

# ***Future of Myeloma Treatment*** ***the roadmap for curing***

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UNIVERSITY OF NAVARRA

# Disclosures

Research Support/P.I.

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Employee

NA

Consultant

Takeda; Janssen; Celgene; Novartis; Sanofi.

Major Stockholder

NA

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Scientific Advisory Board

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# How should we treat Multiple Myeloma?

*Key points to consider*

- ***Currently, Myeloma treatment is highly expensive.***
  - ***The cheapest medicine is the one that is able to CURE the patient.***
  - ***Not to use the best drugs upfront is an expensive and frustrating approach***
-

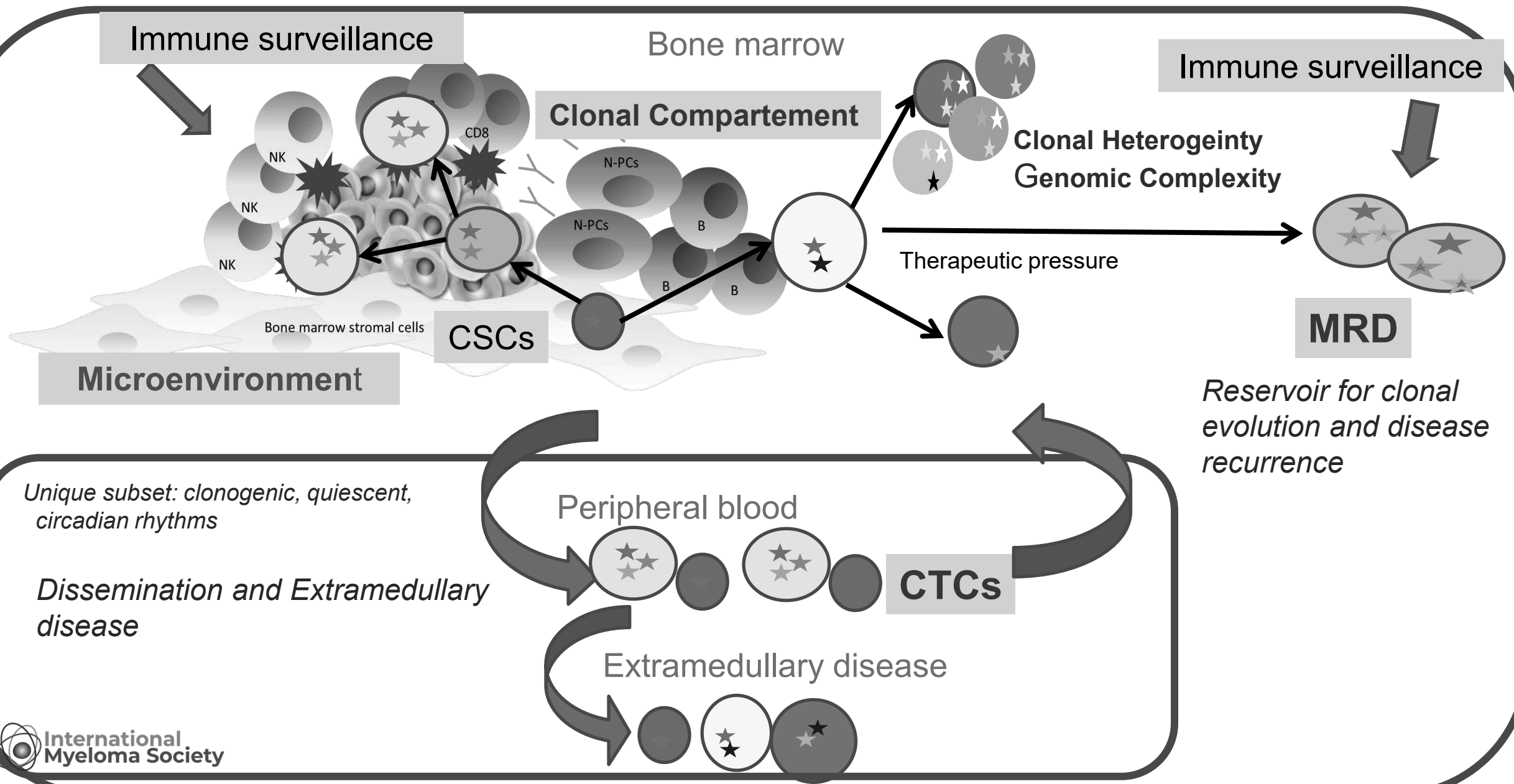
# The roadmap to cure patients with multiple myeloma

- 1) *To Investigate the pathogenesis of MM (identify the signatures of high Risk clones)*
- 2) *To eradicate all tumour cells: high sensitive techniques to evaluate treatment efficacy.*
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- 5) *To investigate experimental therapies upfront in High risk patients.*

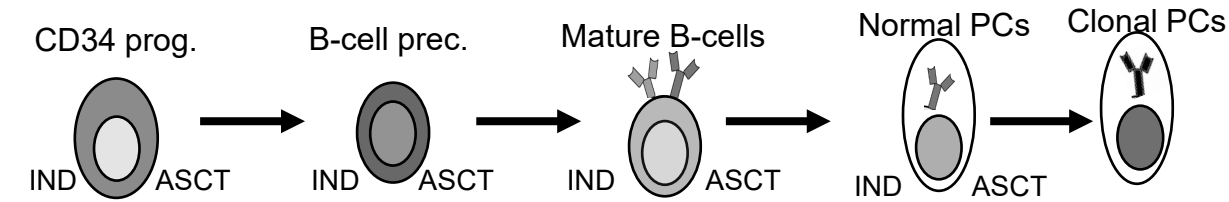


# Myeloma Pathogeneis

To identify signatures of High Risk clones: as tools for understanding disease dissemination & resistance “Achilles’ heel”



# Clonal Compartment: *the pathogenesis of MM is preceded by mutated lymphopoiesis*



POTEE, CCZ1B, SPATA31A3, ORAF21, POTE, NPIP3, LGALS9C and PSG4, GTF2I and AGAP7

POTEE, CCZ1B, SPATA31A3, POTE, NPIP3, LGALS9C and PSG4, GTF2I

Mature B-cells

Normal PCs

B-cell precursors (CD34+ and CD34-)

POTEE, CCZ1B, SPATA31A3, POTE, NPIP3, LRR37A2, LGALS9C and PSG4, GTF2I

CD34 progenitors

POTEE, CCZ1B, SPATA31A3, POTE, NPIP3, LGALS9C and PSG4

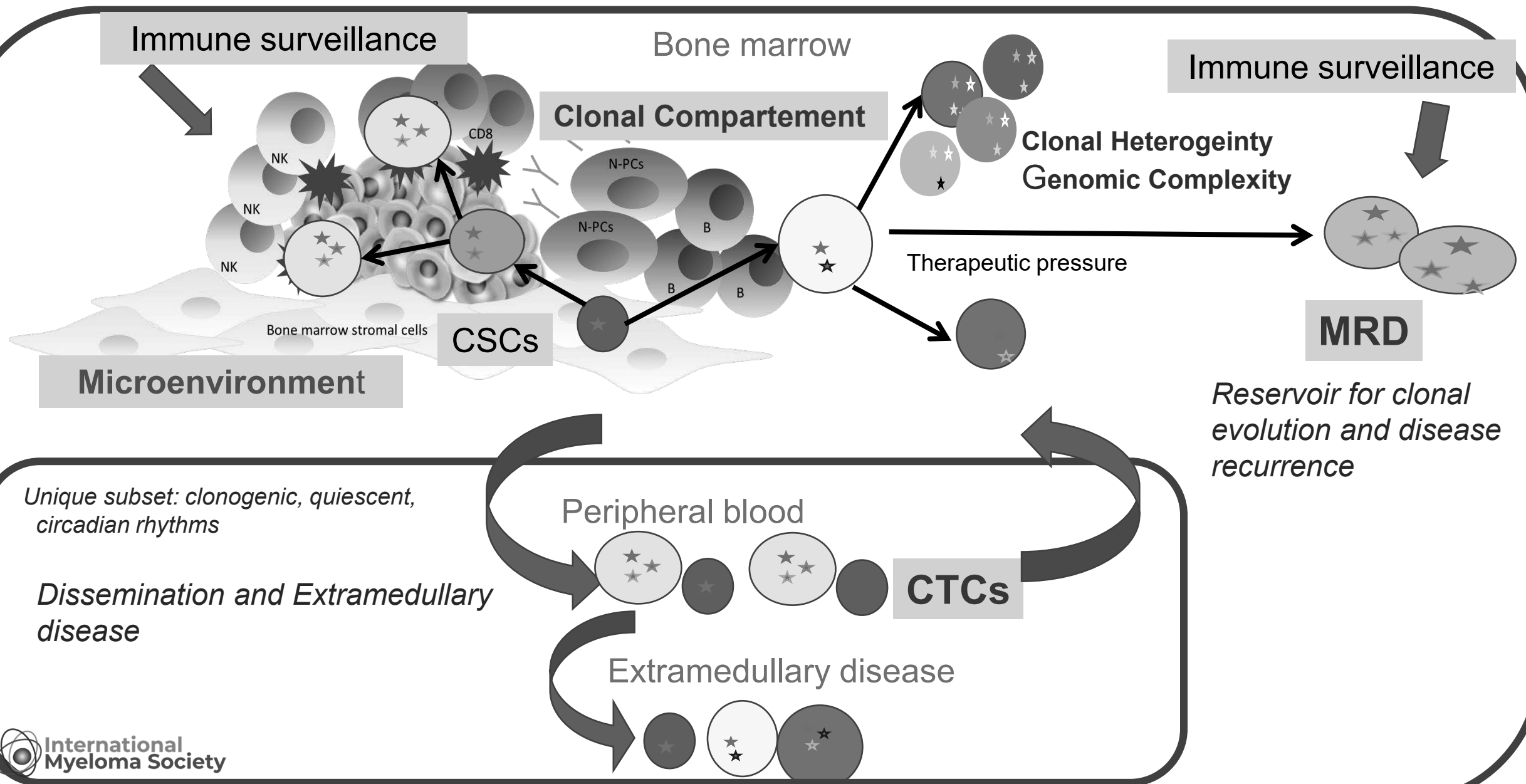
*Normal cells isolated from double negative MRD patients to avoid contamination*

- *Mature B Lymphocytes & normal PC display the same clonal IgG rearrangement observed in clonal PC (at diagnosis) (5/6)*
- *Whole exome sequencing revealed that not only normal PC and mature B cells, **but also** B cell precursors and CD34 progenitors shared with clonal PC some somatic mutations (but not recurrent mutations). **However critical MM driver mutations or copy number alterations were not detected**.....MM patients have somatic mutations in the B cell lineage, likely before the disease onset*
- *Mutated lymphopoiesis may increase risk of developing B cell and PC oligoclonality, which precedes secondary driver mutations or CNV leading to the expansion of MM PCs*
- *Can these cells secrete the same immunoglobulin as MM cells?*

***Our data suggest that there is a clonal B lymphopoiesis that preceded MM***

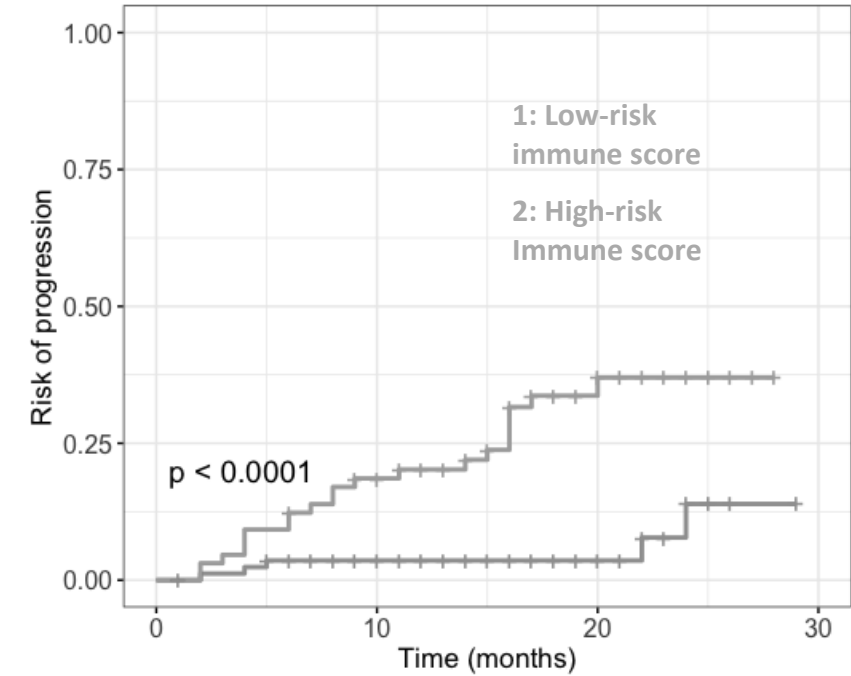
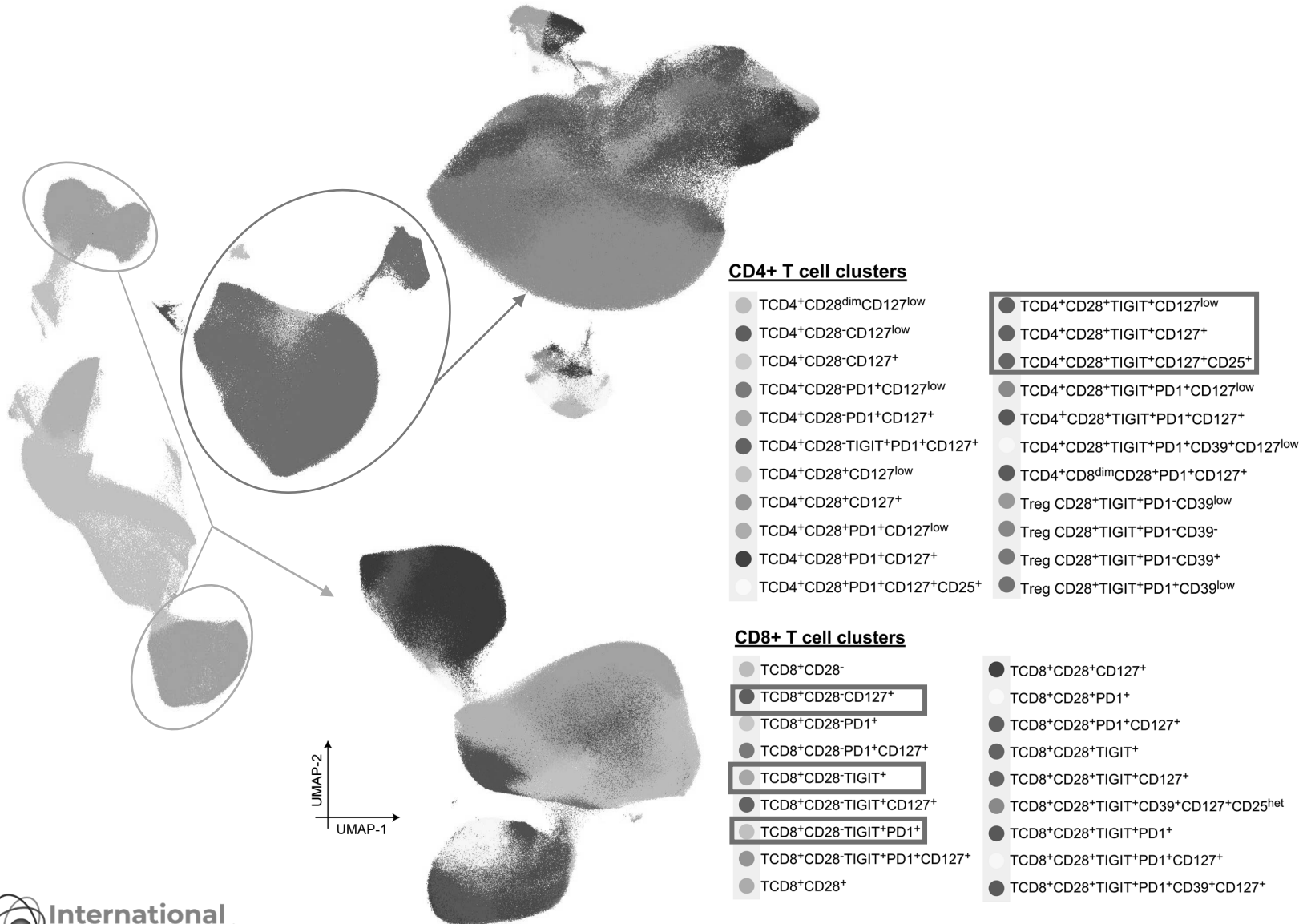
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# T cell subsets in blood associated with the progression of SMM

