

Highly reproducible, sensitive and early detection and characterization of antidrug responses using RNA-seq

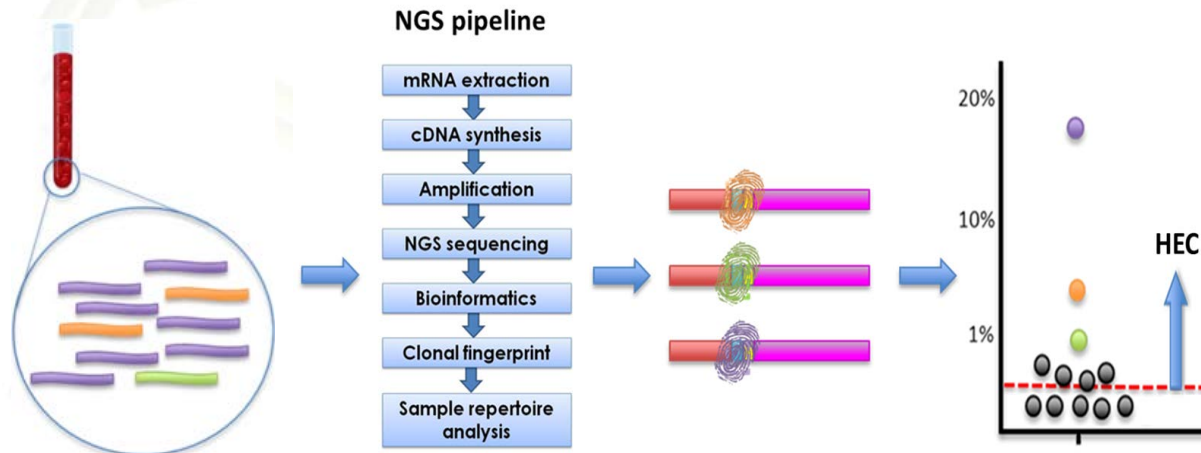
9th Open EIP Scientific Symposium & Final ABIRISK Open conference
November 15th 2017

Niek de Vries, AMC, The Netherlands

To overcome existing hurdles in assessment of antidrug responses we aimed to develop a robust tool for analysis of B- and T-cell responses that allows:

- Reliable assessment of clonal B- and T-cell responses
 - Linking of clonal responses to antigen specificity (epitopes)
 - Linking *in vitro* to *in vivo* clonal responses
- Quantitative Next Gen Sequencing (NGS) with single cell approaches

