



20 ANNI DI EMATOLOGIA
A TREVISO

TREVISO | 18-20 NOVEMBRE 2021
Auditorium Fondazione Cassamarca

La *biopsia liquida* nel Mieloma Multiplo: è un reale salto di qualità?

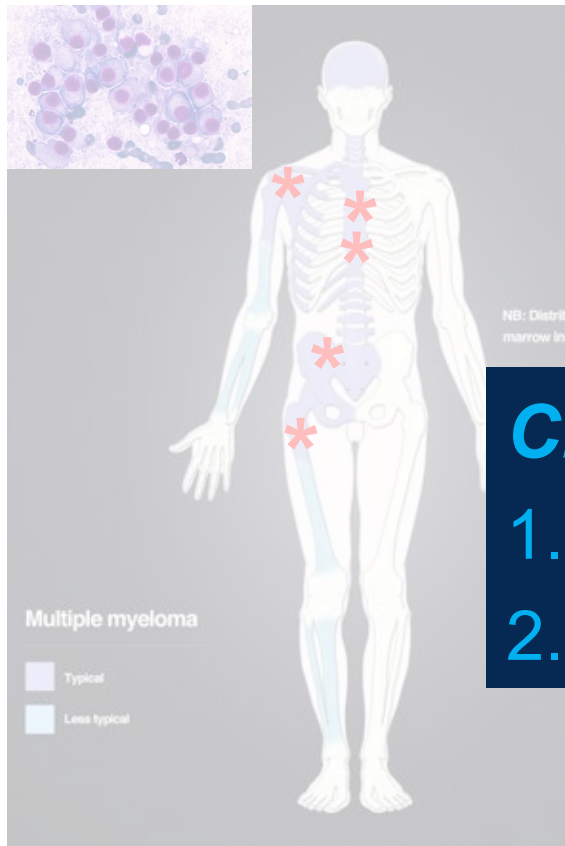
Carolina Terragna

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Disclosures of Carolina Terragna

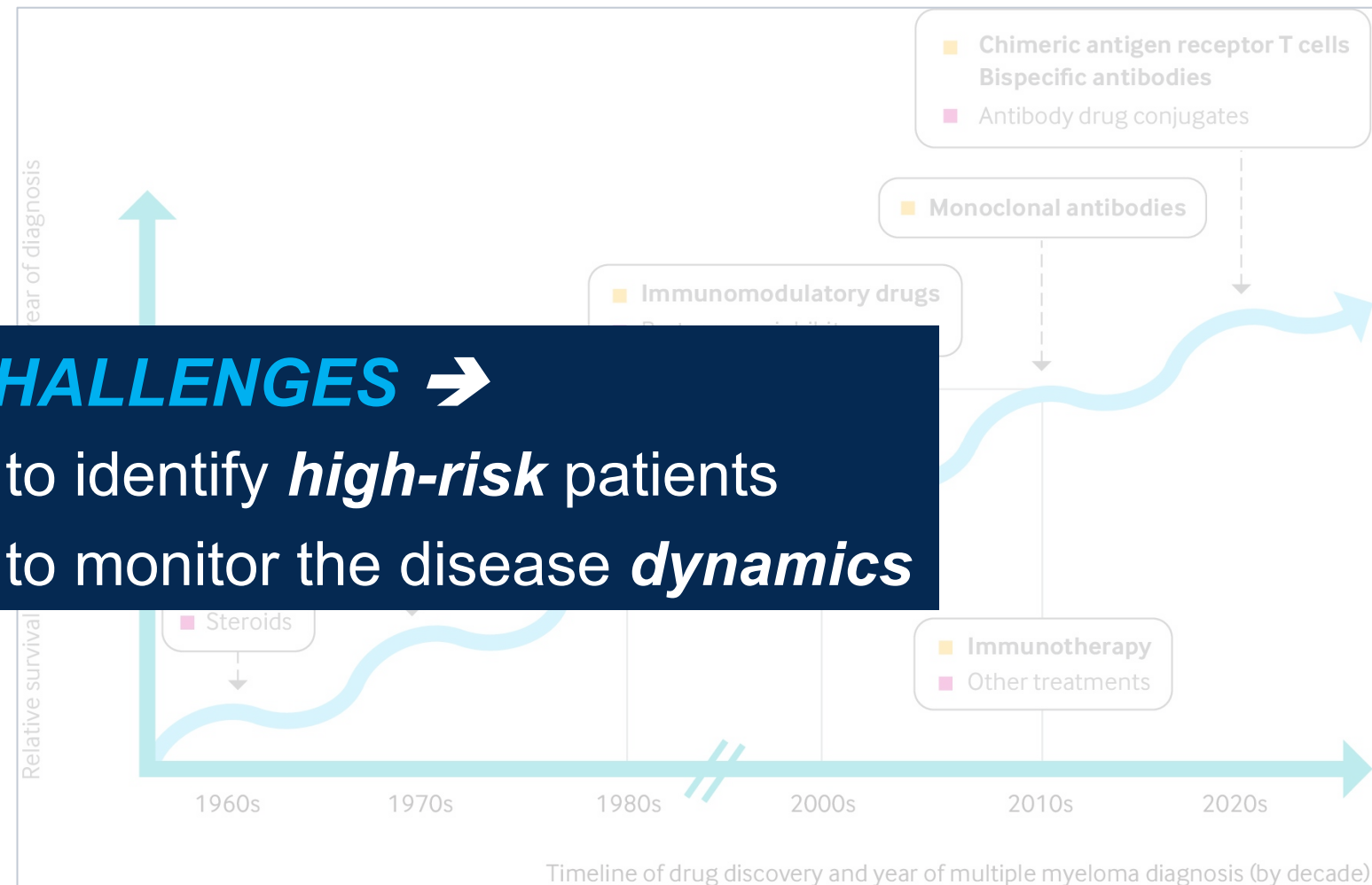
Company name	Research support	Employee	Consultant	Stockholder	Speakers bureau	Advisory board	Other
Janssen			X				
GSK			X				

Multiple Myeloma

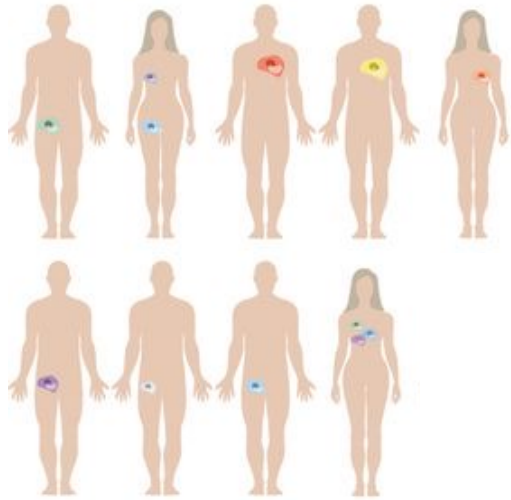


CHALLENGES →

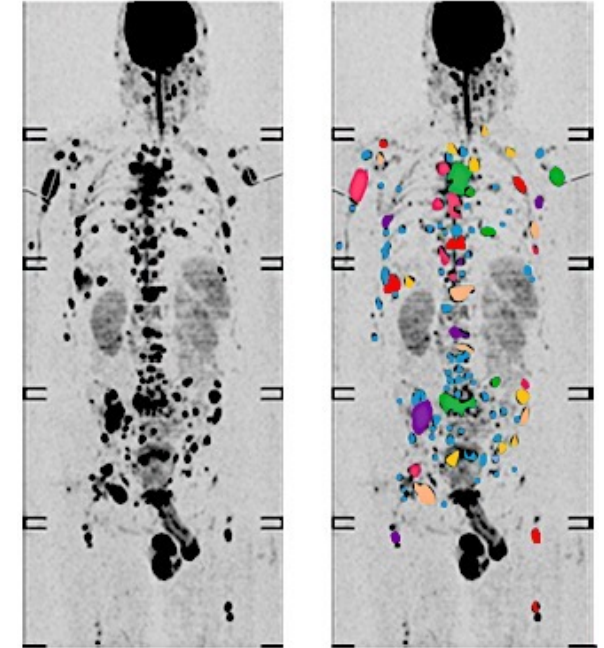
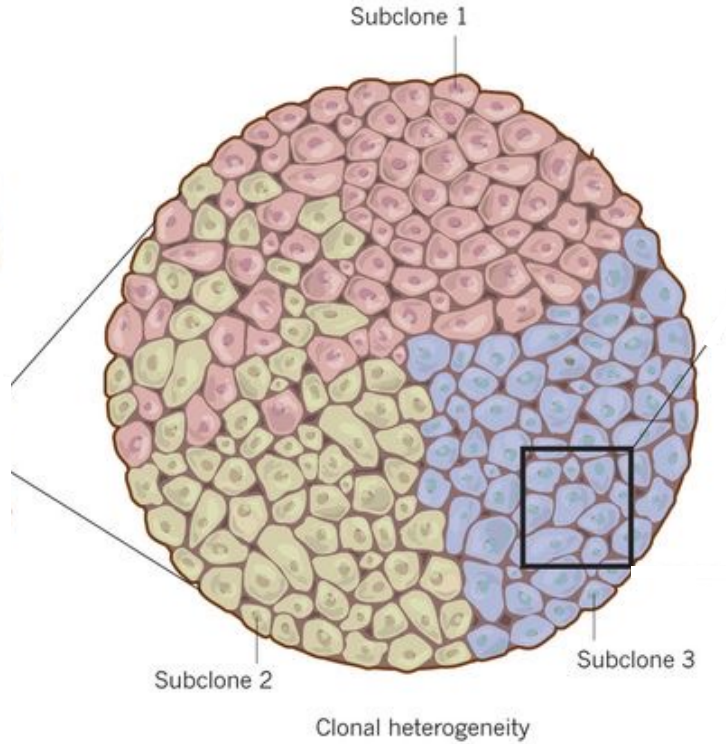
1. to identify *high-risk* patients
2. to monitor the disease *dynamics*



