

## ECCMID Symposium “CRISPR-Cas revolution”

### CRISPR-Cas9 based therapy for persistent virus infections (HIV)



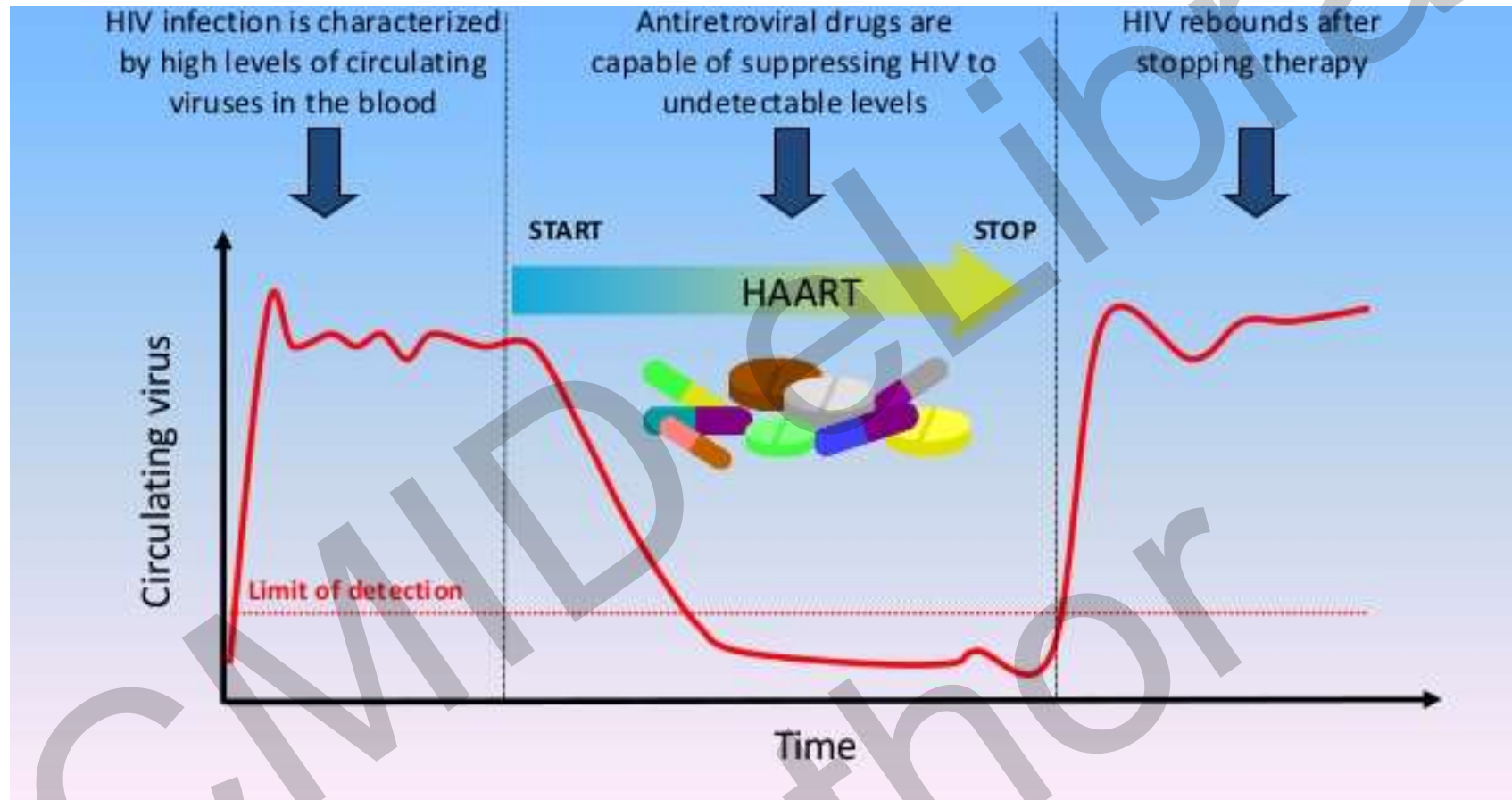
Ben Berkhout  
Laboratory of Experimental Virology  
University of Amsterdam  
The Netherlands

**HIV in the Netherlands** since 1983 (18 million inhabitants)

We have analyzed some 60,992 patient samples since start epidemic

End 2017: 19,582 HIV+ people in care (approx. 2300 don't know their status)  
12,378 MSM, other men (3593) and women (3611)  
around 750 new cases in 2017 (PReP started in risk groups)  
**90%** diagnosed, **93%** on ART, **95%** viral suppression

**Research towards a cure:**  
**Anti-HIV gene therapy (RNAi)**  
**CURE approaches (CRISPR-Cas)**



**Combination drug therapy saves lives:** Durable HIV control possible

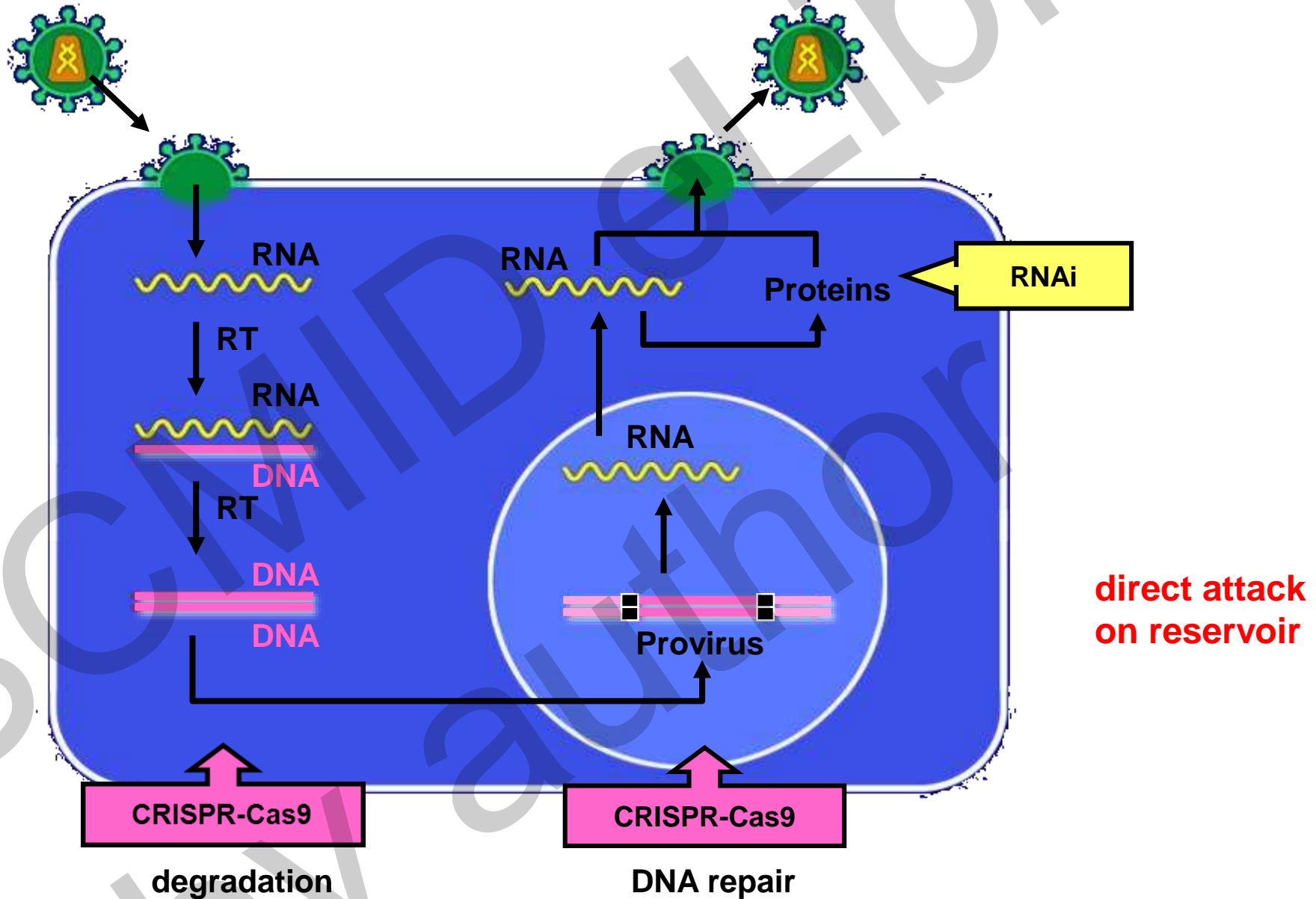
But HIV rebounds rapidly after stopping therapy > **life-long therapy**

