



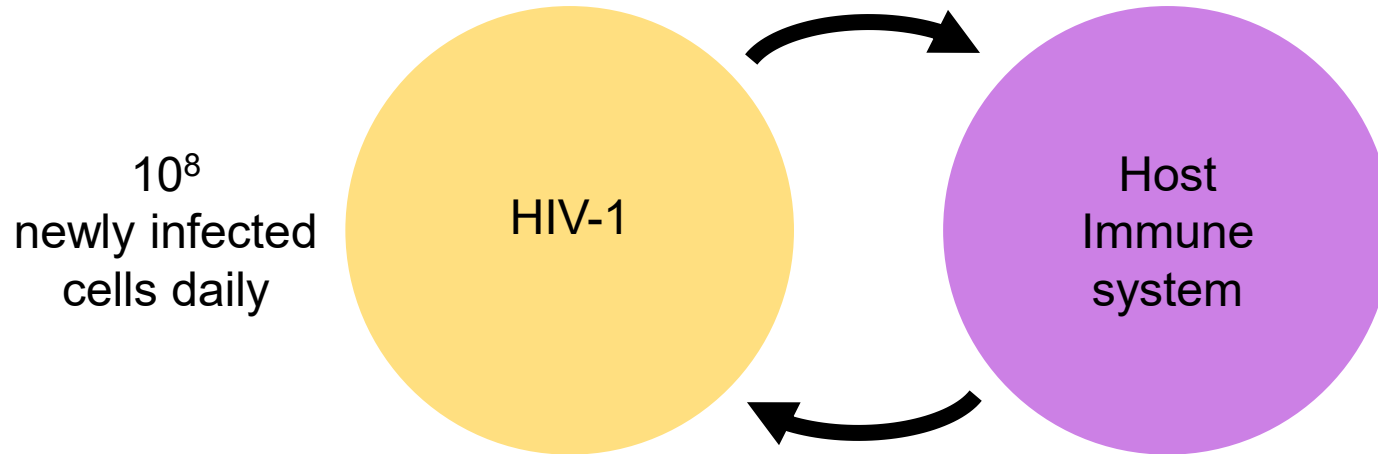
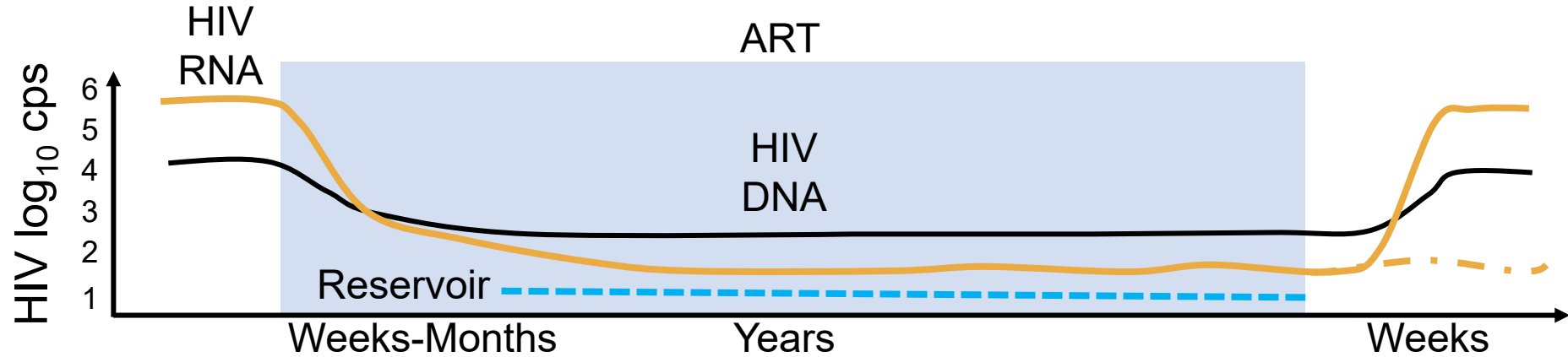
15 Settembre 2022

IL RESERVOIR DI HIV: CREAZIONE, SELEZIONE E MANTENIMENTO

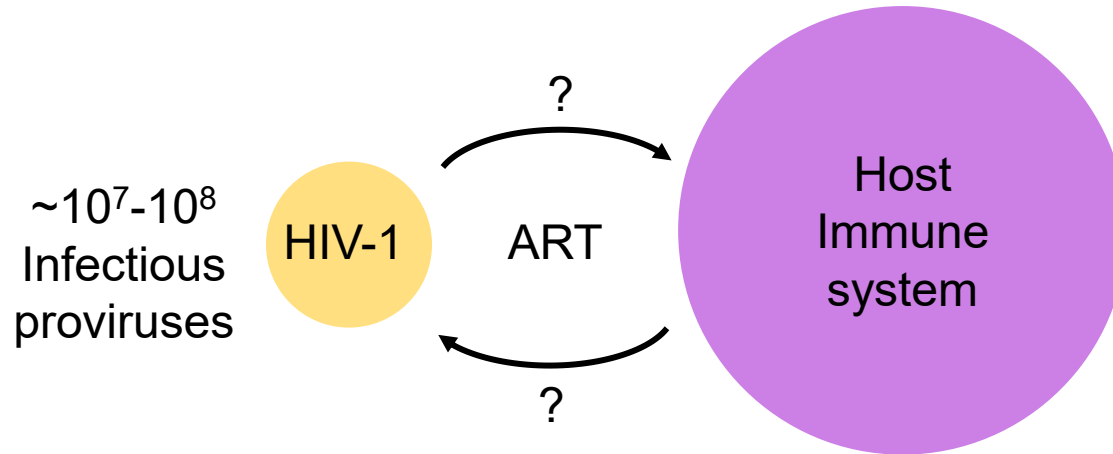
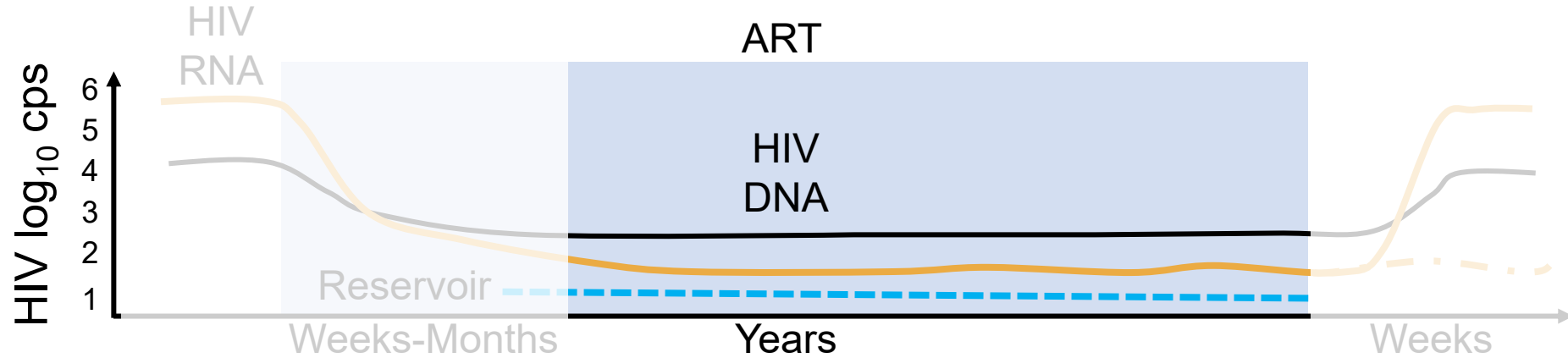
Francesco R Simonetti MD PhD

Johns Hopkins University
Division of Infectious Diseases

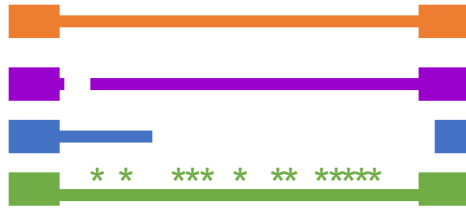
Selection pressures take place before, during, and post ART



Selection pressures take place before, during, and post ART



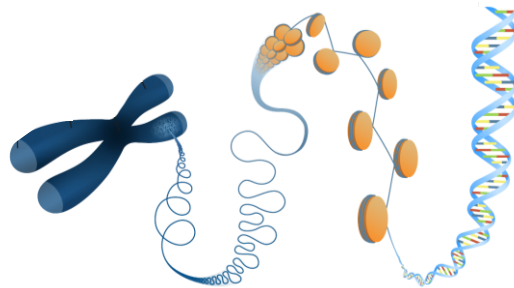
Multi-layered factors shaping HIV-1 persistence



Intact/Defective

Immune escape

Tropism

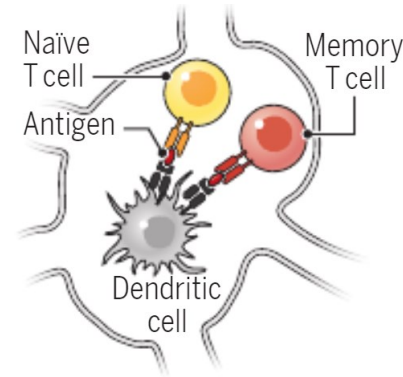


Gene

Epigenetic context

Chromosome

Nuclear architecture



T cell subset

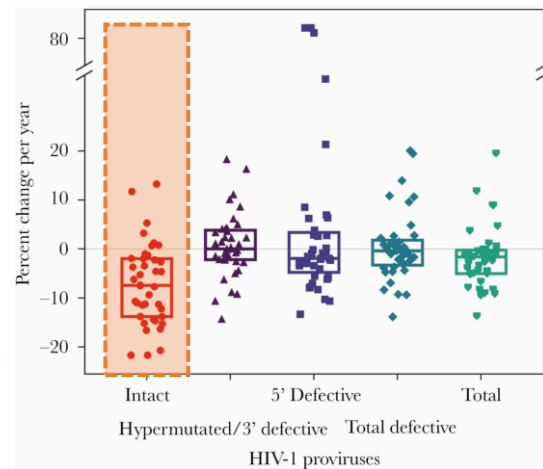
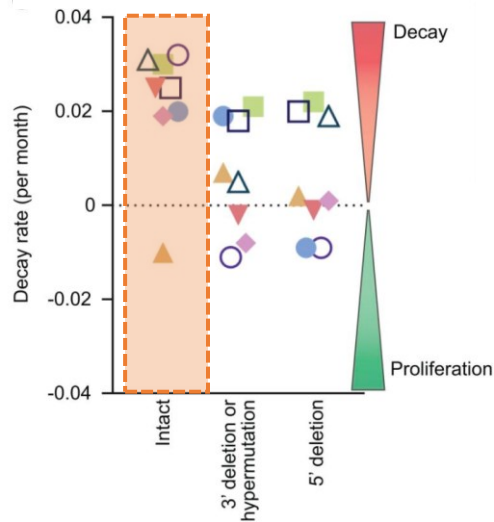
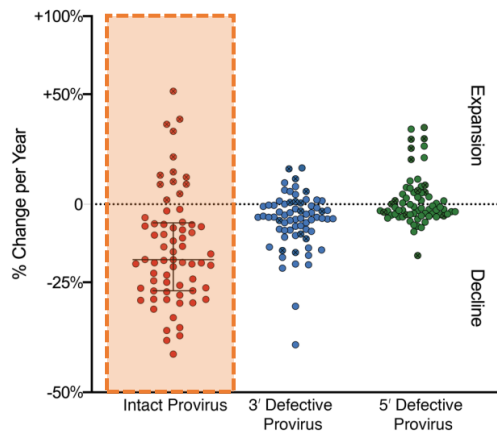
Antigen specificity