MM heterogeneity => *how many layers?*



inter-tumour



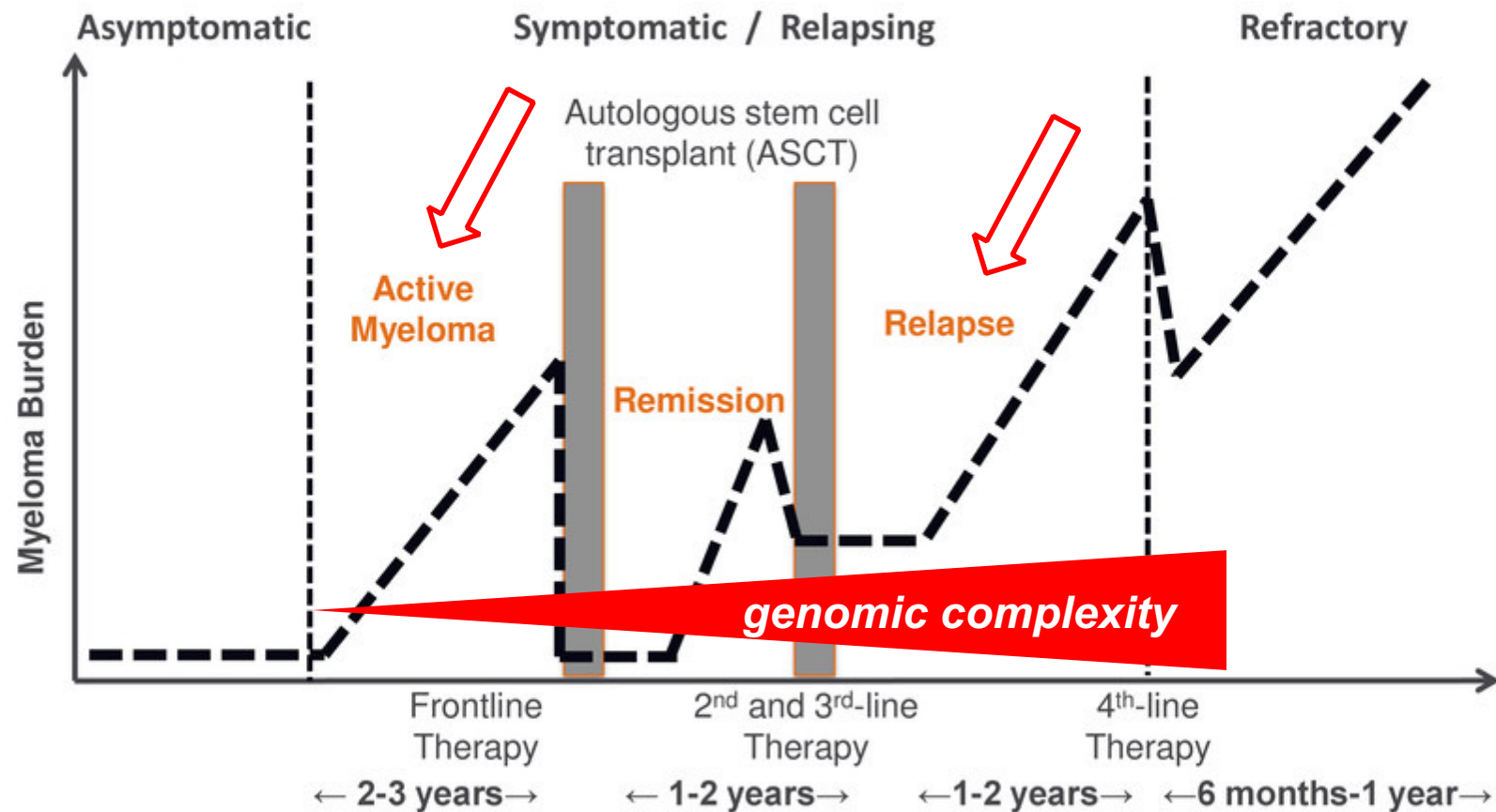
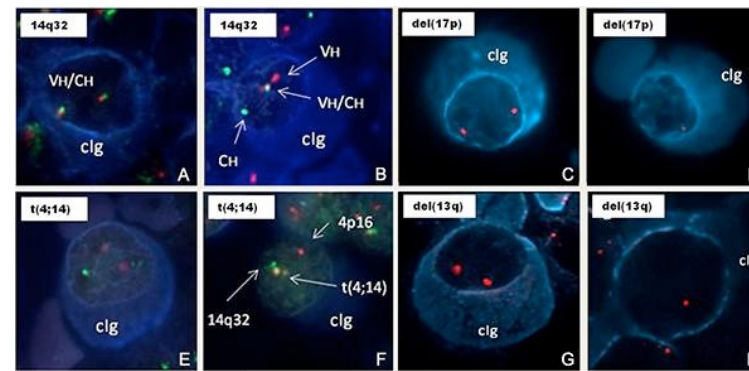
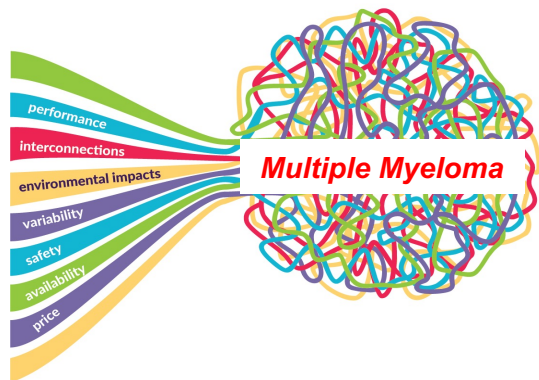
intra-tumour

SPACE

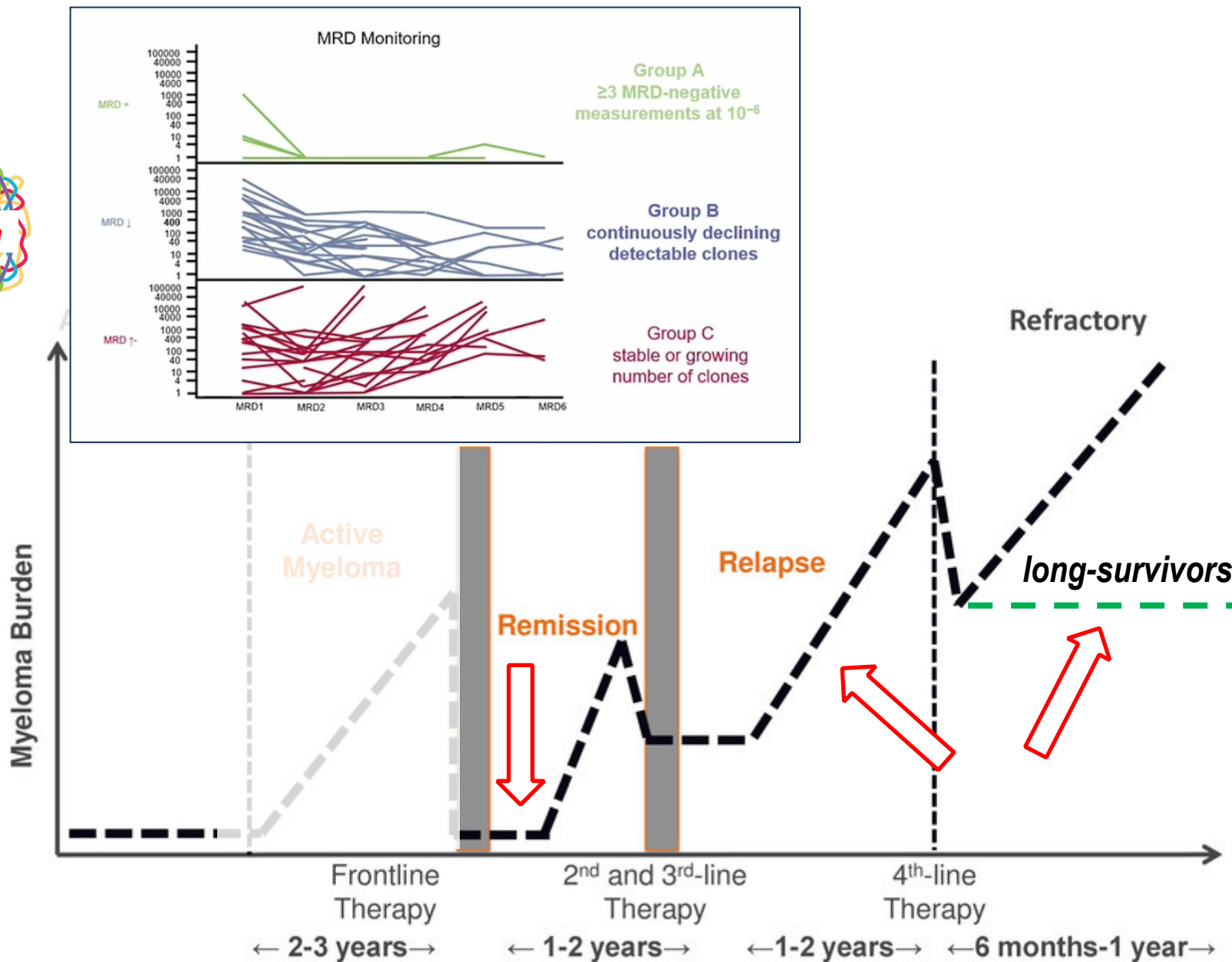
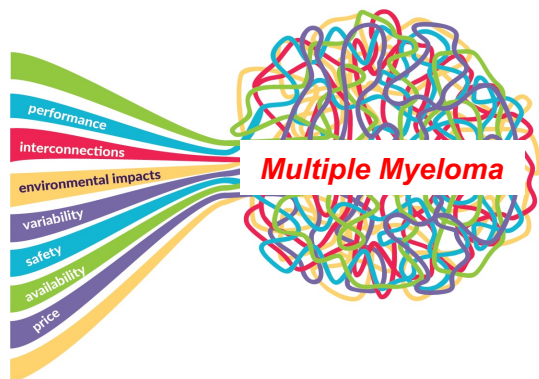
TIME



MM heterogeneity



MM dynamics



sample collection: what? when? how?



