

# WHOLE EXOME SEQUENCING OF PATIENTS WITH ADULT ONSET EVANS SYNDROME: A COHORT OF 120 PATIENTS

**E. Crickx**<sup>1,2</sup>, J. Fadlallah<sup>3</sup>, M. Cheminant<sup>4</sup>, J. Rosain<sup>5</sup>, J. Dion<sup>6</sup>, M. Malphettes<sup>3</sup>, D. Boutboul<sup>7</sup>, C. Gourguechon<sup>8</sup>, M. Ebbo<sup>9</sup>, A.M. Ronchetti<sup>10</sup>, T. Moulinet<sup>11</sup>, D. Gobert<sup>12</sup>, J. Hadjadj<sup>12</sup>, J. Graveleau<sup>13</sup>, M.C. Stolzenberg<sup>1</sup>, B. Godeau<sup>2</sup>, L. Galicier<sup>3</sup>, J.F. Viallard<sup>14</sup>, S. Audia<sup>15</sup>, F. Suarez<sup>4</sup>, E. Oksenhendler<sup>3</sup>, C. Fieschi<sup>3</sup>, O. Hermine<sup>4</sup>, M. Michel<sup>2</sup>, M. Mahevas<sup>2</sup>, F. Rieux-Laucat<sup>1</sup> and the French Evans study group

**1 Imagine Institute, « Immunogenetics of Pediatric Autoimmune Diseases », INSERM U1163, Paris;**

**2 Internal medicine Department, Henri Mondor Hospital, AP-HP, Créteil, France;**

*3 Clinical immunology department, Saint Louis hospital, AP-HP; 4 Hematology department, Necker Hospital, APHP; 5 Centre d'étude des déficits immunitaires (CEDI), Necker Hospital, APHP; 6 Toulouse University Hospital; 7 Hematology department, Cochin Hospital, APHP; 8 Hematology department, Amiens University Hospital; 9 Internal medicine department, Timone University Hospital, Aix-Marseille Université; 10 Hematology department, Sud Francilien hospital; 11 Internal medicine department, Nancy University Hospital; 12 Internal medicine department, Saint Antoine Hospital, APHP; 13 Internal medicine department, Saint Nazaire Hospital; 14 Internal medicine department, Haut-Leveque Hospital; 15 Internal medicine department, Dijon University Hospital;*

*Cities : 1.2.3.4.5.7.12. Paris (F), 6. Toulouse (F), 8. Amiens (F), 9. Marseille (F), 10. Corbeil Essonne(F), 11. Nancy (F), 13. Saint Nazaire (F), 14. Pessac, (F), 15. Dijon (F)*

## Disclosures of Crickx Etienne (unrelated to this presentation)

Company name	Research support	Employee	Consultant	Stockholder	Speakers bureau	Advisory board	Other
Novartis						EC	
UCB						EC	
Sanofi							EC
Amgen							EC



# Introduction

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- Loss of tolerance toward several self-antigens suggests an underlying genetic predisposition
- In children with Evans syndrome (ES), 30-40% have an underlying monogenic disease

*Hadjadj et al., Blood 2019*

- In adult, next generation sequencing is not routinely performed in ES, as diagnosis yield is considered to be low

*Fattizzo et al., Blood Adv 2021*

*Jiang et al., Blood Advance 2023*



# Objectives

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- **Identify genetic variants** responsible for adult onset Evans syndrome
- Study their **association with clinical or biological features**
- Perform functional studies of **new genetic variants**
- **Guide therapeutic strategy** with genetic findings



# Patients and methods

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- **Inclusion criteria** : Adult onset ( $\geq 18$  years) Evans syndrome
  - Defined as at least 2 autoimmune cytopenia among:
    - Immune thrombocytopenia (ITP), warm autoimmune hemolytic anemia (wAIHA), autoimmune neutropenia (AIN)
  - Diagnosed according to international guidelines<sup>1,2</sup>
- **Exclusion criteria** :
  - Systemic lupus (according to Systemic Lupus International Collaborating Clinics criteria<sup>3</sup>)
  - Indolent B cell malignancies at Evans syndrome onset
  - Other causes of cytopenia (drugs)