Proliferation

Resistance

Cell program

Intact proviruses (~5%) decay faster than defective ones



Peluso, 2020

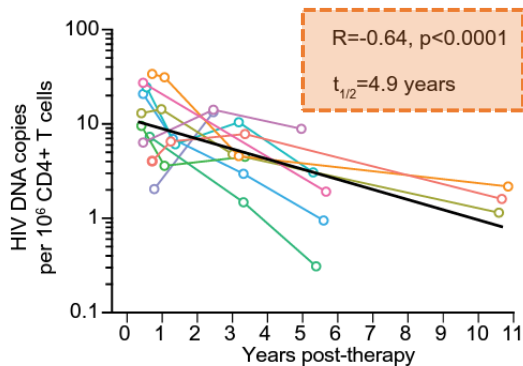
Antar, 2020

Gandhi, 2020

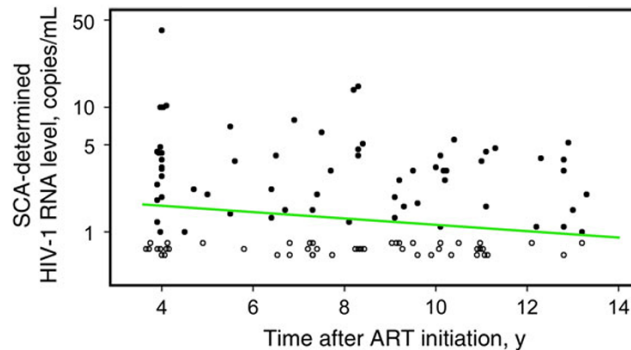
Pinzone, 2019

Cho, 2022

INTACT PROVIRUS



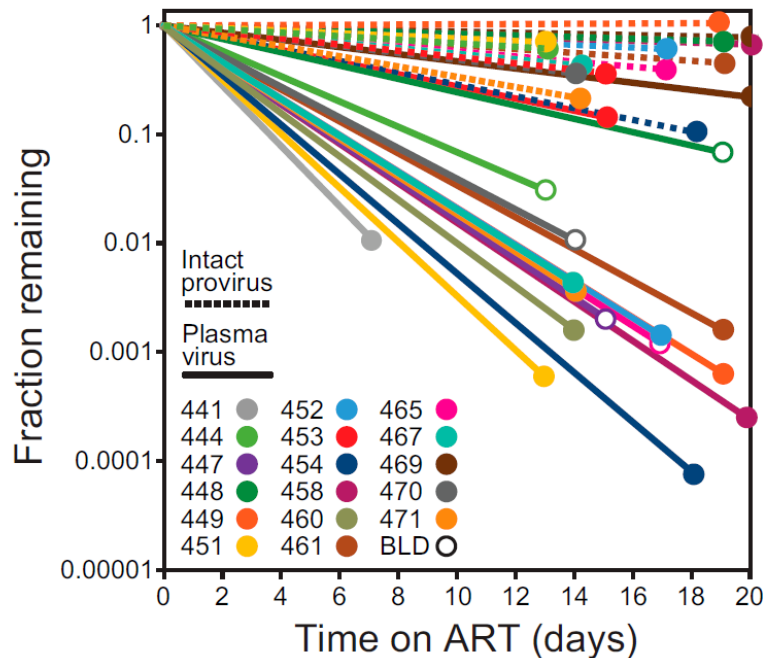
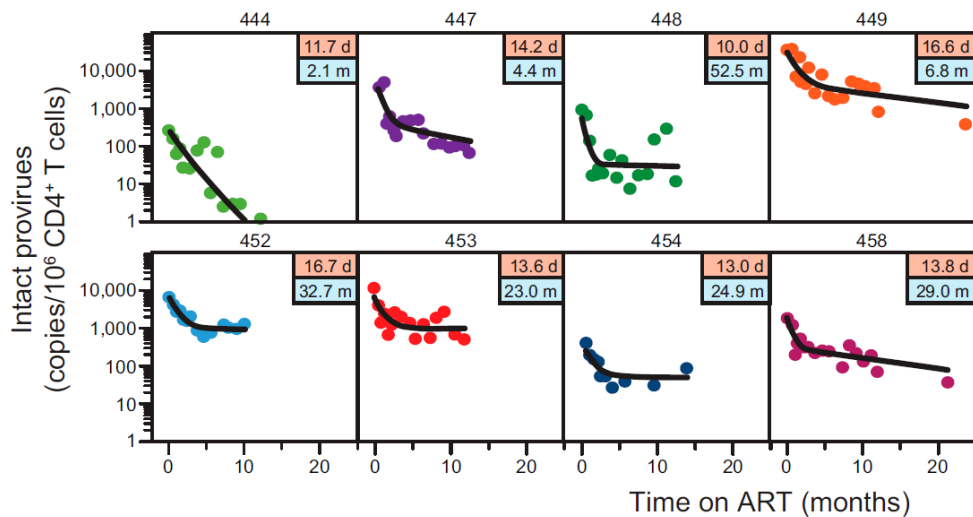
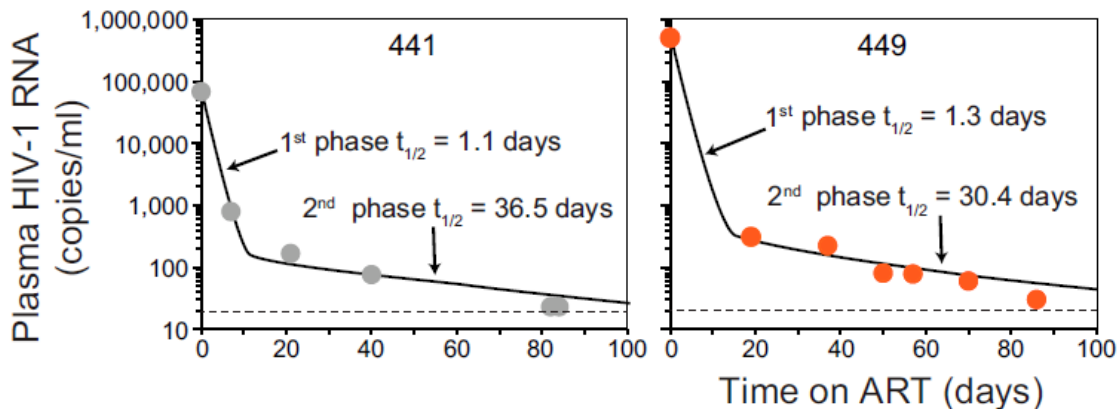
Residual plasma viremia



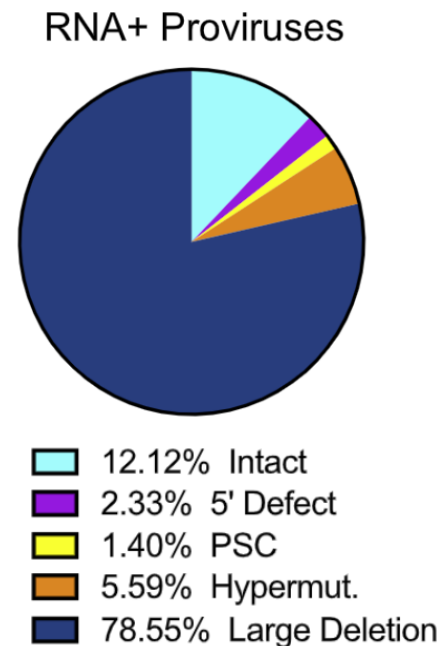
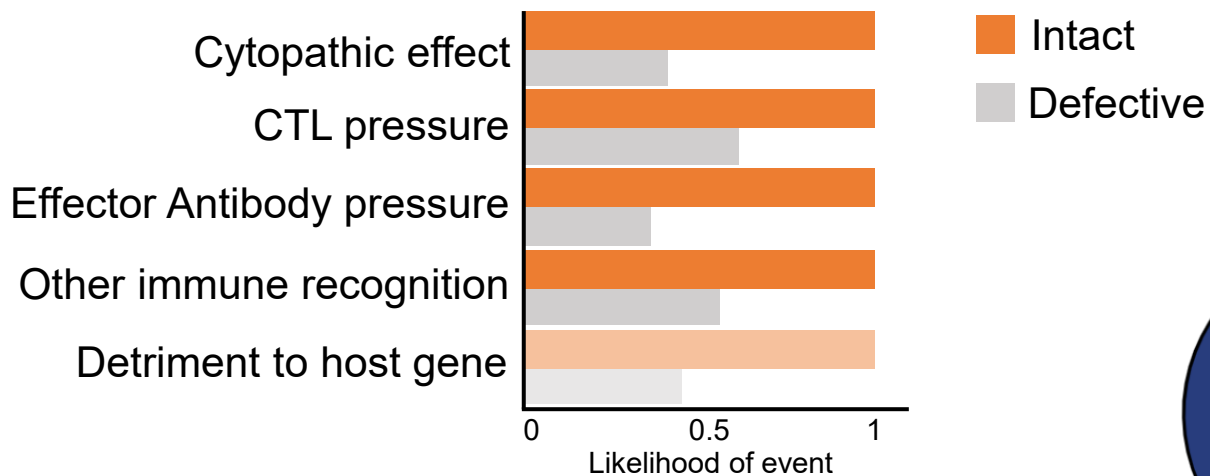
Siliciano, 2003

Riddler, 2016

Intact proviruses in blood have a biphasic but slower decay



Why intact and defective proviruses undergo different selection?



Defective proviruses can produce RNA and proteins

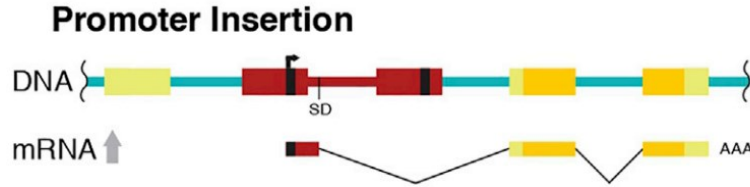
Defective proviruses can be recognized by CTL

RNA expression is often not enough to produce proteins/virions

Little signal for ongoing CTL selection on ART

Genomic context: HIV-1 integration site

HIV-1 affecting surrounding gene expression



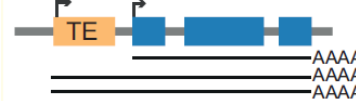
Alteration of splicing



New polyA site



Alternative promoter

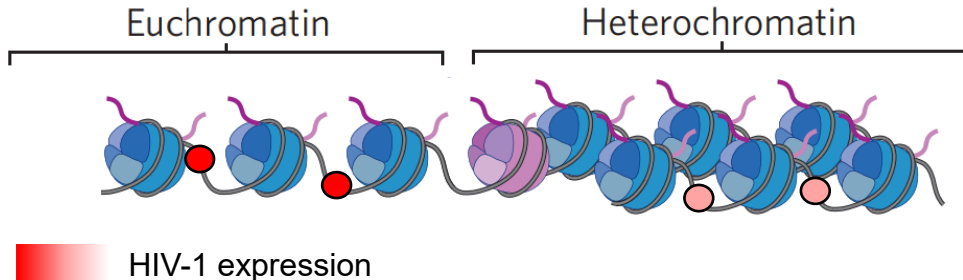


Negative
selection

>>Same orientation of
highly expressed genes

Positive
selection

Surrounding genome affecting HIV-1 expression



Bushman, 2020

Liu, 2020

Yoon, 2020

Mellors, 2021

Lewinski, 2005

Burdick, 2022

Jiang, 2021

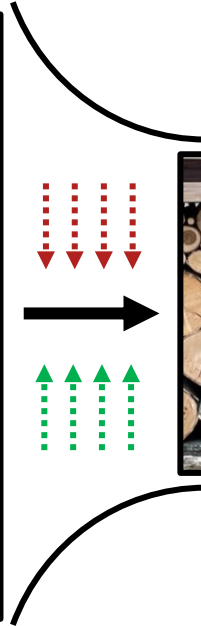
Einkauf, 2022

Role of HIV-1 integration: what is the gold standard?

