

Evoluzione Genomica delle Discrasie Plasmacellulari

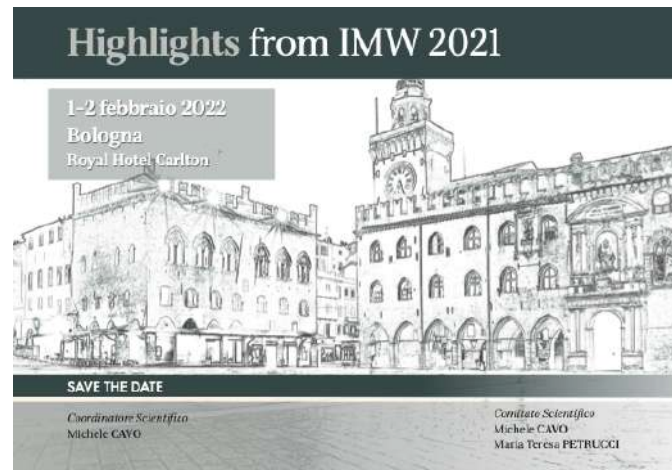
Niccolò Bolli

Università di Milano

Fondazione IRCCS Ca' Granda Ospedale Maggiore Policlinico

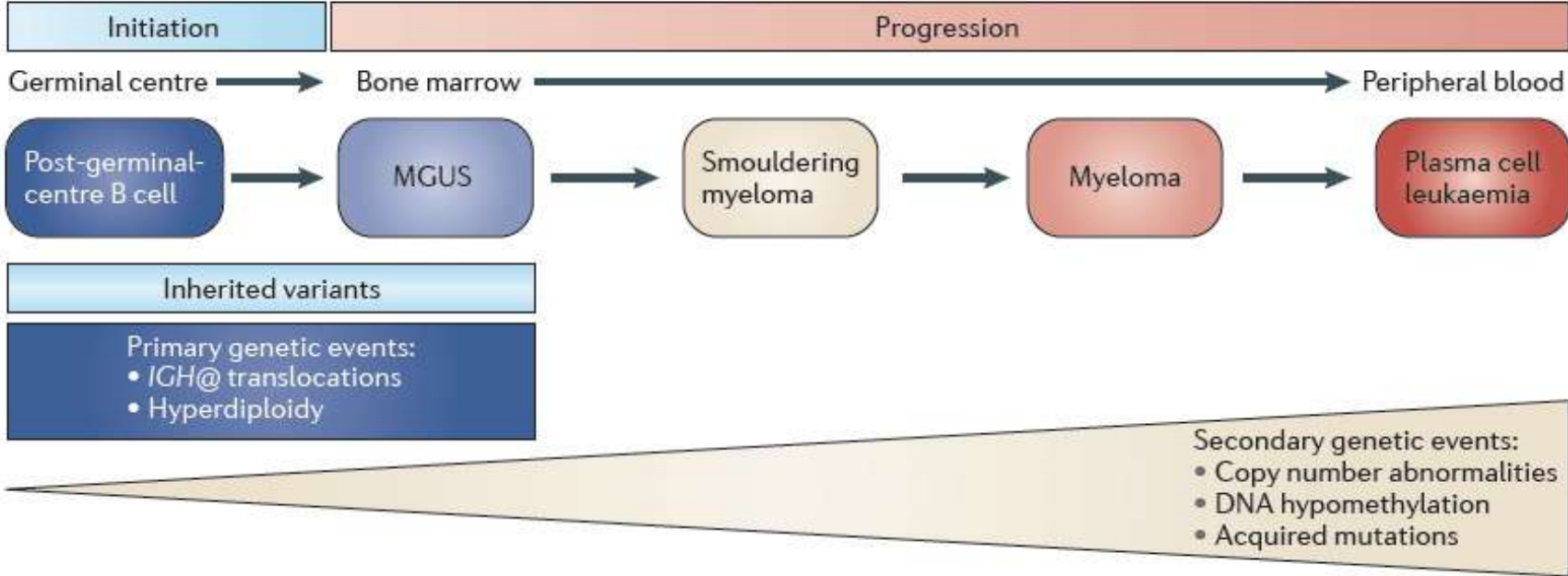


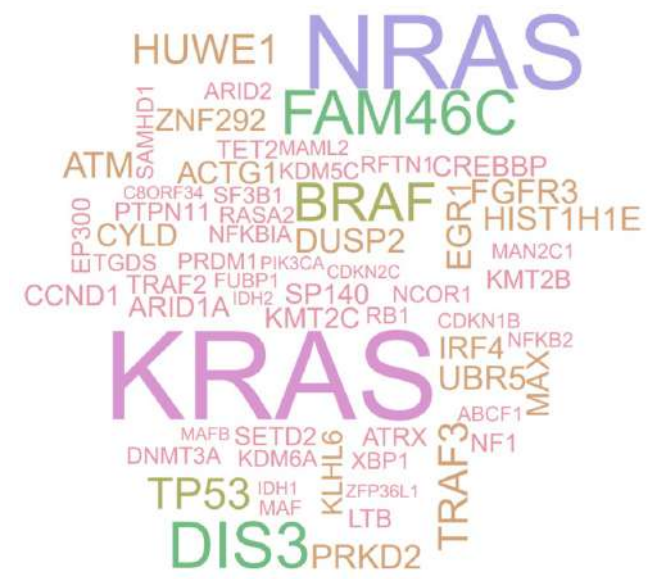
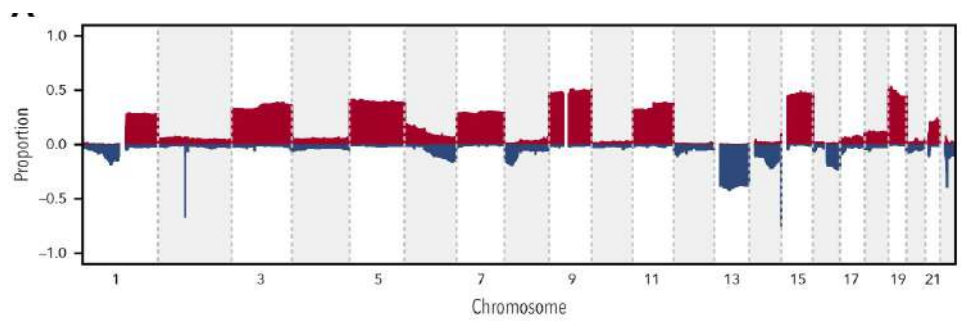
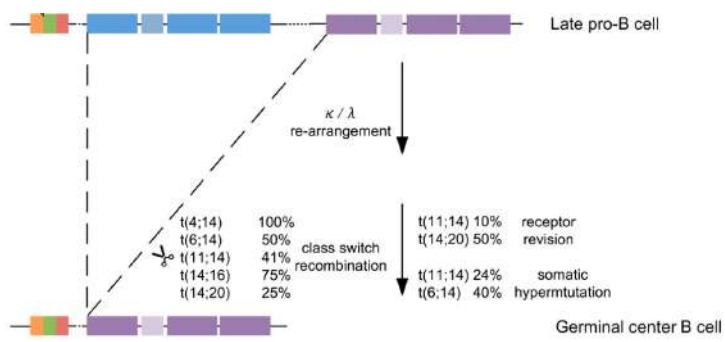
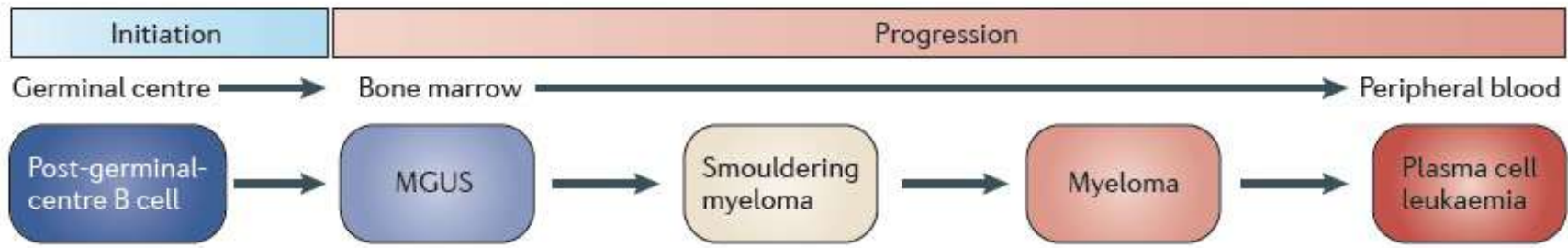