*Expansion of 6 subsets with exhausted phenotype associated with inferior TTP*



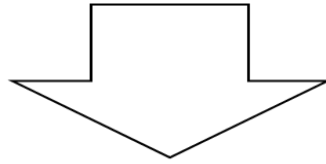
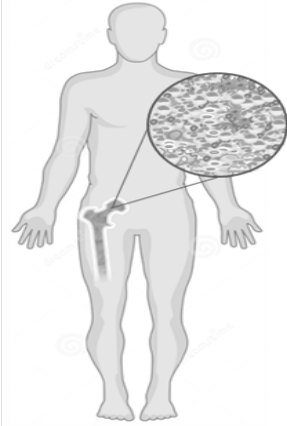
Number at risk

Time (months)	0	10	20	30
1: Low-risk immune score	85	68	28	0
2: High-risk immune score	65	51	20	0

# Biological and clinical significance of dysplastic hematopoiesis

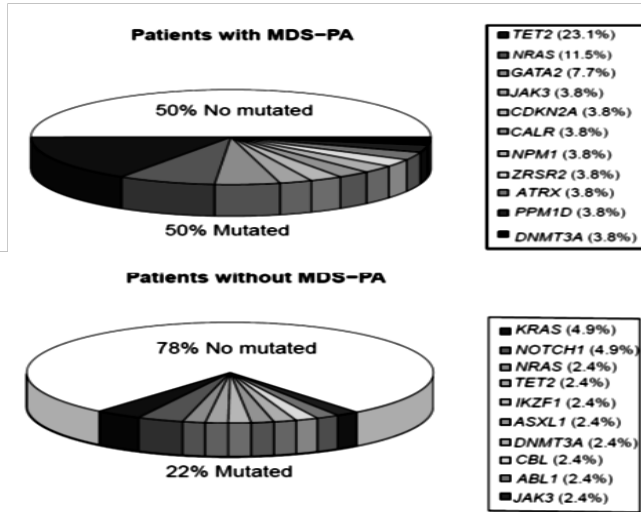
*MDS-PA modify the tumor microenvironment and induce greater risk of hematological toxicity from treatment*

Approximately 1 out of 10 patients with myeloma displays MDS-associated phenotypic abnormalities (MDS-PA) at diagnosis, which...

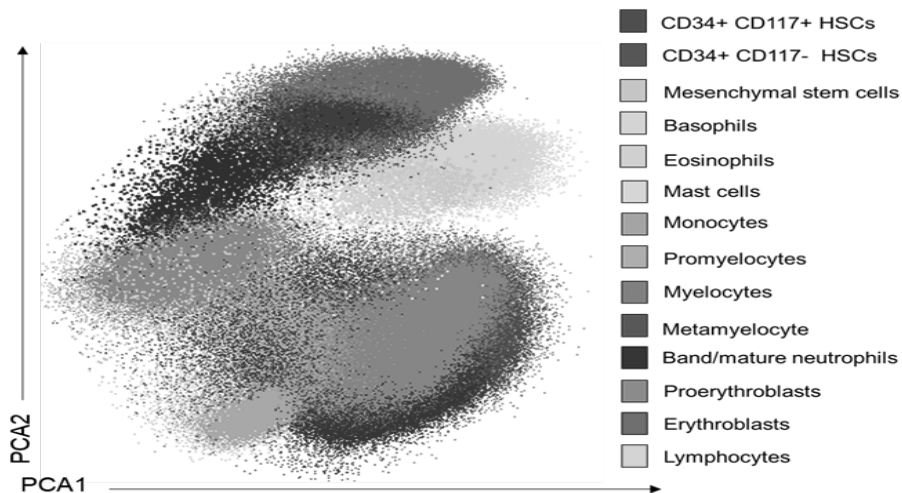


...induce greater risk of hematological toxicity from treatment.

## MDS-PA and clonal hematopoiesis

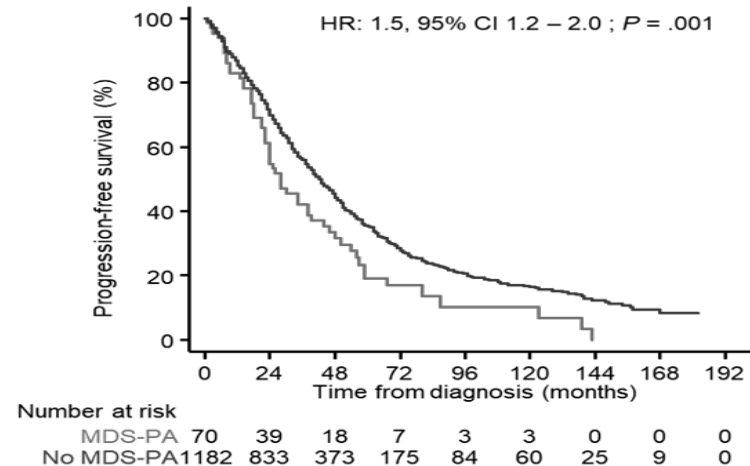


## MDS-PA modify the tumor microenvironment



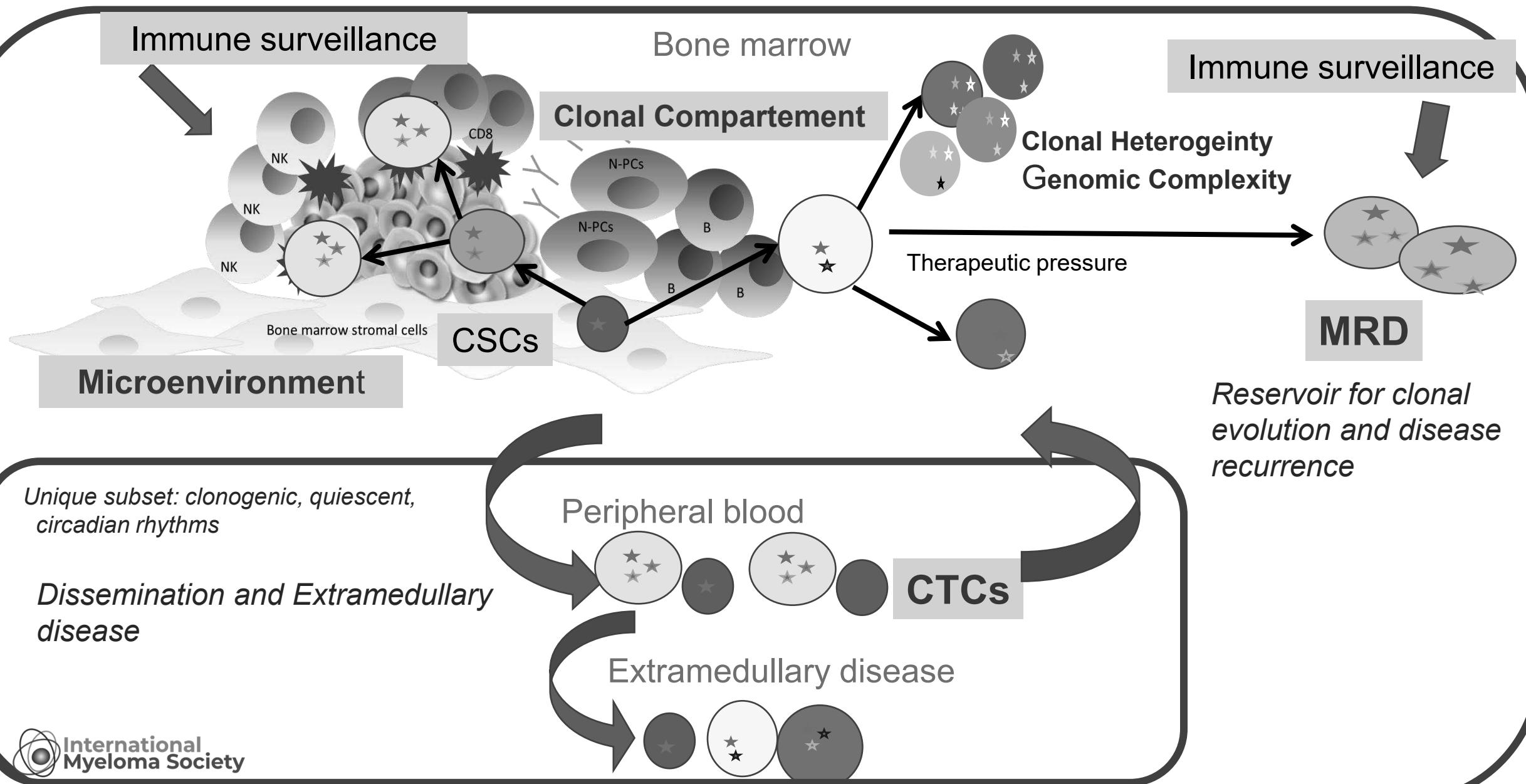
*Higher frequency of T-regulatory cells & maturation blockage in neutrophils*

## MDS-PA at diagnosis was independently associated with inferior progression-free survival



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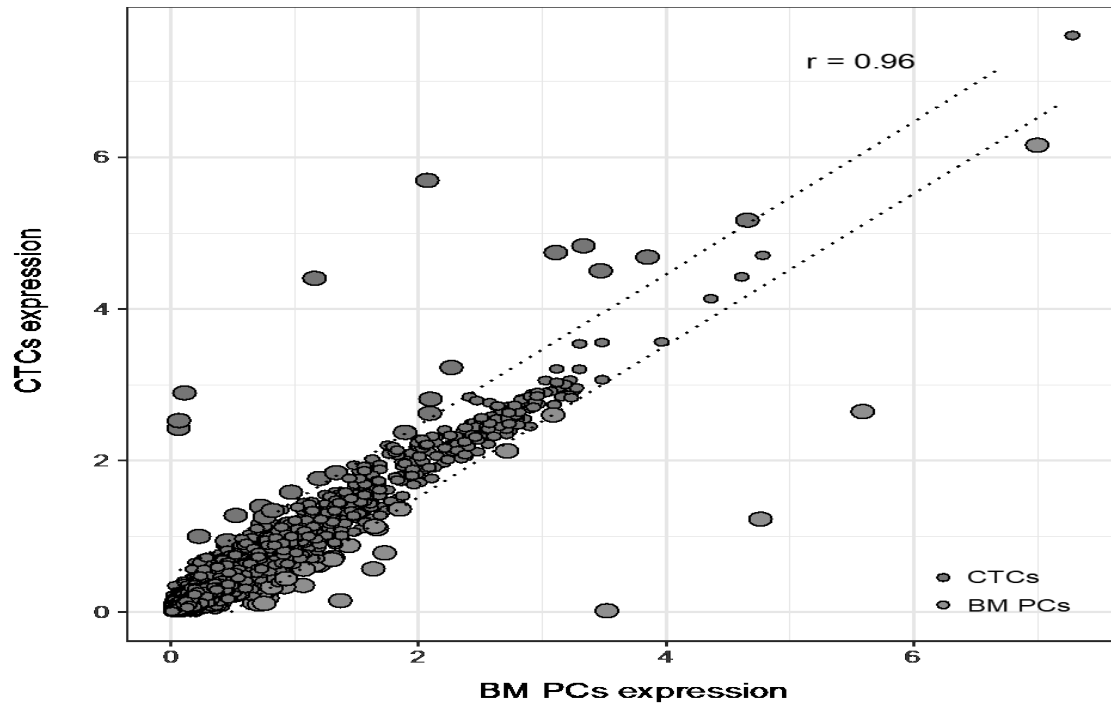


# Biologic characterization of paired CTCs vs BM clonal PCs

## A new model to understand disease dissemination

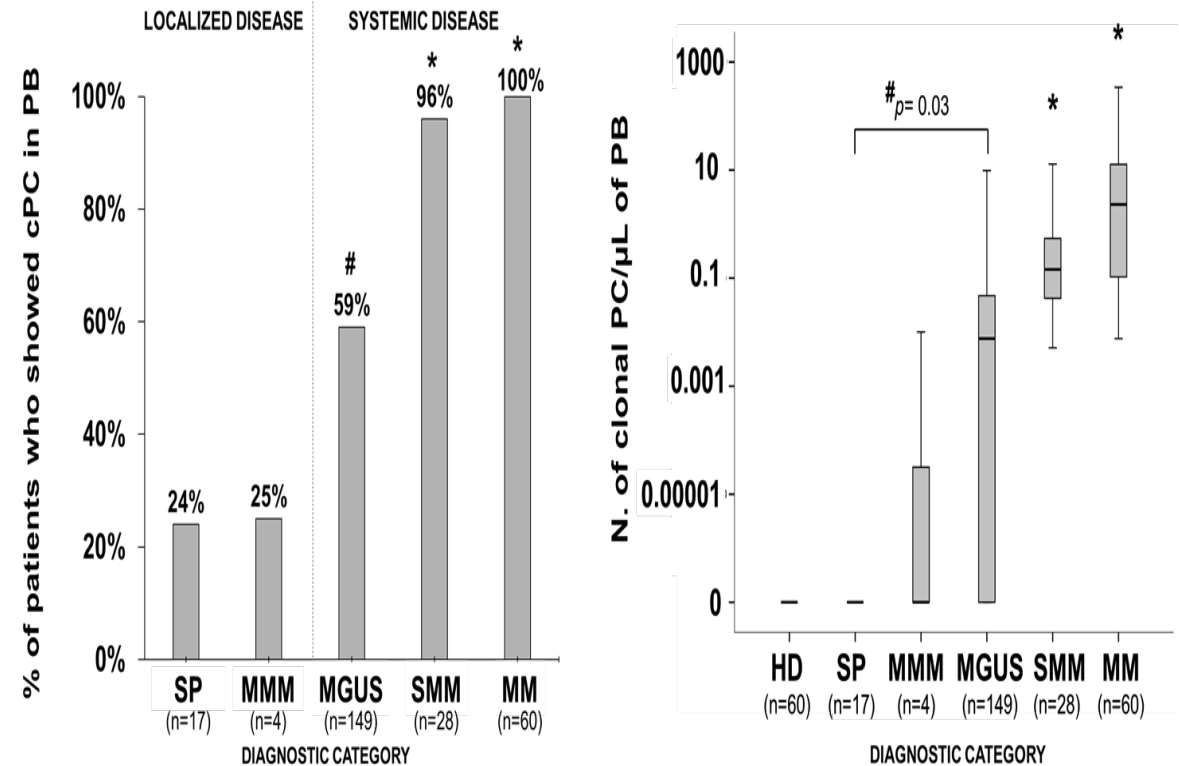
*Transcriptional profile at single cell level & GEP of CTCs and BM clonal PCs highly overlapping*

Only **58 genes significantly deregulated** in CTCs (7 infra- and 51 over-expressed) : some of them: Filanin, WEE1, LAMP3 and SAMD9 prognostic value .