Acute infection *in vivo* or *in vitro*



Initial distribution



Long-term ART



Result of selection

Challenges in detecting HIV-infected clones

Sampled population



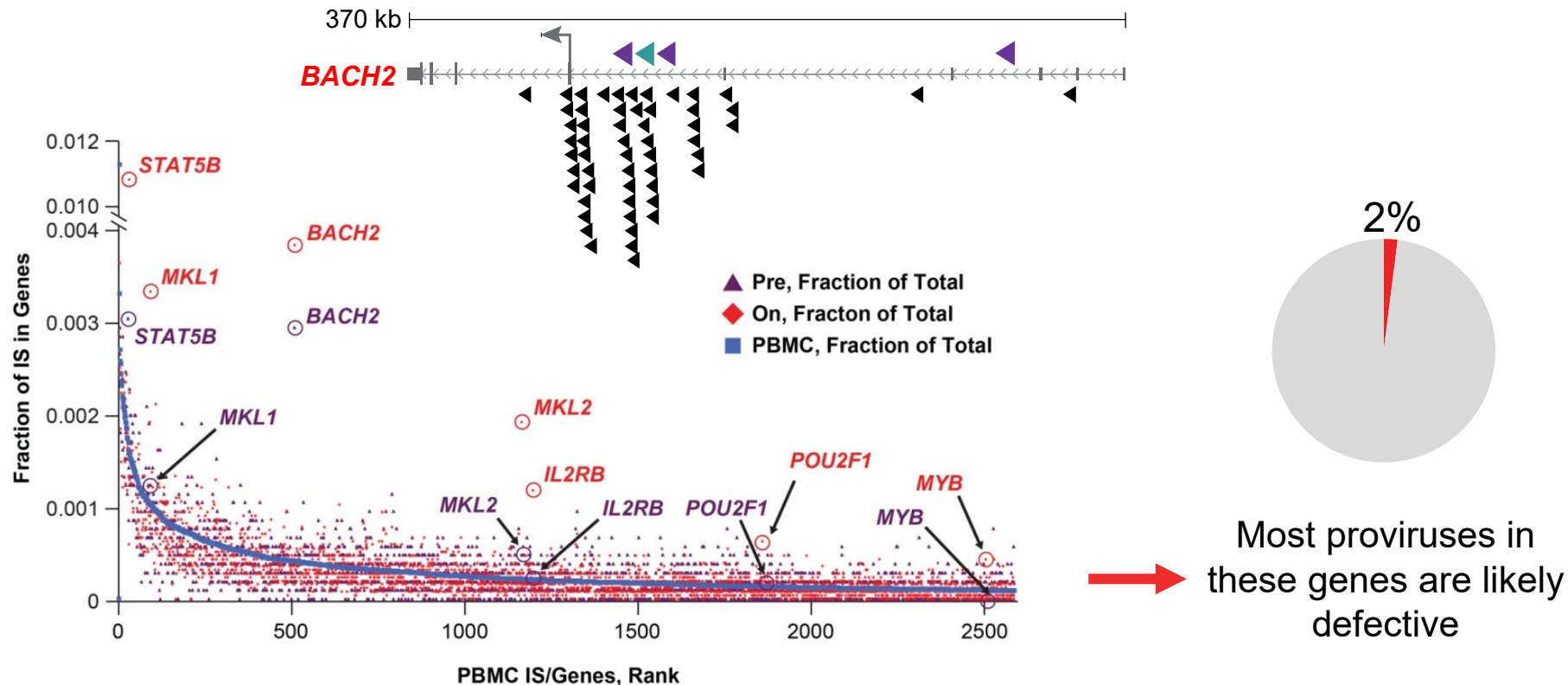
Actual population



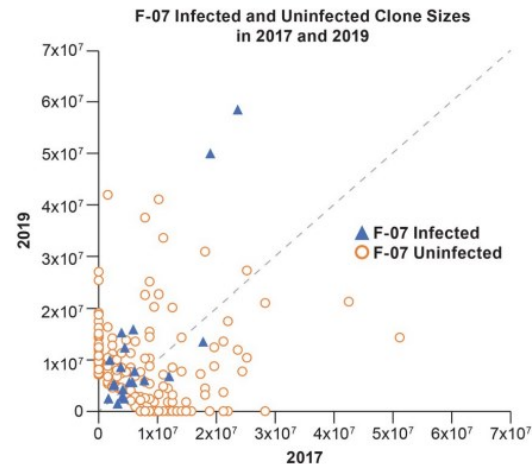
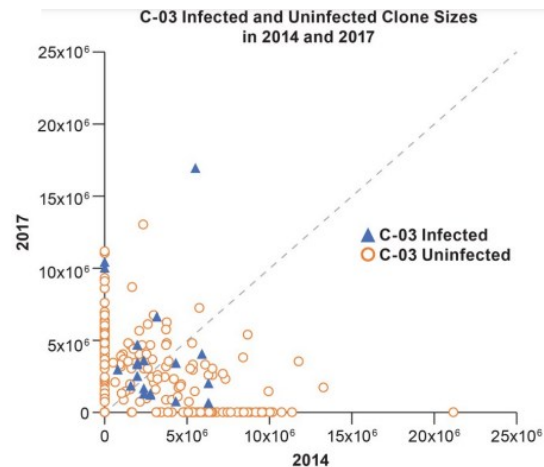
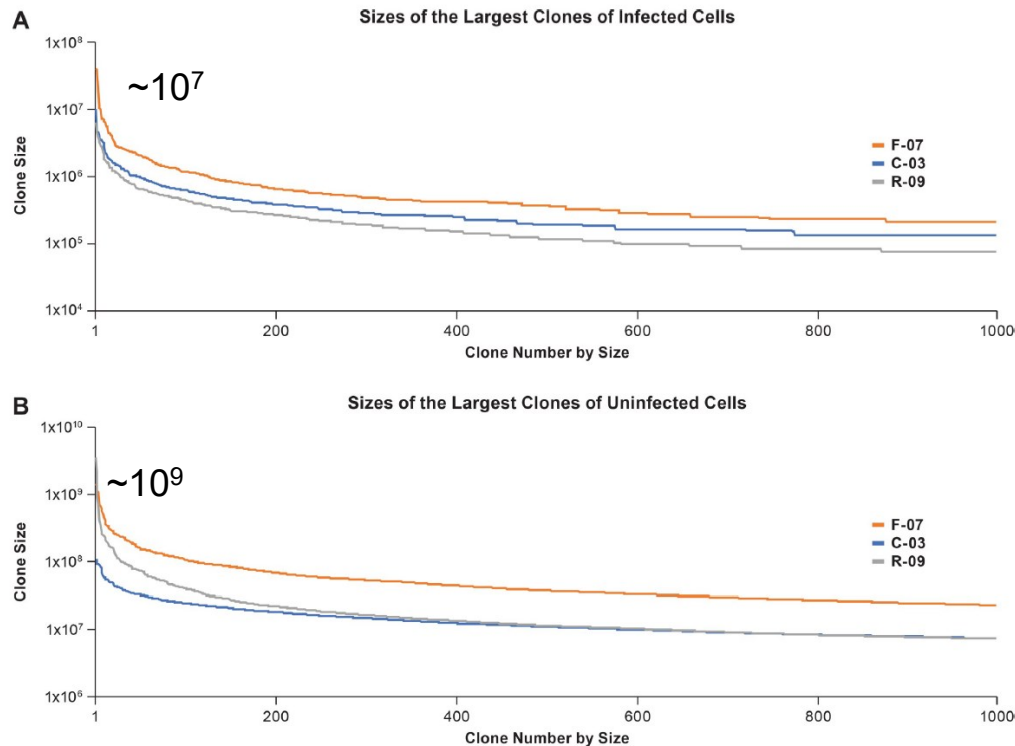
If 1000 integration sites are recovered from one individual only clones $>10^5$ can be detected as clonally expanded.

From Coffin and Hughes

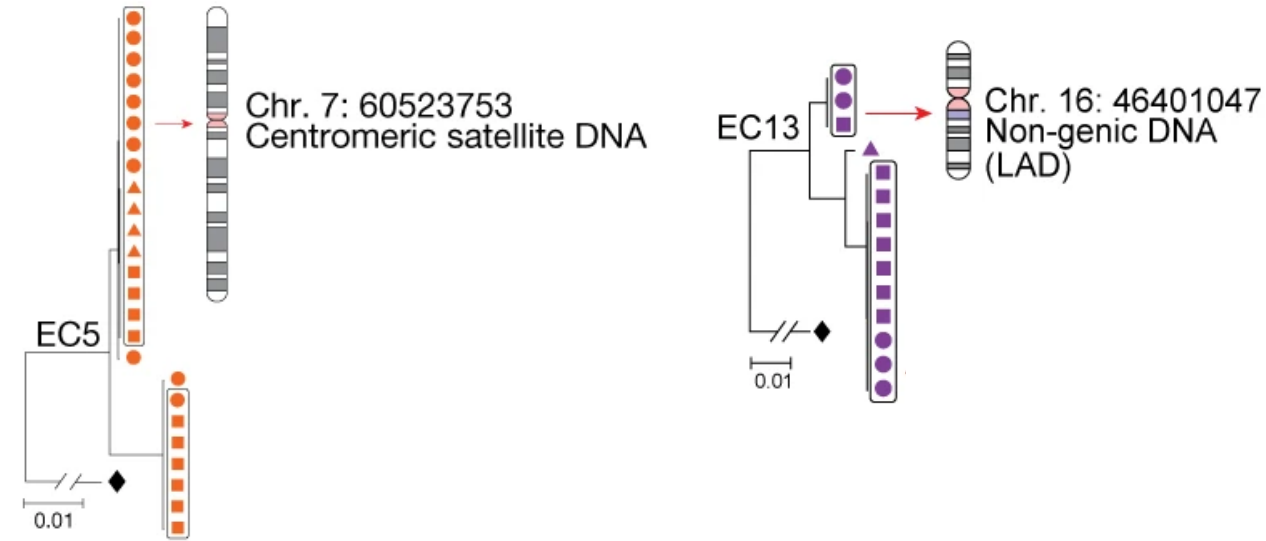
Host gene misexpression leading to positive selection is rare



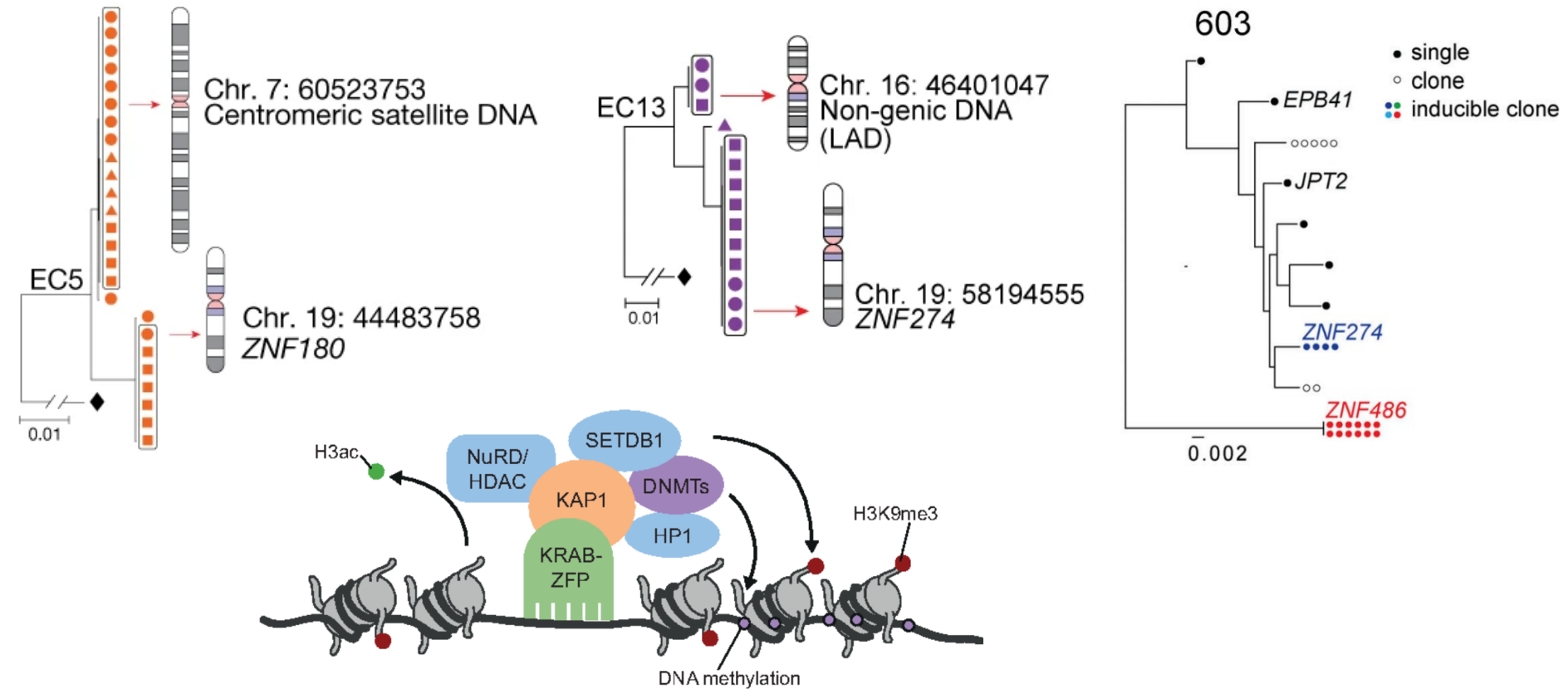
Clones of infected T cells are more stable, compared to all T cell clones



Selection of intact proviruses in loci associated with deeper latency

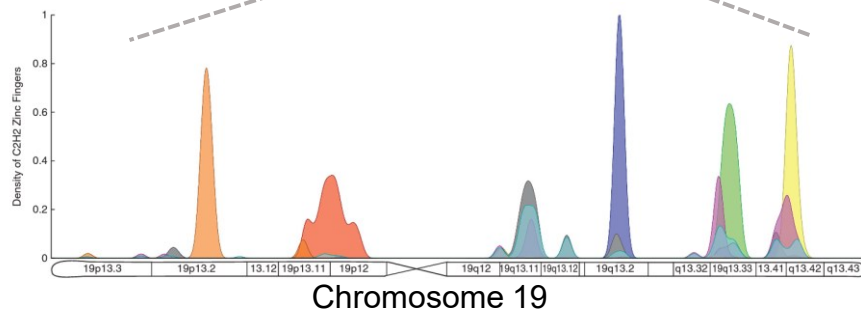
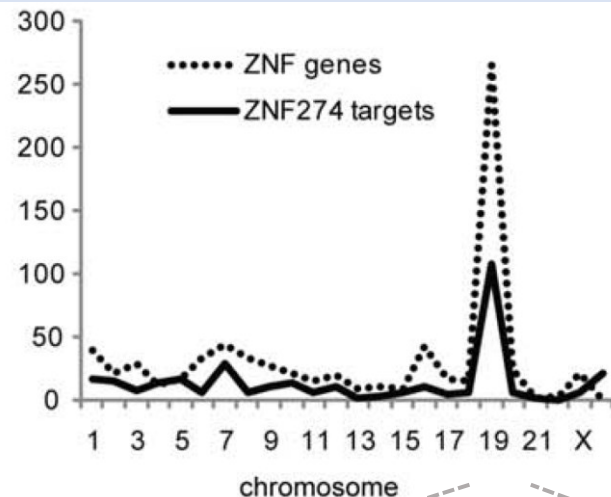