T cell receptor (TCR) and B cell receptor (BCR) repertoire analysis

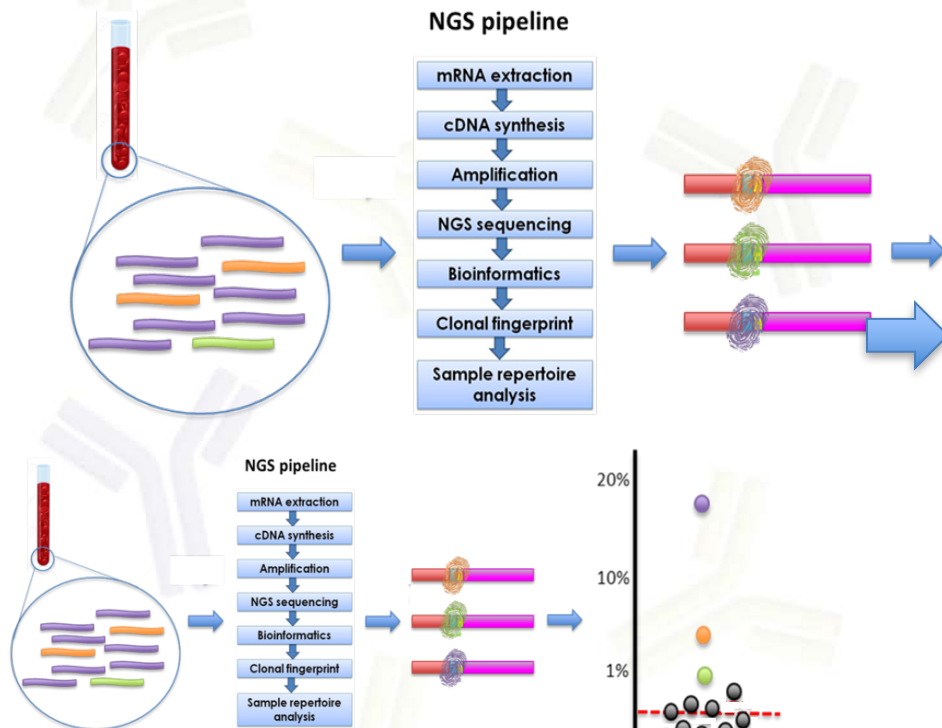


Applications:

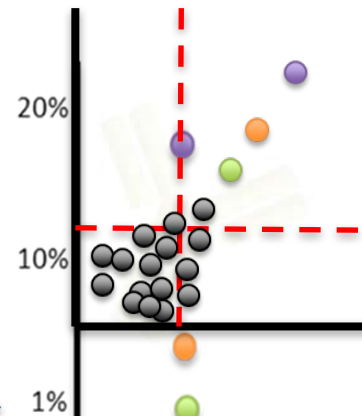
1. Quantify clonal expansion
2. Follow clones over time
3. Compare clonal distributions between different samples

Klarenbeek P.L. et al., *Immunol Lett* 2010

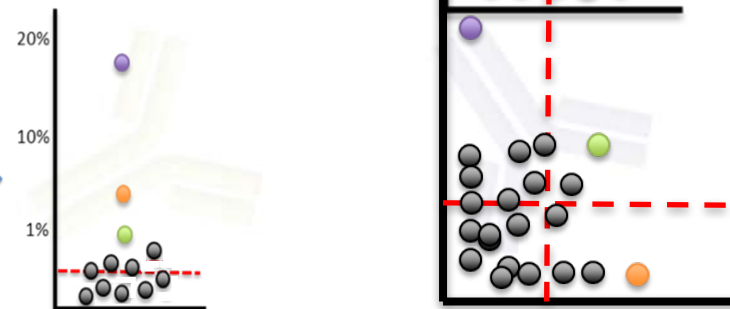
Comparing two samples



Similar clonal distribution



Different clonal distribution



- Chao-Sorensen similarity index
- Top clonal overlap analysis

IgG4-related disease

Tumor formation in different organs, e.g. biliary, retroperitoneum, retro-orbital, salivary glands, thyroid, lungs ...

2/3 have increased serum IgG4

Characteristic histopathological appearance¹

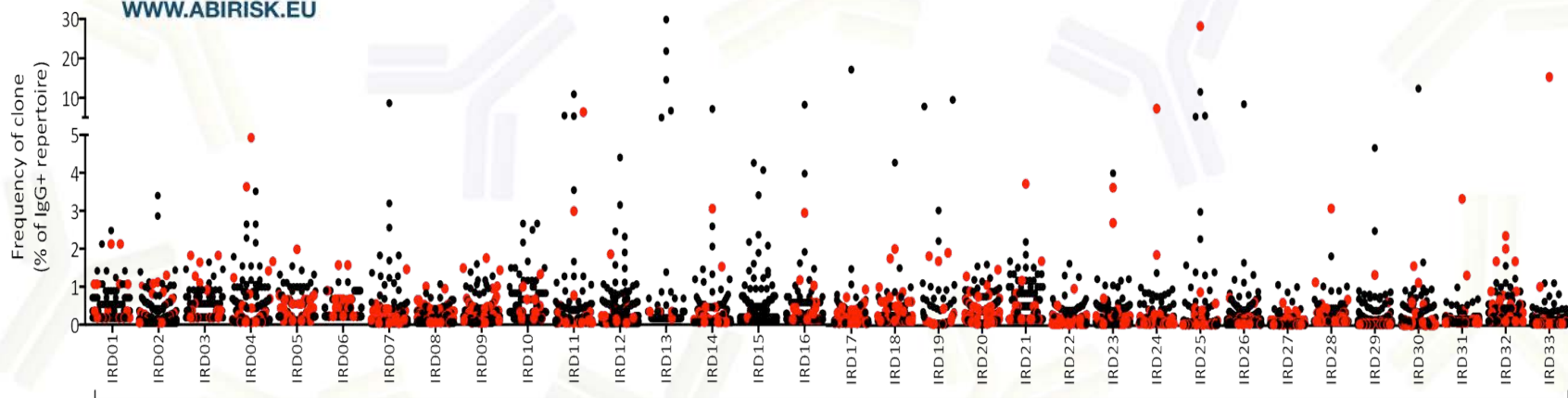
- dense lymphoplasmacytic infiltrate
- storiform pattern of fibrosis
- obliterative phlebitis
- increased numbers of IgG4+ plasma cells

