

What to learn from deep immunological monitoring in phase I/II vaccine trials?

Rodolphe Thiébaud
for the Vaccine Research Institute

INSERM U897, INRIA SISTM, Bordeaux University



VACCINE
RESEARCH
INSTITUTE



Inserm

Institut national
de la santé et de la recherche médicale

université
de **BORDEAUX**

Systems biology



Systems Biology Has its Backers and Attackers

D.F. Dowd Though coined 40 years ago, a lot of people still ask, "What's that?" when the term systems biology comes up. The Scientist - October 6, 2003

Systems Vaccinology

Bali Pulendran,^{1,2,*} Shuzhao Li,¹ and Helder I. Nakaya¹

¹Emory Vaccine Center, Yerkes National Primate Research Center, 954 Gatewood Road, Atlanta, GA 30329, USA

²Department of Pathology, Emory University School of Medicine, Atlanta, GA, USA

*Correspondence: bpulend@emory.edu

DOI [10.1016/j.immuni.2010.10.006](https://doi.org/10.1016/j.immuni.2010.10.006)

516 Immunity 33, October 29, 2010

Objectives

- To address the mechanisms that control immune responses to vaccination
- To identify predictors of vaccine efficacy

Methods

- Using all available information
- Potentially leading to specific experimentations

Systems biology approach predicts immunogenicity of the yellow fever vaccine in humans

Troy D Querec^{1,8}, Rama S Akondy^{1,8}, Eva K Lee², Weiping Cao¹, Helder I Nakaya¹, Dirk Teuwen³, Ali Pirani⁴, Kim Gernert⁴, Jiusheng Deng¹, Bruz Marzolf⁵, Kathleen Kennedy⁵, Haiyan Wu⁵, Soumaya Bennouna¹, Herold Oluoch¹, Joseph Miller¹, Ricardo Z Vencio⁵, Mark Mulligan^{1,6}, Alan Aderem⁵, Rafi Ahmed¹ & Bali Pulendran^{1,7}

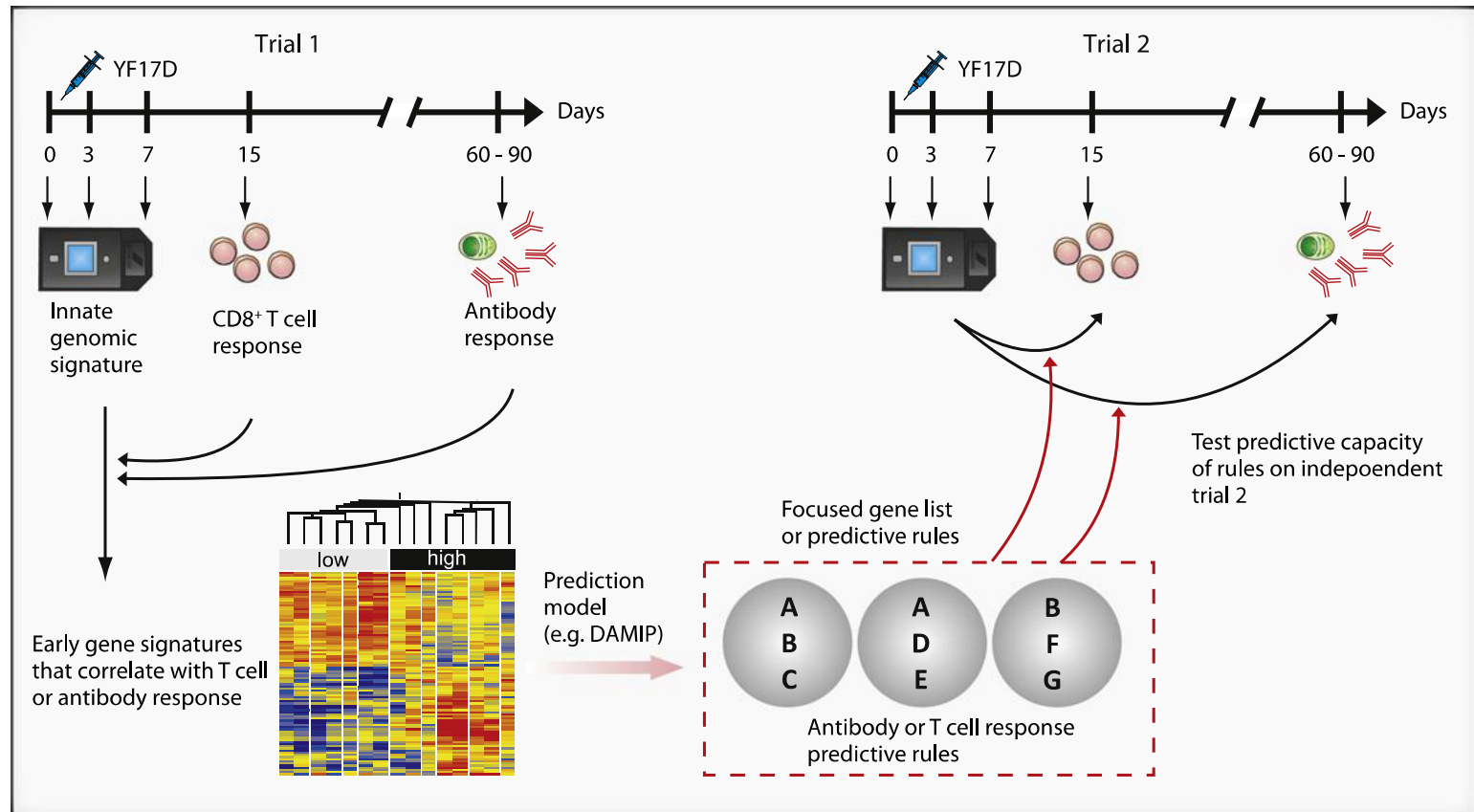
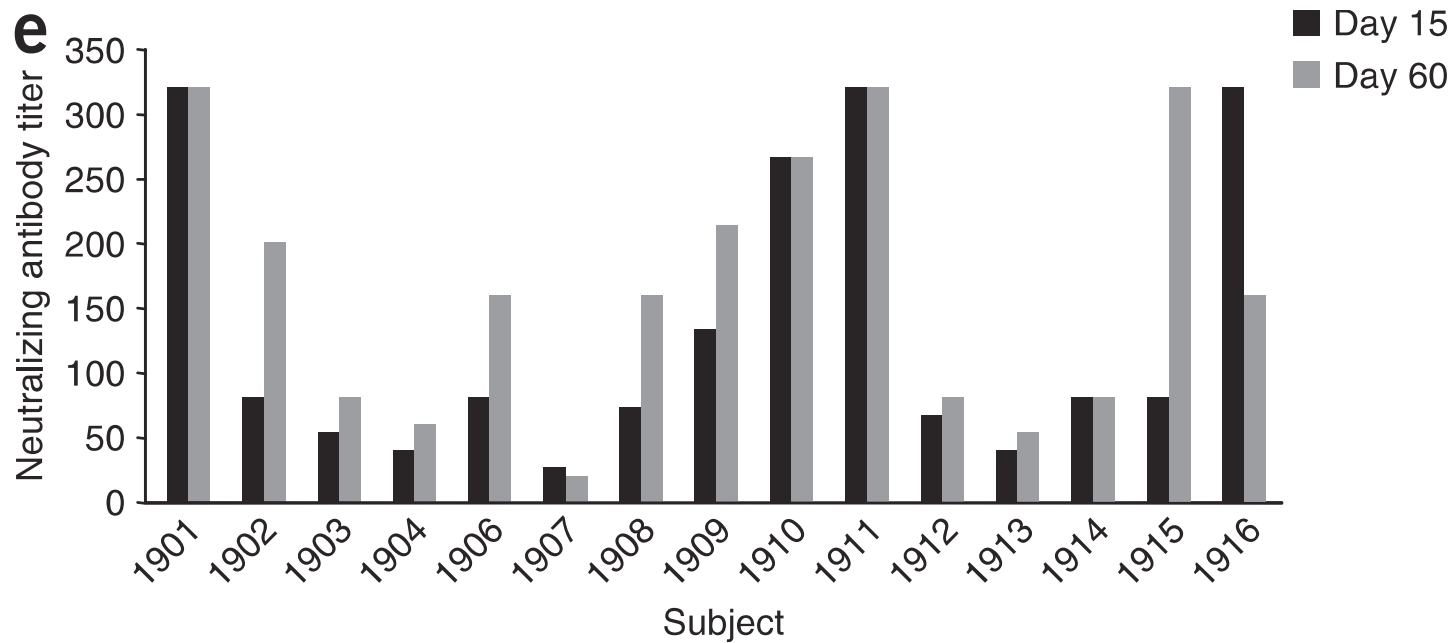
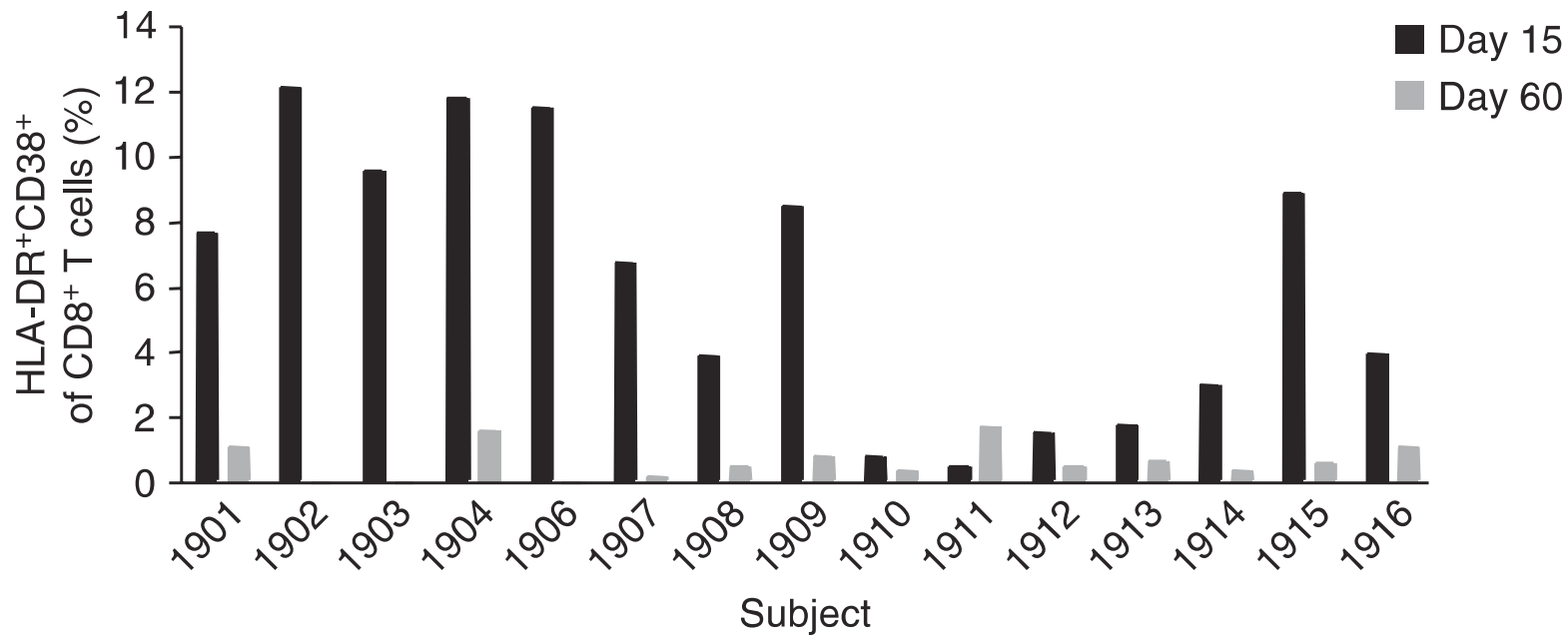


