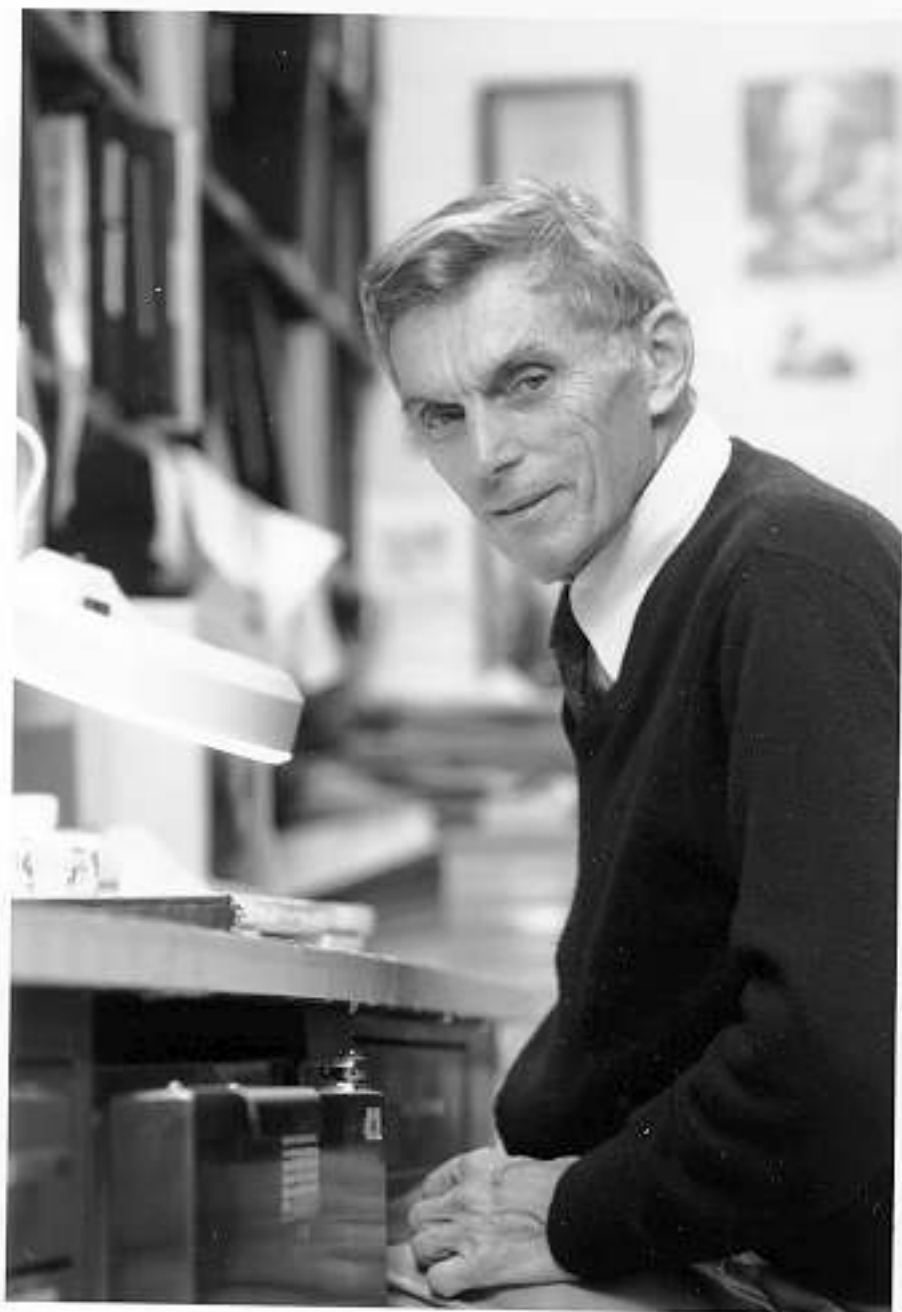


Molecular pathogenesis of plasma cell MGUS and MM

**Michael Kuehl
National Cancer Institute**