<sup>1</sup> Provan D et al., *Blood Adv* 2019

<sup>2</sup> Jäger U et al., *Blood Rev* 2020

<sup>3</sup> Petri M et al., *Arthritis Rheum* 2012



# Patients and methods

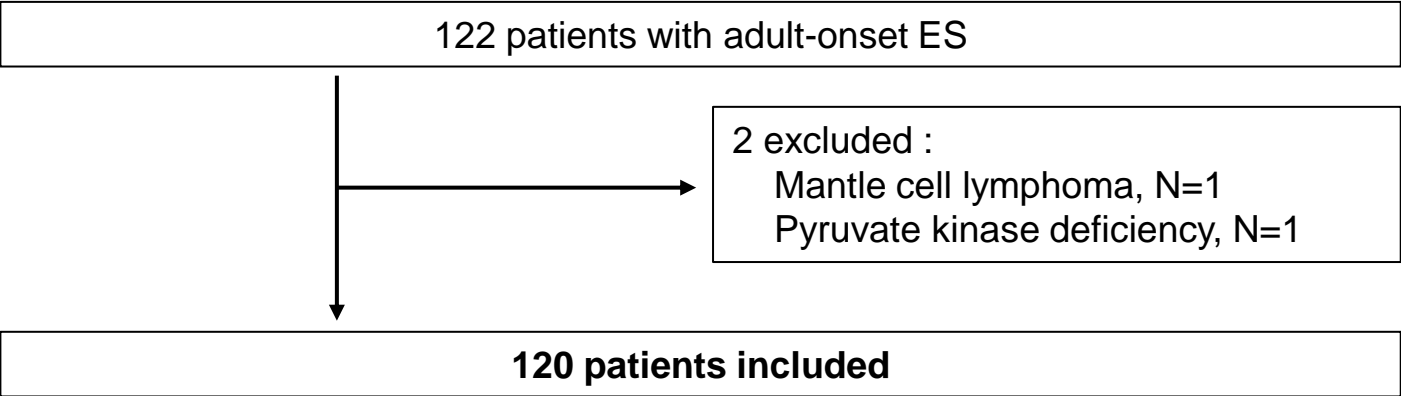
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- Patients identified in France in the network of the national reference center for adult autoimmune cytopenia (CERECAI) from November 2021 to June 2023
- Clinical and biological data were retrospectively collected using a standardized form
- Whole-exome sequencing after written and informed consent was obtained (except for patients with genetic diagnosis already available)
- Gene variants already published and/or with *in vitro* confirmed consequences were considered as genetic diagnoses. Clinical interpretation of variants was performed according to the ACMG guidelines<sup>1</sup>

