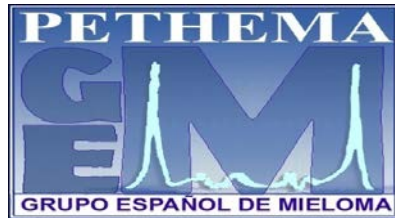


# Dissecting MM: from flow-cytometry to single-cell sequencing



Universidad  
de Navarra

CIMA LAB  
DIAGNOSTICS



**Bruno Paiva**

Flow Cytometry Core - CIMA LAB Diagnostics

Hematology Department - Clinica Universidad de Navarra

Onco-Hematology Research Group – CIMA Universidad de Navarra

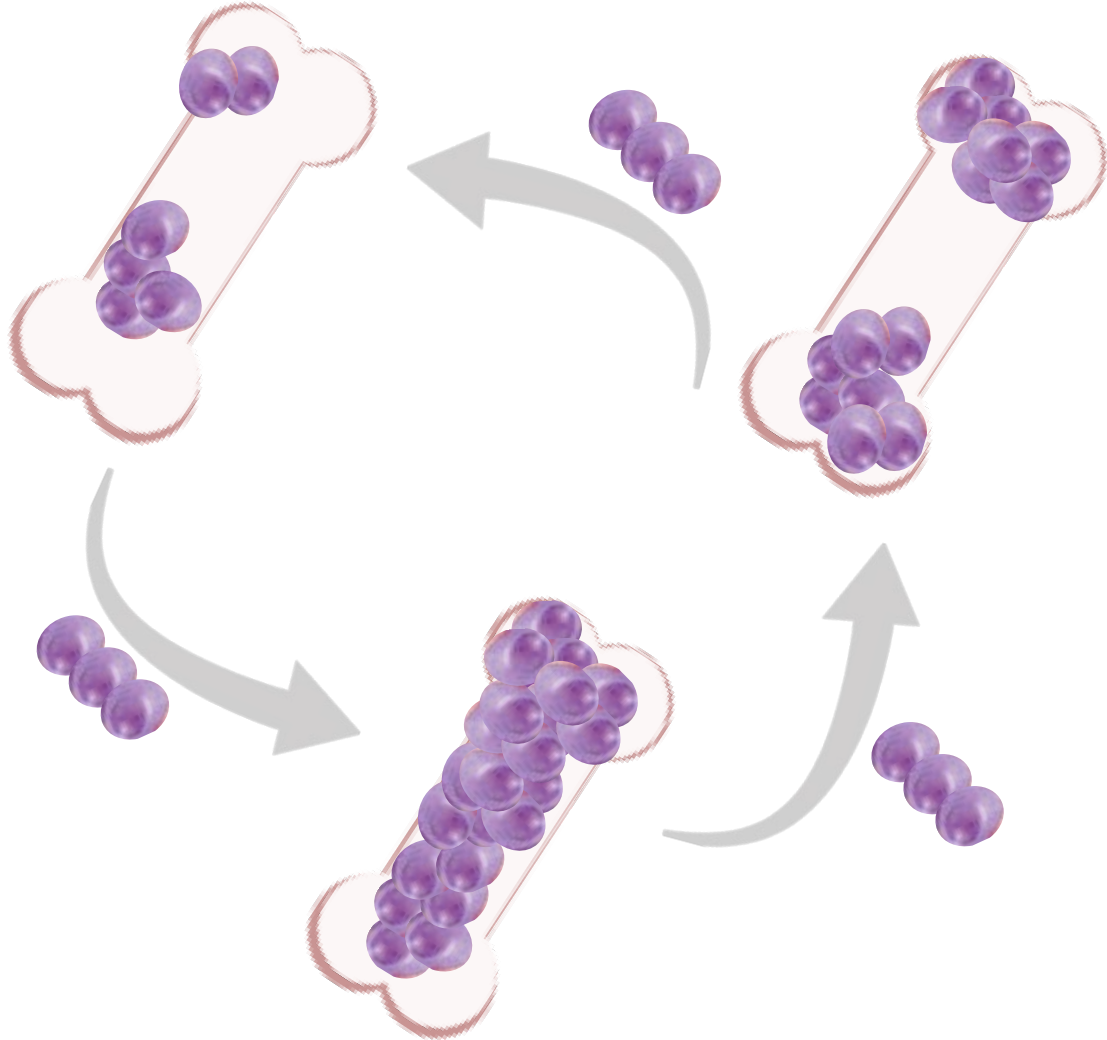
Spanish Myeloma Group (PETHEMA/GEM)

EuroFlow Consortium

# Disclosures

- Honoraria
  - Adaptive, Amgen, Becton Dickinson, Bristol Myers Squibb/Celgene, GSK, Janssen, Sanofi, Takeda
- Research funding (institution)
  - BeiGene, Bristol Myers Squibb/Celgene, GSK, Roche, Sanofi, Takeda
- Advisory board
  - Bristol Myers Squibb/Celgene, GSK, Janssen, Roche, Sanofi
- Consultant
  - Bristol Myers Squibb/Celgene, Janssen, Sanofi, Takeda

# CTC numbers are a potential surrogate of tumor burden, proliferation, niche occupancy and dissemination



There are no unifying genetic events associated with tumor egress from the BM<sup>1</sup>

Fully occupied hypoxic BM niches together with a pro-inflammatory tumor microenvironment force cancer cells to stop proliferating, recirculate in PB and seek other BM niches to continue growing<sup>2</sup>

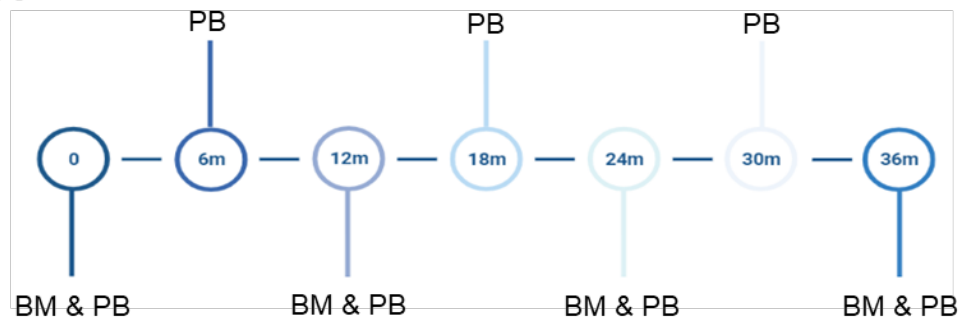
CTCs are a powerful prognostic factor<sup>3-4</sup>

1. Garces JJ, et al. Leukemia. 2020;34(2):589-603.
2. Garces JJ, et al. Leukemia 2020;34(11):3007-3018.
3. Garces JJ, et al. J Clin Oncol. 2022;40(27):3151-3161.
4. Termini R, et al. Clin Cancer Res. 2022;28(21):4771-4781.

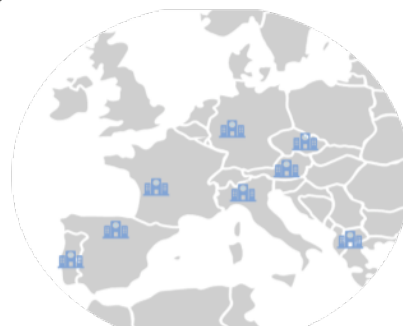
# Tumor and immune blood biomarkers in smoldering MM

## The iMMunocell project

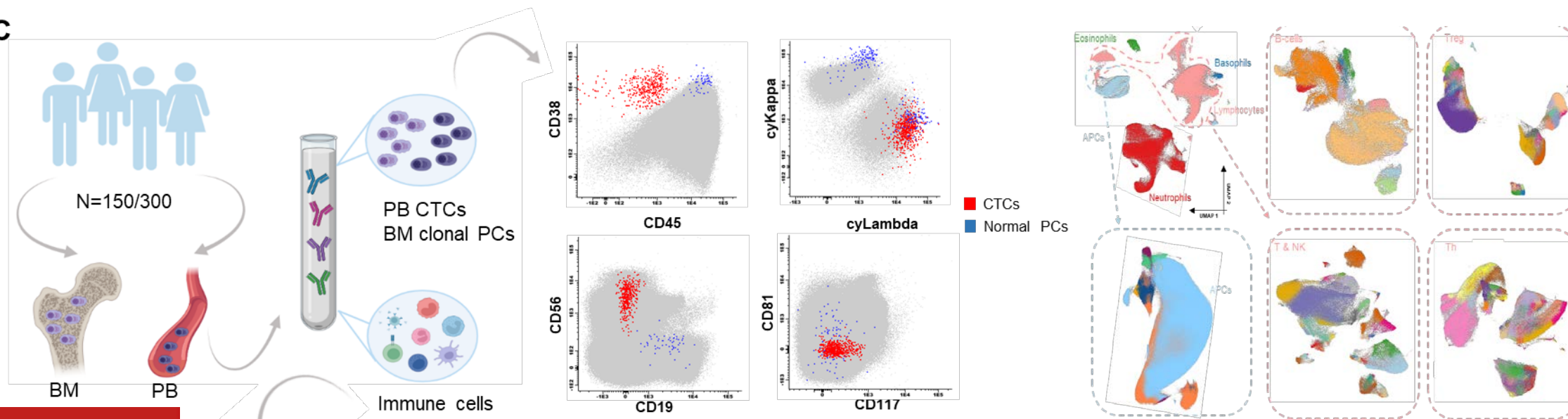
A



B



C

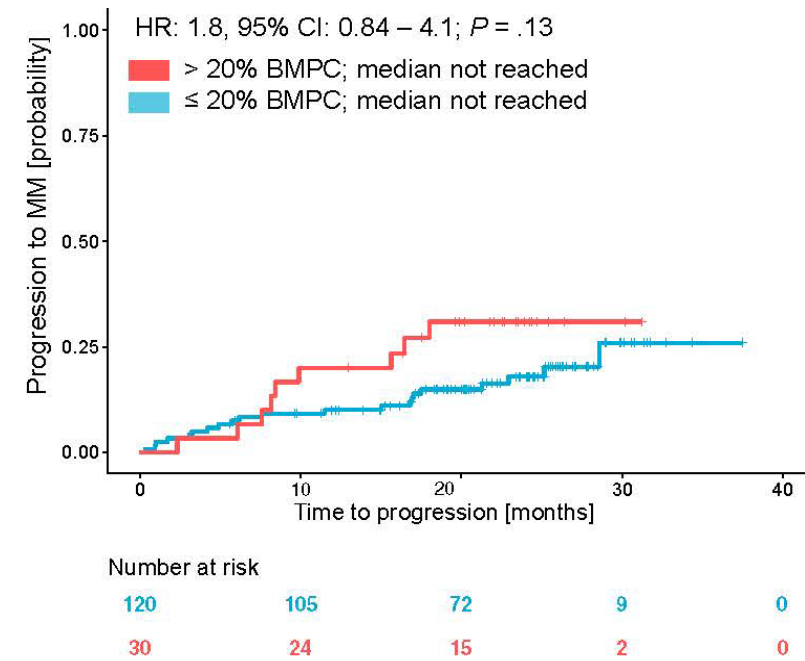


# CTCs outperform BM PCs to predict TTP in SMM

Paving the way for minimally-invasive models

>0.015% CTCs

>20% BM PC

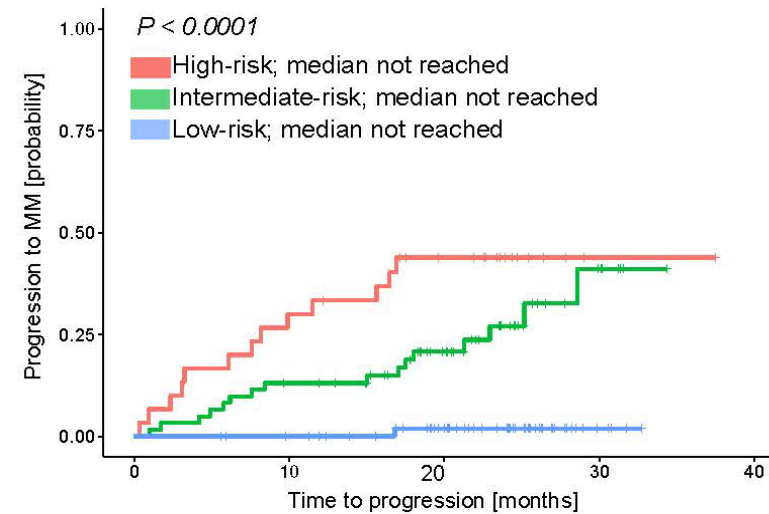


# CTCs can replace BM PCs in the IMWG risk model for SMM

Similar performance between minimally and partially invasive models

2/20/0.015 Model (>0.015% CTCs)