However: Value of each criterion is variable and tissue specific ...

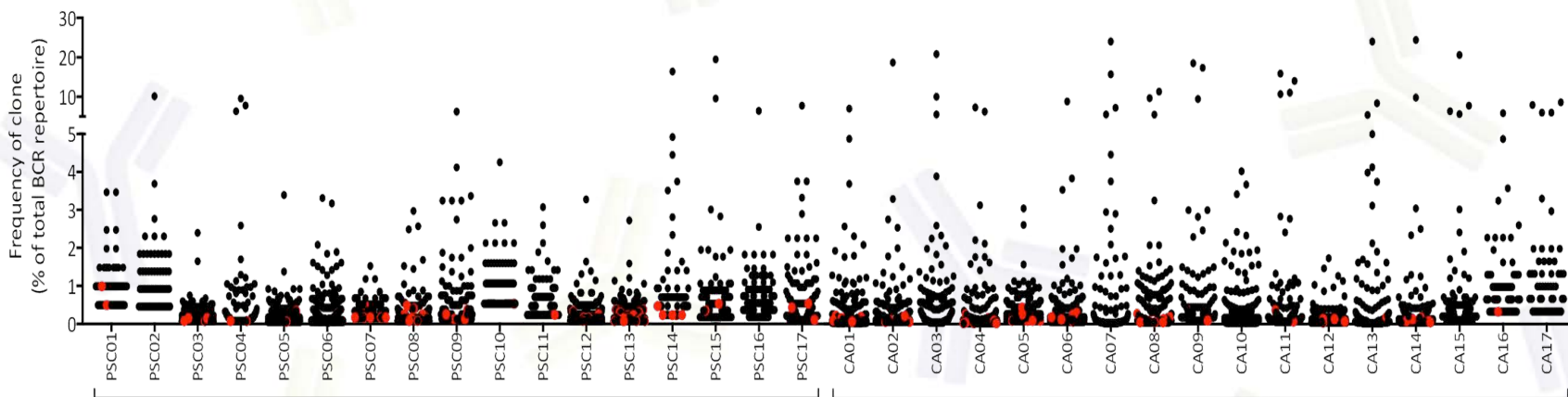
Diagnosis is problematic

¹Consensus statement on the pathology of IgG4-related disease: Deshpande V, et al. Mod Pathol. 2012; 25:1181.

IgG4-RD : PB BCR (red = IgG4)