Figure 1. Using Systems Biology to Predict the Immunogenicity of the YF-17D Vaccine

Schematic representation of the systems biology approach used to predict the T and B cell responses of YF-17D vaccinees (Querec et al., 2009). Healthy humans vaccinated with YF-17D are bled at the indicated time points and the innate and adaptive responses studied. Innate signatures obtained with microarrays are found to correlate with the later adaptive immune responses. The predictive power of such signatures is tested in an independent trial (trial 2).



Gene signatures

CD8 T cell response

Neutralizing antibody response

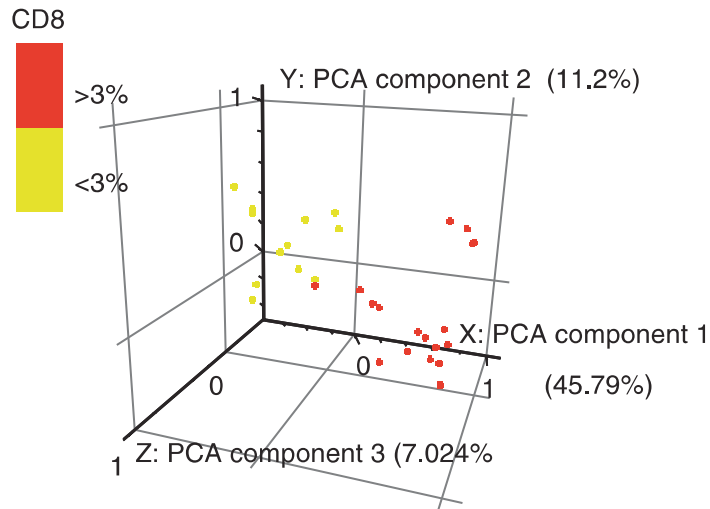


Table 5 RT-PCR validation of genes in the DAMIP models for signatures that predict neutralizing antibody titers