*The transcriptional profile of CTCs vs patient-matched BM clonal PCs identify **gene regulatory networks related to MM dissemination.***

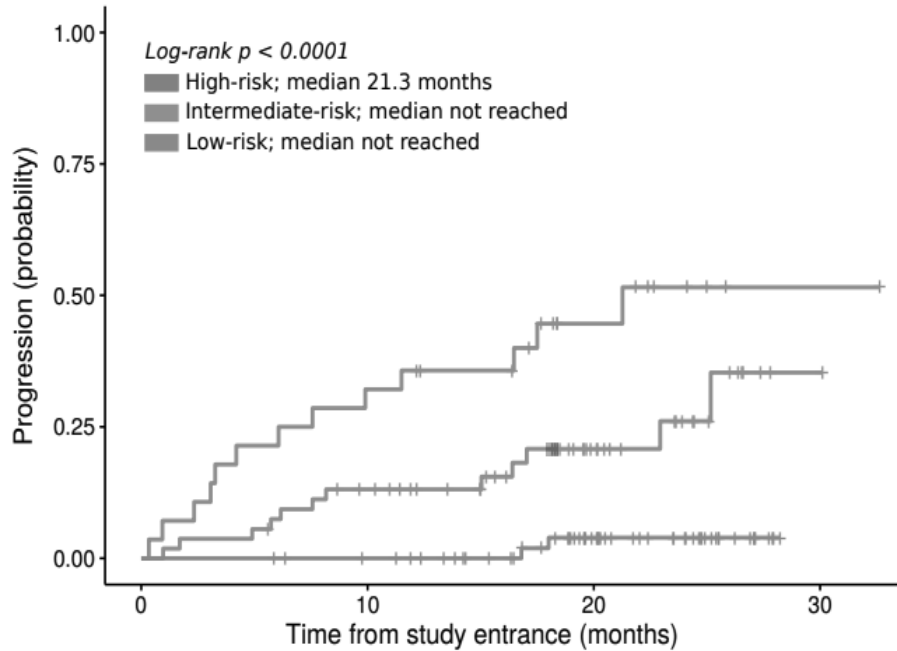
**CTCs detected in half MGUS and virtually all MM patients**  
**Highly significant differences between MGUS vs SMM and active MM**



# CTC predicts risk of progression in SMM: *Risk stratification using CTCs vs BM PCs*

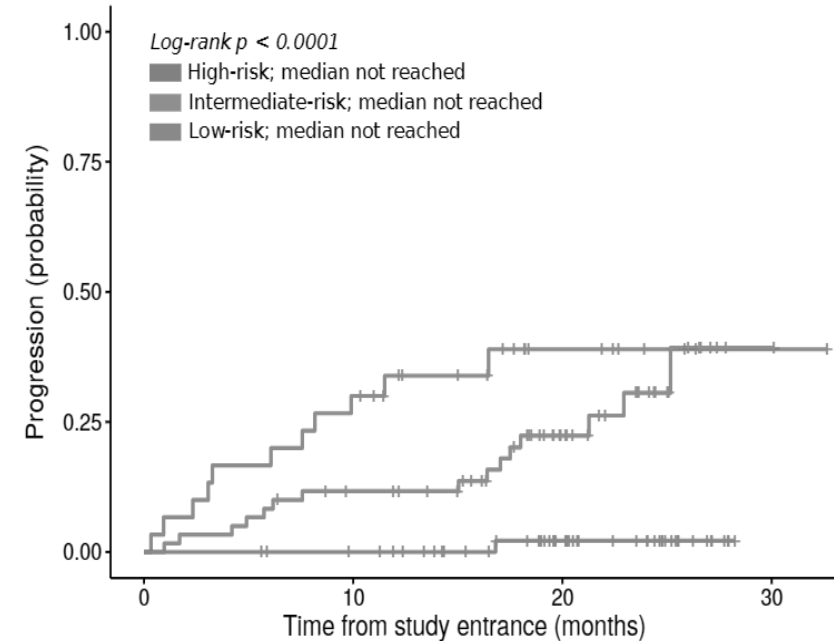
## Minimally invasive vs partially invasive models

**2/20/0.7 Model (CTC/ $\mu$ L >0.7)**



Number at risk				
28	19	8	1	
54	44	20	1	
66	63	37	0	

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



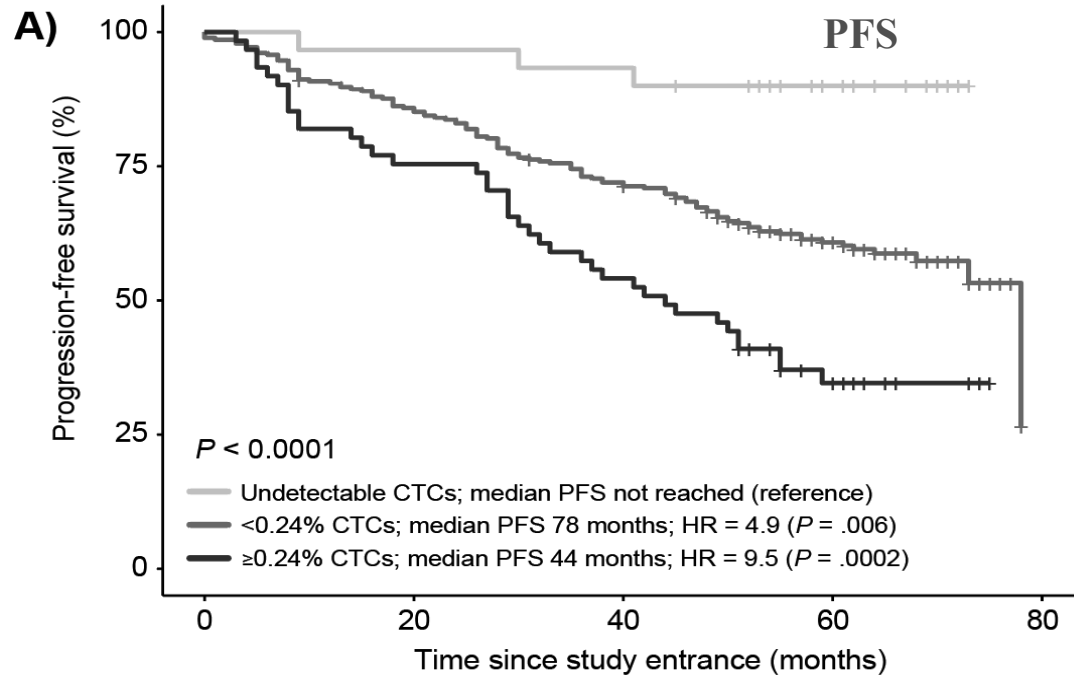
Number at risk				
30	21	7	1	
60	50	25	1	
58	55	33	0	

**Sequential monitoring of CTCs: new and easy to obtain evolving profile in SMM**

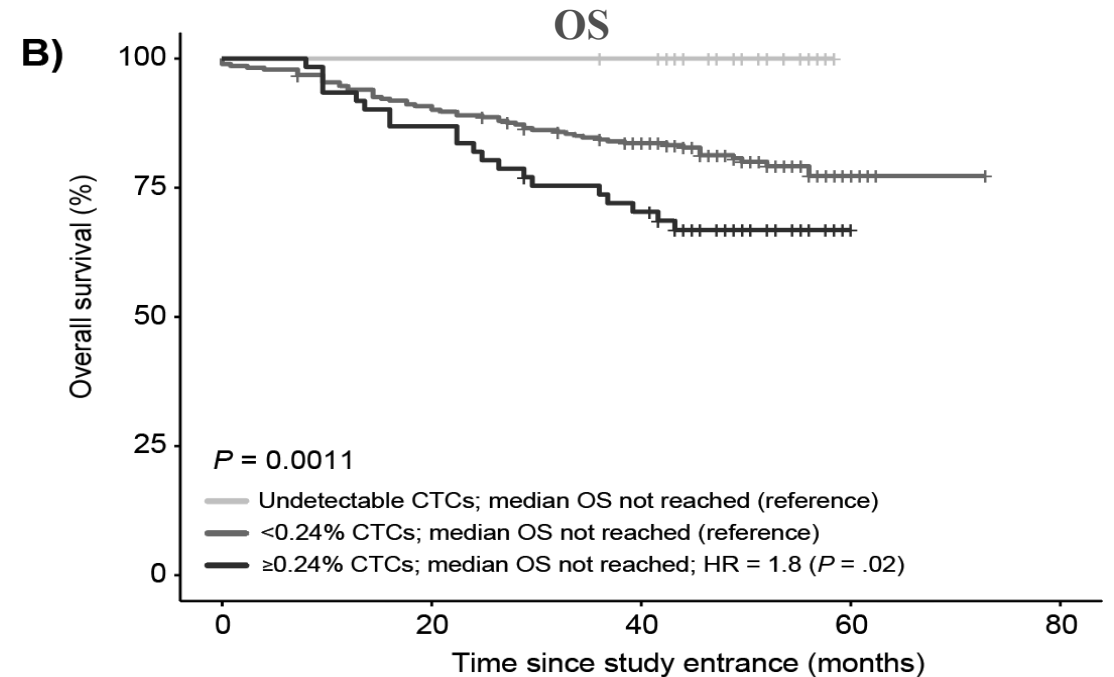


# CTCs are the most relevant diagnostic biomarker in MM (GEM12)

- ❖ Detected by NGF in 92% of patients.
- ❖ Higher number of CTCs were observed in patients with advanced ISS, elevated LDH and high-risk genetics



No. at risk	Undet.	30	29	28	17	0
	<0.24%	283	242	202	104	0
	$\geq 0.24\%$	61	46	33	14	0



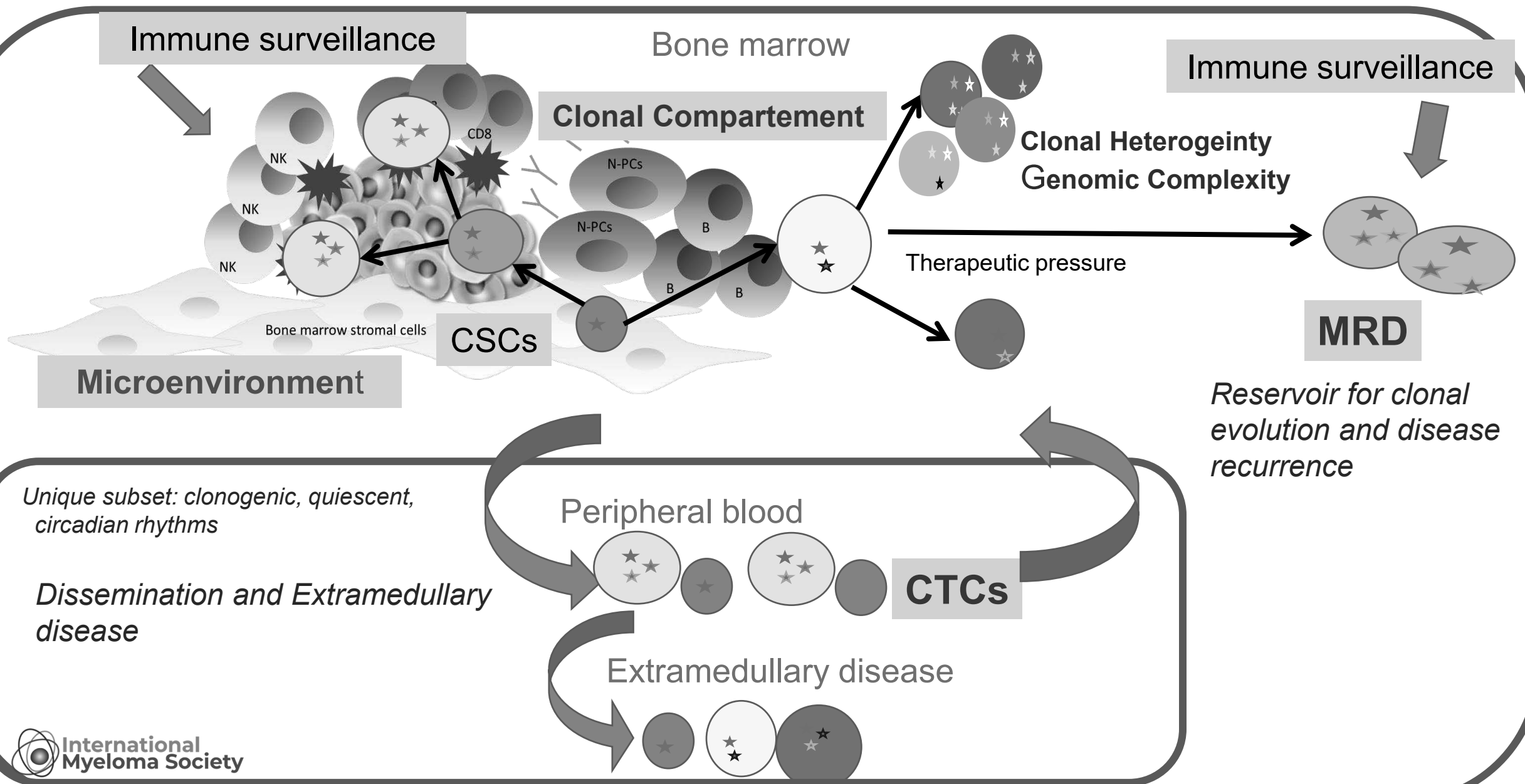
No. at risk	Undet.	30	30	29	0	0
	<0.24%	283	256	228	10	0
	$\geq 0.24\%$	61	53	42	1	0

**CTC levels are the most powerful independent prognostic factor at diagnosis**

*Model for MM dissemination: a high occupancy of hypoxic BM niches + pro-inflammatory microenvironment: force cancer cells to stop proliferating, recirculate in PB and seek other BM niches to continue growing*

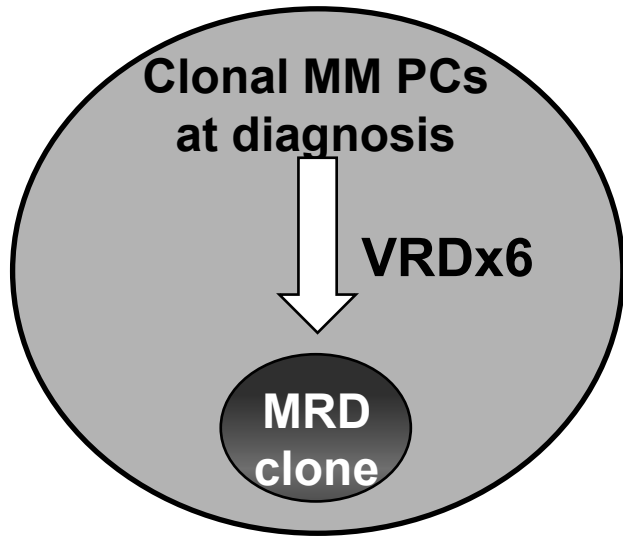
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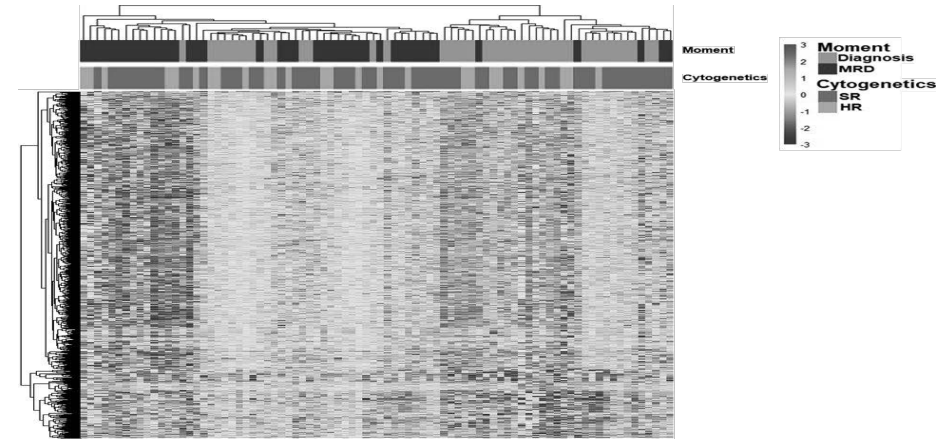
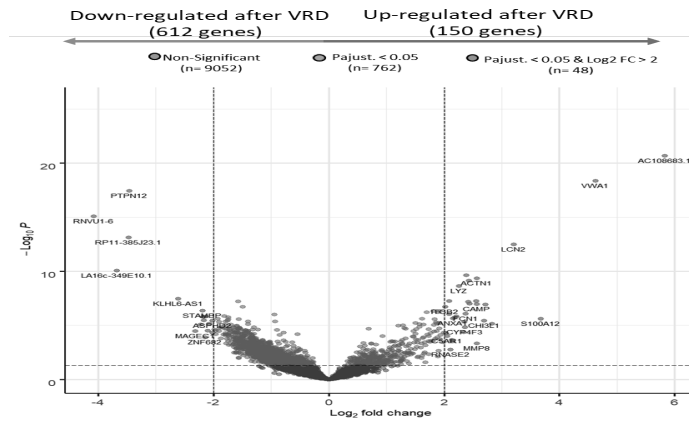


# Transcriptomic comparison: paired diagnostic vs MRD cells following VRD

FACs sorted cells & Massively parallel single-cell RNA-seq (MARSeq)

