

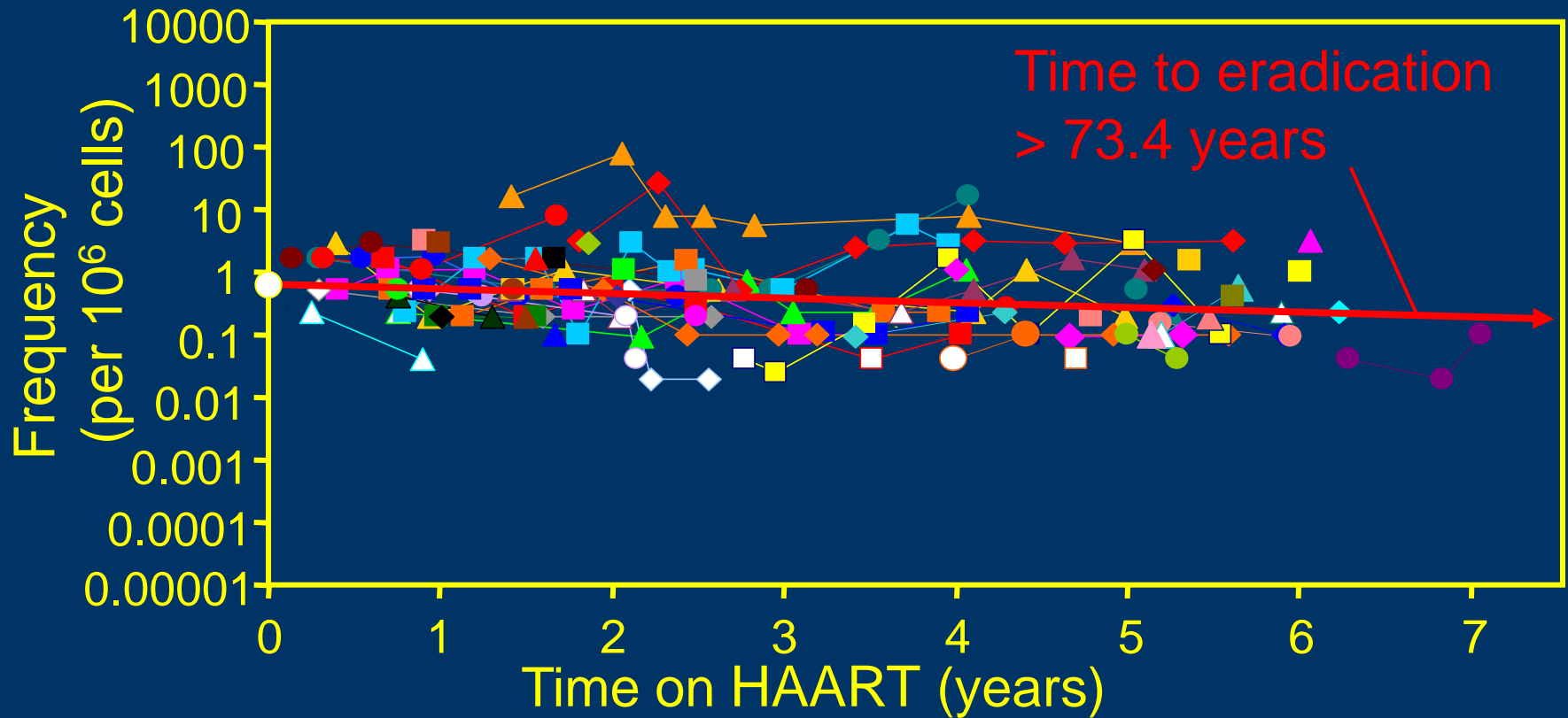
# Comparative Analysis of Measures of Viral Reservoirs in HIV-1 Eradication Studies

**Janet M. Siliciano PhD**  
**Johns Hopkins University**  
**School of Medicine**

Disclosures: None



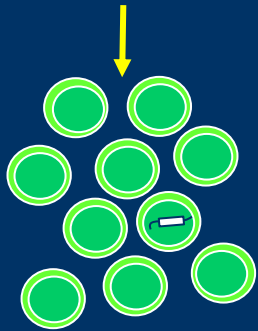
# Slow decay of latently infected CD4<sup>+</sup> T cells



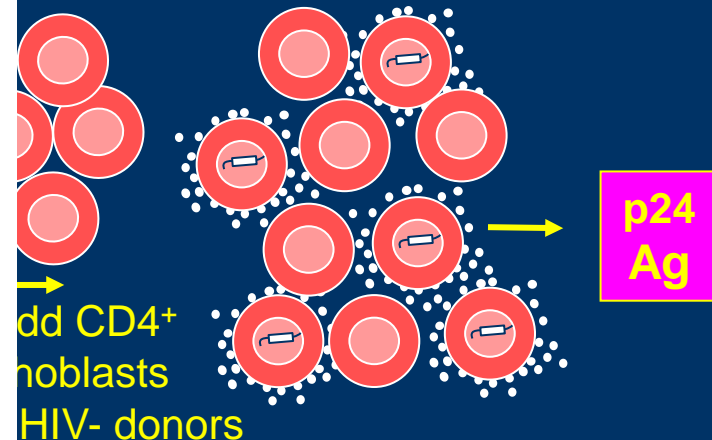
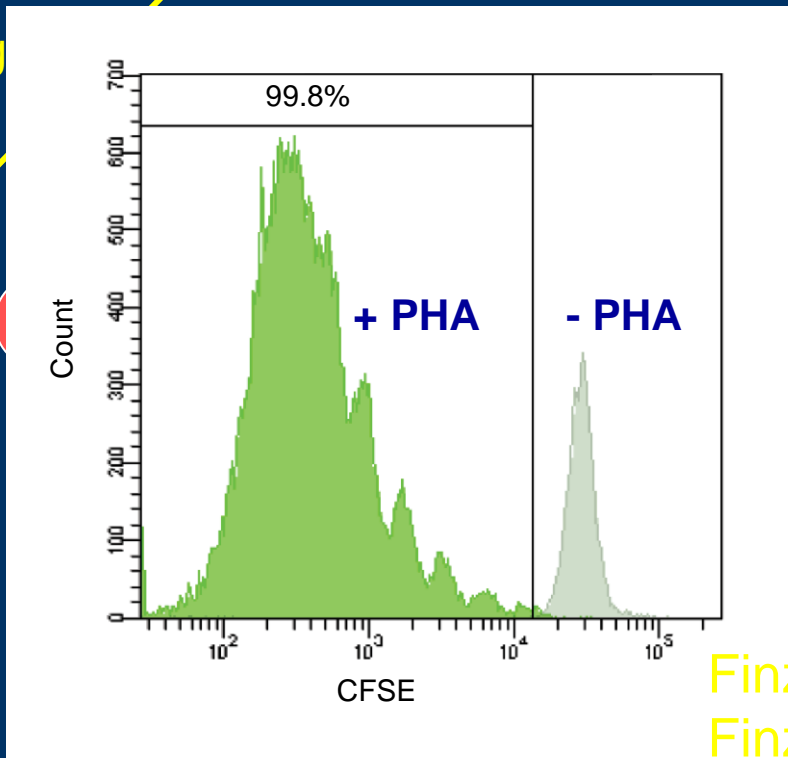
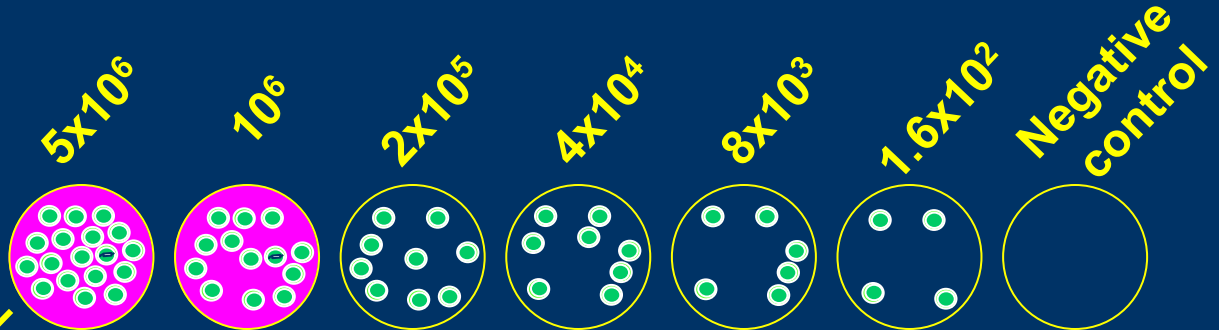
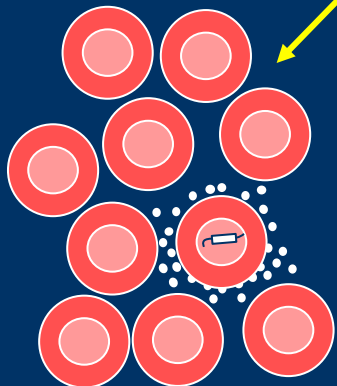
Finzi et al., Nature Med., 1999  
Siliciano et al., Nature Med., 2003

# Virus culture assay for latent HIV-1 in resting CD4<sup>+</sup> T cells

180-200  
ml blood



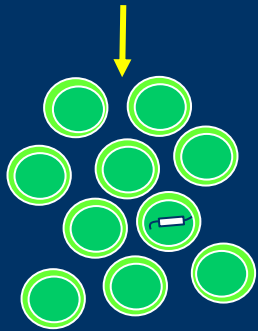
Purified resting  
CD4<sup>+</sup> T cells



Finzi et al, Science 1997  
Finzi et al., Nature Med., 1999  
Siliciano et al., Nature Med., 2003