BM aspirate at D & R:

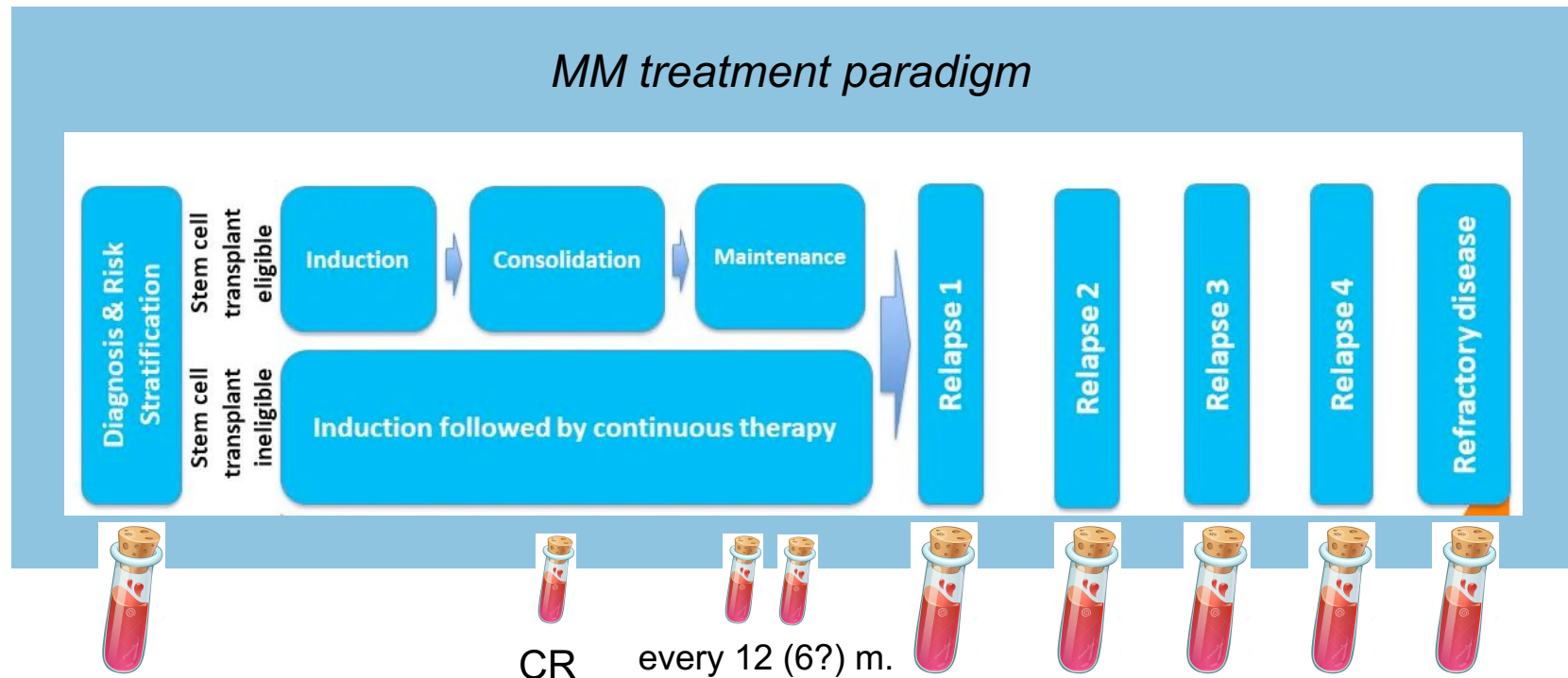
1° => **EDTA**: 5-8 mL

2° => **heparin**: 3-4 mL

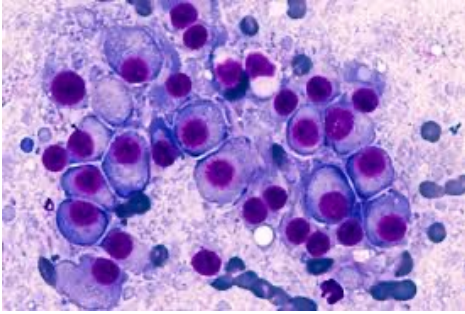
BM aspirate during treatment:

1° => **EDTA**: 5-8 mL

MM treatment paradigm



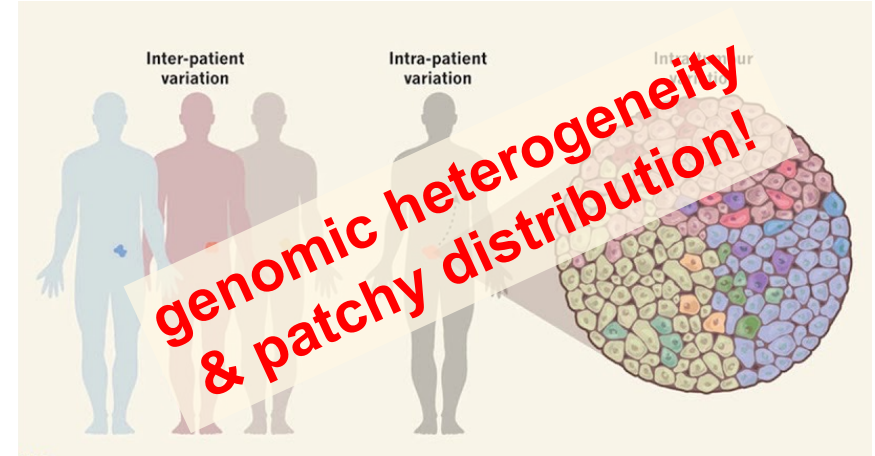
is BM aspirate the *appropriate* approach?



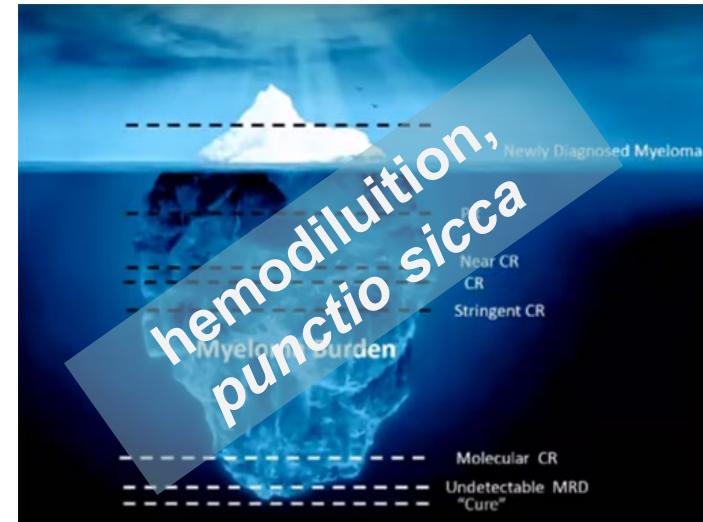
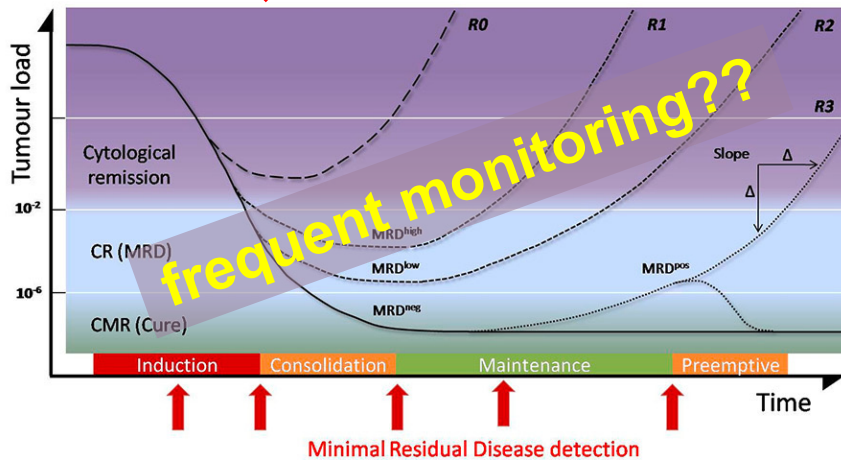
is BM *representative*??

is BM *representative*??

is BM aspirate
frequently feasible?

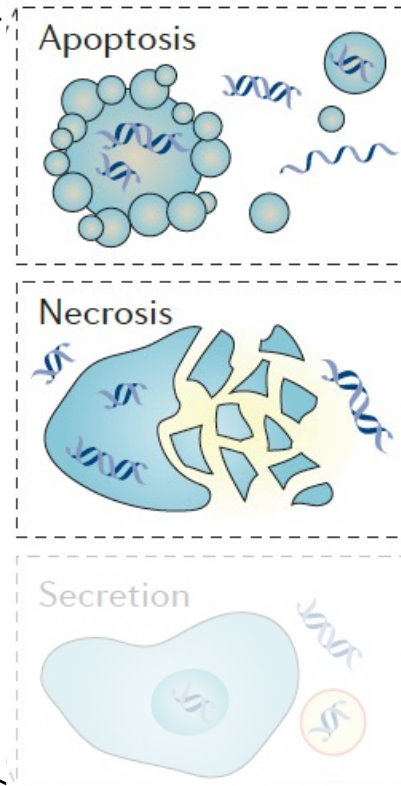
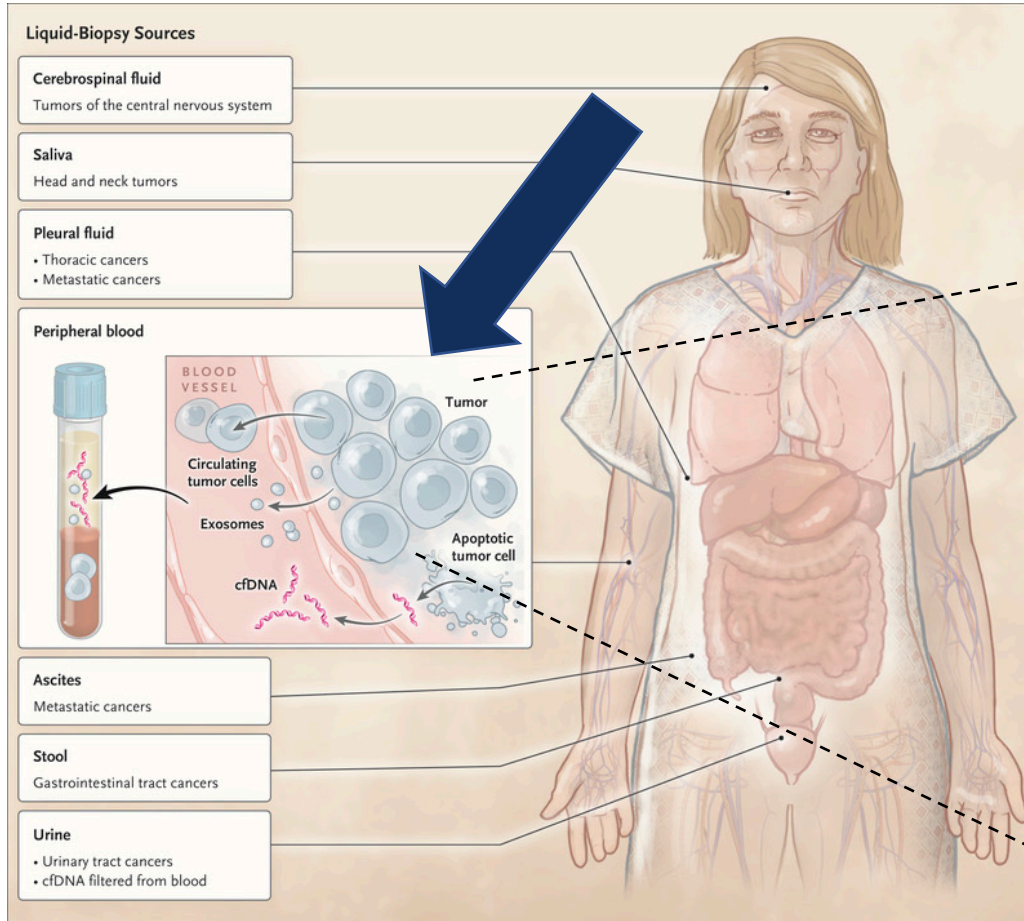