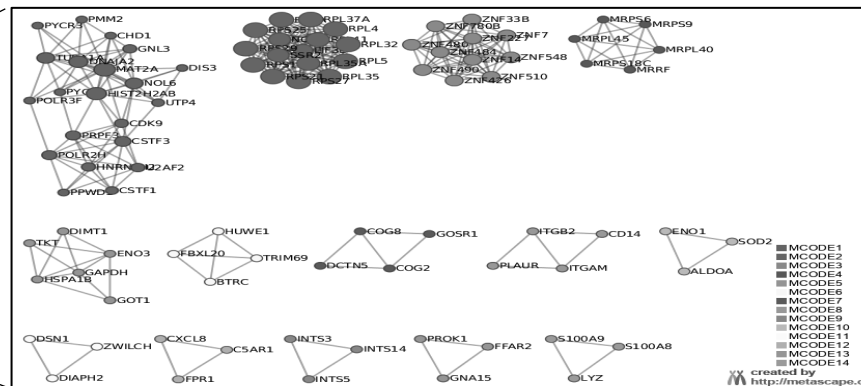
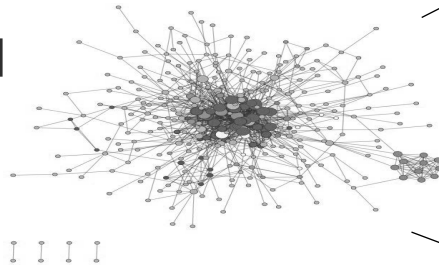


N=40 (28 SR + 12 HR FISH)



MRD cells showed 762 genes significantly deregulated

Derregulated functional networks



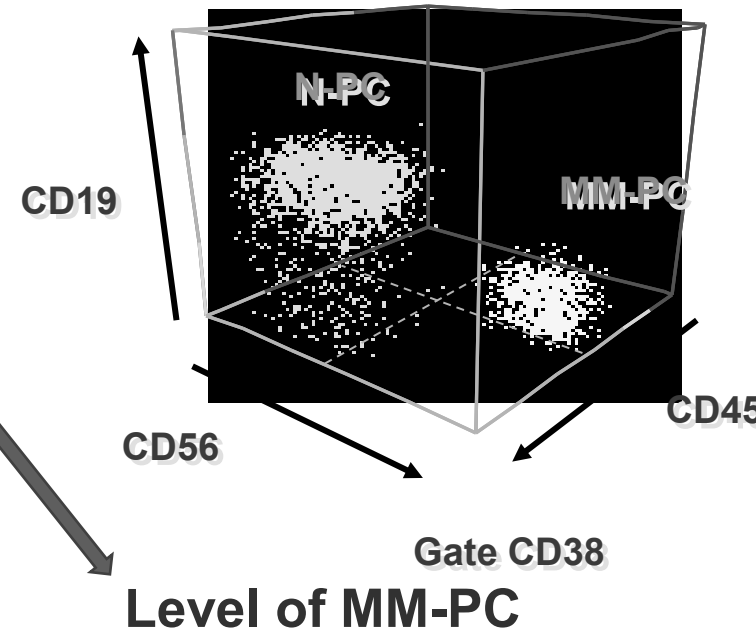
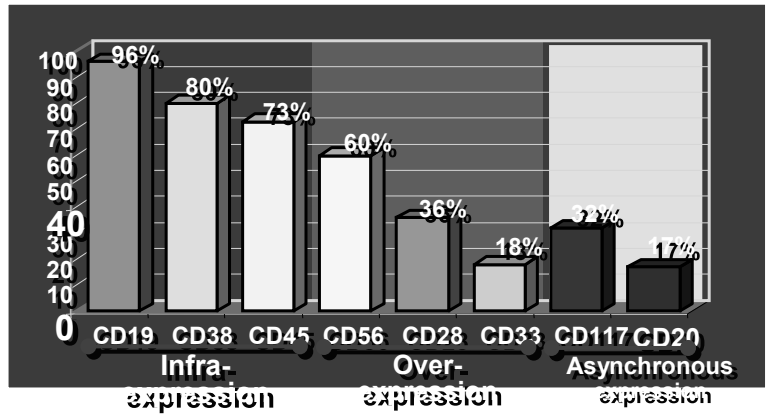
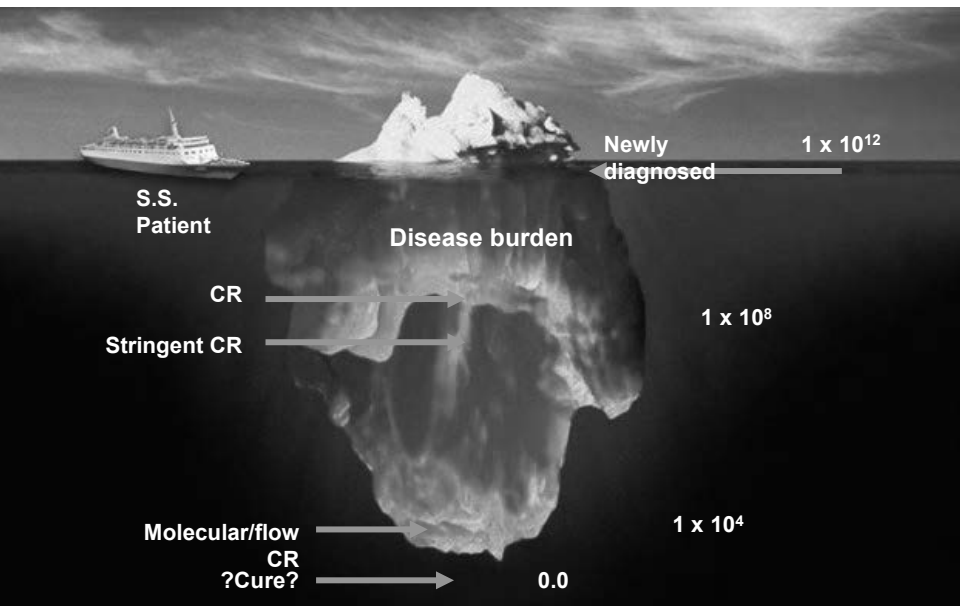
9-fold higher deregulated genes in MRD cells of SR patients compared to HR patients

*In SR, there is a clonal selection or transcriptomic adaptation in order to resist treatment, but in HR, the cytogenetic abnormality may predispose cells to resist treatment*

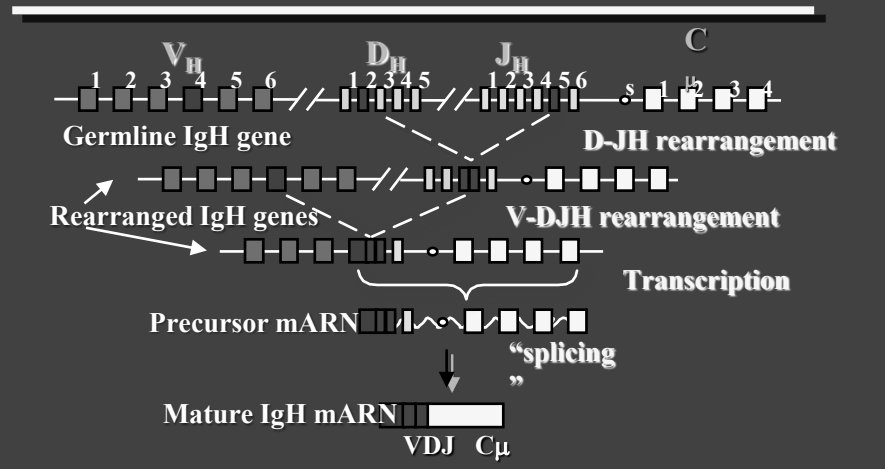
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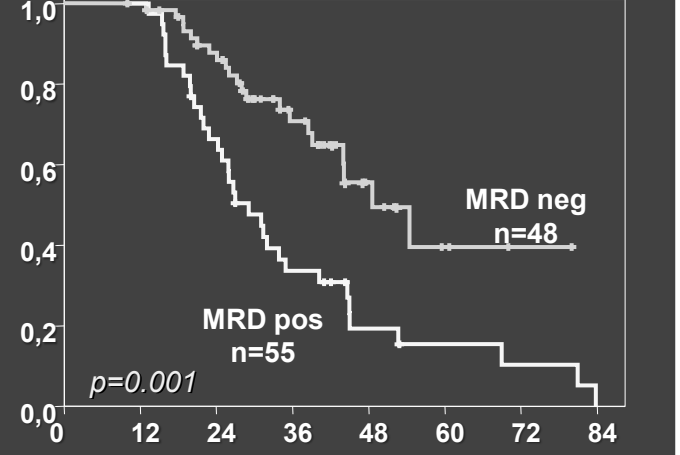
# Response to therapy is the key element to evaluate treatment efficacy and critical for survival ...*But definition of CR in MM is suboptimal*



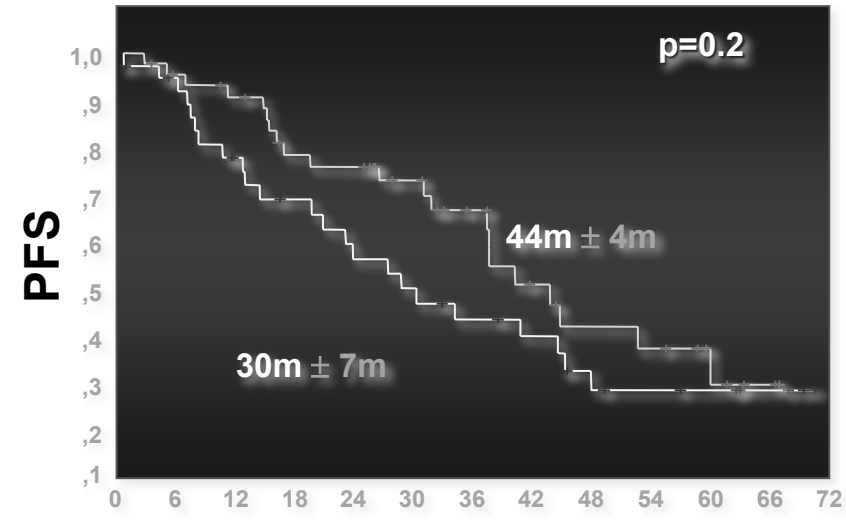
## ASO-PCR: Immunoglobulin heavy (IgH) chain gene rearrangement



## ASO RQ-PCR



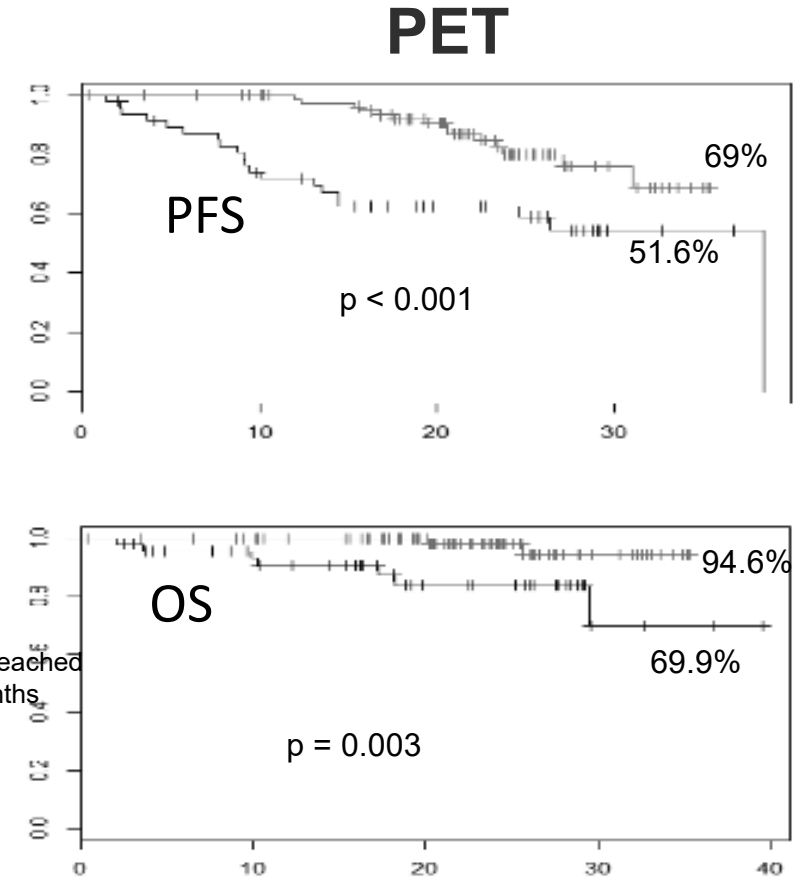
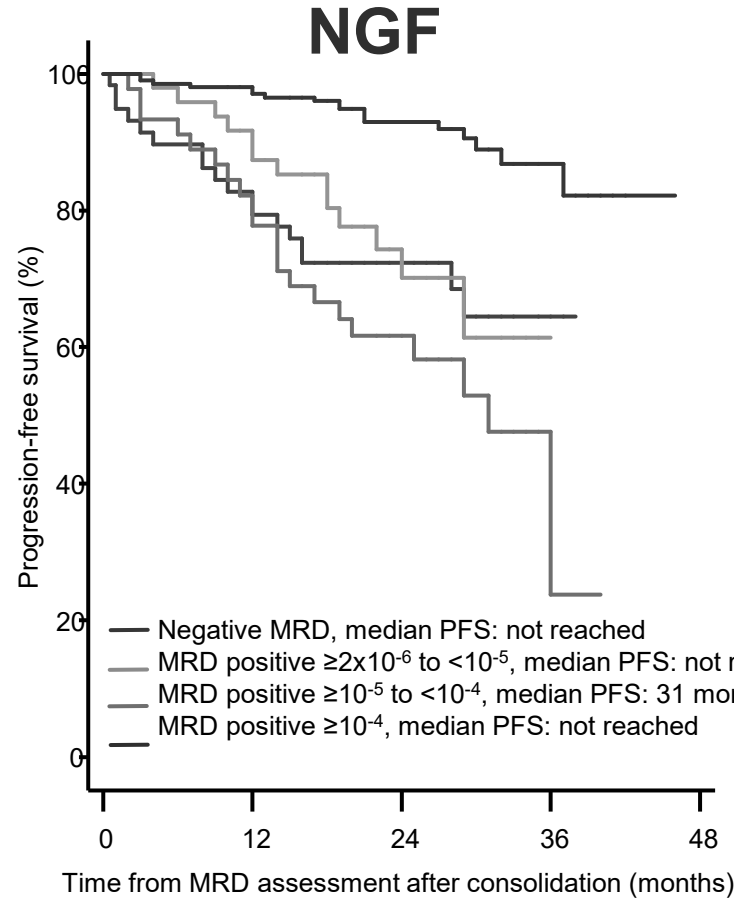
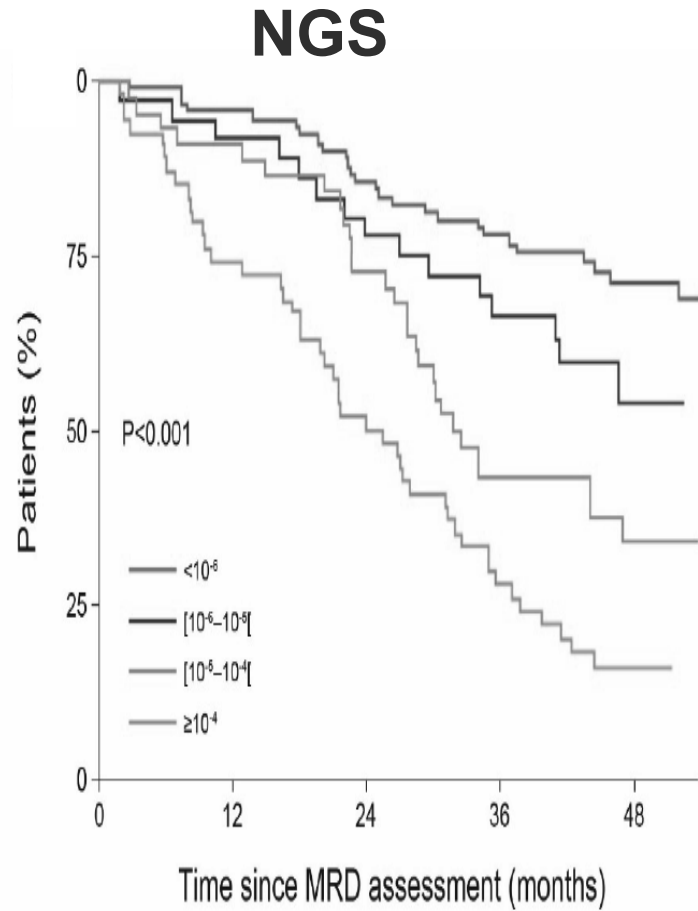
Puig, N Leukemia 201



San Miguel et al Blood 2002:99, p1853-56

# Response to therapy is the key element to evaluate treatment efficacy and critical for survival *Why we do not use to change treatment except in cases of refractory disease?*

## MRD assessment (endpoint)



No. at Risk

Perrot A, et al. Blood 2018;132(23):2456-2464.