# Virus culture assay for latent HIV-1 in resting CD4<sup>+</sup> T cells

180-200  
ml blood

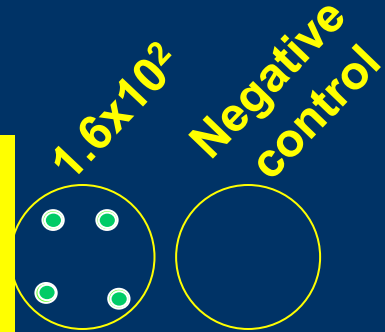


Purified resting  
CD4<sup>+</sup> T cells

- Detects individual latently infected cells
- Detects cells with latent viruses capable of robust growth in vitro in primary CD4<sup>+</sup> T cells
- Does not detect cells with defective viruses
- No other approach has given a higher frequency of cells with replication competent virus
- BUT labor-intensive and costly

d2: add CD4<sup>+</sup>  
lymphoblasts  
from HIV- donors

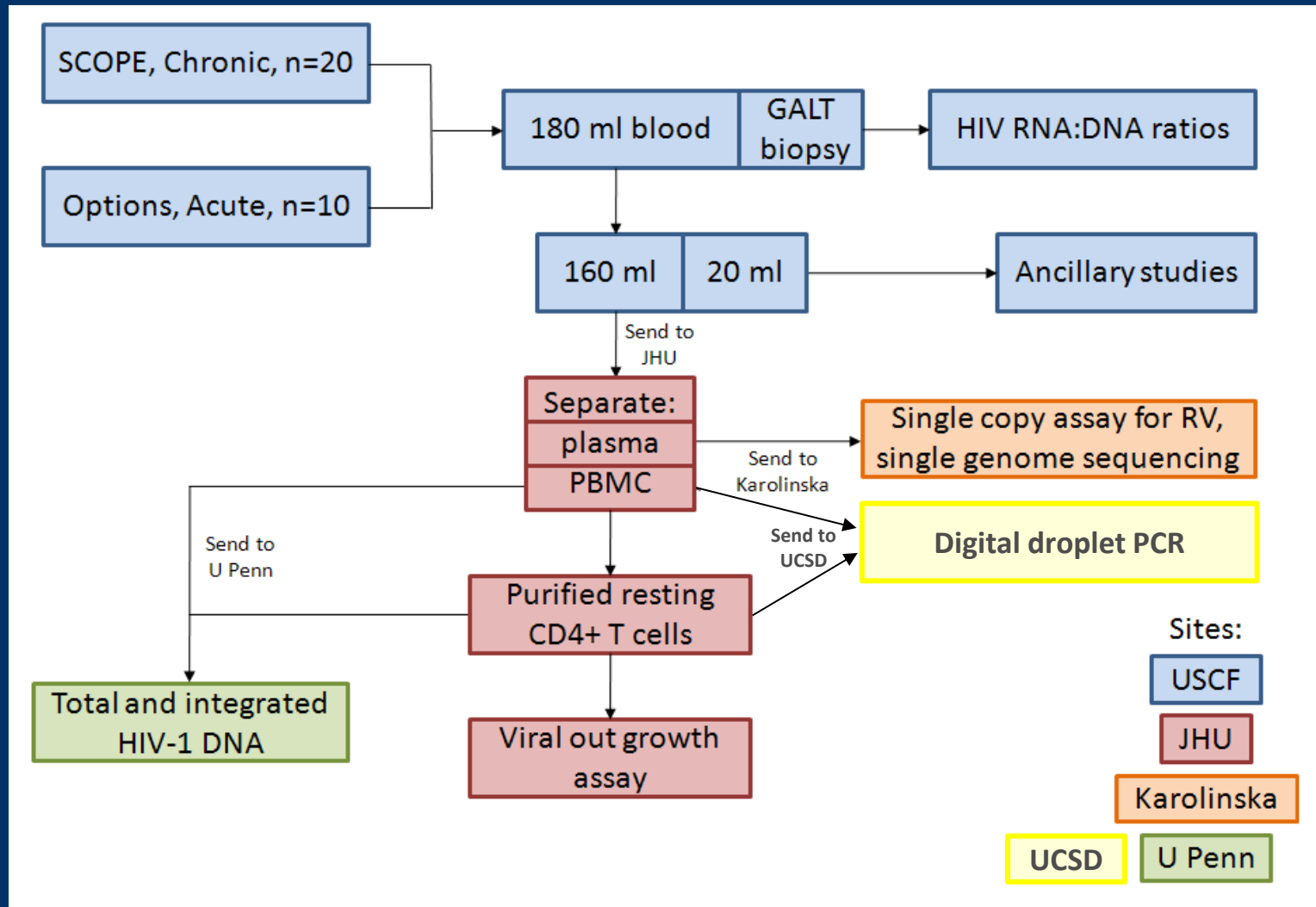
d7: add CD4<sup>+</sup>  
lymphoblasts  
from HIV- donors



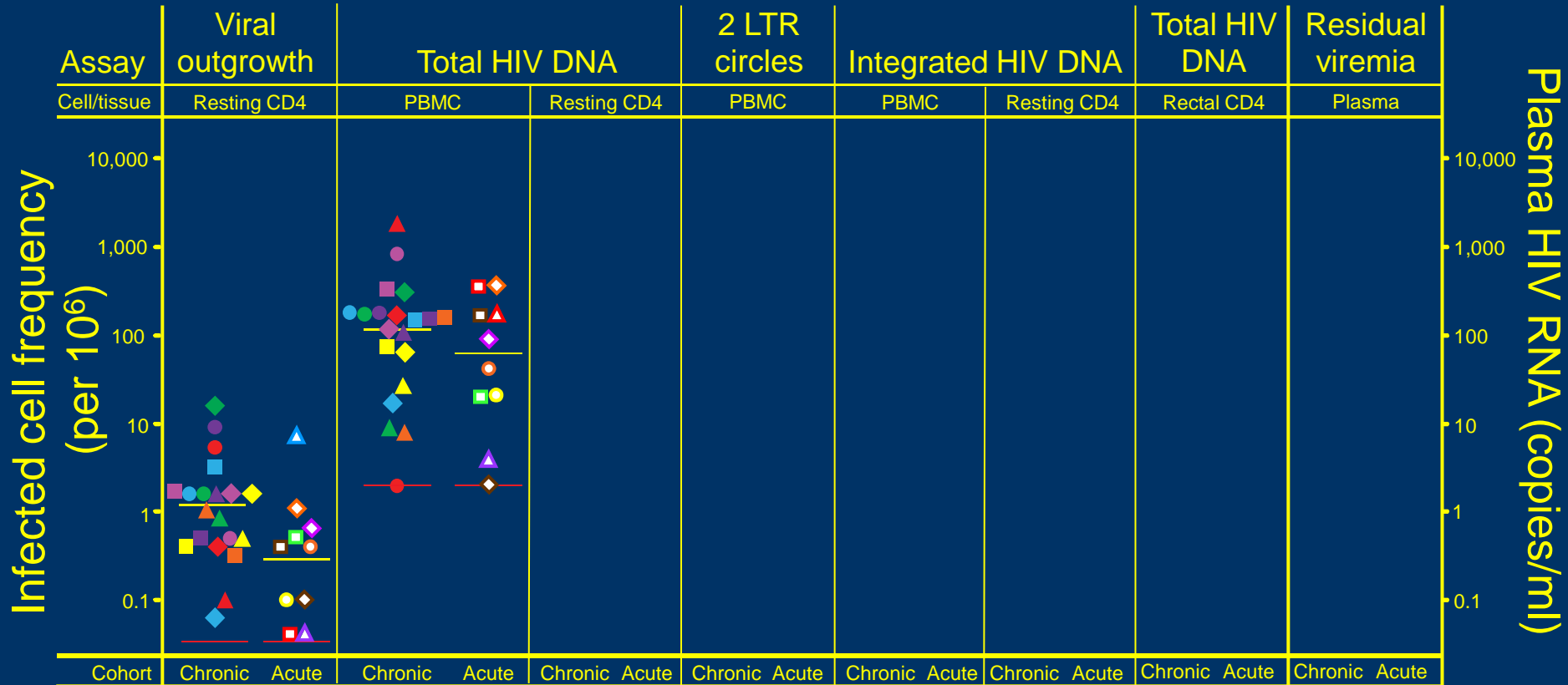
p24  
Ag

Finzi et al, Science 1997  
 Finzi et al., Nature Med., 1999  
 Siliciano et al., Nature Med., 2003