**genomic heterogeneity
& patchy distribution!**



liquid biopsy

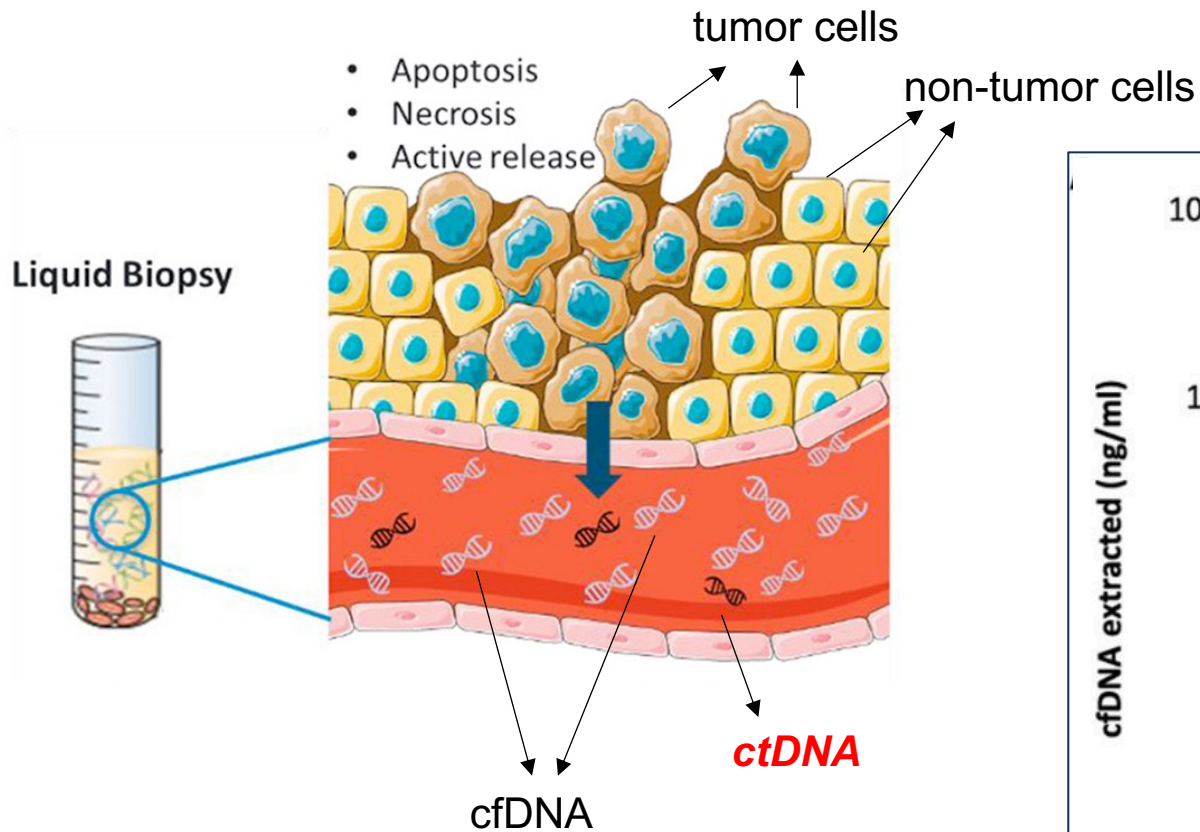
→ **alternative & non-invasive** source of circulating cell-free nucleic acids, proteins and extracellular vesicles, **circulating cells**