Selection of intact proviruses in loci associated with deeper latency



Recurring ZNF genes with integrations of intact proviruses

ZNF gene	Overlap	Chr.	Provirus	Paper
ZNF140		12	intact	Huang, 2021
ZNF274		19	intact	
ZNF486		19	intact	
ZNF721		4	intact	
ZNF460		19	intact	
ZNF557		19	intact	
ZNF141		4	intact	Cole, 2021
ZNF274		19	intact	
ZNF268		12	intact	Halvas, 2020
ZNF721		4	intact	
ZNF721*	ABCA11P	4	intact	Einkauf, 2019
ZNF721	ABCA11P	4	intact	
ZNF140		12	intact	
ZNF84		12	intact	
ZNF274		19	intact	Einkauf, 2022
ZNF140		12	intact	
ZNF180		19	intact	Jiang, 2021
ZNF225		19	intact	
ZNF721	ABCA11P	4	intact	
ZNF407		18	intact	
ZNF274		19	intact	
ZNF350	ZNF350-AS1	19	intact	Veenhuis, 2019
ZNF470		19	not known	



Elite controllers On ART

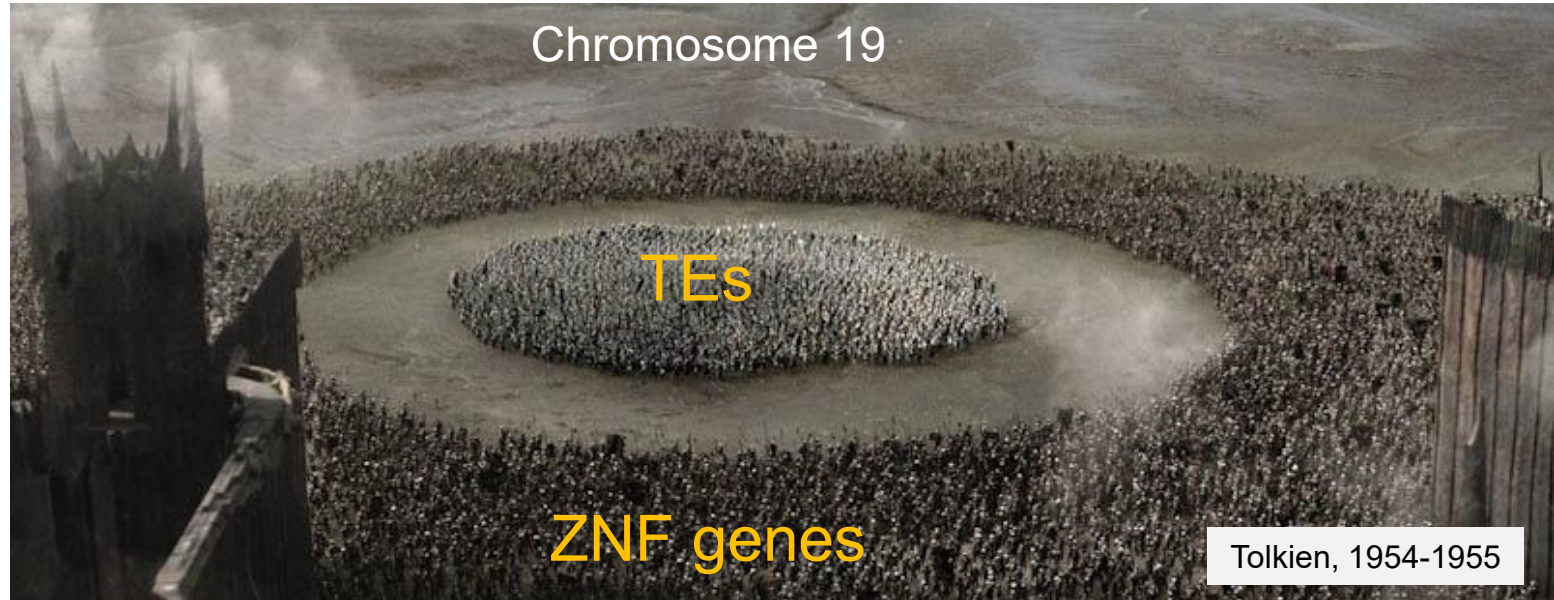
Freitze, 2010

Jakobsson, 2022

Lukic, 2013

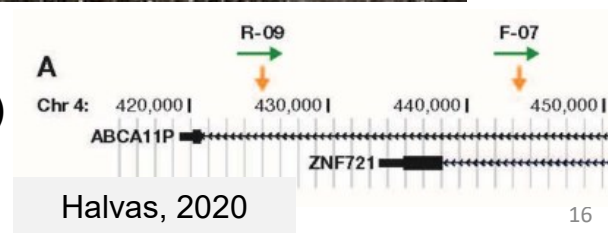
Selection of intact proviruses in a state of deeper latency

Do KRAB-ZNF interact directly with intact proviruses? Or they are simply “trapped”, casualties of an ancient arm race?

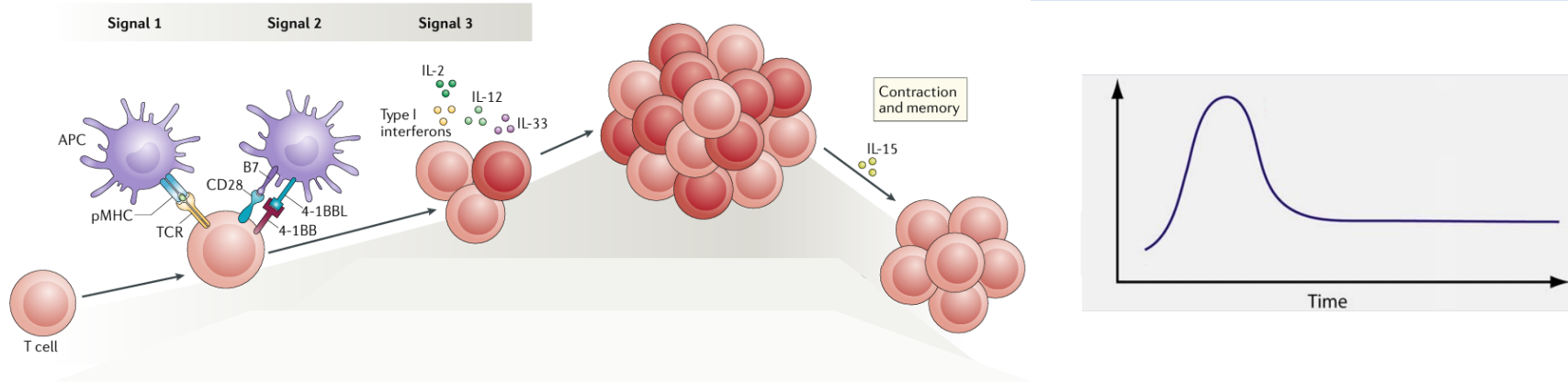


Some intact proviruses in ZNF genes can be induced *ex vivo*

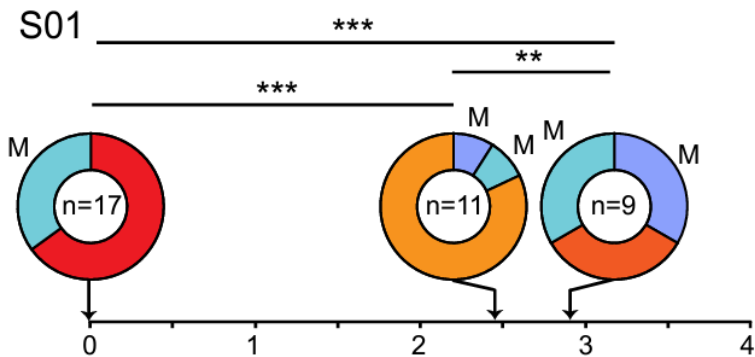
- What about physiological T cell stimulation? (e.g. cognate antigen)
- Can they lead to viral rebound upon treatment interruption?



Reservoir fluctuations resemble T cell response dynamics

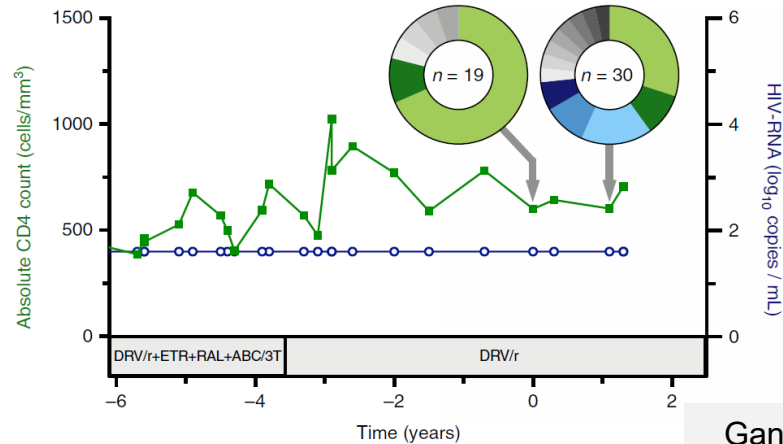


Viral outgrowth



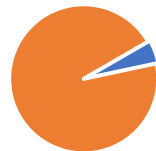
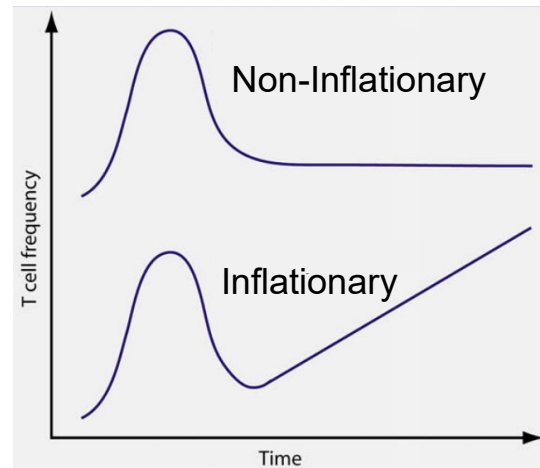
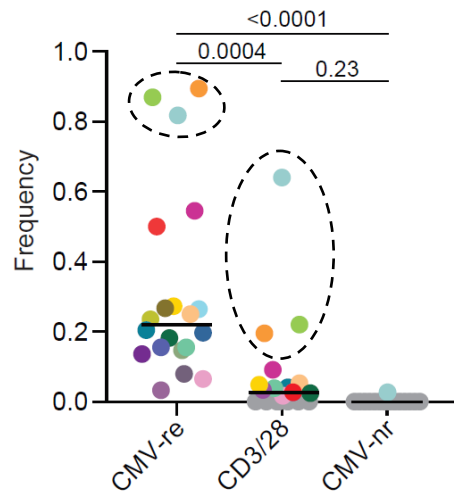
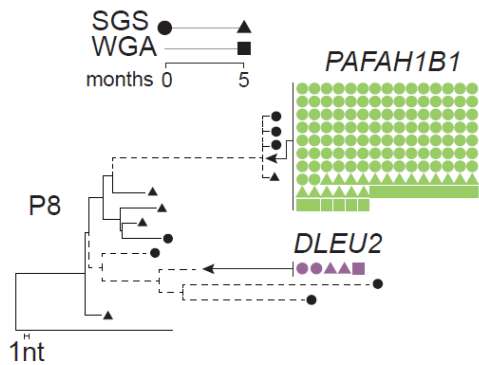
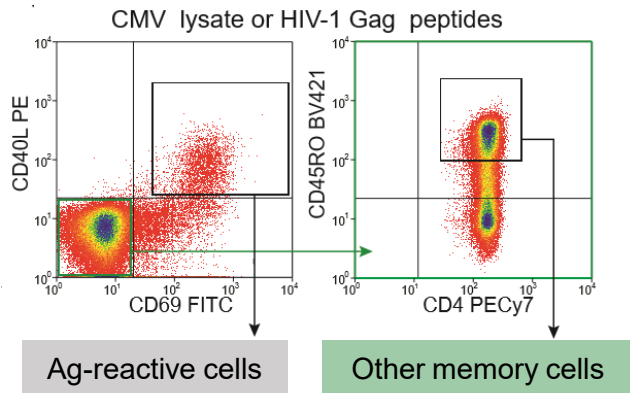
Wang, 2018