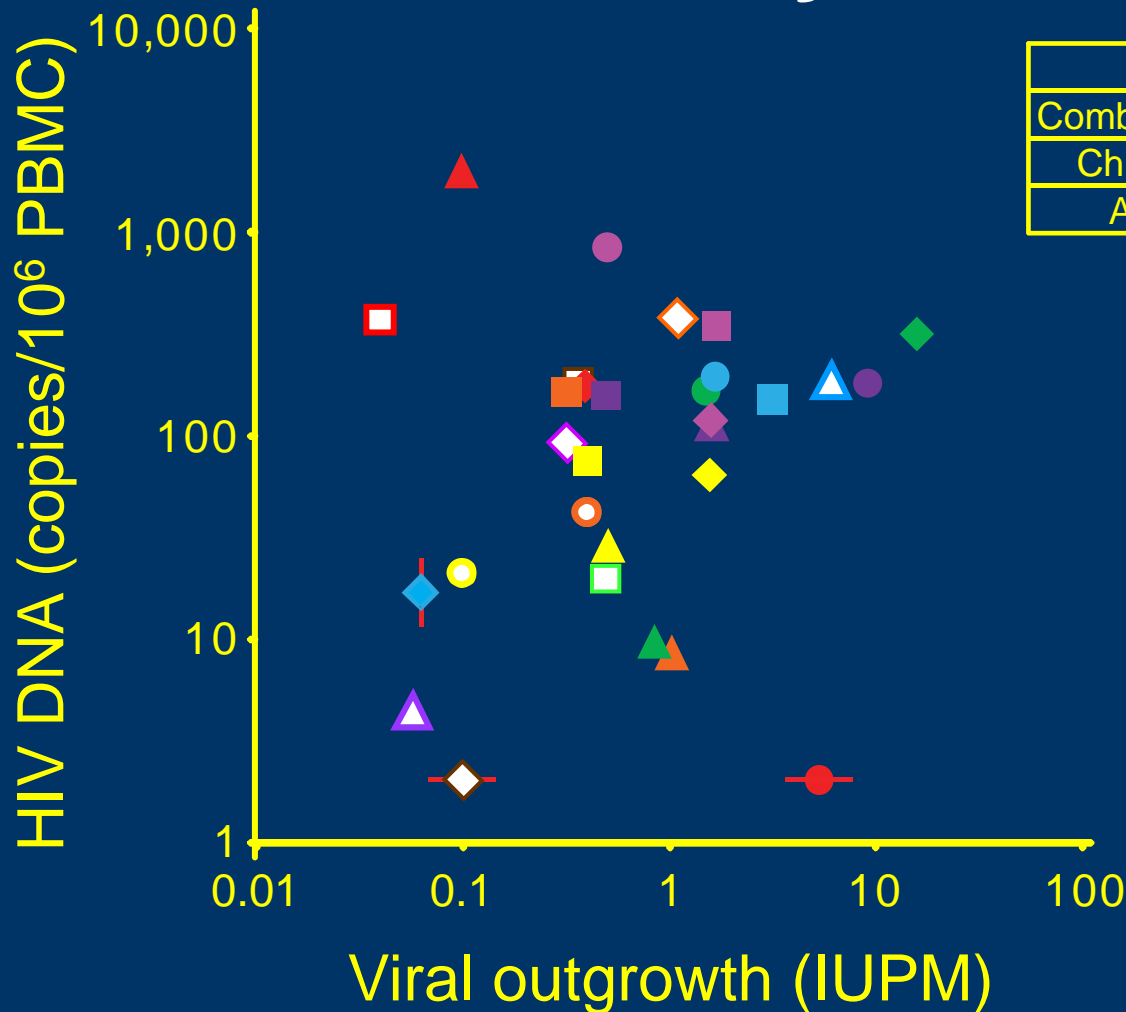
# Comparison of reservoir assays



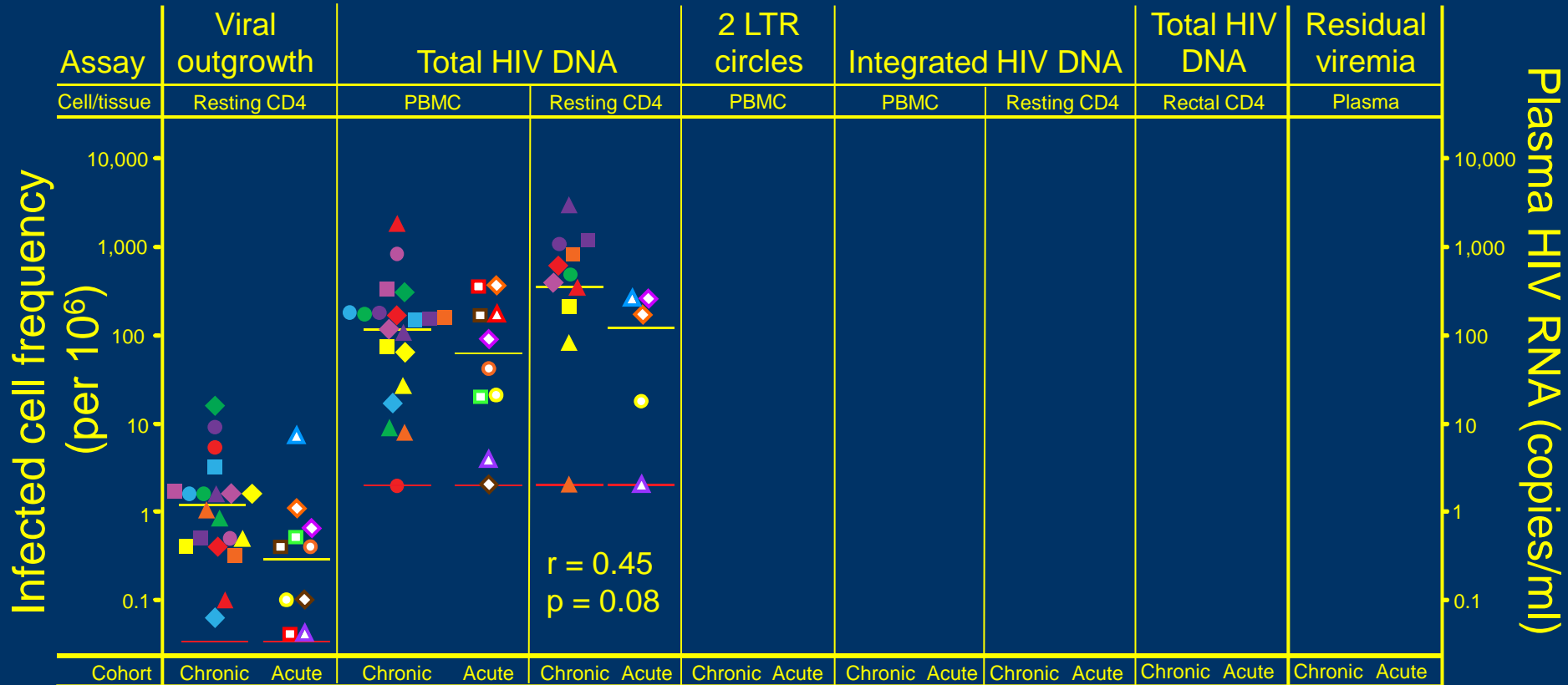
# Assay for persistent HIV in patients on HAART



