



Characterization of the HIV-1 viral reservoir in subtype B early treated individuals

Tine Struyve¹, Marion Pardons¹, Liesbet Termote¹, Jozefien De Clercq¹, Laurens Lambrechts¹, Jerel Vega², Daniel Boden³, Mathias Lichterfeld⁴, Sofie Rutsaert¹, Linos Vandekerckhove¹

¹**HIV Cure Research Center**, Ghent University, Ghent, Belgium; ²Arcturus Therapeutics, Science Center Drive, 92121 San Diego, California; ³Janssen Biopharma, Johnson and Johnson, South San Francisco, USA; ⁴Ragon Institute of MGH, MIT and Harvard, Cambridge, MA, USA

16/12/2022



C O N F L I C T S O F I N T E R E S T

The Tat#1 molecule is provided by Janssen.

Introduction

- Early ART initiation limits the size of the viral reservoir, although it does not prevent viral rebound after treatment interruption

(Archin et al. Proc Natl Acad Sci USA 2012, Buzon et al. J Virol. 2014, Colby et al. Nat Med 2018, Leyre et al. Sci Trans Med 2020)

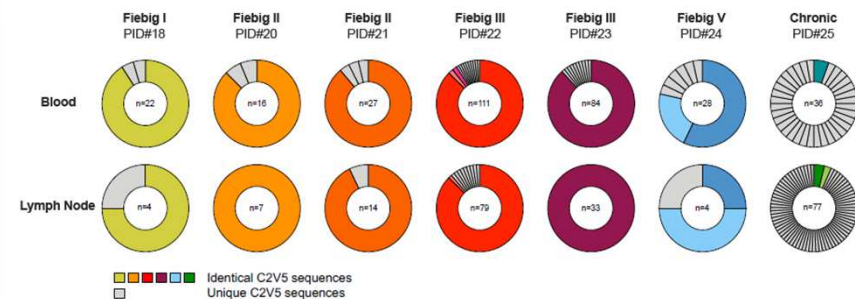
Introduction

- Early ART initiation limits the size of the viral reservoir, although it does not prevent viral rebound after treatment interruption
(Archin et al. *Proc Natl Acad Sci USA* 2012, Buzon et al. *J Virol*. 2014, Colby et al. *Nat Med* 2018, Leyre et al. *Sci Trans Med* 2020)
- Integration site analyses:
 - Clonal expansion is rare during acute infection
(Coffin et al. *JCI Insight* 2019, Wu et al. *JCI Insight* 2020, Gantner et al. *Preprint* 2022)
- Proviral genome analyses:
 - Sequence diversity is low during acute infection
(Bruner et al. *Nat Med* 2016, Lee et al. *Nat Commun* 2019, Gantner et al. *Preprint* 2022)

Table 2. Pre-ART cell-associated HIV DNA, integration sites, and clones in PBMCs from the donors put on ART shortly after infection (groups 1 and 2)

Group	Stage (PID)	HIV DNA ^a	Cells ($\times 10^4$) used for ISA	Unique integration sites	Sites with >1 breakpoint	Clones confirmed
1a	FIII (CH 83-1)	50,000	3	1,409	1	0
	FIII (CH 84-4)	1,700	1.5	176	2	0
	FIV PIT-001	14,000	1.5	149	1	0
	Average per 10 ⁴ cells	22,000		290	0.67	0
	SD FIII-IV	25,000		210	0.51	0
1b	FIV/V (CH 62-1)	18,000	4.5	709	14	9
	FV (CH 68-5)	5,600	1.5	366	1	0
	FV (CH 91-4)	4,800	4.5	416	3	1
	FV (CH 98-6)	1,900	3	179	2	2
	Average per 10 ⁴ cells	7,600		120	1.5	0.87
	SD FIV/V-V	7,100		42	1.2	0.9
2	FV (IDFJ-192)	17,000	1.5	409	3	0
	FV (JRI)	1,500	3	193	1	1
	FV/VI (AVBIO2-14)	4,300	1.5	144	0	0
	FV/VI (AVBIO2-23)	21,000	1.5	405	3	0
	FVI (AVBIO2-07)	2,100	1.5	48	0	0
	Average per 10 ⁴ cells	9,200		130	0.89	0.11
	SD	9,100		120	0.94	0.15

^aPer million cells. F, Fiebig; PID, patient identifier; ISA, integration site analysis.



Gantner et al. *Preprint* 2022

Coffin et al., *JCI Insight* 2019

Aims of the study

In early treated individuals:

- The **integration site** and **intactness** of proviral genomes remain **poorly characterized**.
- The **inducible** viral reservoir has been **understudied** due to the **lack** of **latency reversing agents** (LRA) capable of inducing **potent HIV reactivation**.

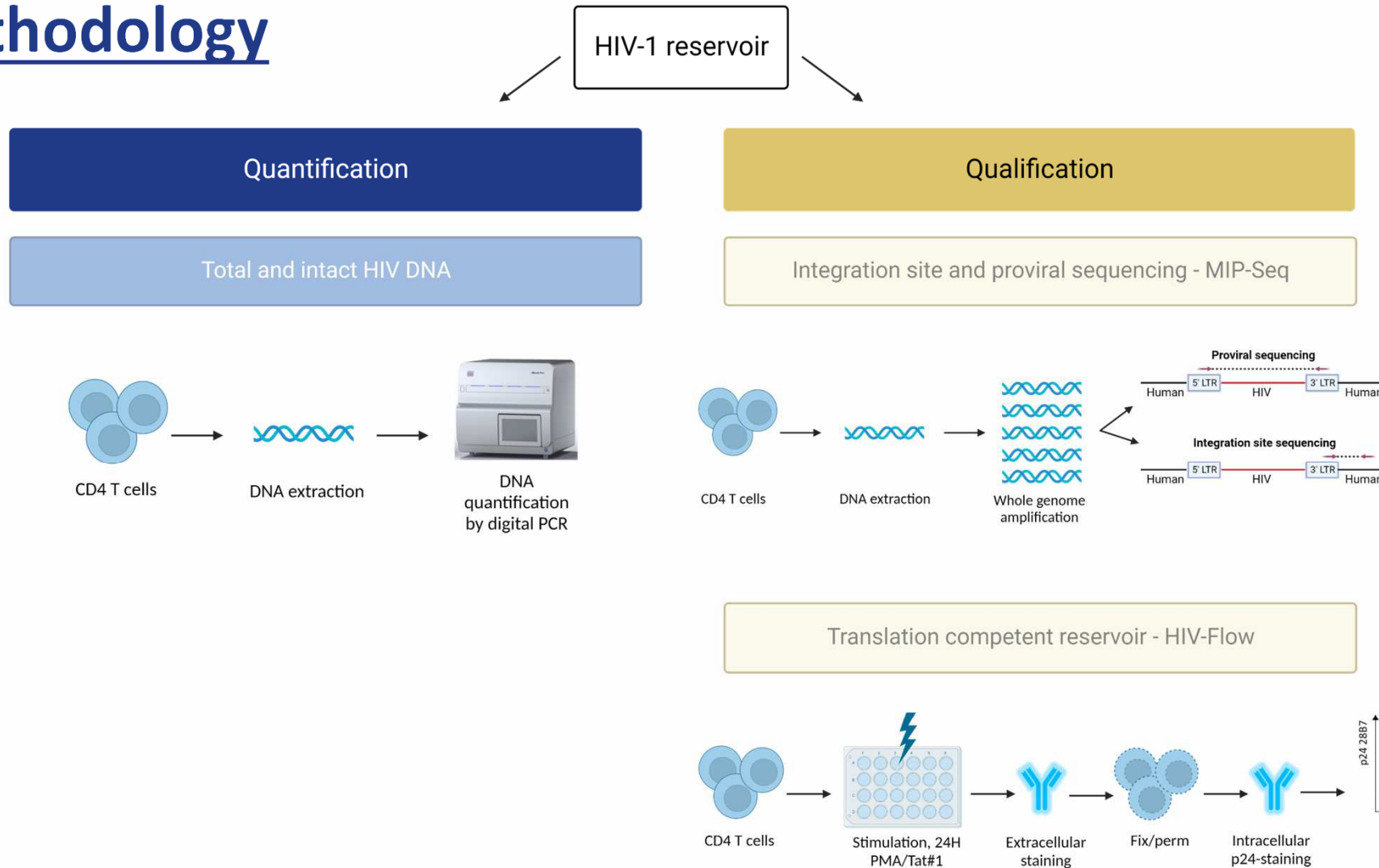
Here, we did an **in-depth assessment** of the **total** and **inducible** viral reservoir in **9 early treated individuals after 1 year of treatment**.