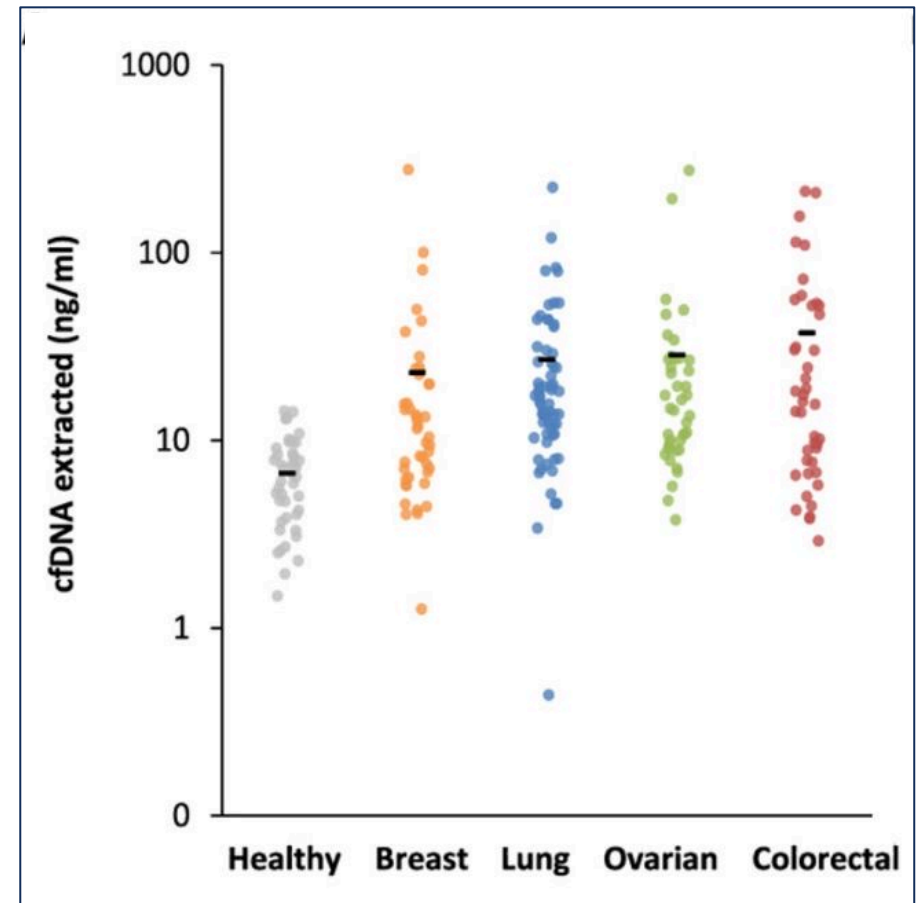
passive release

active release

cfDNA & ctDNA

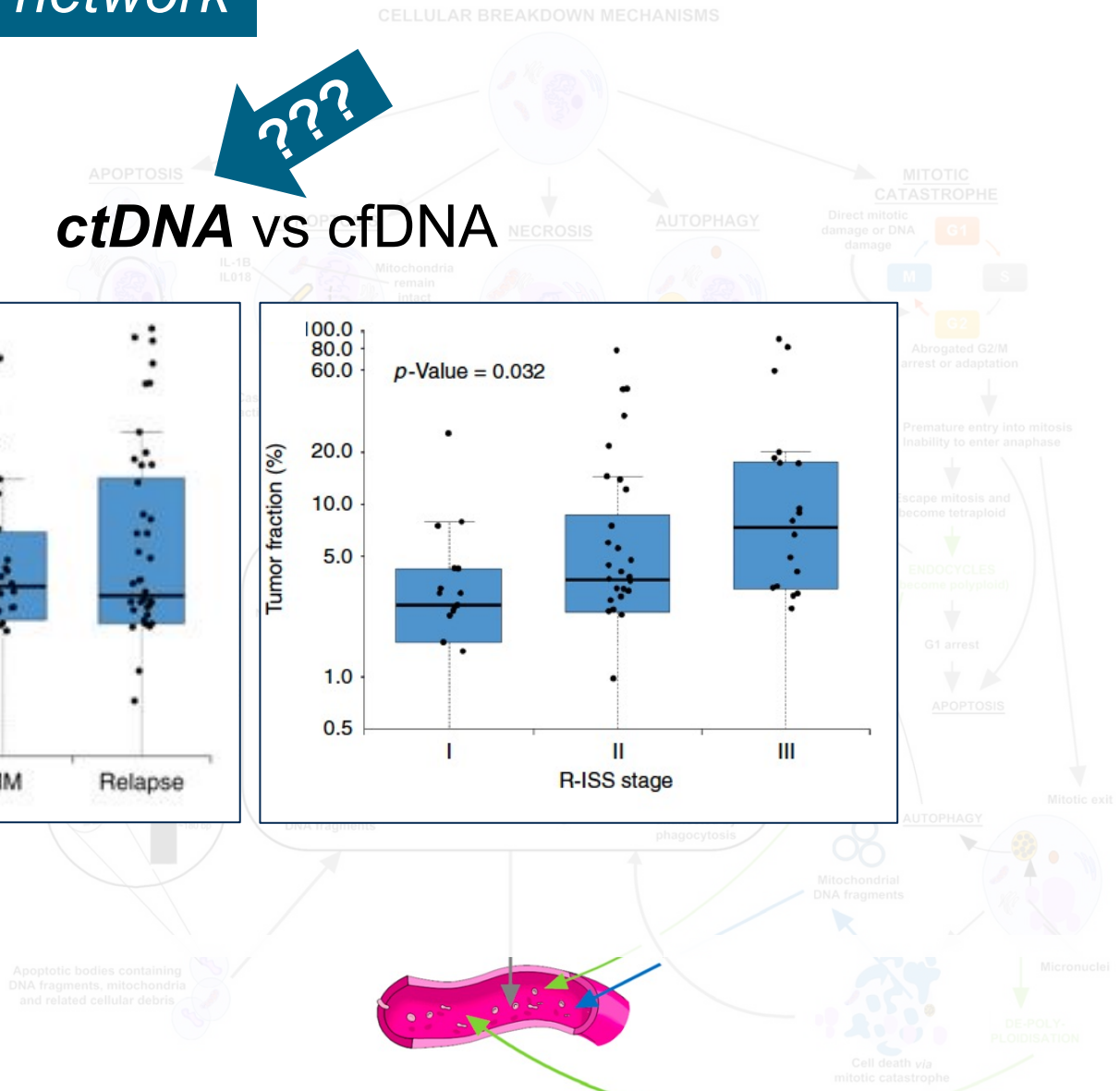
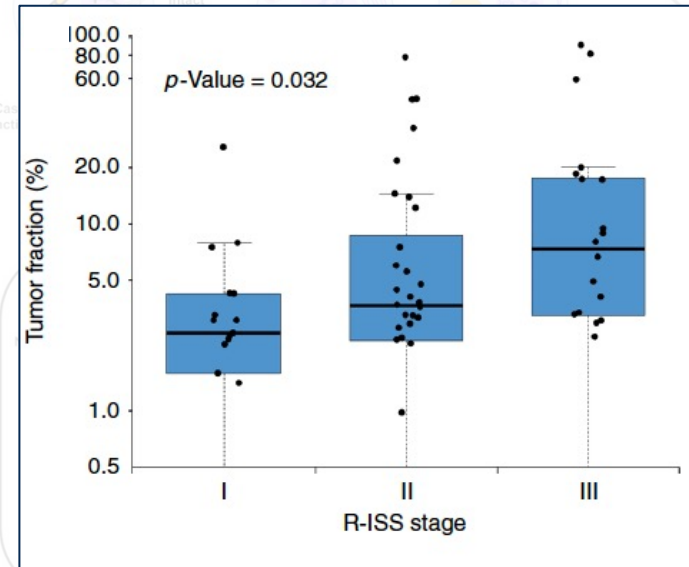
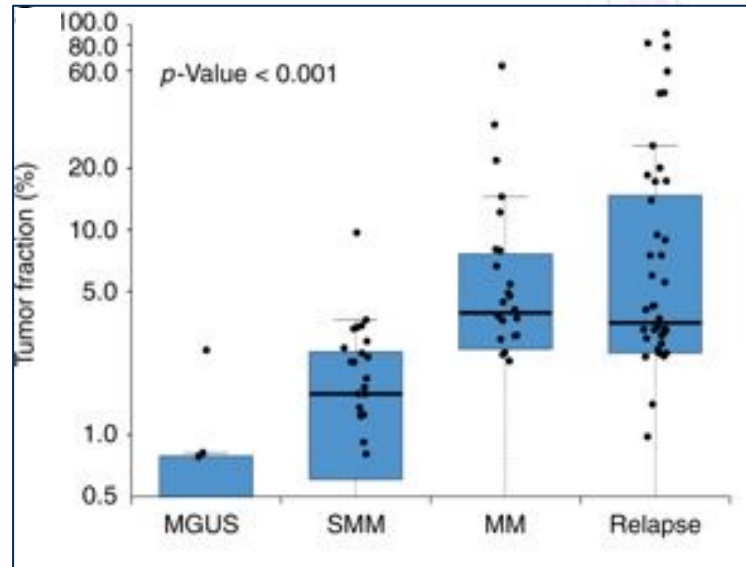


healthy subjects => range: **0** to **100** ng/mL
neoplastic pts => range: **0-5** to **>1000** ng/mL



cfDNA release: a complex network

ctDNA vs cfDNA

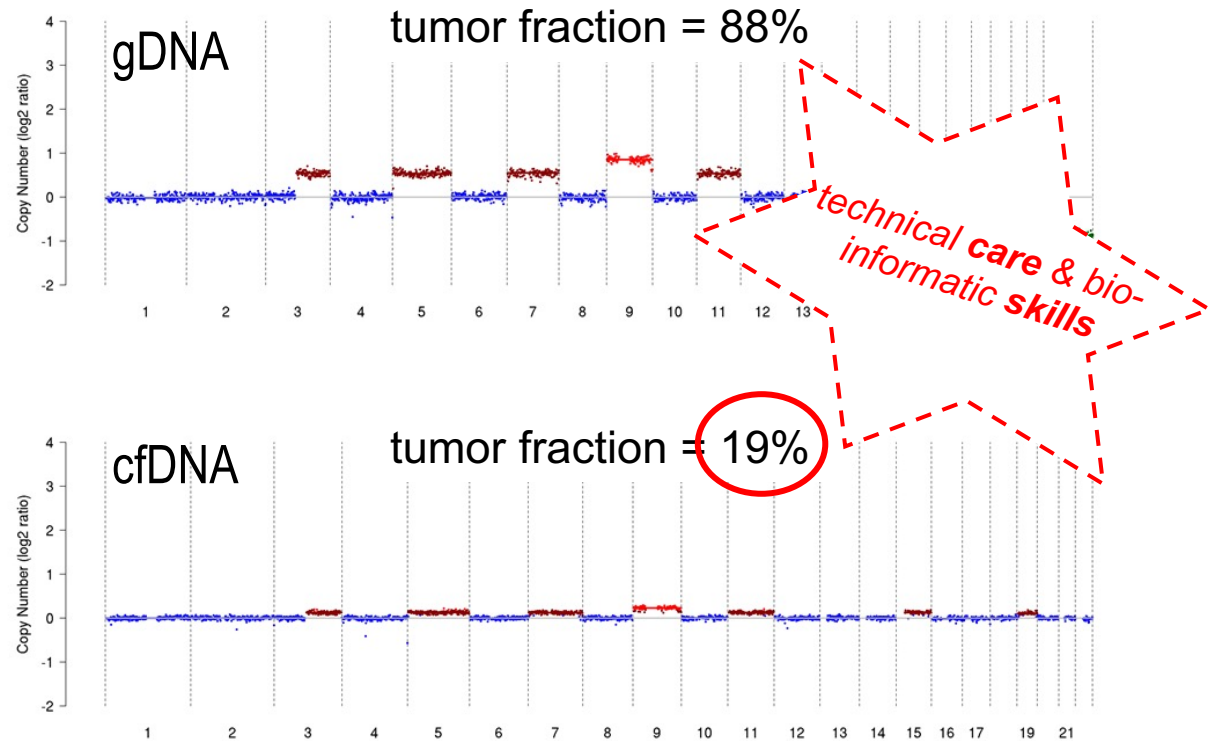
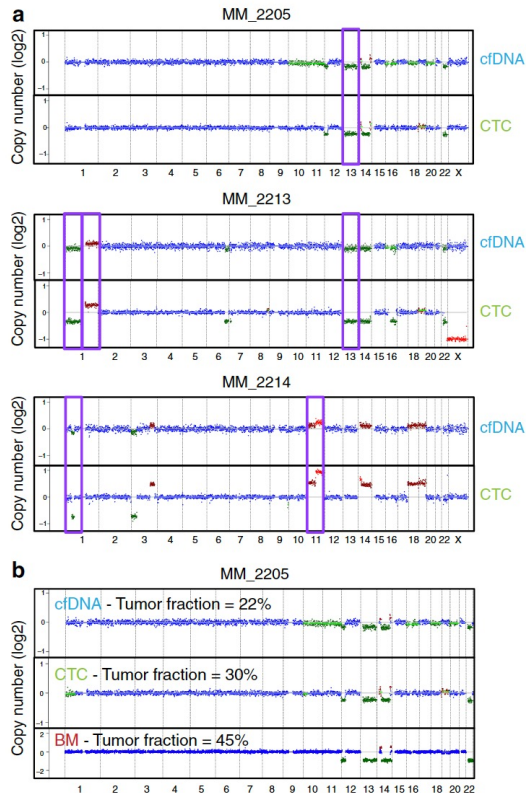


S.Manier et al., Nature Comm. 2018

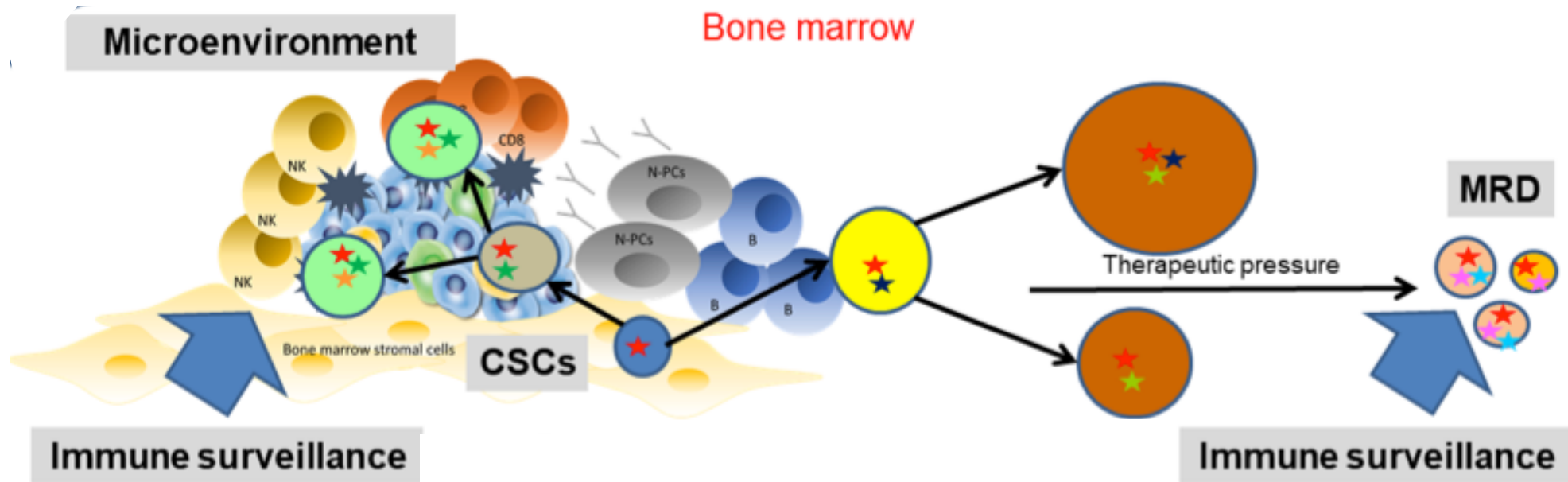
Abel J.B., Biom. Det and Quant (2019)

how can ctDNA be distinguished?