# Correlation between culture and PCR assays

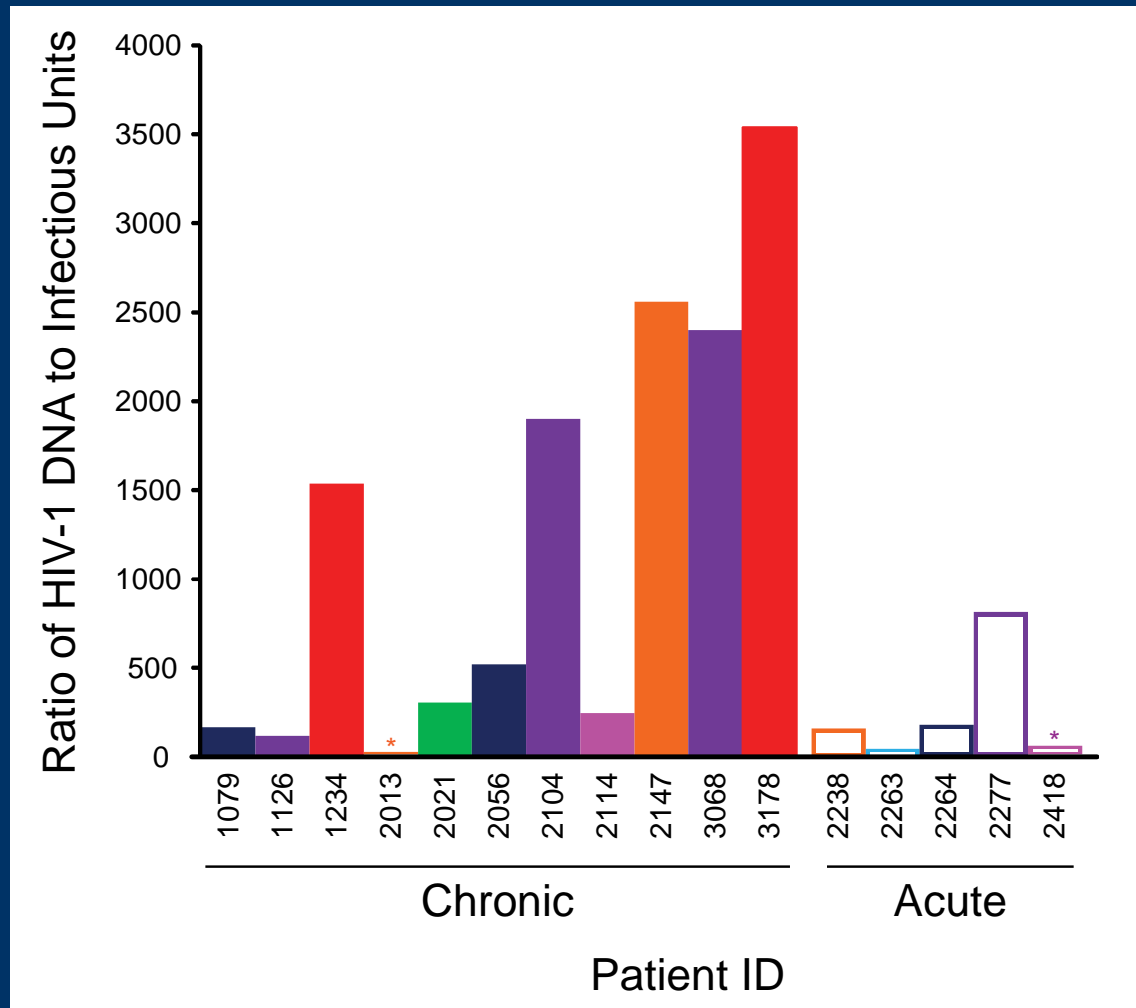


# Assay for persistent HIV in patients on HAART

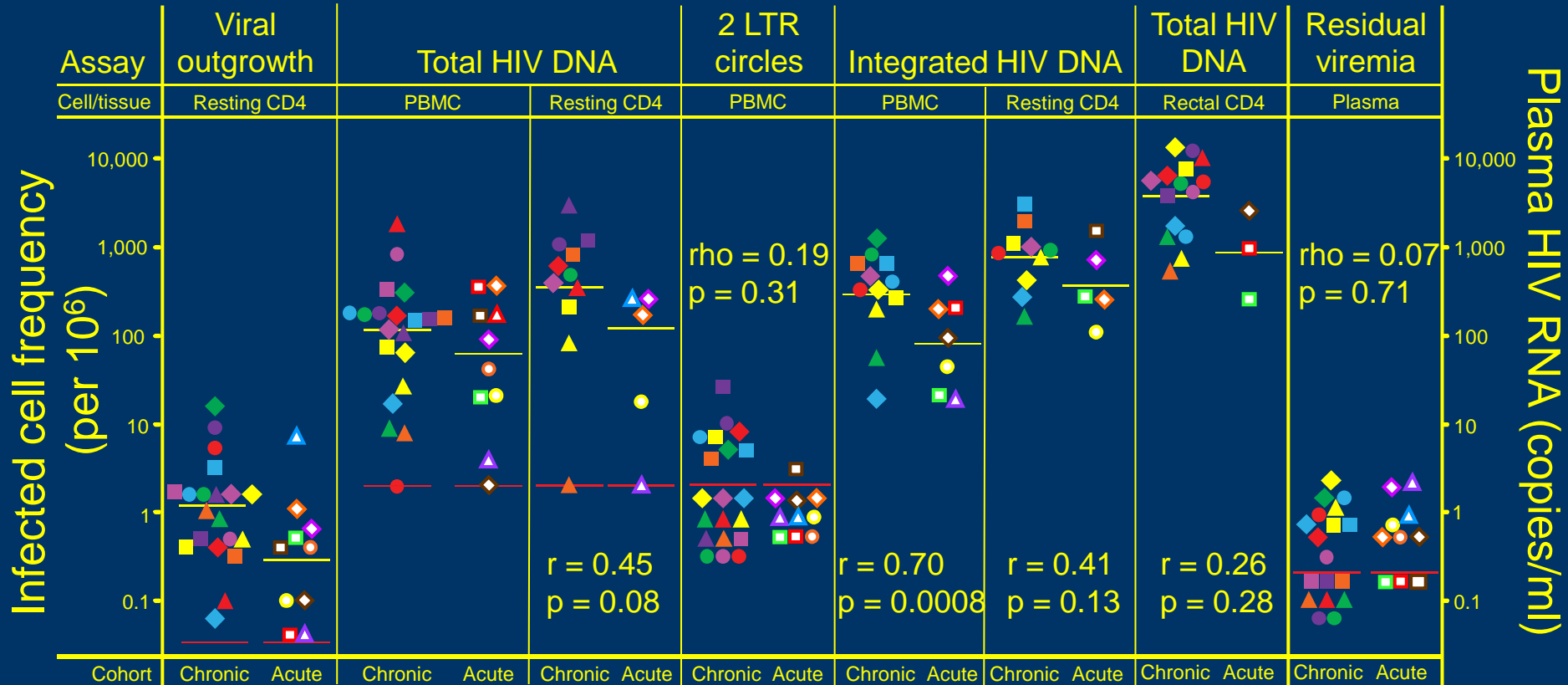




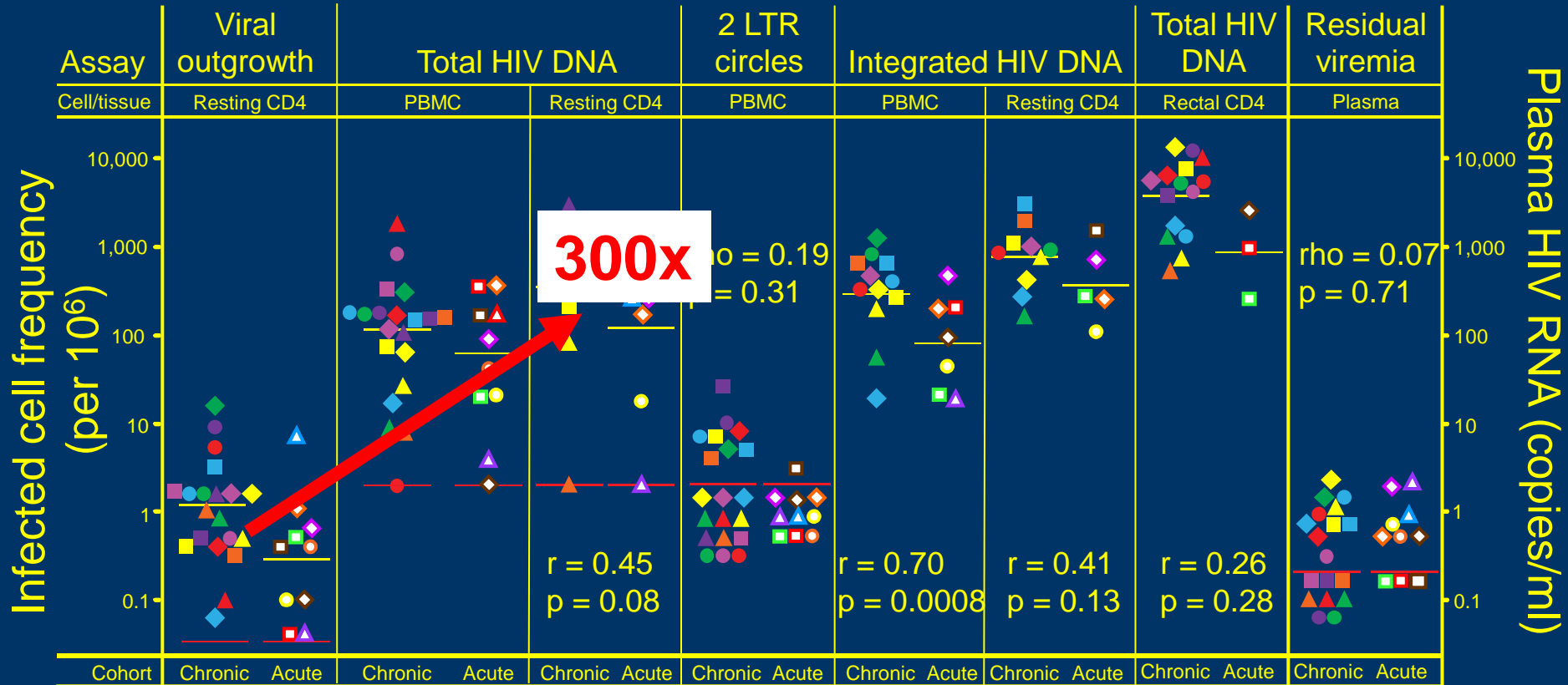
# Ratio of infected cell frequencies by PCR and culture assays



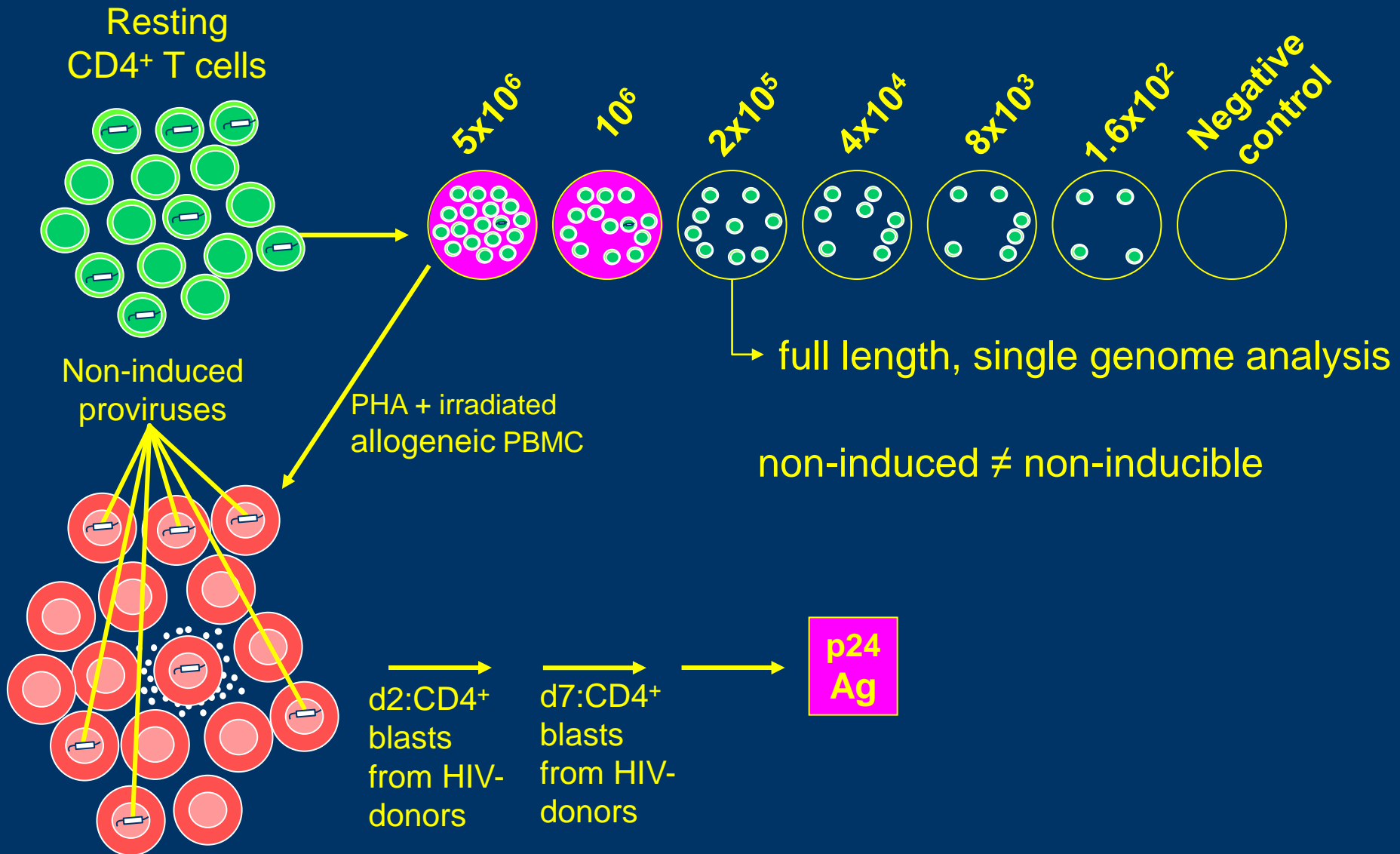
# Assay for persistent HIV in patients on HAART



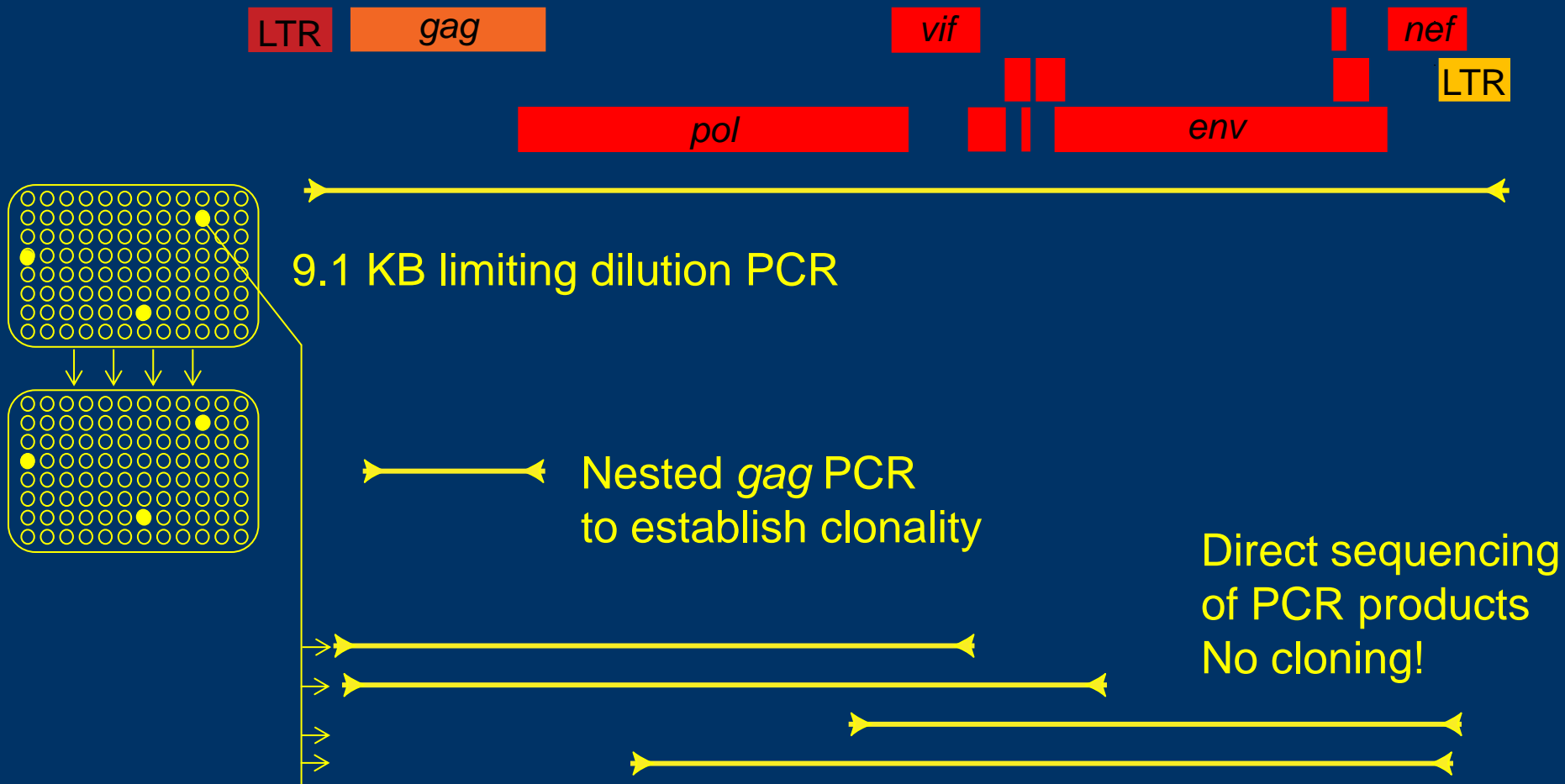
# Which assay should be used?