TCR-seq of p24 positive cells



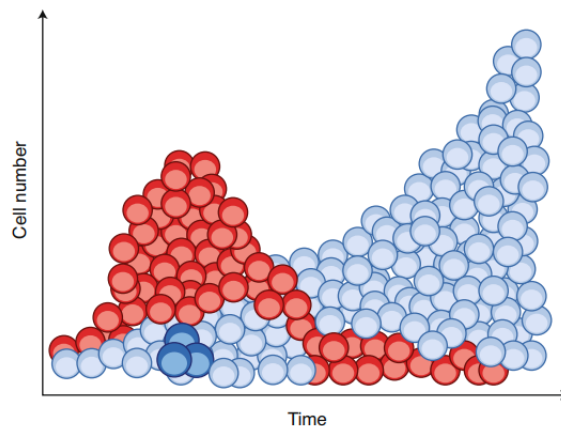
Gantner, 2020

Antigen-driven selection contributes to HIV persistence

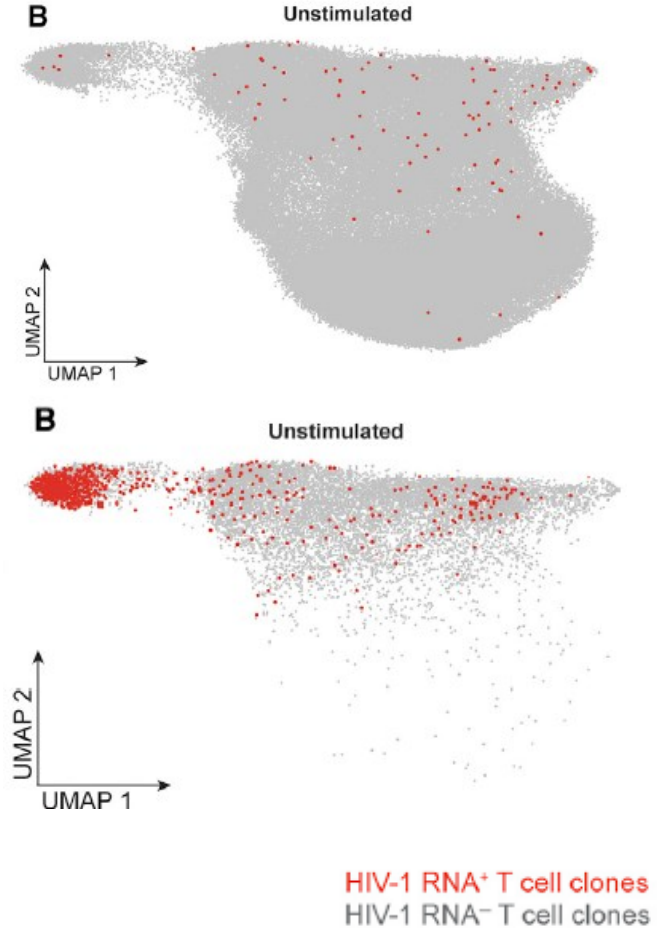
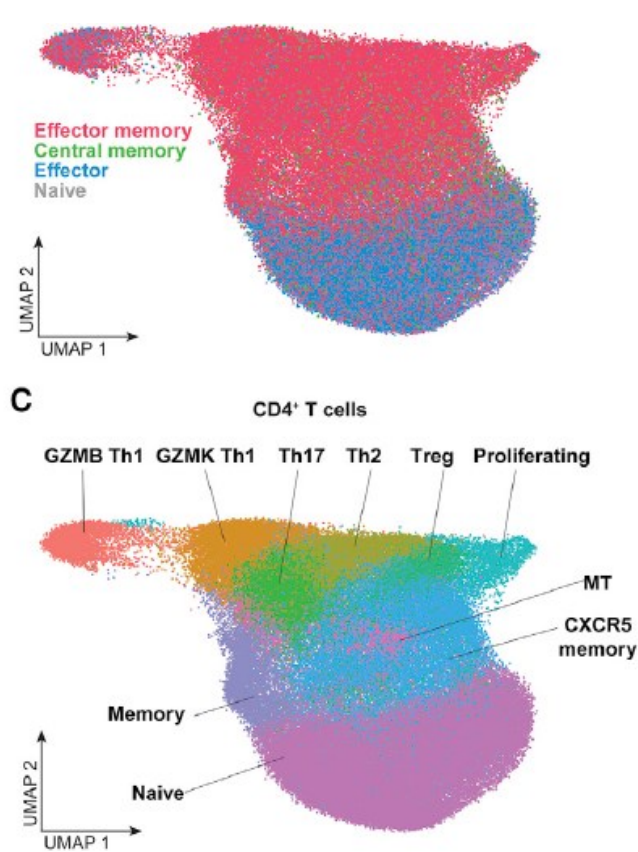
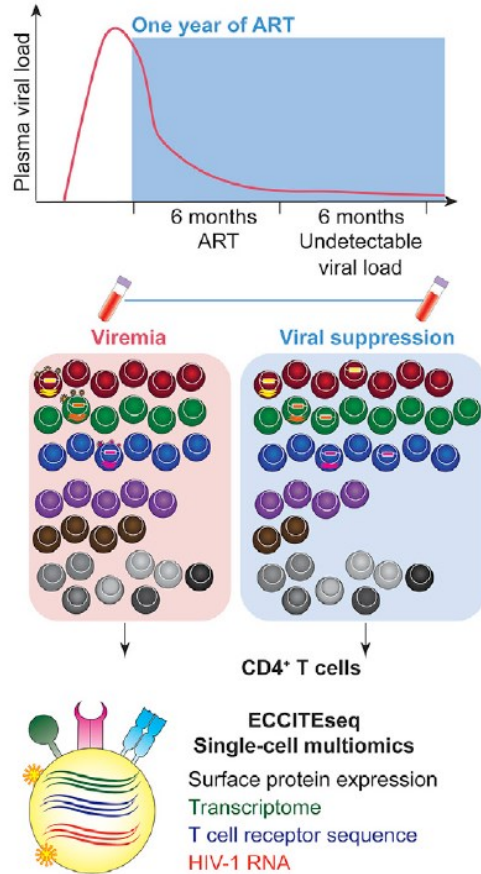


TCM

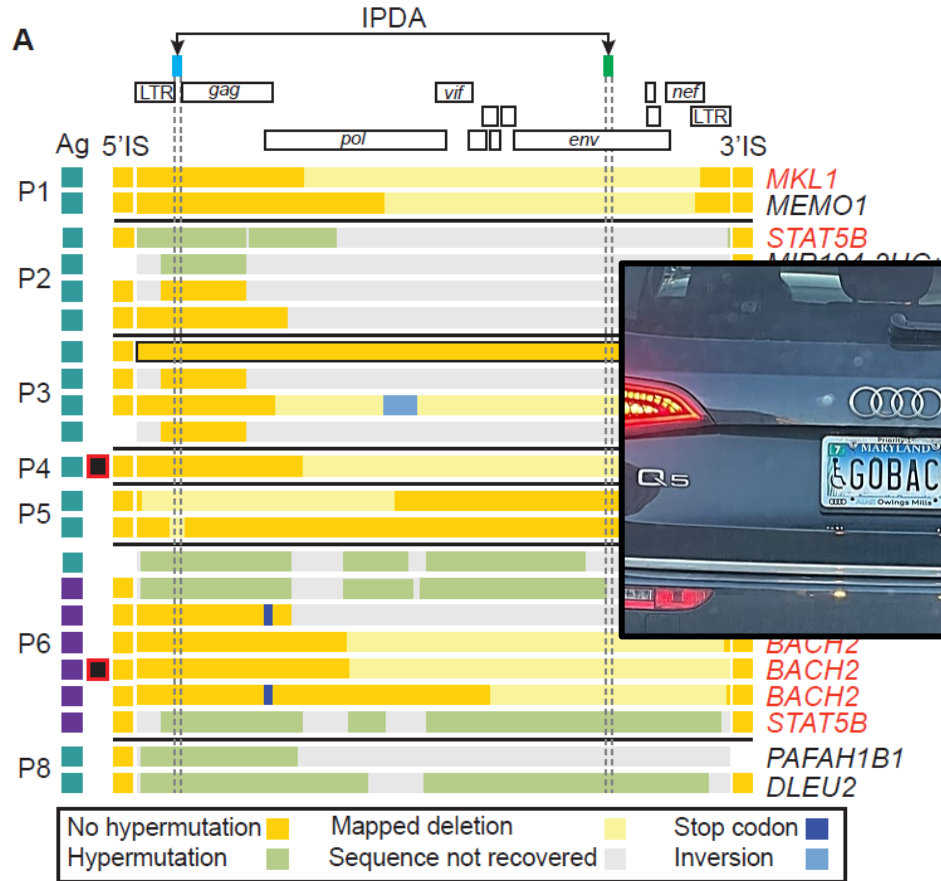
TEM



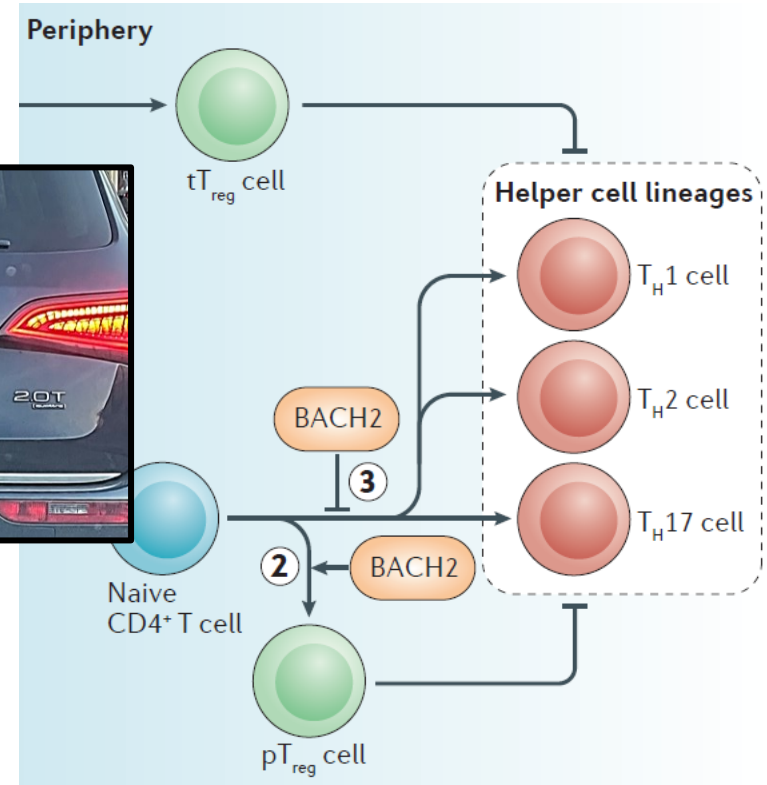
HIV+ expanded clones are enriched in cytotoxic T cells



Possible synergy between HIV integration and immune selection



Simonetti, 2021

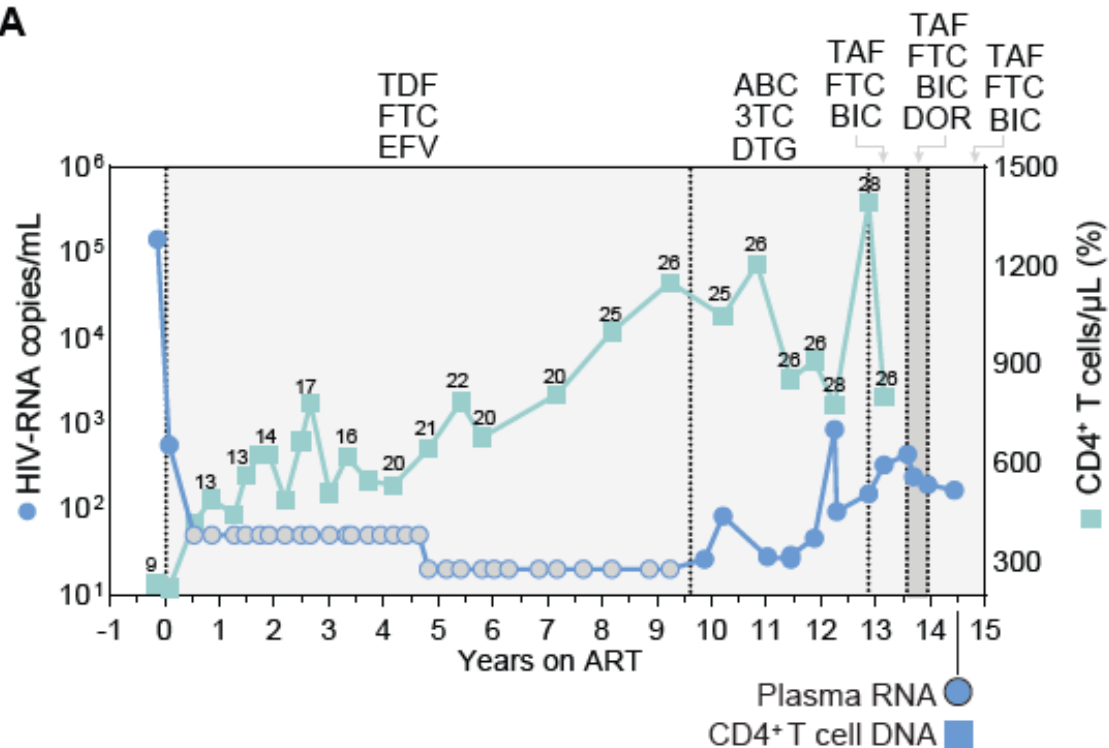


Igarashi, 2017

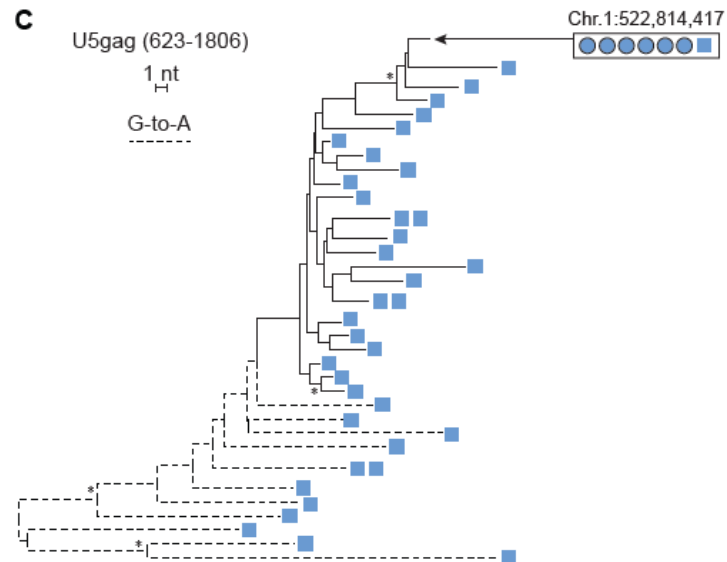
Time for a little digression...