**Alternative:** Gene therapy for durable therapeutic effect (**single treatment**)

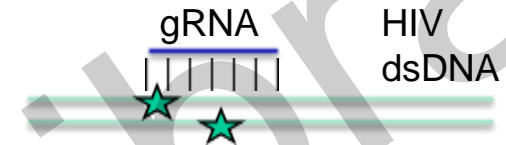
- Protect cells against HIV, use lentiviral vector that stably integrates!
- Express antiviral molecules (RNAi)
- Direct attack on HIV DNA in the reservoir (CRISPR-Cas)

# HIV drug therapy a success, but what about a cure

## Attack on the HIV reservoir







**RNAi**

**versus**

**CRISPR-Cas9**

**Effector**

short hairpin RNA

guide RNA

**Target**

RNA (sequence-specific)

dsDNA (sequence-specific)

**Result**

cleavage

cleavage

**Components**

1 (shRNA)

2 (gRNA + CRISPR-Cas9)

**Viral escape**

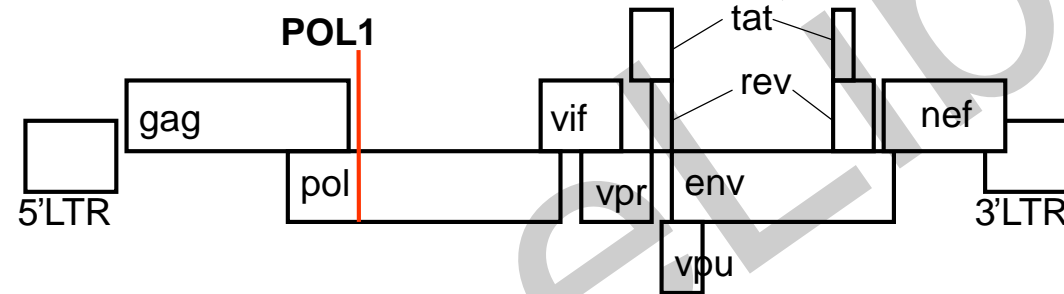
yes (point mutation in target)

no (initial literature)

**Bonus:**  
direct attack on HIV DNA reservoir

Globally similar antiviral approaches  
Yet many **surprising differences**

Cell culture infections: Potent inhibition by some shRNAs  
 But HIV escape, which can be blocked by a combinatorial attack (3 shRNAs)

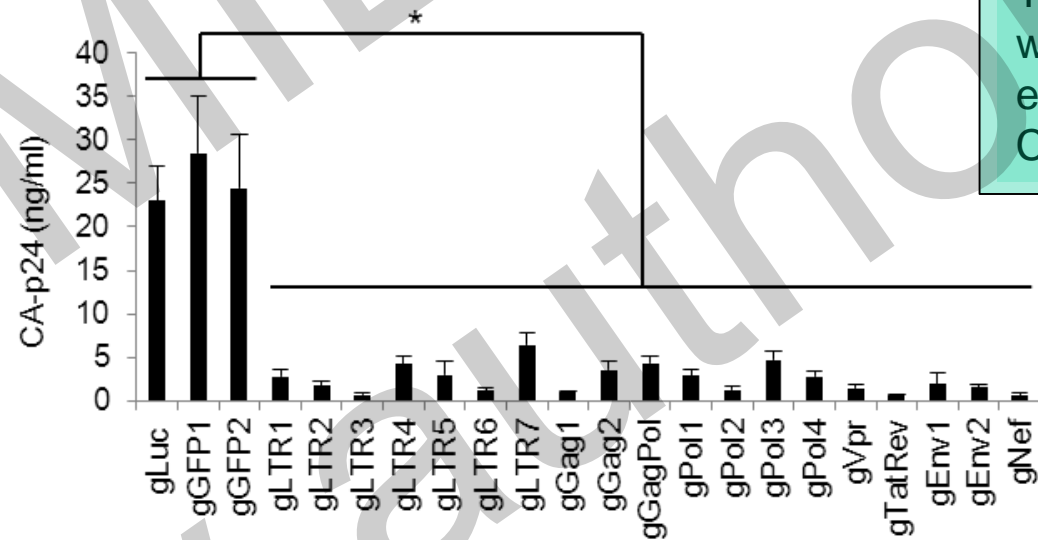
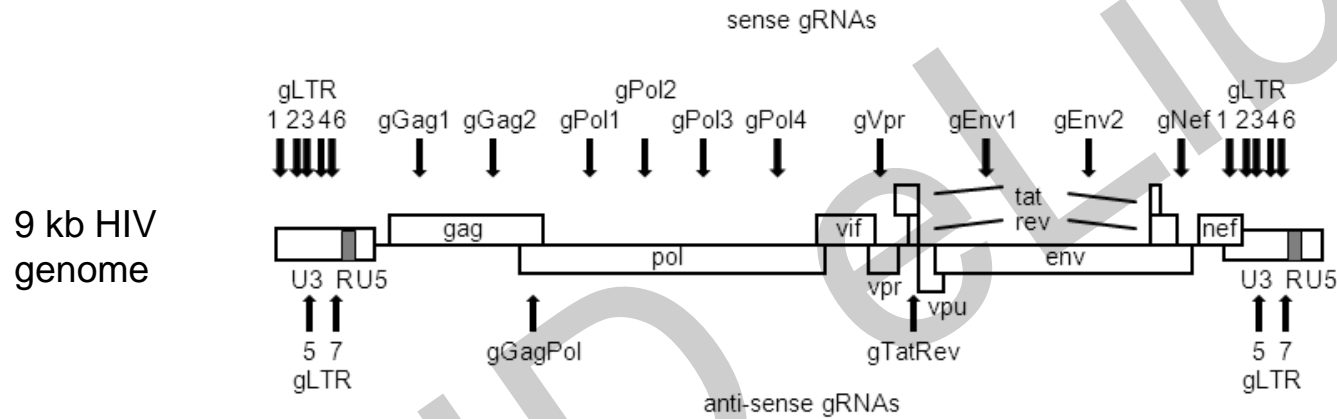


