

#### Transcriptomic profile of gut T follicular helper cells during persistent HIV infection

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Reservoirs & Eradication Strategies Workshop

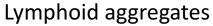
## **CONFLICTS OF INTEREST**

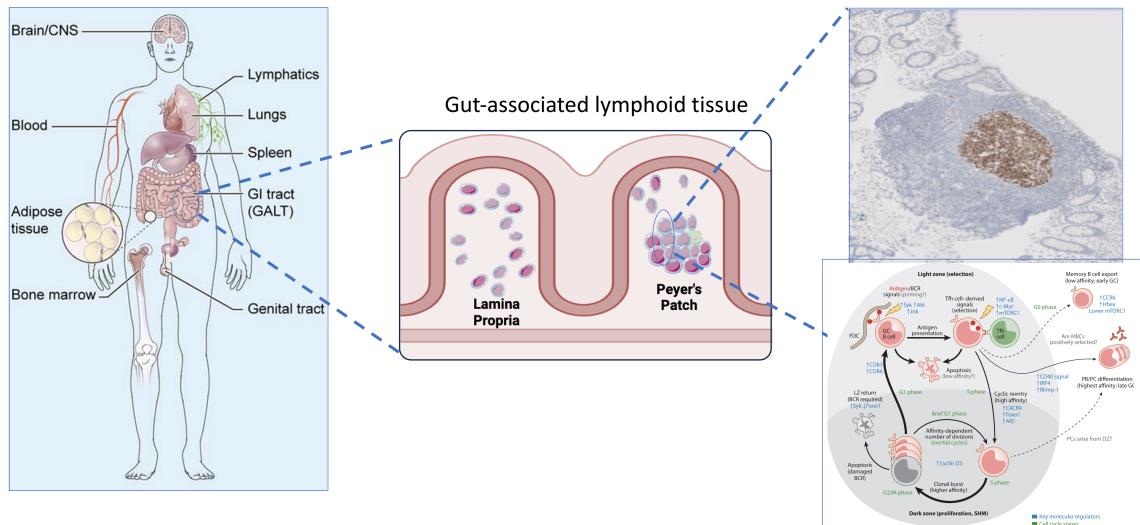
None



### Background and Aim of the Study

#### Anatomical reservoir sites

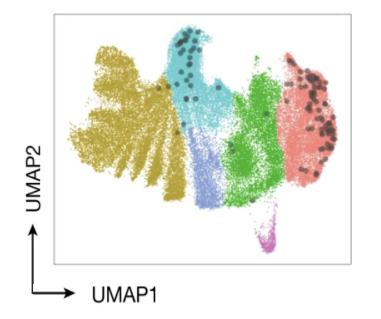


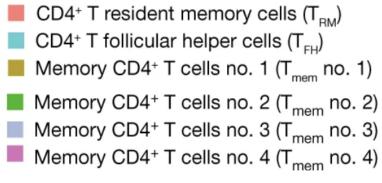


Henderson J.L et al. J Virology 2020, Breitfeld D, et al, JCI 2000. Shulman Z et al Science 2013. Estes JD. et al, Nat Med 2017. Cossarini F. et al, AIDS Res Hum Retroviruses 2023. Victora G. et al, Annu Rev Immunol. 2022

TFH cells in People with HIV:

- Highly susceptible to infection
- Relatively higher frequency compared to other CD4<sup>+</sup> T cell subsets
- Altered transcriptional profile with increased in pro-inflammatory signatures
- Represent a tissue HIV reservoir





Tenner-Racz K. et al, J Eep Med 1998. Connick E. et al, J Immunol 2007. Kohler SL et al, J Immunol. 2016. Lindqvist M et al, JCl 2012, Colineau L et al, PLoSOne 2015. Sun W et al. Nature 2023