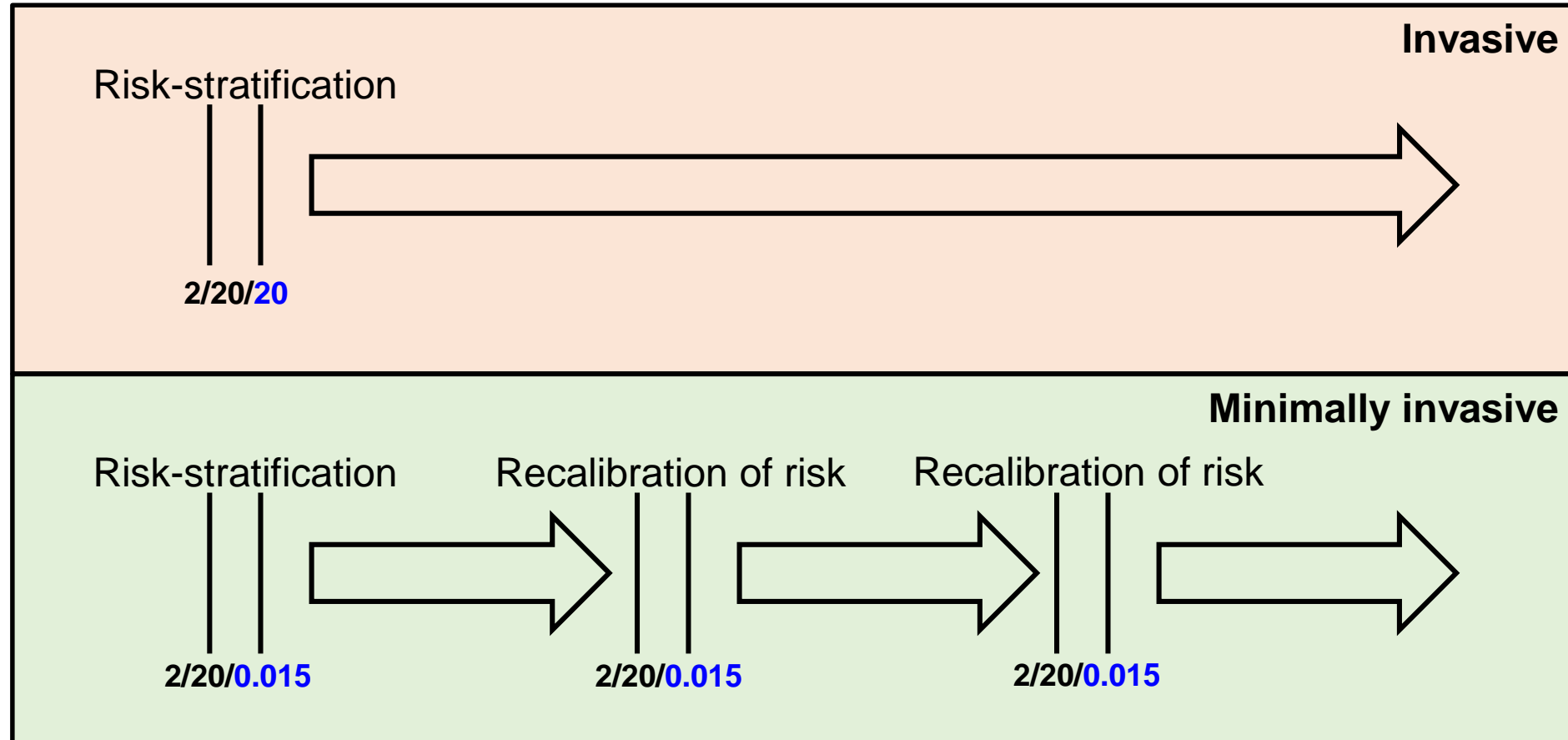
2/20/20 Model (>20% BMPC)





# Possible added value of dynamic risk-stratification in SMM

Replacing invasive by minimally invasive tumor burden assessment in the model



# iMMunocell (sub-analysis in patients with >3 time points)

## Temporal cluster CTC-dynamics (757 assessments)

**Sustained undetectable CTCs**

n= 20

Median n° of observations: 4  
**100% TTP** at 28 months  
 Total assessments: 85

**Detectable CTC values**

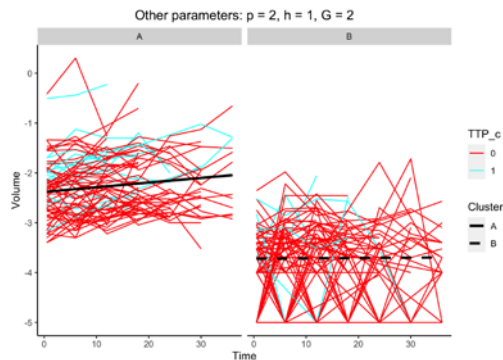
n= 144

Cluster A n= 71

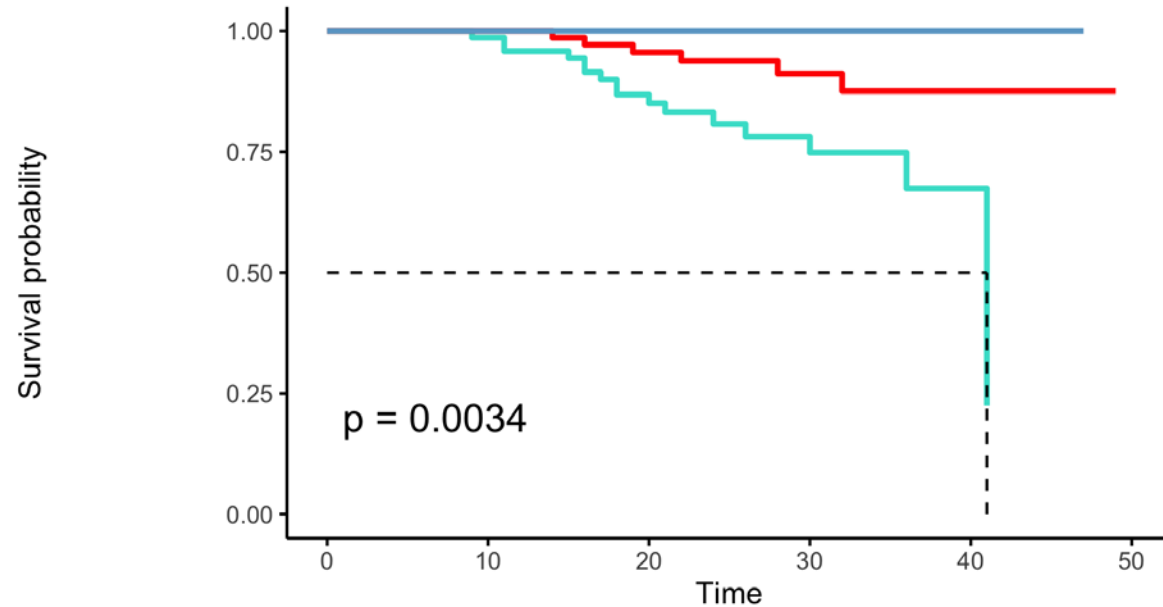
Median n° of observations: 4  
**78% TTP** at 28 months  
 Total assessments: 333

Cluster B n= 71

Median n° of observations: 5  
**91% TTP** at 28 months  
 Total assessments: 339



Strata cluster\_2=A cluster\_2=B cluster\_2=Sustained

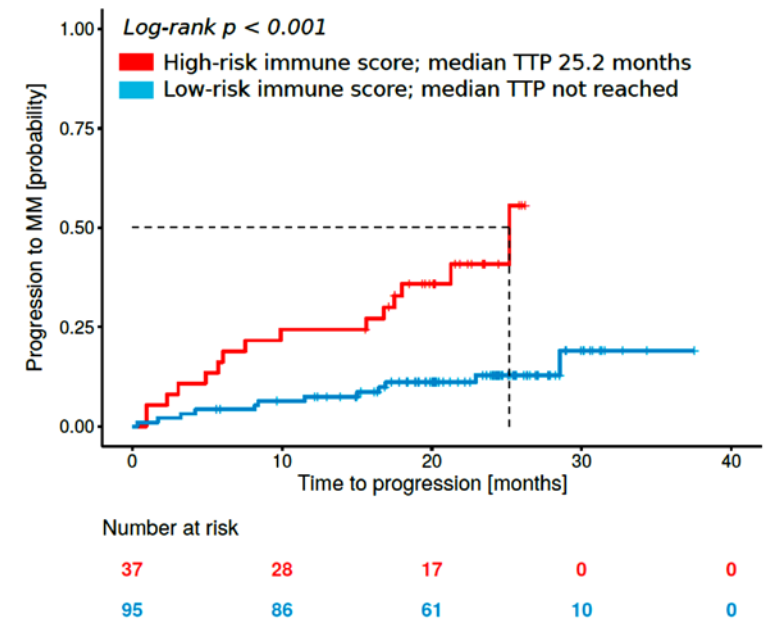
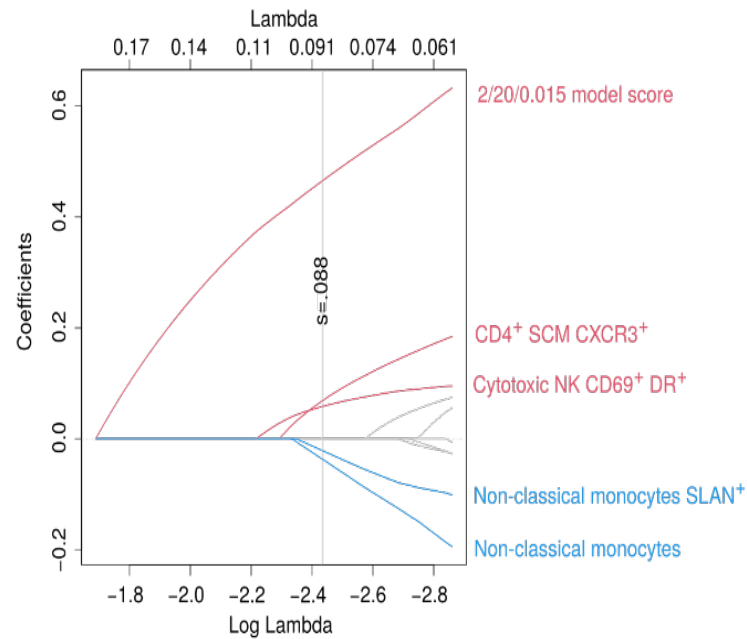
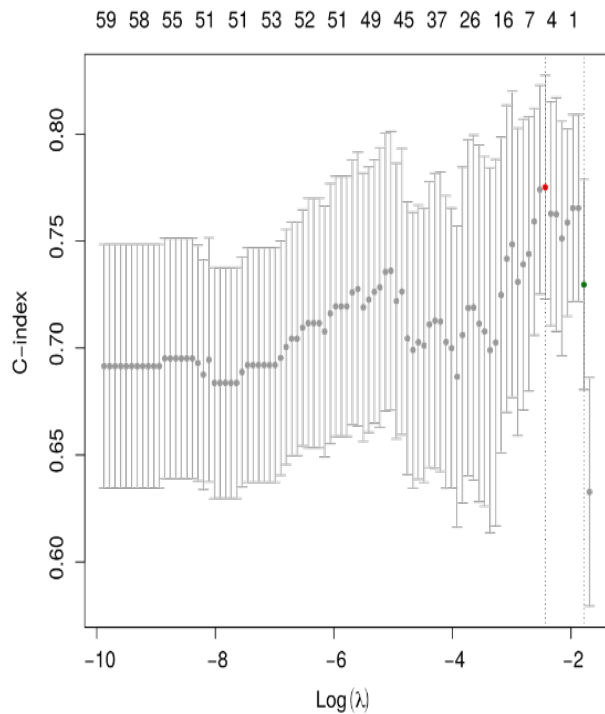


		Number at risk				
		10	20	30	40	50
Strata	cluster_2=A	71	49	24	3	0
	cluster_2=B	71	59	29	3	0
	cluster_2=Sustained	20	15	6	1	0
		10	20	30	40	50



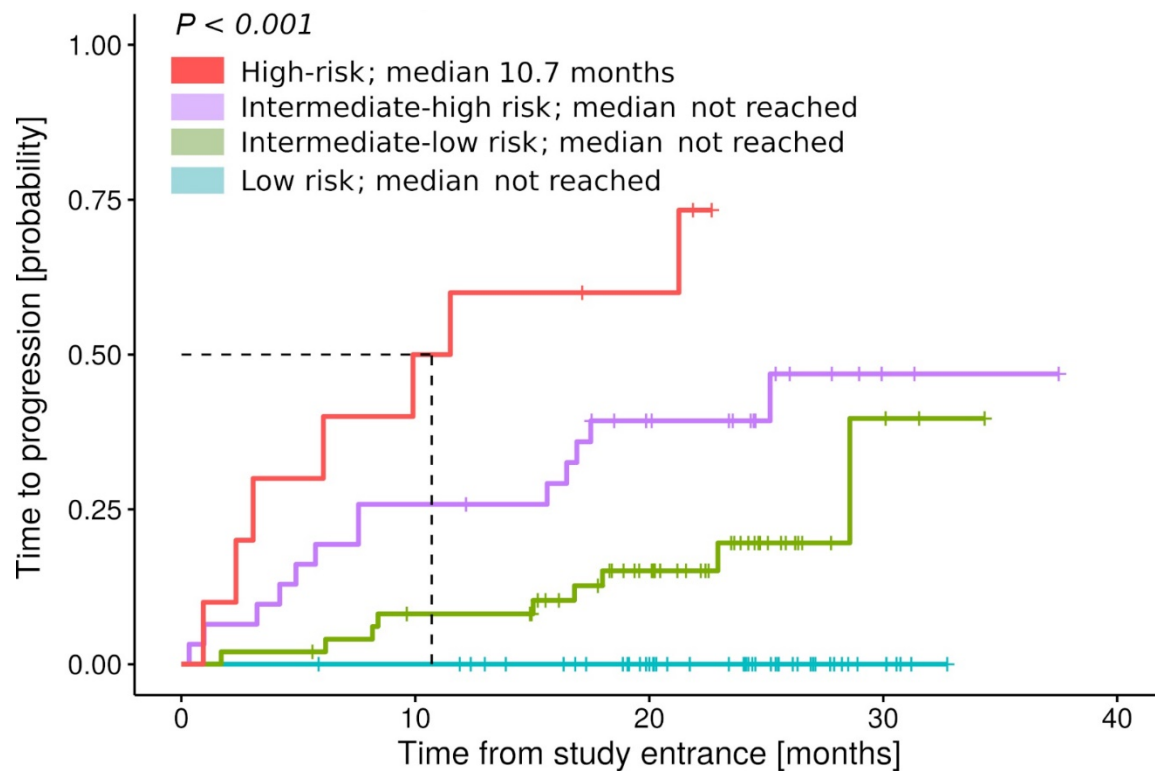
# Immune cell types complementary to the 20/2/0.015 model

Selected by lasso penalized cox model (non-zero coefficient at optimal lambda)



# Minimally invasive tumor and immune model

2/20/2/0.015 risk score (>2 immune risk factor)