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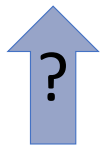
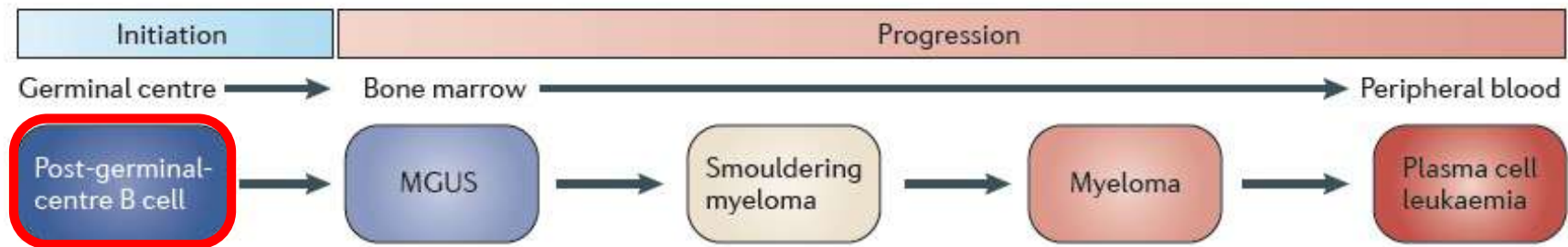
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Outline of clonal PC evolution