13th International Myeloma Workshop

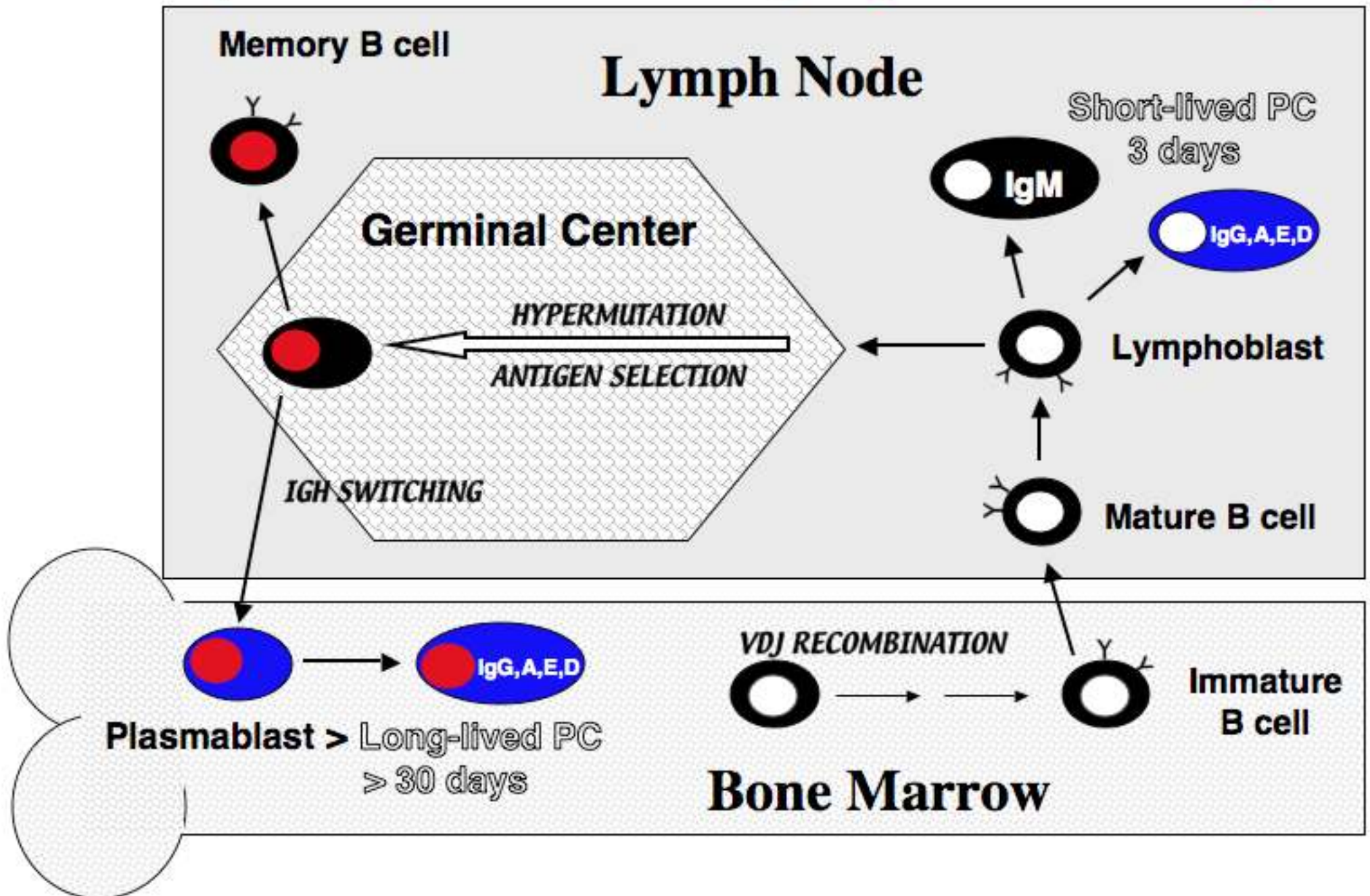


Michael Potter

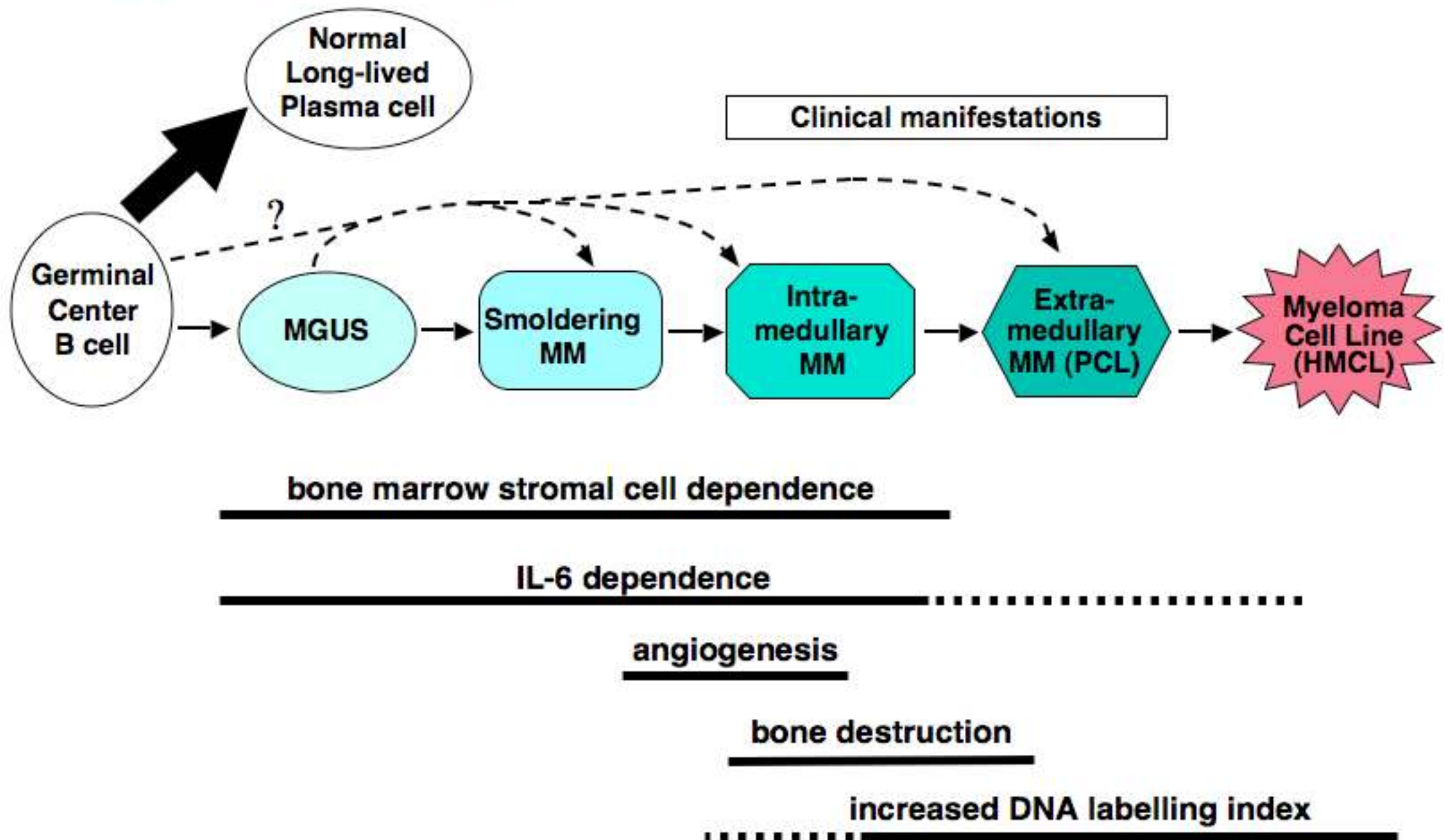


**Leif Bergsagel
1988**