Paiva B, et al. JCO Manuscript in review

Zamagni E, et al. Clin Cancer Res 2015;21(19):4384-90  
Moreau P, et al. Blood 2015 126:395

*The lowest the level of MRD the longer the survival  
MRD in the logarithmic range of  $10^{-6}$  is clinically relevant*

*The concept of PET CR.....Methionine?*

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# Rationale for Early Intervention in High Risk SMM

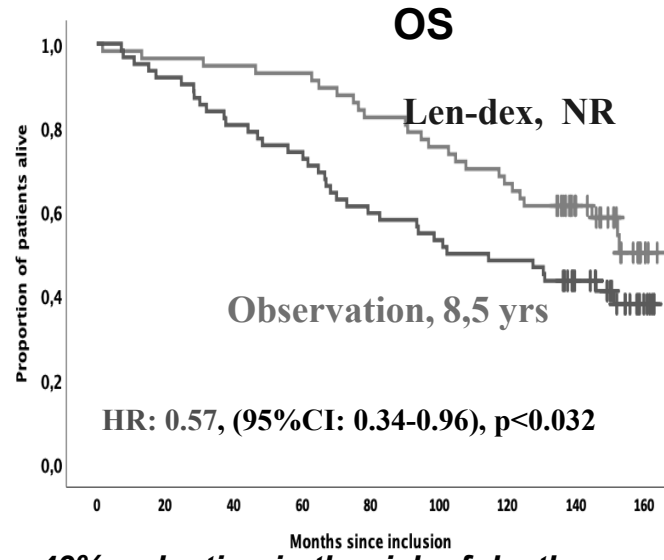
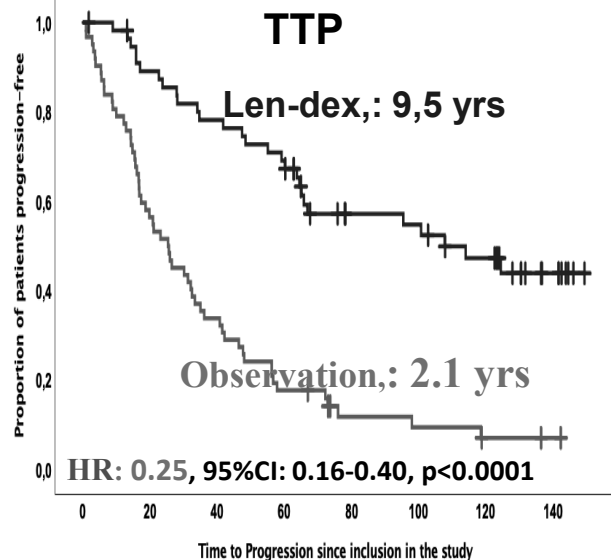
- **To treat the disease early: to achieve cure**
- *Early detection and intervention is a pre-requisite for cure in most malignancies*
- *Why is the standard of care in MM no treatment until CRAB? Risk of harm: clonal selection, toxicities.*

Numerous clinical trials in SMM (~ 75 in clinicaltrials.gov)

TO DELAY THE DISEASE PROGRESSION

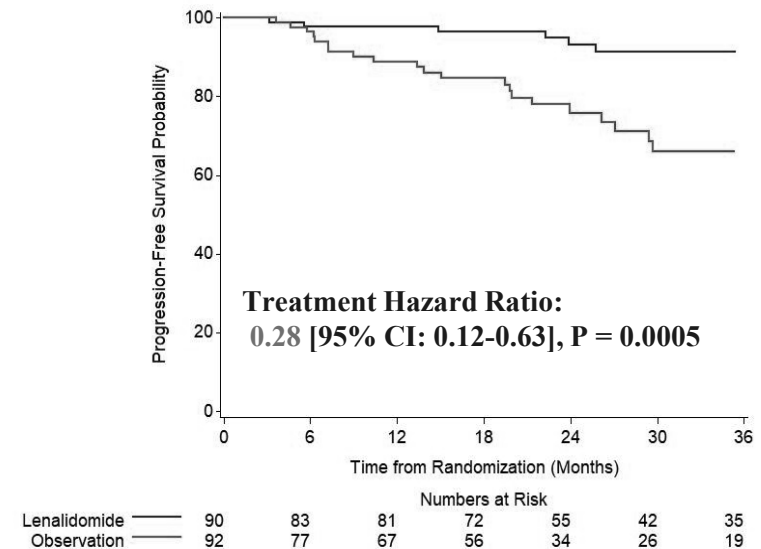
TO CURE THE DISEASE

**Len-Dex vs Observation** (n = 119) Median f/u: 12,8y



**43% reduction in the risk of death**

**Len vs Observation** (n = 182)





# Curative Strategy for High Risk Smoldering (CESAR trial) (n = 90)

High risk definition based on Pethema and/or Mayo models

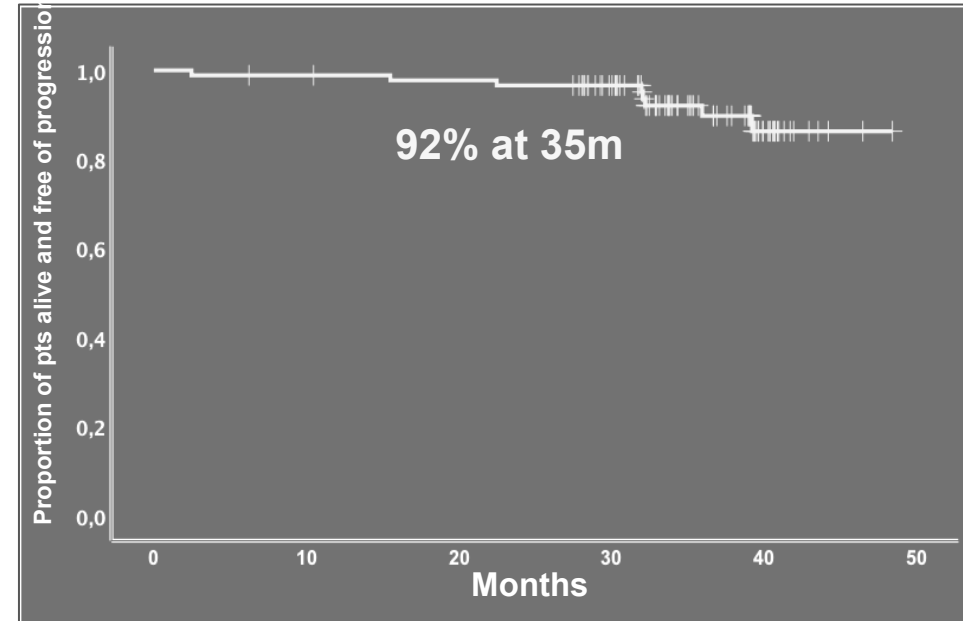
## CR and MRD status

Response, %	Induction (KRd x 6) (n = 77)	HDT- ASCT (n = 77)	Consolida (KRd x 2) (n = 77)	Maintenan (Rd x 1 Yr) (n = 77)
≥ CR	43	63	75	81
MRD negative	33	49	65	62

- 6 pts did progress (In 5 it was biological & 4 were ultra-HR):  
2 during induction; one after ASCT and 4 during maintenance

- Three deaths: Only 1 treatment related death( Ischemic stroke )

## PFS



*Mateos et al. ASH 2019. Abstract 781;*

### Results to date:

- 54 patients accrued
- Median patient age 63 years
- 6% have completed maintenance, 56% consolidation, 80% induction and 17% in induction phase
- ≥1 patient needed a dose modification
- ≥ grade 3 AE seen in 43% of patients

## ASCENT : KRd-Dara

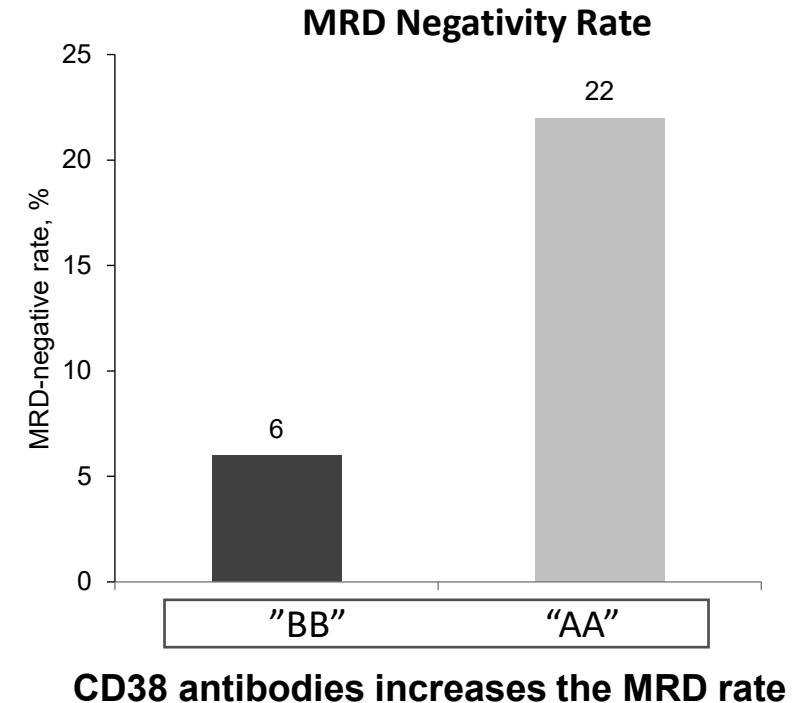
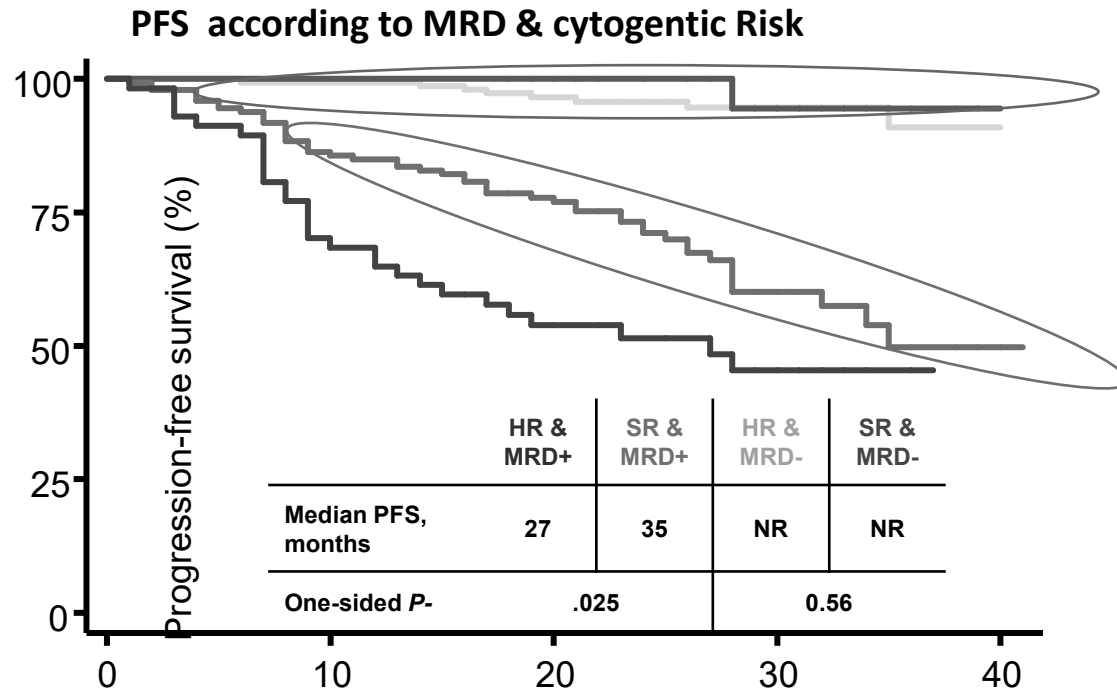
**Quadruplet regimen KRd-D is well tolerated in high-risk SMM**

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# Influence of depth of Response in Standard Risk patients

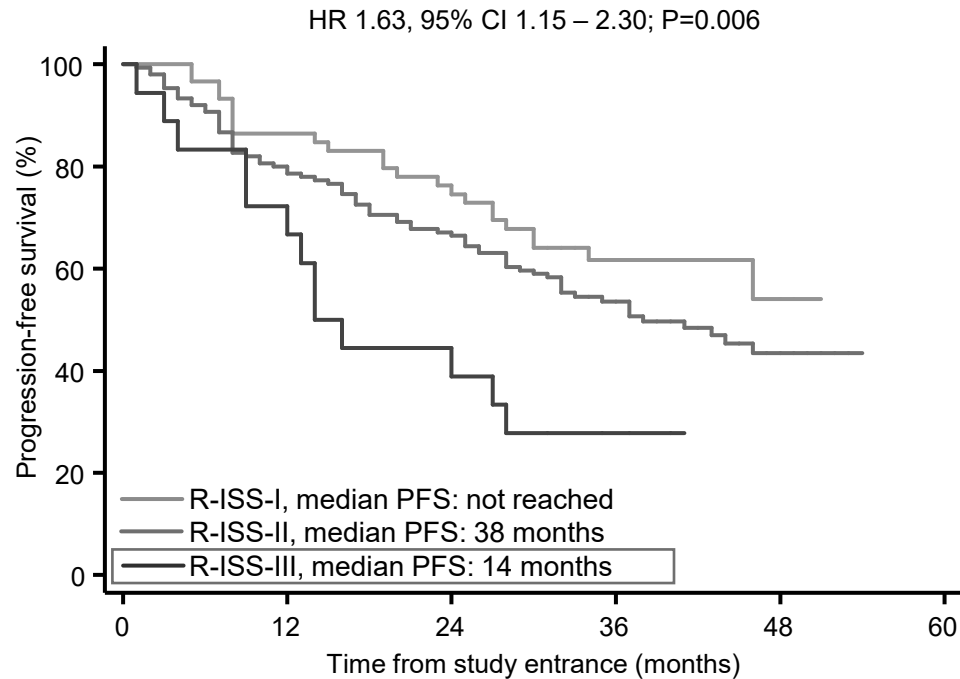
## *Evidences that support MRD directed therapy*



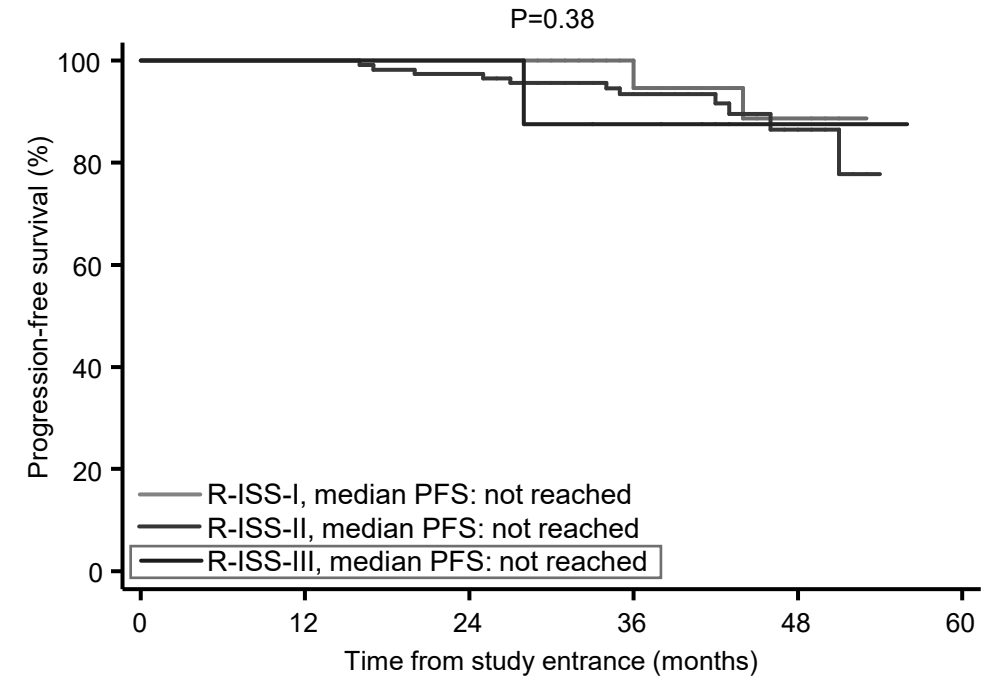
*If cure is the goal : To offer intensive therapies to high-risk patients & a gentle one to standard risk patients.....Wrong philosophical approach?*

# The best pathway to overcome the poor prognosis of high-risk cytogenetics is through the achievement of MRD-negativity: *overcomes poor prognosis of high-risk*

MRD-positive



MRD-negative (Undetectable)



Paiva B, et al. Blood 2017;130: abstract 905

- **Treatment should be adapted in High risk patients in order to eradicate MRD inside and outside BM**
- ❖ *MoAb improve outcome...but does not overcome the adverse prognosis*
- ❖ *Effective treatment may not be a matter of dose intensity..... but of dose density*
- ❖ *Investigate experimental therapies: sequential courses including immunotherapy to avoid early tumour regrowth?.*

# Transplant candidate Patient: *Proposal for today*

## Induction (*VRD or KRD*)+(*CD38 Ab*)

### ASCT (*Tandem in HR*)

MRD-

MRD+

### Consolidation

*Same as induction if CR*

*Different if <CR or HR*

### Maintenance (*Len +/- Carf....Dara??*)

VRD+MoAb

VRD+MoAb

VRD+MoAb

.....