Clonal PCs arise decades before diagnosis

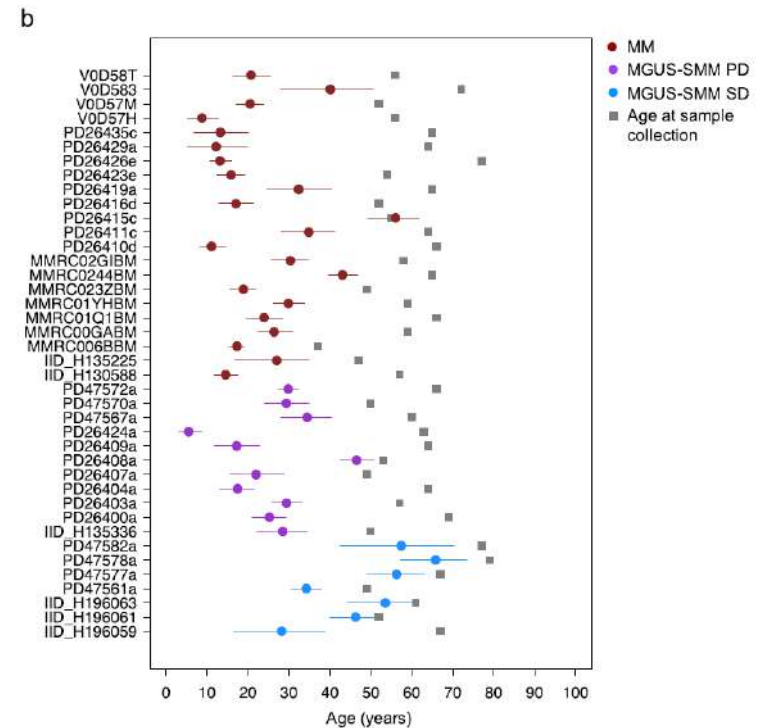


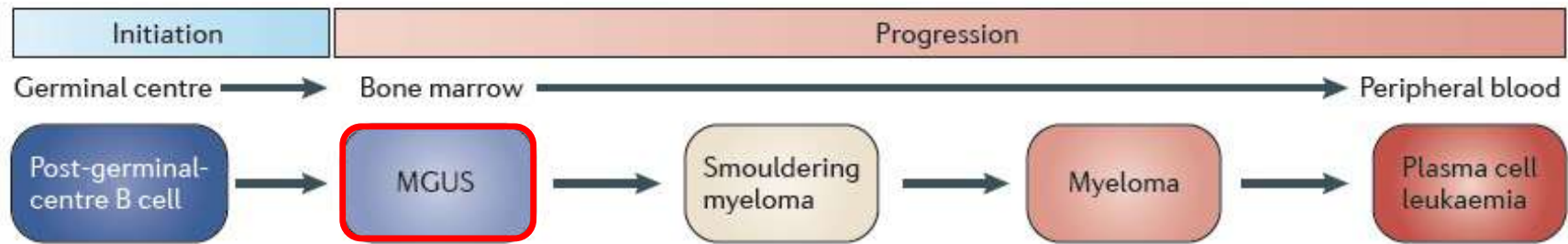
When does MGUS start?

Examine mutation rates

Clock-like mutations correlate with age
Myeloma initiation at 20-30 years of age

Rustad et al. *Nat Commun* 2020
Oben et al. *Nat Commun* 2021





IGH translocations are present

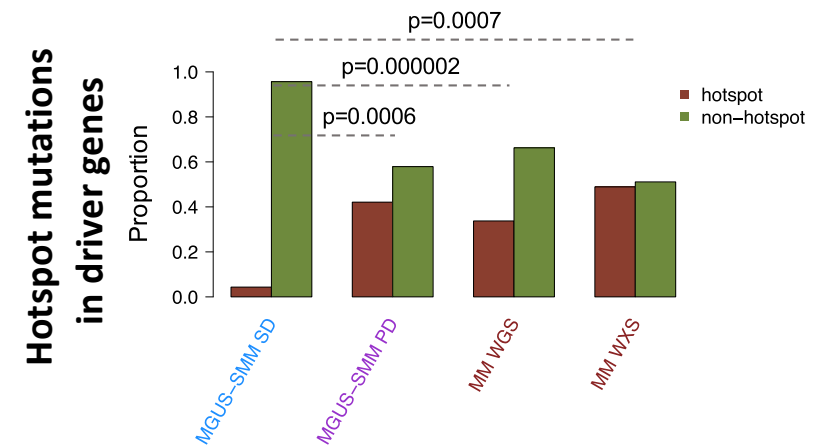
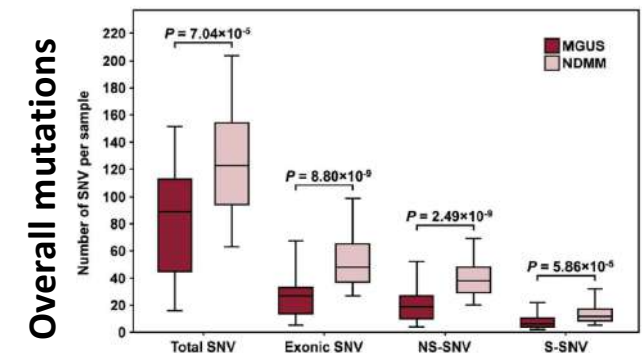
100% of patients have mutations by WGS