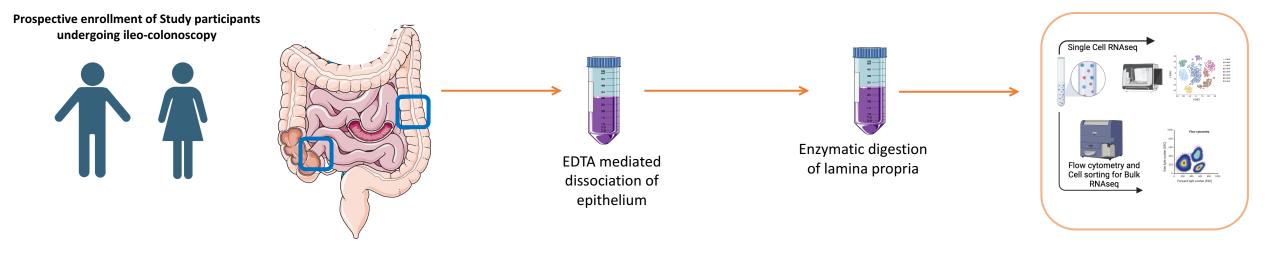


#### Aims of the study

- > Identify intestinal tissue cellular compartment where HIV can be identified at a single cell level
- Characterize the transcriptional profile of intestinal TFH cells in people with HIV with suppressed peripheral viral load
- > Characterize the signatures associated with HIV persistence in intestinal cells



### Methods: sample prep and sc-RNAseq analysis



Sc-RNAseq parameters		Seurat package analysis parameters		
Assay	10X Genomics NextGem 3'v3.1	Total UMI counts threshold	1,000	
Target cell recovery	8,000	Mitochondrial genes fraction threshold	10%	
Target depth sequencing per cell	25,000 reads	Clustering resolution	0.5	