Two kinds of plasma cells: short-lived and post-germinal center long-lived



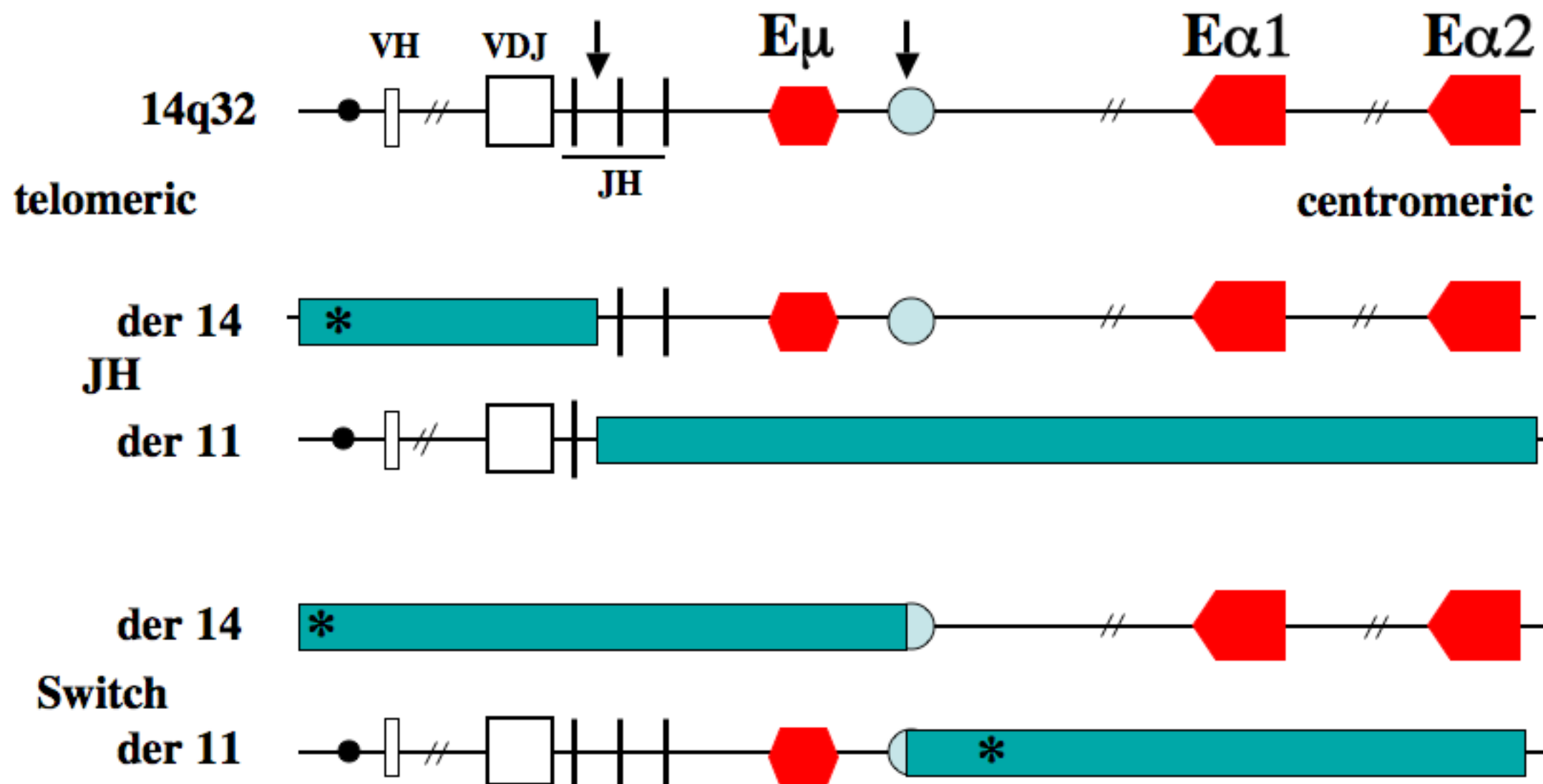
Stages: pre-malignant MGUS > MM > EMM > HMCL