CNAs: amplifications >> deletions

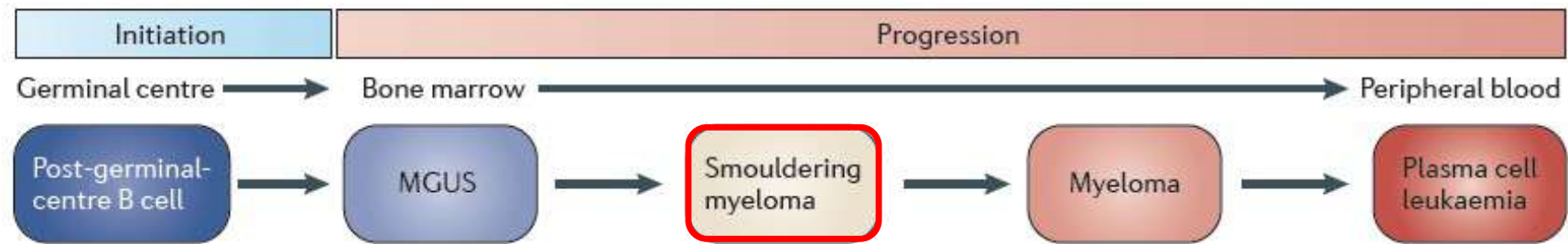
Distinct profile of progressive and non-progressive cases

No biallelic deletions in TSGs.
CDKN2C, *TP53*, *CYLD*, *BIRC2/3*

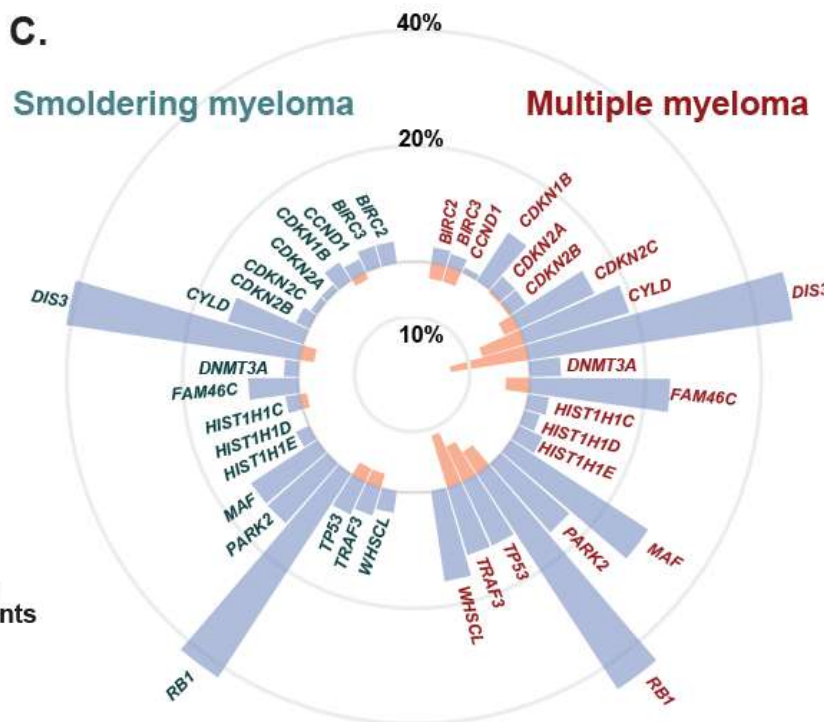
No *TP53* mutations or *MYC* abnormalities