Clinical characteristics of the participants

ID	Age	Gender	Subtype	Fiebig	Time since infection (years)	Time to ART (days)	Time to UD VL (years)	ART duration (years)
ACS002	35	Male	B	Fiebig II-III	1,95	8	1,12	1,93
ACS005	35	Male	B	Fiebig II-III	1,62	7	1,37	1,61
ACS105	33	Male	B	Fiebig II-III	0,79	2	0,32	0,78
ACS107	39	Male	B	Fiebig V	0,97	6	0,75	0,96
ACS108	43	Male	B	Fiebig II-III	0,98	14	0,27	0,94
ACS114	43	Male	B	Fiebig IV	0,52	10	0,16	0,49
ACS404	58	Male	B	Fiebig II-III	0,40	NA	NA	NA
ACS405	46	Male	B	Fiebig II-III	0,48	NA	NA	NA
ACS408	28	Male	B	Fiebig II-III	0,32	NA	NA	NA

- All participants are men and subtype B
- Mostly Fiebig II-III
- ART duration: 0.49 - 1.93 years

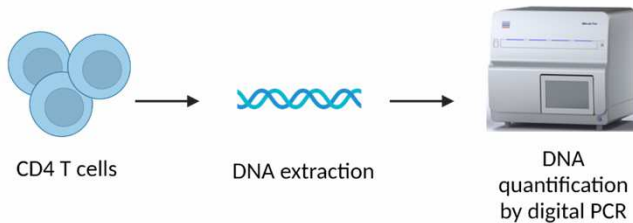
Methodology



Quantification of the viral reservoir: methodology

Quantification

Total and intact HIV DNA

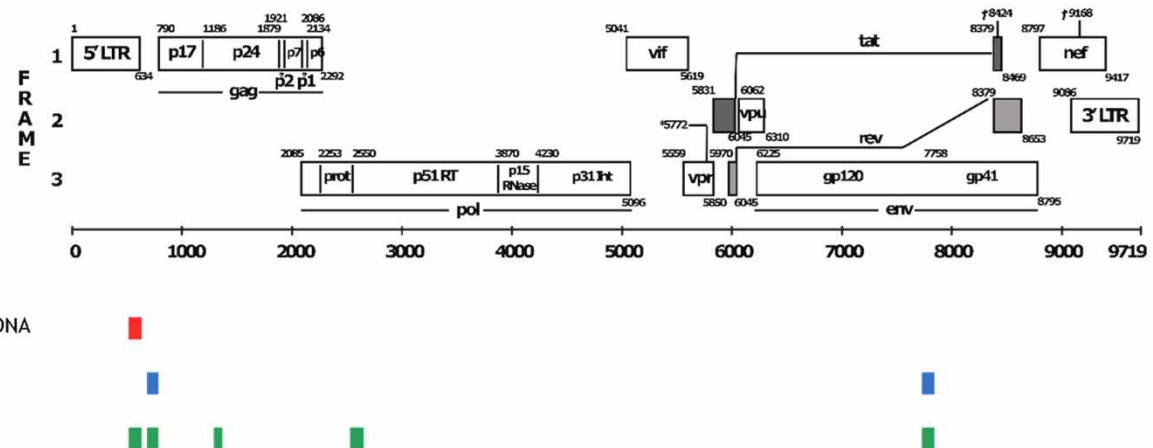


QIAcuity (Qiagen)

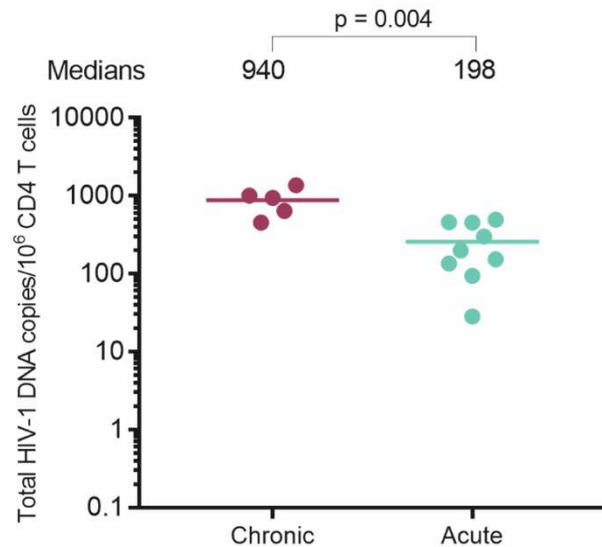
Yun 2002 - Total HIV DNA

Bruner 2019 - IPDA

Delparte - Rainbow

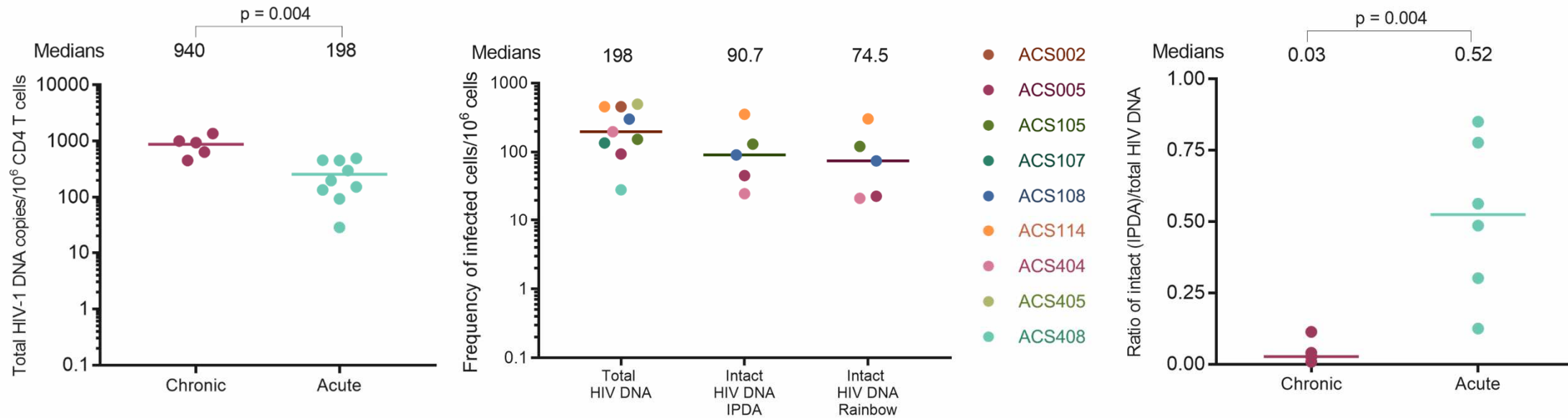


Early ART initiation limits the size of the viral reservoir



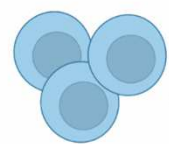
- In early treated individuals, **the frequency of total HIV-1 DNA copies per million CD4 T cells is lower** than in individuals who initiated ART in chronic infection.