nr	Pol, Protease															AA sequence								
	A	C	A	G	G	A	G	C	A	G	A	T	G	A	T	A	C	A	G	T	G	A	D	D
8x	-	-	-	-	-	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
7x	-	-	-	-	-	-	-	-	-	-	-	-	-	C	-	-	-	-	-	-	-	-	-	-
4x	-	-	-	-	-	-	-	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3x	-	-	-	-	-	-	-	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2x	-	-	-	-	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2x	-	-	-	-	-	-	-	-	-	-	-	A	-	-	-	-	-	-	-	-	-	-	N	-
1x	-	-	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Regular RT-induced mutations  
 Preference for silent mutations (25/27)

## Targeting HIV DNA (conserved sites only)

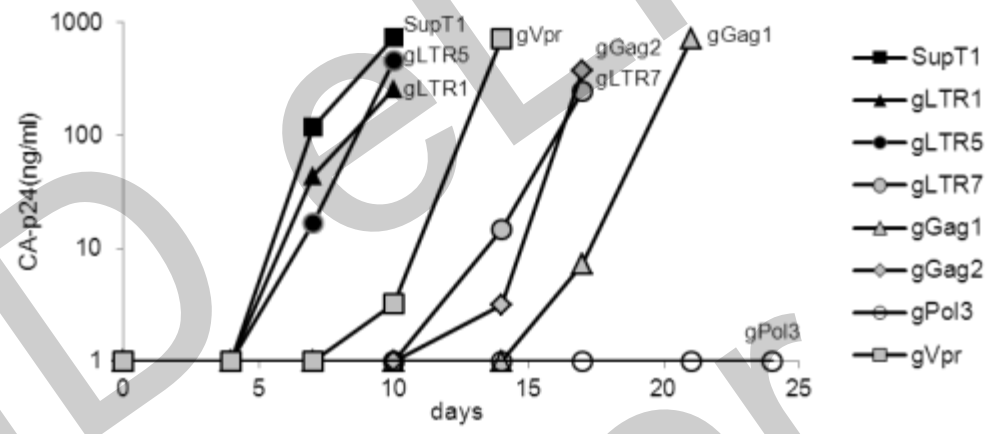
profound inhibition of viral gene expression by **each gRNA** (unlike shRNAs)



Transfect 293T cells with plasmids encoding CRISPR-Cas, gRNA and HIV

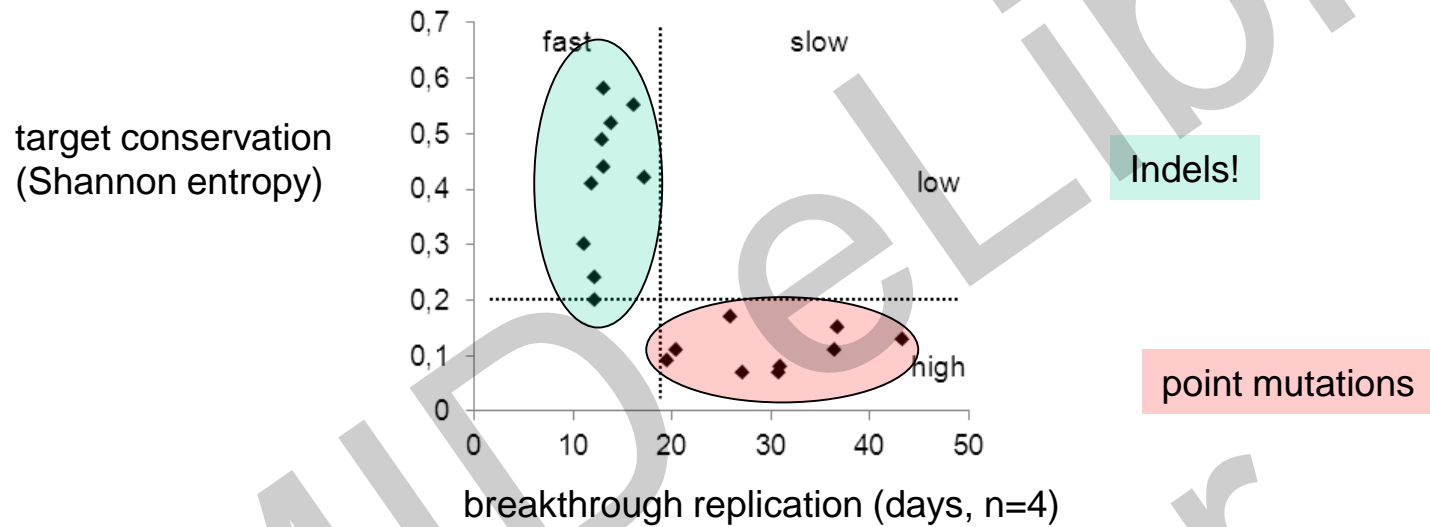


Transduce T cell line  
with LV-Cas-gRNA  
Infect with HIV LAI isolate



Good inhibition of HIV replication  
But sometimes **immediate** virus escape?