Distinct mutational profile of SMM and MM

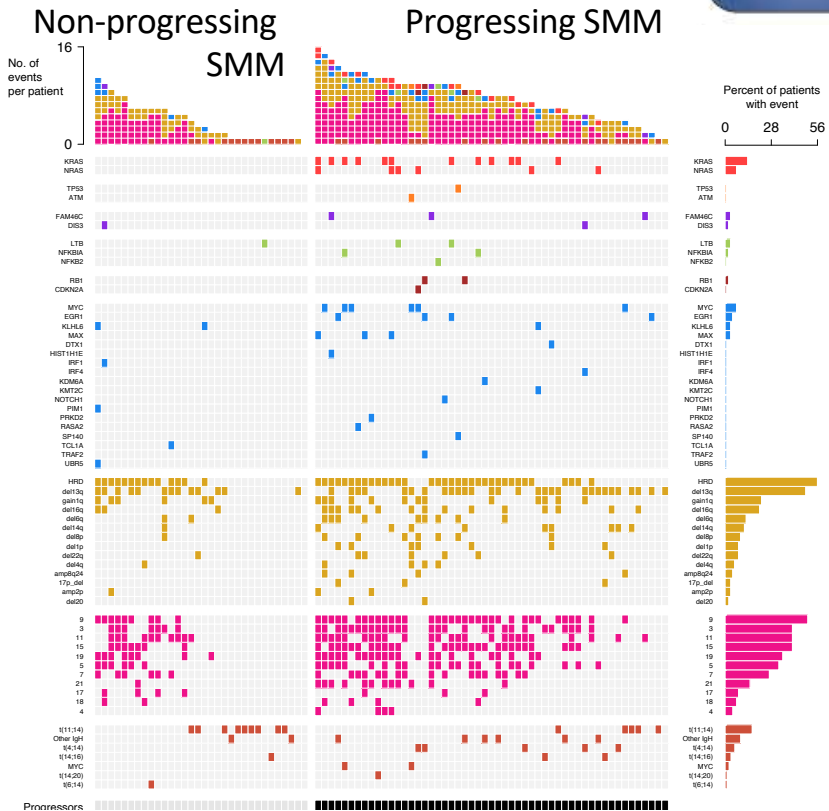
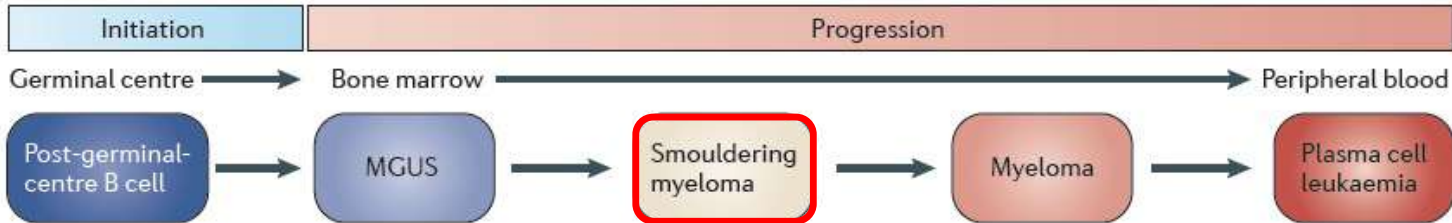


C.



- Total of 103 (64/223 pts) biallelic events identified in MM, compared to 8 (8/82 pts) in SMM, $\chi^2=10.9$, $p=0.001$
- 1.2% SMM patients with Biallelic *TP53*, compared to 8.1% in MM
- 2% SMM with Biallelic *DIS3*, compared to 5% in MM
- Biallelic inactivation may be a hallmark mechanism in the transition to MM