Early ART initiation limits the size of the viral reservoir



- In early treated individuals, **the frequency of total HIV-1 DNA copies per million CD4 T cells is lower** than in individuals who initiated ART in chronic infection.
- Early ART initiation does not prevent the establishment of the intact viral reservoir.

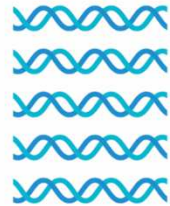
IS and proviral sequencing: methodology



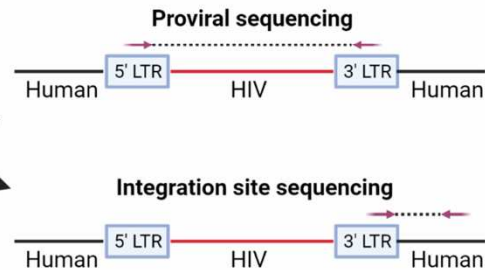
CD4 T cells



DNA extraction



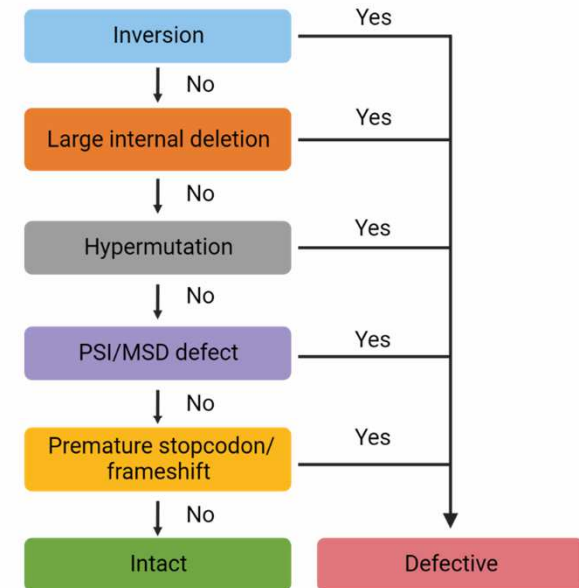
Whole genome amplification



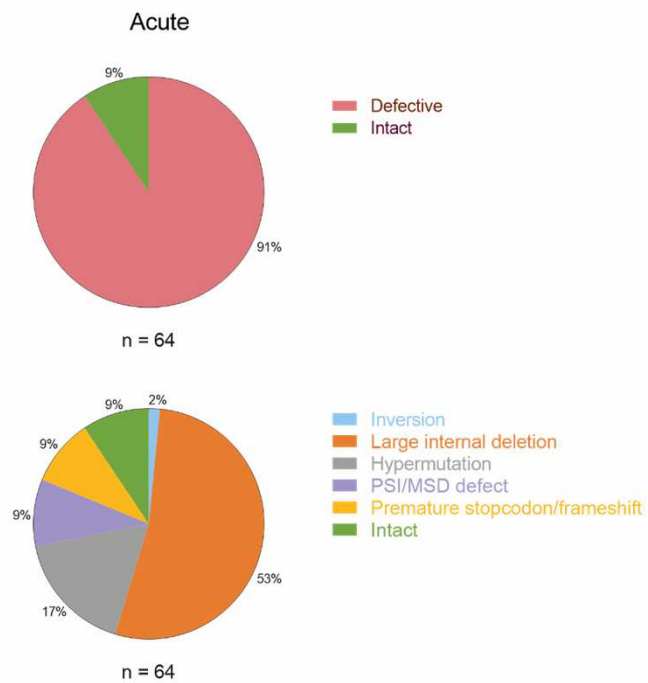
Qualification

Integration site and proviral sequencing - MIP-Seq

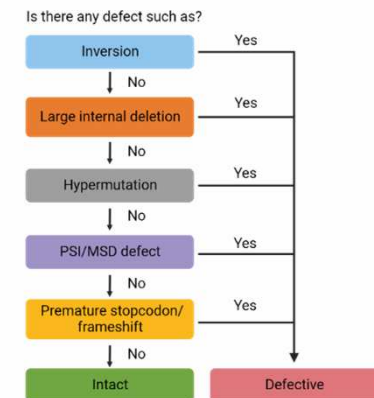
Is there any defect such as?



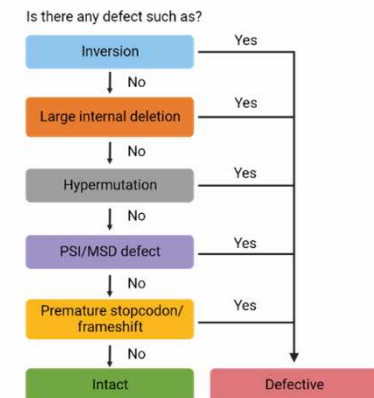
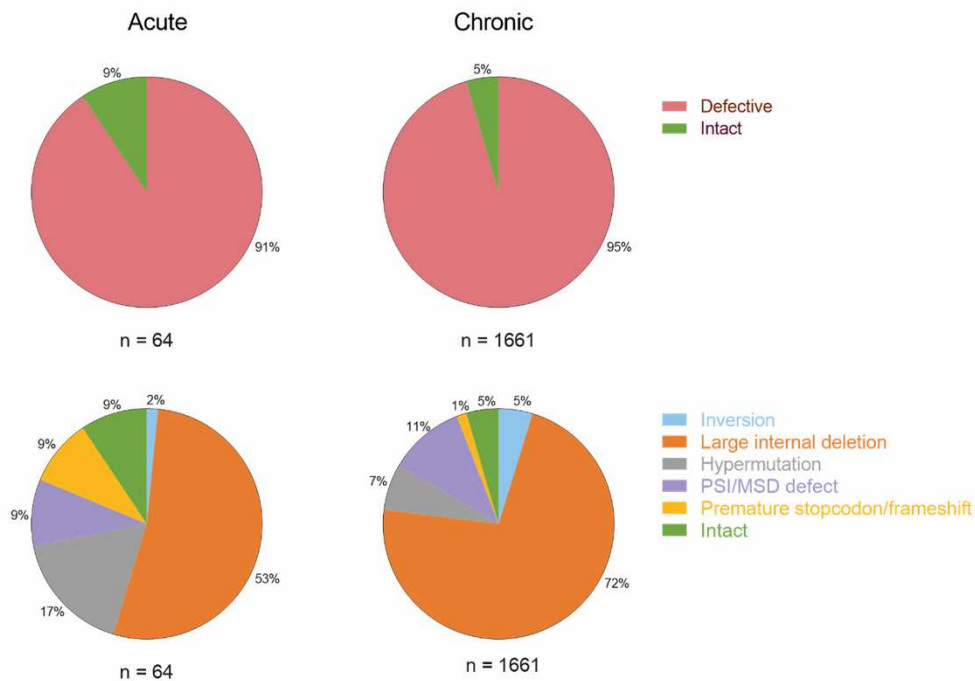
Proviral classification



- After a median of 0.96 years [0.49-1.93y] of ART, 9% of proviruses are intact.