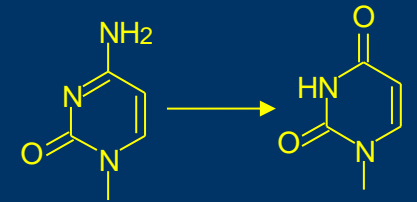
# Non-induced proviruses



# Clonal analysis of non-induced proviruses



# Non-induced proviral clones (n=213)



TGG → TAG  
Trp Stop

Hypermuted  
32.4%

# 32.4% of non-induced proviruses have G→A hypermutation

B.FR.83.HXB2_LAI_IIIB_BRU_K034	ATGGGTGCGAGAGCGTCAGTATTAAAGCGGGGGAGAATTAGATCGATTGGEAAAAAATTCGGTTAAGGCCAGGGGGAAA
9CC3_31E5_gag_hypermut	.A.....A.....A.....A..A.....C.....A.....
9CC3_31E11_gag_hypermut	.AA.....A.....AA.....A..AA.....A..C.....AAA.....
20CB4_36D12_gag_hypermut	.A.....C.....A..A.....G.....A.....
20TB1_33C3_gag_hypermut	.A.....C.....A..A.....G.....A.....
20TB1_33C9_gag_hypermut	.A.....C.....A..A.....G.....A.....
20TB3_33G10_gag_hypermut	.A.....AA..C.....A..A.....AA.....



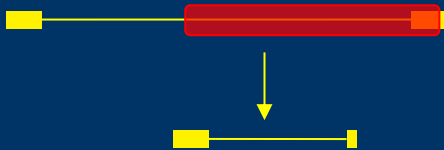
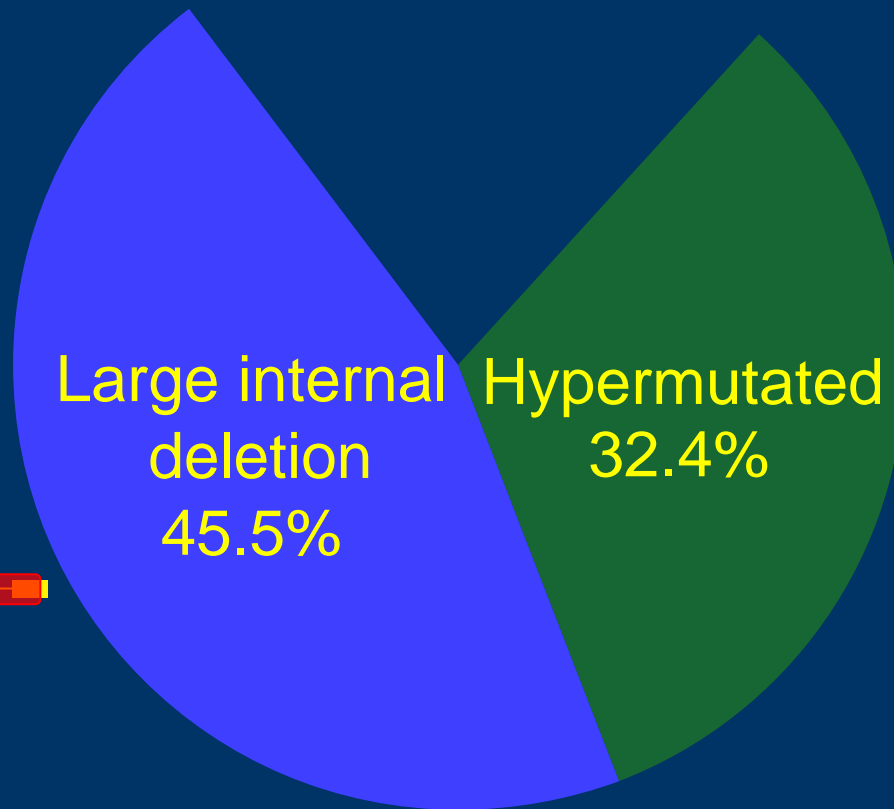
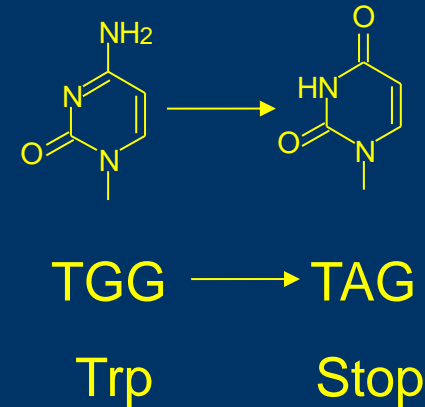
ATG → ATA  
M→I  
start codon mutation

TGG → TAA, TAG, TGA  
Tryptophan → stop codon  
nonsense mutation

B.FR.83.HXB2_LAI_IIIB_BRU_K034	MGARASVLSGGELDFWEKIRLRPGGKKKYKLVHIVASRELERFAVNPGLLLETSEGCQRQILGQIQPSL
9CC3_31E5_gag_hypermut	I...I..E...*.....L..G.....A.....
9CC3_31E11_gag_hypermut	IS...I..R...*...Q..K.....L.*GK.....S...A.....R.....
20CB4_36D12_gag_hypermut	I.....Q...*R.....N.R.....AG.....E...A..
20TB1_33C3_gag_hypermut	I.....Q...*R.....N.R.....AG.....E...A..
20TB1_33C9_gag_hypermut	I.....Q...*R.....N.R.....AG.....E...A..
20TB3_33G10_gag_hypermut	I.....R.Q...*.....E.N.R.....K.....AG.....E...A..

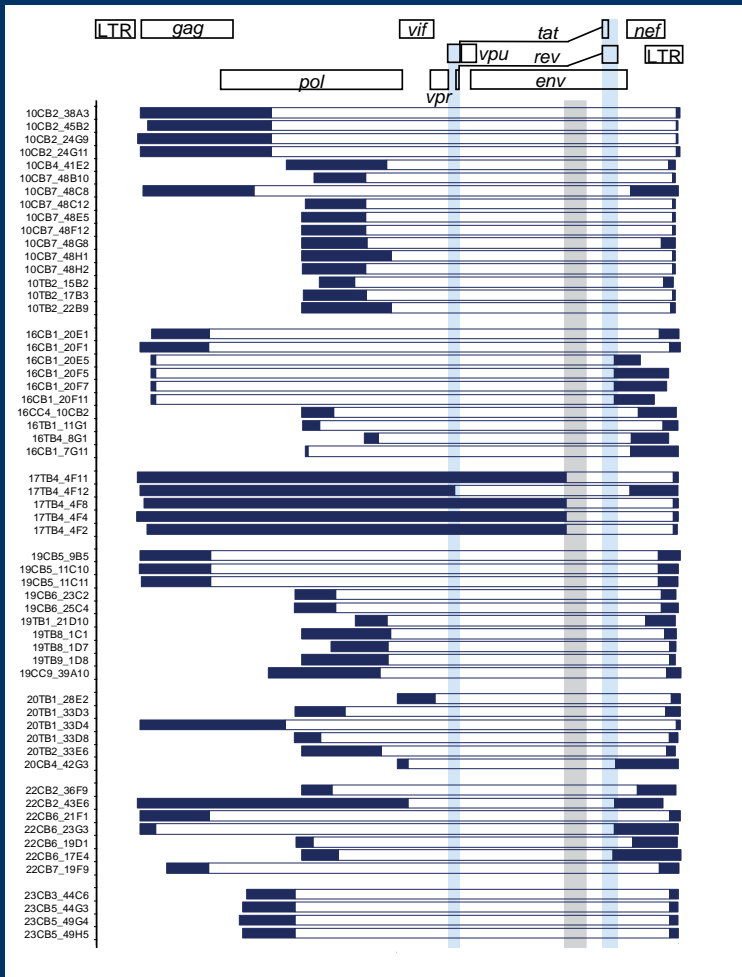


# Non-induced proviral clones (n=213)





# 45.5% of non-induced proviruses have large internal deletions



# Non-induced proviral clones (n=213)

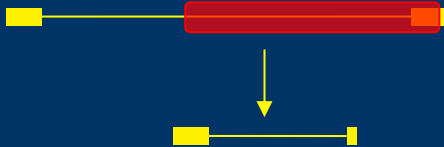
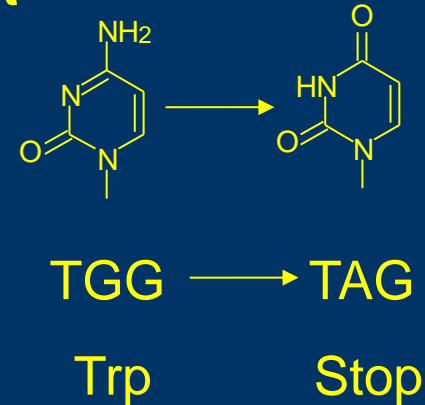
Nonsense mutations/  
INDELS 3.8%

