* Stem Cell transplant monitoring – May 2016
- \* Qiagen CMV RGQ MDX Kit (Artus)
  - \* Qiagen EZ1 Extraction Instrument
  - \* Roto-Geen Q MDX Instrument
  - \* Solid Organ transplant monitoring – June 2014
- \* Nothing currently available for other clinical CMV infections {Diagnosis??}

# Questions?