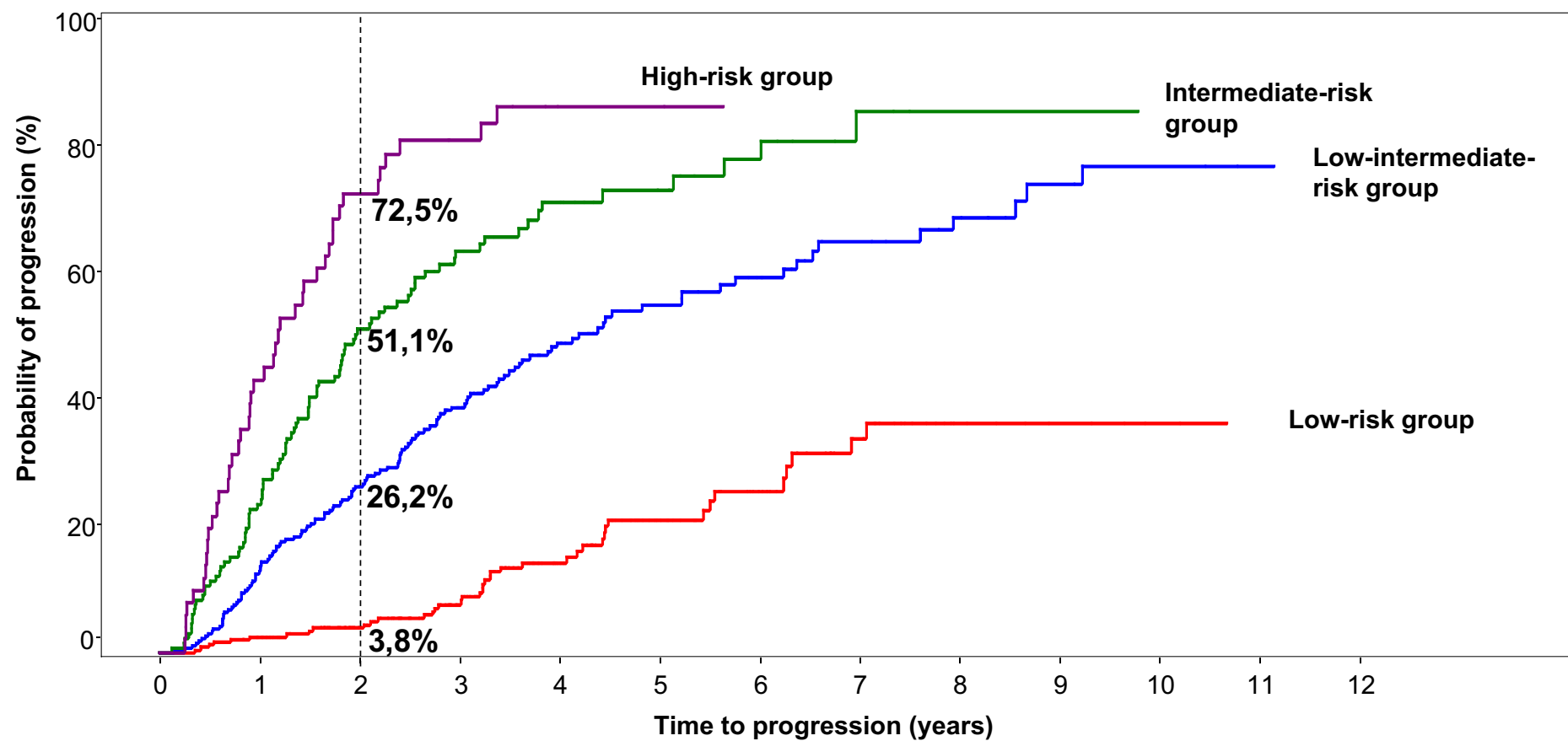
Genomic features can help prognostication in SMM



Term	No. (%)	Estimate (95% CI)	P
DNA repair pathway			
Wild type	80 (94)	Reference	
Mutation	5 (6)	5.54 (1.96 to 15.64)	.001
MYC			
Wild type	79 (93)	Reference	
Mutation	6 (7)	4.53 (1.74 to 11.82)	.002
MAPK pathway			
Wild type	70 (82)	Reference	
Mutation	15 (18)	3.84 (1.90 to 7.74)	< .001
t(4;14)			
Wild type	80 (94)	Reference	
Mutation	5 (6)	2.58 (0.92 to 7.27)	.072
Mayo 18			
Low	23 (27)	Reference	
Intermediate	22 (26)	1.91 (0.66 to 5.47)	.23
High	40 (47)	4.47 (1.63 to 12.26)	.004