IgG4-related disease



primary sclerosing cholangitis

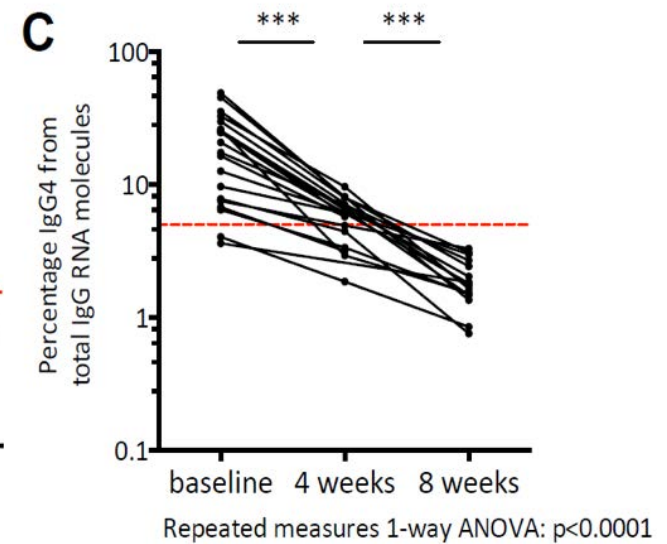
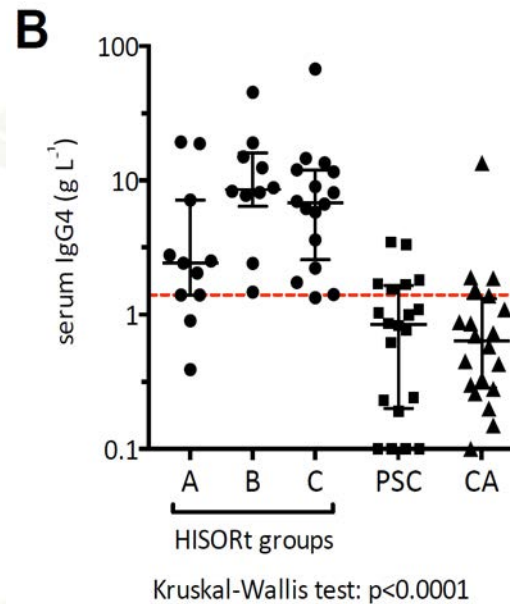
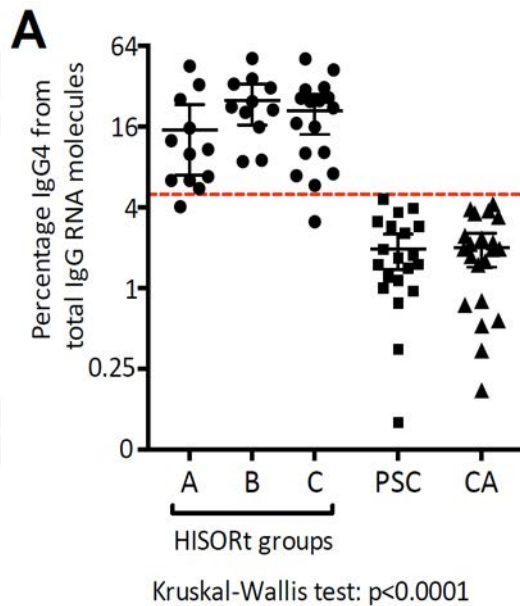
carcinoma

