

# Personalized mass spectrometry as a tool for minimal residual disease detection in the blood of myeloma patients

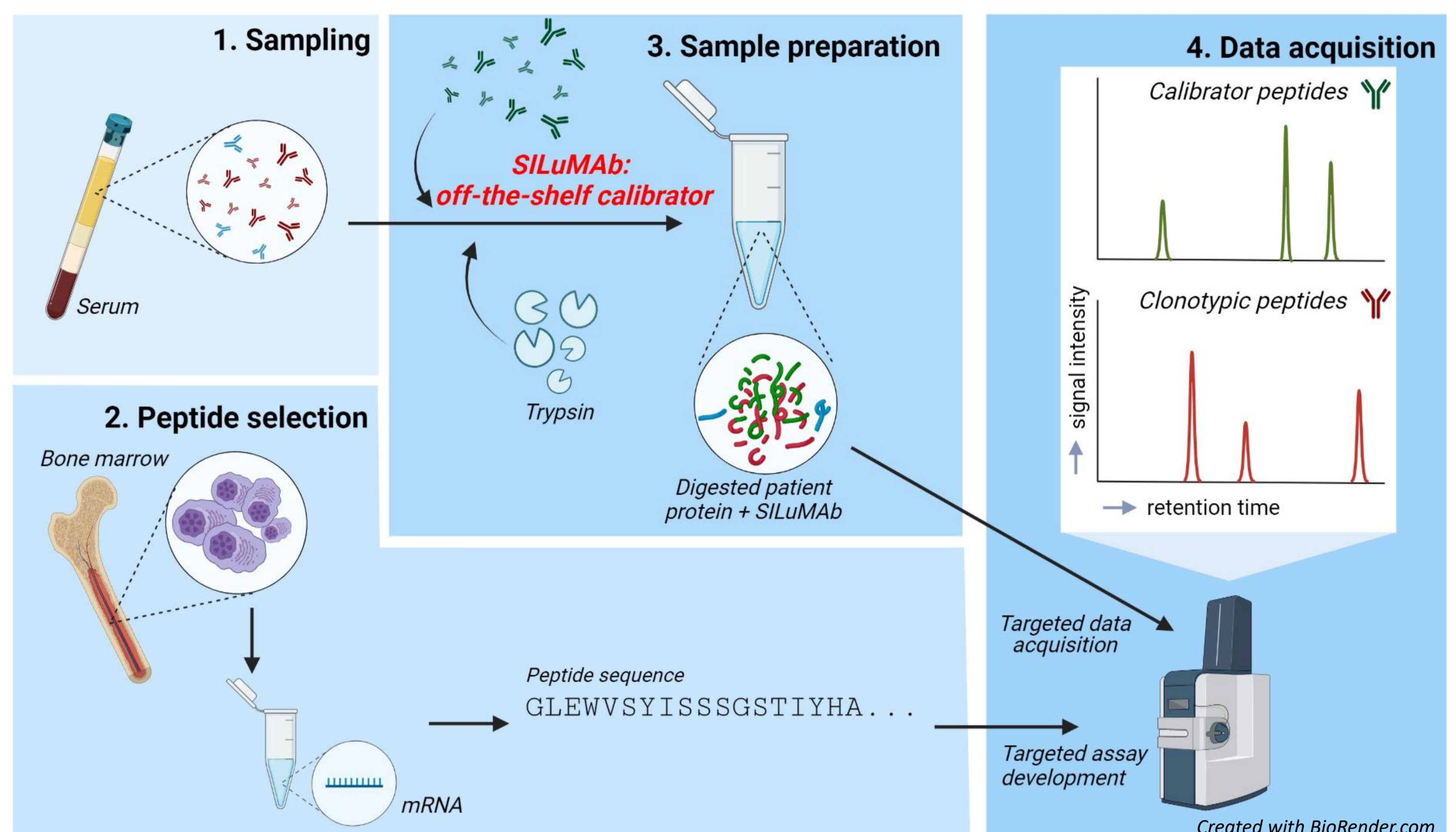
Wijnands C.<sup>a</sup>, Noori S.<sup>b</sup>, Langerhorst P.<sup>a</sup>, Gloerich J.<sup>c</sup>, Bonifay V.<sup>d</sup>, Sonigo P.<sup>d</sup>, Touzeau C.<sup>e</sup>, Corre J.<sup>f</sup>, Perrot A.<sup>g</sup>, Moreau P.<sup>h</sup>, Caillon H.<sup>i</sup>, Luider T.<sup>b</sup>, van Gool A.<sup>c</sup>, Dejoie, T.<sup>i</sup>, VanDuijn, M.<sup>b</sup>, Jacobs J.<sup>a</sup>