Number at risk

46	45	33	5	0
50	44	29	3	0
31	23	15	2	0
10	5	3	0	0

# Prognostic value of CTCs in newly diagnosed active MM

5 independent studies published in 2022 at the J Clin Oncol

## More Than 2% of Circulating Tumor Plasma Cells Defines Plasma Cell Leukemia–Like Multiple Myeloma

Tomas Jelinek, MD, PhD<sup>1</sup>; Renata Bezdekova, PhD<sup>2</sup>; David Zihala, PhD<sup>1</sup>; Tereza Sevcikova, PhD<sup>1,2</sup>; Anjana Anilkumar Sithara, MSc<sup>1,2</sup>; Lenka Pospisilova, MSc<sup>4</sup>; Sabina Sevcikova, PhD<sup>5</sup>; Petra Polackova, MSc<sup>2</sup>; Martin Stork, MD, PhD<sup>6</sup>; Zdenka Knechtova, MSc<sup>6</sup>; Ondrej Venglar, MSc<sup>3</sup>; Veronika Kapustova, MSc<sup>1</sup>; Tereza Popkova, MD<sup>1</sup>; Ludmila Muronova, MD<sup>1</sup>; Zuzana Chyra, PhD<sup>1</sup>; Matous Hrdinka, PhD<sup>1</sup>; Michal Simicek, PhD<sup>1</sup>; Juan-Jose Garcés, PhD<sup>7</sup>; Noemi Puig, MD, PhD<sup>8</sup>; Maria-Teresa Cedena, MD, PhD<sup>9</sup>; Artur Jurczynszyn, MD, PhD<sup>10</sup>; Jorge J. Castillo, MD, PhD<sup>11</sup>; Miroslav Penka, MD<sup>2</sup>; Jakub Radocha, MD, PhD<sup>12</sup>; Maria Victoria Mateos, MD<sup>8</sup>; Jesús F. San-Miguel, MD, PhD<sup>7</sup>; Bruno Paiva, PhD<sup>7</sup>; Ludek Pour, MD, PhD<sup>5</sup>; Lucie Rihova, PhD<sup>2</sup>; and Roman Hajek, MD, PhD<sup>1</sup>

## Identification of High-Risk Multiple Myeloma With a Plasma Cell Leukemia-Like Transcriptomic Profile

Davine Hofste op Bruinink, MD, MSc<sup>1,2</sup>; Rowan Kuiper, PhD<sup>1,3</sup>; Mark van Duin, PhD<sup>1</sup>; Tom Cupedo, PhD<sup>1</sup>; Vincent H.J. van der Velden, PhD<sup>2</sup>; Remco Hoogenboezem, MSc<sup>1</sup>; Bronno van der Holt, PhD<sup>4</sup>; H. Berna Beverloo, PhD<sup>5</sup>; Erik T. Valent, PhD<sup>2</sup>; Michael Vermeulen, BSc<sup>1</sup>; Francesca Gay, MD, PhD<sup>6</sup>; Annemiek Broijl, MD, PhD<sup>1</sup>; Hervé Avet-Loiseau, MD, PhD<sup>7</sup>; Nikhil C. Munshi, MD, PhD<sup>8</sup>; Pellegrino Musto, MD<sup>9</sup>; Philippe Moreau, MD<sup>10</sup>; Sonja Zweegman, MD, PhD<sup>11</sup>; Niels W.C.J. van de Donk, MD, PhD<sup>11</sup>; and Pieter Sonneveld, MD, PhD<sup>1</sup>

## Circulating Tumor Cells for the Staging of Patients With Newly Diagnosed Transplant-Eligible Multiple Myeloma

Juan-Jose Garcés, MSc<sup>1</sup>; Maria-Teresa Cedena, MD<sup>2</sup>; Noemi Puig, MD, PhD<sup>3</sup>; Leire Burgos, PhD<sup>1</sup>; Jose J. Perez, PhD<sup>3</sup>; Lourdes Cordon, PhD<sup>4</sup>; Juan Flores-Montero, MD, PhD<sup>5,6</sup>; Luzalba Sanoja-Flores, PhD<sup>7</sup>; Maria-Jose Calasanz, PhD<sup>1</sup>; Albert Ortiol, MD<sup>8</sup>; Maria-Jesús Blanchard, MD<sup>9</sup>; Rafael Rios, MD, PhD<sup>10</sup>; Jesus Martin, MD<sup>7</sup>; Rafael Martinez-Martinez, PhD<sup>11</sup>; Joan Bargay, MD, PhD<sup>12</sup>; Anna Sureda, MD, PhD<sup>8,13</sup>; Javier de la Rubia, MD<sup>4,14,15</sup>; Miguel-Teodoro Hernandez, MD, PhD<sup>16</sup>; Paula Rodriguez-Otero, MD, PhD<sup>1</sup>; Javier de la Cruz, MD<sup>2</sup>; Alberto Orfao, MD, PhD<sup>5,6</sup>; Maria-Victoria Mateos, MD, PhD<sup>3</sup>; Joaquin Martinez-Lopez, MD<sup>2,17</sup>; Juan-Jose Lahuerta, MD<sup>2</sup>; Laura Rosiñol, MD, PhD<sup>18</sup>; Joan Blade, MD, PhD<sup>18</sup>; Jesus F. San-Miguel, MD, PhD<sup>1</sup>; and Bruno Paiva, PhD<sup>1</sup>

## High Levels of Circulating Tumor Plasma Cells as a Key Hallmark of Aggressive Disease in Transplant-Eligible Patients With Newly Diagnosed Multiple Myeloma

Luca Bertamini, MD<sup>1</sup>; Stefania Oliva, MD, PhD<sup>1</sup>; Delia Rota-Scalabrini, MD<sup>2</sup>; Laura Paris, MD<sup>3</sup>; Sonia Morè, MD<sup>4</sup>; Paolo Corradini, MD<sup>5</sup>; Antonio Ledda, MD<sup>6</sup>; Massimo Gentile, MD<sup>7</sup>; Giovanni De Sabbata, MD<sup>8</sup>; Giuseppe Pietrantonio, MD<sup>9</sup>; Anna Pascarella, MD<sup>10</sup>; Patrizia Tosi, MD<sup>11</sup>; Paola Curci, MD<sup>12</sup>; Milena Gilestro, BSc<sup>1</sup>; Andrea Capra, MScEng<sup>1</sup>; Piero Gallieni, MD<sup>13</sup>; Francesco Pisani, MD<sup>14</sup>; Ombretta Annibaldi, MD, PhD<sup>15</sup>; Federico Monaco, MD<sup>16</sup>; Anna Marina Liberati, MD<sup>17</sup>; Salvatore Palmieri, MD<sup>18</sup>; Mario Luppi, MD, PhD<sup>19</sup>; Renato Zambello, MD<sup>20</sup>; Francesca Fazio, MD<sup>21</sup>; Angelo Belotti, MD<sup>22</sup>; Paola Tacchetti, MD, PhD<sup>23</sup>; Pellegrino Musto, MD<sup>12,24</sup>; Mario Boccadoro, MD<sup>1</sup>; and Francesca Gay, MD, PhD<sup>1</sup>

Circulating Plasma Cells in Newly Diagnosed Multiple Myeloma: Prognostic and More

# CTCs are one of the most relevant prognostic factors in MM

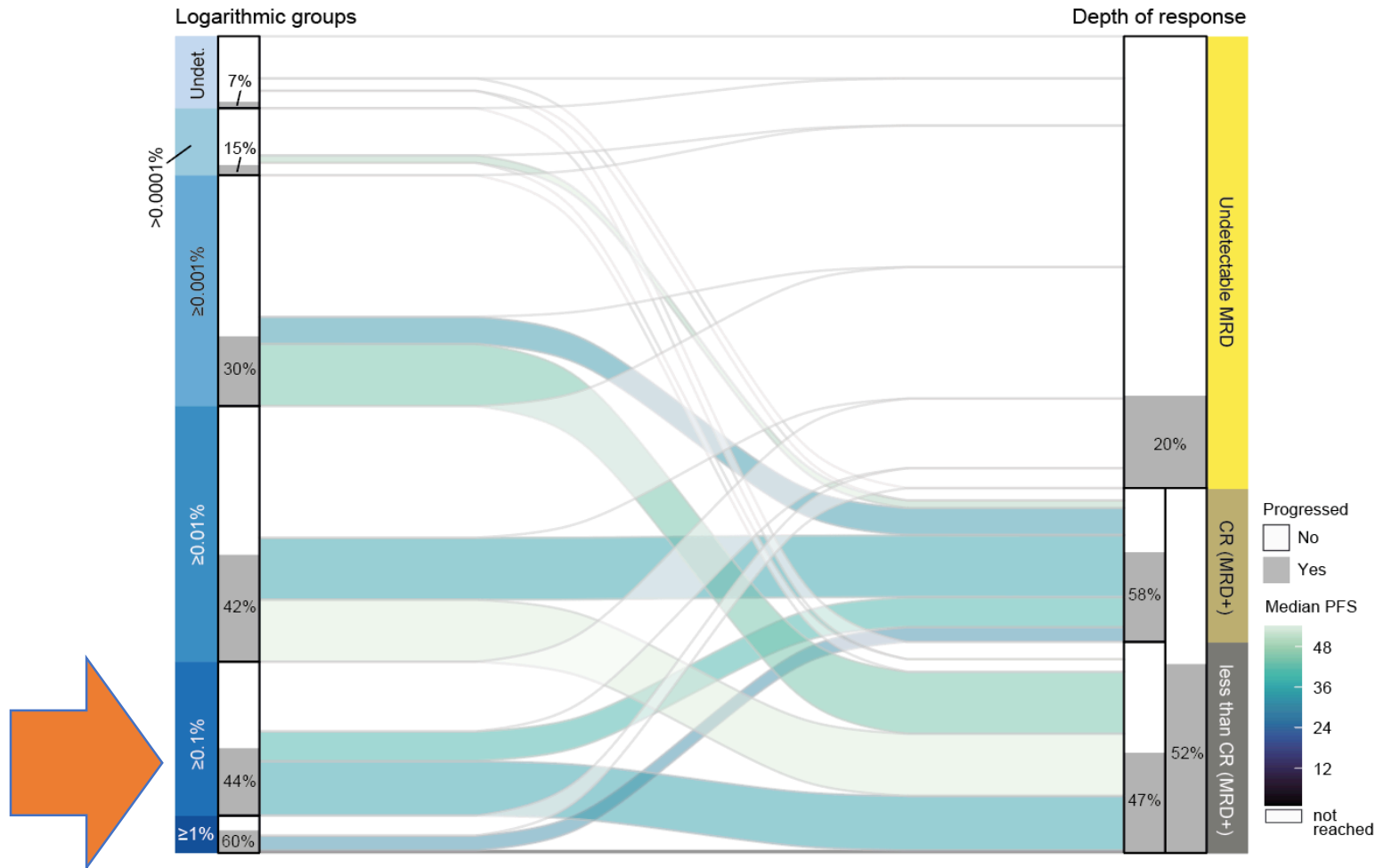
Independent of treatment-related and other risk factors

	HR (95% CI)	sig.
<0.2% CTCs (vs undet.)	2.61 (1.15-5.94)	0.022*
≥0.2% CTCs (vs undet.)	4.44 (1.87-10.55)	0.001**
ISS II (vs ISS I)	1.01 (0.72-1.43)	0.943
ISS III (vs ISS I)	1.12 (0.77-1.62)	0.552
Elevated LDH	1.56 (1.1-2.22)	0.013*
HR cytogenetics	1.64 (1.21-2.24)	0.002**
Transplant-eligibility	3.0 (2.13-4.21)	<0.001***

▶ The detection of **high-CTC** levels resulted in 4-fold increment in the risk of progression and/or death

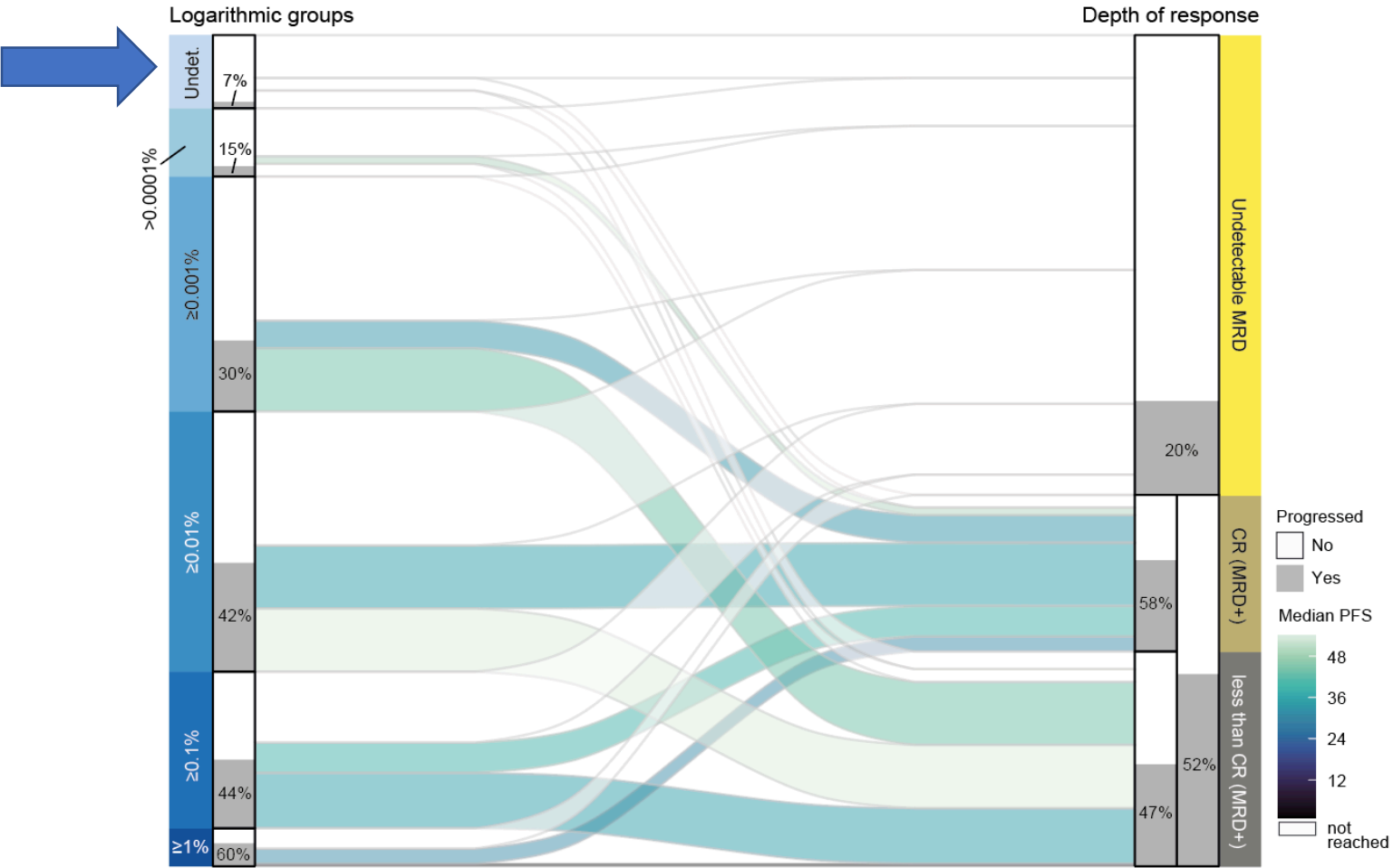
# >0.1% CTCs defines a hidden PC leukemia