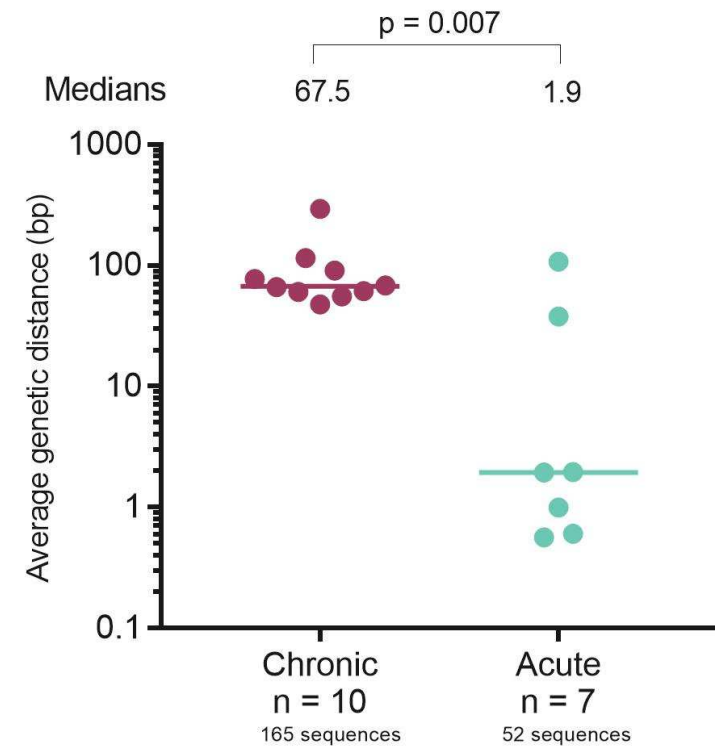
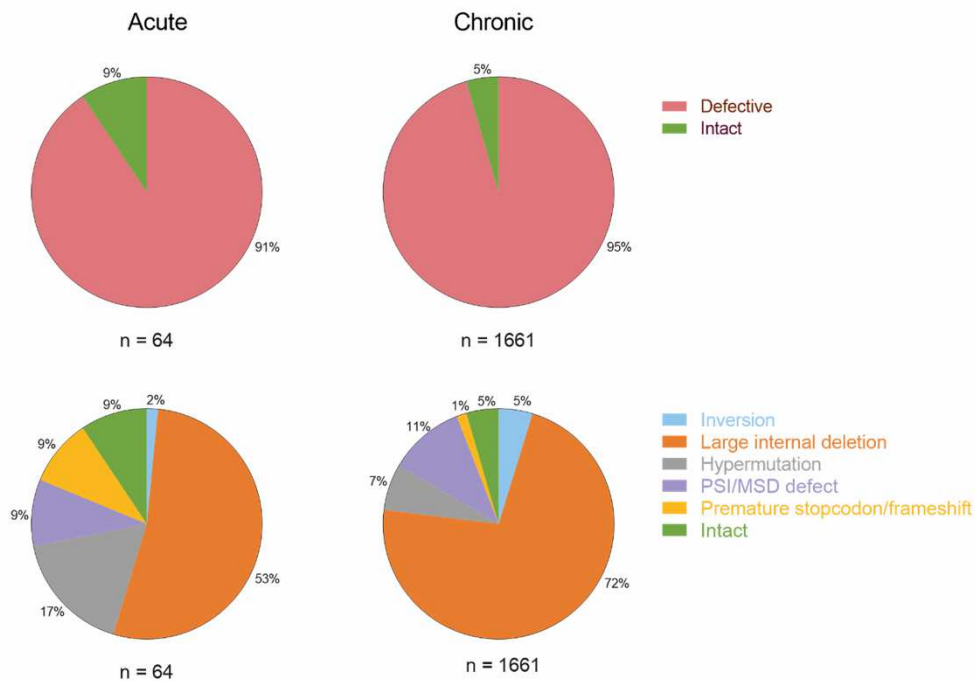


Proviral classification



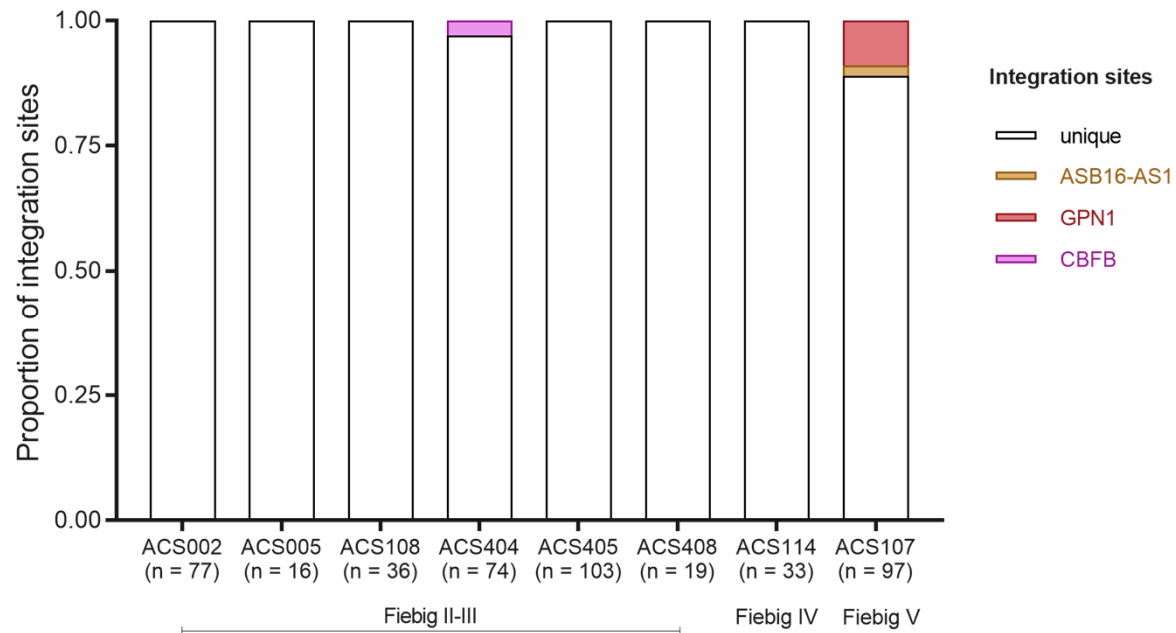
- After a median of 0.96 years [0.49-1.93y] of ART, 9% of proviruses are intact.
- Early treated individuals have a **higher fraction of intact and hypermutated proviruses**, and a **lower fraction of deleted proviruses** compared to chronically treated individuals.