## Background

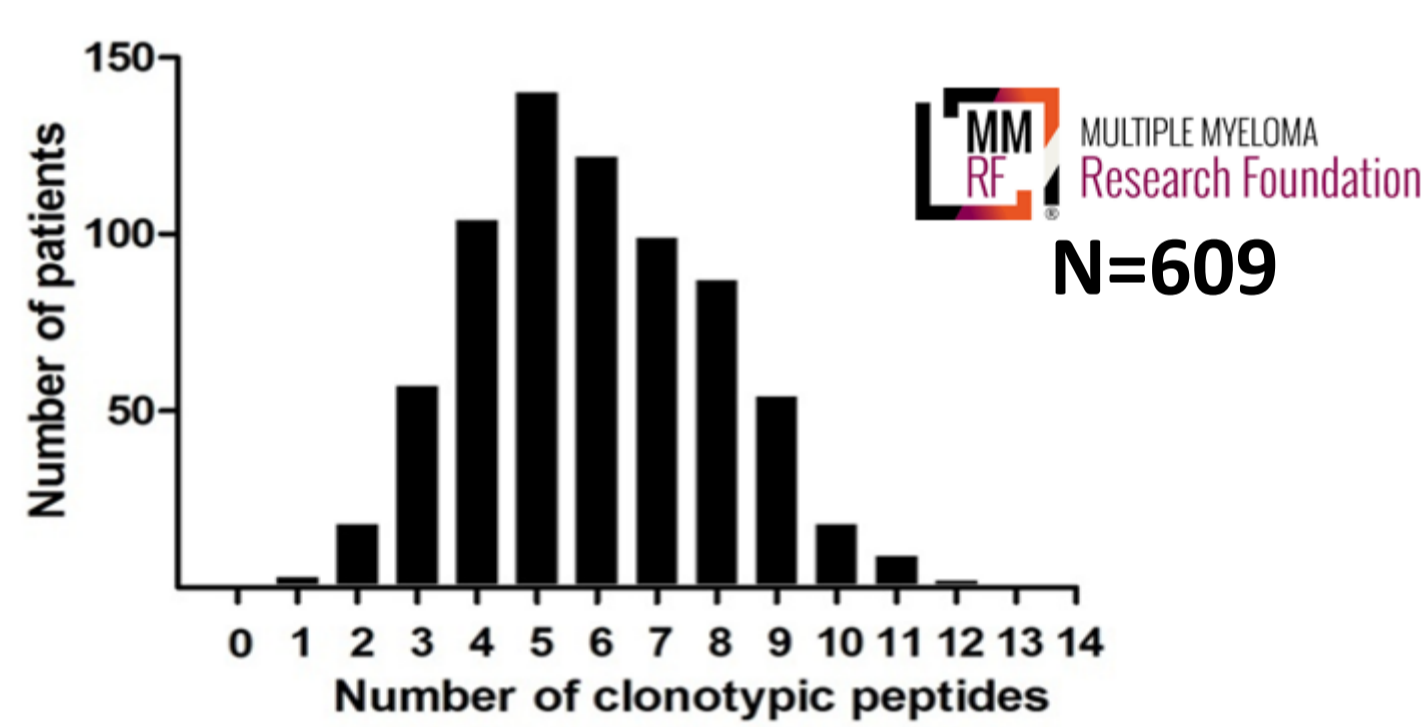
- **Multiple Myeloma (MM)** is characterized by a clonal expansion of plasma cells, which overproduce a monoclonal immunoglobulin (**M-protein**).
- The M-protein provides a patient specific biomarker that is important for diagnosis and disease monitoring.
- Serum Protein Electrophoresis (SPE) is used in routine diagnostics, but lacks **sensitivity** to measure low disease activity (**Minimal Residual Disease, MRD**).
- Current MRD-detecting methods all rely on **bone marrow biopsies**. This is a highly invasive procedure, making it unsuitable for frequent sampling, but it can also lead to sampling bias due to the heterogeneous nature of MM cells.
- **MS-MRD** is an ultrasensitive **targeted mass spectrometry blood-test**. Furthermore, MS-MRD is a **personalized assay**, because unique peptides originating from the variable region of the M-protein are targeted.
- Quantification of MS-MRD data is usually performed using Stable Isotope Labeled (SIL) peptides. They offer the best possible reference for M-protein peptides. However, using SIL peptides is time-consuming and expensive. We have developed an MS-MRD method that uses a **universal calibrator (SILuMAB)** to quantify M-protein concentrations in all patients.