New onset low level viremia is usually caused by a single, rare provirus

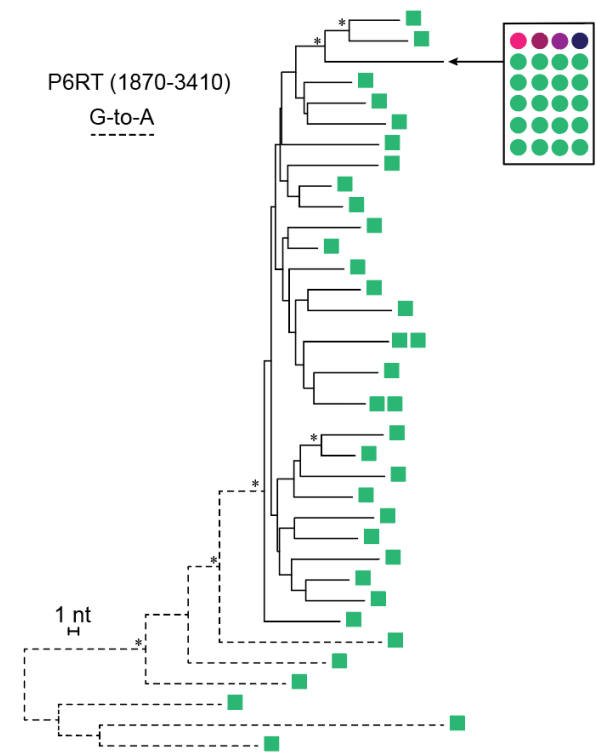
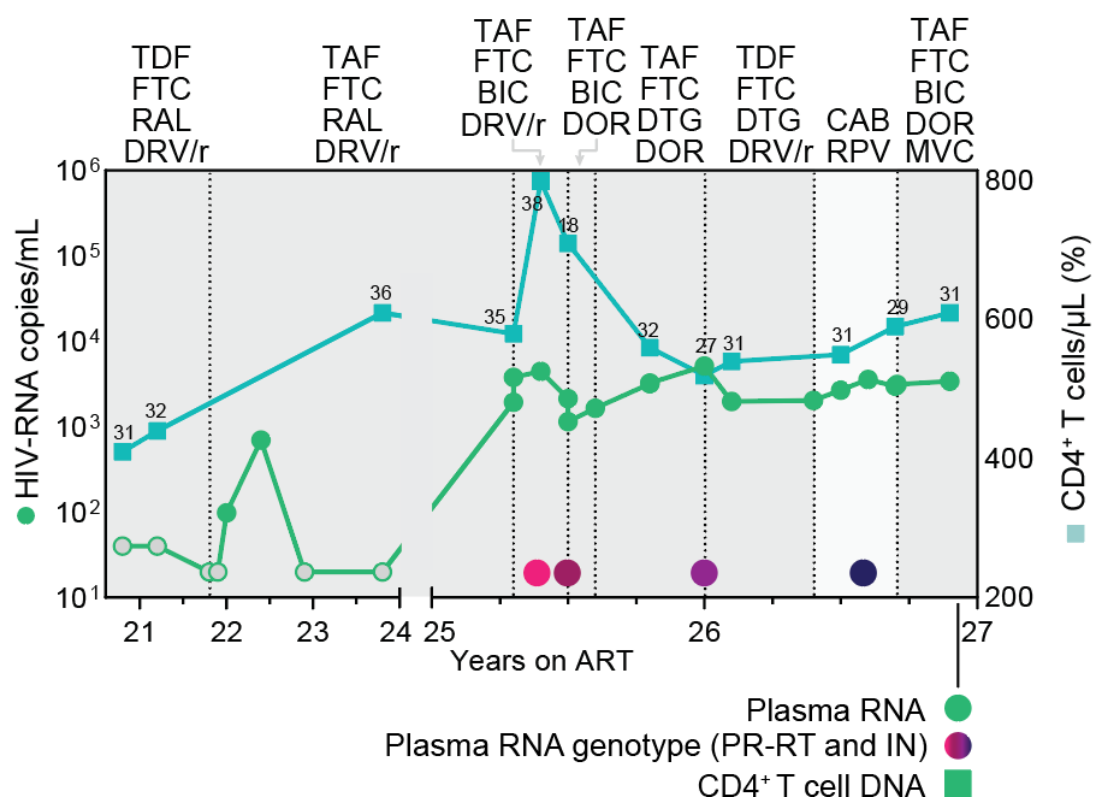
A



C

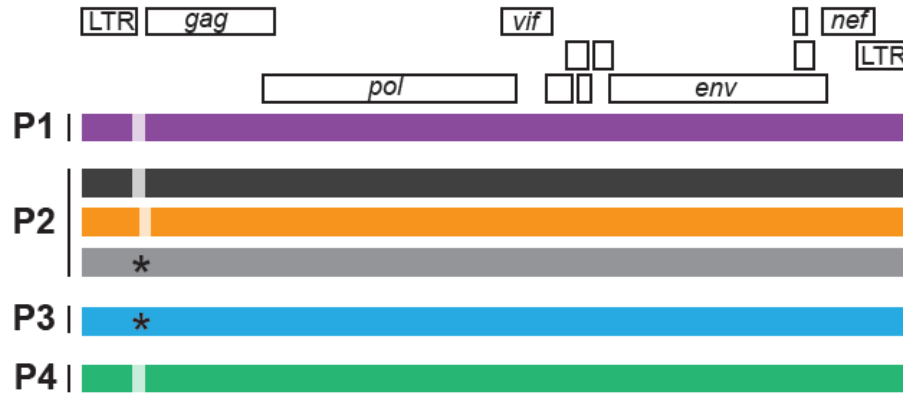


~3000 copies/mL of plasma HIV RNA caused by a single drug-sensitive variant



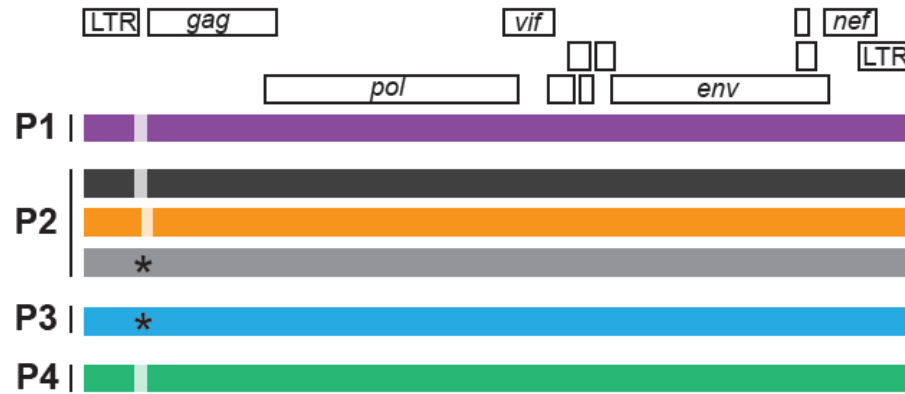
Provirus cause of NSV show defects in the 5' leader

A



Provirus cause of NSV show defects in the 5' leader

A

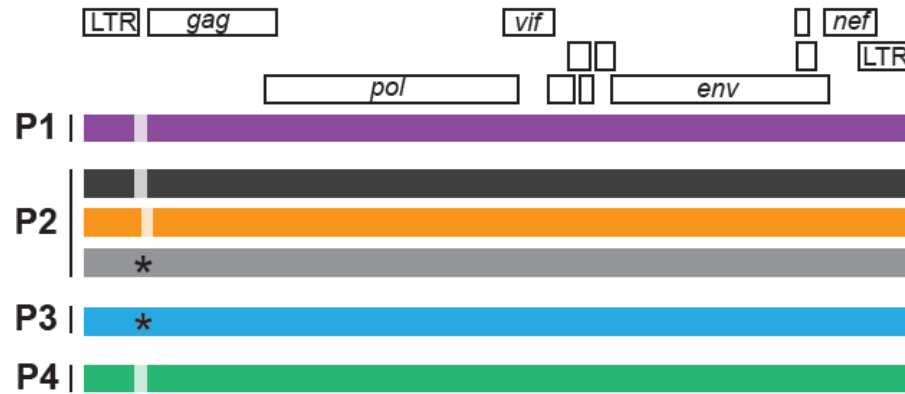


B

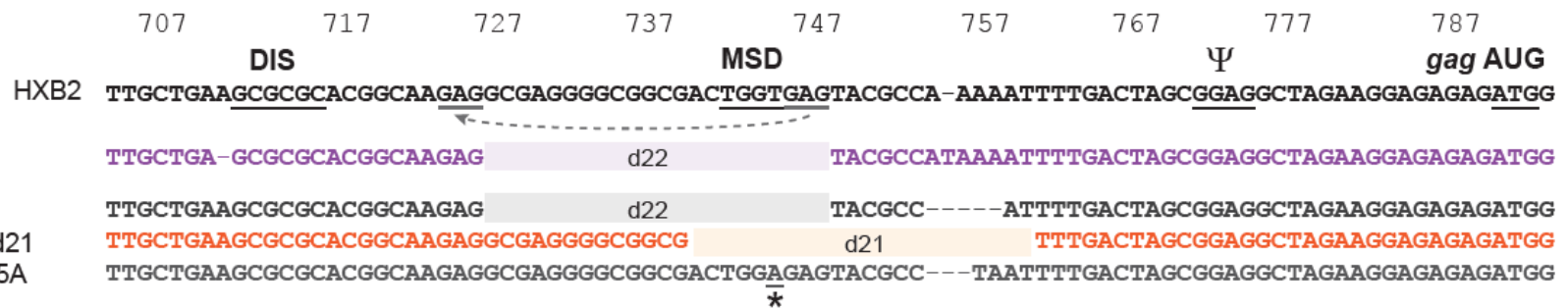


Provirus cause of NSV show defects in the 5' leader

A

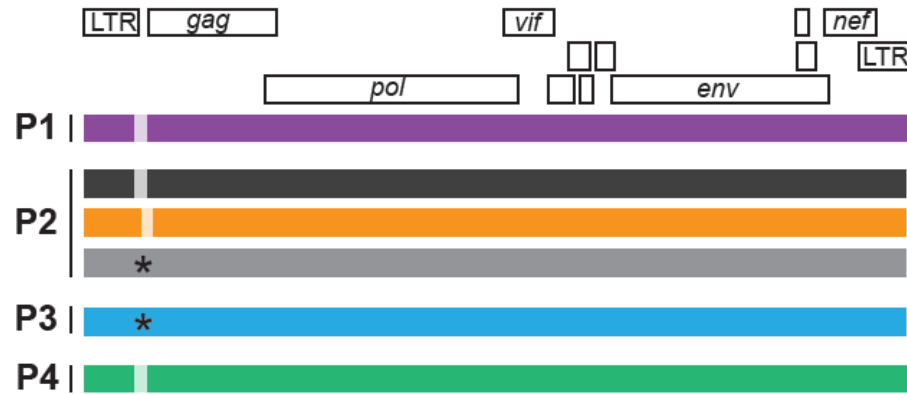


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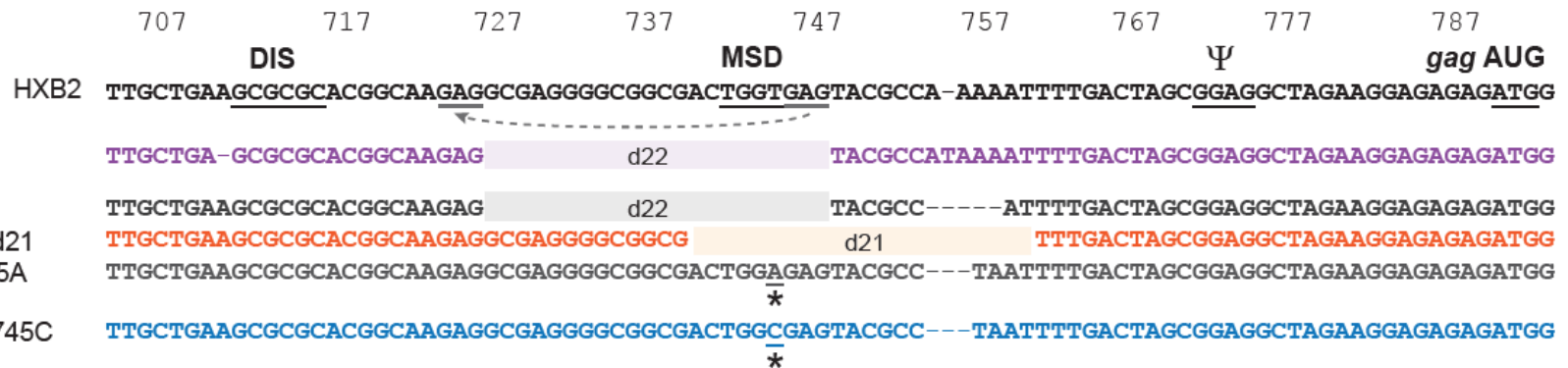


Provirus cause of NSV show defects in the 5' leader

A



B



Provirus cause of NSV show defects in the 5' leader

The diagram illustrates the HIV-1 genome organization and the four proviruses (P1, P2, P3, P4) in the proviral DNA. The HIV-1 genome is shown at the top with LTR, gag, pol, vif, vpr, vpx, env, and nef genes. Below, four proviruses are shown: P1 (purple), P2 (orange), P3 (blue), and P4 (green). P1 and P2 have a small deletion at the 5' end. P3 and P4 have a small deletion at the 3' end. An asterisk (*) marks the deletion site in P2, P3, and P4.