<sup>1</sup> Richards S et al., Genet Med 2015

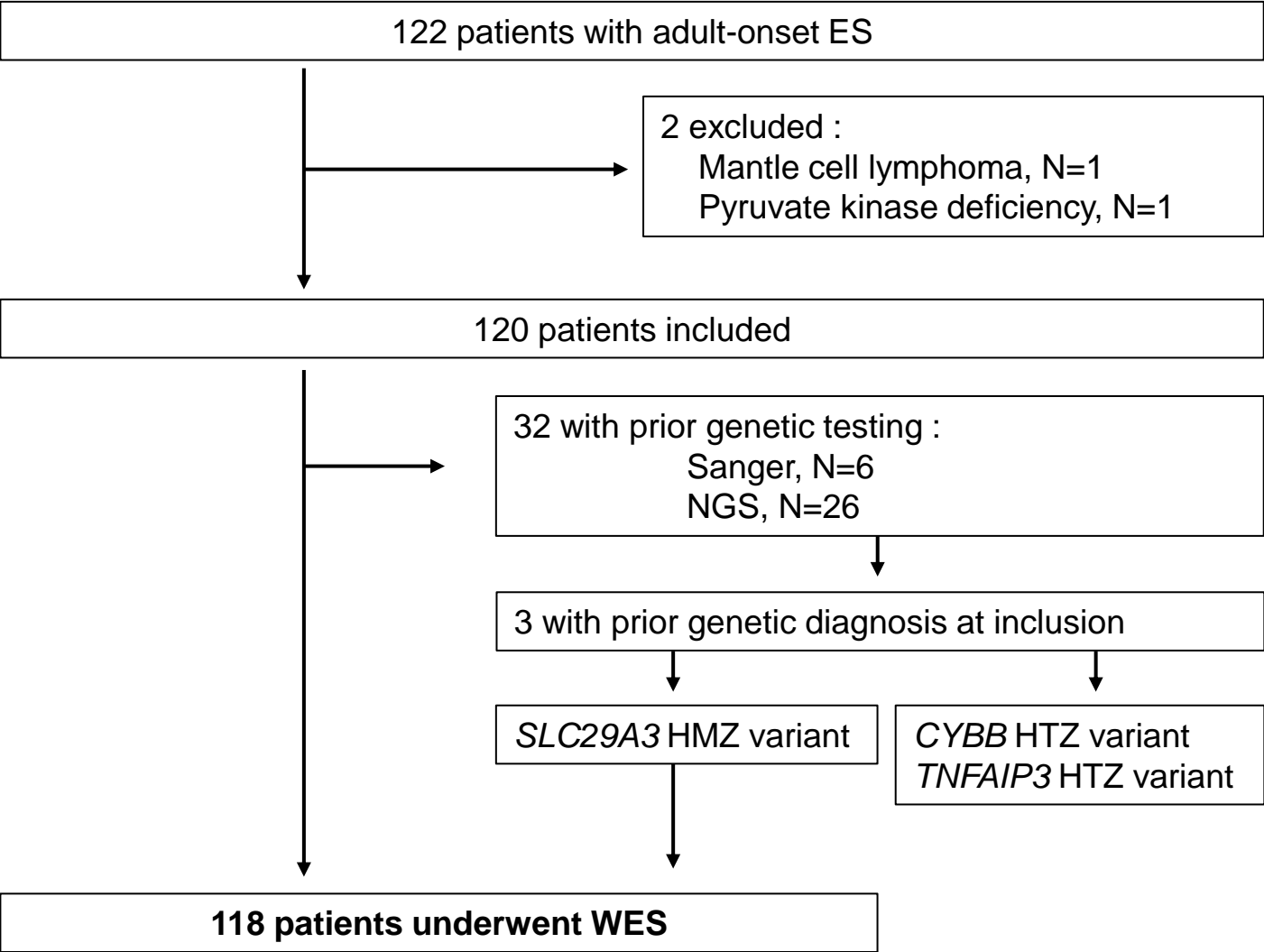


# Flow Chart of study





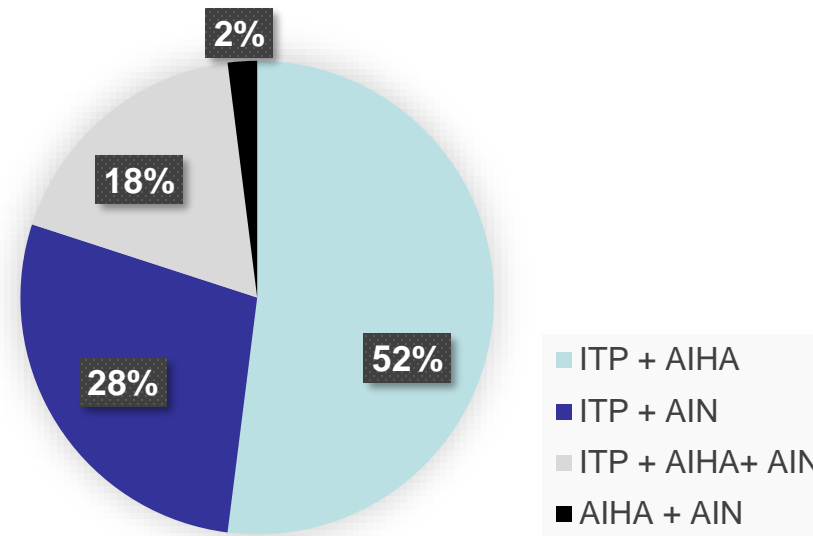
# Flow Chart of study





# Patients characteristics

	All patient (N=120)
Female	44 (37)
Age at Evans syndrome diagnosis (median, range)	33 [18 - 80]
Age at first cytopenia (median, range)	30 (1 - 80)



# Patients characteristics

	All patient (N=120)
Age < 18 at first cytopenia	19 (16)
Immunopathologic manifestations in first-degree relatives	24 (20)
Severe and/or recurrent infections	31 (26)
Humoral immune deficiency	30 (25)
CVID-like	20 (17)
IgA deficiency	3 (3)
IgG subclass deficiency	2 (2)
Secondary humoral immune deficiency	5 (4)
Organomegaly	64 (53)
Adenomegaly	48 (40)
Splenomegaly	37 (31)
Hepatomegaly	12 (10)
Tissue lymphocyte infiltration	7 (6)
Malignancies	13 (11)
Associated immunopathologic manifestations	40 (33)
Antinuclear antibody (titer $\geq$ 1/160)	37 (31)