Patients with dismal outcome that should be candidates to innovative therapies



# Undetectable CTCs defines a unique subgroup in active MM

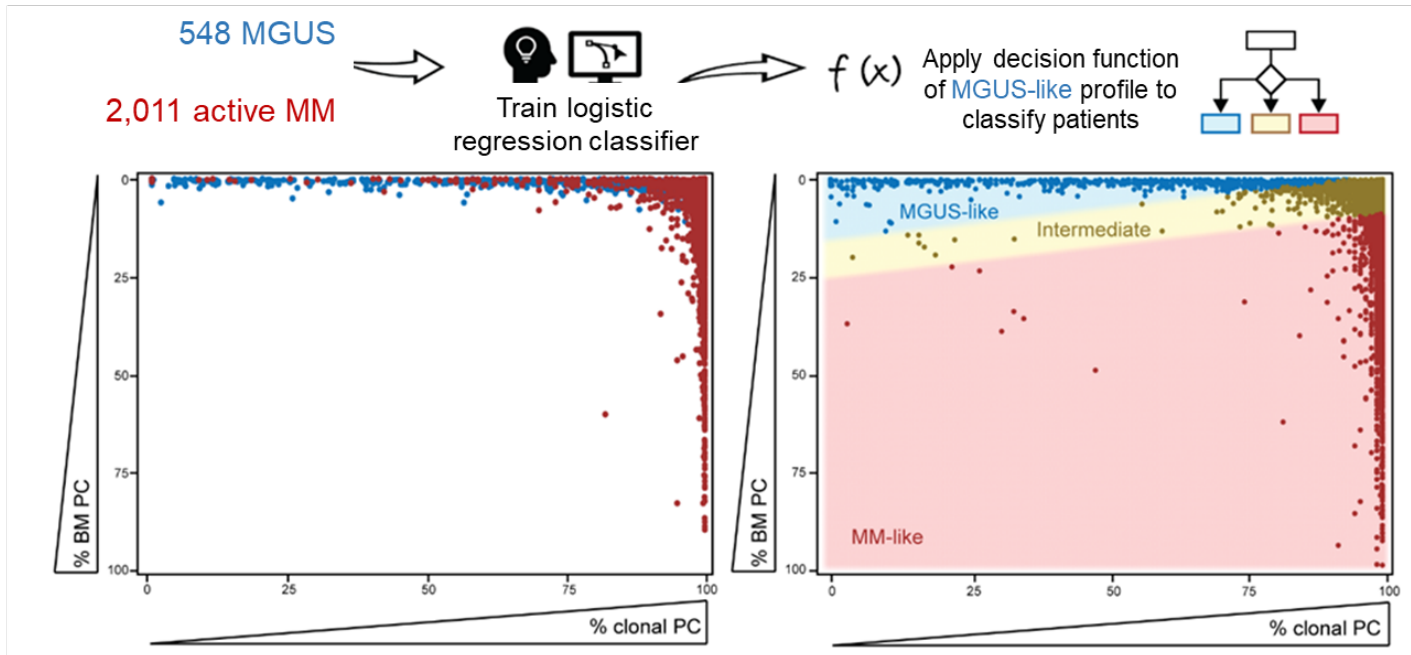
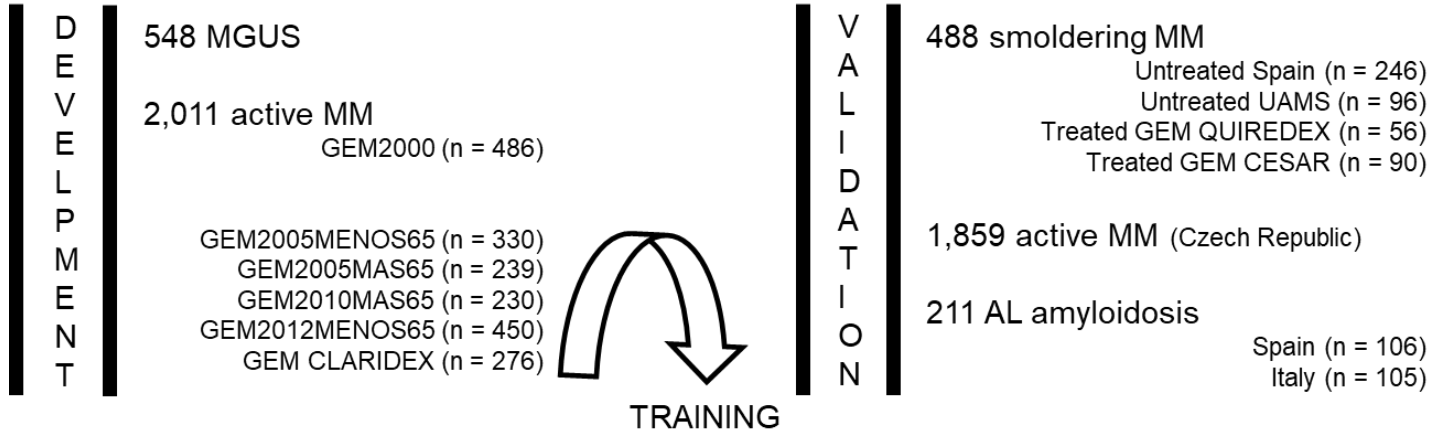
Favorable outcome regardless of the depth of response (MGUS-like phenotype)



***Using big data to provide simple solutions***

# Definition and clinical significance of the MGUS-like phenotype

## A study in 5,117 patients with monoclonal gammopathies





# Open access tool available at [www.mgus-like.com](http://www.mgus-like.com)

## MGUS-like calculator

% BM PCs

*Example: 1.5*

% clonal BM PCs (from the PC compartment)