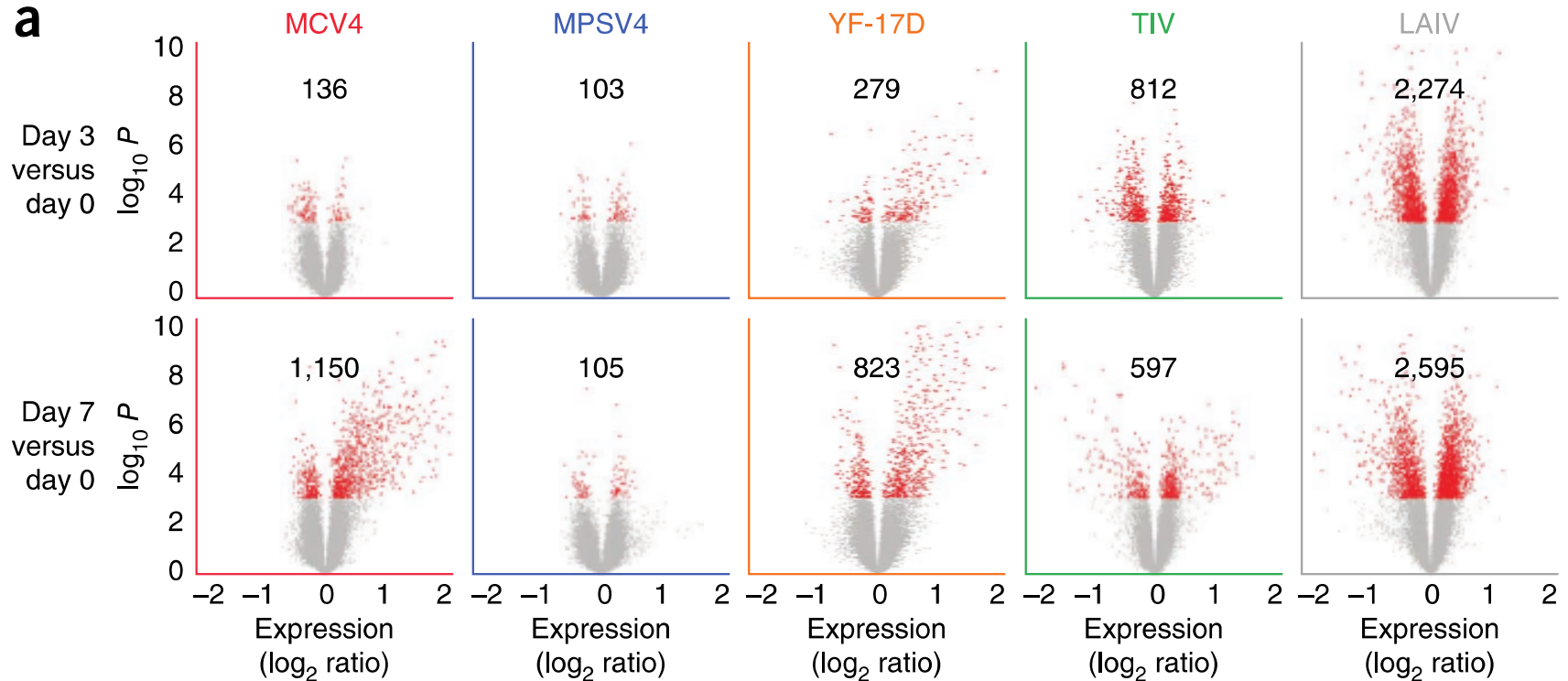
Symbol	UniGene	Day	Pearson r	P -value
<i>BEND4</i>	Hs.120591	7	0.764	0.00002
<i>KBTD7</i>	Hs.63841	7	0.543	0.02510
<i>TNFRSF17</i>	Hs.2556	7	0.784	0.000001
<i>TPD52</i>	Hs.368433	7	0.530	0.00667

Complement protein C1qB
and eukaryotic translation
initiation factor 2 alpha
kinase 4

TNFRSF17 (which encodes the receptor for the B cell growth factor BAFF) is highly predictive of the later antibody response

Molecular signatures of antibody responses derived from a systems biology study of five human vaccines

Shuzhao Li^{1,2,10}, Nadine Rouphael^{1,3,10}, Sai Duraisingham^{1,2,10}, Sandra Romero-Steiner⁴, Scott Presnell^{5,6}, Carl Davis^{1,7}, Daniel S Schmidt⁴, Scott E Johnson⁴, Andrea Milton⁴, Gowrisankar Rajam⁴, Sudhir Kasturi^{1,2}, George M Carlone⁴, Charlie Quinn^{5,6}, Damien Chaussabel^{5,6}, A Karolina Palucka⁶, Mark J Mulligan^{1,3,7}, Rafi Ahmed^{1,8}, David S Stephens^{1,7}, Helder I Nakaya^{1,2,9} & Bali Pulendran^{1,2,9}



Geneset approach

- Geneset analysis*: analysing change of gene expression of functional groups of genes defined with prior biological knowledge
 - Single-gene analysis may miss important effects on pathways
- Chaussabel's modules** : 260 groups of genes defined
- Blood transcription modules (BTM)

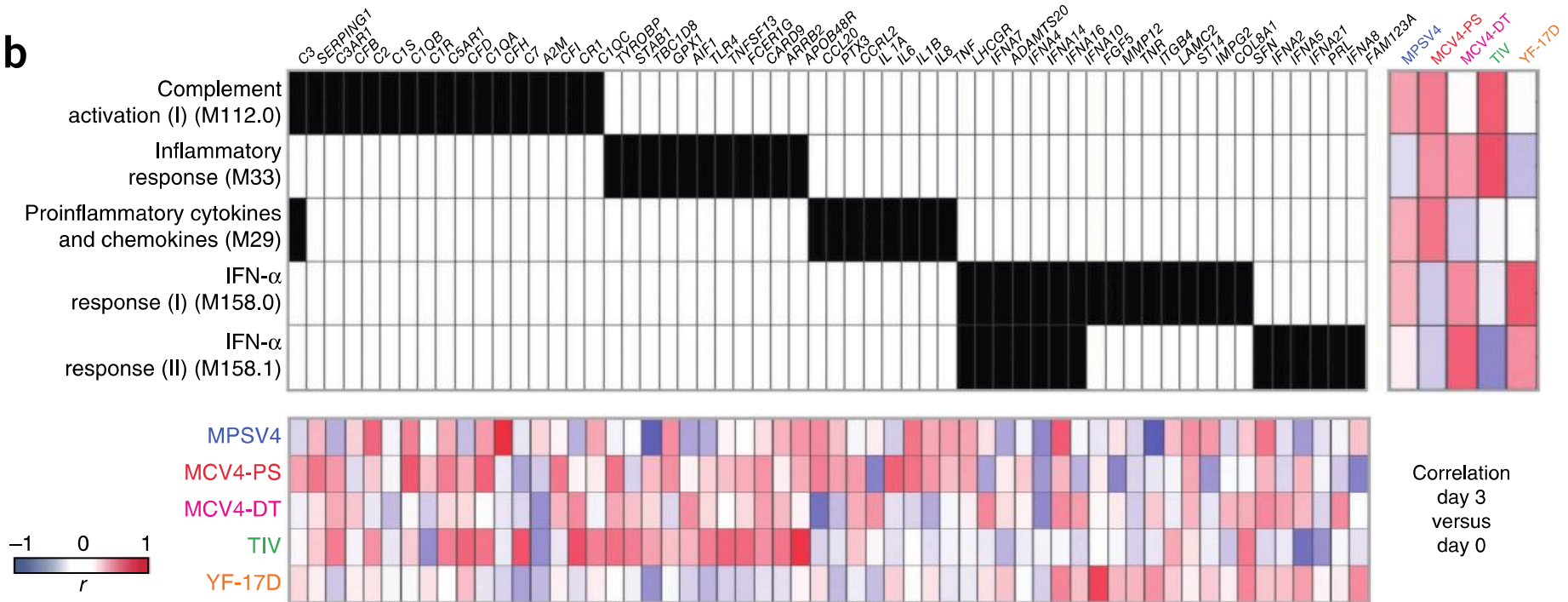
* Subramanian et al. PNAS 102:15545 (2005)