# Patients characteristics

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<b>Age &lt; 18 at first cytopenia</b>	<b>19 (16)</b>
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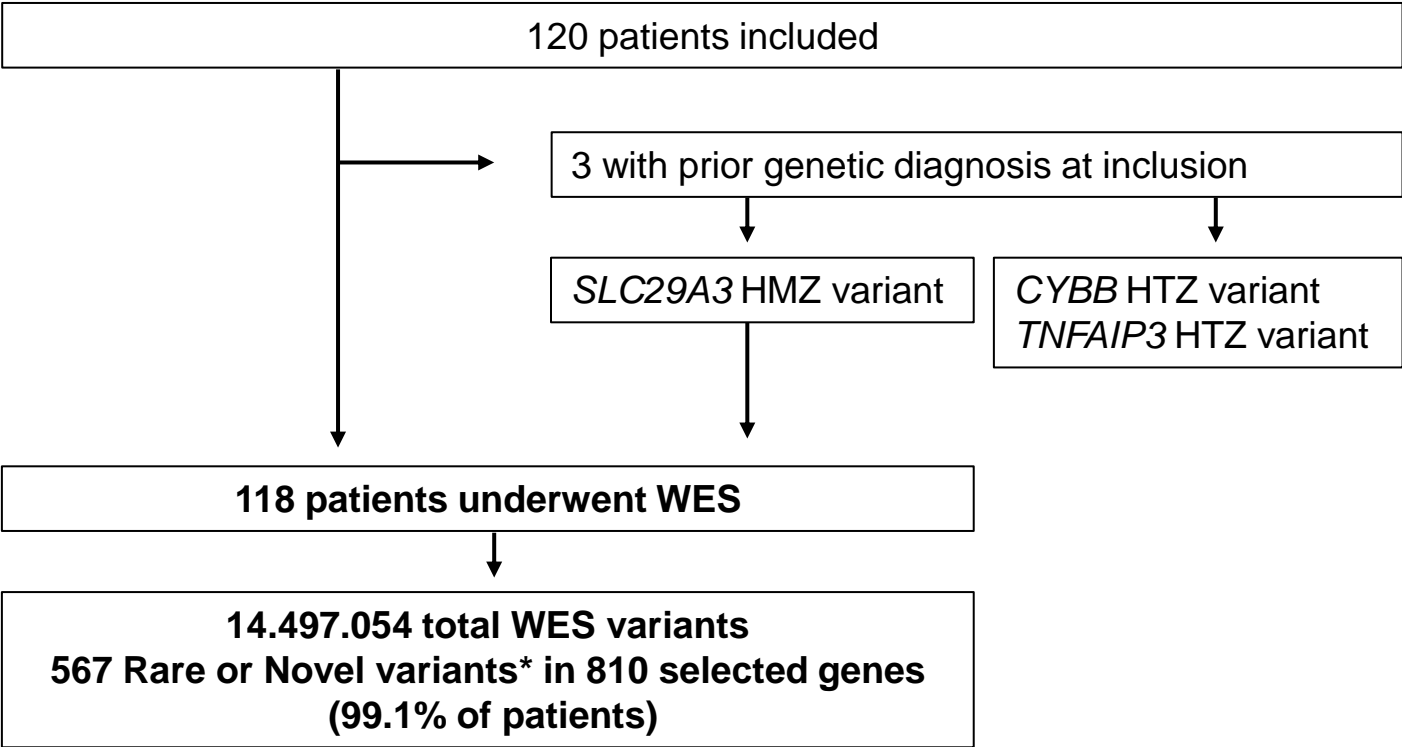
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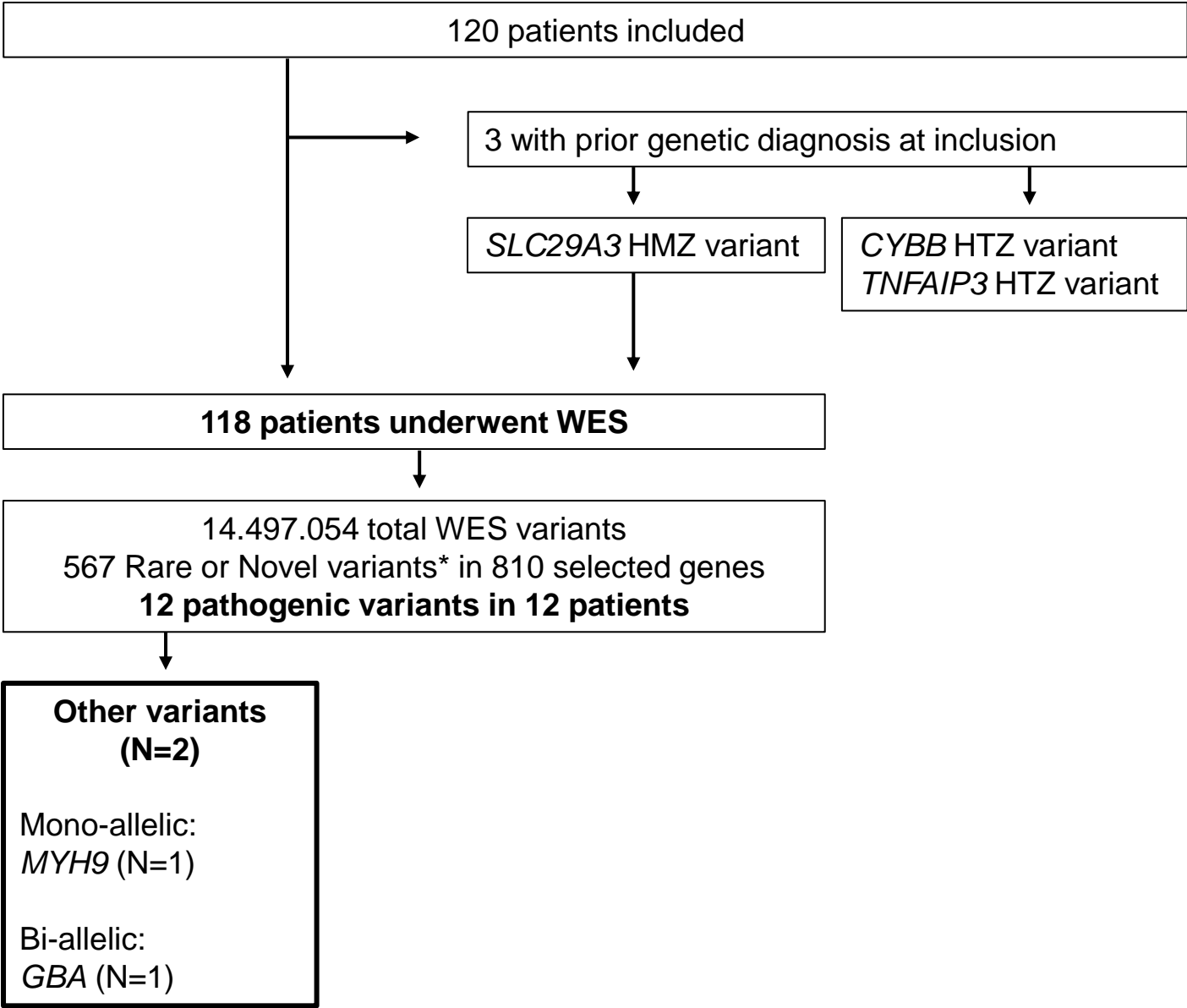
# Genetic testing