Limited genetic diversity after 1 year of ART



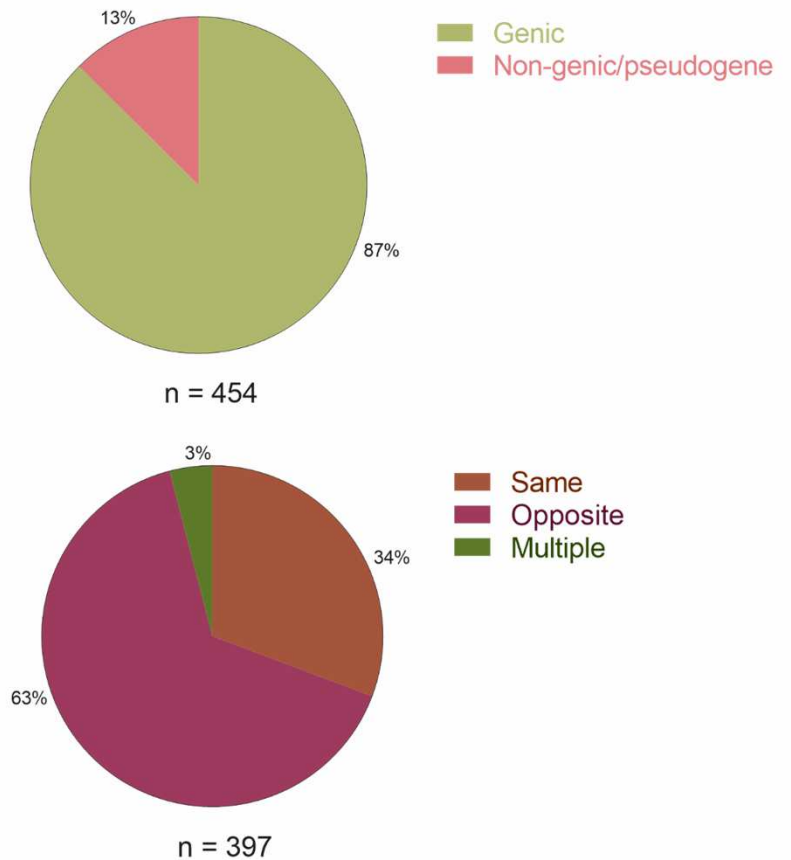
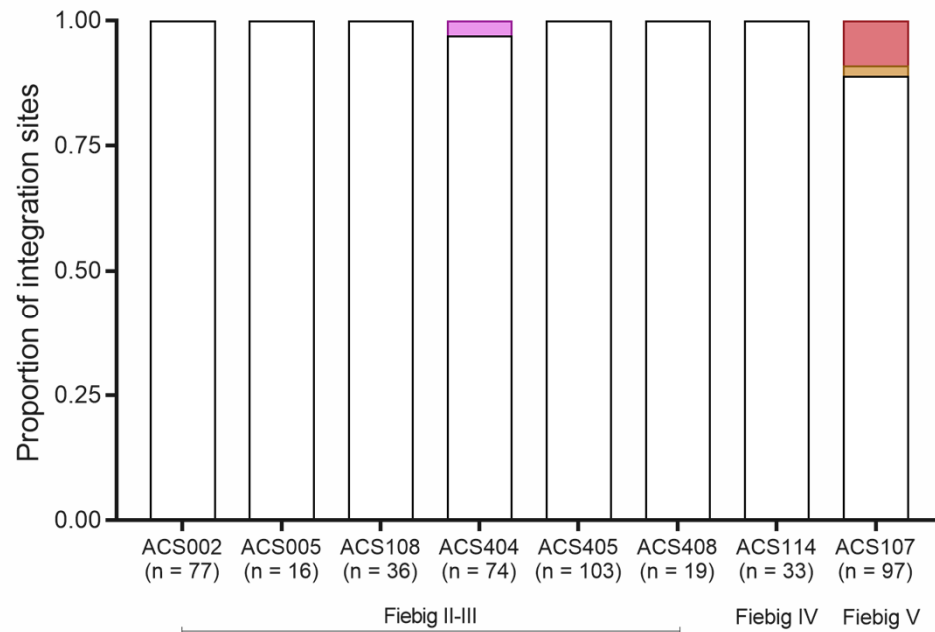
- After a median of 0.96 years [0.49-1.93y] of ART, 9% of proviruses are intact.
- Early treated individuals have a **higher fraction of intact and hypermutated proviruses**, and a **lower fraction of deleted proviruses** compared to chronically treated individuals.
- The analysis of a 4.5 kb region at the 3' end of the provirus revealed that the **intra-individual genetic diversity is limited**.

Minimal clonal expansion after 1 year of ART



- The majority of integration sites are unique (97%).
- Clonally expanded cells were retrieved in only 2 out of 8 participants and accounted for 3% of total integration sites.

Minimal clonal expansion after 1 year of ART

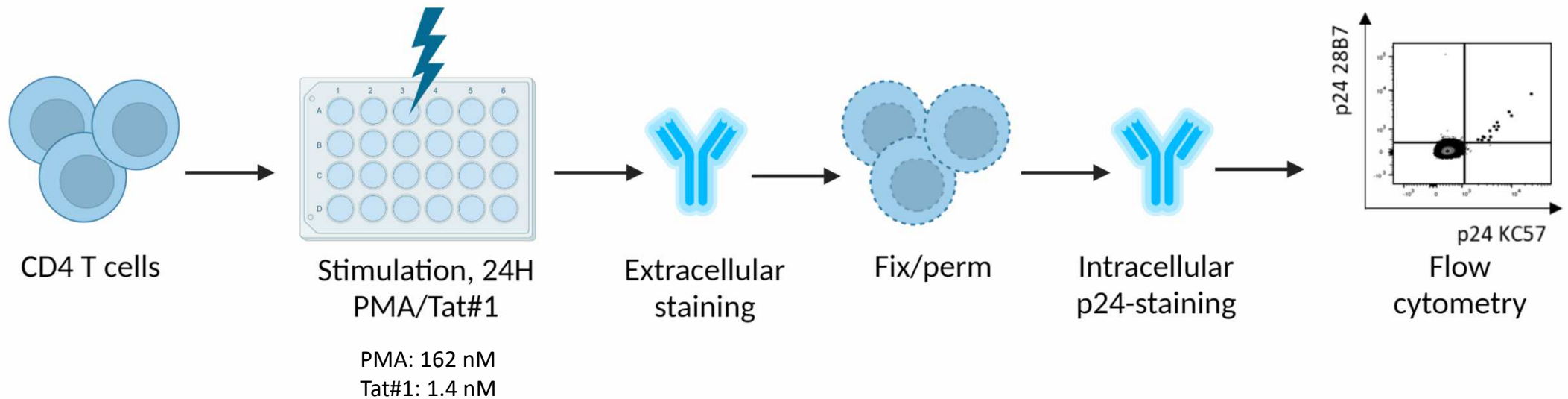


- The majority of integration sites are unique (97%).
- Clonally expanded cells were retrieved in only 2 out of 8 participants and accounted for 3% of total integration sites.
- Among proviruses integrated in genes, opposite orientation relative to the host gene was approximately twice as common as same orientation