Phoenix, Arizona November 2010

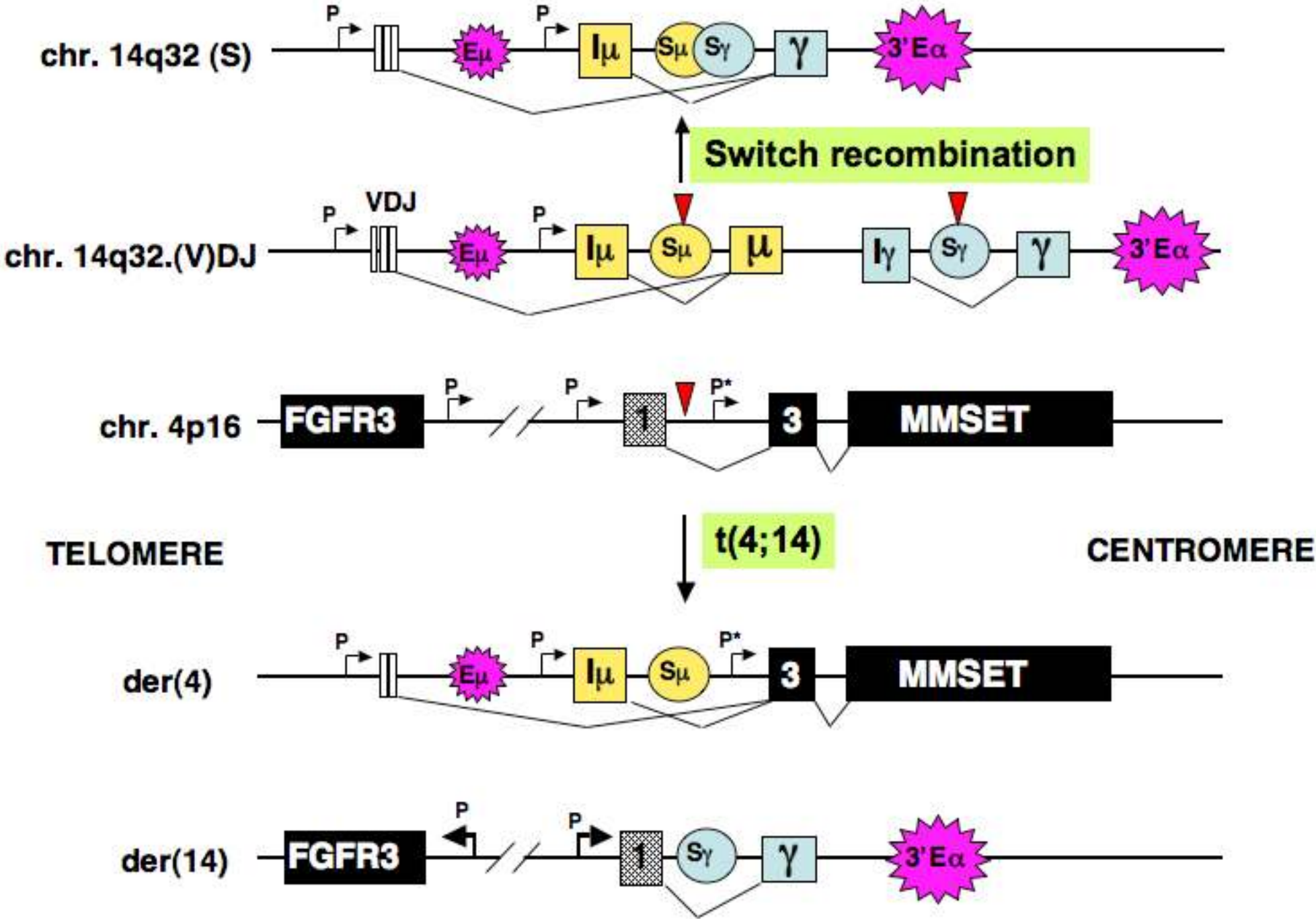


14q32 translocation breakpoints: JH vs SWITCH



*** Oncogene dysregulated by E μ and/or E α ***

Figure 3. Anatomy of t(4;14)(p16;q32) chromosome translocation



Marta Chesi



Three primary IgH translocation groups In MGUS and 40% of MM tumors

CYCLIN D group **18%**

11q13 (CYCLIN D1)	15
6p21 (CYCLIN D3)	3
12p13 (CYCLIN D2)	< 1

MAF group* **7%**

16q23 (c-MAF > CYCLIN D2)	4
20q11 (MAF B > CYCLIN D2)	2
8q24.3 (MAF A > CYCLIN D2)	< 1

MMSET/FGFR3 (4p16) **15%**

* MAFs are transcription factors for Cyclin D2

Rafael Fonseca



Chromosome content indicates 2 pathogenic pathways, each occurring in ~50% of both MGUS and MM tumors

Hyperdiploid (HRD) (48-75 chromosomes)

- **multiple trisomies selectively involving 8 chromosomes (3, 5, 7, 9, 11, 15, 19, 21)**
- **primary IgH translocations in ~10%**

Non-hyperdiploid (NHRD) (<48 and/or >75 chromosomes)

- **primary IgH translocations in ~ 70%**

MYC locus complex rearrangements in MM: a late progression event

- **Selective expression of L-MYC, N-MYC or one parental MYC allele (11) in all 13 informative HMCL**
- **MYC rearrangements by FISH**
 - 84% HMCL**
 - 48% advanced MM**
 - 15% newly diagnosed MM**
 - rarely - if ever - in MGUS or SMM**
- **Heterogeneity of MYC rearrangements frequent in MM**

Progression by secondary (Ig) translocations

What translocations are secondary?

MYC: c- >> N- >> L-

OTHER secondary translocations

IgH(non-recurrent or rare partner)

IgL (κ >> λ)

rarely IgH with one of seven recurrent partners

	PRIMARY	SECONDARY
TIMING	very early	anytime*
B CELL SPECIFIC MECHANISM	yes**	no (off in PC)
STRUCTURE	simple	complex
PREVALENCE	70%NHRD;10%HRD	NHRD = HRD
HETEROGENEITY	no	sometimes