To summarize IgG4-RD

Excellent diagnostic marker

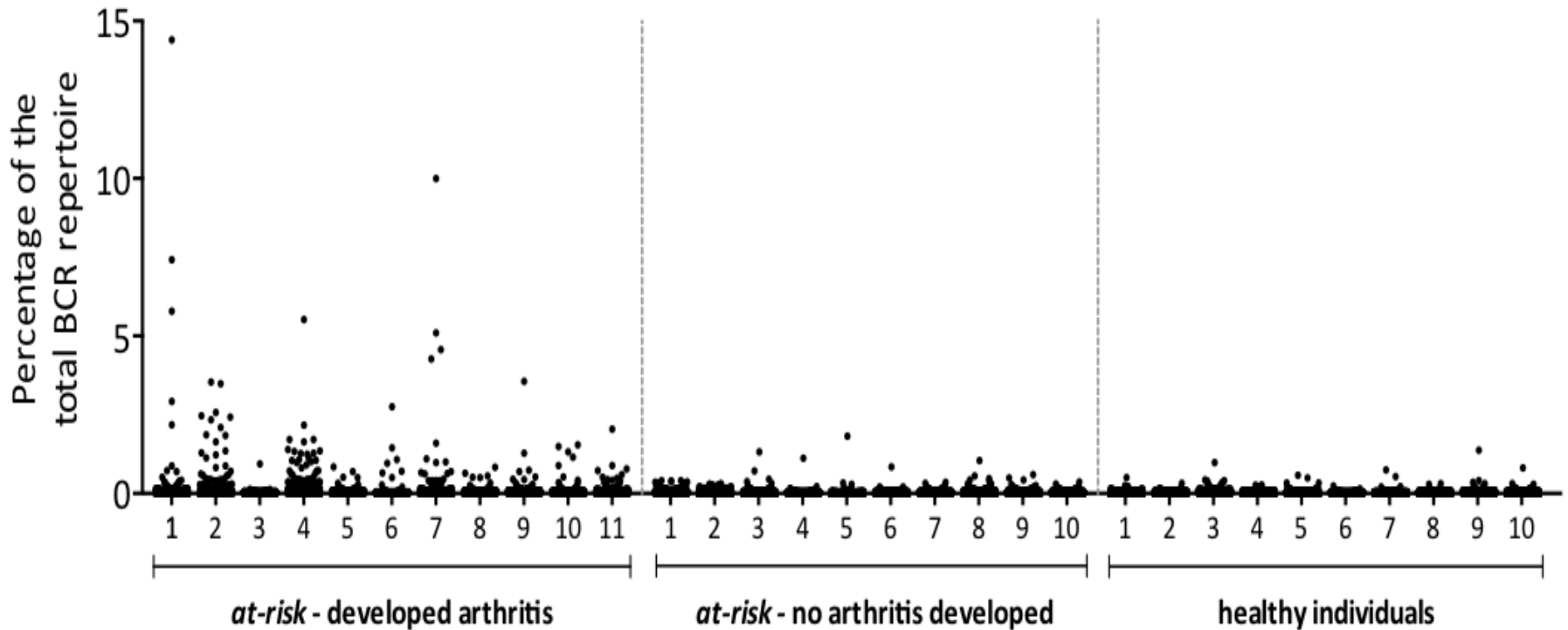
Outperforms IgG4 serum protein

Reflects disease activity



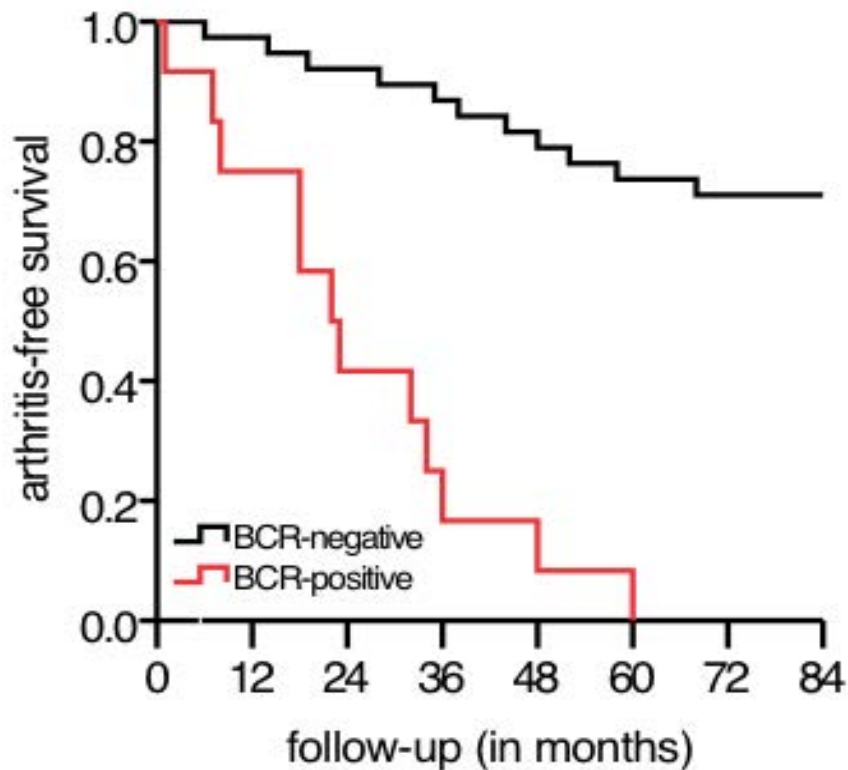
Doorenspleet et al. Hepatology 2016

PB BCR in arthralgia with IgM-RF or anti-CCP2 antibodies



Increased number of dominant BCR clones heralds imminent onset of (rheumatoid) arthritis