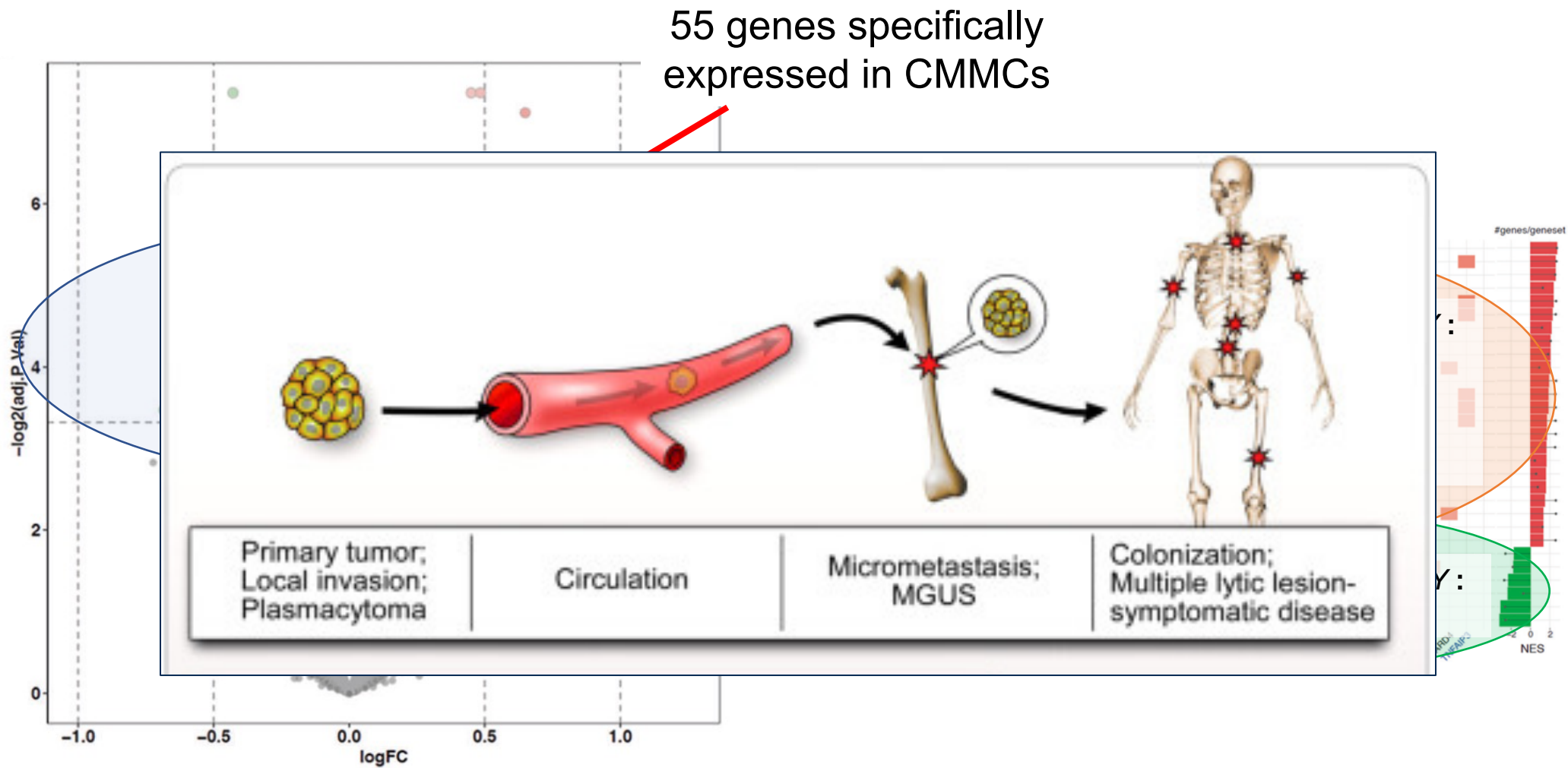
→ by taking advantages of **cancer-specific** mutations, structural rearrangements, CNAs, epigenetic modifications or gene fusions to separate tumour-derived fragments from normal cfDNA



Circulating Multiple Myeloma Cells (CMMCs)



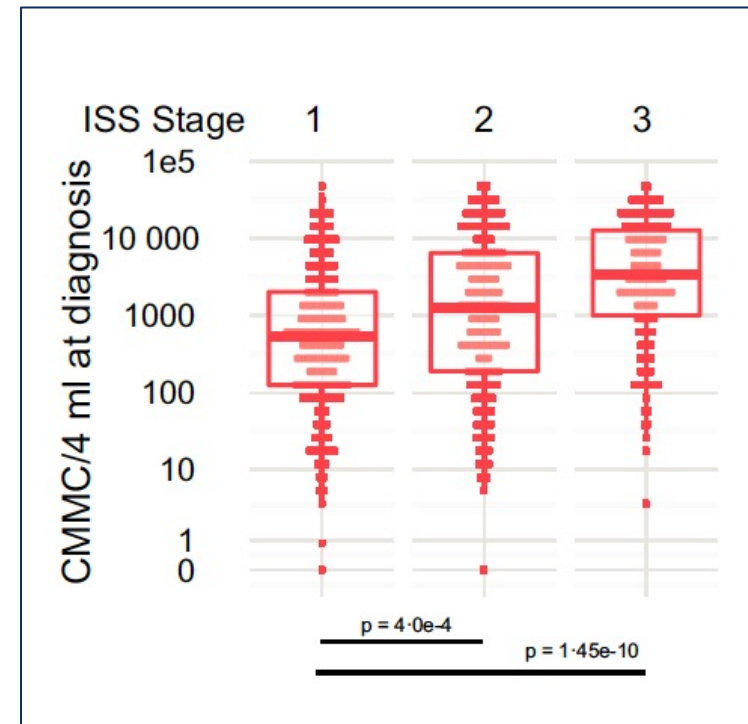
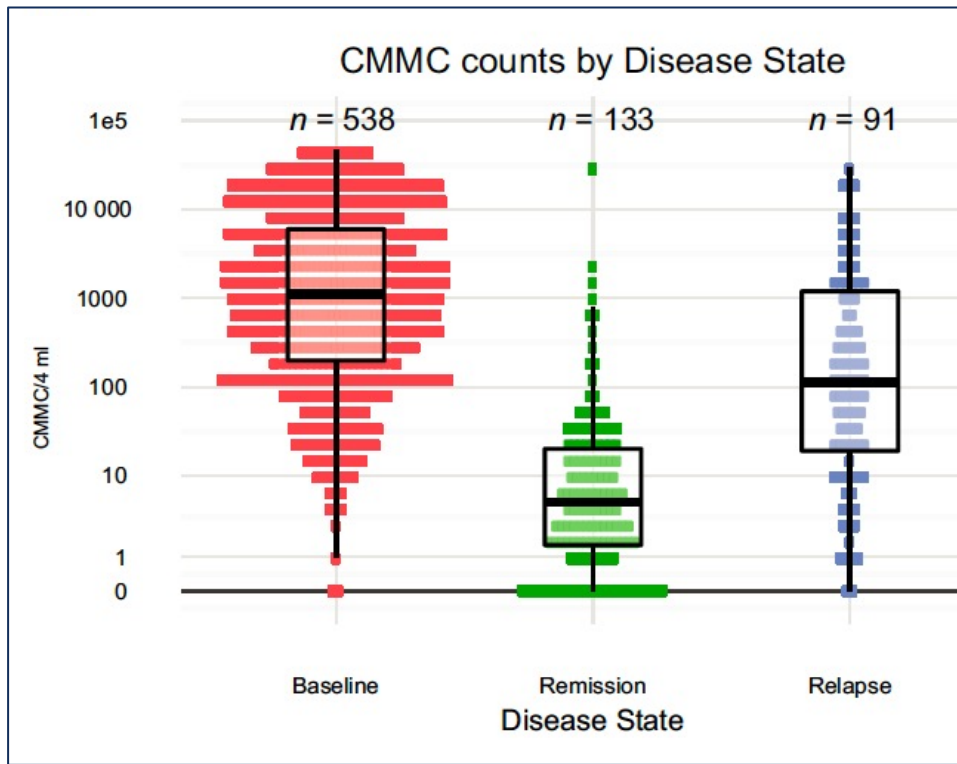
“myeloma as a model of the process of *metastasis*” (?)



J.J. Garcés et al., *Leukemia* 2020

I.Ghobrial, *Blood* 2012

CMMCs & disease stage



- significant correlation between disease CMMCs count
 “*dissemination*” (prognostic significance?)
 - in different disease **stages**

B.Foulk et al, Br.J.Haem. 2017

MM disease *dynamics* => ***rationale*** for the use of liquid biopsy

→ a ***good correlation*** exists between circulating elements (ctDNA and/or CMMCs) and tumour burden