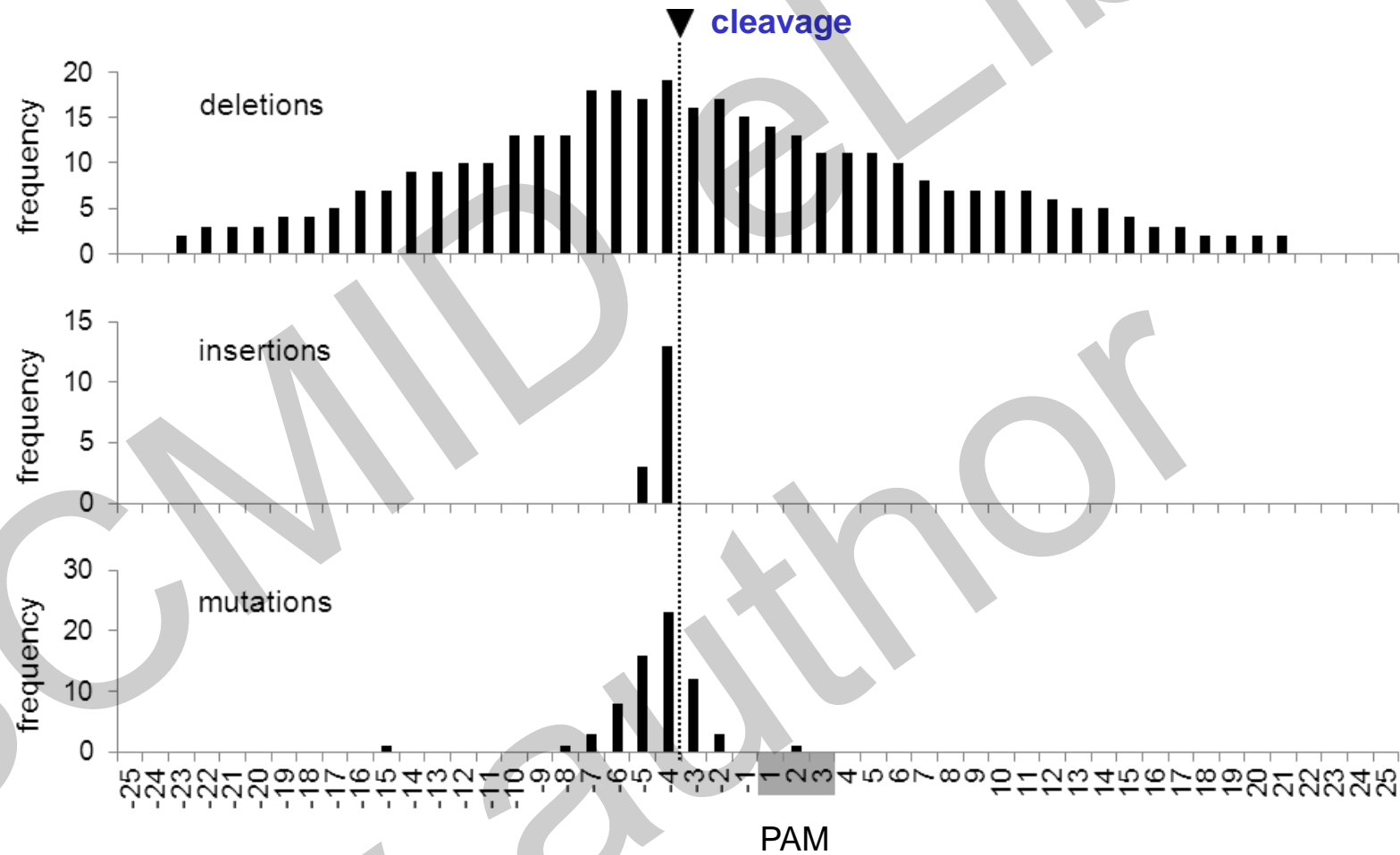


Variable targets (high Shannon) = rapid escape by indels ..... **mechanism?**

Well-conserved targets (low Shannon) = slow escape by (regular) point mutations  
indels not compatible with function

All occurs around the cleavage site: CRISPR-Cas9 mediates DNA cleavage, but subsequent DNA repair by the **NHEJ pathway** (non-homologous end joining) creates indels that allows viral escape

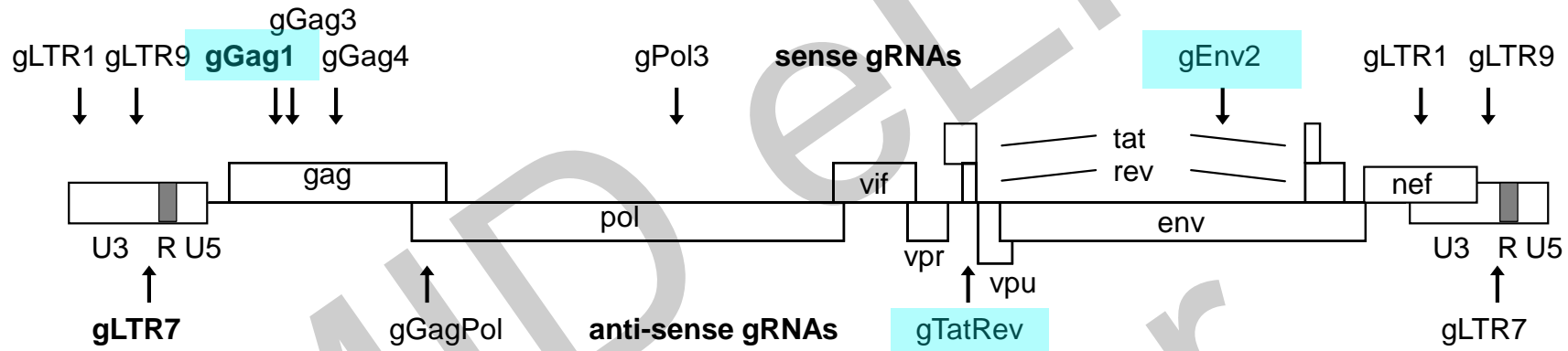
**HIV escapes with help from the host (NHEJ)**



# Combinatorial CRISPR attack

1. Better inhibition
2. Higher threshold for resistance

Possible bonus: **excision** of sequences between 2 cleavage sites (LTRs)