*Example: 98*

Revised-ISS

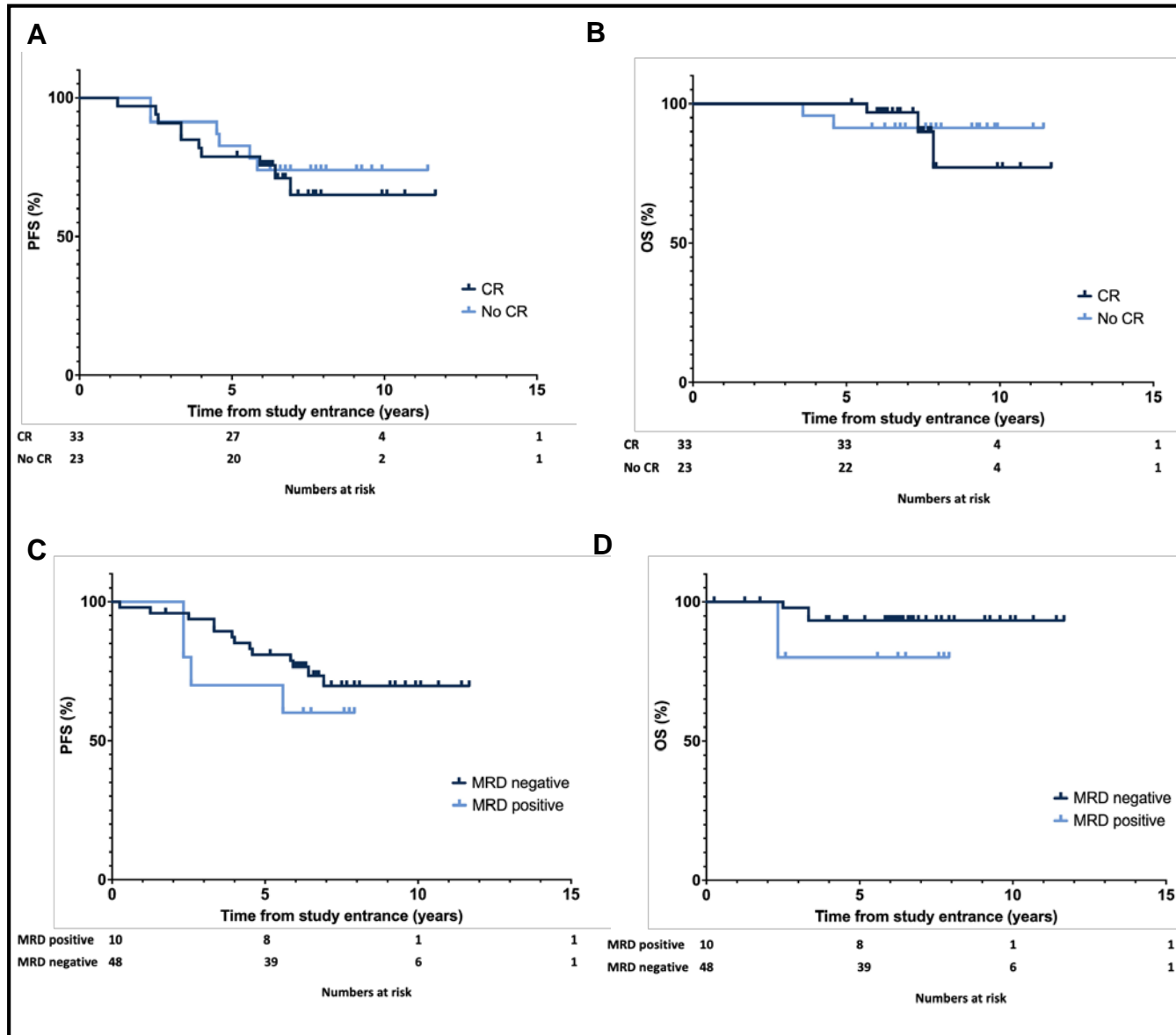
Transplant eligibility

Depth of response

Calculate & Estimate

# Long-term survival of MGUS-like patients regardless of response

## Outcomes according to CR and MRD status

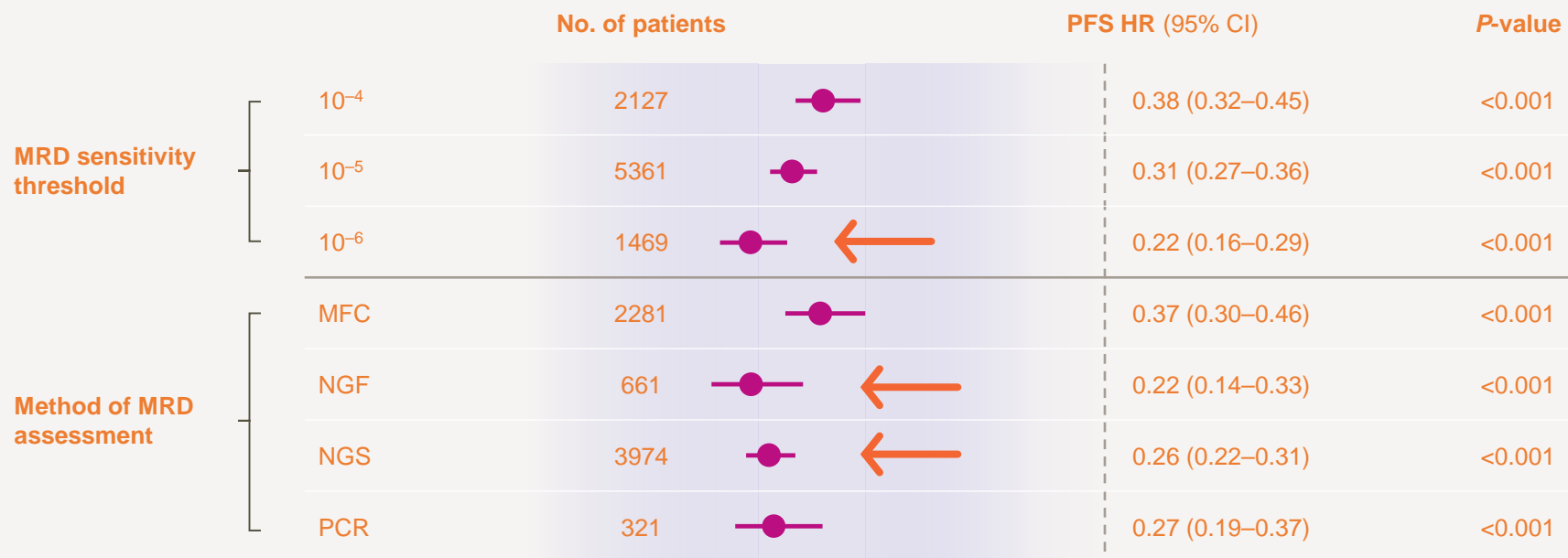


# ***MRD & Myeloma***

# Sensitivity matters

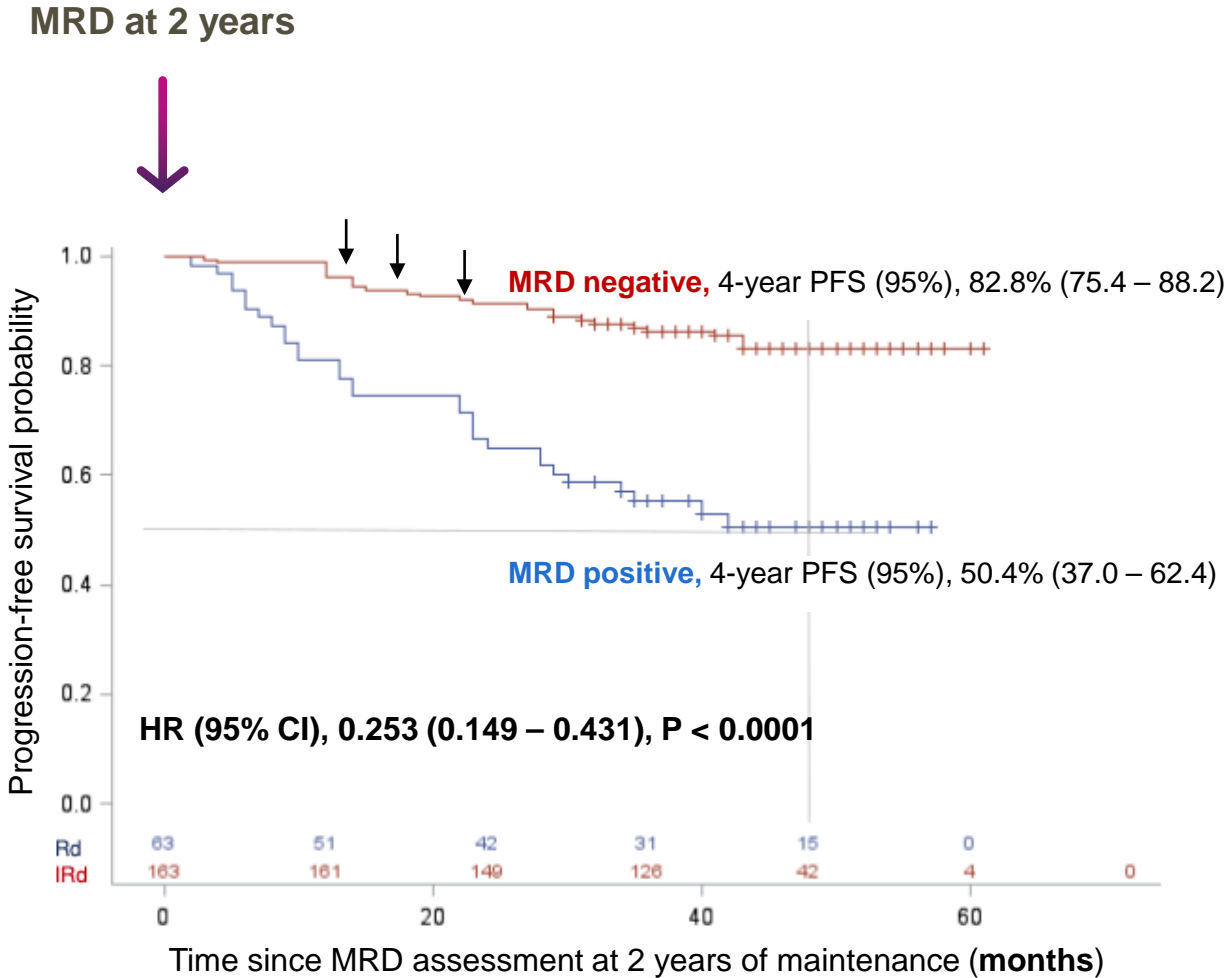
## Importance of standardized assessment of MRD

Association of MRD negativity with PFS in various subgroups



# Can MRD be used to interrupt or prolong treatment?

## Results from the GEM2014MAIN trial

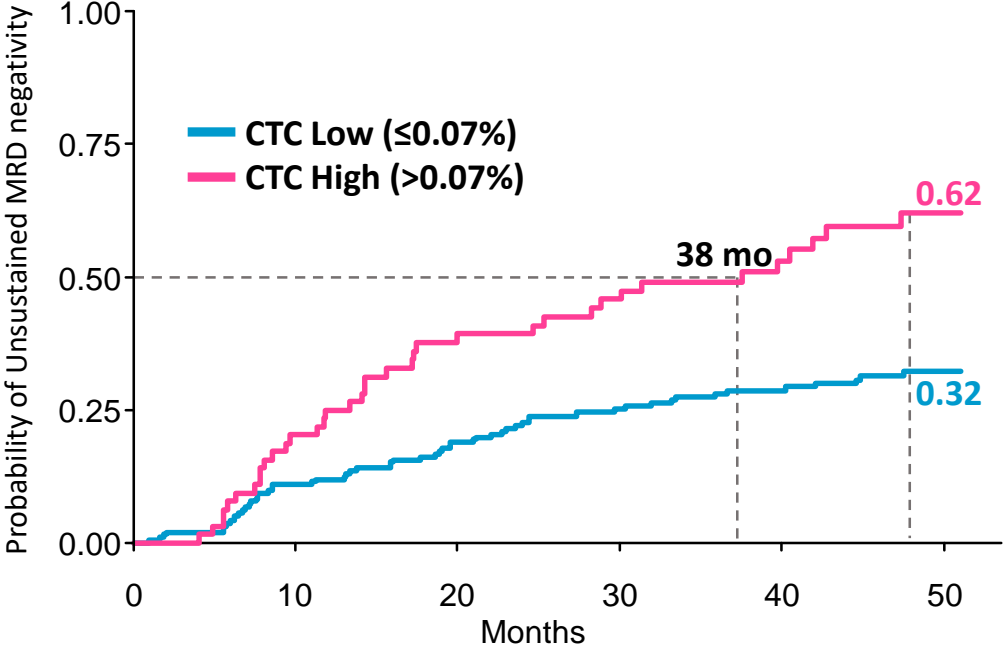


# High CTC levels at diagnosis predict unsustained negative MRD

Potentially valuable information before treatment interruption

## FORTE<sup>1</sup>

CTC High vs. Low: HR 1.86, 95% CI 1.17 – 2.96, P=0.0086



Low	195	167	151	133	116	64
High	64	51	38	33	22	12

Number at risk

## GEM2014MAIN<sup>2</sup>

**A**

%CTC  $\geq 0.01$  vs  $< 0.01$ ;  
HR 2.29, 95% CI 1.5 - 3.5, P = 0.0002



%CTC  $< 0.01$   
%CTC  $\geq 0.01$

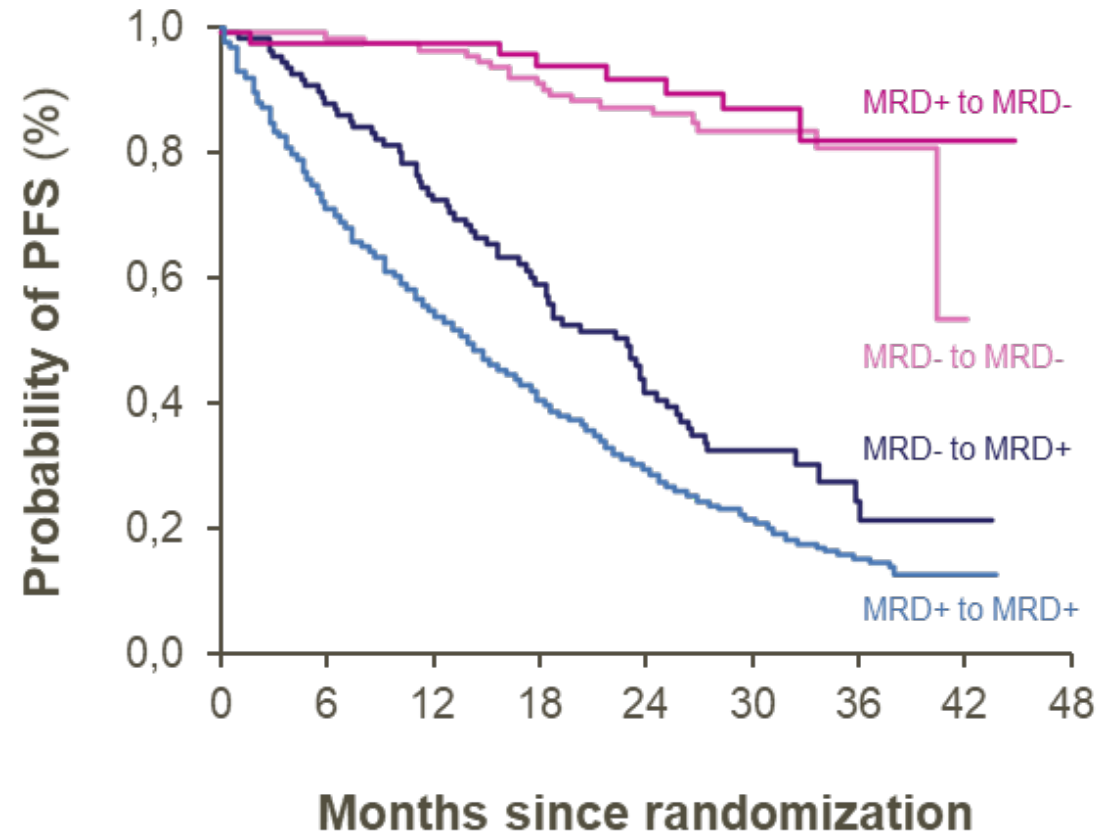
	0	20	40	60	80
%CTC $< 0.01$	99	88	77	69	26
%CTC $\geq 0.01$	109	89	64	51	15

1. D'Agostino M, et al. IMS 2022;OAB-11

2. Guerrero C, et al. IMS 2023

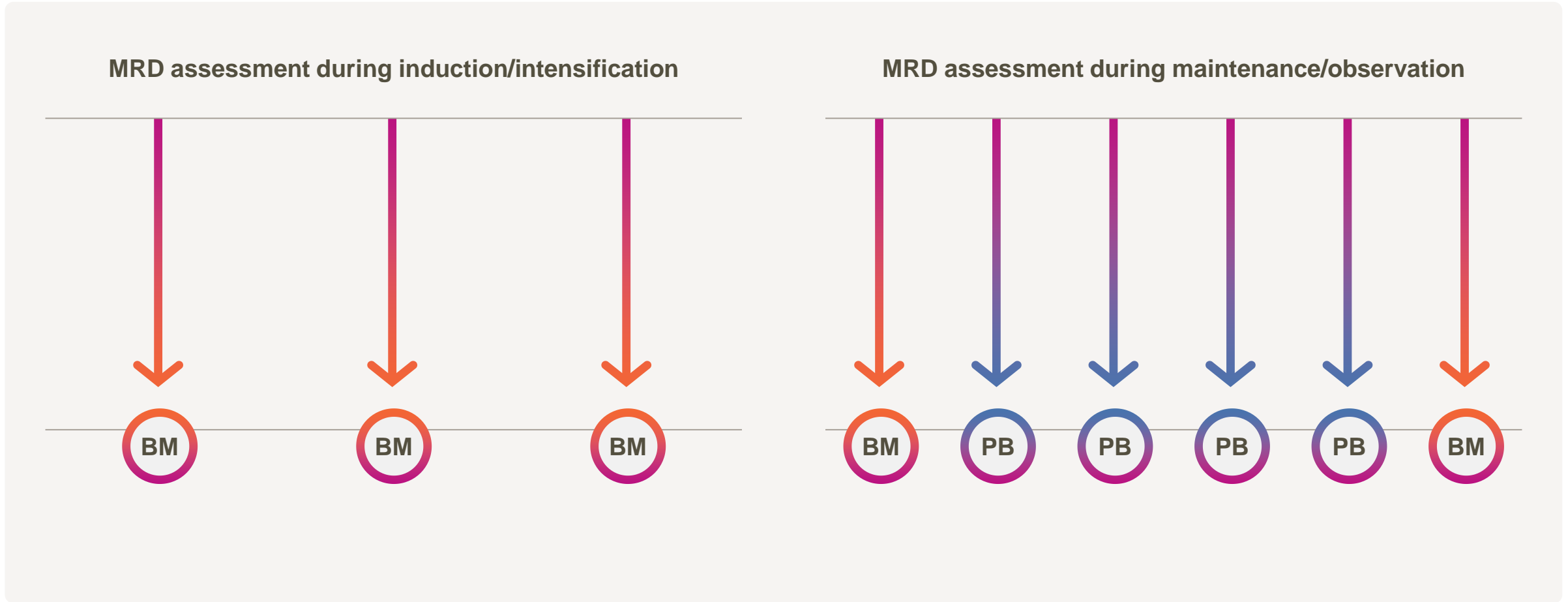
# The problem of MRD is that a single “snapshot” is not enough!