\*frequency <1/10.000 (gnomAD)  
and CADD score ≥ 20



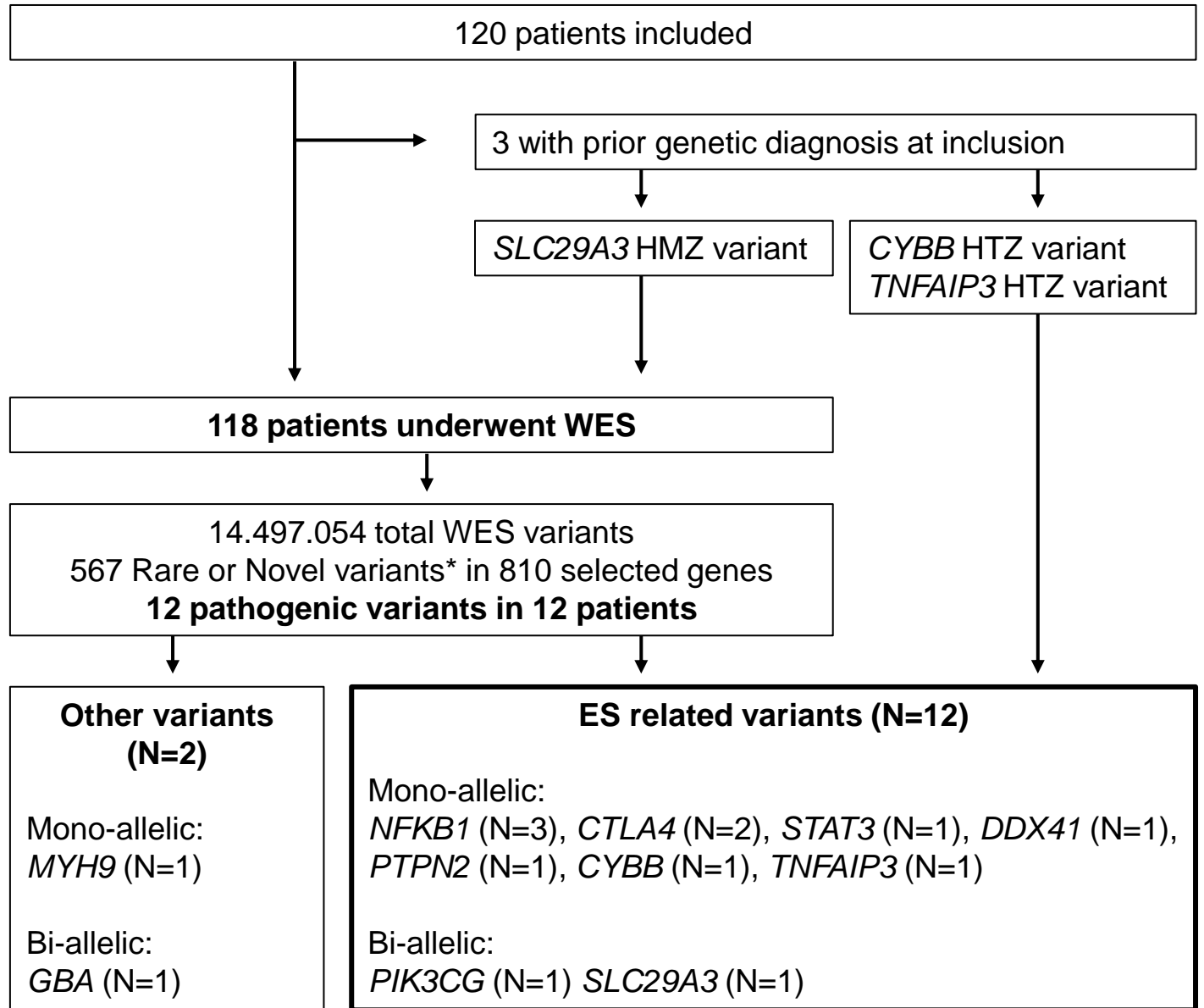