* MYC rare in MGUS but OTHER 2° TLC not rare in MGUS

** mostly IgH switching; sometimes somatic hypermutation

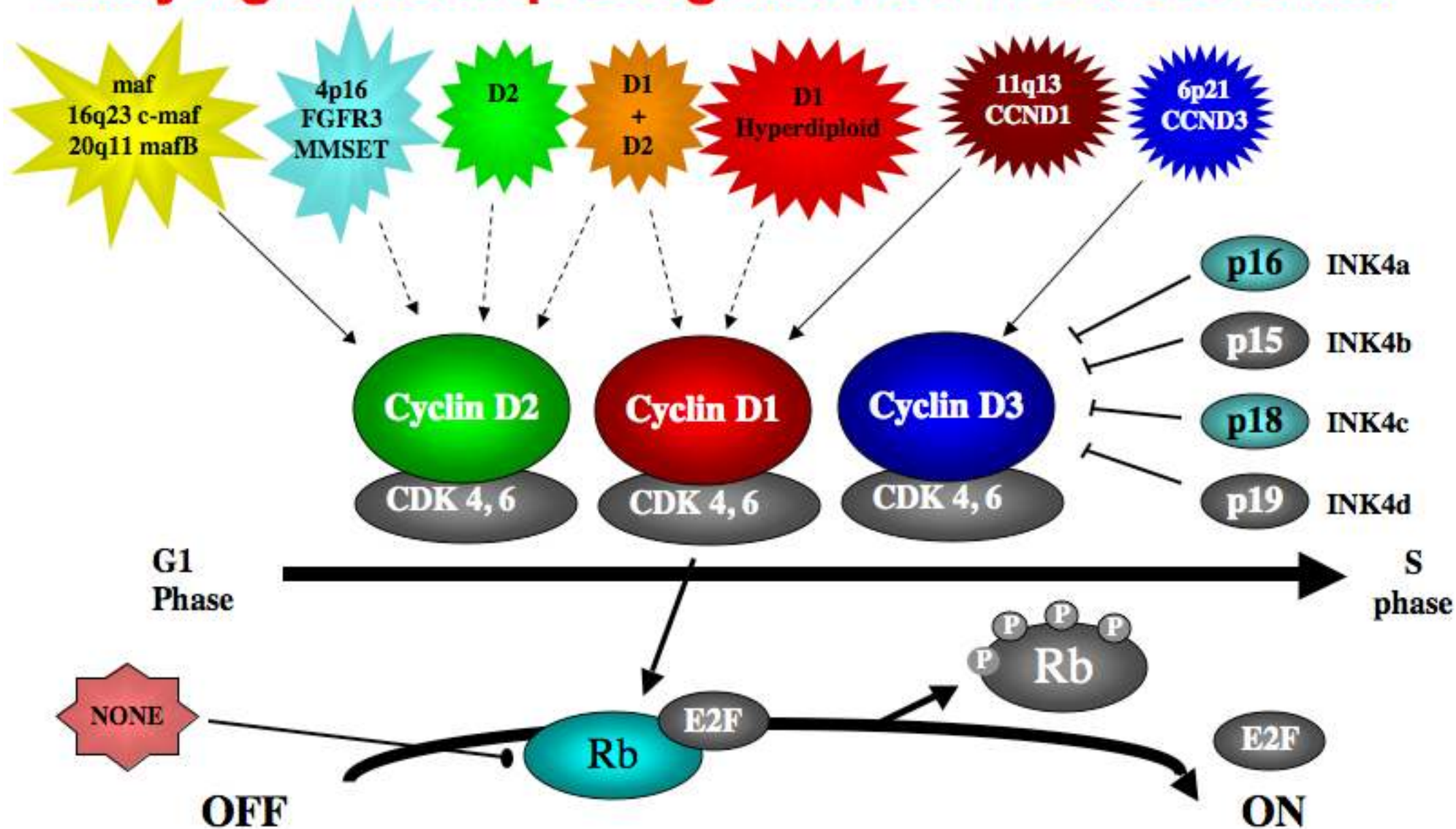
John Shaughnessy



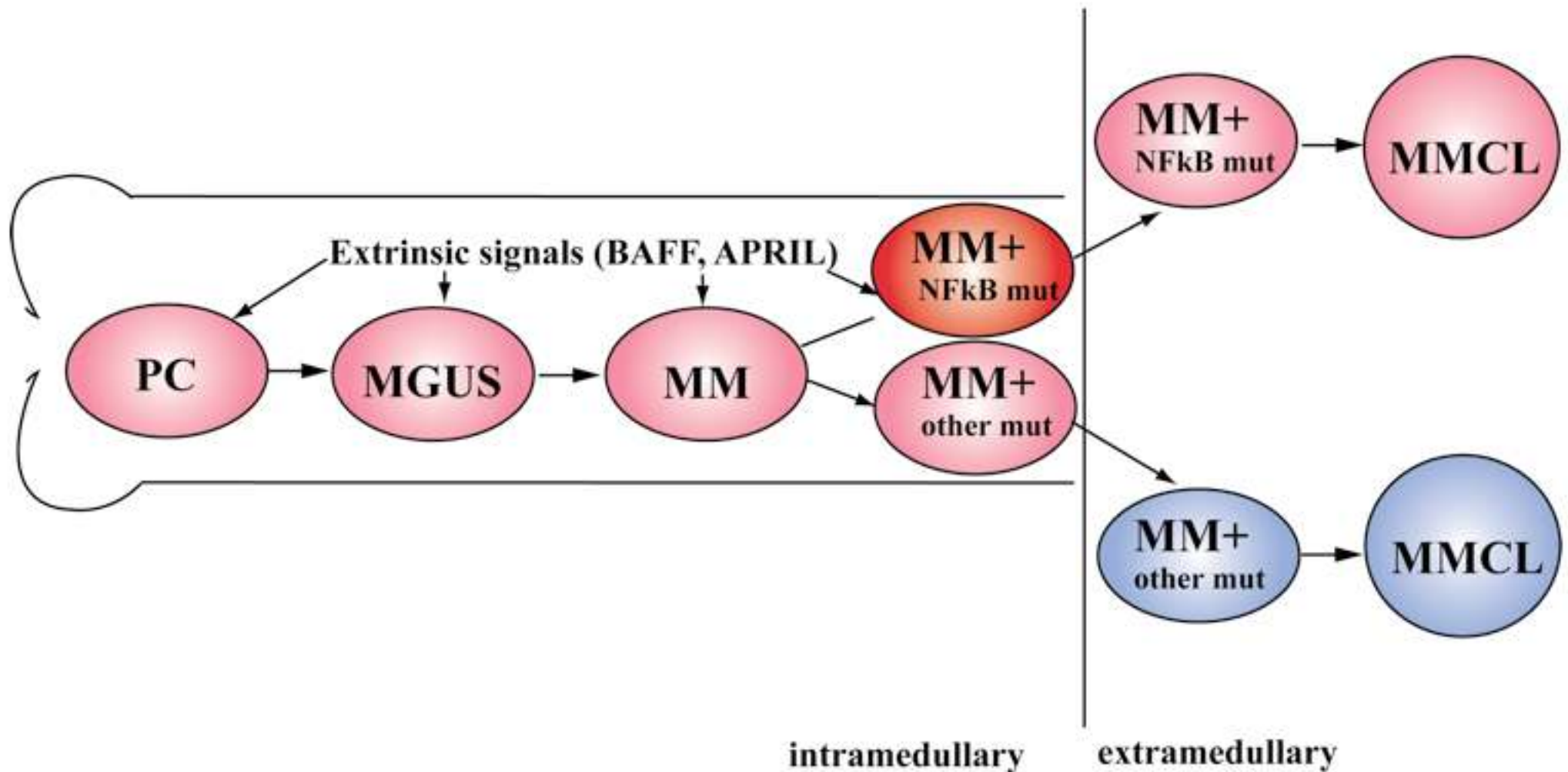
Bart Barlogie