Deletion in  $\psi$ /  
MSD site 6.5%

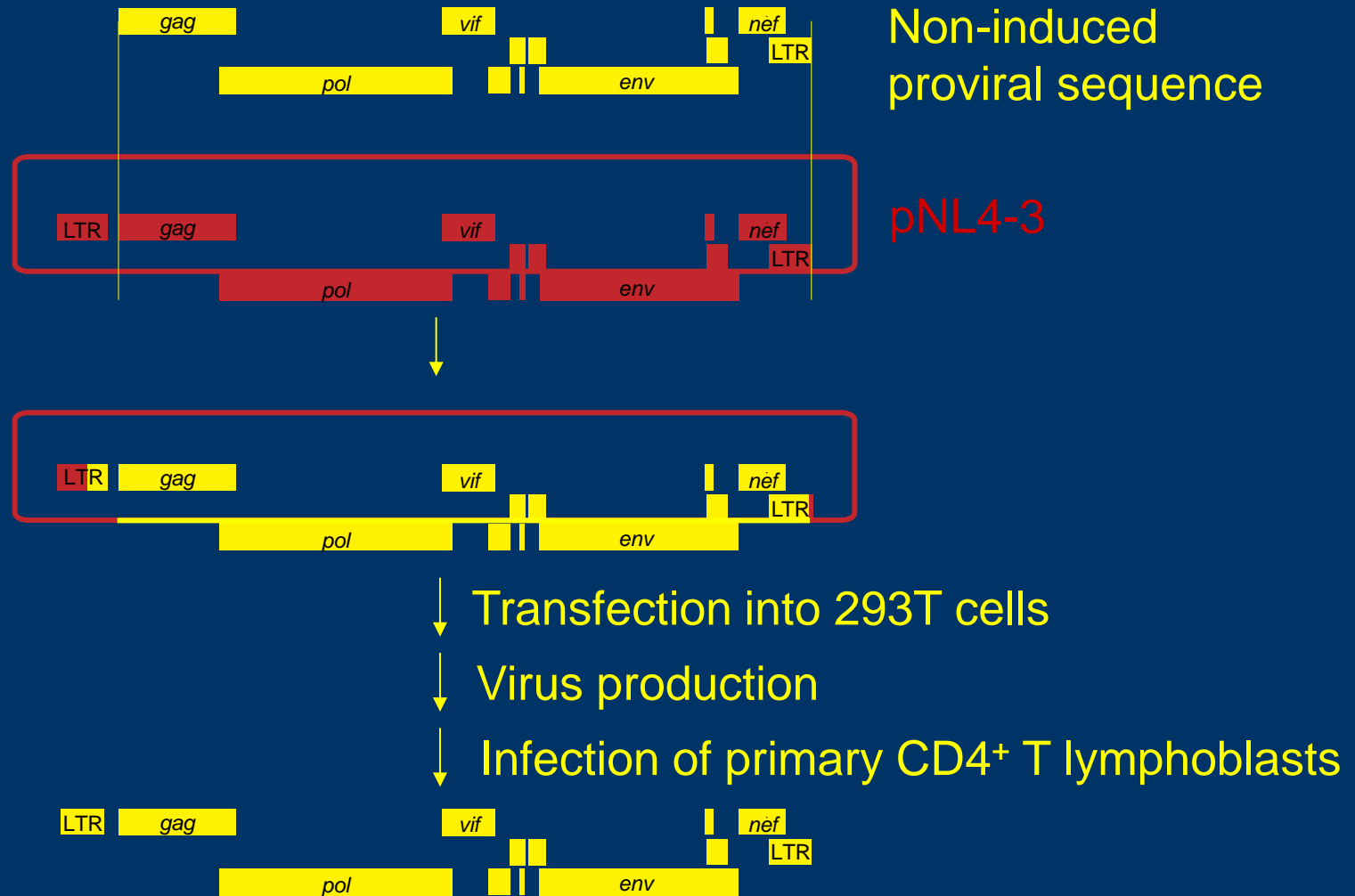
11.7% Intact  
genome

Large internal  
deletion  
45.0%

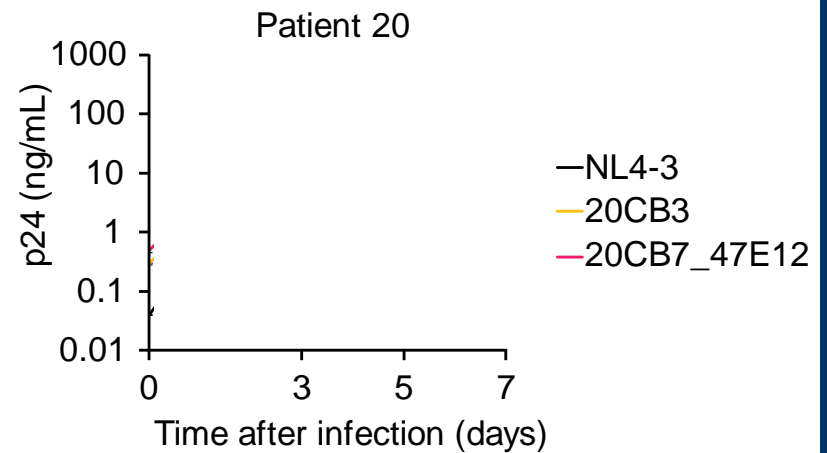
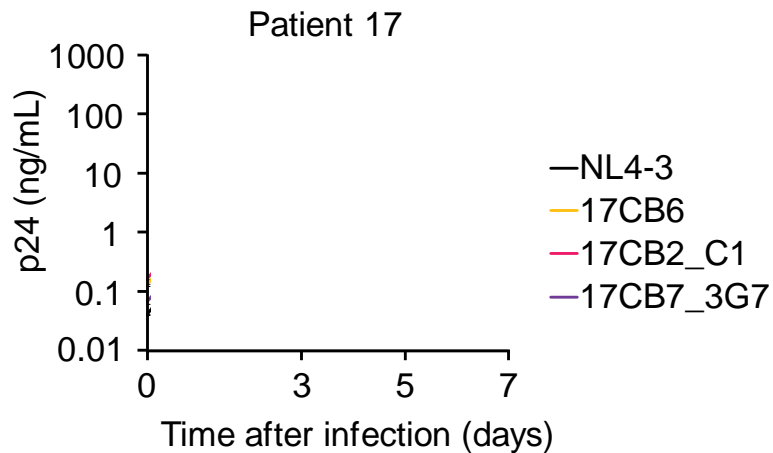
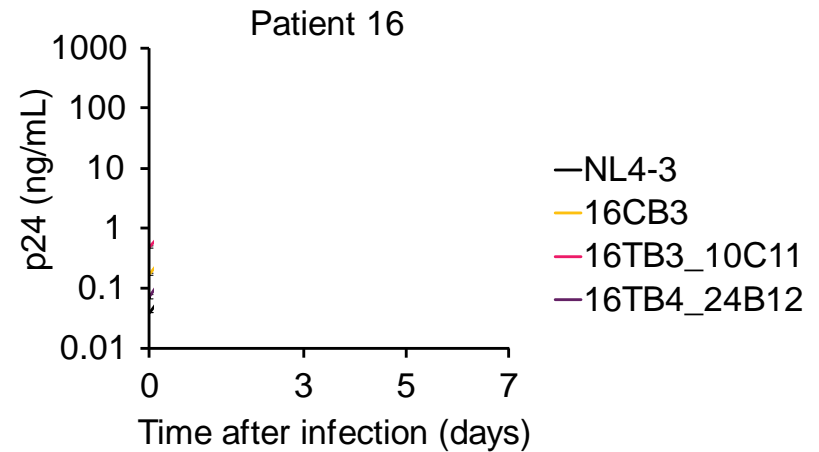
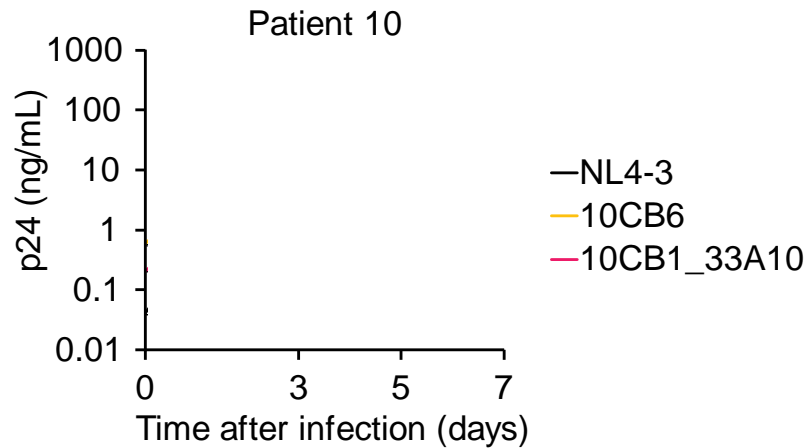
Hypermuted  
32.4%



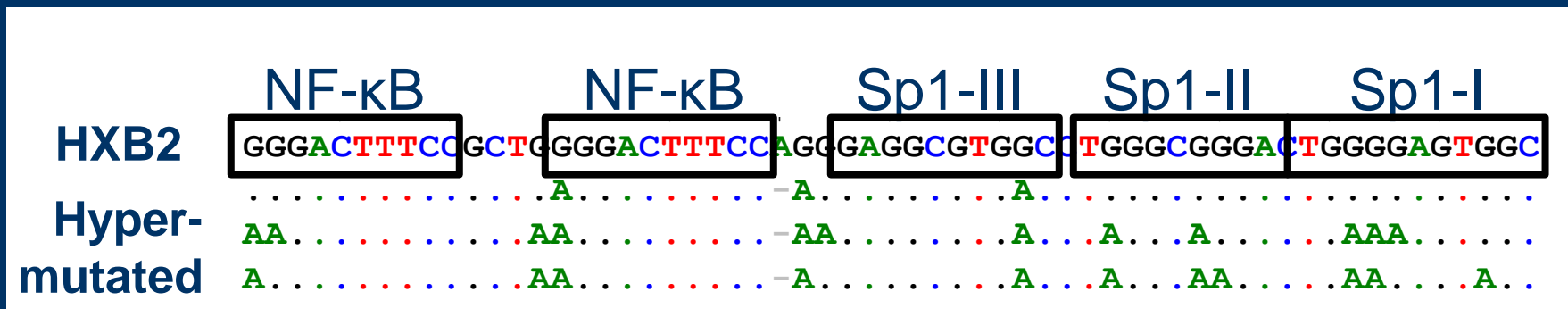
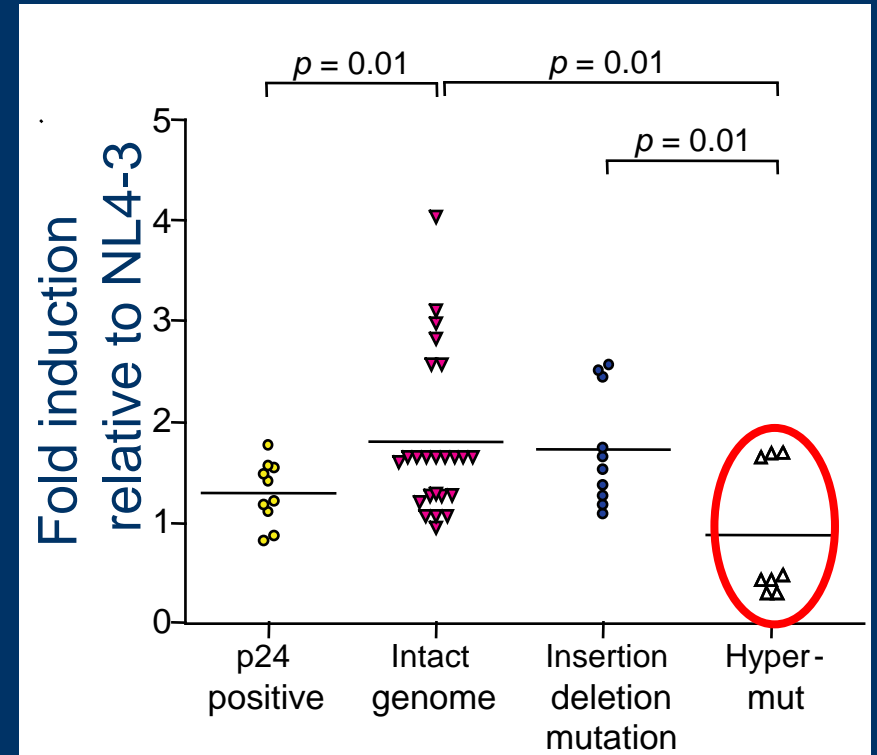
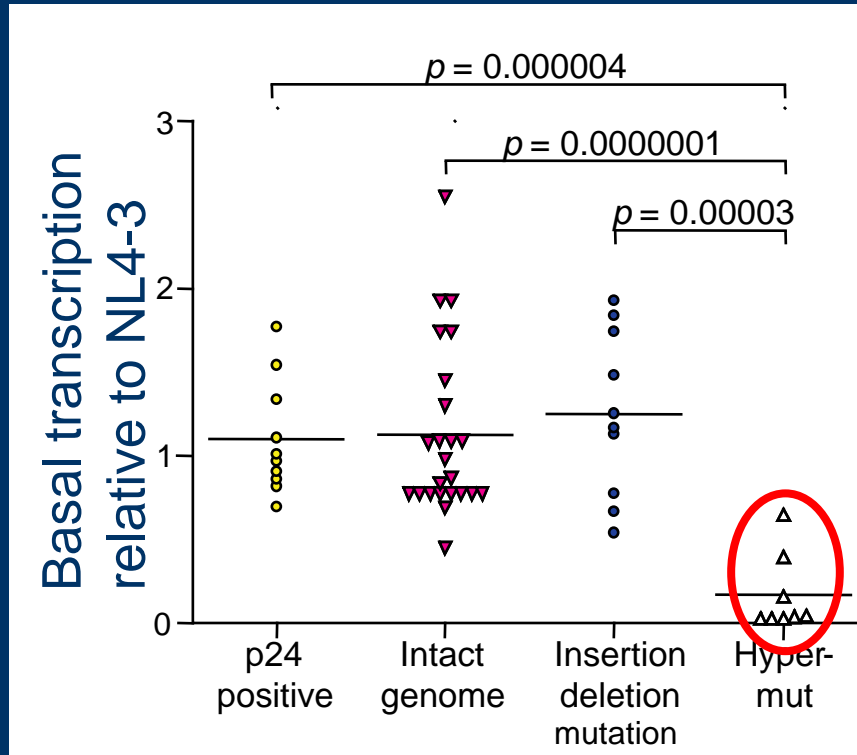
# Replication-competence of non-induced proviruses



