# 335 HIV-2 VIRAEMIA

# HIERARCHICAL CLUSTERING SHOWS B-CELL PERTURBATIONS INDEPENDENT OF Emil Johansson<sup>1\*</sup>, Priscilla F. Kerkman<sup>2,3</sup>, Lydia Scharf<sup>4</sup>, Jacob Lindman<sup>5</sup>, Zsófia Ilona Szojka<sup>1</sup>, Fredrik Medstrand<sup>6</sup>, Hans Norrgren<sup>5</sup>, Marcus Buggert<sup>8</sup>, Annika C. Karlsson<sup>4</sup>, Mattias N.E. Forsell<sup>2,†</sup>,

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### BACKGROUND

Time to AIDS in HIV-2 infection is approximately twice as long compared to in HIV-1 infection<sup>1</sup>. Still, and despite reduced viraemia, HIV-2 infected individuals display signs of chronic immune activation<sup>2</sup>. In HIV-1 infected individuals, the expansion of hyperactivated B-cells, characterized by the expression of the transcription factor T-bet, is driven by continuous antigen exposure<sup>3</sup>. However, the contribution of viraemia to B-cell perturbations in HIV-2 infected individuals remains largely unexplored.

Here we set out to determine if B-cell hyperactivation is viraemia dependent during HIV-2 infection, as it has been described for HIV-1 infection, and if aviraemic individuals display signs of virus replication in tissue.



Figure 1. Flow cytometry and mass spectrometry-based profiling of **study participants.** Study participants were enrolled from an occupational cohort in Guinea-Bissau. B-cells were immunophenotyped using flow cytometry and blood plasma was profiled using mass-spectrometry basedproteomics. Tissue damage was assessed using differentially expressed proteins and a previously published list of tissue-enriched genes<sup>4</sup>.

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Plasma proteomic profiling

**B-cell** cluster analysis

Pseudotime trajectory analysis

### CONCLUSIONS

Aviraemic HIV-2 infected individuals display elevated frequencies of T-bethigh B-cells.

Hyperactivated T-bethigh B-cells are located at the terminal end of the pseudotime trajectory.

Aviraemic HIV-2+ individuals also display colon tissue damage, suggesting virus replication and antigen release





hierarchical cluster analysis of flow cytometry data, using the FlowSOM algorithm, identified 12 clusters of B-cells. B) Frequencies of cluster 8, containing T-bet<sup>high</sup>CD95<sup>+</sup>CD27<sup>int</sup> hyperactivated B-cells, was elevated among both viraemic and aviraemic HIV-2 infected individuals.

# hyperactivated



Figure 3. Hyperactivated T-bethigh B-cells are located at the terminal end of a pseudotime trajectory. A) UMAP plot displaying the differentiation of B-cells from transitional B-cell to hyperactivated T-bethigh B-cells along a pseudotime trajectory, created using the slingshot algorithm. B) Density plot demonstrating the enrichment of B-cells from HIV infected individuals at the terminal end of the pseudotime trajectory.

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