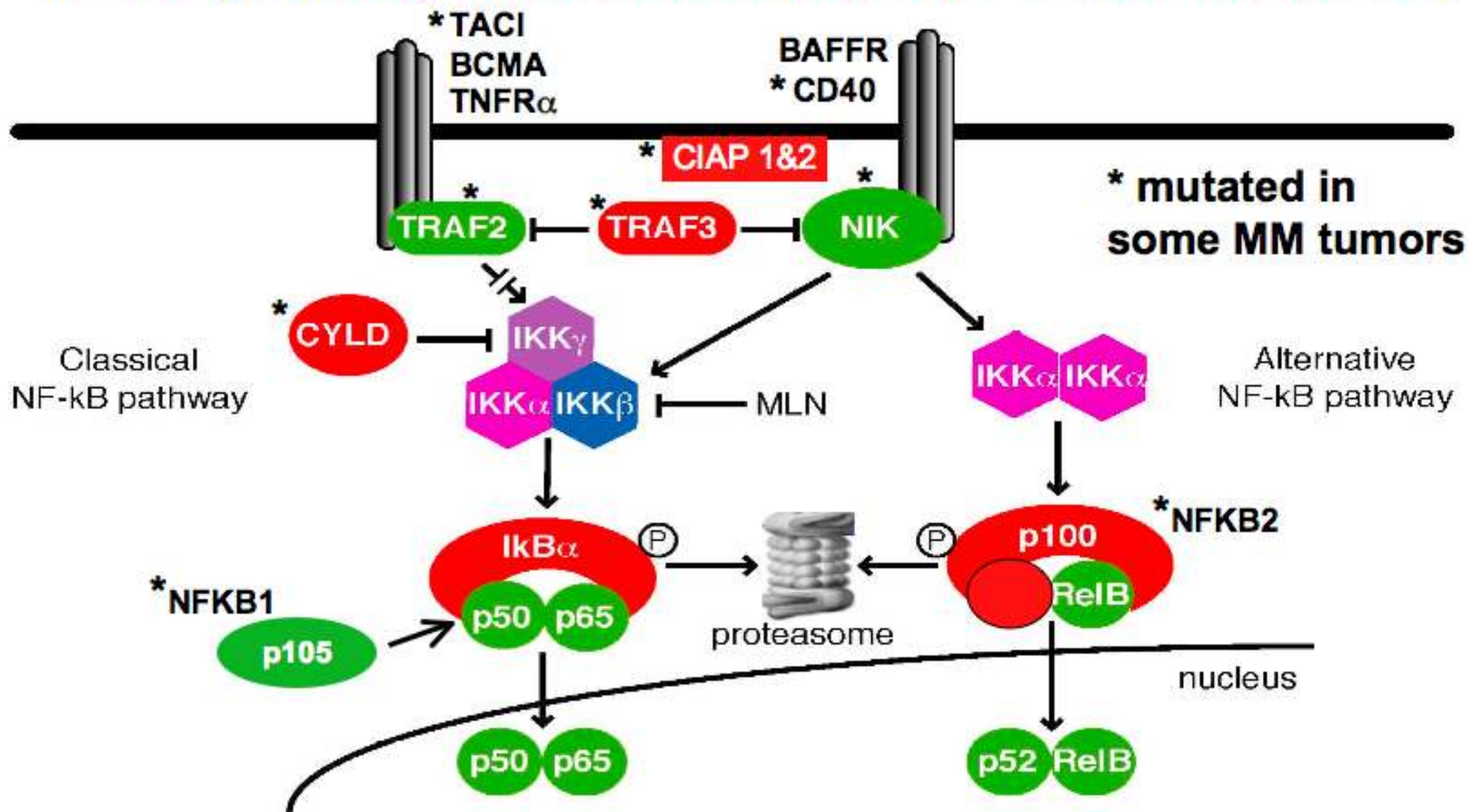
Dysregulation of a CYCLIN D gene is early, and unifying event in pathogenesis of MGUS and MM