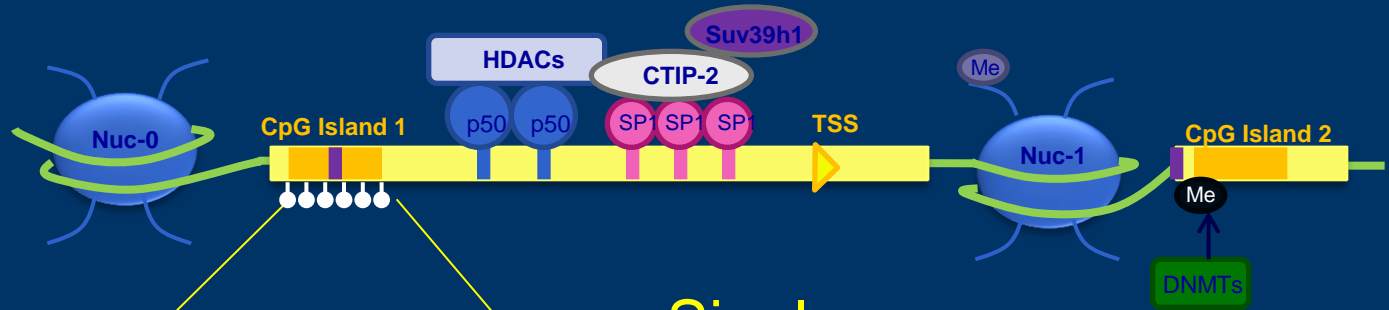
# Replication of non-induced proviruses clones



# Non-induced proviruses have functional LTRs except for hypermutated clones



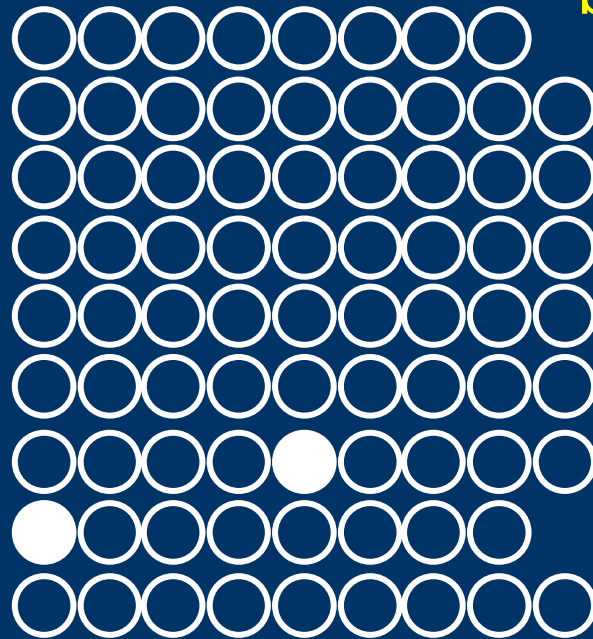
# Clonal analysis of DNA methylation



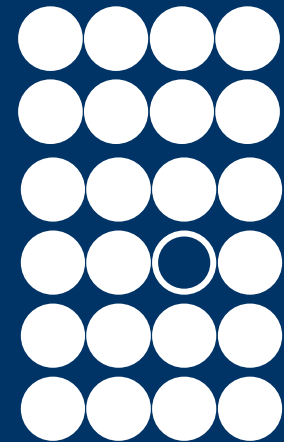
Single genome  
bisulfite sequencing

Patient 20

Cells from  
p24 negative  
co-culture  
well



*env*



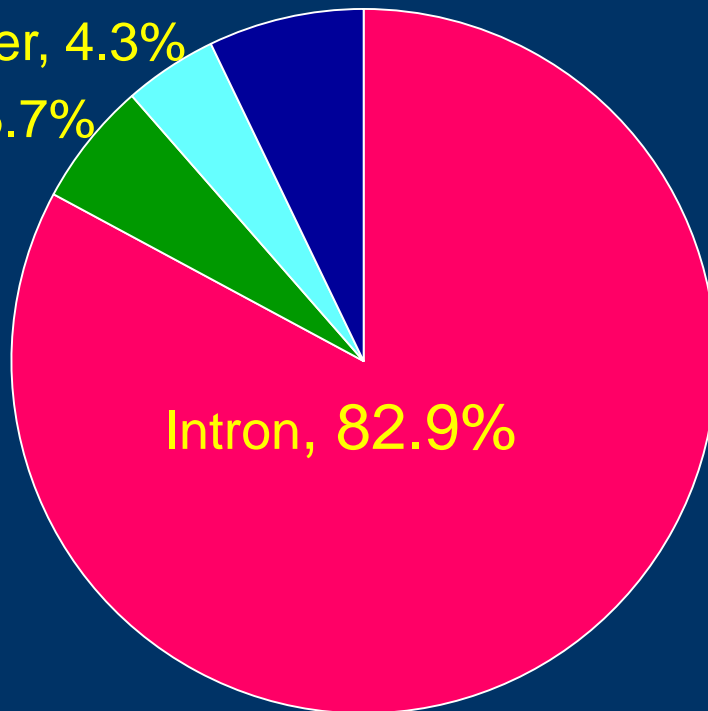
# Non-induced proviruses integrate into active transcription units

- Location

Intergenic space, 7.1%

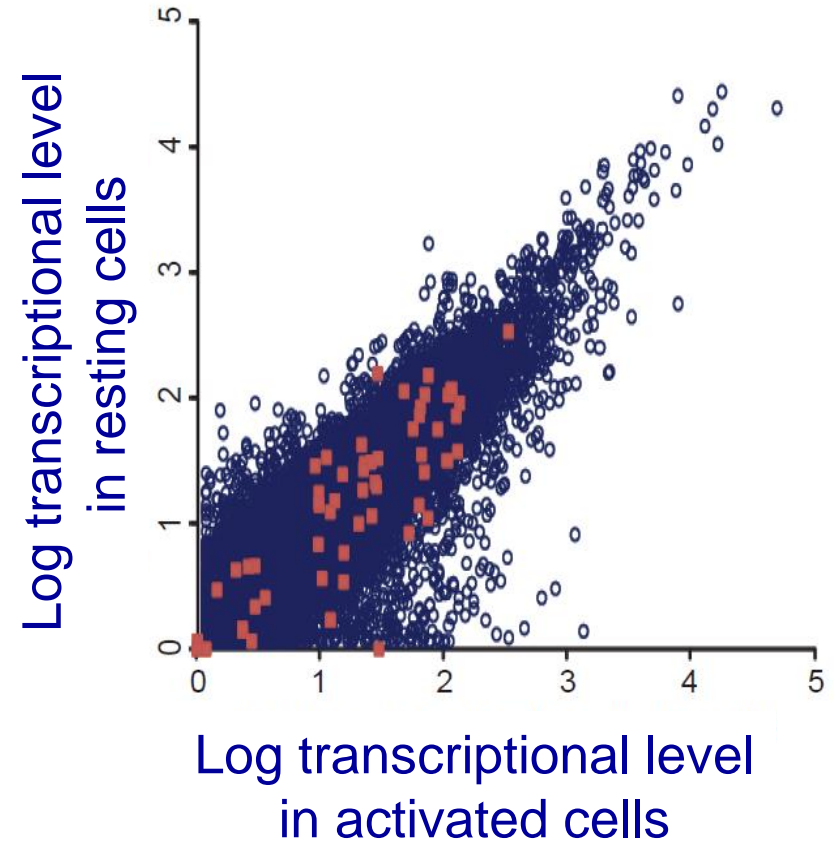
Other, 4.3%

Exon, 5.7%

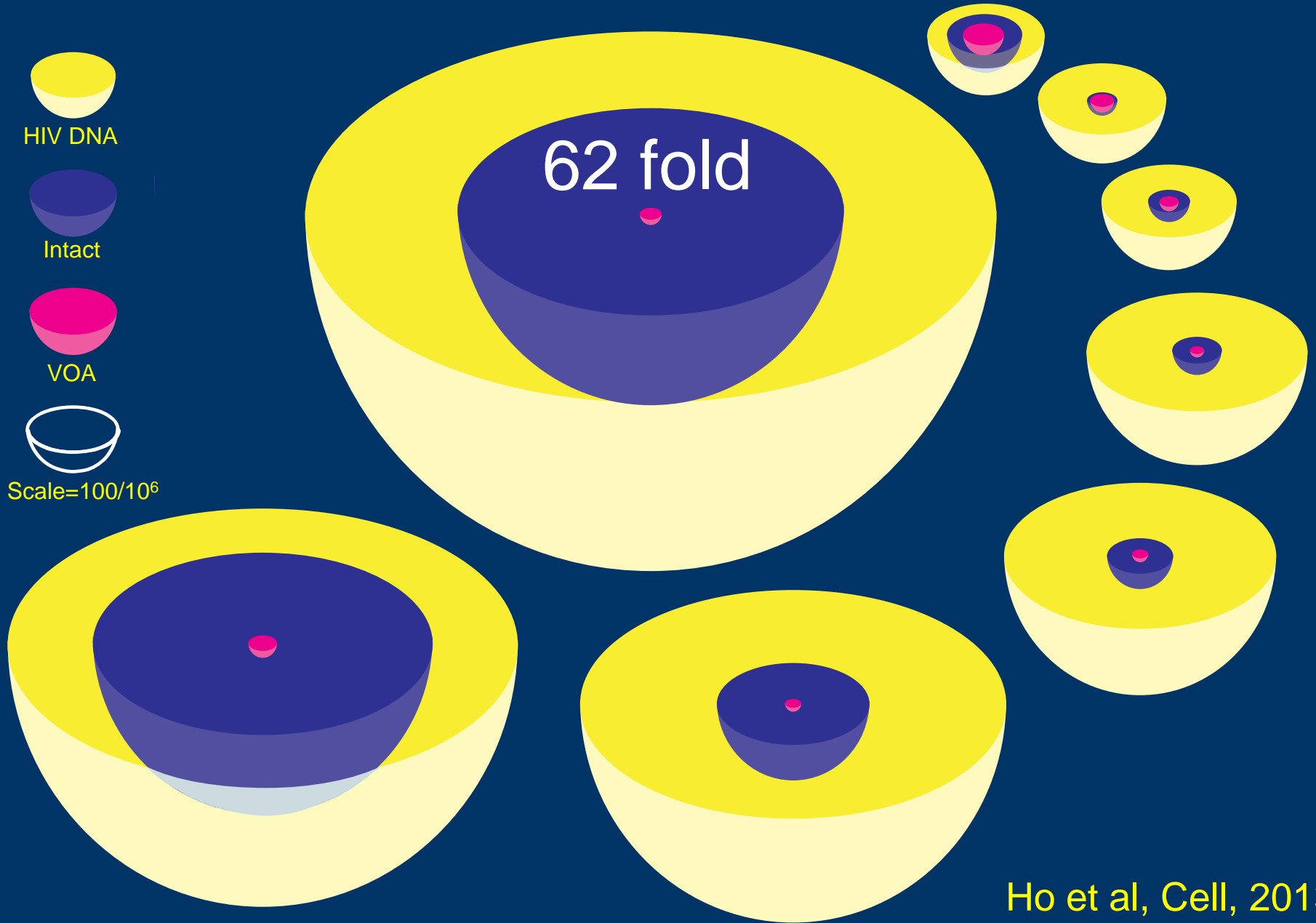


Transcription units: 92.9% (65/70)