<sup>a</sup> Laboratory Medical Immunology, Department of Laboratory Medicine, Radboud university medical center, Nijmegen, The Netherlands  
<sup>b</sup> Department of Neurology, Erasmus University Medical Center, Rotterdam, The Netherlands  
<sup>c</sup> Translational Metabolic Laboratory, Department of Laboratory Medicine, Radboud university medical center, Nijmegen, The Netherlands  
<sup>d</sup> Sebia, Lisses, France  
<sup>e</sup> Centre Hospitalier Universitaire de Nantes, Nantes, France  
<sup>f</sup> Unite de Genomique du Myelome, Institut universitaire du cancer de Toulouse Oncopole, Toulouse, France  
<sup>g</sup> Institut Universitaire du Cancer de Toulouse-OncoPole, Toulouse, France  
<sup>h</sup> Hematology, University Hospital Hôtel-Dieu, Nantes, France  
<sup>i</sup> Biochemistry Laboratory, Hospital of Nantes, Nantes, France

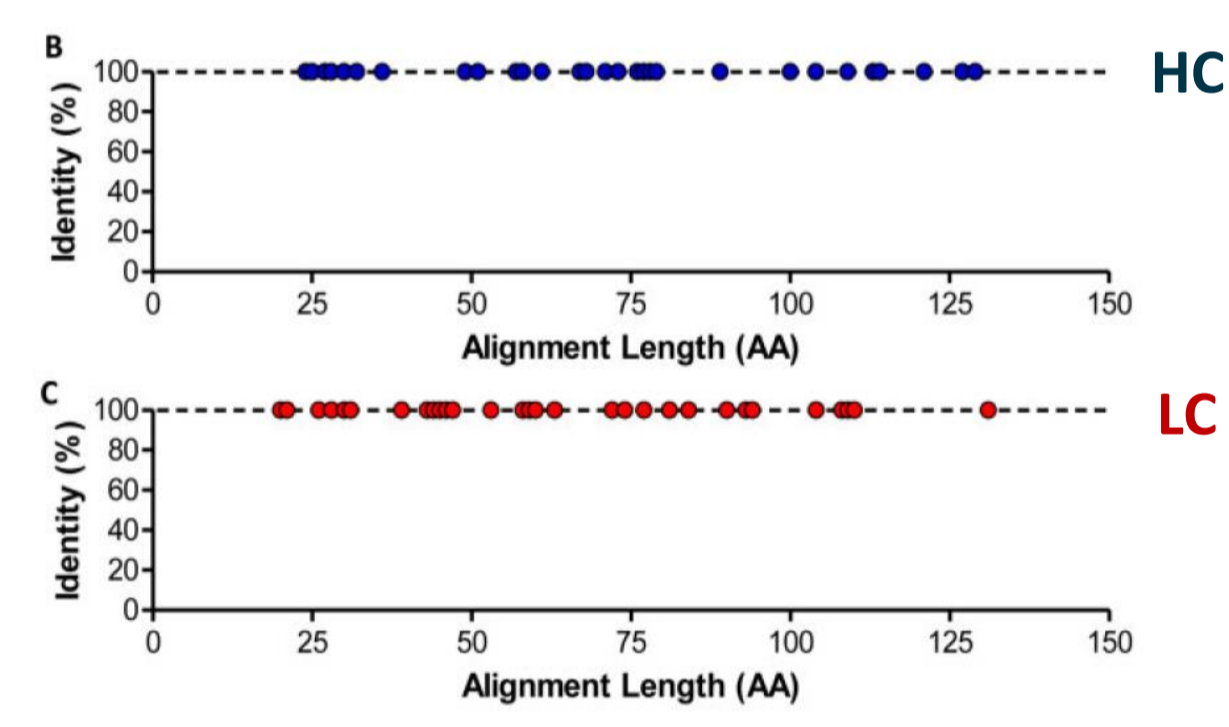
## Materials and Methods: MS-MRD



## MS-MRD feasible in 100% MM patients

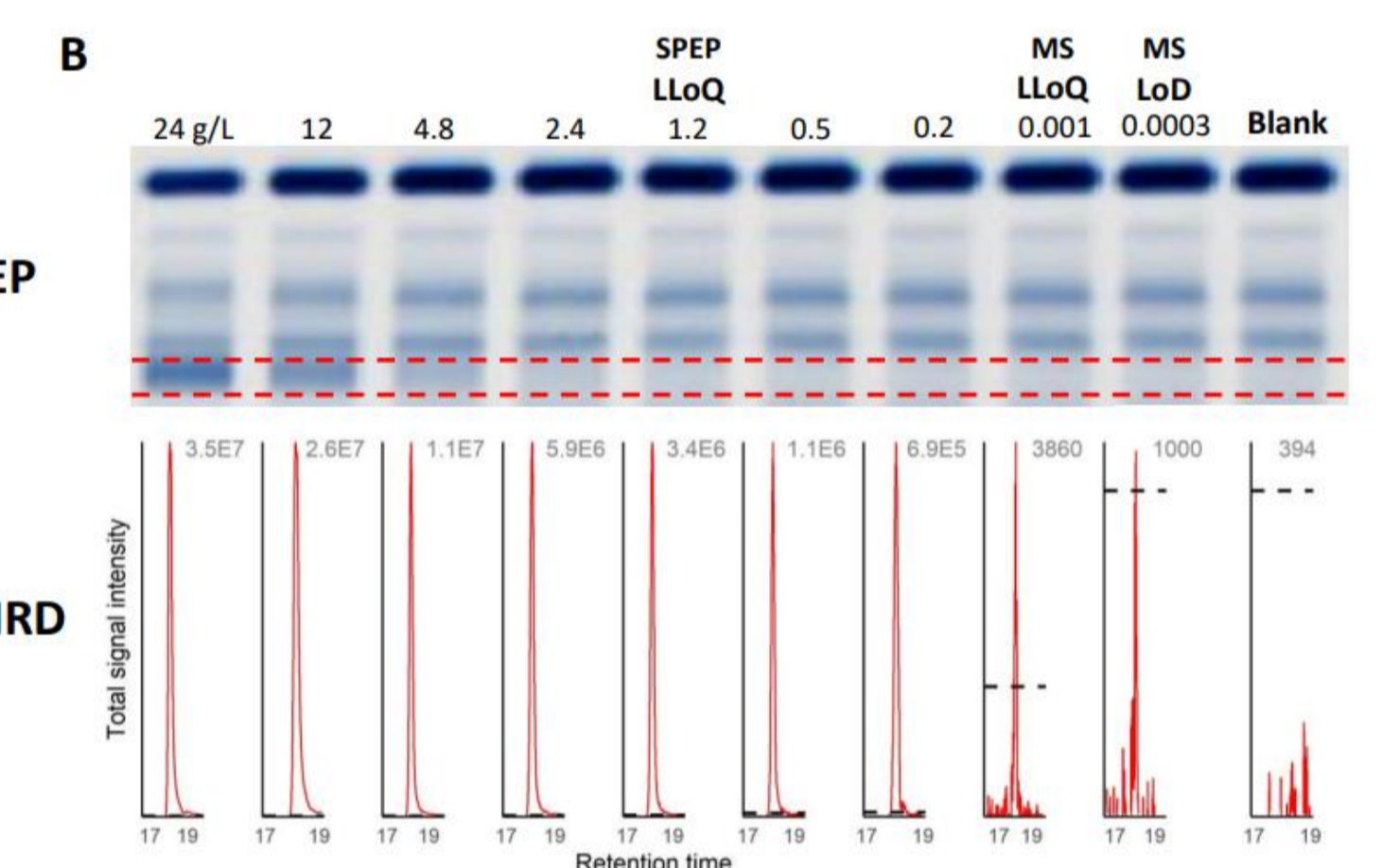
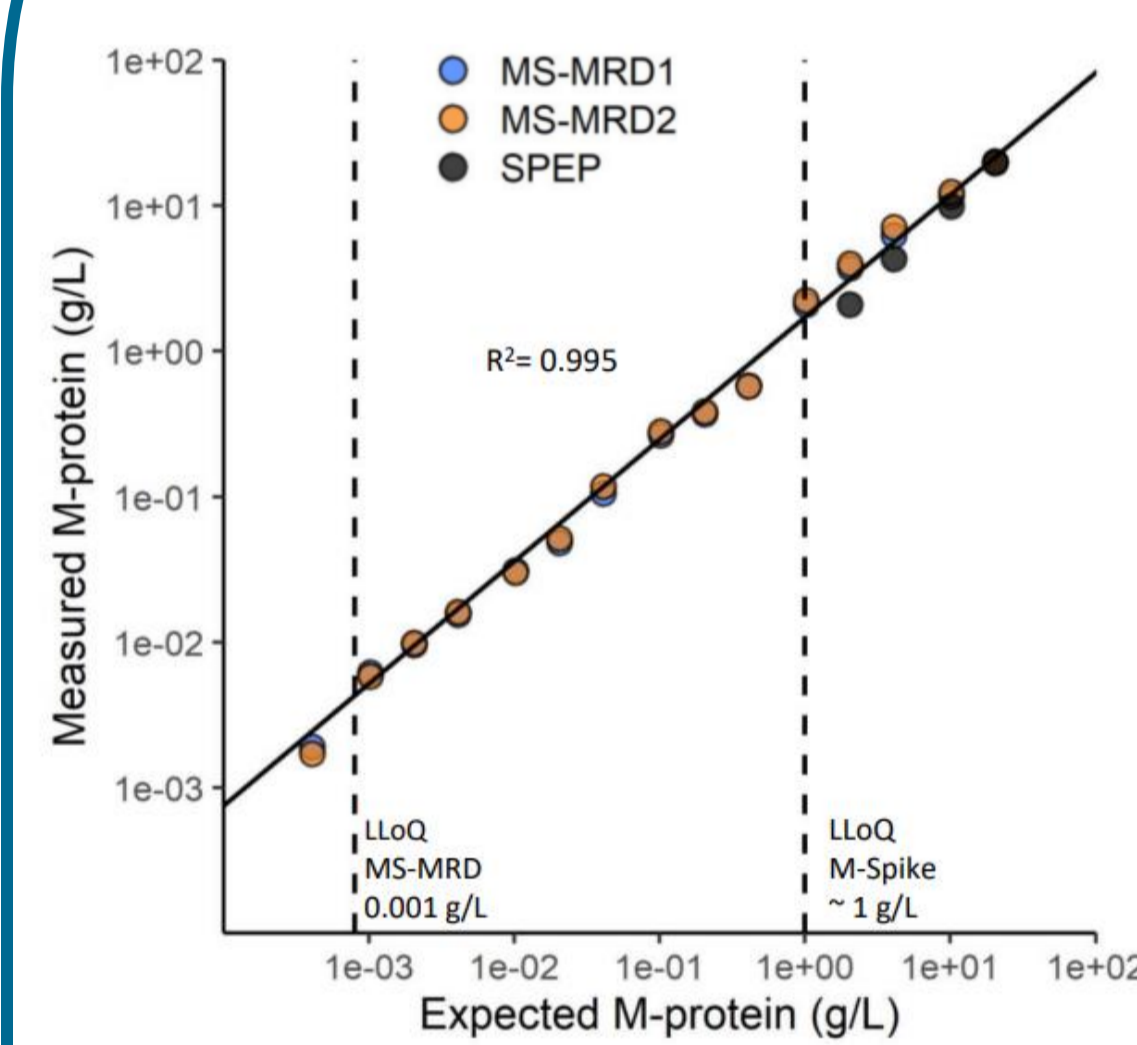