** Chaussabel et al. Immunity 29:150 (2008)

Molecular signatures of antibody responses derived from a systems biology study of five human vaccines

Shuzhao Li^{1,2,10}, Nadine Rouphael^{1,3,10}, Sai Duraisingham^{1,2,10}, Sandra Romero-Steiner⁴, Scott Presnell^{5,6}, Carl Davis^{1,7}, Daniel S Schmidt⁴, Scott E Johnson⁴, Andrea Milton⁴, Gowrisankar Rajam⁴, Sudhir Kasturi^{1,2}, George M Carlone⁴, Charlie Quinn^{5,6}, Damien Chaussabel^{5,6}, A Karolina Palucka⁶, Mark J Mulligan^{1,3,7}, Rafi Ahmed^{1,8}, David S Stephens^{1,7}, Helder I Nakaya^{1,2,9} & Bali Pulendran^{1,2,9}

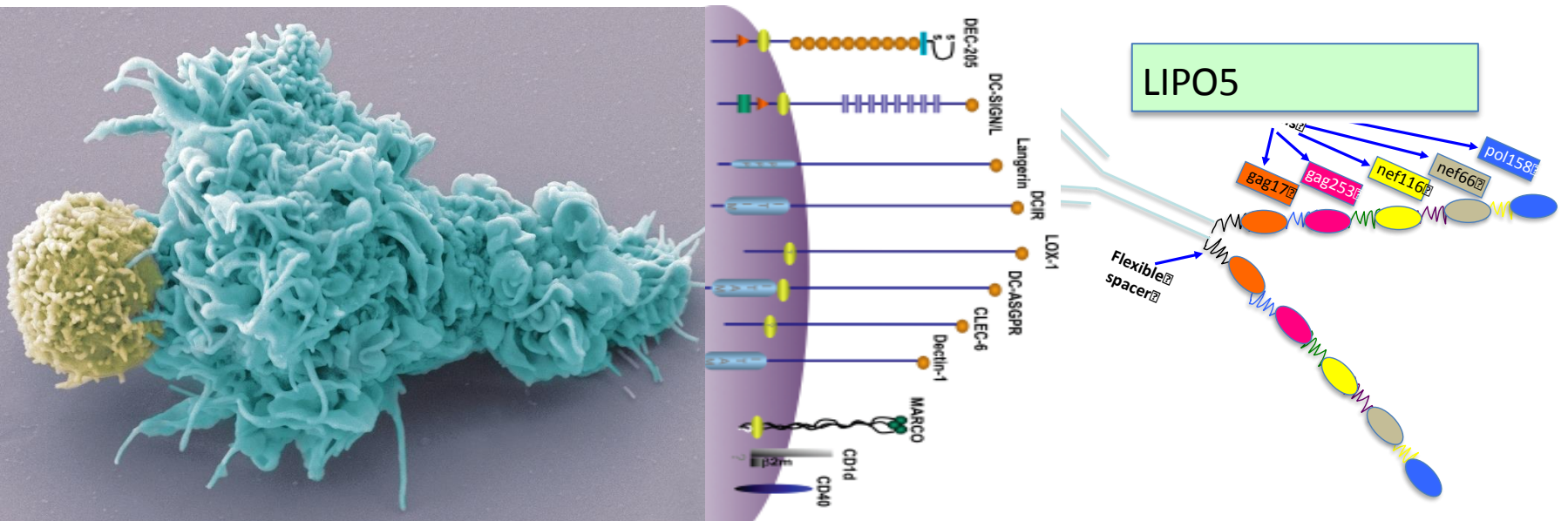
b





Dendritic cell based vaccine

- Therapeutic vaccine in HIV-infected patients
- Dendritic Cells are loaded with 5 HIV peptides