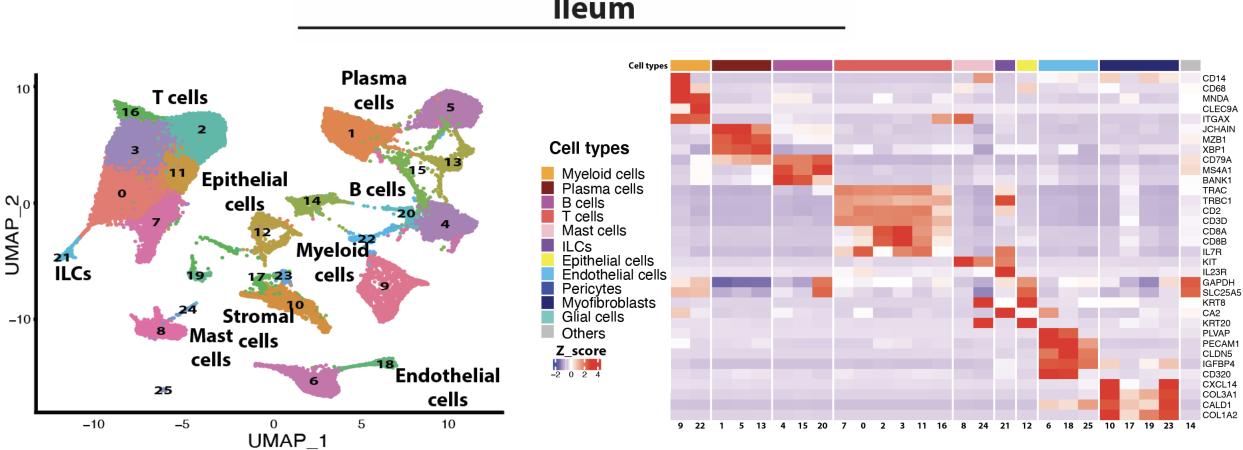


Study participants

Student t-test or Chi-square as appropriate



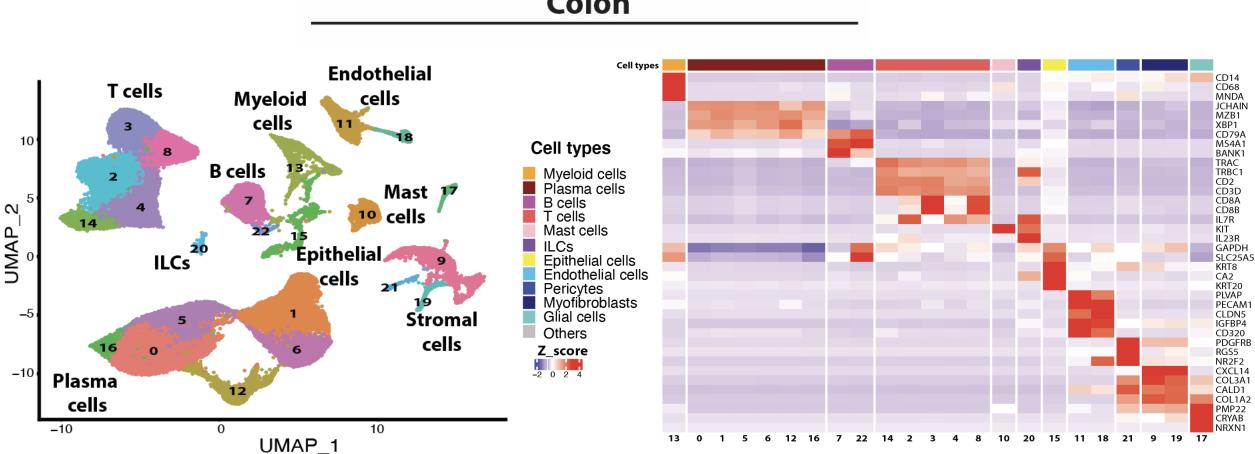
## Identification of immune and non-immune cells via sc-RNAseq