MRD status is dynamic and must be reassessed periodically



# Hypothetical scenario to assess MRD in BM and PB

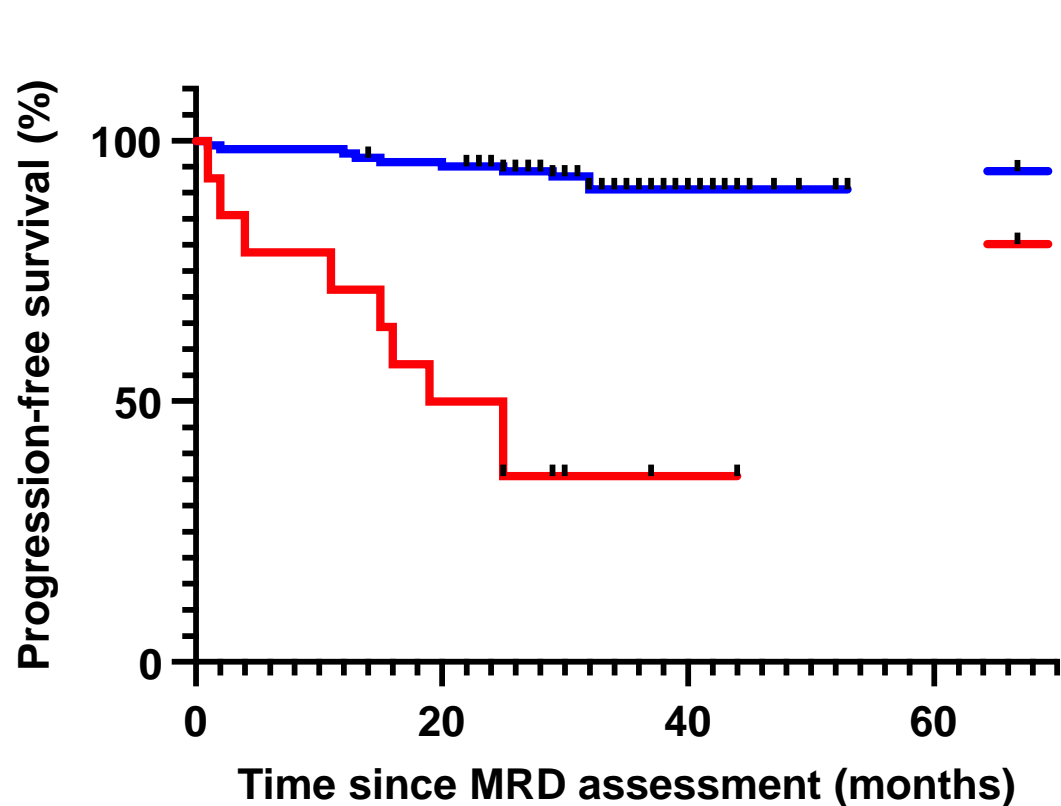
Imaging, Mass-spec and BloodFlow for minimally invasive MRD





# Prognostic value of MRD assessment in PB using NGF

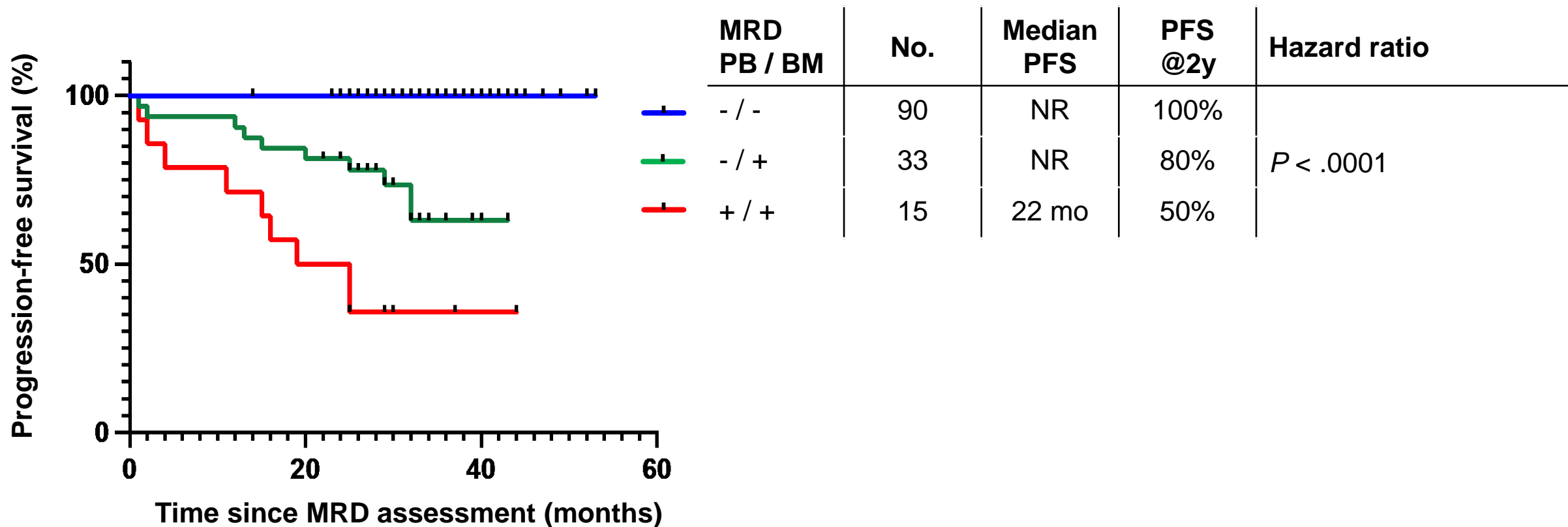
GEM2014MAIN trial (n = 138)



MRD	No.	Median PFS	PFS @2y	Hazard ratio
Negative	123	NR	98%	11.7 ( $P < .0001$ )
Positive	15	22 mo	50%	

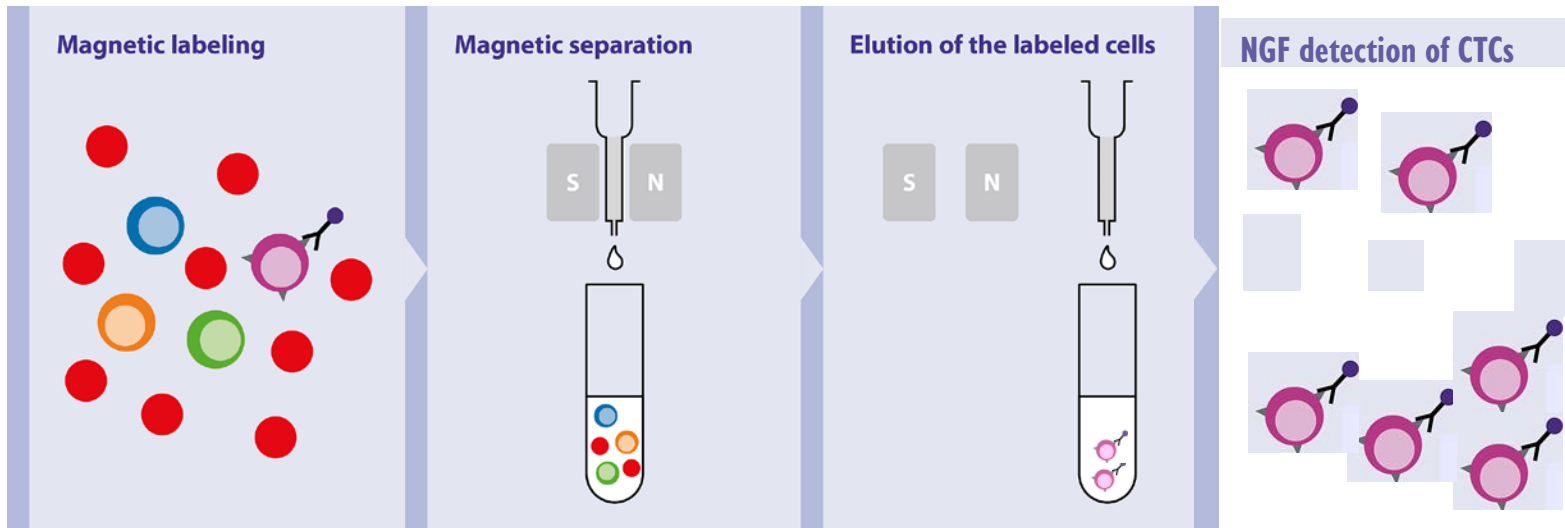
# Prognostic value of MRD assessment in PB & BM using NGF

GEM2014MAIN trial (n = 138)



# BloodFlow

## Immunomagnetic enrichment using MACS® MicroBeads prior NGF



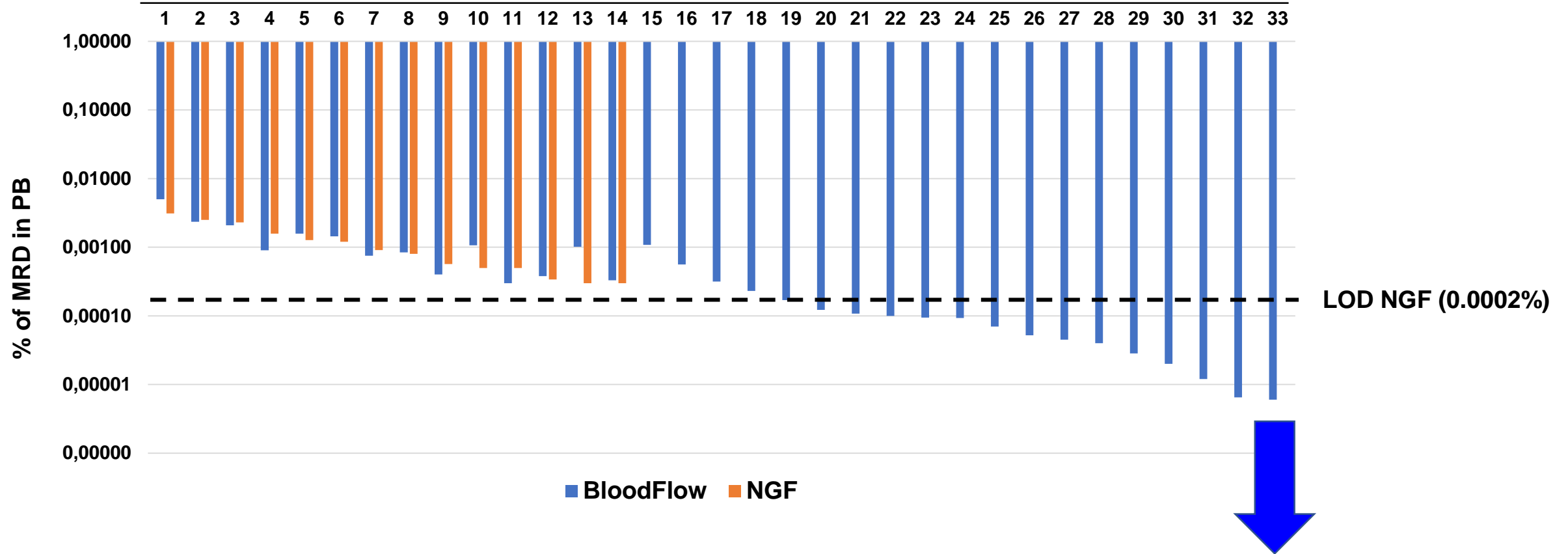
- A minimum sensitivity of  $10^{-7}$  requires analyzing  $\geq 2 \times 10^8$  cells (~50mL of PB)
- Large (~50mL) PB volumes were magnetically labeled and processed via MACS® columns, and ~100 $\mu$ L aliquots enriched with circulating PC were analyzed using EuroFlow NGF



# Performance of BloodFlow vs NGF in PB (n = 353 samples)

BloodFlow detected MRD in 33/353 (9%); 19/33 (58%) were negative by NGF

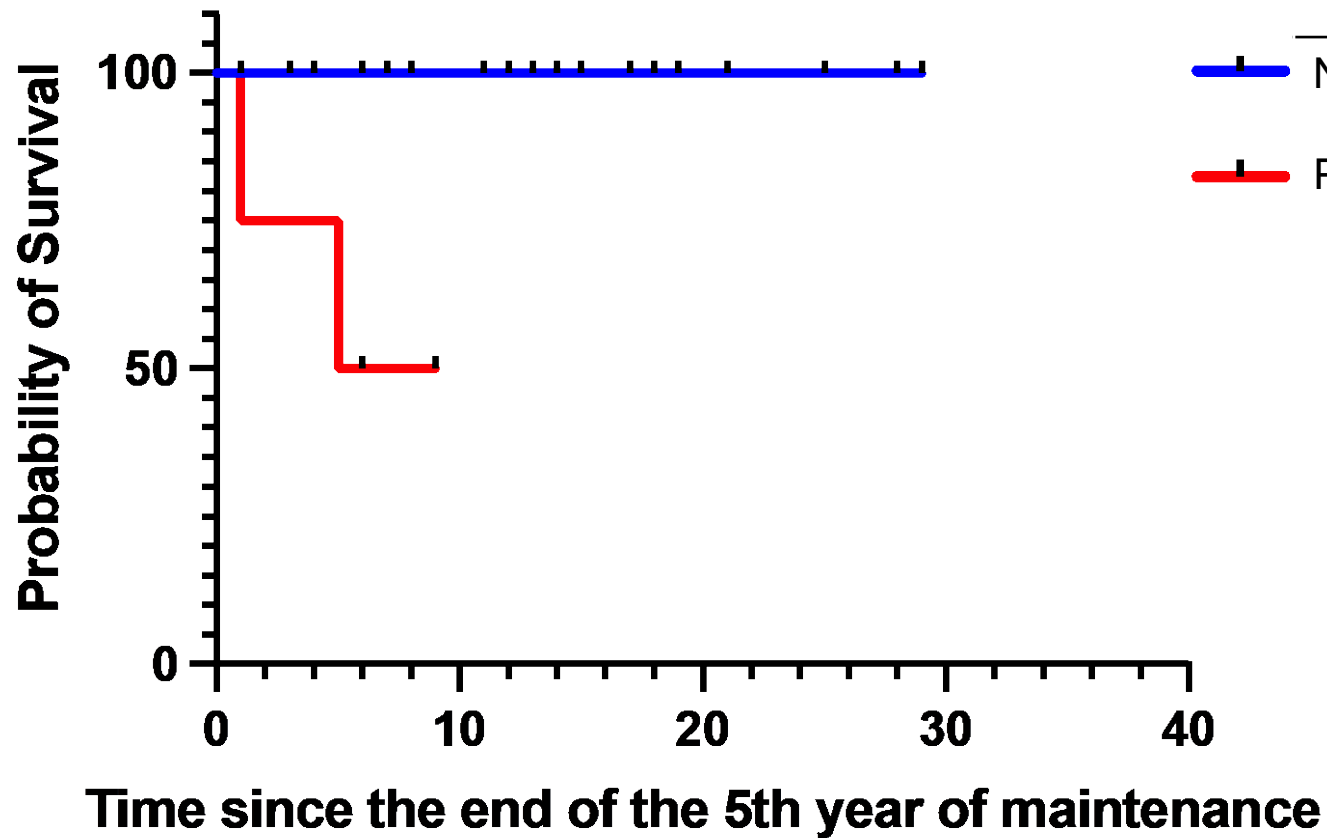
Patients with positive MRD in PB using BloodFlow



The lowest MRD level was  $6 \times 10^{-8}$

# Prognostic value of MRD assessment in PB using BloodFlow

GEM2014MAIN trial (n = 33)



MRD	N.	Median PFS	<i>p</i> value
Negative	29	NR	<i>p</i> < .0001
Positive	4	7 mo	

## ***Immune profiling and the challenge ahead...***

Staging  
Genetic risk

Depth of response  
MRD

Immune  
Profiling  
?