Suitable clonotypic peptides are found in 100% of MM patients

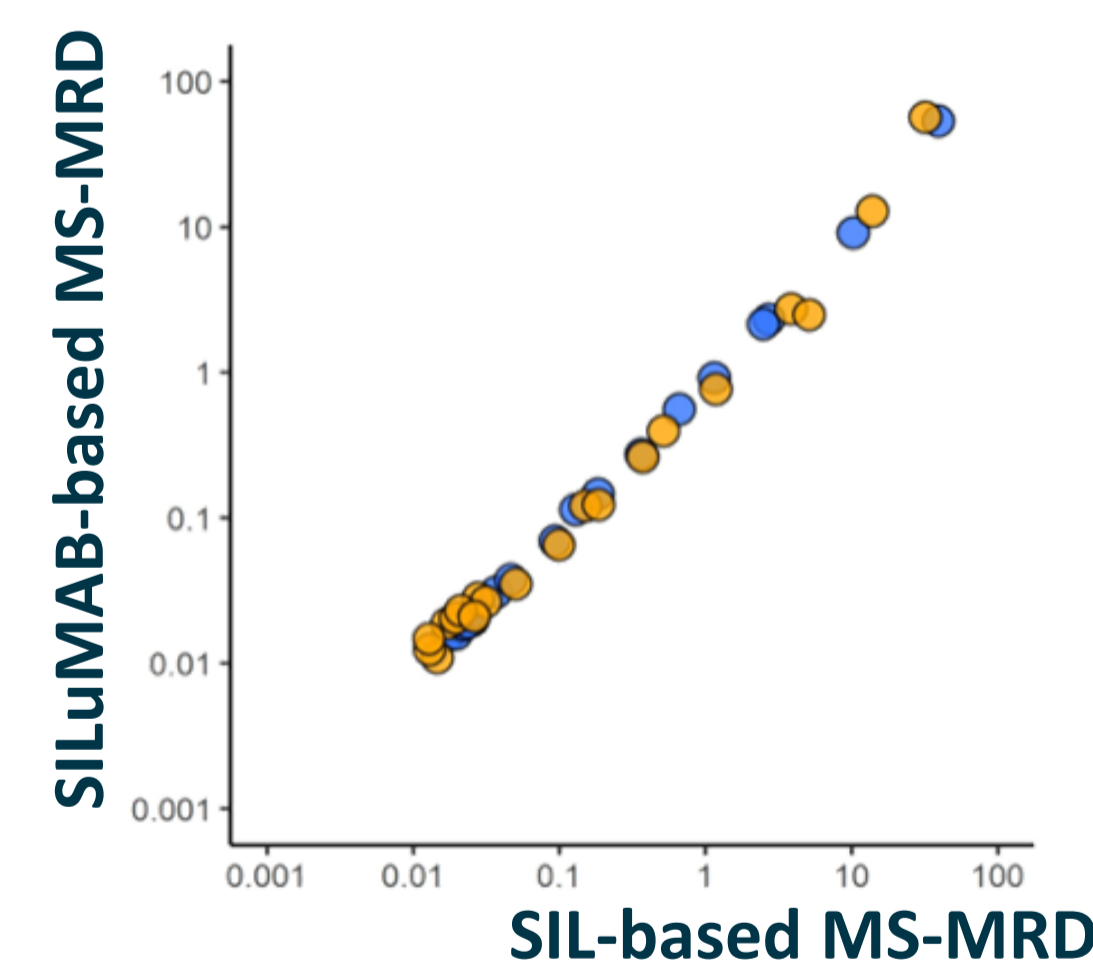


Clonotypic peptides are stable in 100% of MM patients

## MS-MRD with off-the-shelf calibrator

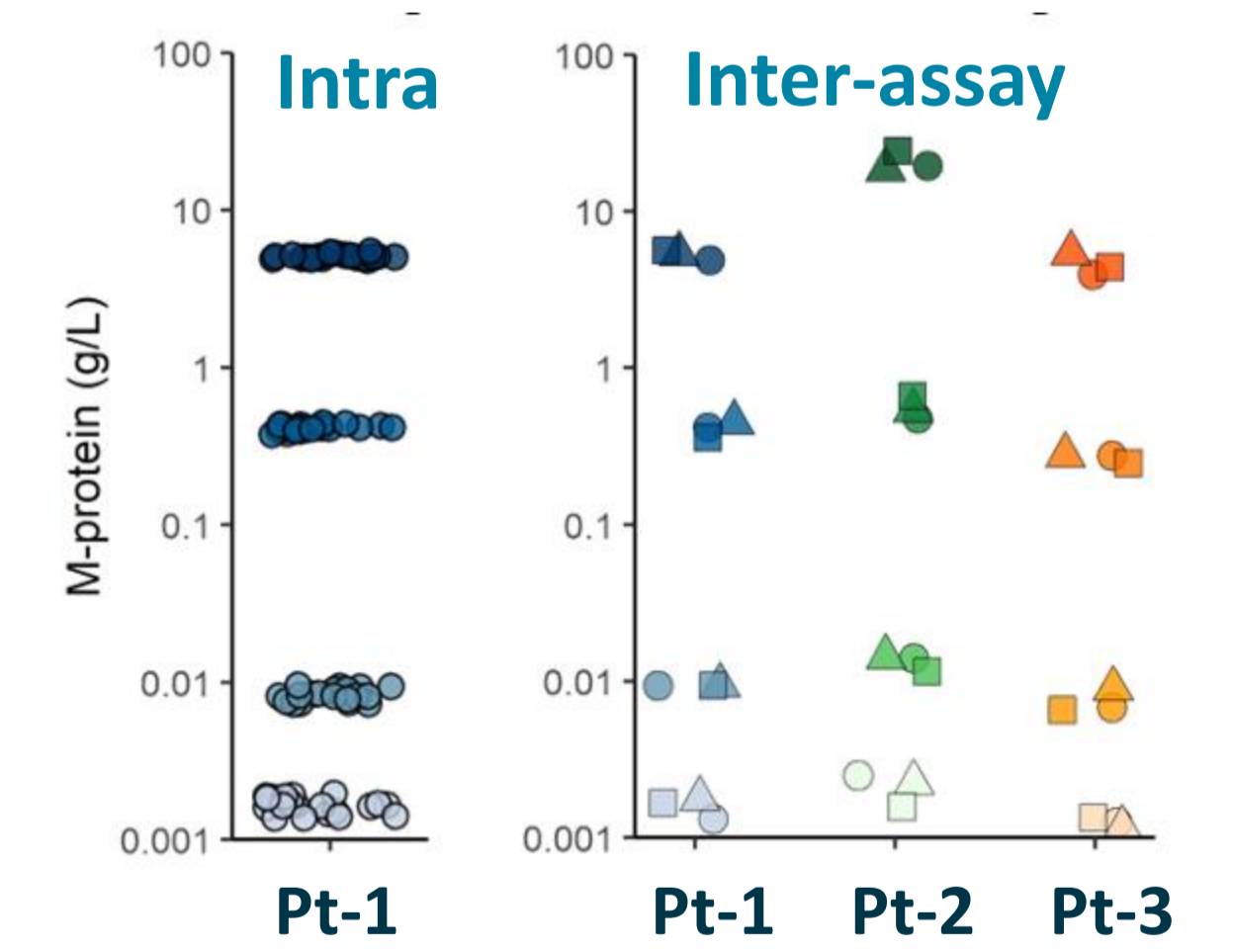