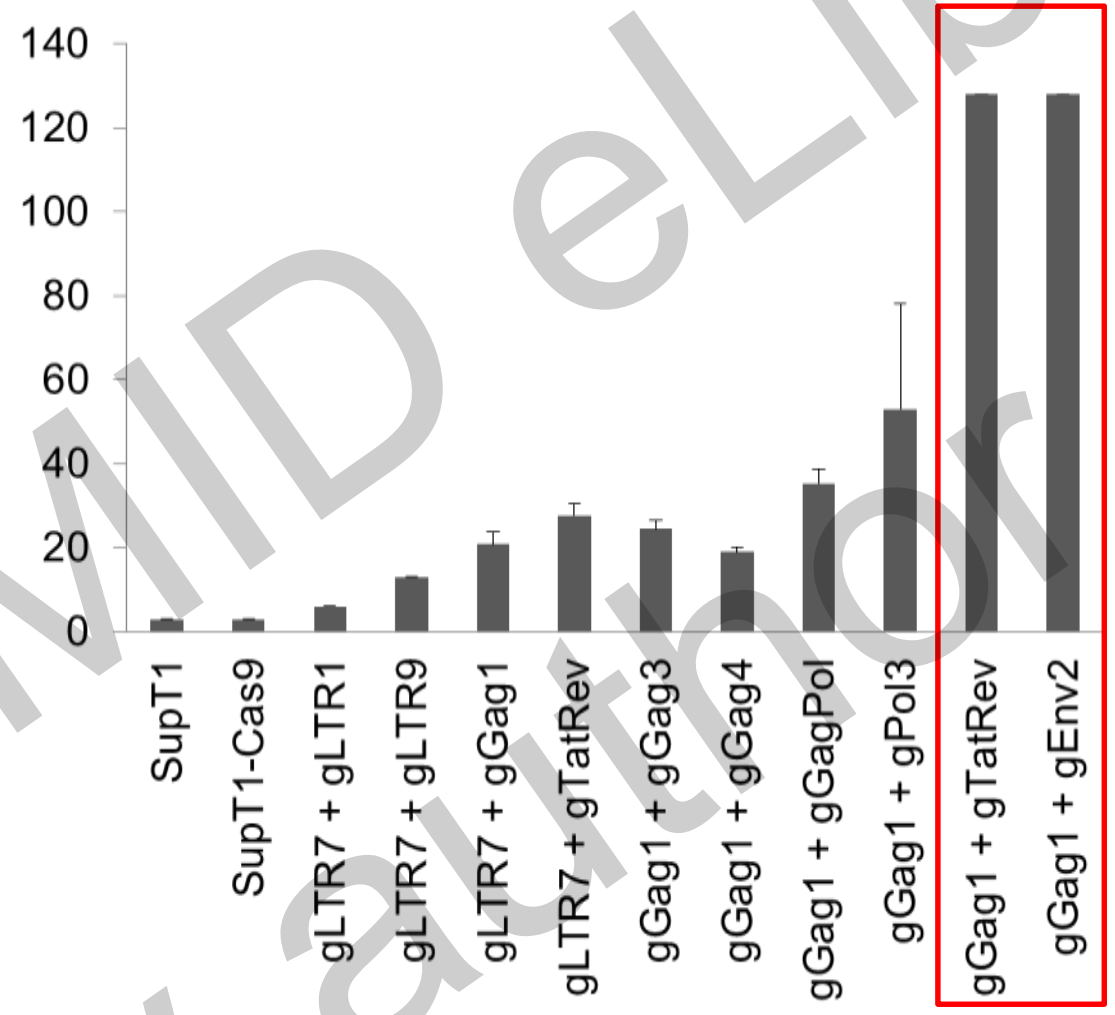
gRNA I	gRNA II	distance (bp)
	gLTR9	22, 8810
<b>gLTR7</b>	gLTR1	322, 9110
	gGag1	988, 8145
	gTatRev	5590, 3542

gRNA I	gRNA II	distance (bp)
	gGag3	91
	gGag4	438
<b>gGag1</b>	gGagPol	888
	gPol3	2796
	<b>gTatRev</b>	4602
	<b>gEnv2</b>	6452

# HIV replication: two combi's prevent viral escape

gGag1+gTatRev and gGag1+gEnv2 (very conserved targets)

Time to "HIV breakthrough"  
(days, average 4 cultures)



< no escape at end experiment

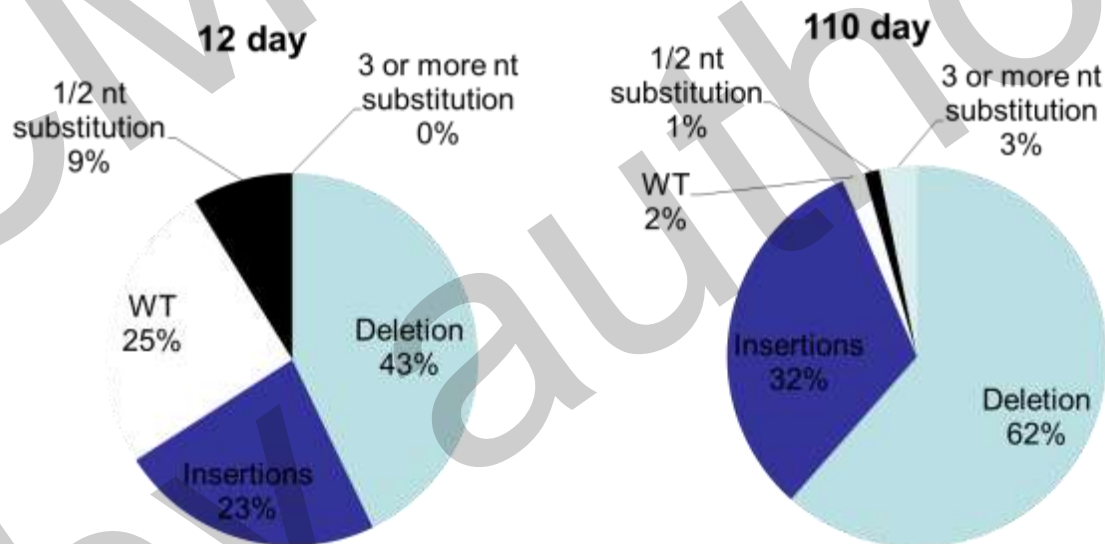
HIV sterilization???

When escape: regular NHEJ  
signature in both targets

# wild-type HIV proviruses disappear over time

gRNAs	target region	wild-type sequence frequency (%)	
		day 12	day 110
gGag1 + gTatRev	gGag1	8 / 21 (38.1)	2 / 38 (5.3)
	gTatRev	7 / 28 (25.0)	0 / 39 (0.0)
gGag1 + gEnv2	gGag1	8 / 21 (38.1)	1 / 37 (2.7)
	gEnv2	0 / 21 (0.0)	0 / 43 (0.0)

A shift from minor to major mutations (repeated Cas action)



# Ultra-sensitive screen for infectious HIV

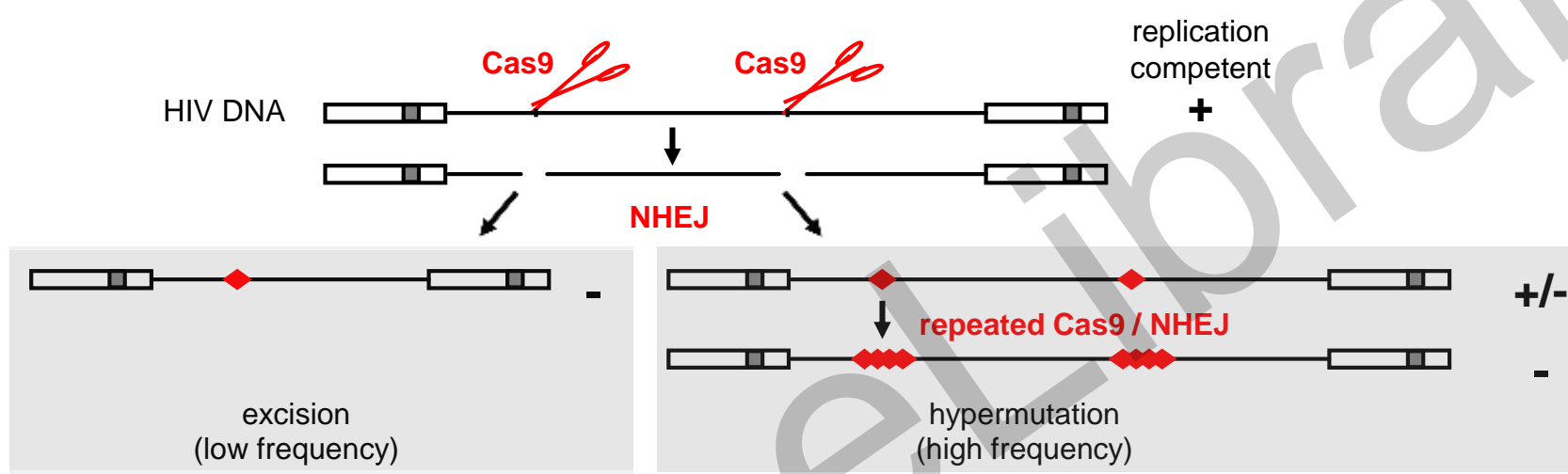
gRNAs	Culture	virus rescue			
		day 16	day 41	day 69	day 97
gGag1 + gTatRev	1	+	-	-	-
	2	+	-	-	-
	3	+	-	-	-
	4	+	-	-	-
gGag1 + gEnv2	1	+	+	+	-
	2	+	+	-	-
	3	+	+	+	-
	4	+	+	+	-