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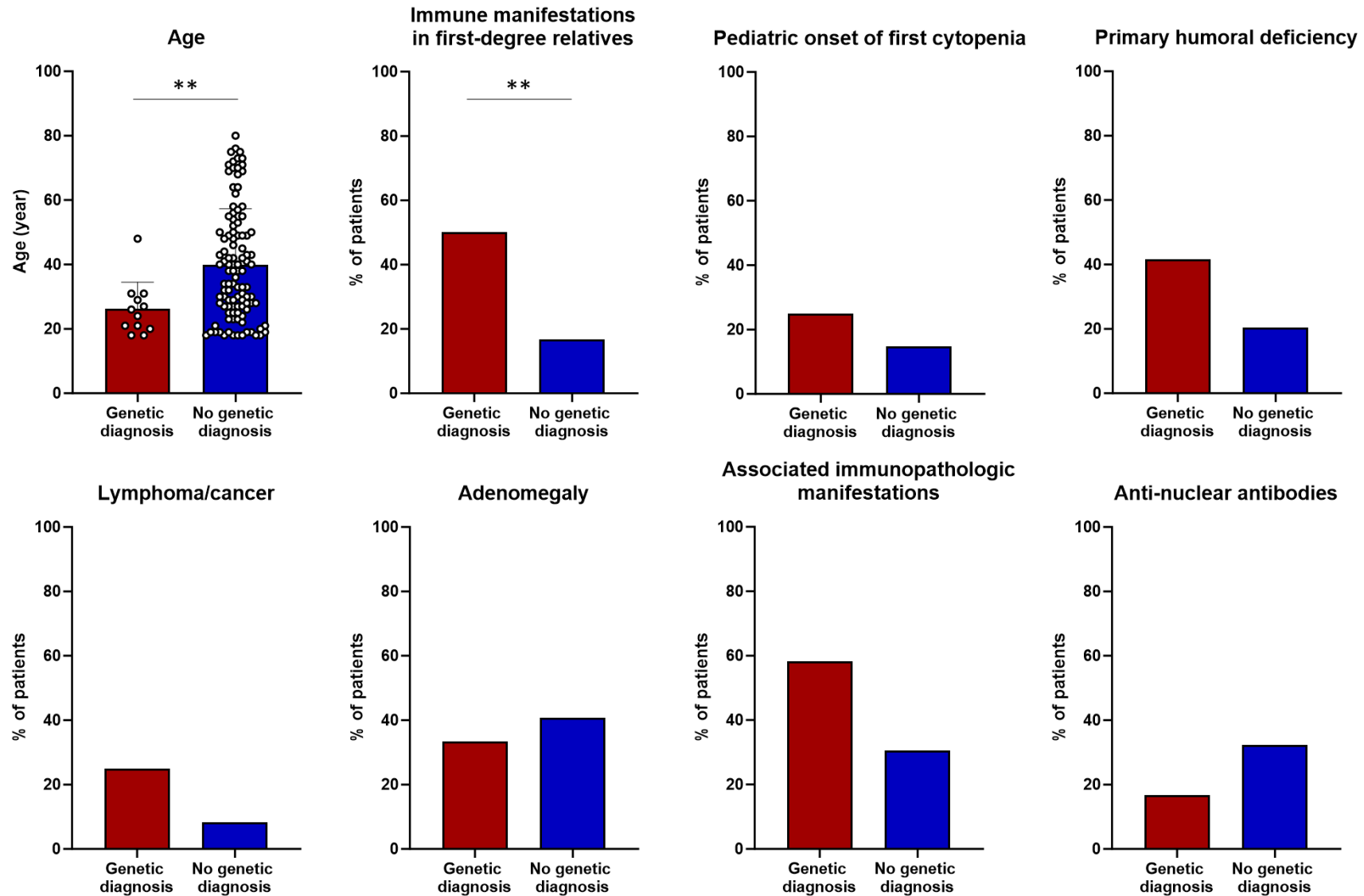