HIV-Flow: methodology

Qualification

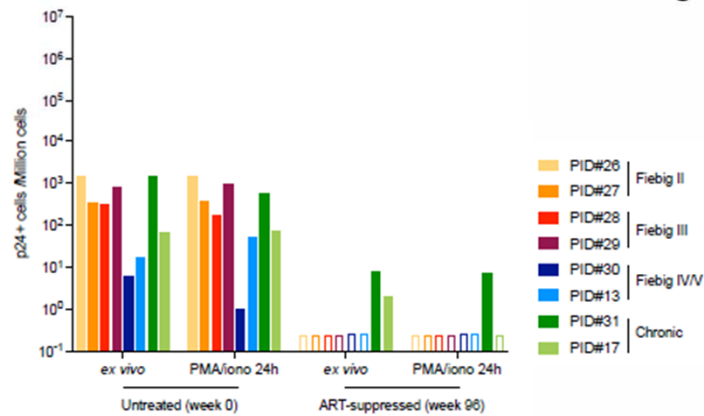
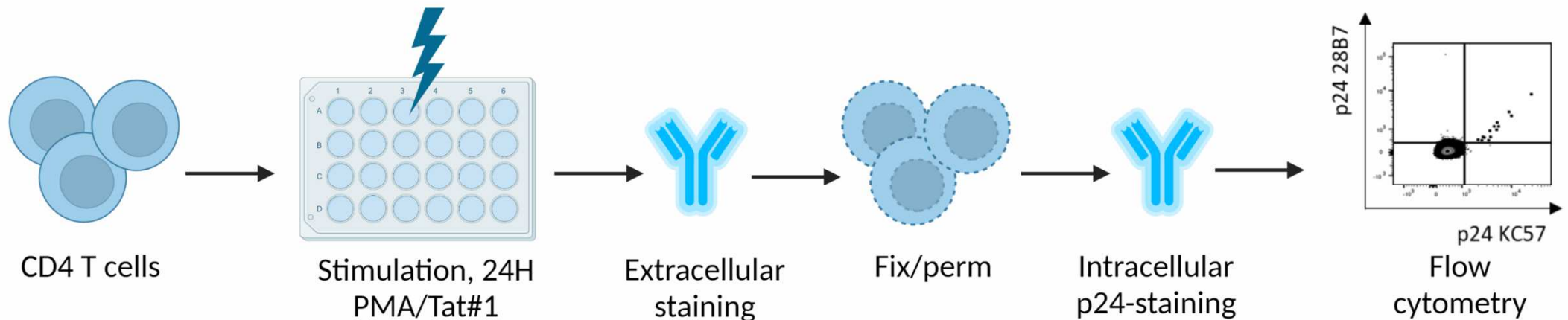
Translation competent reservoir - HIV-Flow