707 717 727 737 747 757 767 777 787

DIS MSD Ψ gag AUG

HXB2 TTGCTGAAGCGCGCACGGCAAGAGSCGAGGGGCGGCGACTGGTGAGTACGCCA-AAAATTTTGACTAGCGGAGGCTAGAAGGAGAGAGATGG

TTGCTGA-GCGCGCACGGCAAGAG d22 TACGCCATAAAATTTTGACTAGCGGAGGCTAGAAGGAGAGAGATGG

TTGCTGAAGCGCGCACGGCAAGAG d22 TACGCC-----ATTTTGACTAGCGGAGGCTAGAAGGAGAGAGATGG

121 TTGCTGAAGCGCGCACGGCAAGAGSCGAGGGGCGGCG d21 TTTGACTAGCGGAGGCTAGAAGGAGAGAGATGG

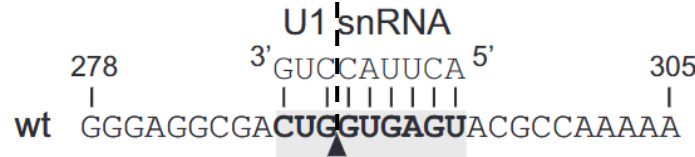
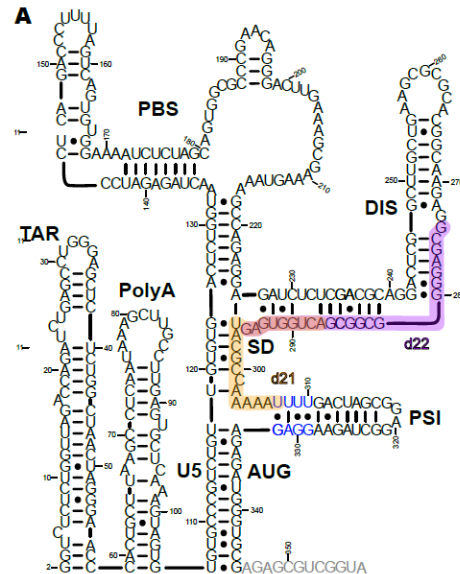
5A TTGCTGAAGCGCGCACGGCAAGAGSCGAGGGGCGGCGACTGGAGAGTACGCC---TAATTTTGACTAGCGGAGGCTAGAAGGAGAGAGATGG

745C TTGCTGAAGCGCGCACGGCAAGAGSCGAGGGGCGGCGACTGGCGAGTACGCC---TAATTTTGACTAGCGGAGGCTAGAAGGAGAGAGATGG

2 TTGCTGAAGCGCGCACGGCAAGAG d22 TACGCC-AAAATTTTTGACTAGCGGAGGCTAGAAGGAGAGAGATGG

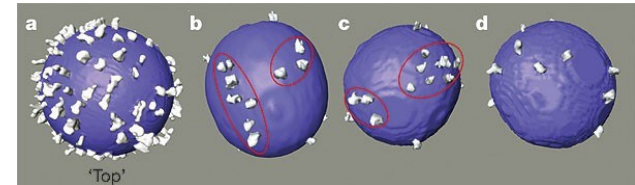
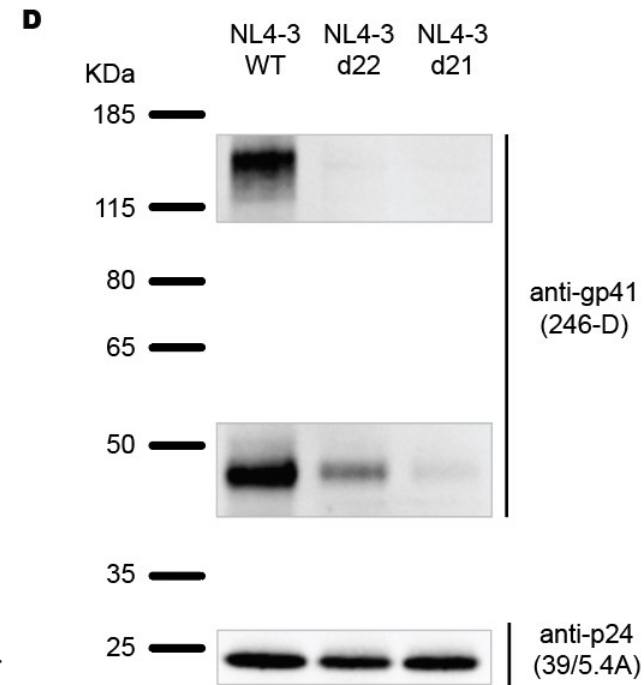
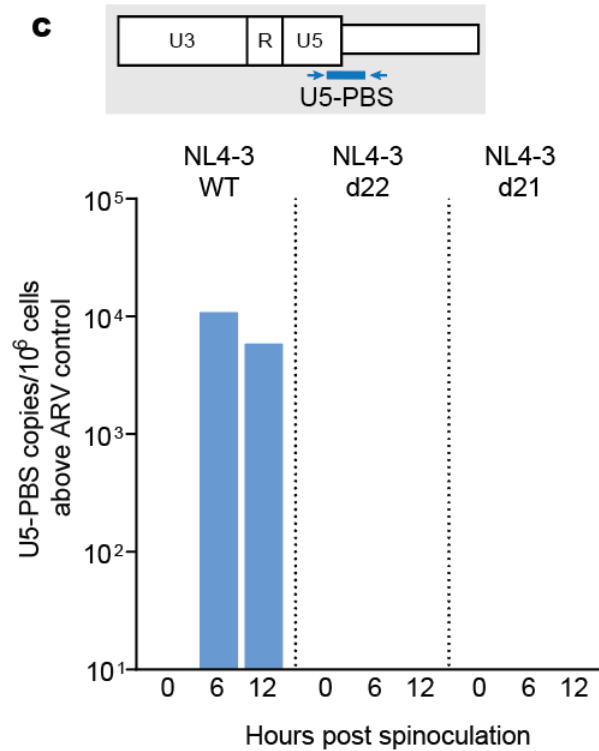
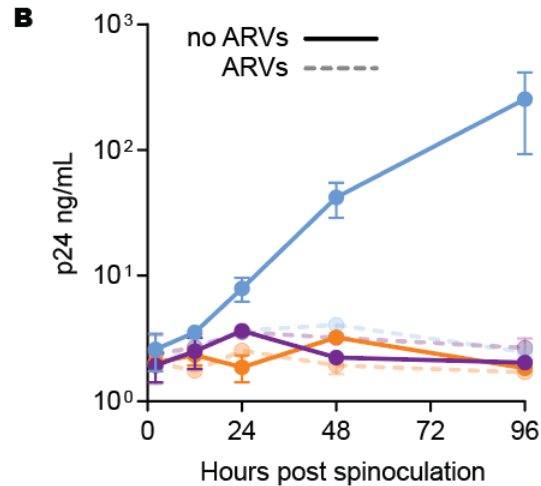
Provirus cause of NSV show defects in the 5' leader

		DIS	MSD	Ψ	<i>gag</i> AUG
	HXB2	TTGCTGAAGCGCGCACGGCAAGAGAGGCGAGGGGCGGCGACTGGT	GAGTACGCCA-AAAATTTTGACTAGCGGAGGCTAGAAGGAGAGAGATGG		
P1	ADK.d22	TTGCTGA-GCGCGCACGGCAAGAG	d22	TACGCCATAAAATTTTGACTAGCGGAGGCTAGAAGGAGAGAGATGG	
P2	AAK1.d22	TTGCTGAAGCGCGCACGGCAAGAG	d22	TACGCC-----ATTTTGACTAGCGGAGGCTAGAAGGAGAGAGATGG	
	DNAJB14.d21	TTGCTGAAGCGCGCACGGCAAGAGAGGCGAGGGGCGGCG	d21	TTTGACTAGCGGAGGCTAGAAGGAGAGAGATGG	
	RRM1.T745A	TTGCTGAAGCGCGCACGGCAAGAGGCGAGGGGCGGCGACTGGAGAGTACGCC---		TAATTTTGACTAGCGGAGGCTAGAAGGAGAGAGATGG	
P3	ZFYVE9.T745C	TTGCTGAAGCGCGCACGGCAAGAGAGGCGAGGGGCGGCGACTGGCGAGTACGCC---		TAATTTTGACTAGCGGAGGCTAGAAGGAGAGAGATGG	
P4	CCND3.d22	TTGCTGAAGCGCGCACGGCAAGAG	d22	TACGCC-AAAATTTTTGACTAGCGGAGGCTAGAAGGAGAGAGATGG	

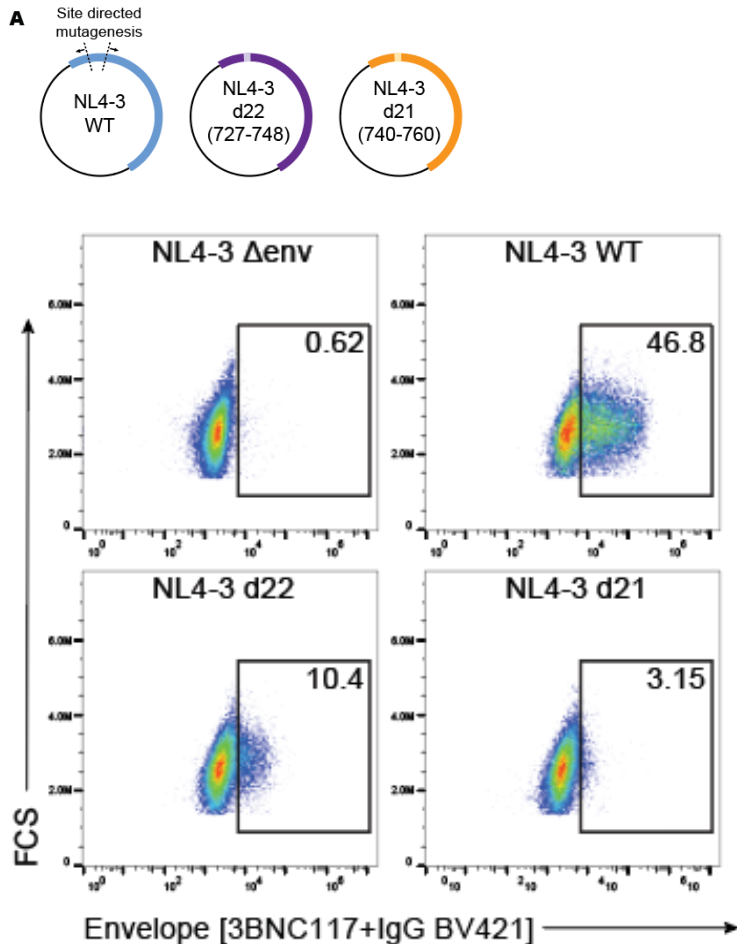


Mueller, 2014

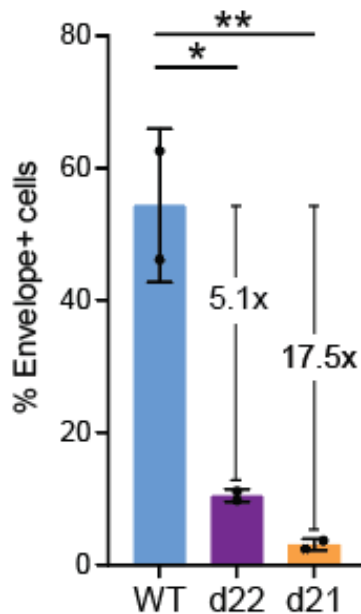
Small 5' leader deletion lead to noninfectious viral particles



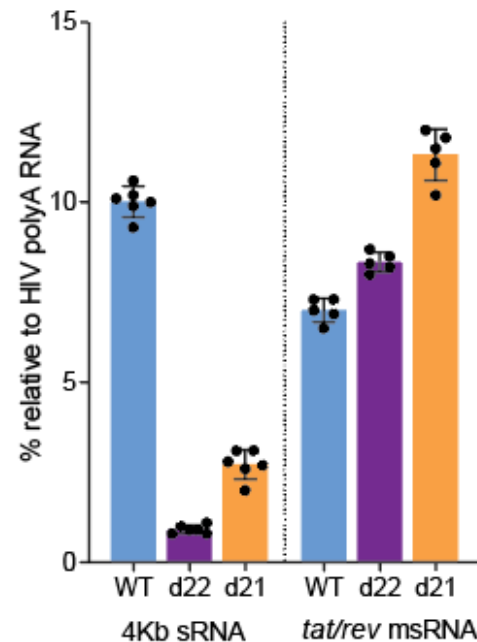
293 cells transfected with 5'L defective vector express lower Envelope