DALIA-1 trial design

TREATMENT

HAART + DC-HIV LIPO-5 vaccine

FOLLOW-UP

Cd4 < 350 cells/ mm³ → HAART

Interrupt HAART

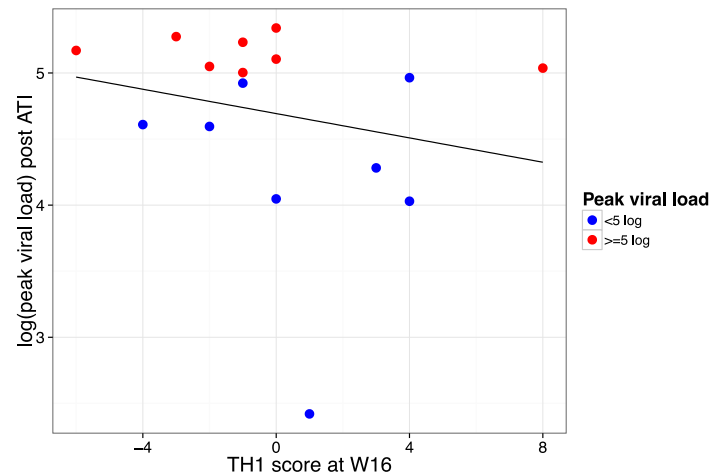
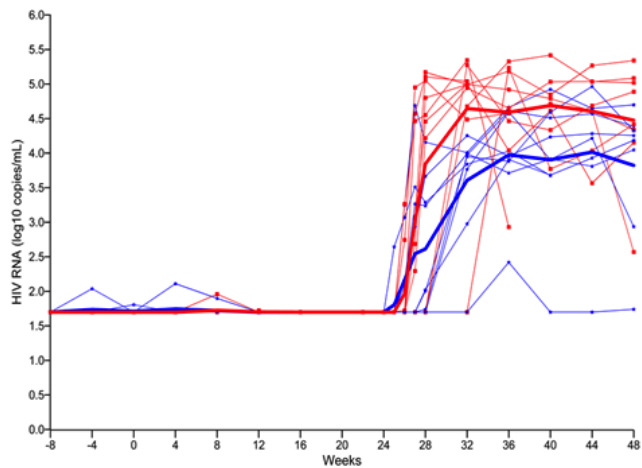
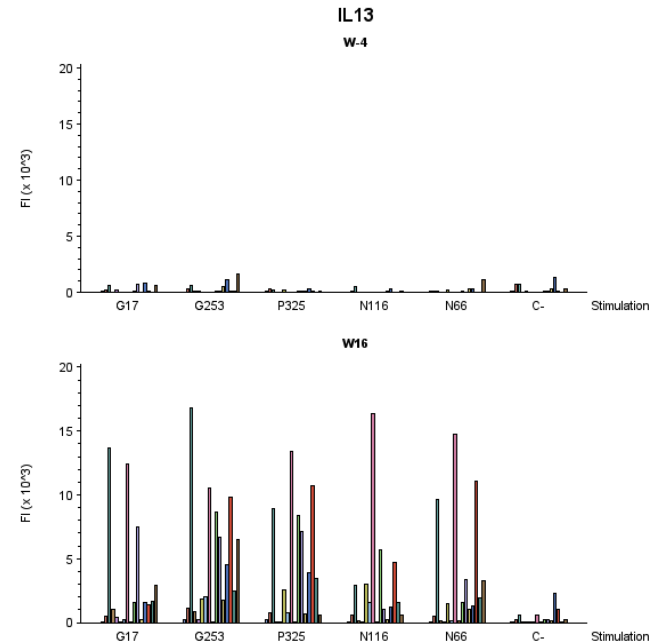
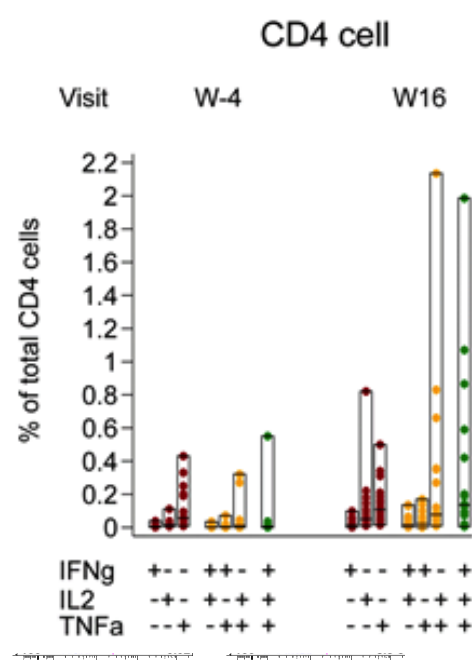
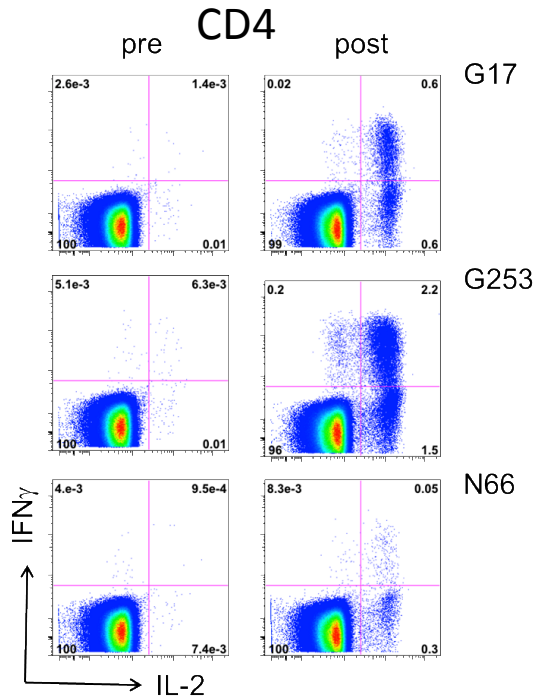
Vaccinations

19 HIV+ pts





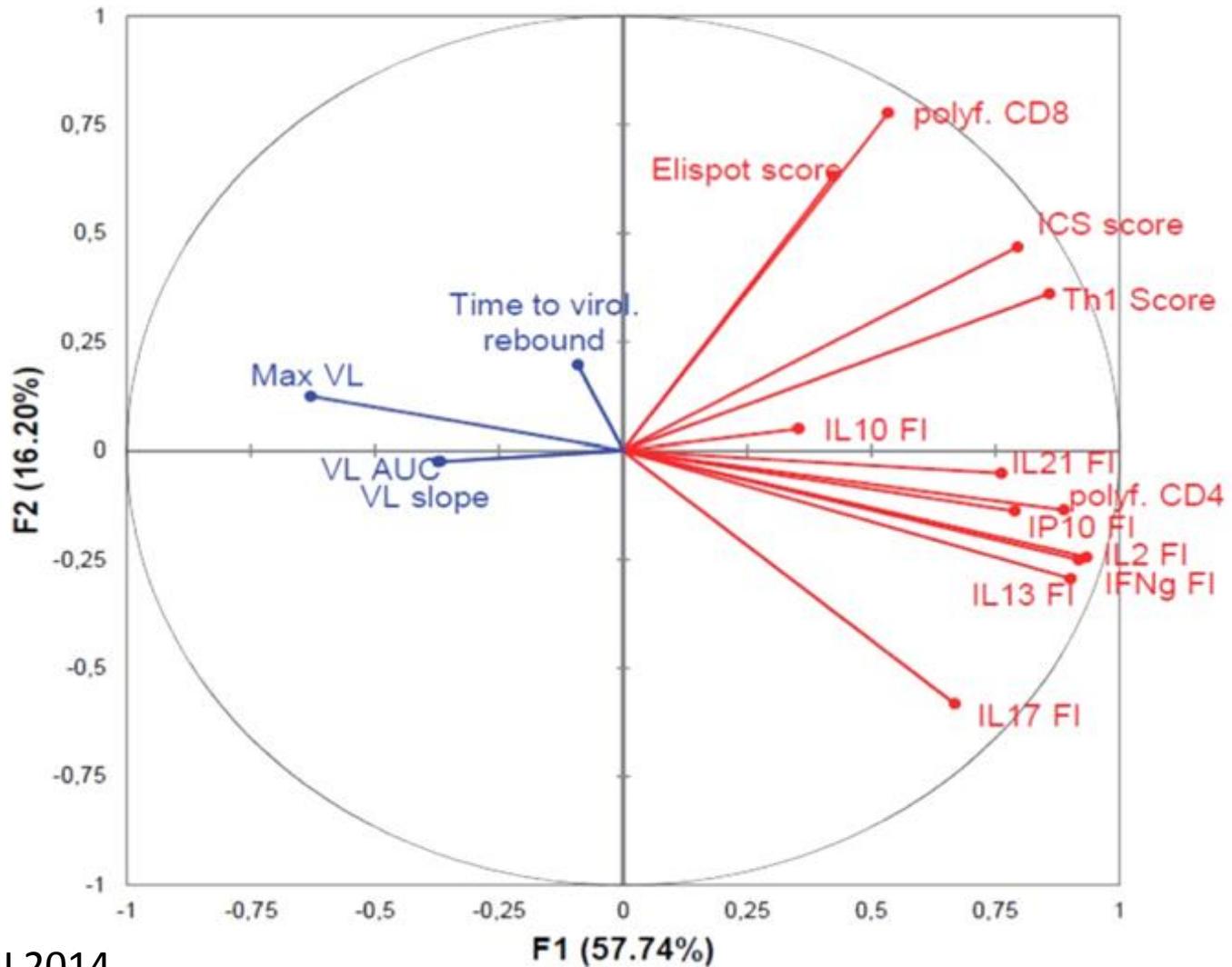
DALIA-1 trial results





DALIA-1 trial results

Variables (axes F1 and F2: 73.94%)



