

# Multomics Profiling Links Galectin-9 and Interferon Signaling to Inflammation-Driven Comorbidities

**Claudio Díaz-García<sup>1\*</sup>**, Laura Martín-Pedraza<sup>1\*</sup>, Javier Martínez-Sanz<sup>1</sup>, Ana del Amo-de Palacios<sup>1</sup>, Eloisa Yuste<sup>2</sup>, Laura Luna<sup>1</sup>, Carmen Elena Gómez Rodríguez<sup>3</sup>, Sara Saiz-Baggetto<sup>1</sup>, María Fons<sup>1</sup>, María Tasia Pitarch<sup>4</sup>, Alexandre Pérez-González<sup>5</sup>, Rafael Rodríguez-Rosado<sup>6</sup>, Santiago Moreno<sup>1</sup>, Elena Moreno<sup>1\*</sup>, Sergio Serrano-Villar<sup>1\*</sup>, *on behalf of Cohort of the Spanish HIV/AIDS Research Network (CoRIS)*  
<sup>1</sup>Hospital Universitario Ramón y Cajal, IRYCIS, CIBERINFEC, Universidad de Alcalá, Madrid, Spain, <sup>2</sup>National Microbiology Center, Institute of Health Carlos III (ISCIII), CIBERINFEC, Madrid, Spain, <sup>3</sup>Centro Nacional de Biotecnología, Consejo Superior de Investigaciones Científicas, CIBERINFEC, Madrid, Spain, <sup>4</sup>Hospital Universitario y Politécnico de La Fe, Valencia, Spain, <sup>5</sup>Galicia Sur Health Research Institute (IIS Galicia Sur), SERGAS-UVIGO, Vigo, Spain, <sup>6</sup>Hospital Universitario Severo Ochoa, Madrid, Spain.

**Inflammatory and immune activation markers remain elevated** in people with HIV (PWH) despite early antiretroviral therapy (ART) and sustained viral suppression.

Although biomarkers such as IL-6, D-dimer, and CD4/CD8 ratio predict severe non-AIDS events (SNAEs), their clinical interpretation and underlying biological pathways remain **incompletely defined**.

We hypothesized that **distinct, outcome-specific inflammatory patterns during suppressive ART predict differential risks** of cardiovascular events and malignancies.

## Galectin-9 identified PWH at increased risk of SNAEs within a type I interferon-enriched inflammatory network, supporting its prioritization as a biomarker and potential therapeutic target to mitigate persistent immune activation under ART

Participants were predominantly middle-aged (mean 46.5 years) with similar baseline characteristics at baseline and a median follow-up of 63 months (IQR 42–82) in cases and 94 months (IQR 62–133) in controls.

**Author contact information**  
 claudio.diaz@salud.madrid.org  
 sergio.serrano@salud.madrid.org

Follow us!  
 @einlabryc

**Acknowledgements**

We would like to thank all the participants in this study, and the support and collaboration of the Infectious Diseases team of the Hospital Ramón y Cajal.

**Funding**

This study was funded by MSD (Investigator Studies Program 101305) and Gilead Sciences (CO-ES-985- 6728).

**Cohort of the Spanish AIDS Resarch Network (CORIS)**  
 N = 18,573 PWH

**Nested case-control study**  
 on ART, virologically suppressed, follow-up > 2 years

**Cases/controls - 1:1 matching by propensity score**  
 age, sex, risk factor for HIV transmission, AIDS history, level of education, country of origin, smoking, CD4/CD8 ratio at year 2, ART regimen, total cholesterol, HDL cholesterol

**89 cases and 89 controls**  
 Primary outcome: 1) nonaccidental death (n = 22) or 2) severe cardiovascular event (n = 28) or 3) non-AIDS cancers (n = 61) from year 2 through year 10

**Proximity Extension Assay (Olink Proteomics) on plasma RNA-seq from PBMC**  
 Outcomes through **year 10** since ART initiation  
 Samples obtained from patients **on ART for 24 ± 6 months**

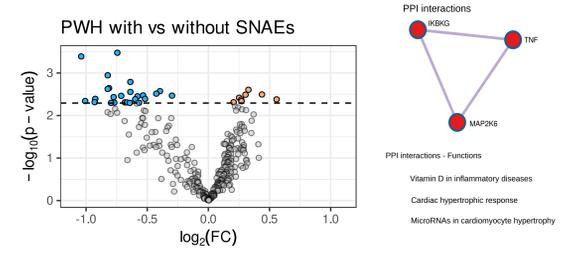
Proteomic assay of 368 inflammatory proteins