HIV-Flow: methodology

Qualification

Translation competent reservoir - HIV-Flow

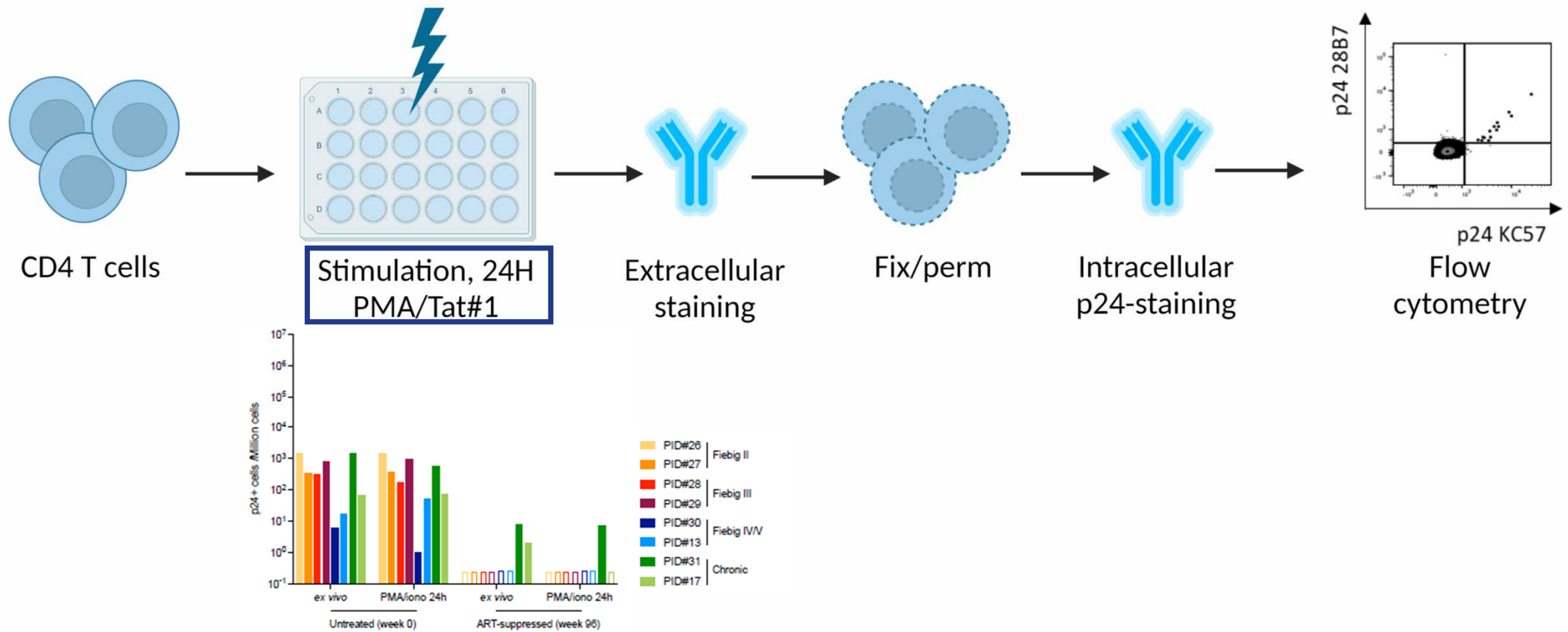


Gantner et al. Preprint 2022

HIV-Flow: methodology

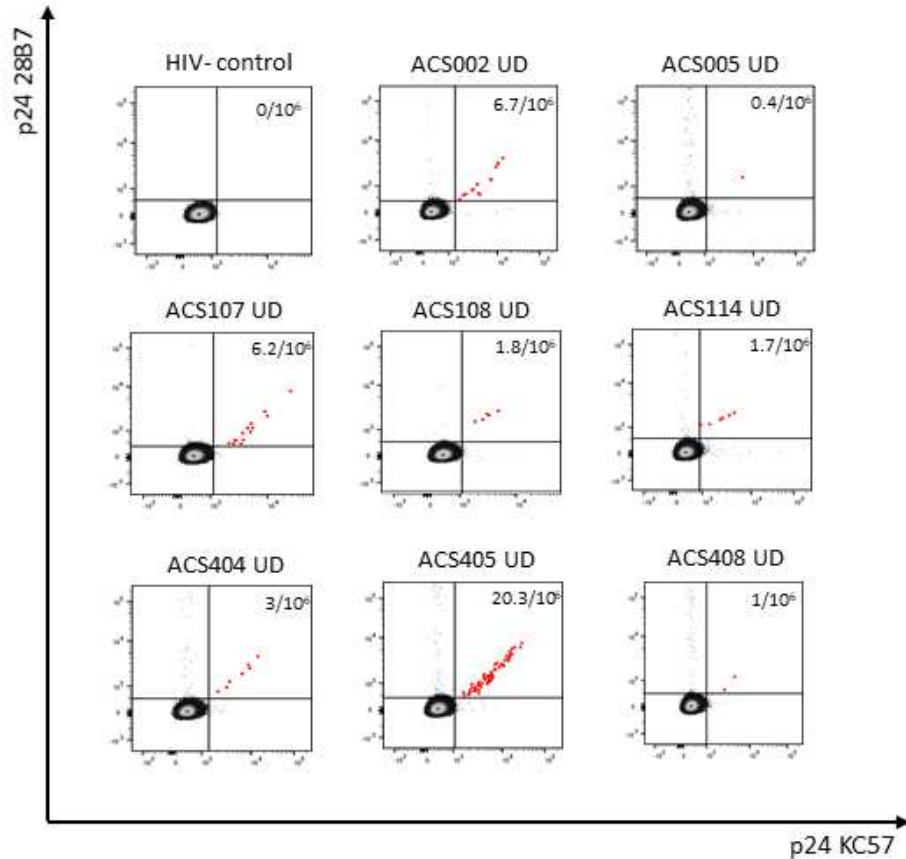
Qualification

Translation competent reservoir - HIV-Flow



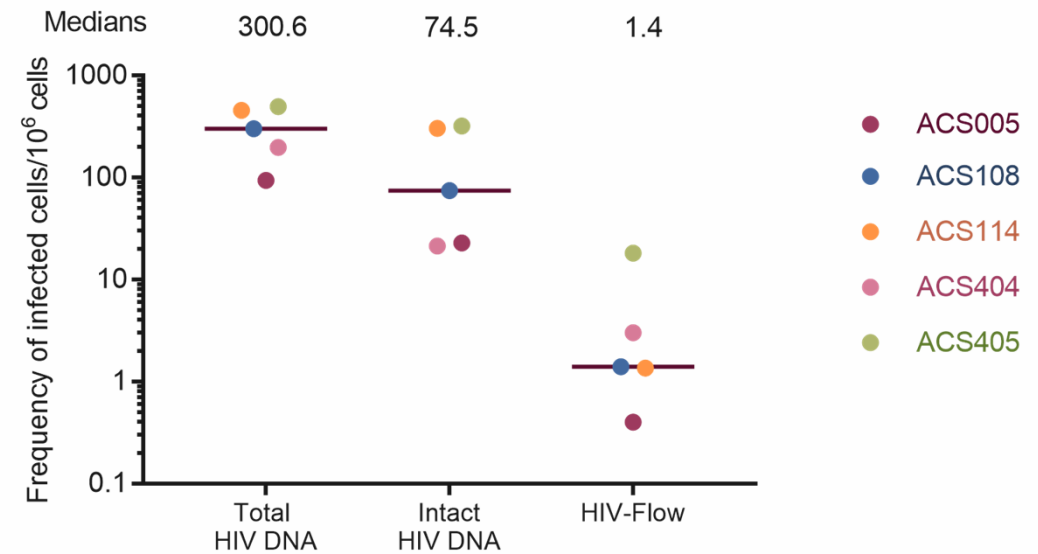
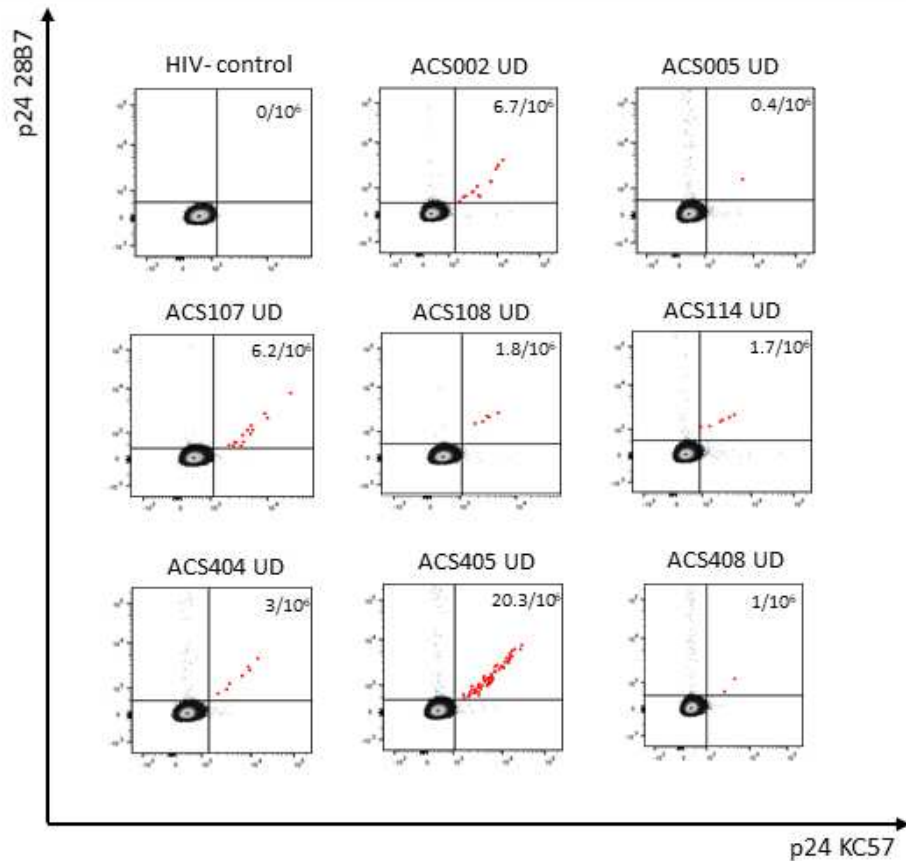
Gantner et al. Preprint 2022

Frequencies of p24+ cells



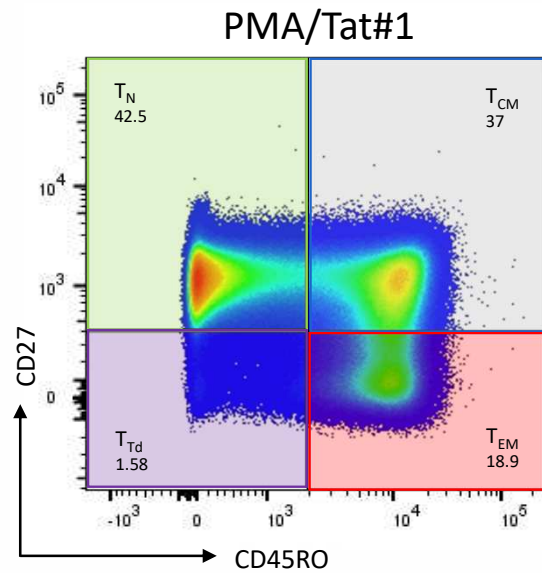
- Following PMA/Tat#1 stimulation, the frequency of p24+ cells ranges between 0.4-20 p24+ cells.