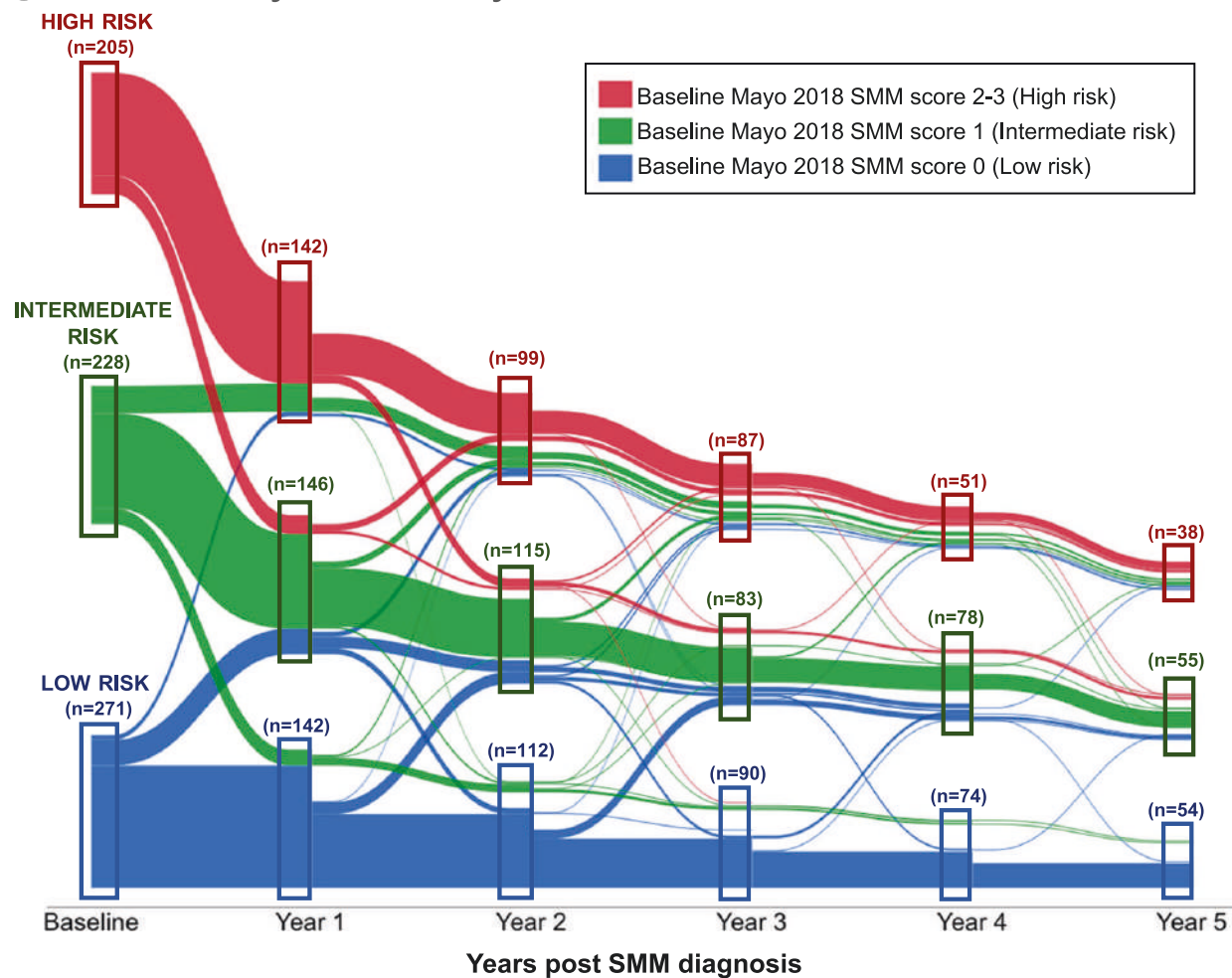
Bustoros et al, JCO 2020

IMWG model for risk stratification of SMM incorporating FISH



Possible added value of dynamic risk-stratification in SMM

Replacing invasive by minimally invasive tumor burden assessment in the model?



Aims of the iMMunocell study group

- Compare the prognostic value of PC quantification in bone marrow (BM) vs the evaluation of circulating tumor cells (CTCs) in peripheral blood (PB) of SMM patients
- Define immune signatures predictive of time-to progression (TTP) in SMM to identify patients with stable tumor burden, but at risk of progression due to lost immune surveillance

Conclusions

- MM initiation decades before diagnosis
- Continuum of genomic features – more studies needed for classification and prognosis
- CTC numbers may have greater prognostic value than BM PC counts
 - Rationale for future dynamic models
- Tumor microenvironment is a key player in disease progression

Evviva i meetings in presenza!