Cultures of cells were effectively **sterilized!**

gGag1+gTatRev faster than gGag1+gEnv2

**The host (NHEJ) helps to inactivate HIV-1**





## Provirus excision only? (“HIV Excision” Meeting, NIH)

Prominent product in PCR, but in fact occurs surprisingly little

Instead, most HIV genomes are inactivated by NHEJ-hypermutation !

Why? DNA repair is simply too fast

1st break repaired before 2nd break occurs

no 2 breaks simultaneously > no excision

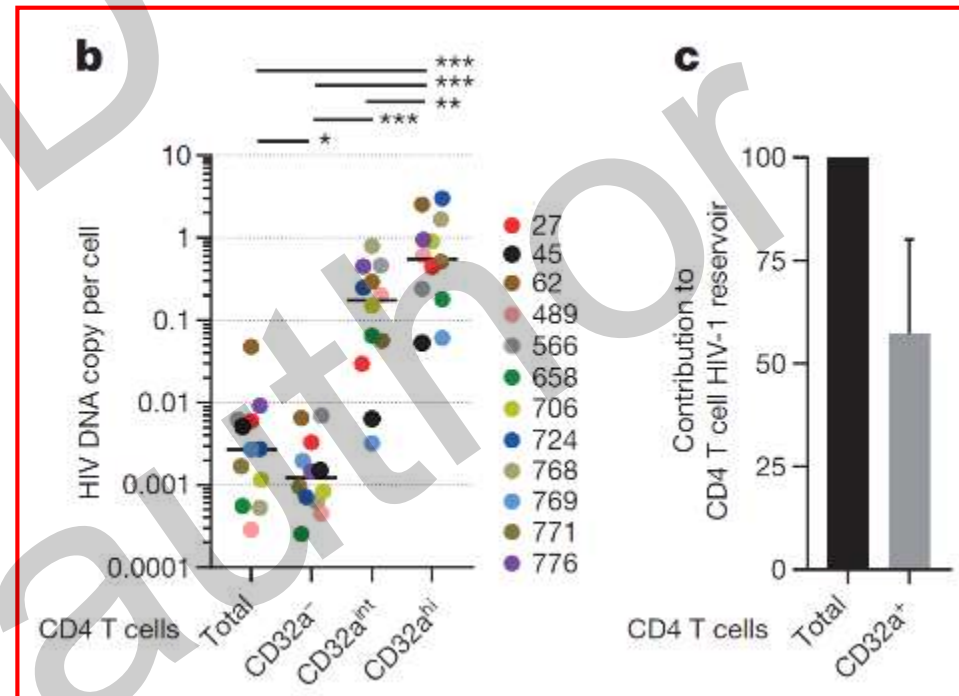
We can sterilize HIV .... but can we find the HIV reservoir in humans?

## CD32a is a marker of a CD4 T-cell HIV reservoir harbouring replication-competent proviruses

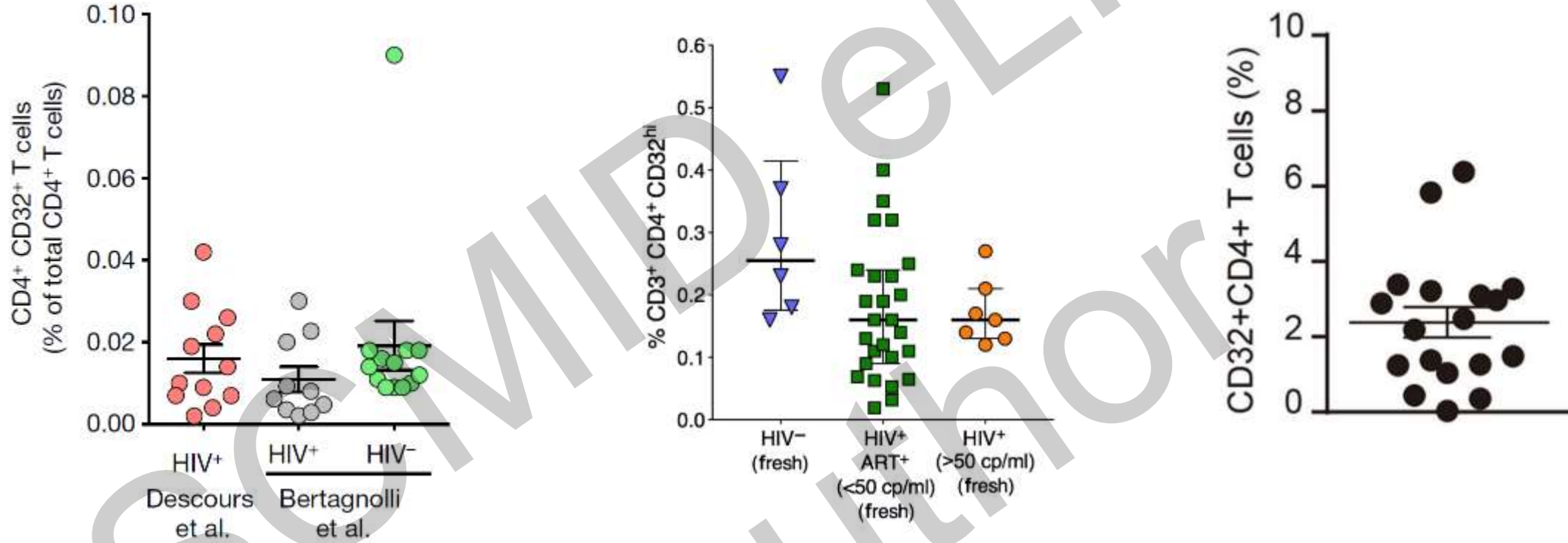
Benjamin Descours<sup>1\*</sup>, Gaël Petitjean<sup>1\*</sup>, José Luis López Zaragoza<sup>2,3,4</sup>, Timothée Bruel<sup>2,5</sup>, Raoul Raffel<sup>1</sup>, Christina Psomas<sup>6</sup>, Jacques Reynes<sup>6</sup>, Christine Lacabaratz<sup>2,3,4</sup>, Yves Levy<sup>2,3,4</sup>, Olivier Schwartz<sup>2,5</sup>, Jean Daniel Lelievre<sup>2,3,4</sup> & Moncef Benkirane<sup>1</sup>