Frequencies of p24+ cells

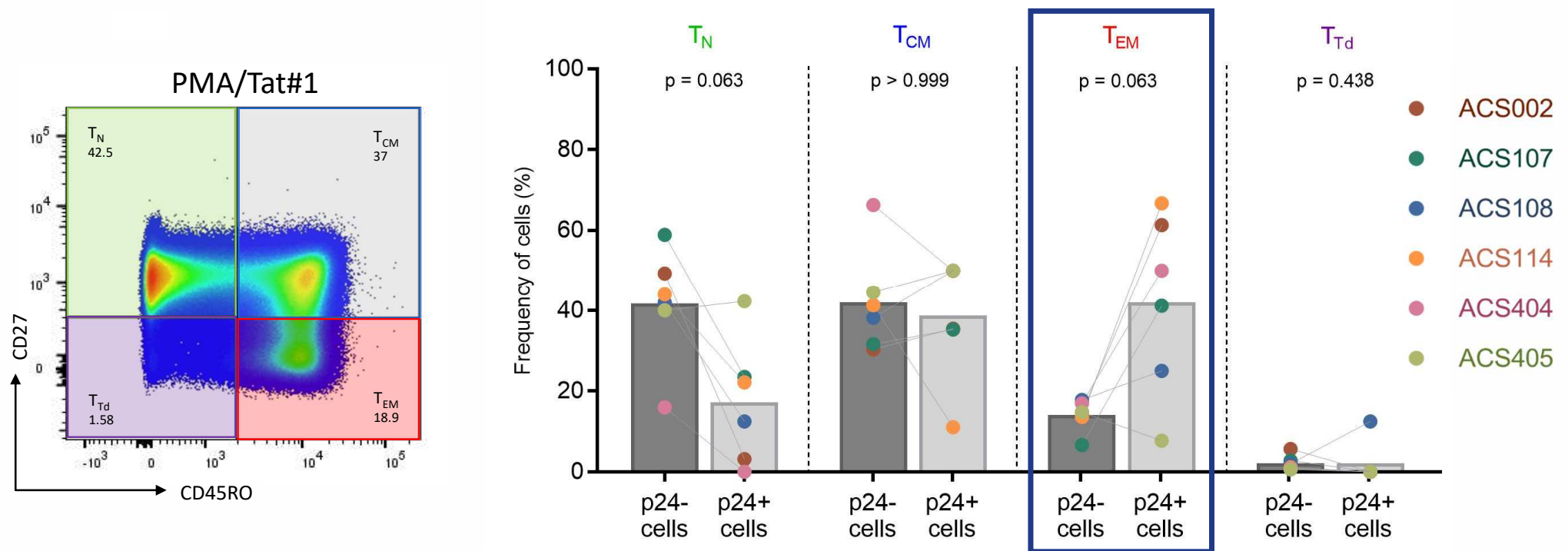


- Following PMA/Tat#1 stimulation, the frequency of p24+ cells ranges between **0.4-20 p24+ cells**.
- The median frequency of p24+ cells is lower than the frequency of cells harboring intact HIV DNA, indicating not all proviruses are inducible.

Phenotype of p24+ cells during ART

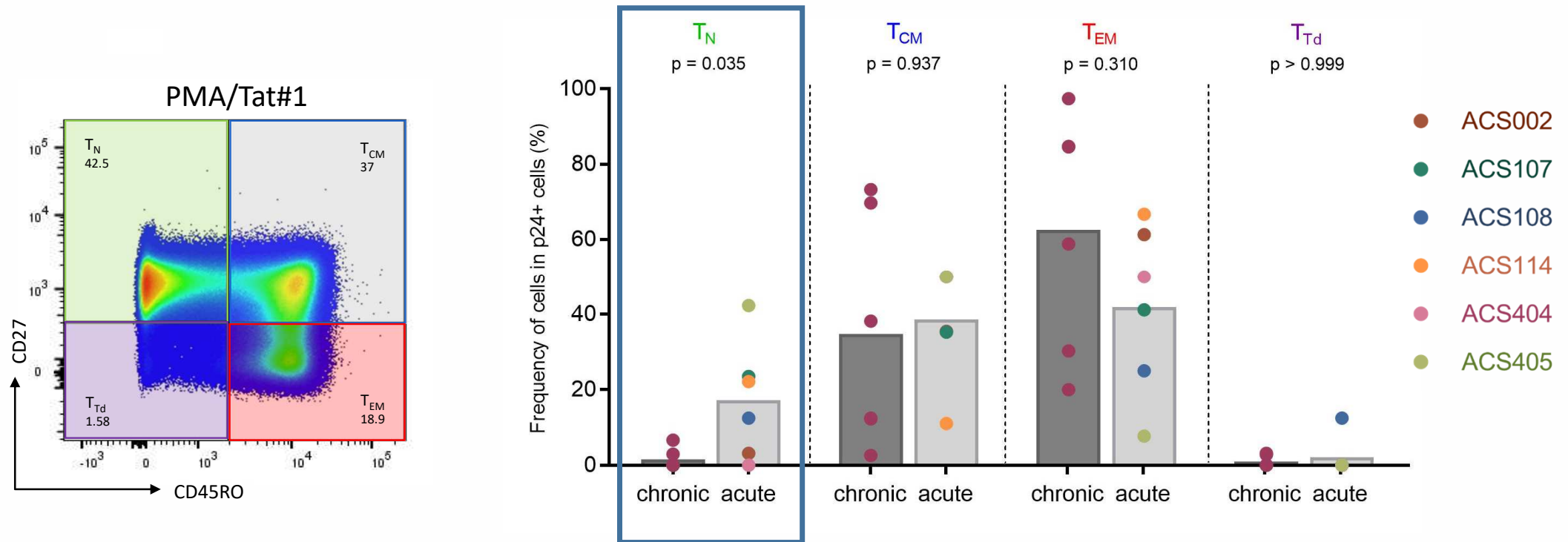


Phenotype of p24+ cells during ART



- p24+ cells reactivated by PMA/Tat#1 tend to be enriched in the **TEM** fraction

Phenotype of p24+ cells during ART



- In early treated individuals, a significantly **higher frequency of p24+ cells** resides in the **naïve T cell fraction** compared to chronically treated individuals.



COMMUNITY SUMMARY

What is the impact of early ART initiation on the viral reservoir?

- **Early ART** does **not prevent** the **establishment of the viral reservoir** (9% of viral genomes are intact).
- After a median of 0.96 years of ART, the majority of infected cells are clonotypically unique.
→ **Minimal contribution** of **clonal expansion** to persistence of the viral reservoir
- The **genetic diversity** of early treated individuals is **limited** compared to chronically treated individuals.
- **PMA/Tat#1** is a potent combination of LRA, which enables to study the **translation-competent reservoir** in early treated individuals.

What are the next steps?

- Study the translation-competent reservoir more in-depth
- How does the viral reservoir evolve over time in early treated individuals?

**HCRC**

Sofie Rutsaert
Marion Pardons
Liesbet Termote
Jozefien De Clercq
Laurens Lambrechts
Ytse Noppe
Linos Vandekerckhove

Janssen

Ellen Van Gulck
Erik Nijs
Daniel Boden

Arcturus Therapeutics

Jerel Vega
Jinho Park



HIV Cure Research Center

FACULTY OF MEDICINE
AND HEALTH SCIENCES**All the participants from the study**

Flow cytometry core from Ghent University and NXTGNT
sequencing core

National Institutes
of HealthResearch Foundation
Flanders
Opening new horizons