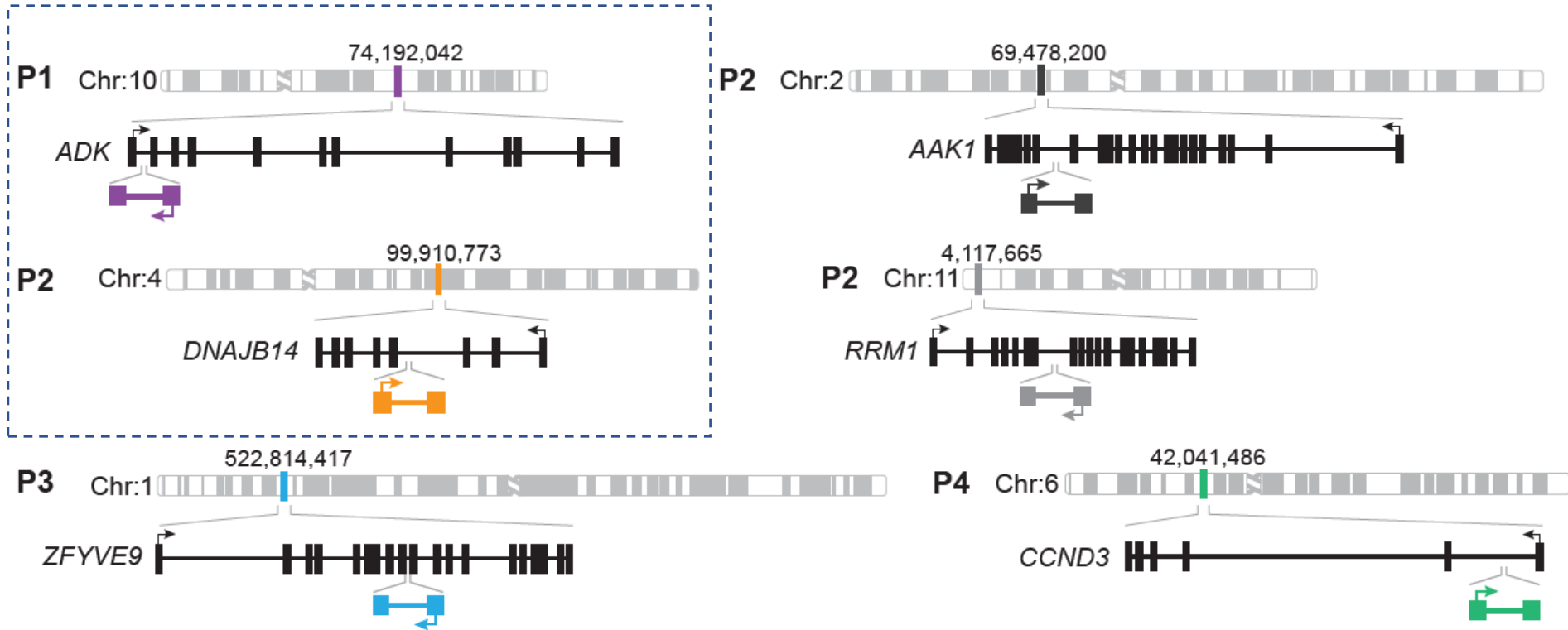
Reduced Envelope production



Disrupted spliceosome composition

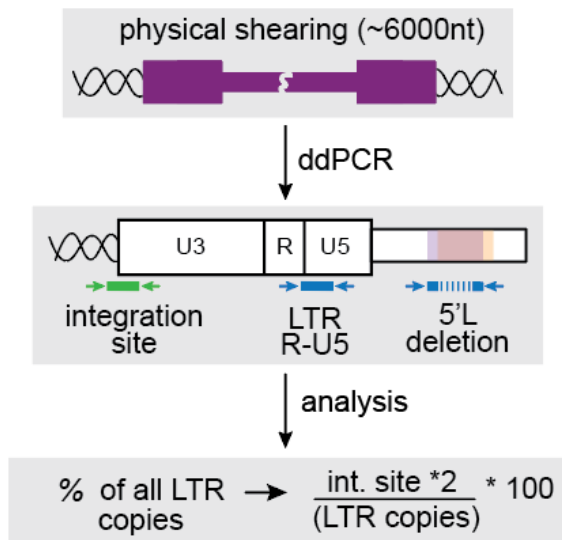


Defective proviruses causing low level viremia are located within genes not linked to HIV insertional mutagenesis



Clones expanded around onset of NSV and are stable over time

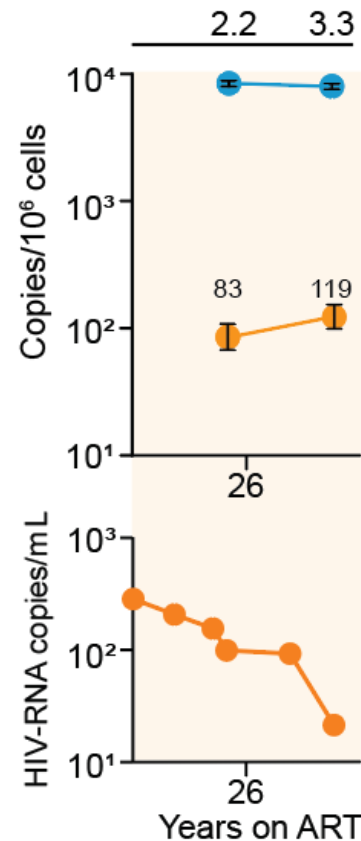
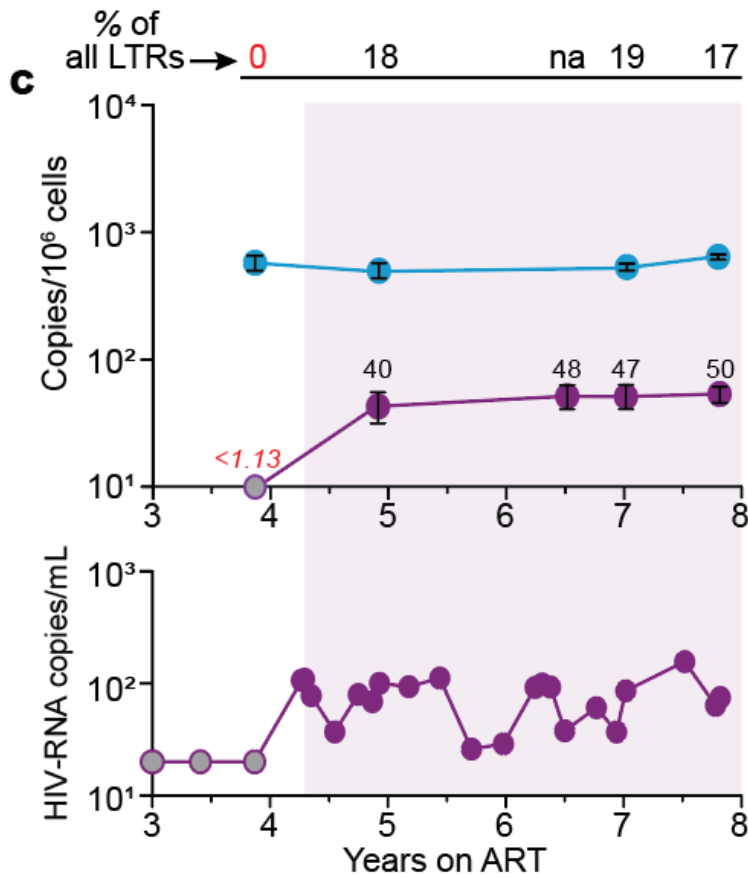
A



Total LTR

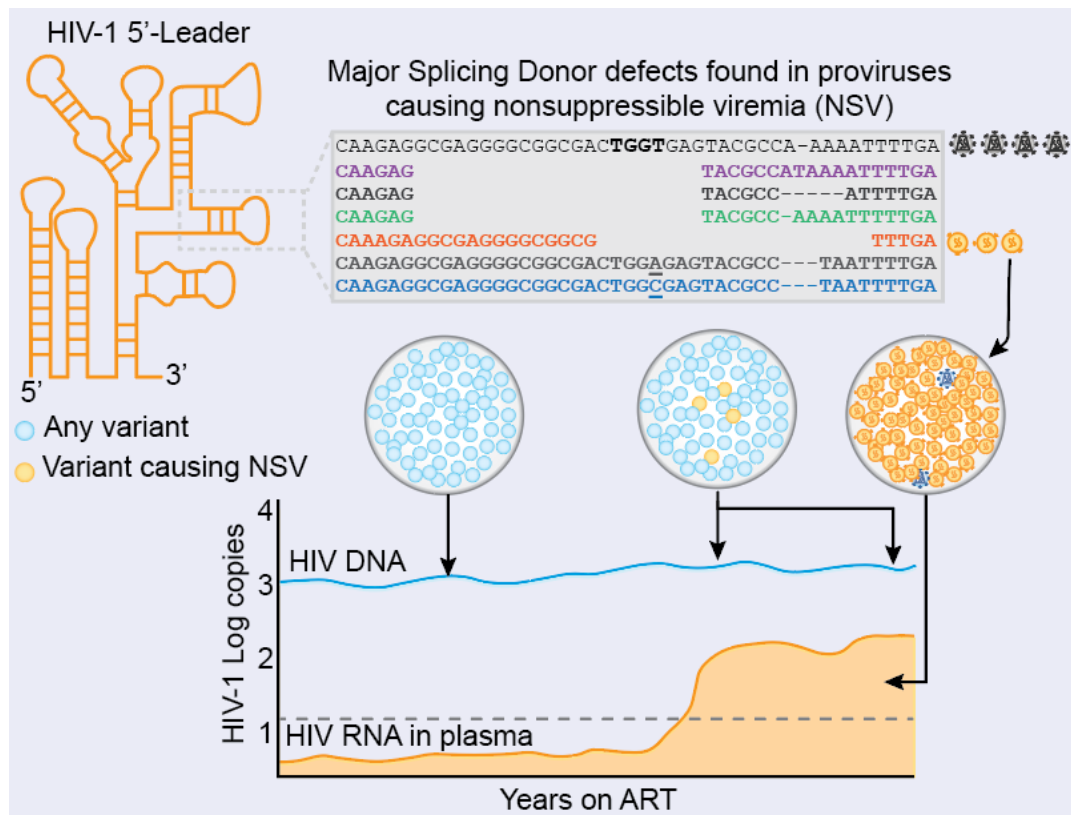
ADK.d22

DNAJB14.d21



ADK.d22 ~10 million CD4⁺ T cells
DNAJB14.d21 ~32 million CD4⁺ T cells

Non-infectious viremia is common among those with LLV



Clinical ultrasensitive assays should be developed to rule out altogether drug resistance and 5' leader defects

What makes one of these clones constantly produce virus?

- type of stimulation?
- recognition of an antigen that is always present?

- commensal pathogens?
- chronic virus?
- HIV itself?
- self?

White, Wu, *et al.*, submitted

Putting everything together...

Provirus persist in those cells that are meant to persist
(expansion, immune response, stimuli, cell program, resistance to death, ...)

Detriment

HIV+ cells

Advantage

HIV
integration

Host gene
misexpression

Deeper
Latency

Host gene
misexpression

Provirus

Avg Intact

Avg Defective

More viral RNA/Ag
expressed

Sensitive to
immune clearance

Less viral RNA/Ag
expressed

Resistant to
immune clearance

Erosion

Persistence

Putting everything together...

Provirus persist in those cells that are meant to persist
(expansion, immune response, stimuli, cell program, resistance to death, ...)

Detriment

Advantage

HIV+ cells

HIV
integration

Provirus

Host gene
misexpression

Deeper
Latency

Host gene
misexpression

Avg Intact

Avg Defective

More viral RNA/Ag
expressed

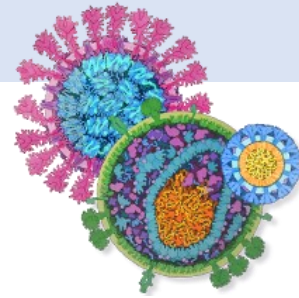
Sensitive to
immune clearance

Less viral RNA/Ag
expressed

Resistant to
immune clearance

Erosion

Persistence



- There are **multiple, layered factors** shaping the HIV reservoir. No single factor can explain the persistence of every HIV-infected cell.
- On average, intact and defective **proviruses are expressed at similar, low frequencies**.
- **Integration** provides a selective advantage in only few infected cells.
- Clonal expansion is mostly driven by **immune stimuli**.
- **Large, sharable, datasets are needed**. Additional data on paired proviral structures and integration sites will help understanding the persistence of intact proviruses caused by specific chromosomal locations (e.g. ZNF genes).
- **Defective proviruses** with specific defects **can cause low-level viremia** and complicate art management. Their role in pathogenesis remains unclear.

Acknowledgments

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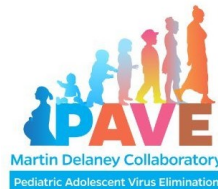
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BEAT-HIV
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