Validation : Kaplan Meier curve



These dominant clones:

- Are not present in the synovium in the arthralgia stage
- But are present in the synovium during onset of arthritis

Tak PP, et al. Ann Rheum Dis. 2017 Aug 8

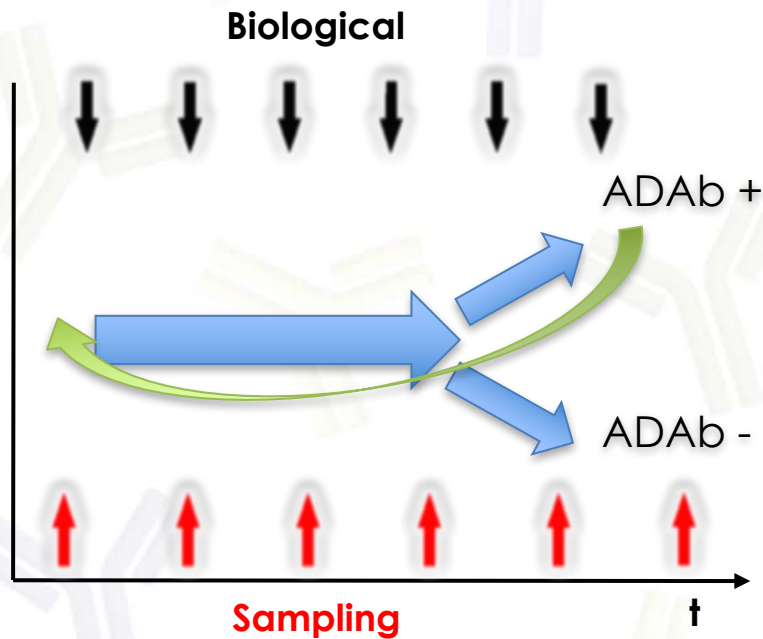
Main points to emphasize:

1. **Cells are not static** : they differentiate and migrate
2. **Cells \neq antibodies** : Different kinetics, give different representations of the same immunological response
3. **Cellular B cell responses correlate with immunological activity**
4. **Antibodies \neq active disease**

NGS-based cellular analysis can help:

1. Direct assessment of cellular ADR
2. Identification of drug characteristics contributing to cellular B/T-cell responses and subsequent (humoral) immunogenicity
3. Sensitive assessment of active antidrug responses & epitope spreading in patients

Molecular fingerprinting of anti-drug responses



1. Identify and fingerprint anti-drug T- and B-cell responses
2. Show development of anti-drug responses over time
3. Phenotype/Genotype drug-responsive cells early on

Predictive tools for anti-drug immunogenicity
 Novel targets for preventing anti-drug responses

- Technological advances and preliminary results on NGS-based analysis of B- and T-cell receptor repertoires were discussed
- Manuscripts in preparation

Overall conclusions

- Reliable sensitive quantitative assessment of clonal B- and T-cell responses introduces statistical evaluation of immune responses at the clonal level
- Allows:
 - Linking of clonal responses to antigen specificity (epitopes)
 - Linking *in vitro* to *in vivo* clonal responses & phenotypes
- Can be used to
 - detect and monitor active immune responses resulting in immunogenicity
 - Characterize cells involved using single cell approaches
- May find application in:
 - Sensitive detection of immunogenicity issues in preclinical research
 - Rapid epitope mapping



Acknowledgements

Laboratory for Genome Analysis, AMC

Linda Koster & Frank Baas

Clinical Epidemiology, Biostatistics and
Bioinformatics

Aldo Jongejan, **Barbera van Schaik**,
Antoine van Kampen

Institute of Biology and Technologies

CEA-Saclay, France

Marie de Bourayne & Bernard Maillère

Sabrina Pollastro
Anne Musters

Aram Al-Soudi

Giulia Balzaretta

Marieke Doorenspleet

Rebecca Esveldt

Isthu Hageman

Paul Klarenbeek

Ilse Niewold