- Activity of genes



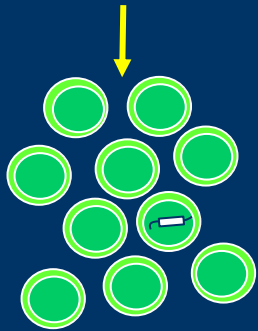
# Intact vs induced proviruses





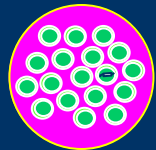
# Can intact non-induced proviruses be induced?

180-200 ml blood

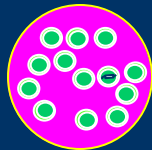


Purified resting CD4<sup>+</sup> T cells

$5 \times 10^6$



$10^6$



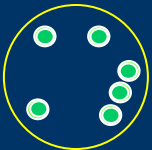
$2 \times 10^5$



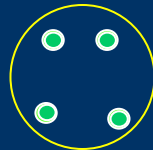
$4 \times 10^4$



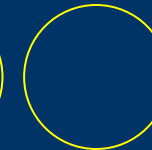
$8 \times 10^3$



$1.6 \times 10^2$

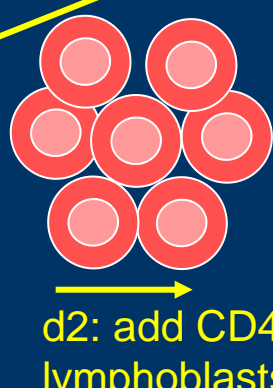
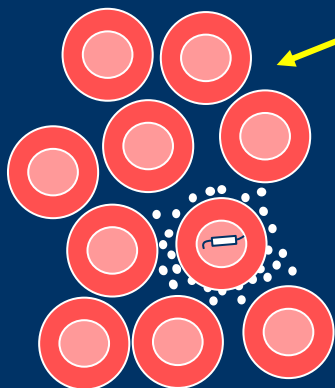


Negative control

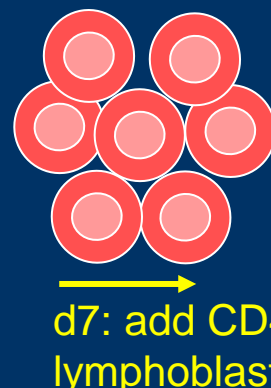
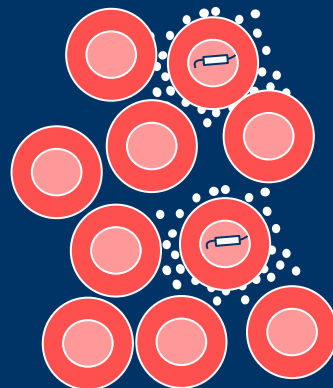


PHA + irradiated allogeneic PBMC

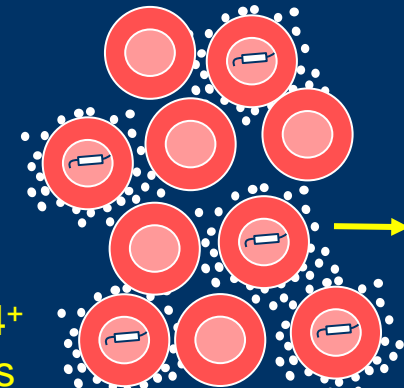
Recover cells from negative wells



d2: add CD4<sup>+</sup> lymphoblasts from HIV- donors

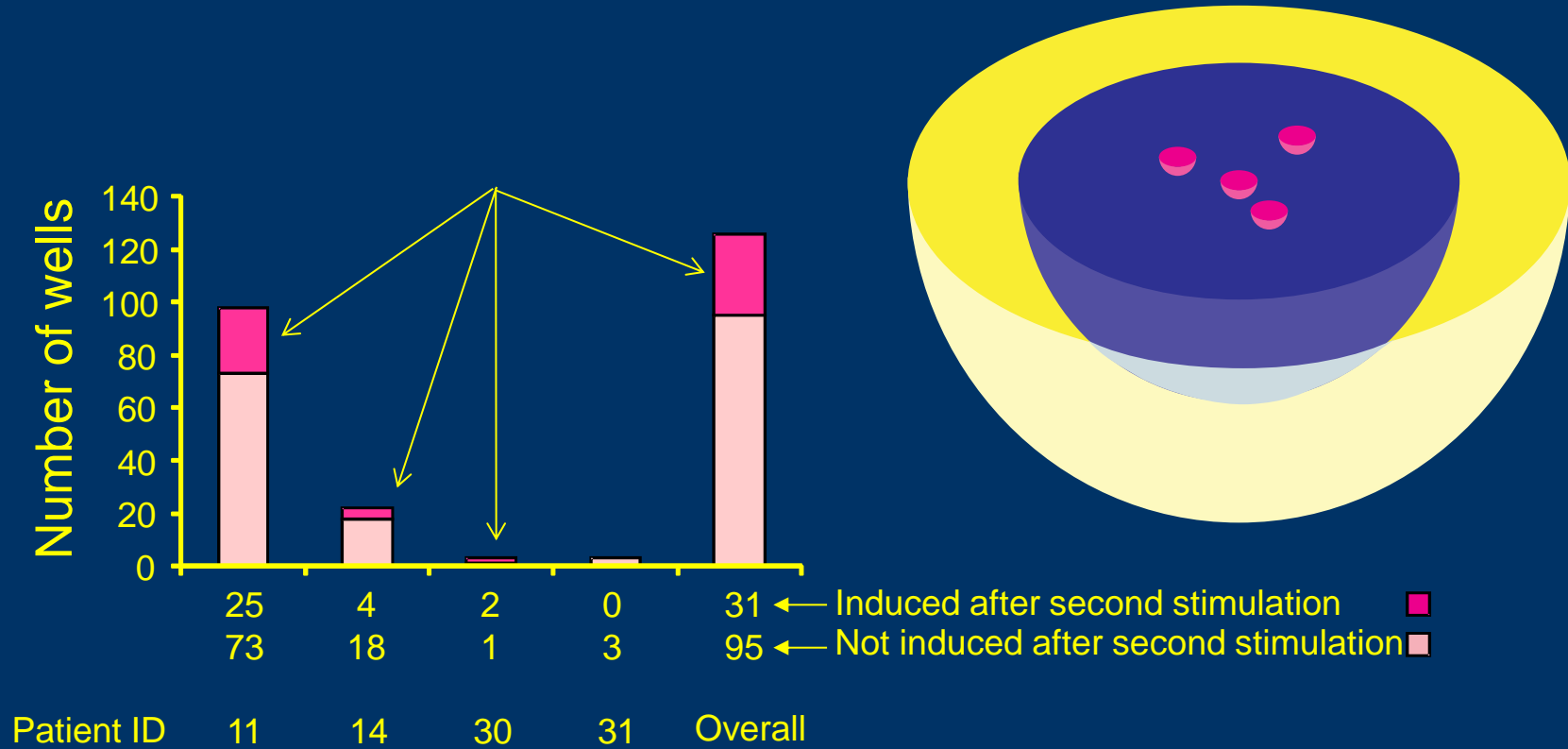


d7: add CD4<sup>+</sup> lymphoblasts from HIV- donors



p24 Ag

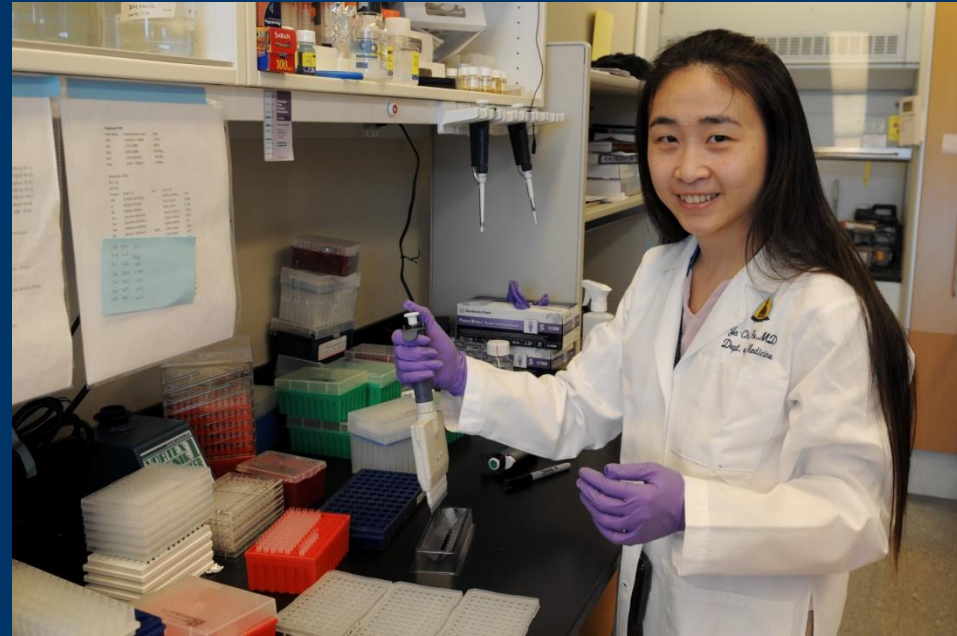
# Can intact non-induced proviruses be induced?



# Thanks

## Collaborators

Robert Siliciano    Matt Strain  
Steve Deeks        Sarah Palmer  
Dave Margolis     Una O'Doherty  
Doug Richman      Joe Wong  
Jon Karn            Steve Yuki  
Martin Nowak



## Funding

Foundation for AIDS Research  
(amFAR): ARCHE  
NIH: Martin Delaney Collaboratories  
CARE and DARE  
Johns Hopkins Center for AIDS  
Research  
Howard Hughes Medical Institute