lleum

Total #cells analyzed 14,299

## Identification of immune and non-immune cells via sc-RNAseq

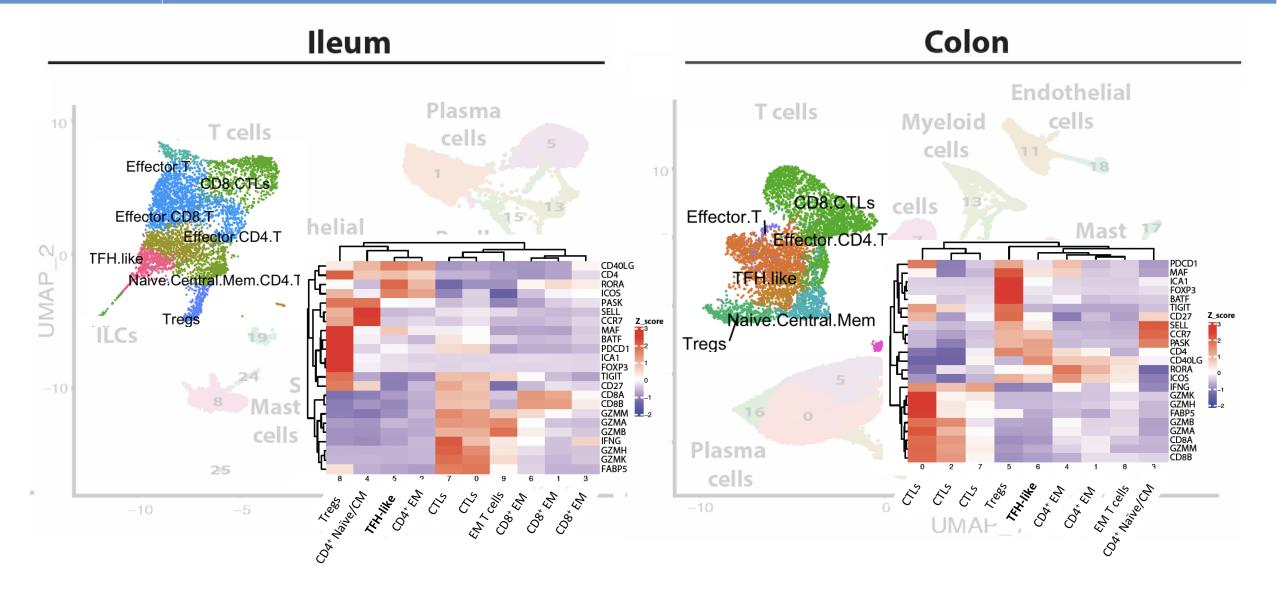


Colon

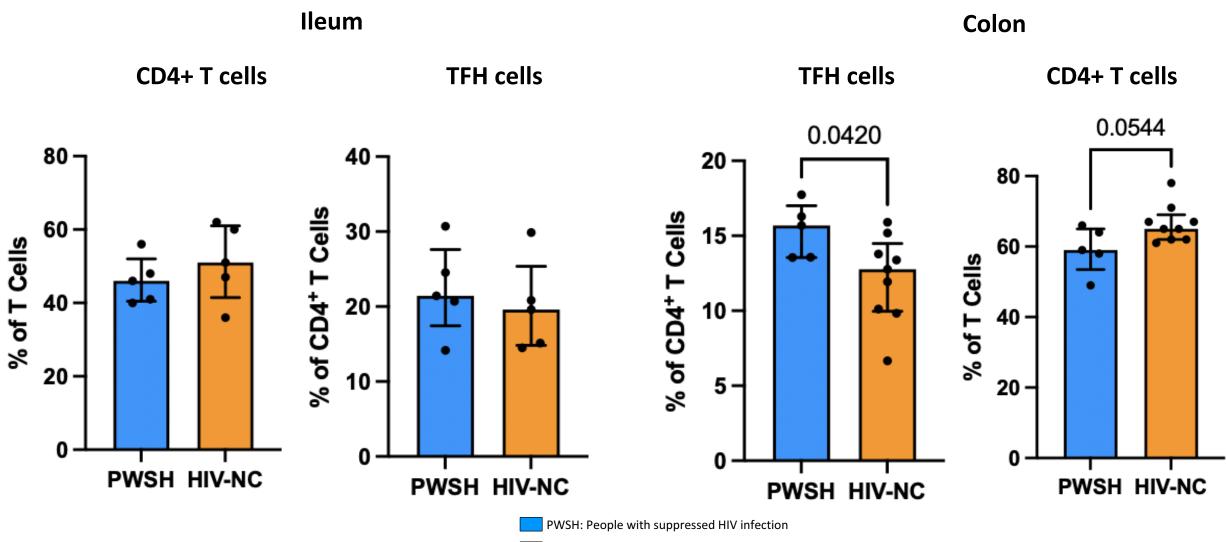
Total #cells analyzed 16,610



## Identification of T cell subsets via sc-RNAseq



## Preserved proportion of TFH cells in PWSH compared to HIV-NC



HIV-NC: HIV-negative Controls

Interferon alpha/beta signaling Signaling by FGFR4 in disease **RHO GTPases activate IOGAPs** MASTL Facilitates Mitotic Progression **Regulation of IFNA signaling** TRAF3-dependent IRF activation pathway Signaling by cytosolic FGFR1 fusion mutants Regulation of necroptotic cell death Interleukin-6 signaling CASP8 activity is inhibited Regulation by c-FLIP **Dimerization of procaspase-8** WNT5A-dependent internalization of FZD2, FZD5 and ROR2 Mitotic Telophase/Cytokinesis AMER1 mutants destabilize the destruction complex AXIN mutants destabilize the destruction complex, activating WNT signaling Establishment of Sister Chromatid Cohesion IRF3-mediated induction of type I IFN Retrograde neurotrophin signalling mean PW.Z score Endosomal/Vacuolar pathway -0.2 -0.10 0.1 0.2 Folding of actin by CCT/TriC NC PWSH