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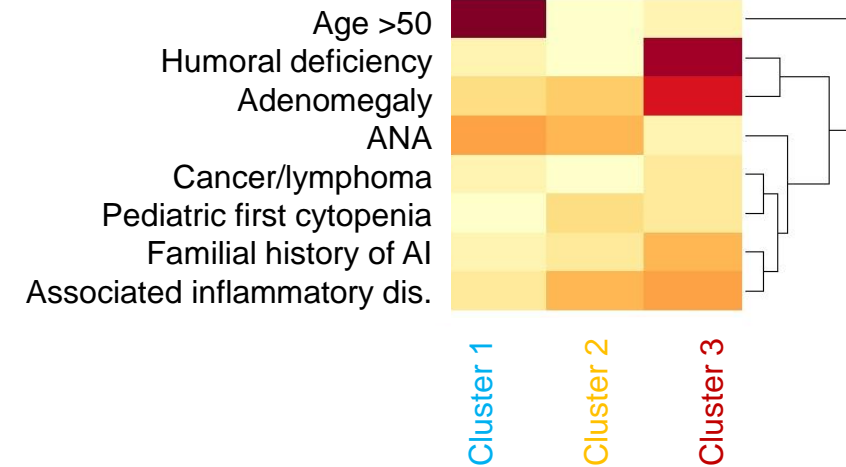
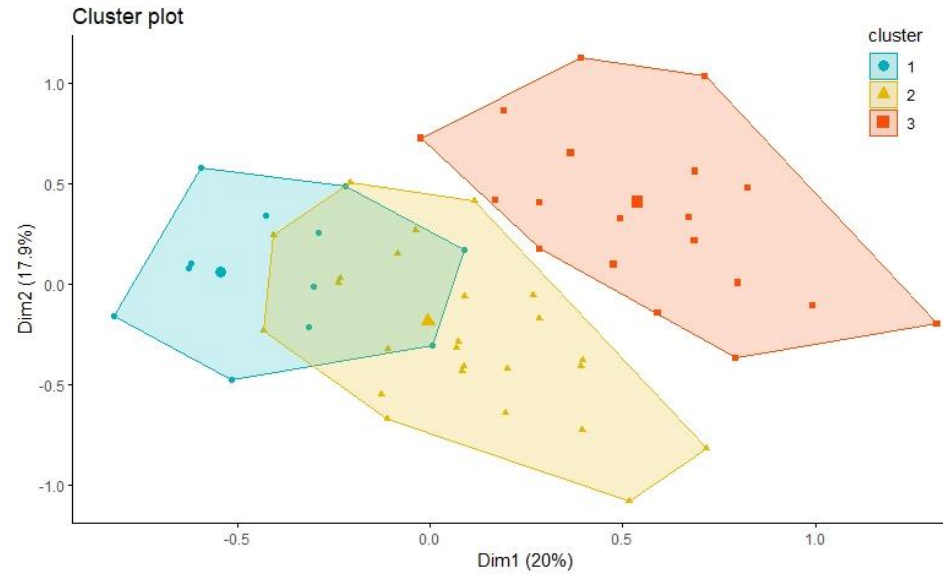
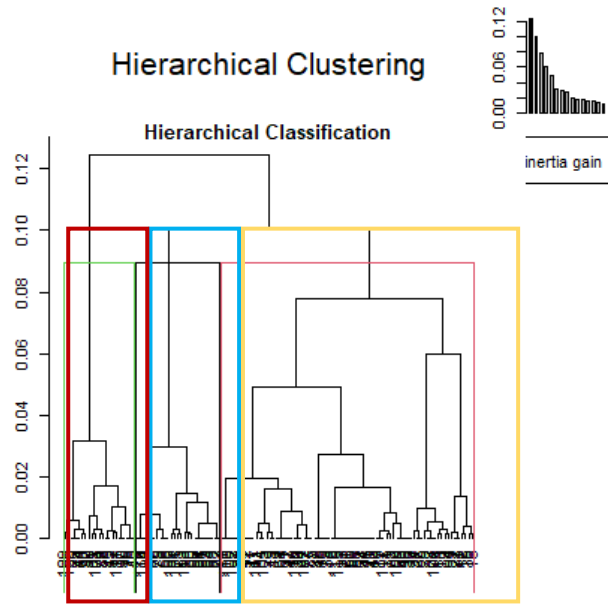


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# Clinical and biological features of patients with or without genetic diagnosis

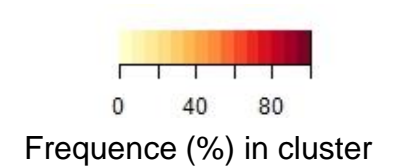


# Hierarchical clustering of patients (multiple correspondence analysis)



Pathogenic variants:

- Cluster 1: N=0
- Cluster 2: N= 7
- Cluster 3: N= 5



# Discussion

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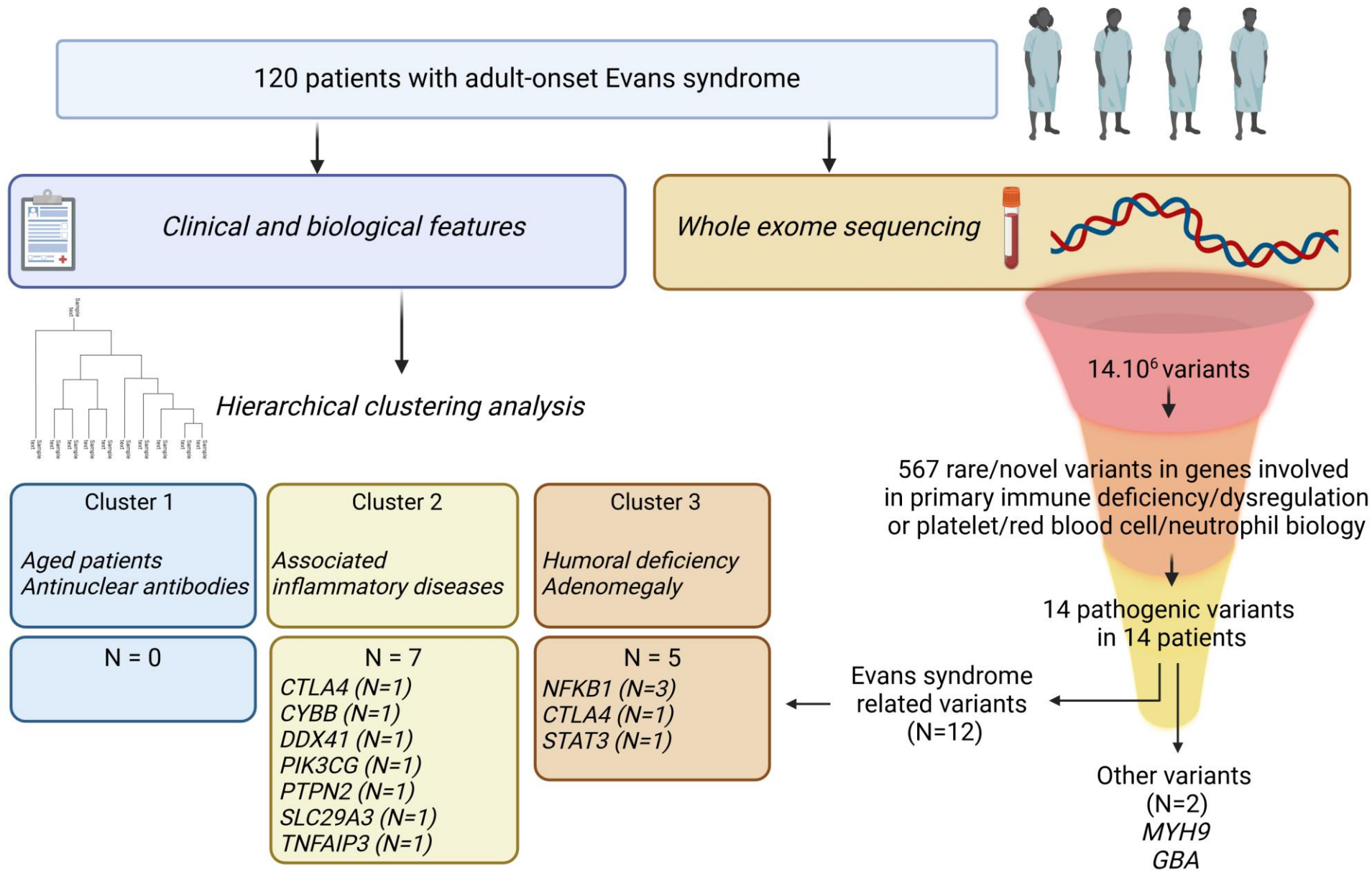
- Large cohort of adult patients with ES and genetic testing, with **genetic diagnosis in 10%**
- Led to **targeted therapy** in some patients<sup>1</sup>, **screening of relatives** (*NFKB1* families), and **new variants description** (e.g. *PTPN2*<sup>2</sup>)
- Limitations include « solo » exome (can miss genetic diagnoses), and assessment of rare variants with high impact only
- Patients with genetic diagnosis were younger and had more immune manifestations in first-degree relatives
- Overall these results suggest that genetic testing should be considered in every adult patient diagnosed with ES

<sup>1</sup> Fischer et al., JACI 2023

<sup>2</sup> Jeanpierre et al., JEM 2024







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**FRL team « Immunogenetics of Pediatric Autoimmune Diseases » :**

- **Frédéric Rieux-Laucat**
- Aude Magerus
- Bénédicte Neven
- Marie-Claude Stolzenberg
- Victor Michel
- Malak Fakih
- Duong Ho-Nhat

**CEDI Necker**

- Capucine Picard
- Jérémie Rosain

**Patients and their families**

**CERECAL network – French Evans study group**

- Matthieu Mahévas, Bertrand Godeau, Marc Michel, Laetitia Languille (Créteil)
- Lionel Galicier, Claire Fieschi, Jehane Fadlallah, Marion Malphettes, David Boutboul, Laurence Gérard, Eric Oksenhendler (St Louis, Paris)
- Olivier Hermine, Morgane Cheminant, Felipe Suarez (Necker, Paris)
- Jérémie Dion, Thibault Comont, Guillaume Moulis (Toulouse)
- Clement Gourguechon (Amiens)
- Mikael Ebbo, Benoit Fauger (Marseille)
- Anne Marie Ronchetti (Corbeil)
- Thomas Moulinet (Nancy)
- Delphine Gobert, Jerome Hadjadj (Saint Antoine, Paris)
- Julie Graveleau (Nantes)
- Jean-Francois Viillard (Bordeaux)
- Sylvain Audia (Dijon)
- Marie Goussef (Vannes)
- Louis Terriou (Lille)
- Antoine Dossier (Bichat, Paris)
- Adrien Bigot (Tours)