Receptor for IgG  
antibodies

Average  
HIV DNA enrichment of  
**~1000-fold**



# Several groups have shown CD32 expression on a small subset of CD4+ T cells



# So far nobody could confirm HIV DNA enrichment in CD32+ cells

SCIENCE TRANSLATIONAL MEDICINE | RESEARCH ARTICLE

HIV

## CD32 is expressed on cells with transcriptionally active HIV but does not enrich for HIV DNA in resting T cells

Mohamed Abdel-Mohsen,<sup>1\*</sup> Leticia Kuri-Cervantes,<sup>2\*</sup> Judith Grau-Exposito,<sup>3\*</sup> Adam M. Spivak,<sup>4</sup> Racheal A. Nell,<sup>4</sup> Costin Tomescu,<sup>1</sup> Surya Kumari Vadrevu,<sup>1</sup> Leila B. Giron,<sup>1</sup> Carla Serra-Peinado,<sup>3</sup> Meritxell Genescà,<sup>3</sup> Josep Castellví,<sup>5</sup> Guoxin Wu,<sup>6</sup> Perla M. Del Rio Estrada,<sup>7</sup> Mauricio González-Navarro,<sup>7</sup> Kenneth Lynn,<sup>1,2,8</sup> Colin T. King,<sup>9</sup> Sai Vemula,<sup>6</sup> Kara Cox,<sup>6</sup> Yanmin Wan,<sup>10</sup> Qingsheng Li,<sup>10</sup> Karam Mounzer,<sup>8</sup> Jay Kostman,<sup>8</sup> Ian Frank,<sup>2</sup> Mirko Paiardini,<sup>9</sup> Daria Hazuda,<sup>6</sup> Gustavo Reyes-Terán,<sup>7</sup> Douglas Richman,<sup>11</sup> Bonnie Howell,<sup>6</sup> Pablo Tebas,<sup>2</sup> Javier Martínez-Picado,<sup>12,13,14</sup> Vicente Planelles,<sup>4</sup> Maria J. Buzon,<sup>3†</sup> Michael R. Betts,<sup>2†</sup> Luis J. Montaner<sup>1†</sup>

frontiers  
in Immunology

ORIGINAL RESEARCH  
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## CD32-Expressing CD4 T Cells Are Phenotypically Diverse and Can Contain Proviral HIV DNA

Genevieve E. Martin<sup>1†</sup>, Matthew Pace<sup>1†</sup>, John P. Thornhill<sup>1,2†</sup>, Chansavath Phetsouphanh<sup>1</sup>, Jodi Meyerowitz<sup>1</sup>, Margane Gossaz<sup>1</sup>, Helen Brown<sup>1</sup>, Natalia Olejniczak<sup>1</sup>, Julianne Lwanga<sup>3</sup>, Gita Ranjee<sup>1</sup>, Pontiano Kaleebu<sup>4</sup>, Khofouf Porter<sup>6</sup>, Christian B. Willberg<sup>1,2</sup>, Paul Klennerman<sup>1,2</sup>, Nneka Nwokolo<sup>5†</sup>, Julie Fox<sup>2†</sup>, Sarah Fidler<sup>2†</sup> and John Frater<sup>1,2,3†</sup> On Behalf of the CHERUB Investigators

nature  
COMMUNICATIONS

ARTICLE

DOI: 10.1038/s41467-016-05157-w OPEN

## CD32 expression is associated to T-cell activation and is not a marker of the HIV-1 reservoir

Roger Badia<sup>1</sup>, Ester Bailana<sup>1</sup>, Marc Castellví<sup>1</sup>, Edurne García-Vidal<sup>1</sup>, Maria Pujantell<sup>1</sup>, Bonaventura Clotet<sup>1</sup>, Julia G. Prado<sup>1</sup>, Jordi Puig<sup>1</sup>, Miguel A. Martínez<sup>1</sup>, Eva Riveira-Muñoz<sup>1</sup> & José A. Esté<sup>1</sup>

The Journal of Infectious Diseases

MAJOR ARTICLE

IDSAA  
Infectious Disease Society of America

hivma  
HIV Medicine Association

CD32016

## The Latent Human Immunodeficiency Virus (HIV) Reservoir Resides Primarily in CD32<sup>-</sup>CD4<sup>+</sup> T Cells in Perinatally HIV-Infected Adolescents With Long-Term Virologic Suppression

Adit Dhumrakupt<sup>1</sup>, Lilly V. Siems<sup>1</sup>, Dolly Singh<sup>1</sup>, Ya Hui Chen<sup>1</sup>, Thuy Anderson<sup>1</sup>, Aleisha Collinson-Streng<sup>1</sup>, Hao Zhang<sup>2</sup>, Purvish Patel<sup>2</sup>, Allison Agwu<sup>1</sup> and Deborah Persaud<sup>1</sup>

- All CD32+ cell purifications based on FACS
- Purity of the CD32 cell fraction a problem