Objectives

- Signature: to look at changes in gene expression* in peripheral blood induced by the vaccination
- Correlates: to look at any association between gene expression and vaccine elicited immunological responses (by Elispot, ICS, Luminex) and viral dynamics after ATI

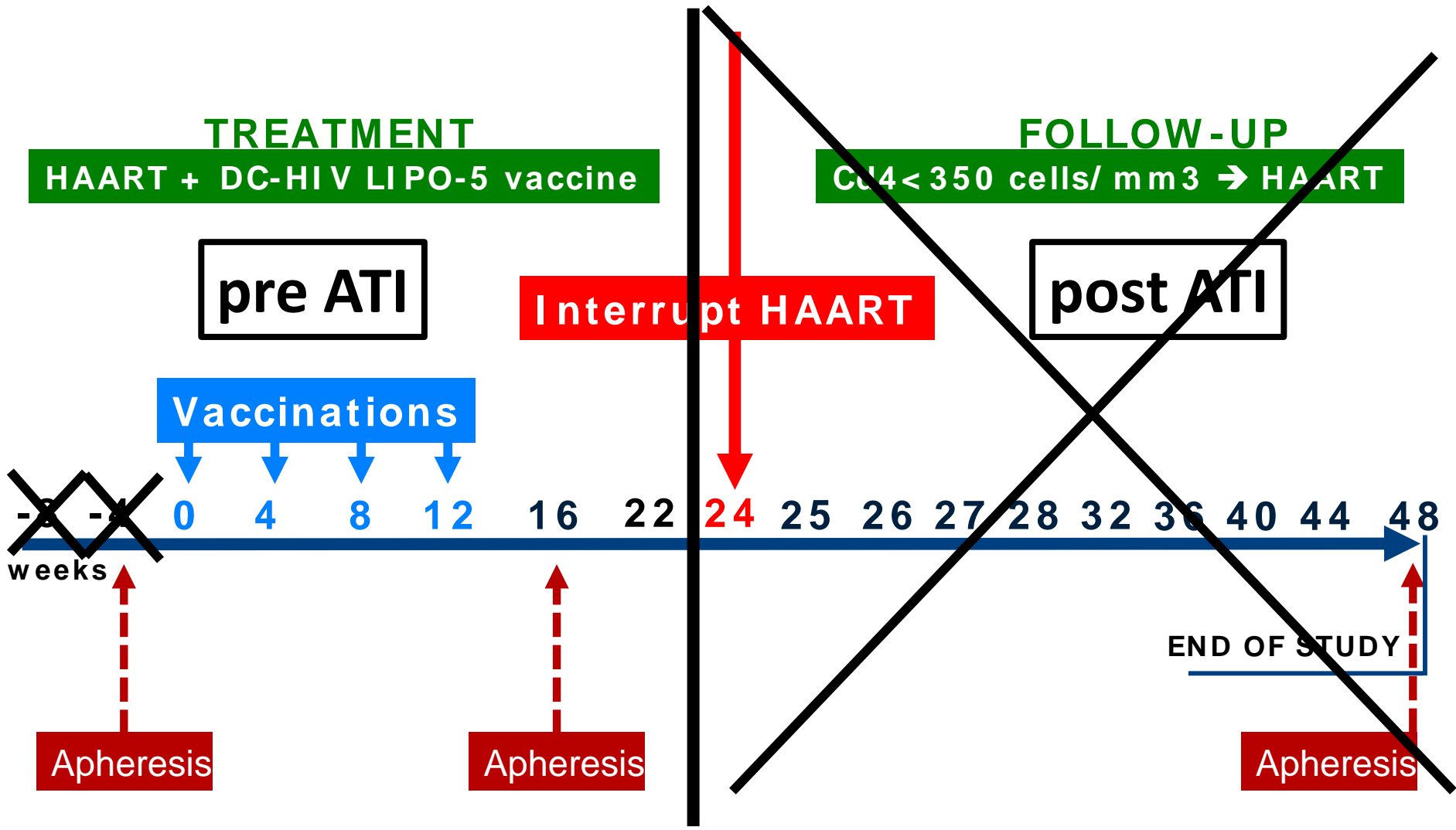
* Illumina HT-12 V4 beadchips



VACCI
NE RESE
ARCH I
NSTITUTE

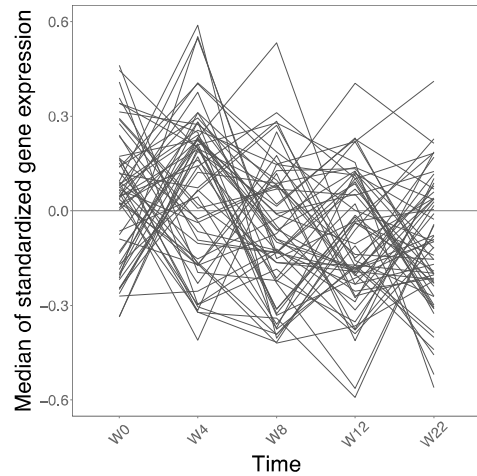
DALIA-1 trial design

Longitudinal transcriptomic analysis

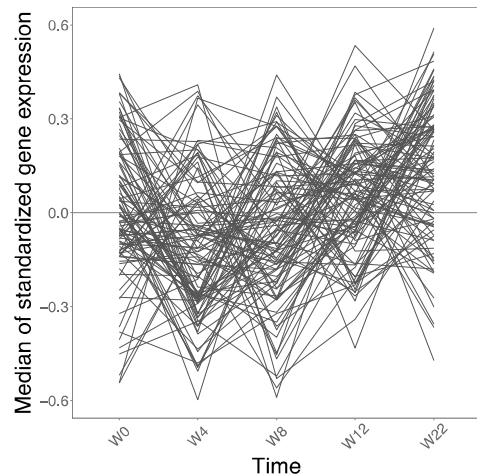
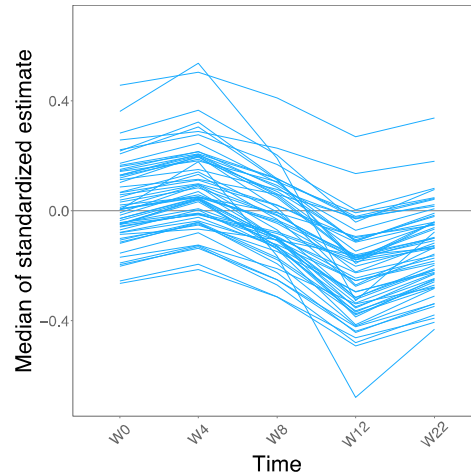