***...cost-effective, standardized and predictive biomarker***

# Immune profiling and the challenge ahead...

## 1. Greater knowledge

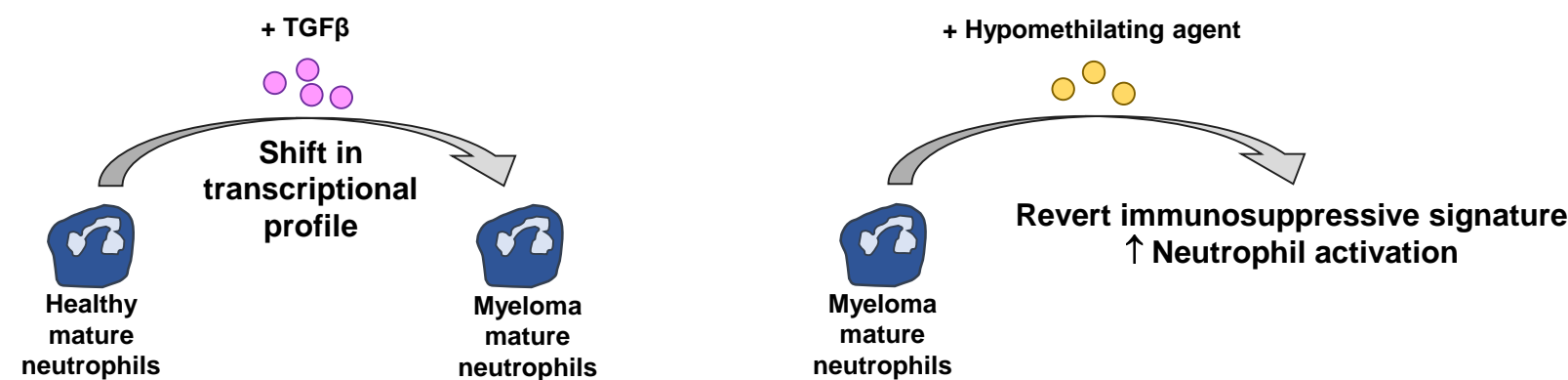
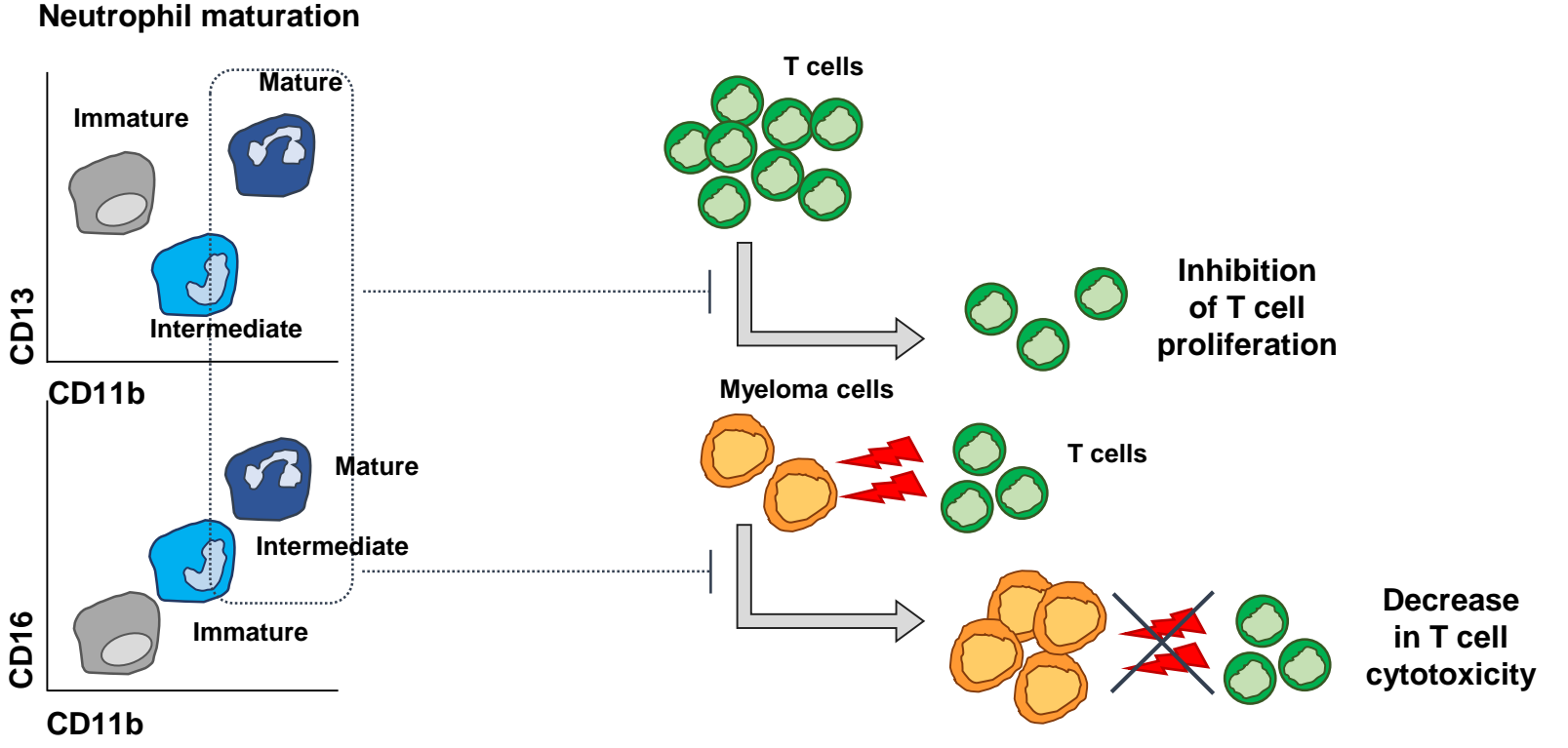
- Better understanding of the mode of action of immunotherapies
- Well-defined immunophenotype of key immune cell types
- Bone marrow vs peripheral blood

## 2. Computational analysis

## 3. Integrated datasets with tumor, immunological, treatment and outcome

# Markers for optimal monitoring of G-MDSCs in MM

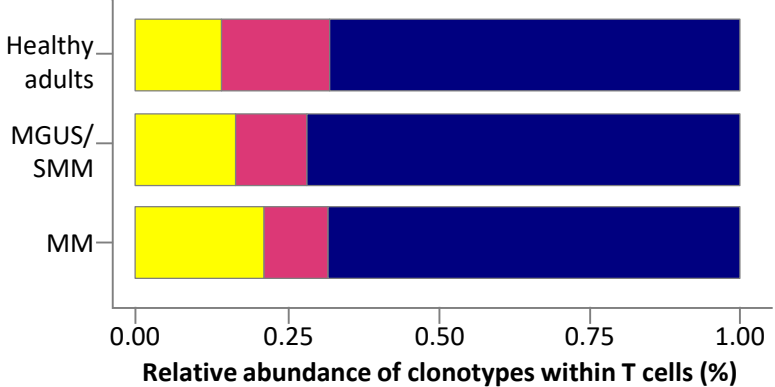
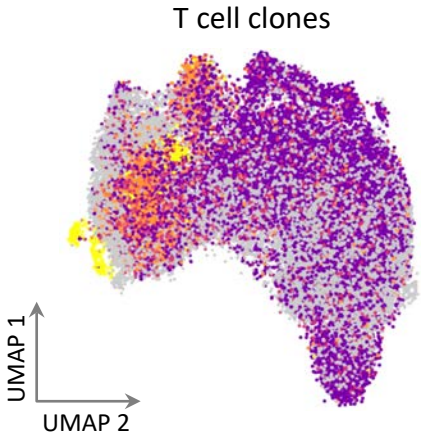
## Biological and clinical significance



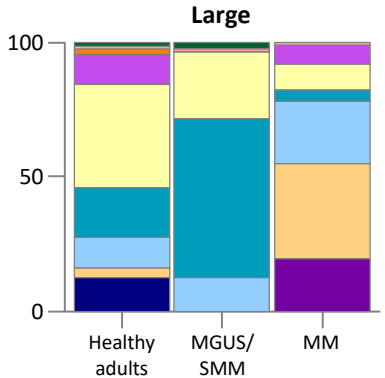
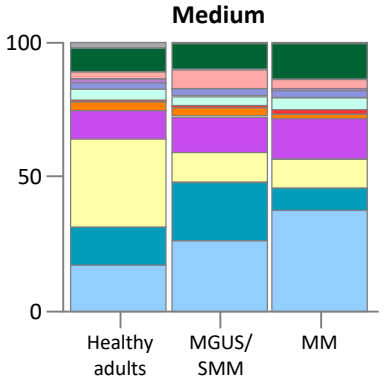
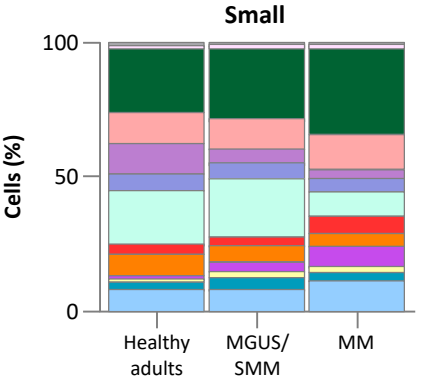


# Disease progression is associated with dysfunction of large T cell clones

scRNA/TCR-seq data (N = 22)



■ Small ( $0 < x \leq 0.01$ ) ■ Medium ( $0.01 < x \leq 0.1$ ) ■ Large ( $0.1 < x \leq 1$ )

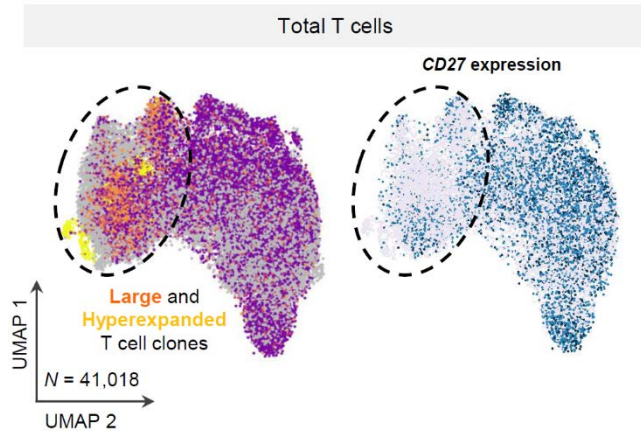
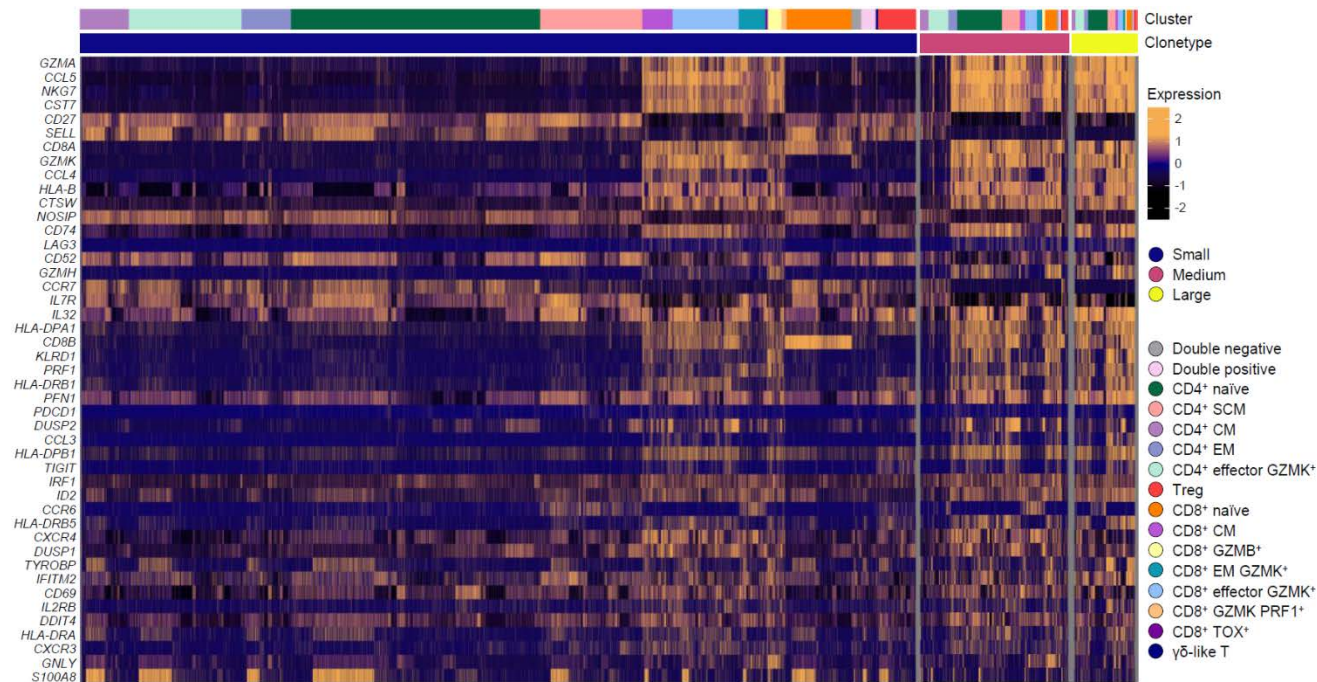


■ Double negative  
 ■ Double positive  
 ■ CD4+ naive  
 ■ CD4+ SCM  
 ■ CD4+ CM  
 ■ CD4+ EM  
 ■ CD4+ effector GZMK+  
 ■ Treg  
 ■ CD8+ naive  
 ■ CD8+ CM  
 ■ CD8+ GZMB+  
 ■ CD8+ EM GZMK+  
 ■ CD8+ effector GZMK+  
 ■ CD8+ GZMK+ PRF1+  
 ■ CD8+ TOX+  
 ■  $\gamma\delta$ -like T