**Blood from HIV-infected individuals**



**PBMCs**



**Alternative purification scheme  
2x negative selection (magnetic sorting)**

**CD4<sup>+</sup> T cells**



**3x positive selection (magnetic sorting)**

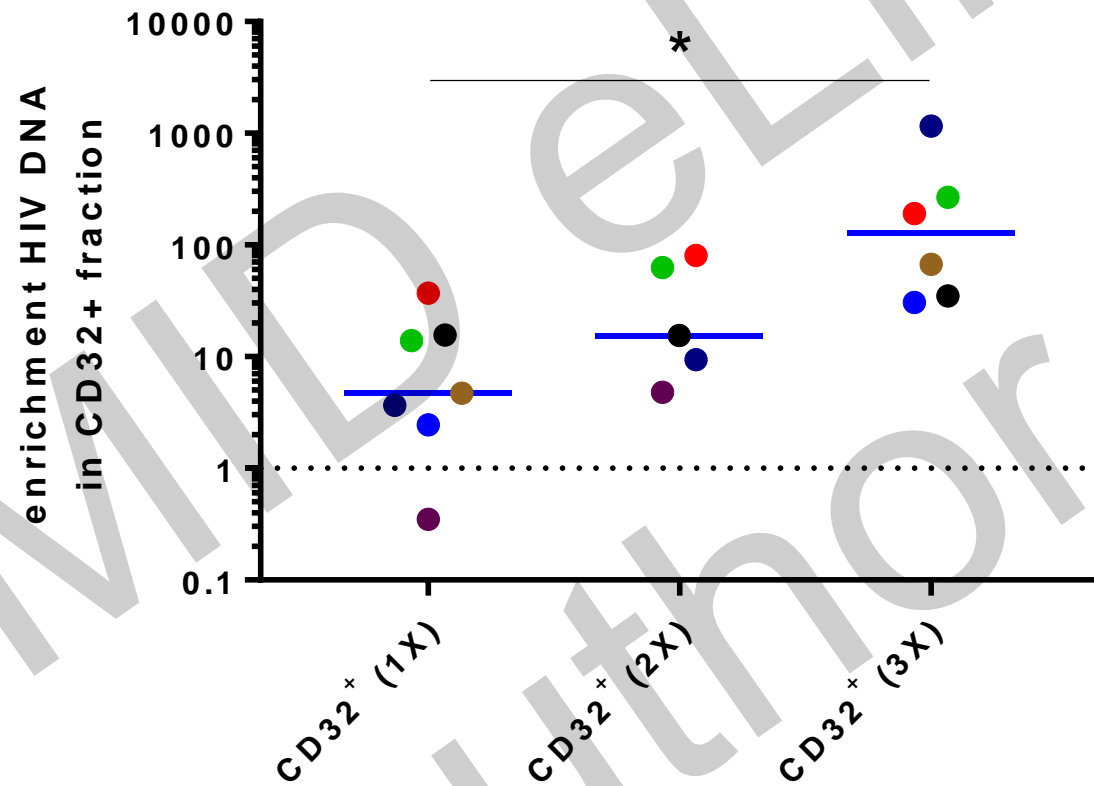
**CD32<sup>+</sup>CD4<sup>+</sup> T cells**

**CD32<sup>-</sup>CD4<sup>+</sup> T cells**



**HIV-1 DNA and RNA measurements**

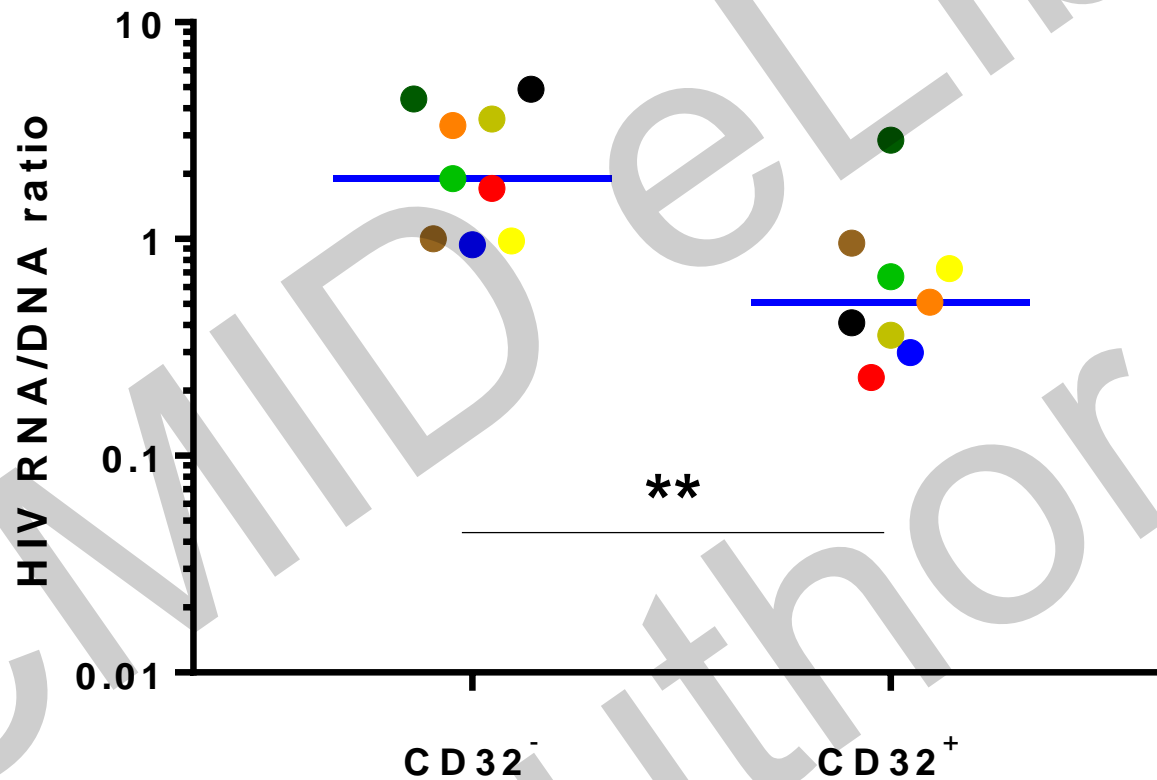
Extra two rounds of CD32<sup>+</sup> positive selection resulted in high (up to ~1000-fold) enrichment in HIV DNA in CD32<sup>+</sup> fraction



Mean enrichment: 11.1x 34.5x 292.4x

HIV DNA load reached 0.53 copies per cell

No enrichment in HIV RNA was observed and HIV RNA/DNA ratio was significantly lower in the CD32+ fraction, indicating that HIV in these cells is mostly transcriptionally silent



**CD32 remains a bona fide candidate marker of the HIV reservoir and a promising target for therapeutic cure strategies**

## **CRISPR-Cas:**

Gang Wang

Zhao Na

Bep Klaver

Gilles Darcis

Zongliang Gao

Elena Herrera Carrillo

Yme van der Velden

Caroline Binda

Minghui Fan

Atze Das

## **CD32:**

Gilles Darcis

Neeltje Kootstra

Berend Hooibrink

Margreet Bakker

Suzanne Jurriaans

Kevin Groen

Thijs Montfort

Carine van Lint

Alexander Pasternak

European Conference of Virology - Rotterdam April 2019



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## Human germline editing in the news

Jianku He (Shenzhen, China)

Out of the blue:

Not published

Not controlled by ethics committees

University employer did not know

Informed consent on vaccination

Protect the unborn child of a HIV-positive father during in vitro fertilization with his sperm and (?) later in life by germline removal of the main receptor for HIV: CCR5

- fertilized oocyte treated with anti-CCR5 CRISPR-Cas
- 9 months later the twins Lulu and Nana were born
- wt gene still present in one baby? (mosaicism)

### Prevention?

No absolute protection (CXCR4-using strains)

Safe alternative means available: sperm washing!

### Safe??

It is in germline!

Off target effects excluded?

R5 really not needed in life? (altered West Nile Virus susceptibility .....)

Too early for oocyte or baby experiments!