### Method comparison



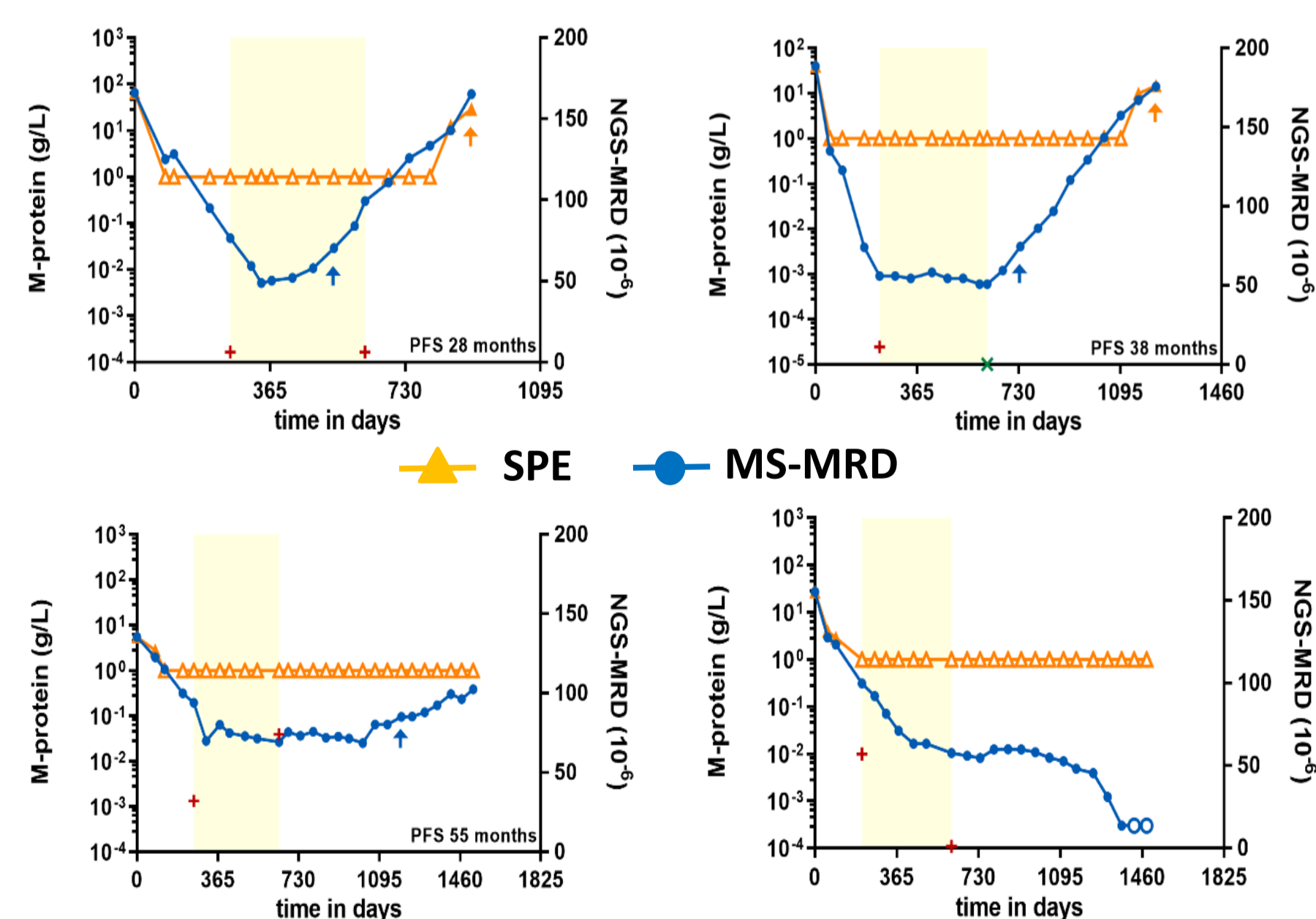
- SILuMAB universal calibrator provides excellent linearity over 4 log scales.
- Average intra-assay CV = 9%; Average Inter-assay CV = 15%

