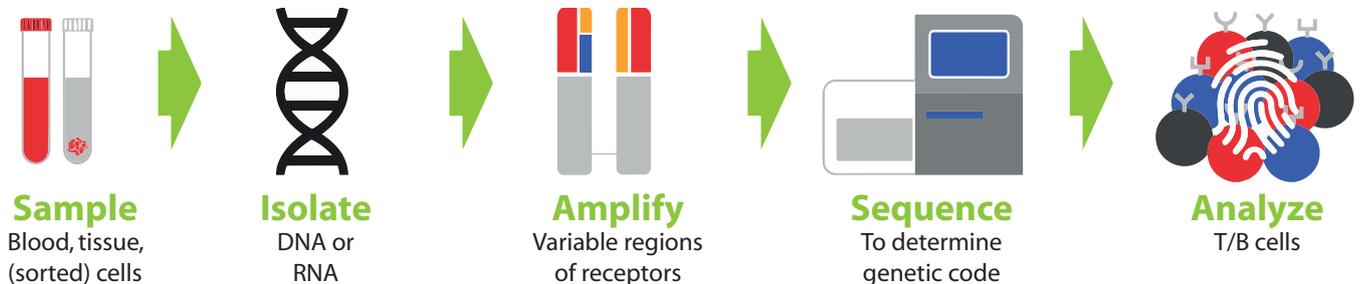# Viroclinics

A Cerba Research Company

B/T-cell immune repertoire sequencing

Advancing your research with full-service immune repertoire sequencing and analysis

High-throughput repertoire sequencing has created an unprecedentedly high-resolution picture of dynamic changes in TCR and BCR repertoire diversity. This data is being used in target discovery (e.g. T-cell based therapies), vaccine development (antibody selection) or to monitor treatment in patients. Viroclinics-DDL, together with ENPICOM, have joined forces to offer full-service immune repertoire sequencing and analyses.

PROCESS AT A GLANCE

Sample
Blood, tissue, (sorted) cells

Isolate
DNA or RNA

Amplify
Variable regions of receptors

Sequence
To determine genetic code

Analyze
T/B cells

- Bulk T-and B- cell receptor next-generation sequencing
- Unbiased RNA amplification thanks to 5' RACE amplification
- Error correction through unique molecular identifiers (UMIs)
- Intuitive analysis software (Enpicom IGX Platform)

COMMON SAMPLE TYPES

Sample type	Recommended sample amount per isolation	Min – max sample amount
Peripheral blood mononuclear cells (PBMCs)	5 million cells	1-10 million cells
(sorted*) B- or T-cells	1 million cells	10.000 – 3 million cells
RNA	40-80 ng/μL	50-1000 ng

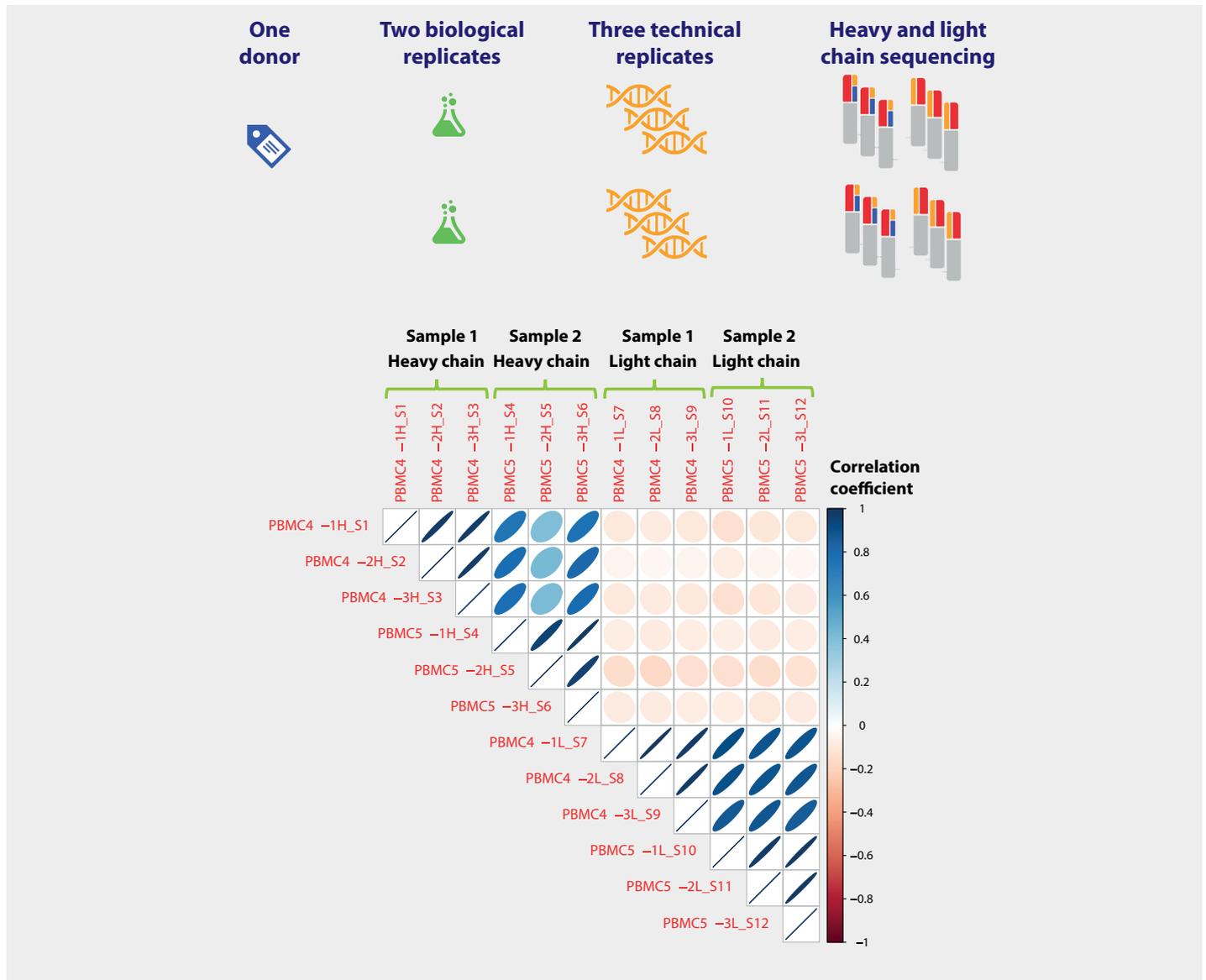*cell sorting service available*

DATA ANALYSIS
- The ImmunoGenomiX (IGX) Platform
- Platform designed to analyze, visualize, and interpret immune repertoire sequencing data
- Example analyses:
  - Gene usage (VDJ)
  - Diversity analysis (richness, Shannon entropy)
  - Overlap in clones between samples
  - Lineage analysis (receptor phylogeny, mutation quantification)

ENPICOM
DECODING THE IMMUNE SYSTEM

IGX
PLATFORM

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DATA: TECHNICAL AND BIOLOGICAL SAMPLE CORRELATION

- Bulk B-cell receptor repertoire sequencing
- Experimental set-up:

One donor **Two biological replicates** **Three technical replicates** **Heavy and light chain sequencing**

Correlation coefficient

CONCLUSION

- High correlation for technical replicates
- Light and heavy chains not correlated (as expected, no cross-contamination)
- Correspondance between abundant clones in biological replicates

CONTACT OUR EXPERT TEAM TO DISCUSS THE POSSIBILITIES

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