liquid biopsy in MM : (1) to *profile* the genomic landscape

Cohort	BM analysis			Sample ID	KRAS			NRAS			BRAF			EGFR			PIK3CA		
	Clinical Lab	CoMpass	5-gene panel		Protein change	ctDNA allele fraction	Tumour allele fraction	Protein change	ctDNA allele fraction	Tumour allele fraction	Protein change	ctDNA allele fraction	Tumour allele fraction	Protein change	ctDNA allele fraction	Tumour allele fraction	Protein change	ctDNA allele fraction	Tumour allele fraction
Training	◆	◆	◆	MYL-018	p.A146T	2.0%	22%												
	◆	◆	◆	MYL-026	p.Q61H	2.0%	29%												
	◆	◆	◆	MYL-030	p.G13D	11%	42%												
	◆	◆	◆	MYL-031	p.K117N	28%	49%												
	◆	◆	◆	MYL-020	p.Q61H	0.53%	2.8%												
					p.G12V	1.0%	6.4%												
					p.G12D	negative	1.3%												
	◆			MYL-023	p.Q61H	1.5%	5.0%				p.V600E	1.0%	2.9%	p.A859S [†]	0.41%	0.8%			
	◆				p.G13C	0.86%	1.4%				p.D594G	8.5%	14%						
	◆			MYL-012	p.A146V	7.2%	8.0%							p.C620W	0.48%	13%			
	◆			MYL-007	p.G13C	0.50%	14%												
	◆	◆	◆	MYL-002				p.G13D	0.25%	0.93%									
	◆	◆	◆	MYL-003				p.Q61K	1.3%	45%									
	◆	◆	◆	MYL-003(2)				p.Q61K	20%	61%									
	◆	◆	◆	MYL-019				p.G13R	15%	61%									
	◆	◆	◆	MYL-022				p.Q61R	1.2%	27%									
	◆	◆	◆	MYL-039				p.Q61K	1.9%	34%									
	◆	◆	◆	MYL-028				p.Q61R	24%	47%									
								p.Q61K	0.72%	1.4%							p.I841V	23%	26%
	◆	◆	◆	MYL-001				p.Q61K	32%	39%							p.Y207*	0.28%	negative
	◆	◆	◆	MYL-027										p.E551K	41%	16%			
	◆	◆	◆	MYL-004															
	◆	◆	◆	MYL-005															
	◆	◆	◆	MYL-016															
	◆	◆	◆	MYL-033															
	◆	◆	◆	MYL-033(2)															
	◆	◆	◆	MYL-034															
	◆	◆	◆	MYL-036															
	◆	◆	◆	MYL-037															
Validation	◆	◆	◆	MYL-043	p.G13D	20%	8.5%												
	◆	◆	◆	MYL-043(3)	p.G13D	1.4%	1.1%												
	◆	◆	◆	MYL-046	p.G13R	6.4%	42%												
	◆	◆	◆	MYL-051	p.Q61H	3.4%	41%												
	◆	◆	◆	MYL-054	p.G12V	negative	1.3%												
	◆	◆	◆	MYL-068	p.G13D	46%	76%				p.D594N	15%	32%	p.E513E	2.9%	7.6%			
	◆	◆	◆	MYL-058	p.G12V	20%	48%				p.D594G	8.2%	15%						
	◆	◆	◆	MYL-012(2)*	p.A146V	7.6%	8.0%				p.G469V	0.39%	3.5%						
	◆	◆	◆	MYL-070	p.Q61H	3.4%	41%							p.C624Y	2.9%	5.7%			
	◆	◆	◆	MYL-044	p.G13D	17%	41%							p.V674F	0.64%	negative			
	◆	◆	◆	MYL-063	p.Q22K	4.6%	38%												
	◆	◆	◆	MYL-055				p.Q61K	4.4%	40%									
	◆	◆	◆	MYL-022(2)*				p.Q61R	3.0%	42%									
	◆	◆	◆	MYL-084				p.G13R	0.73%	46%									
	◆	◆	◆	MYL-001(2)*				p.Q61K	26%	47%							p.I841V	22%	not tested
																	p.Y207*	1.4%	not tested
	◆	◆	◆	MYL-056							p.D594N	2.6%	45%						
	◆	◆	◆	MYL-027(2)*							p.A322T	45%	50%						
	◆	◆	◆	MYL-049										p.E551K	46%	52%			
	◆	◆	◆	MYL-049(2)													p.H59P	40%	41%
																	p.E545K	1.0%	negative
	◆	◆	◆	MYL-017													p.H59P	38%	36%
	◆	◆	◆	MYL-050													p.E545K	2.1%	negative
	◆	◆	◆	MYL-053															
	◆	◆	◆	MYL-077										p.A1201T	0.31%	not tested			

mutations observed
just in ctDNA!!

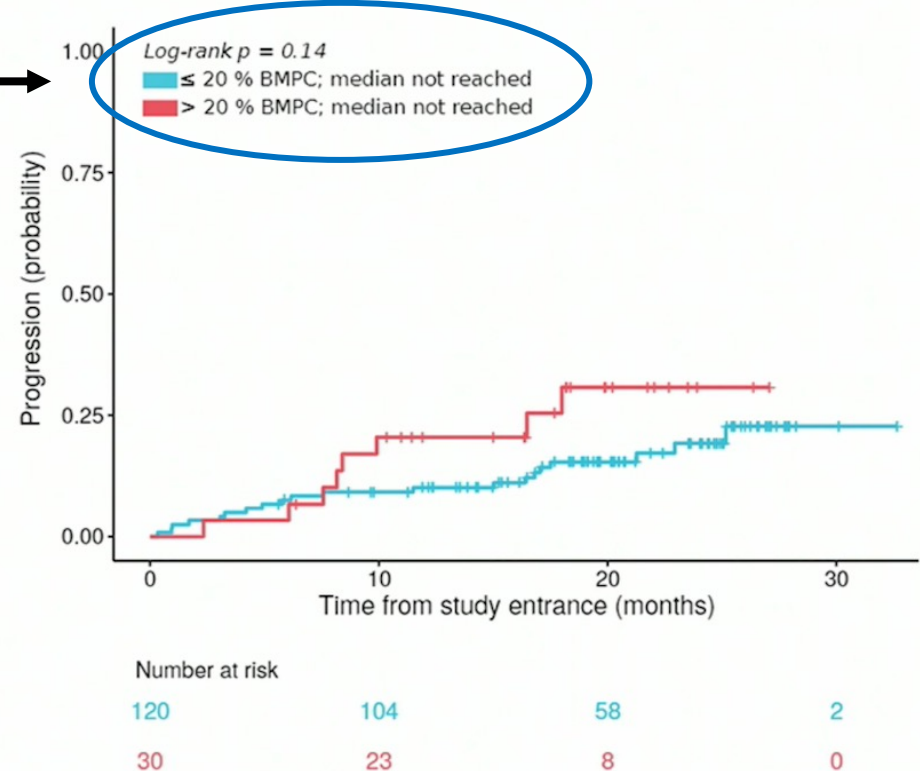
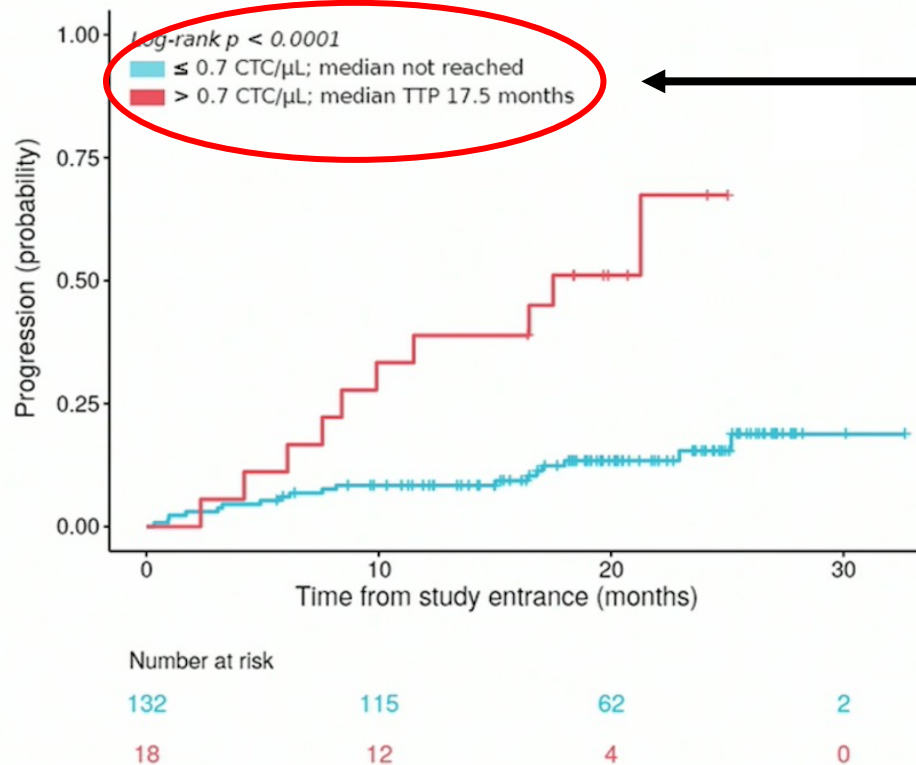
Kis O. et al. Nat. Comm.(2017)

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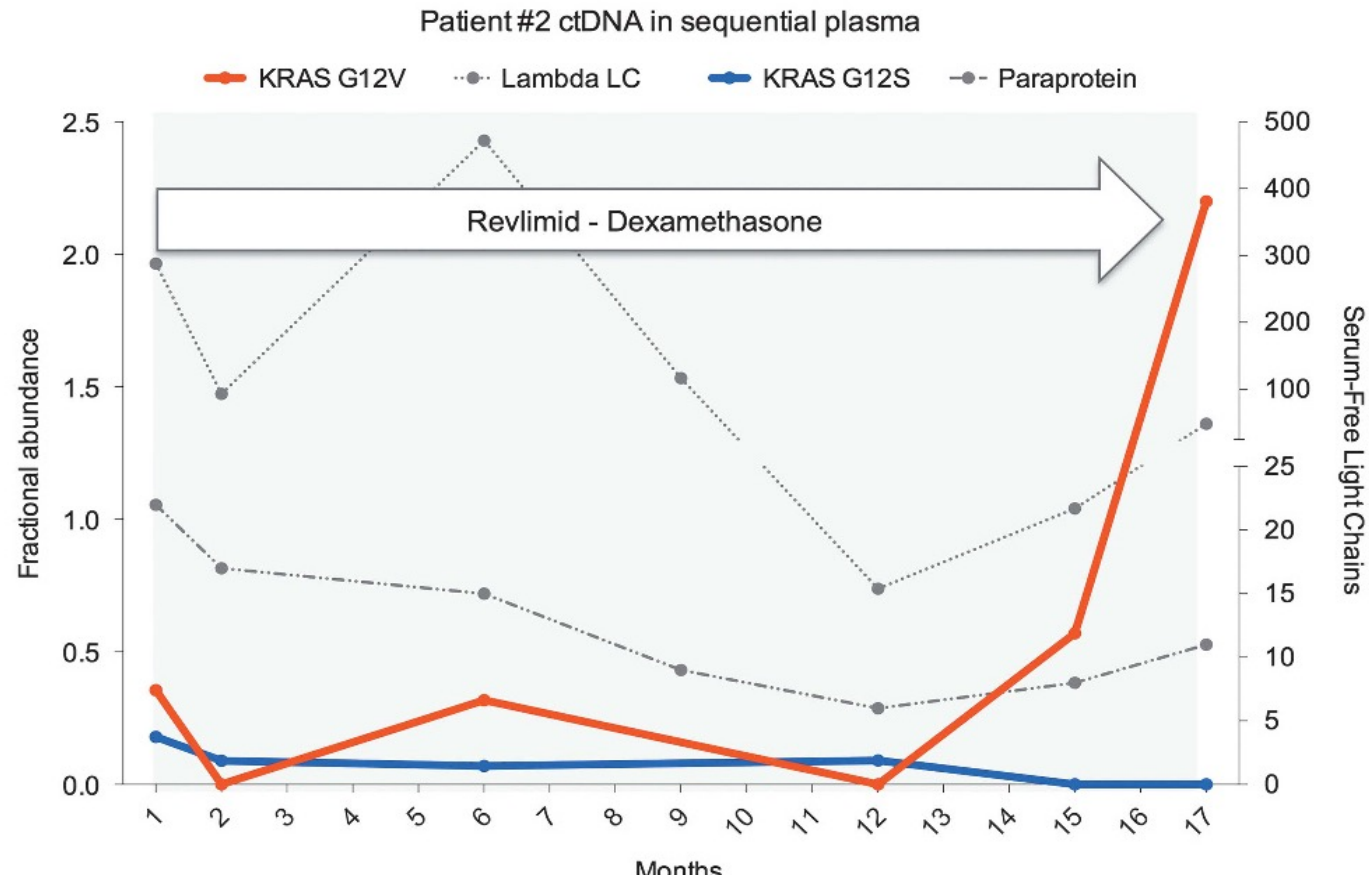
liquid biopsy in MM : (2) to *monitor* the disease dynamics