NC: HIV negative controls PWSH: People with suppressed HIV

PERSISTENCE



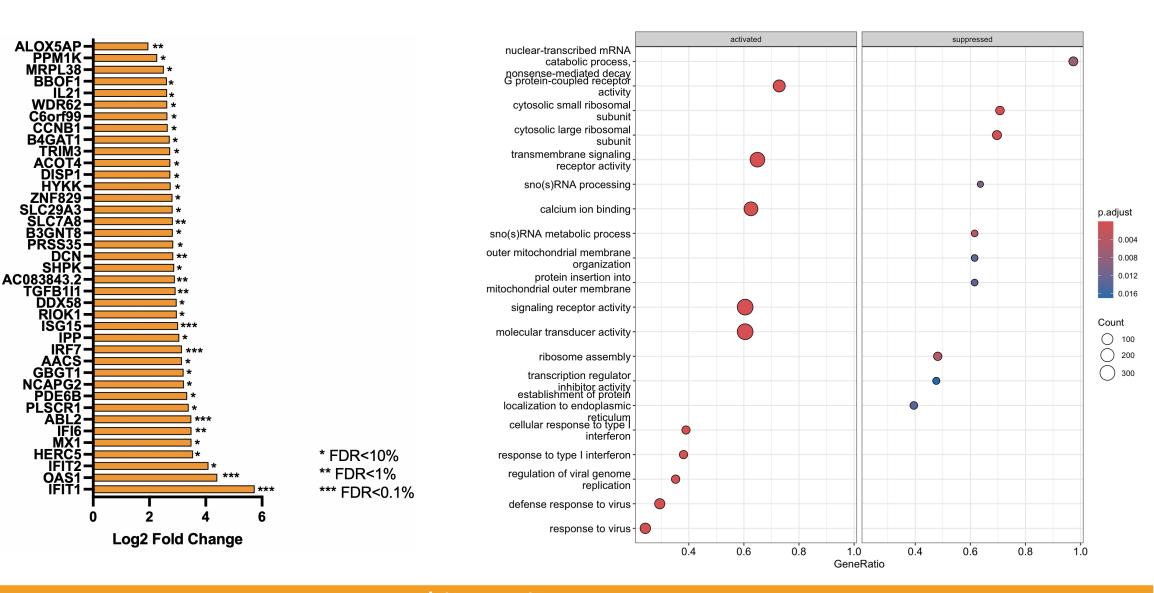
		TFH	CD4⁺ Effector Memory	Tregs	Naïve/Central Memory
lleum	HXB2+	1	2	0	0
	HXB2-	498	767	335	585

		TFH	CD4⁺ Effector Memory	Tregs	Naïve/Central Memory
Colon	HXB2+	2	2	0	0
	HXB2-	437	1394	464	574

Increase in antiviral responses and cellular signaling signatures in cells harboring HIV transcripts

PERSISTENCE

Gene identity





- Amongst intestinal CD4+ T cell subsets, HIV transcripts are primarily found in TFH cells and Effector Memory cells.
- In line with previous data from other tissues, intestinal TFH cells continue to harbor HIV transcripts during virological suppression.
- Despite not being depleted in frequency, Intestinal TFH cells in PWSH show persistently altered transcriptional profile compared to TFH cells from people without HIV.
- HIV+ cells showed upregulated signatures of antiviral response and cell-signaling compared to cells where no HIV transcripts were found.

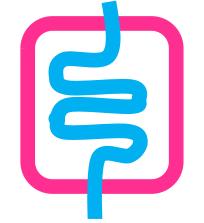
Initial landscape analysis of intestinal tissue at a single-cell level resolution offers additional insights on the characterization of the intestinal tissue reservoir

## Acknowledgements





#### **Mehandru Laboratory**



#### Mehandru Laboratory Saurabh Mehandru Divya Jha **Pablo Canales-Herrerias** Alexandra Livanos Minami Tokuyama Gustavo Martinez-Delgado Michael Tankelevich Matthew Taylor **Keshav Sharma** Louise Leyre Mathieu Uzzan

#### Genetic and Genomics Institute Francesca Petralia Azra Krek



#### ID Division

Judith Aberg Benjamin Chen Rachel Chasan Michelle Cespedes Michael Cruz Ifeoma Opkaleke

#### **HIMC: Human Immune Monitoring Center**

Travis Dowson **Darwin D'souz**a Seunghee Kim-Schulze



Funding Sources NIH



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All study participants @ Mount Sinai Hospital