### Reproducibility



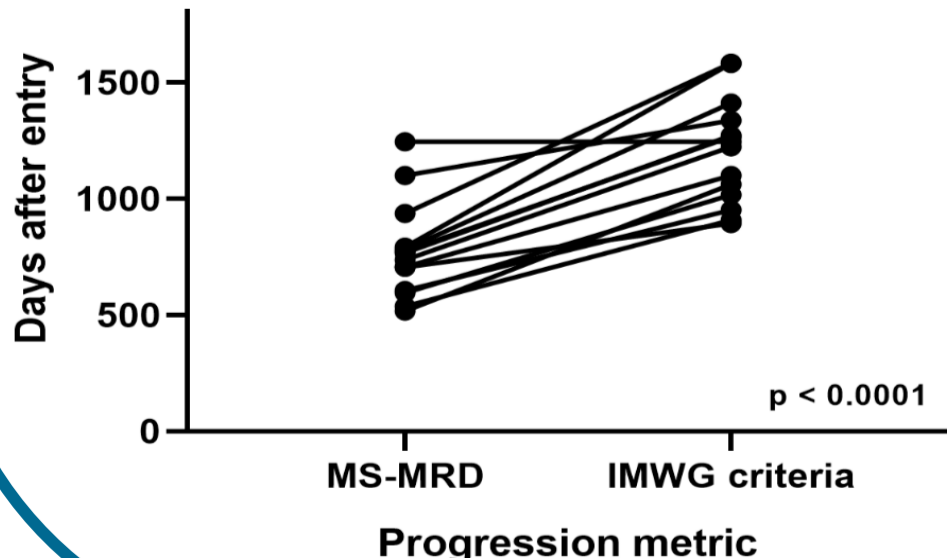
## Dynamic monitoring in serum at MRD level

- MS-MRD validated on 926 follow-up sera of 41 patients from the IFM2009 trial.



- Absolute M-protein quantification feasible.
- 1000-fold increased sensitivity compared to SPE.
- Longitudinal monitoring revealed unique kinetics of disease activity.
- M-protein levels frequently changed following changes in treatment regimen.

- MS-MRD detects relapse on average 455 days earlier than routine M-protein diagnostics.



## Conclusions

- MS-MRD is feasible in 100% of patients with MM.
- The MS-MRD blood-test is 1000-fold more sensitive compared to currently used M-protein diagnostics.
- Dynamic MS-MRD monitoring reveals biochemical relapse on average 455 days earlier compared to SPE.
- SILuMAB can be used as off-the-shelf calibrator for MS-MRD M-protein quantification.

## References

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