ASCT if <MRD+@ 10-12 cycles  
Otherwise ASCT at late relapse

# *In Myeloma treatment there is a high attrition rate, particularly in the elderly population.... therefore front line is critical*

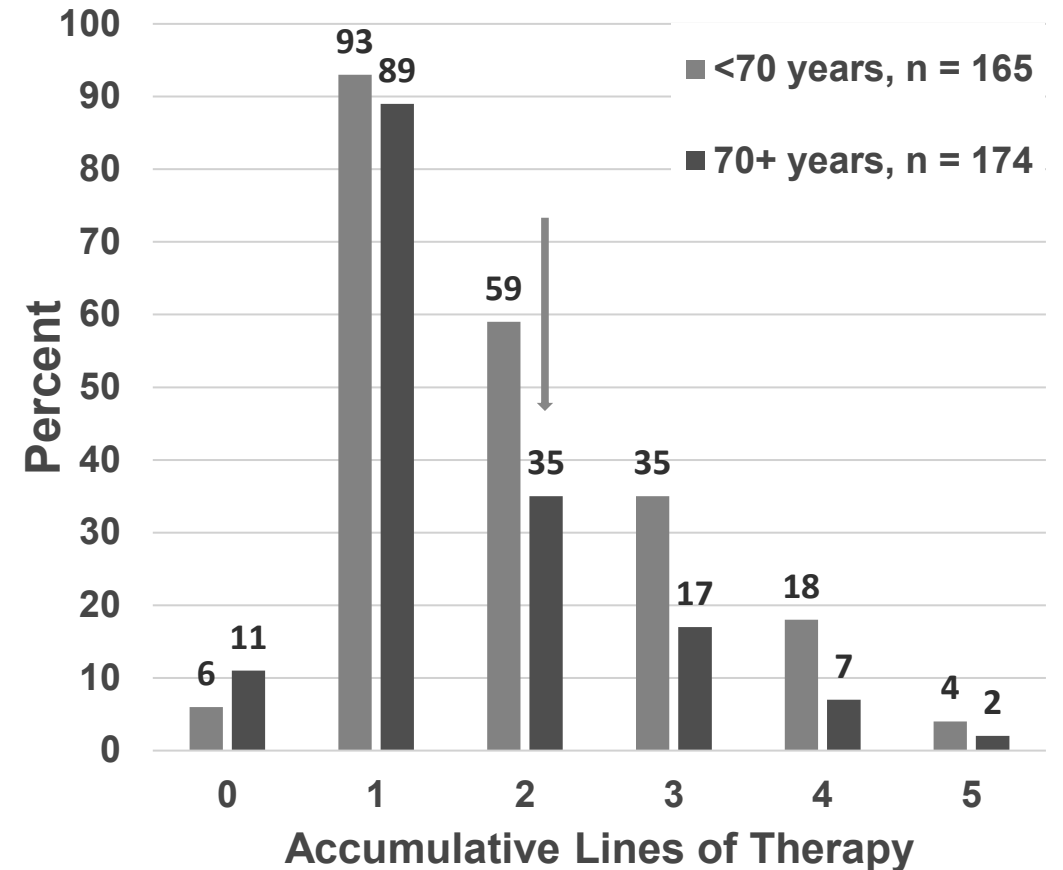
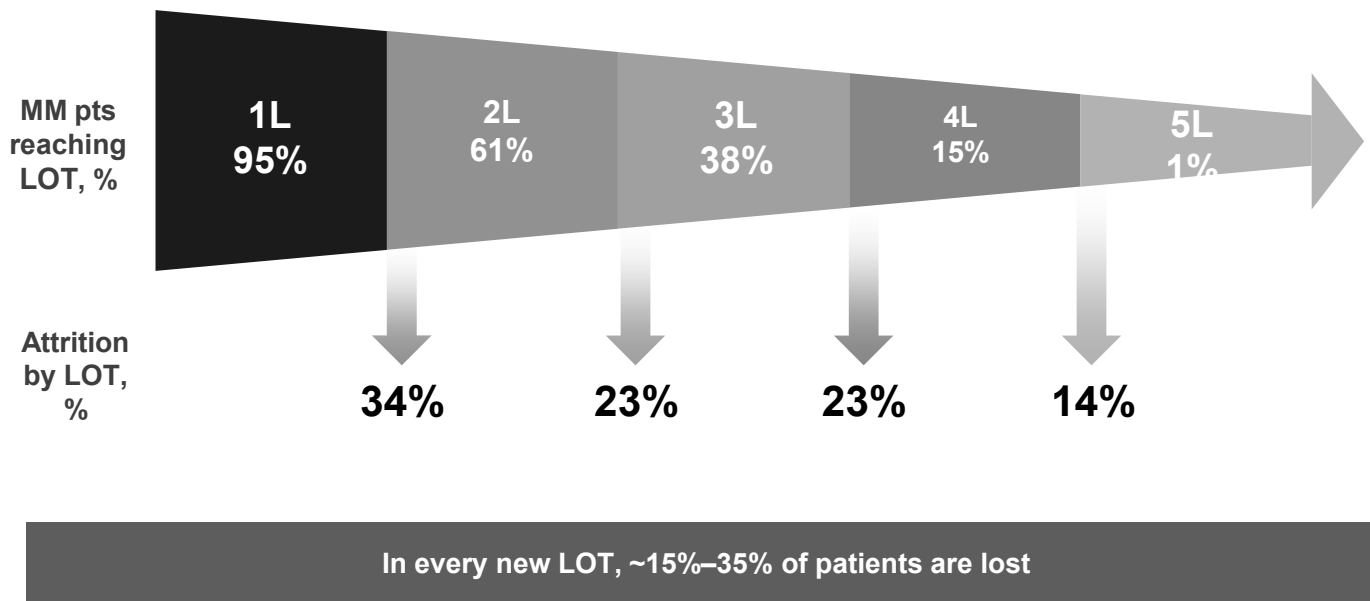
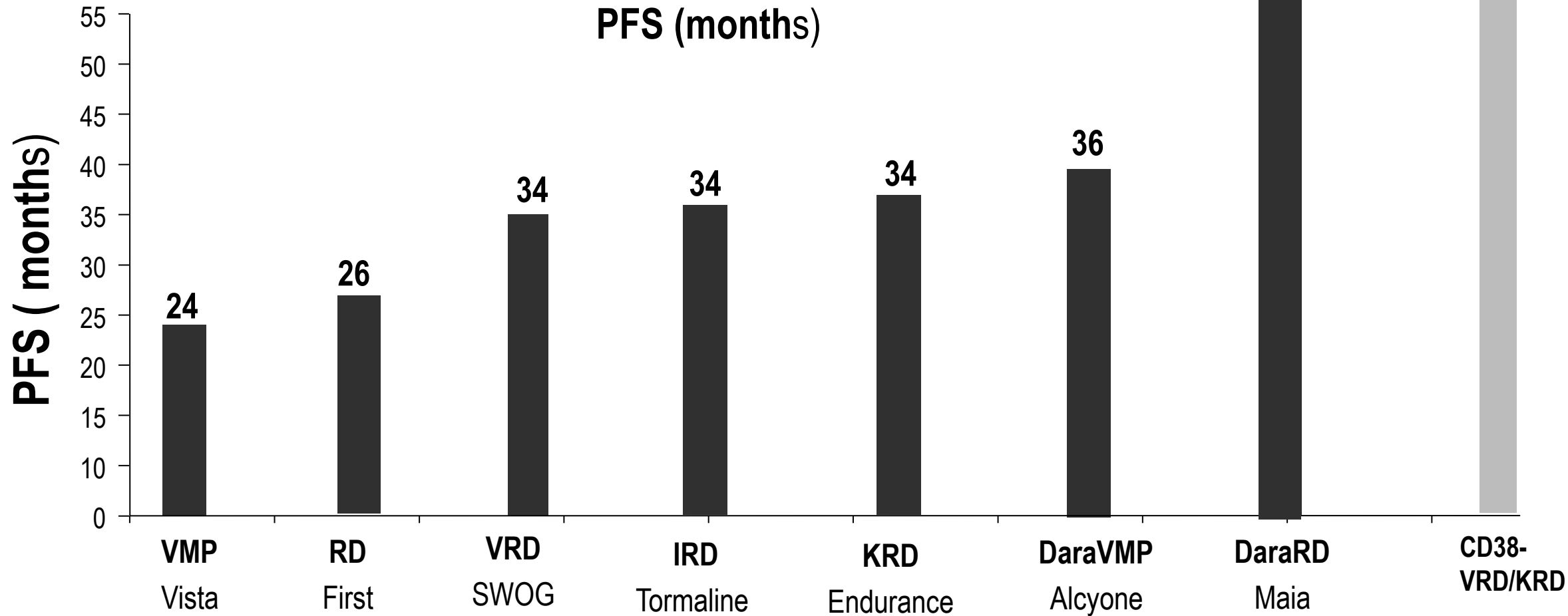


Figure adapted from: Yong K et al. *Br J Haematol* 2016;175(2):252-264.

LOT, line of therapy.



# What are the Optimal Regimens In non- transplant candidates?



1. San Miguel J, et al. N Engl J Med 2008;359:906–17; 2. Benboubker L, et al. N Engl J Med 2014;371:906–17 3. Durie. Lancet. 2017;389:519. 4. Kumar. ASCO 2020 Abstr LBA3; 5. Facon T et al. ASH 2020. Abstract 551 6. Mateos. ASH 2019. Abstr 859. 7. Facon. NEJM. 2019;380:2104

# If cure is the goal.....We need to improve.....*Future Perspectives*

*Many unsolved questions.... Absence of robust data to guide treatment decision*

- ✓ High Risk Cytogenetics ( particularly R-ISS3 & Double Hit)
- ✓ Early Relapses or Primary Refractory disease
- ✓ Extramedullary disease: efficacy of novel agents remains controversial

## Therefore.....

- ❖ *New strategies .....since conventional approaches are suboptimal*
- **Adapted treatment approach upfront to eradicate MRD**
- **Early Rescue Interventions (ERI): based on early detection of resistance**
- **Immunotherapy (Biespecific T-cell engagers and CAR-Ts) may be the way to improve the outcome in this high risk patient population.**

✓ **Early relapses:** OS for R-ISS 3 in early relapses post-ASCT is **1.5 years** (Gopalakrishnan S et al. BBMT 2018).

✓ In **Primary Refractory** Patients, to move into HDM/ASCT is inadequate (PFS:6m; OS:13m) Rosiñol L et al. Haematologica 2012

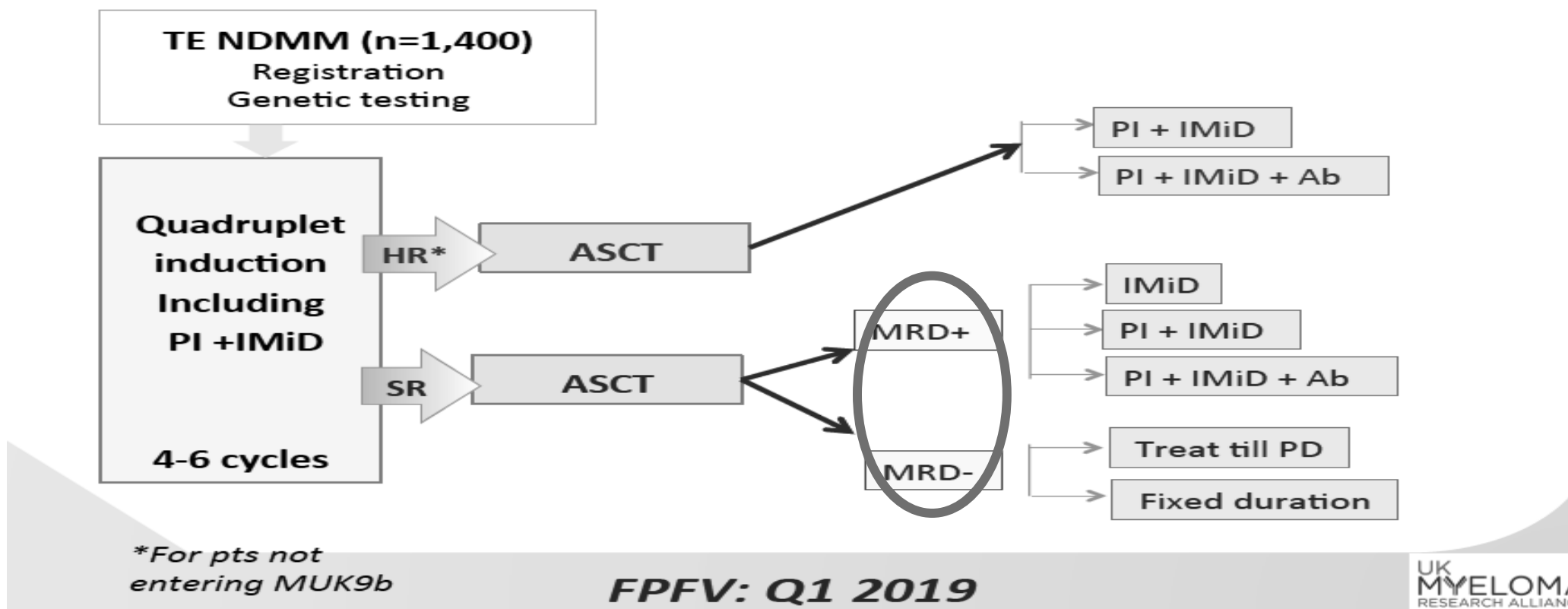


# IFM 2021

IFM 2019 : HR Trial	IFM 2019: Non-HR Trial (Phase III, n= 1 100)	
	Randomisation	
	Non-Adapted Therapy	Adapted Therapy
<b>KRD-Dara x 6</b>	<b>IRD-Dara x 6</b>	<b>IRD-Dara x 6</b>
<i>MRD1</i>	<i>MRD1</i>	<i>MRD1</i>
	--      +	--      +
<b>HDM</b>	<b>HDM</b>	<b>HDM</b>
<b>KRD-Dara x 4</b>	<b>IRD-Dara x 4</b>	<b>IRD-Dara x 4</b> <b>KPD-Dara x4</b>
<i>MRD2</i>	<i>MRD2</i>	<i>MRD2</i>
	--      +	--      +
<b>HDM</b>		<b>HDM</b>
<b>Rev + Dara 2 years</b>	<b>Rev 2 years</b>	<b>Rev 2 years</b> <b>Rev + Dara 2 years</b>
<b>TEP</b>	<b>TEP</b>	<b>TEP and optional tomotherapy of residual targets</b>
<i>MRD3 (end of therapy)</i>	<i>MRD3 (end of therapy)</i>	<i>MRD3 (end of therapy)</i>
<i>MRD 4, 5, 6 (each year)</i>	<i>MRD 4, 5, 6 (each year)</i>	<i>MRD 4, 5, 6 (each year)</i>
<b>Phase II-PO: 30% increase of PFS as compared with HR in the IFM 2009 trial</b>	<b>PO:MRD3 from 45% to 55% with adapted therapy. SO:PFS, OS, Operational cure (ie: MRD3+4+5+6=Neg), Stringent-MRD (ie: MRD3 + TEP = Neg)</b>	