SMM patients with > 0.7 CTCs/ μL showed inferior TTP

CTC assessment yielded greater risk-stratification when compared to BM PCs



liquid biopsy in MM : (2) to *monitor* the disease dynamics



Mithraprabhu S. et al. Leukemia (2017)

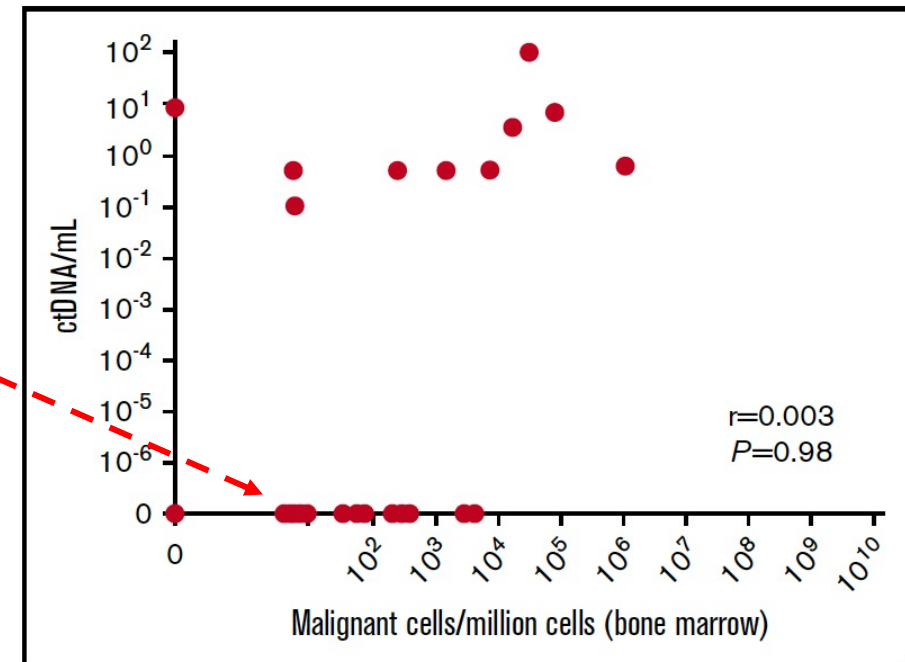
ctDNA & IgH– MRD monitoring

42 patients with BM & ctDNA: 10 D samples + 37 FUP samples

=> **IgH/ κ / λ** analysis for MRD-NGS (Adaptive): *sensitivity 10^{-6} (?)*

Table 1. Comparison of MRD status obtained in plasma and in bone marrow

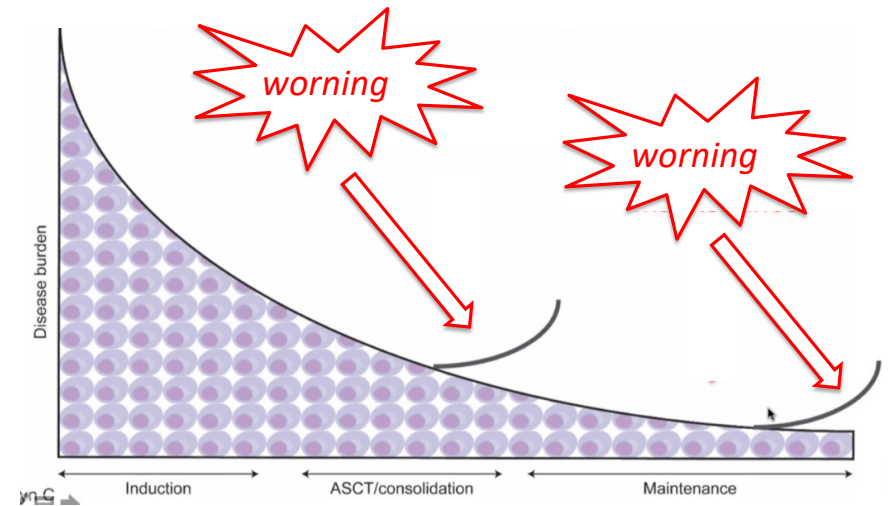
	Key Points	
	<ul style="list-style-type: none">There is no correlation between ctDNA and bone marrow for MRD by NGS using only immunoglobulin gene rearrangements in myeloma patients.	
Bone marrow	plasma negative	Total
Bone marrow	18	26
Bone marrow	10	11
Total	plasma = 36%)	37
NPV _{plasma} , negative predictive value; PPV _{plasma} , positive predictive value		



Mazzotti C. Blood Adv. (2018)

take-home message

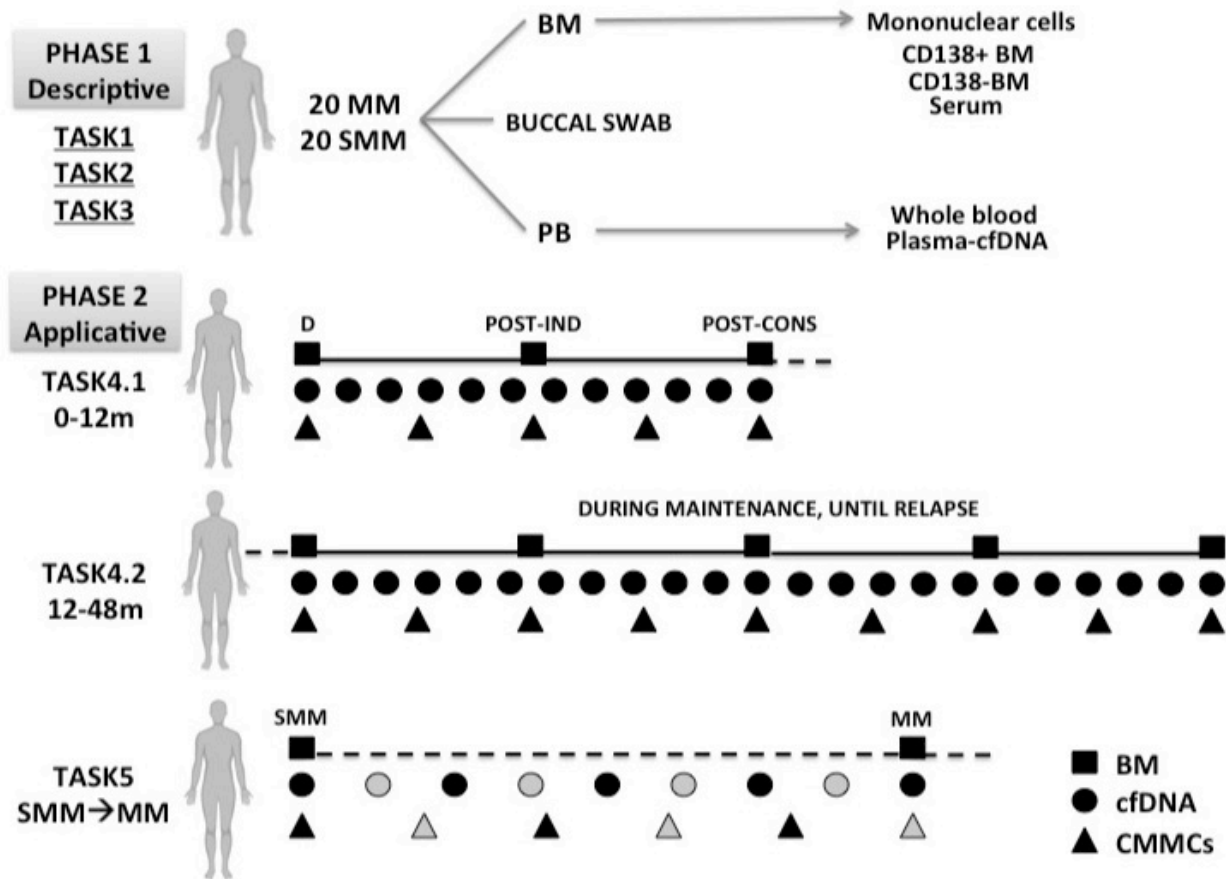
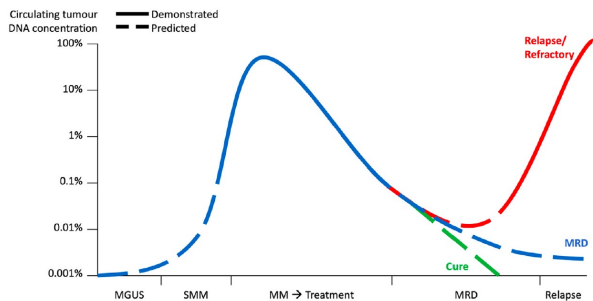
1. liquid biopsy is an alternative and reliable method to measure the disease dynamics in MM, as being **feasible** and **meaningful**
2. liquid biopsy either **collects information** from the different disease locations or inform about the disease **spread** => overall, is very **informative**
3. liquid biopsy is **low invasive** and can be repeatedly performed, thus allowing a strict disease monitoring, aimed at **preventing** disease recurrence



“StreaMMing” project

AIRC IG2019

«StreaMMing: the dynamics of Multiple Myeloma minimal residual disease in the peripheral blood stream»



thanks!!



Multiple Myeloma Research Unit

prof. Michele Cavo



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