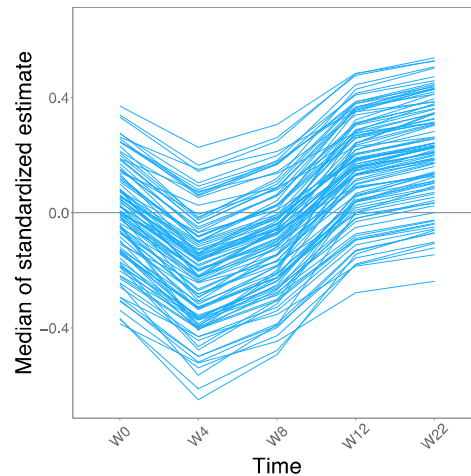
Time course geneset analysis



M 4.1: T cell – 86th percentile



M 4.6: Inflammation – 96th percentile



M3.2[99th pctile]: Inflammation 1/1

M1.1[99th pctile]: Platelets 1/1

M4.13[98th pctile]: Inflammation 1/1

M5.10[97th pctile]: Mitochondrial Respiration 1/1

M4.6[96th pctile]: Inflammation 1/1

M5.6[96th pctile]: Mitochondrial Stress / Proteasome 1/1

M3.5[95th pctile]: Cell Cycle 1/1

M5.7[94th pctile]: Inflammation 1/1

M3.1[94th pctile]: Erythrocytes 1/1

M2.3[94th pctile]: Erythrocytes 1/1

M7.1[93th pctile]: Inflammation 1/1

M6.2[93th pctile]: Mitochondrial Respiration 1/1

M4.3[91th pctile]: Protein Synthesis 1/1

M4.11[91th pctile]: Plasma Cells 1/3

M4.11[91th pctile]: Plasma Cells 2/3

M4.11[91th pctile]: Plasma Cells 3/3

M6.13[90th pctile]: Cell Death 1/1

M4.5[89th pctile]: Protein Synthesis 1/1

M4.14[88th pctile]: Monocytes 1/1

M4.2[88th pctile]: Inflammation 1/1

M4.7[87th pctile]: Cell Cycle 1/1

M4.1[86th pctile]: T cell 1/1

M3.6[85th pctile]: Cytotoxic/NK Cell 1/1

M5.9[84th pctile]: Protein Synthesis 1/1

M5.15[82th pctile]: Neutrophils 1/1

M4.15[81th pctile]: T cells 1/1

M6.6[80th pctile]: Apoptosis / Survival 1/1