# UK group: RADAR study. Risk adapted therapy according to response. NDMM transplant eligible

**UKMRA Myeloma XV (RADAR: Risk Adapted therapy Directed According to Response in newly diagnosed patients with multiple myeloma (NDMM) suitable for stem cell translation (TE))** Kwee Yong, Mark Cook

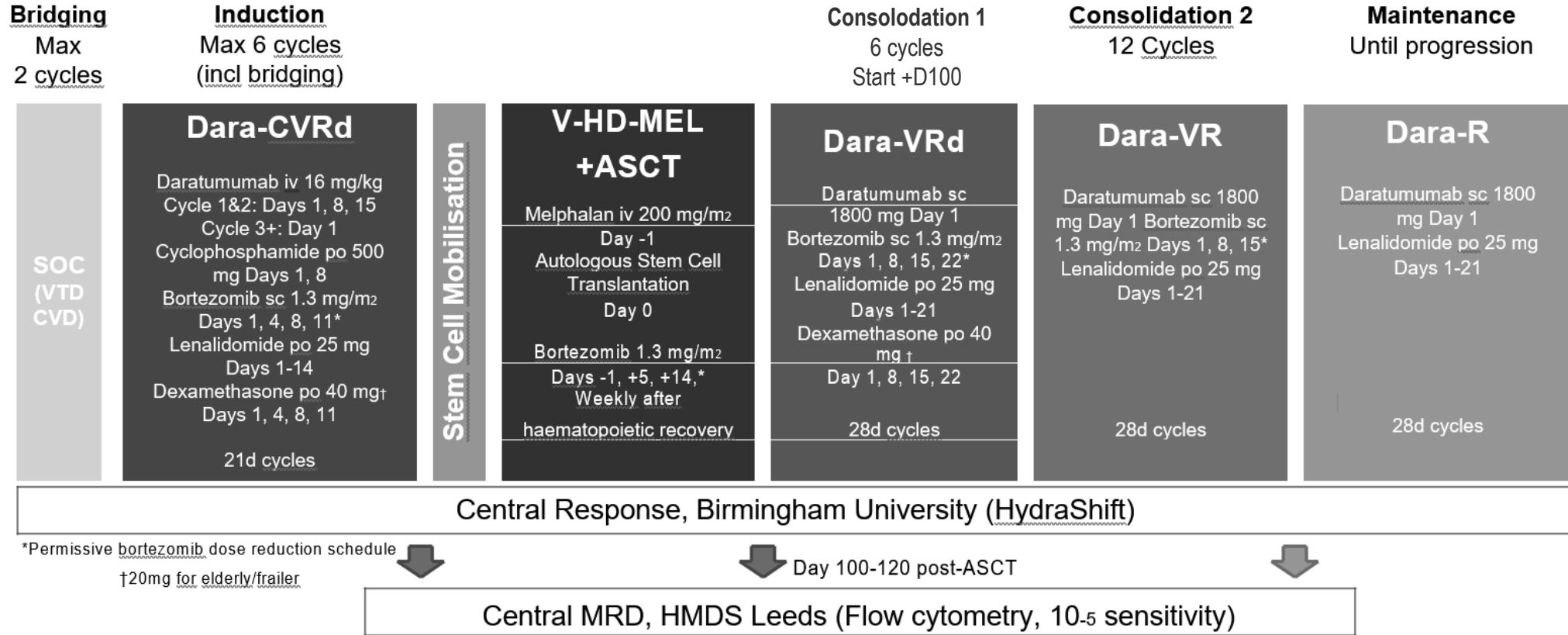


\*For pts not entering MUK9b

FPFV: Q1 2019

UK MYELOMA RESEARCH ALLIANCE

# UK Trial in ULTRA-High Risk MM



From a total of 462 Pts, 128 were Ultra-High Risk\* ( 107 included in the study....102 evaluable for response)

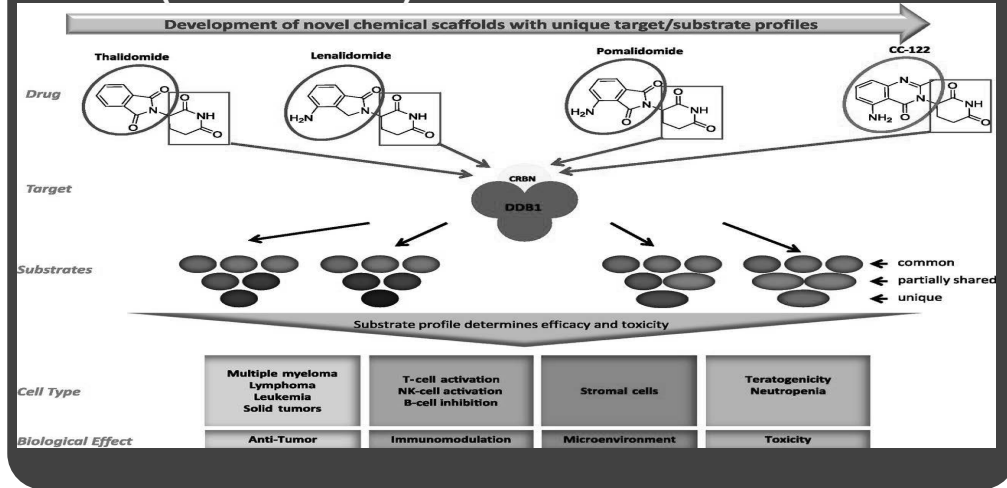
VGPR post induction and Post ASCT: 84% and 87%

MRD-ve post induction and Post ASCT: 50% and 88%

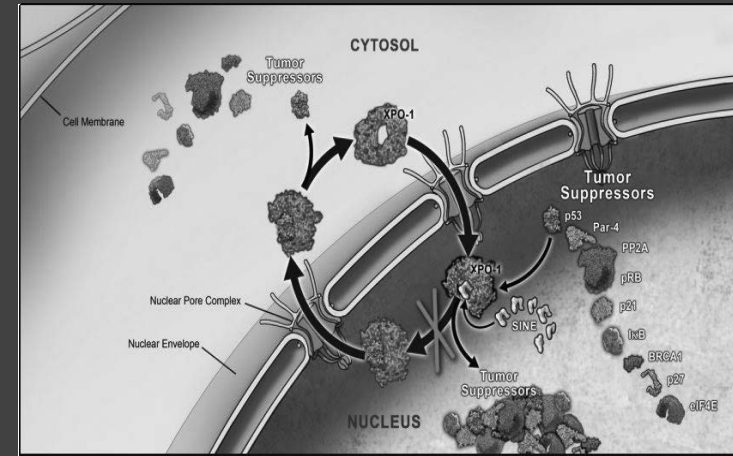
\* 27% : 11% GEP+ Double hit & 16% GEP or Double hit

# New agents

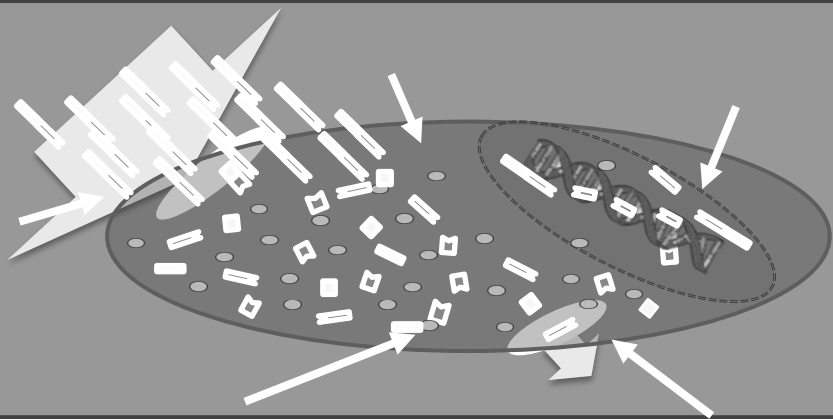
## CC-220(Iberdomide) New IMiDs CC-92480



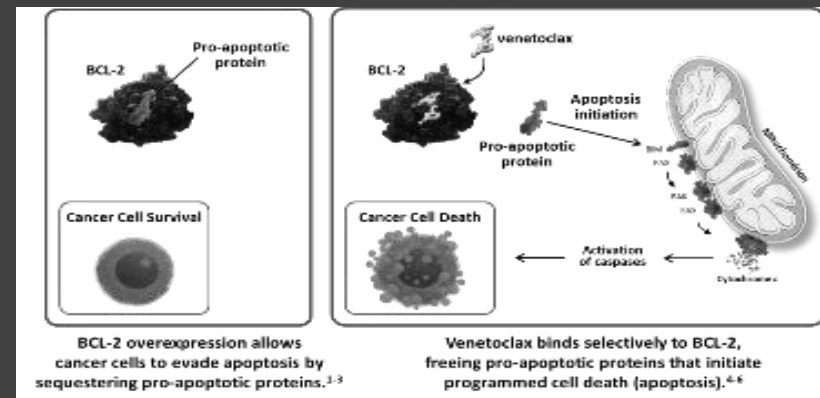
## Selinexor: XPO-1 inhibitor



## Melflufen is a new alkylator



## Venetoclax



# Monoclonal antibodies: New perspectives

*To overcome the limitations of an immunosuppressive tumour microenvironment by linking CTLs with the tumour cell.*

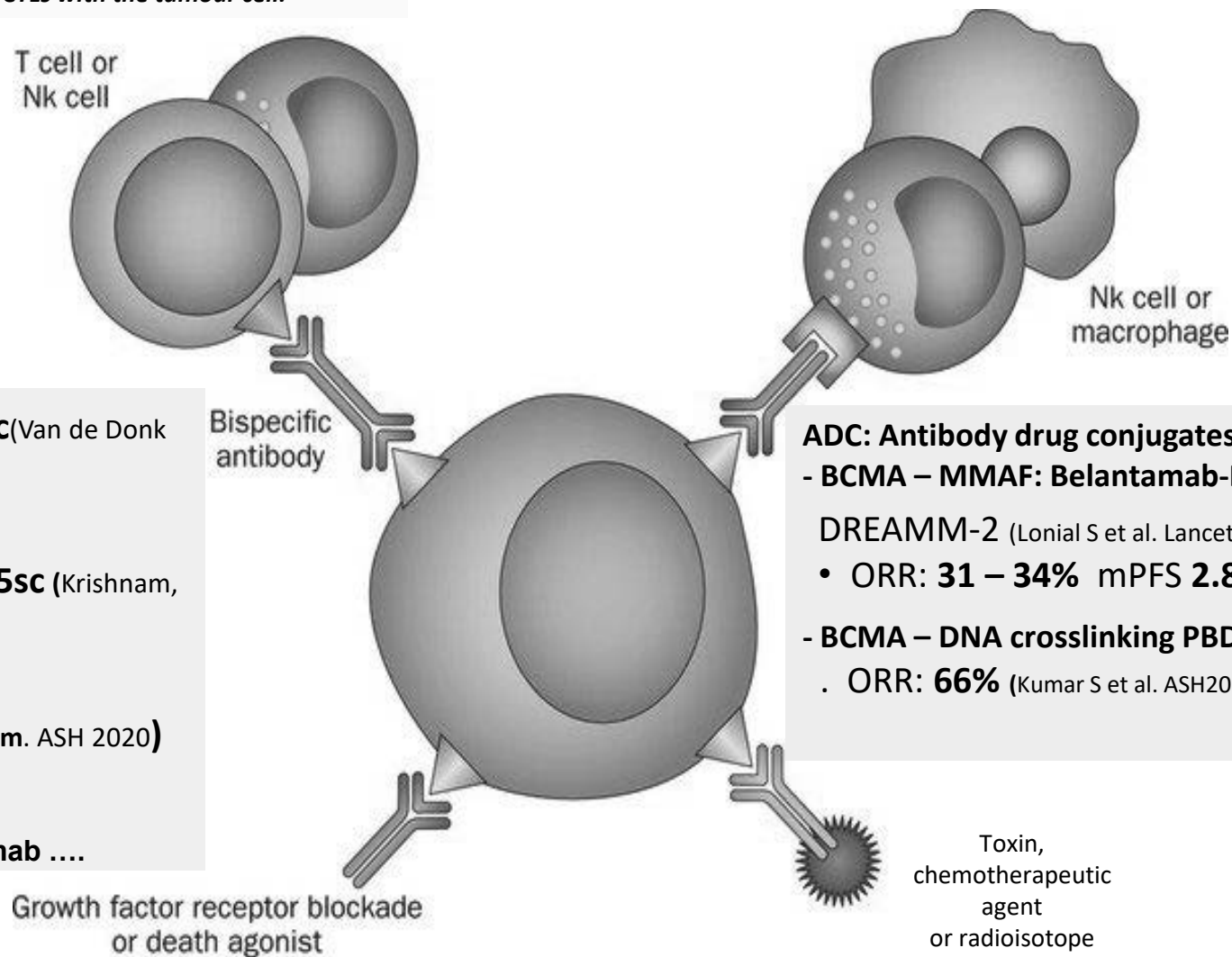
**Bispecific T cell engagers:**  
BCMA & Others –CD3 Phase I trials

**-Teclistamab (BCMA) Pts: 157, 75sc** (Van de Donk EHA 2021) **ORR 65% (58%VGPR)**

**- Talquetamb (GPC5D). Pts: 184, 75sc** (Krishnam, EHA2021) **ORR 70.9% (60%VGPR)**

**-Cevostamab (FcRH5). Pts: 80** (Cohem. ASH 2020) **ORR 61% (17%VGPR)**

**CC-93269; REG 5458, TNB3838, Elranatamab ....**



**ADC: Antibody drug conjugates**

**- BCMA – MMAF: Belantamab-Mafodotin**

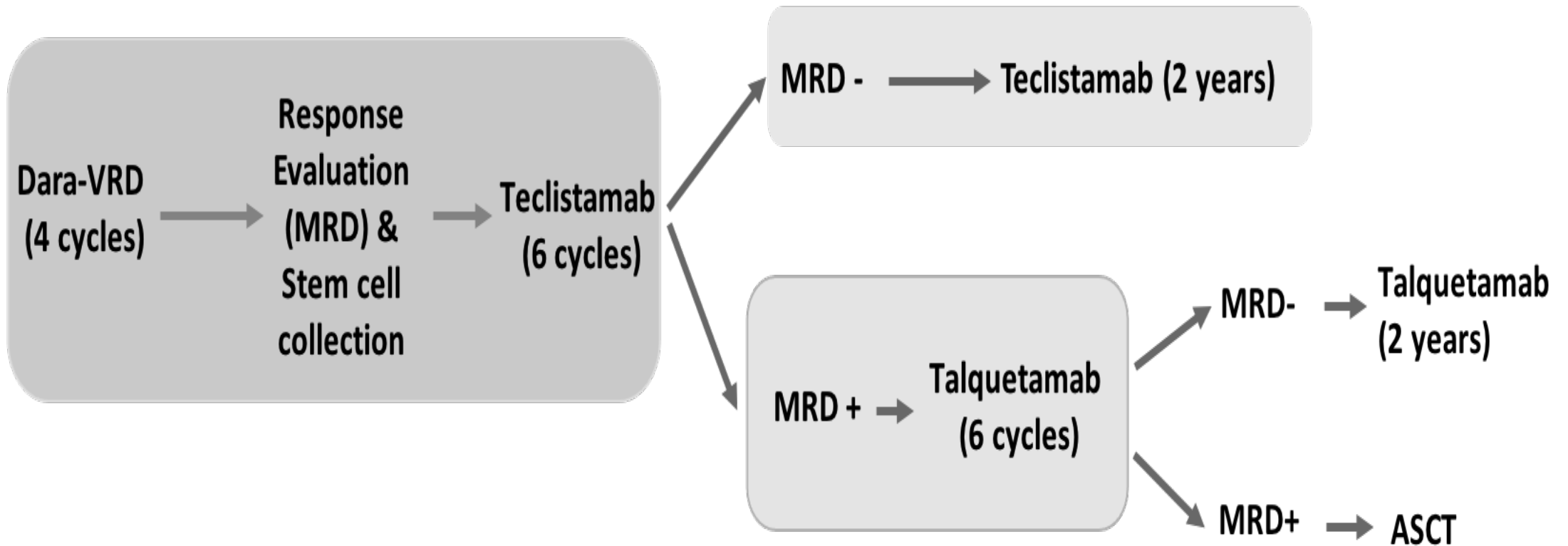
DREAMM-2 (Lonial S et al. Lancet Oncol 2019)

• **ORR: 31 – 34% mPFS 2.8 m – 4.9 m**

**- BCMA – DNA crosslinking PBD : MEDI2228**

• **ORR: 66%** (Kumar S et al. ASH2020 Abst #179)

# PETHEMA/GEM: High Risk MM Patients 2021



**Patient population: High-risk transplant & Fit non-Trx candidates**

-FISH: del(17p), t(4;14), t(14;16) and 1q amplifications .