Transcriptomic analysis

Data integration

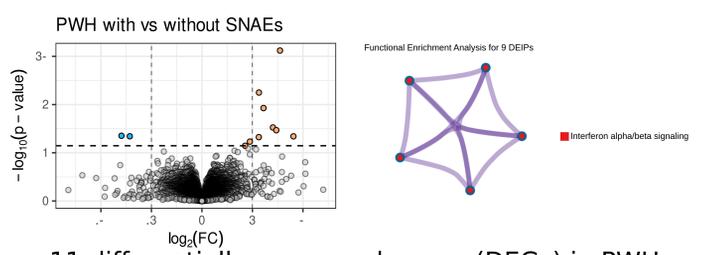
ELISA validation of 4 targets

**1) Proteomic screening identifies inflammatory signatures associated with SNAEs and mortality**



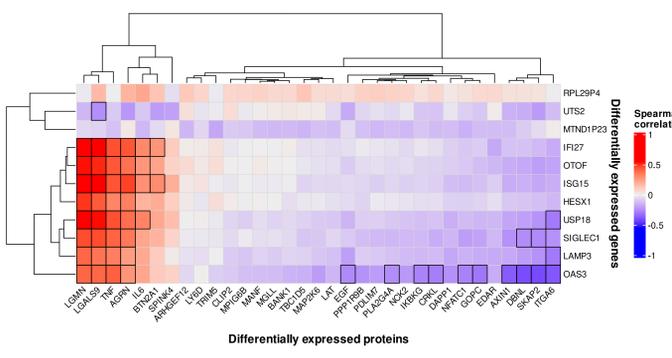
- 33 differentially expressed proteins (DEPs) in PWH with vs without SNAEs
- 52 DEPs in PWH with vs without neoplasia
- 7 DEPs in PWH with vs without mortality

**2) Transcriptomic profiling revealed a shared type I interferon signature associated with SNAEs and mortality**



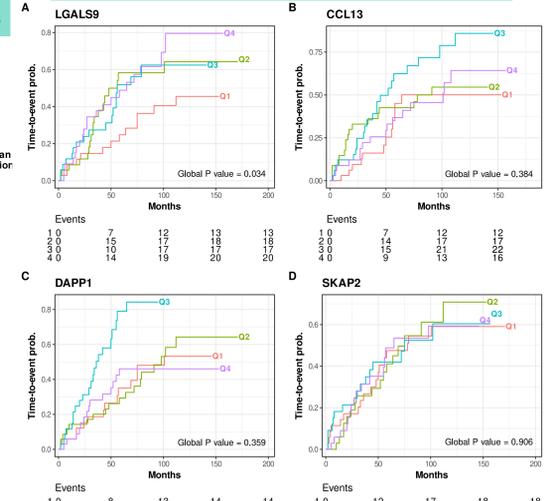
- 11 differentially expressed genes (DEGs) in PWH with vs without SNAEs
- 15 DEGs in PWH with vs without neoplasia
- 32 DEGs in PWH with vs without CV events
- 10 DEGs in PWH with vs without mortality

**3) Cross-omic correlations between differentially expressed genes and proteins**



Higher levels of inflammatory proteins including LGMN, LGALS9, TNF, AGRN, IL6, and BTN2A1 showed positive correlations with interferon-stimulated genes such as IFI27, OTOF, ISG15, HESX1, USP18, SIGLEC1, LAMP3, and OAS3.

**4) Predictive ability of selected inflammatory proteins**



Higher LGALS9 levels were associated with increased SNAEs risk over the full follow-up (HR per quantile increase = 1.25, 95% CI 1.02 - 1.54; p = 0.034).

Unlike conventional biomarker studies immediately preceding clinical events, we identified an **early inflammatory signature during suppressive ART associated with subsequent SNAEs**.

This signature supports a coherent **interferon-galectin-9 axis linked to adverse outcomes**, while revealing substantial biological heterogeneity across non-AIDS complications and arguing against a one-size-fits-all model of residual risk.

**Further research** is needed to:

- Determine whether interferon signalling or the galectin-9/Tim-3 pathway represents a modifiable driver of risk or a stable correlate of immune dysfunction.
- Refine predictive strategies to identify individuals who may benefit from targeted monitoring and preventive interventions.

**PLAIN LANGUAGE SUMMARY**

In people whose HIV is successfully treated, hidden immune system activity may still predict future illness or death. A molecule called galectin-9 stood out as a reliable warning signal in the blood.