M5.1[74th pctile]: Inflammation 1/1

DALIA-1 trial design

Integrative Analysis

TREATMENT

HAART + DC-HIV LIPO-5 vaccine

FOLLOW-UP

Cd4 < 350 cells/mm³ → HAART

Interrupt HAART

Vaccinations

-8 -4 0 4 8 12 16 22 24 25 26 27 28 32 36 40 44 48

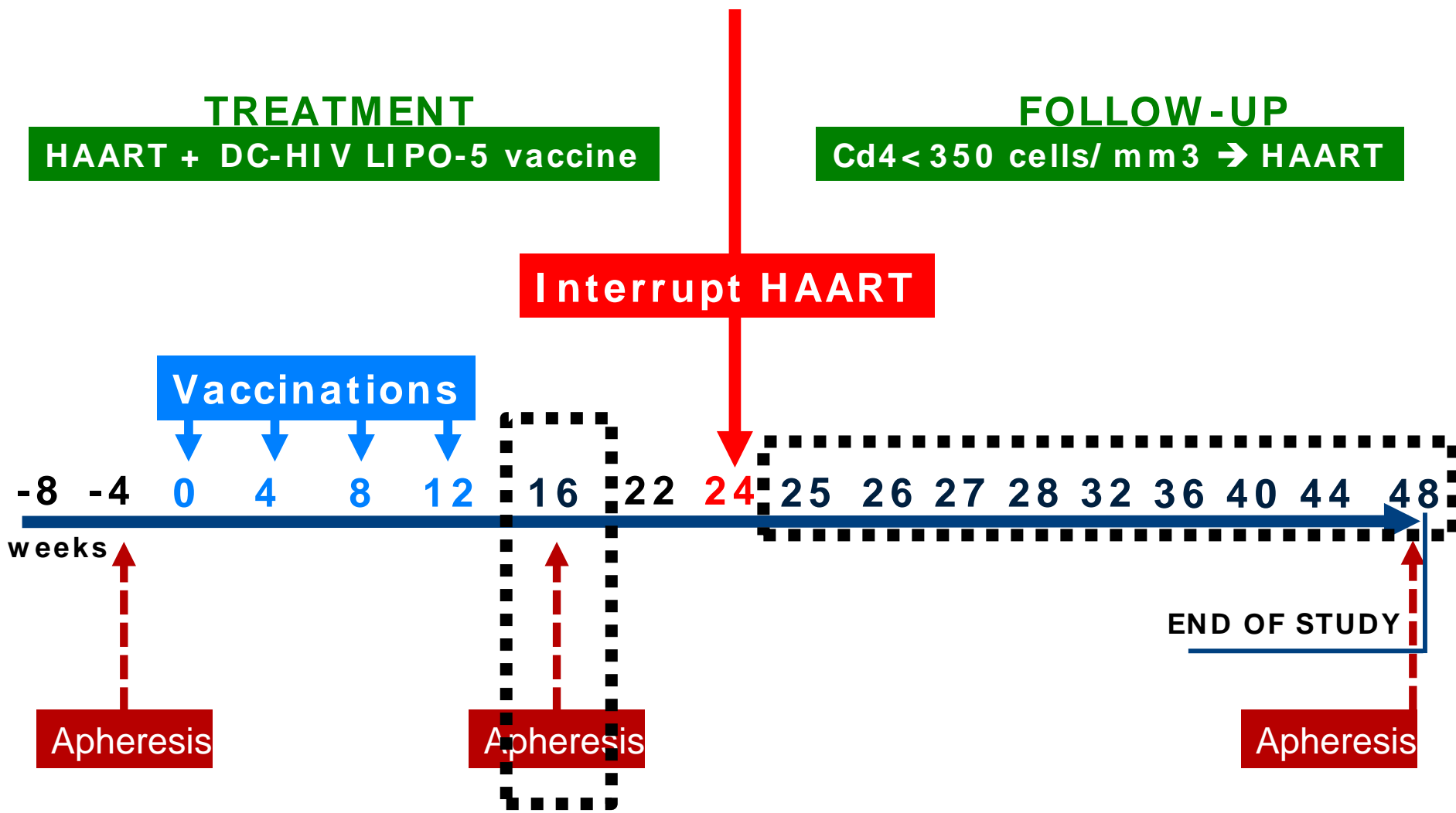
weeks

Apheresis

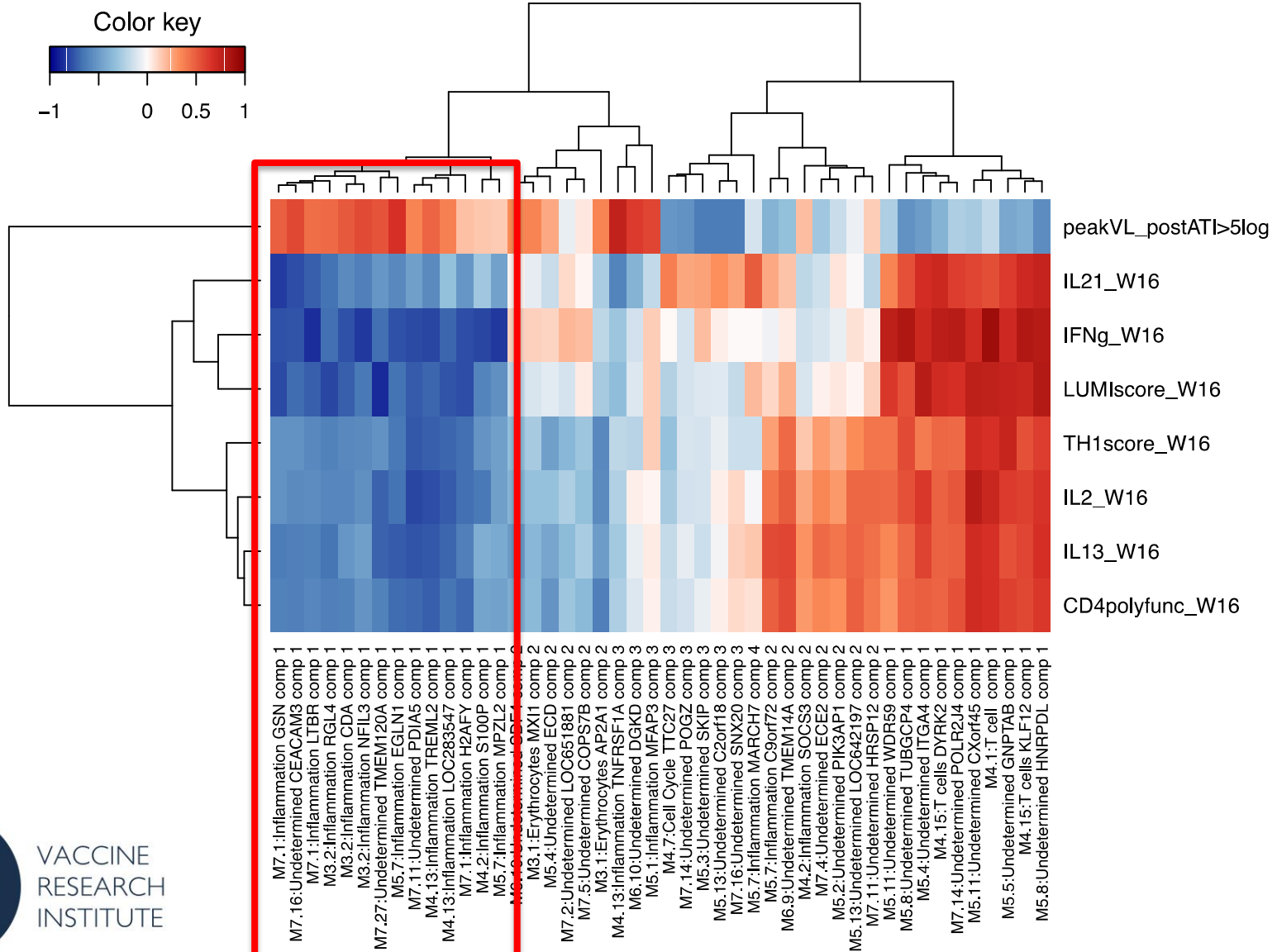
Apheresis

Apheresis

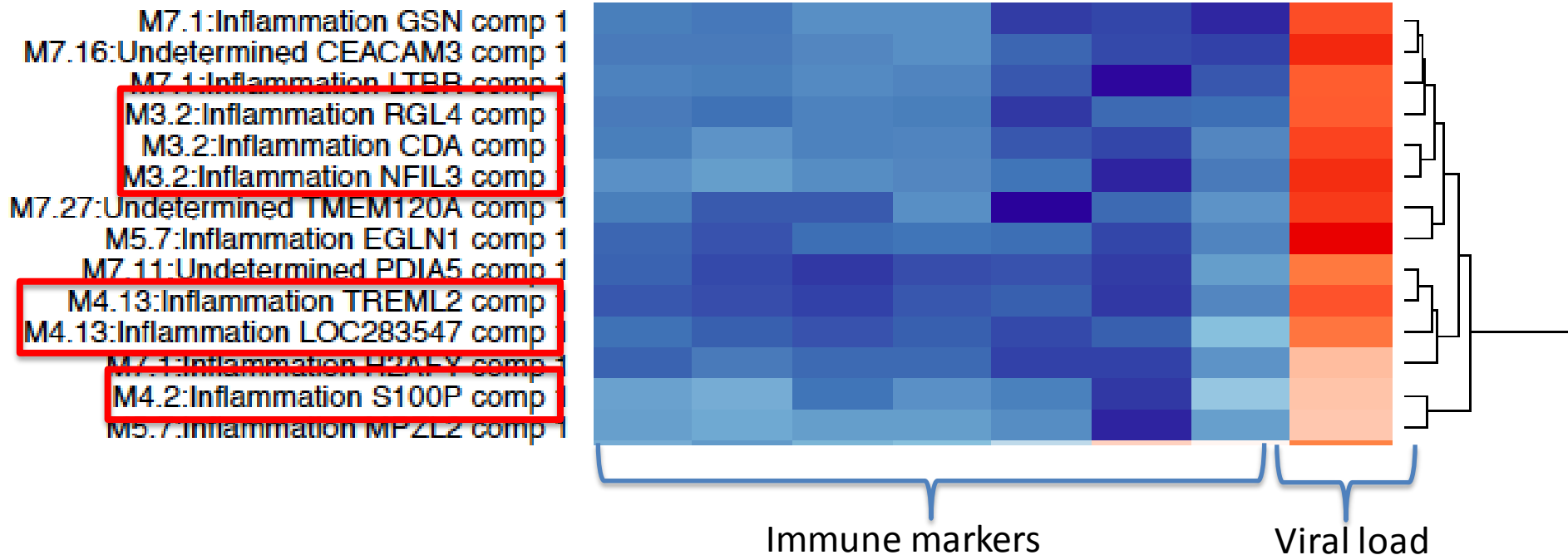
END OF STUDY



Correlations with immune response (W16) and peak of viral load (post ATI)



Correlations with immune response (W16) and peak of viral load (post ATI)



Conclusion

- The goals of the systems vaccinology approach: understanding and predicting the response to vaccine
- The requirements:
 - Early harvest times (innate response)
 - Whole blood (signature) vs. selected cell populations (mechanism)
 - Several assays at the same time (flow cyto, ICS...)
- Opportunity to learn more about the Ebola vaccine (substudies)



VACCINE
RESEARCH
INSTITUTE

Acknowledgments



Jason Skinner, Baylor Institute for Immunology Research, Dallas TX, US;
Yves Levy, Jacques Branchereau, INSERM U955, Equipe 16, UPEC, Créteil
Boris Hejblum, INSERM U897, INRIA SISTM, Univ. Bordeaux



EHESP