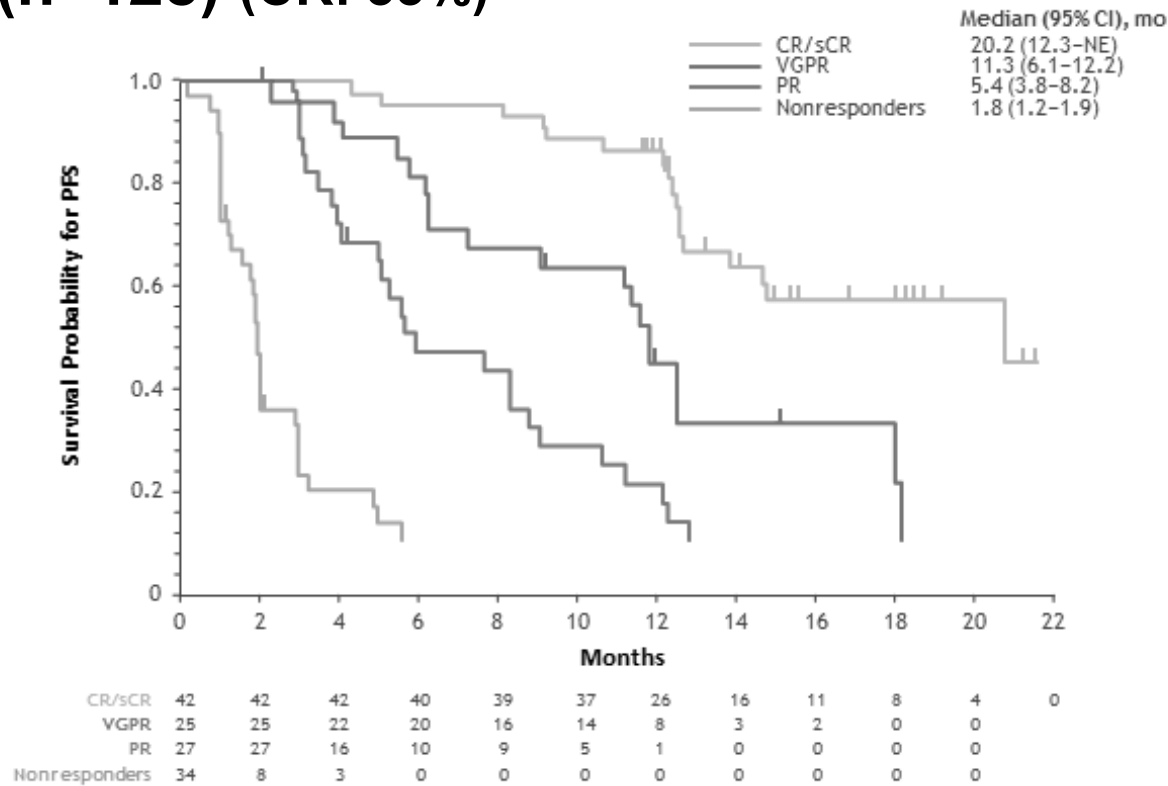
-R-ISS 3

-Presence of extramedullary disease

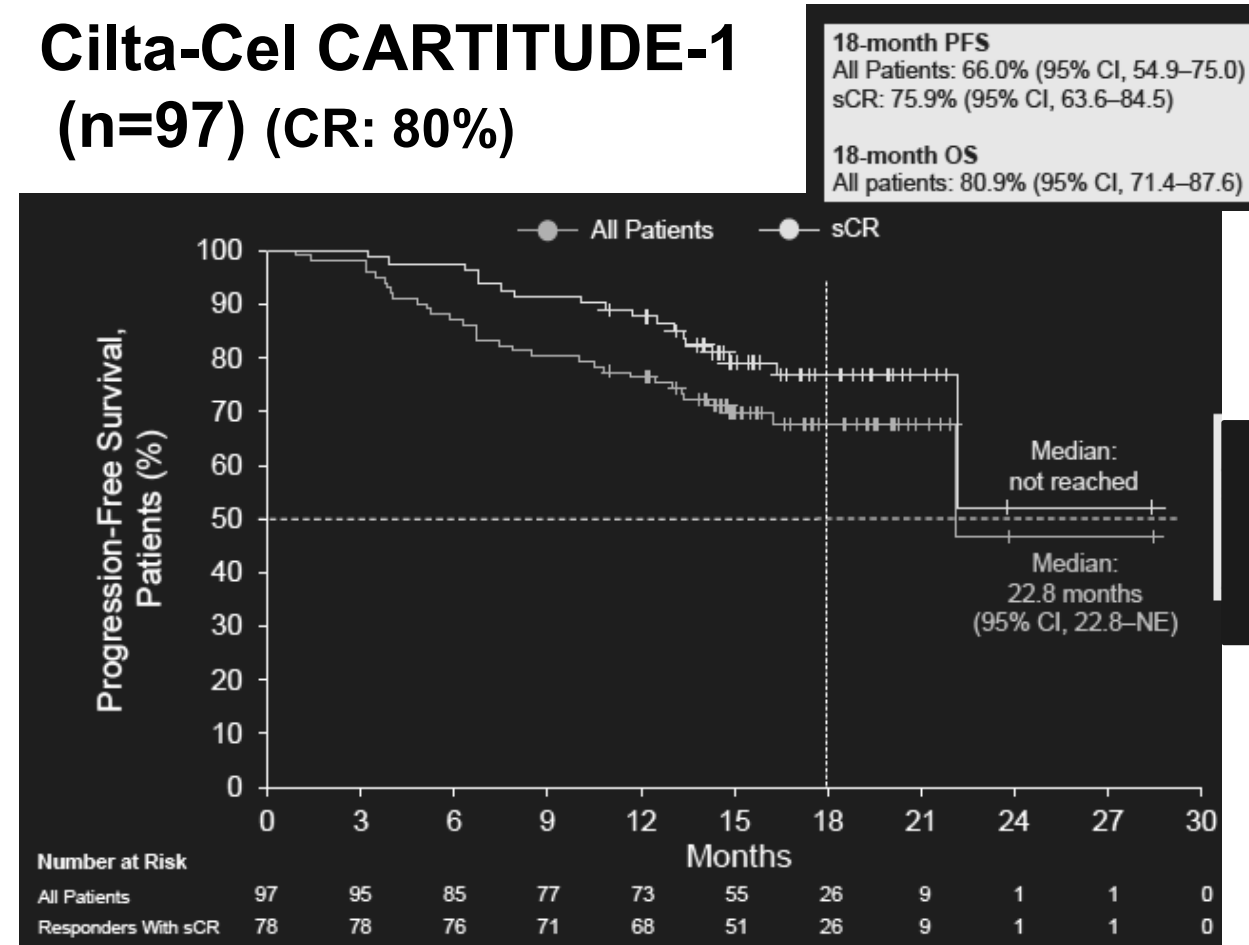
# Outcomes with current BCMA-directed CAR T cells in CR patients

## *The importance of depth of response with CAR T cell treatment*

### Ide-cel KarMMa (n=128) (CR: 33%)



### Cilta-Cel CARTITUDE-1 (n=97) (CR: 80%)



# Future of CAR-T cell therapy

- **Early relapse**
  - CARTITUDE 4 (1-3 PL Len-ref).....*cilta-cel vs SoC*
  - KarMMa-3 (2-4 PL, prior antiCD38).....*Ide-cel vs SoC*
- **Frontline setting**
  - CARTITUDE-5: NDMM not intended for ASCT (Ph 3 randomized): *VRD+Cilta-cel vs VRD-Rd*
  - KarMMa-4: NDMM R-ISS 3: *induction + ide-cel + Len maintenance*
  - BMT-CTN SOSS 2021 Concept: HR-NDMM
- **Suboptimal response after ASCT& 6m Maint: BMT-CTN 1902**
- **Combinations trying to improve the outcomes**
  - KarMMa-7: *ide-cel + Iberdomide /+ gammasecretase inhibitor /+ DPd or PVd*
  - *Fine-tuning the infusion product: increase % of memory like T-cells, armoured CARs, etc.*
  - *Dual targeting*

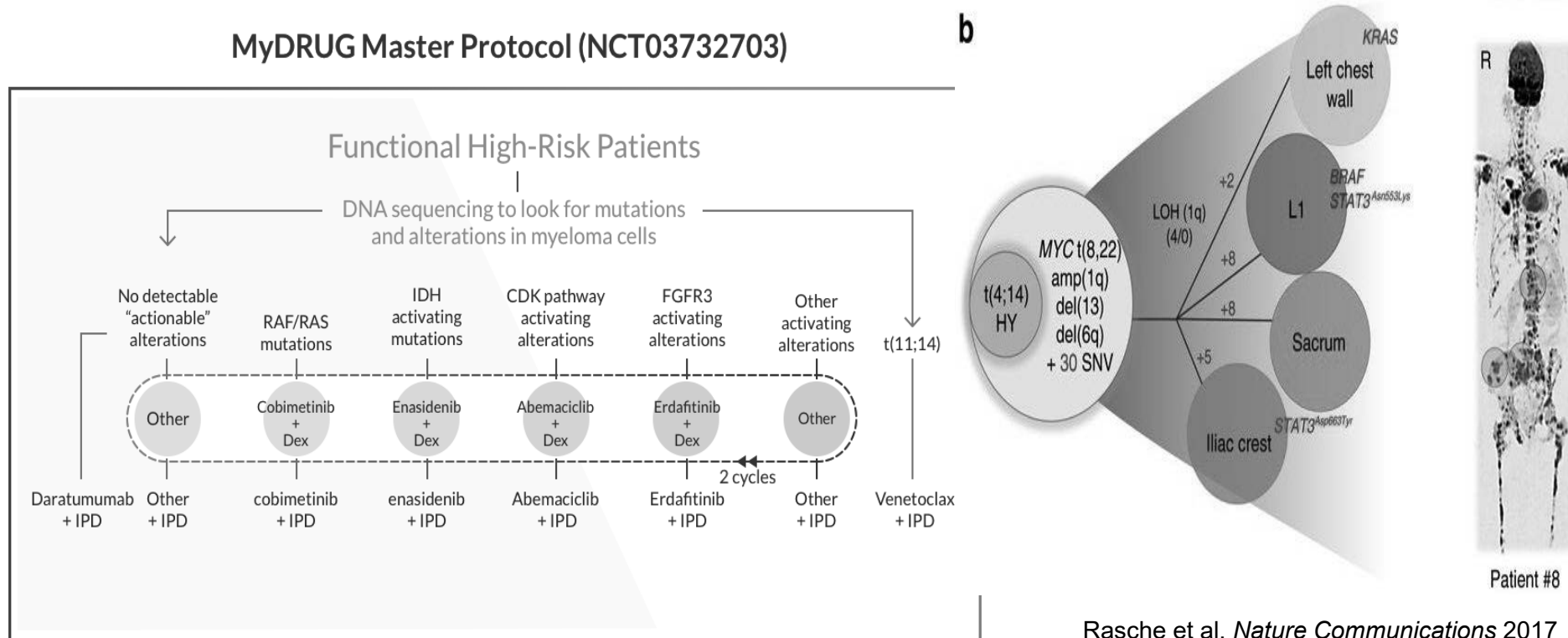


# Optimizing Clinical Trials for MM Patients Individualized therapies

## ➤ Targeted Therapy: Molecular lesions predicting\* response

- **Venetoclax** : for t(11;14) and high BCL2 patients
- **Targeted agents**: RAS/MAPK pathway inhibitors, IDH inhibitors...*But*  
.....*clonal heterogeneity*: KRAS in Chest; STAT3 & BRAF in L1

\* PROGNOSTIC/ PREDICTIVE

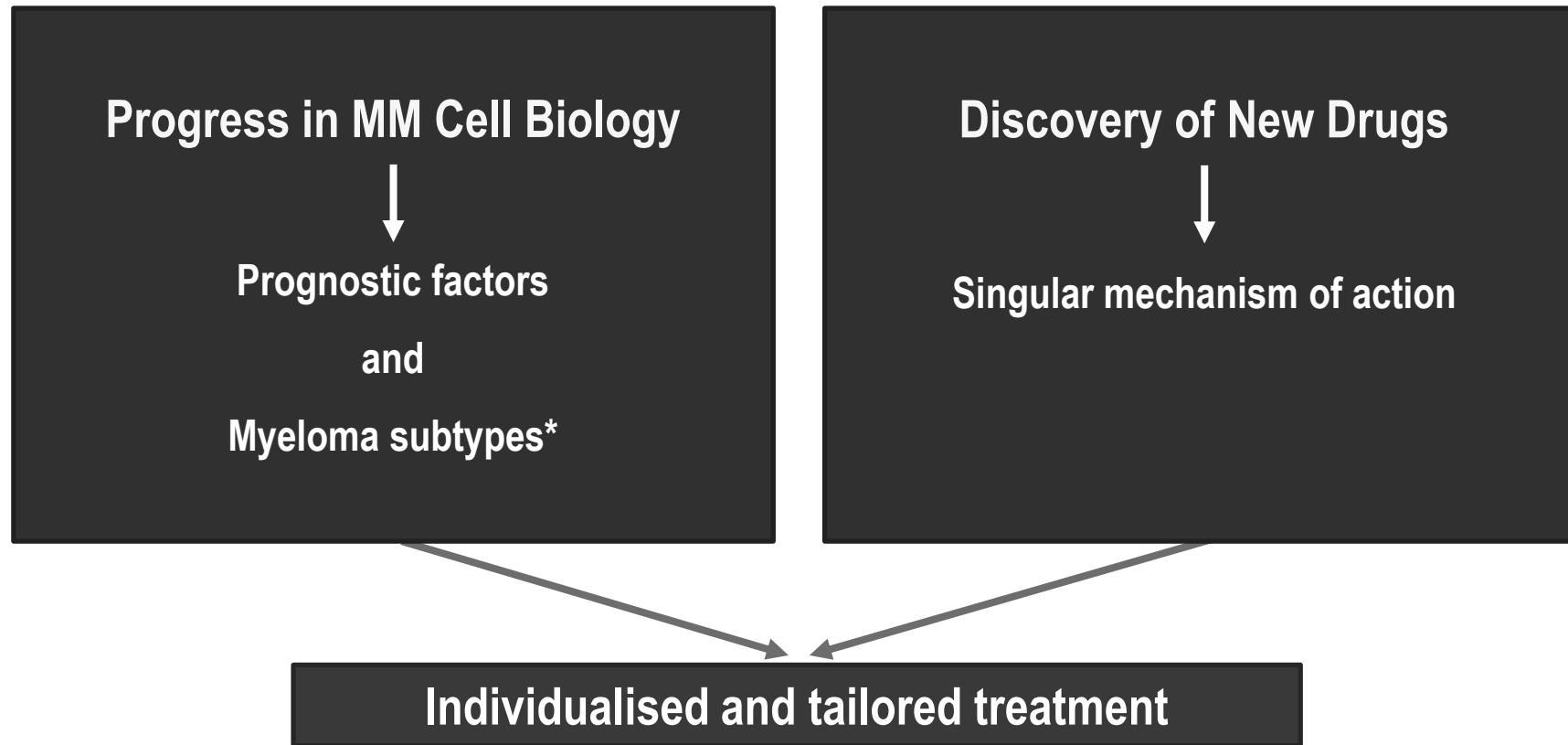


Rasche et al, *Nature Communications* 2017



# MULTIPLE MYELOMA

A model for scientific and clinical progress from biology to therapeutics



\*MM should not be considered a single entity.

# We will beat myeloma!!



# The Real Future