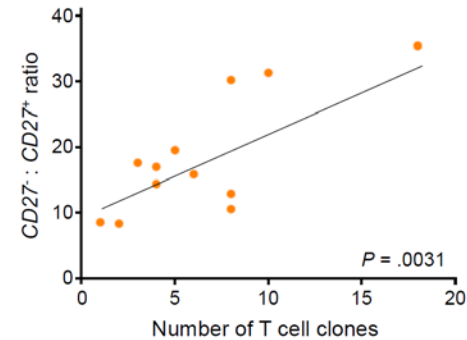


# Large T cell clones do not express CD27

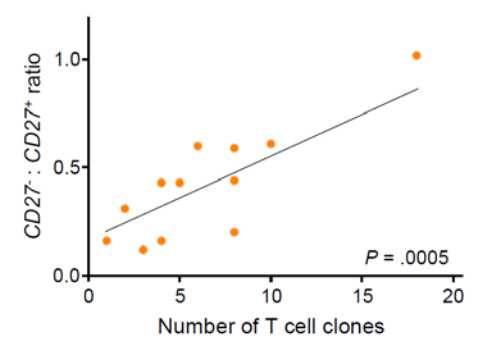
CD27<sup>-</sup> / CD27<sup>+</sup> ratio as a surrogate of T cell clonality in the marrow



CD27<sup>-</sup> : CD27<sup>+</sup> ratio measured by scRNA-seq



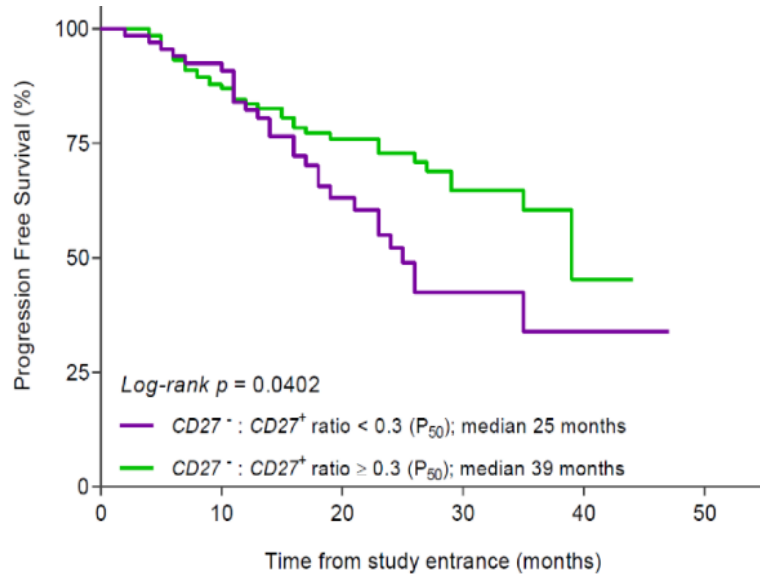
CD27<sup>-</sup> : CD27<sup>+</sup> ratio measured by MFC



# CD27<sup>-</sup> / CD27<sup>+</sup> T cell ratio is prognostic before IMiDs

## Potential role of IMiDs in restoring functionality of large T cell clones

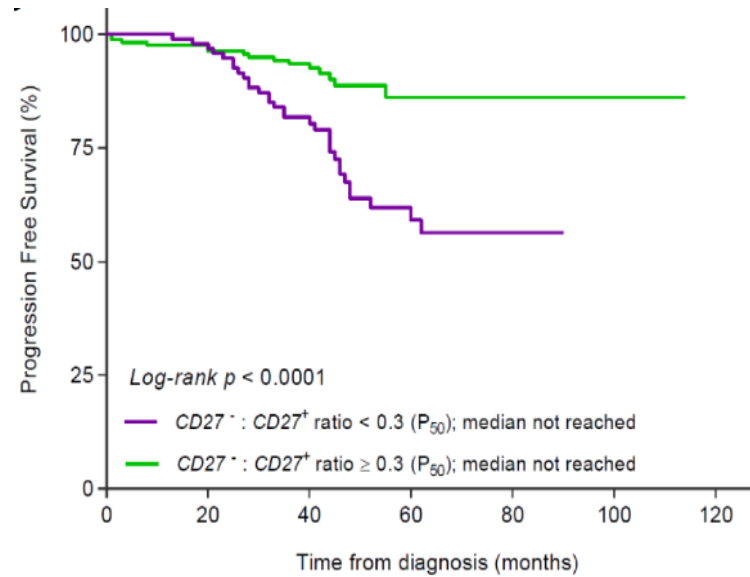
### Transplant-ineligible



Number of subjects at risk

91	73	33	14	3	0
180	137	73	34	5	0

### Transplant-eligible

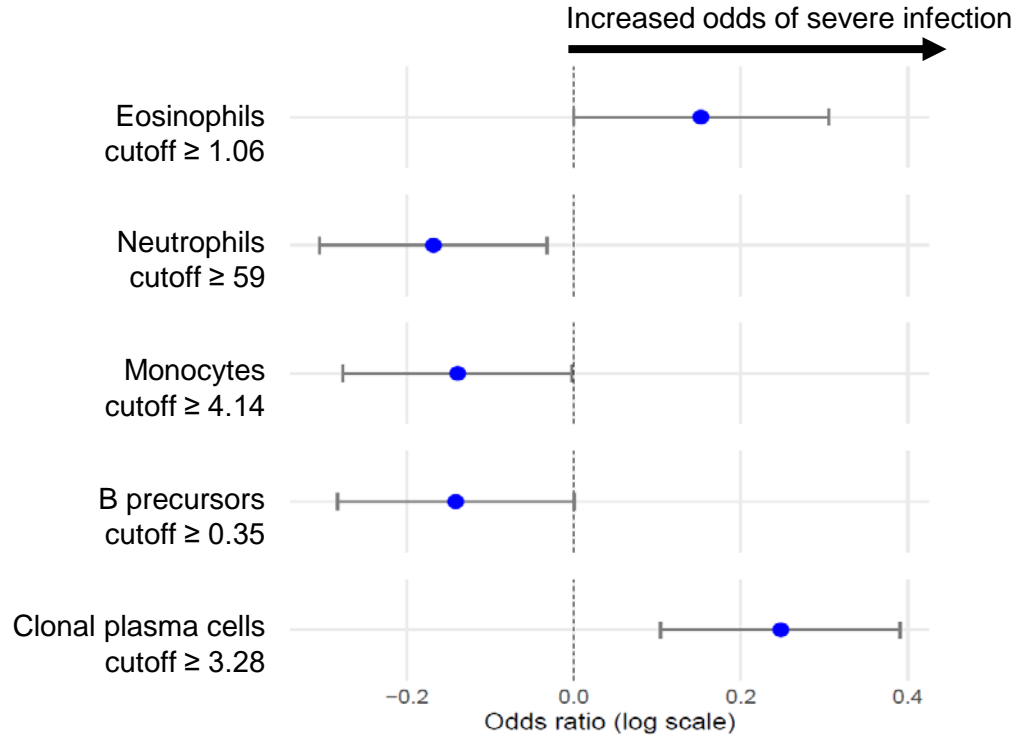
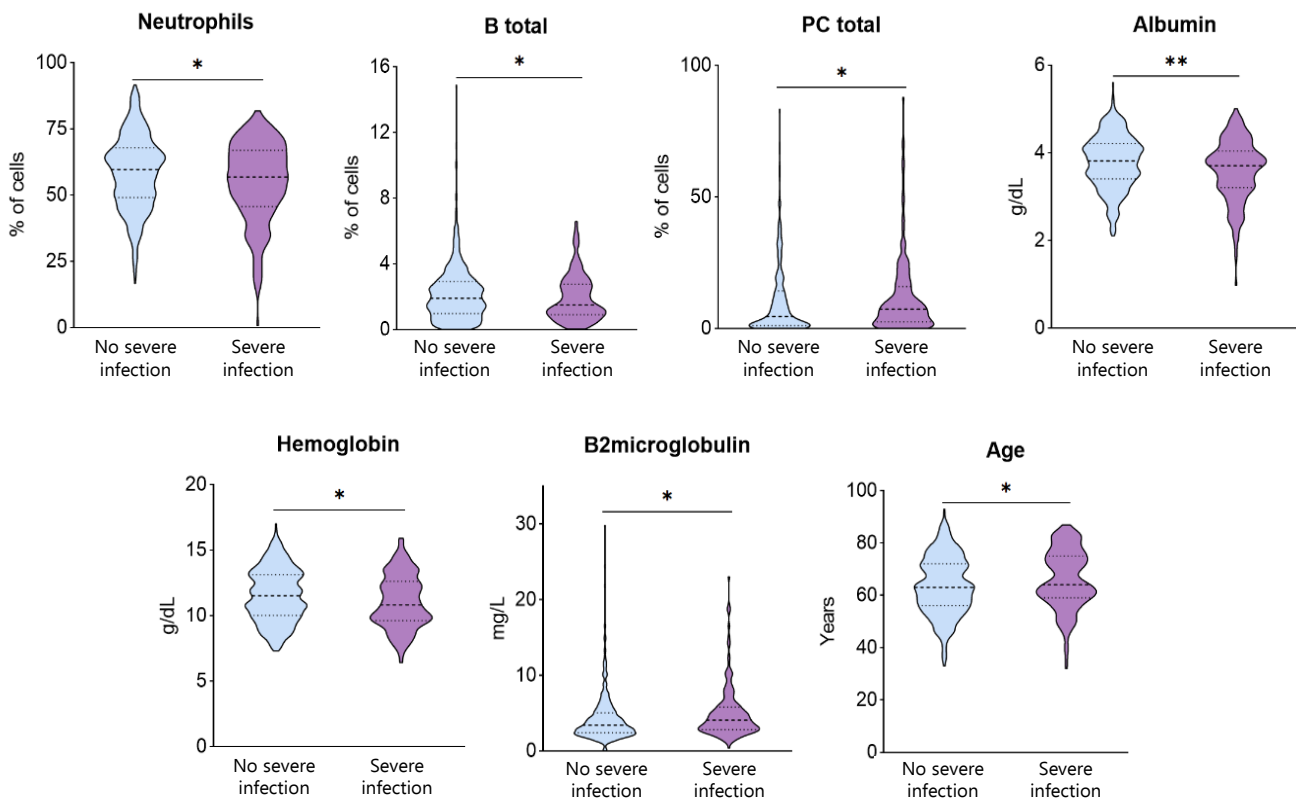


Number of subjects at risk

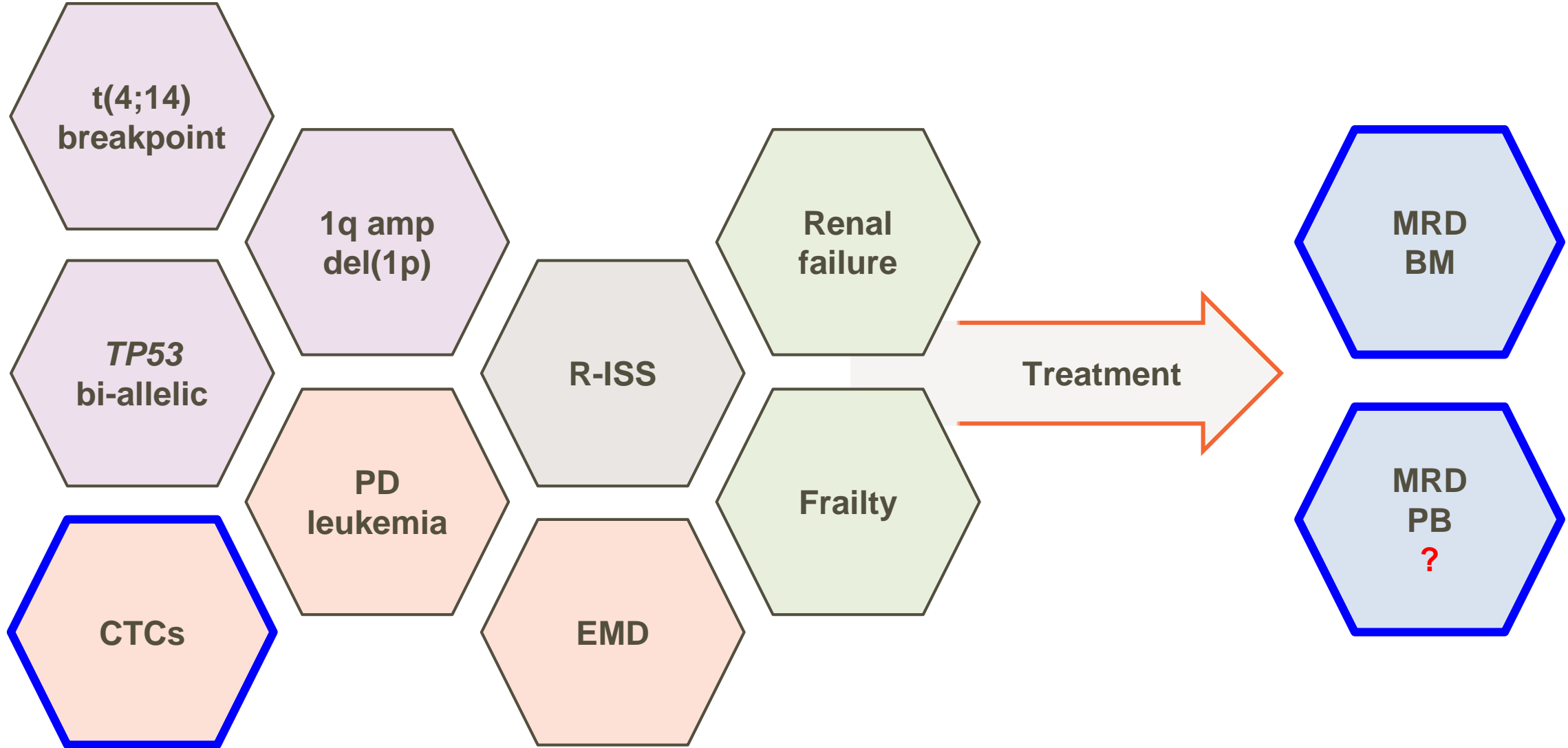
102	91	59	23	2	0	0
170	150	94	28	5	3	0

# Immune biomarkers of severe infection across the spectrum of MM

NGF (N = 984 patients)



# There is no precision medicine without precision diagnostics



Immune profiling?



# Acknowledgments