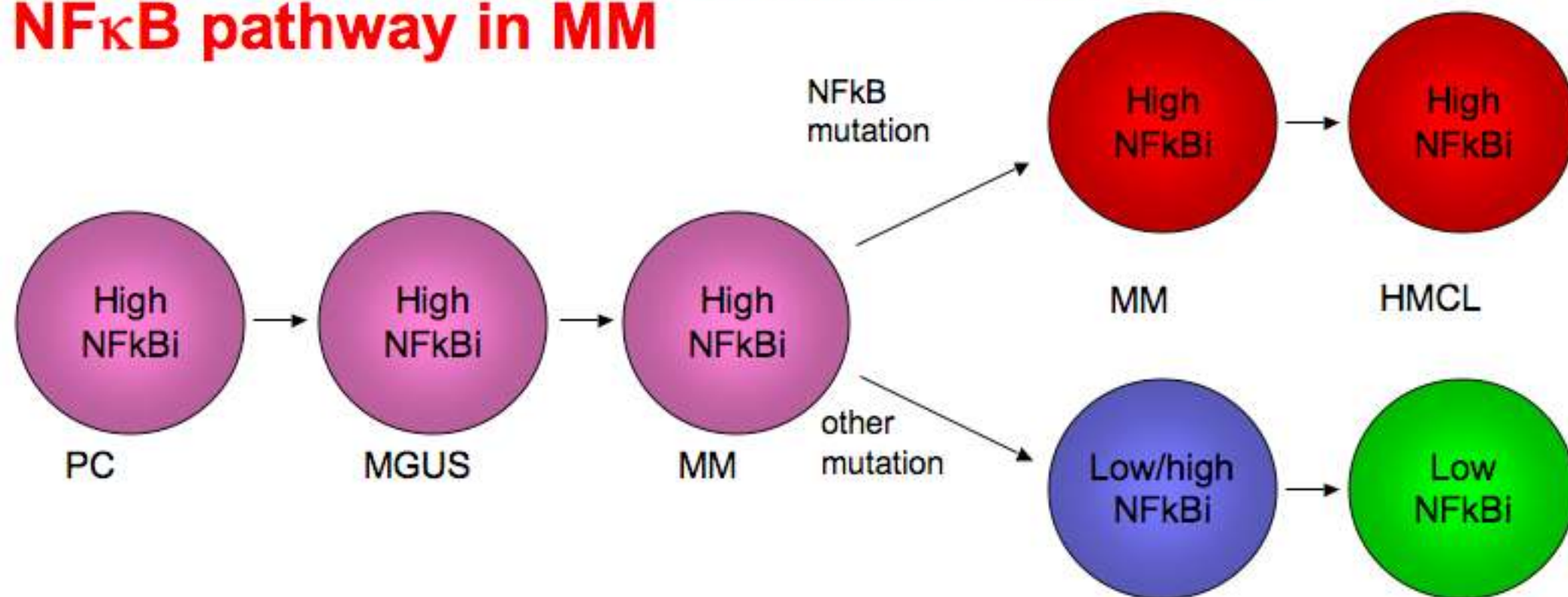
**NFkB pathway is activated by extrinsic signals in PC, MGUS, MM:
activating mutations during progression contribute to less
dependence of MM tumor cells on bone marrow microenvironment**



Mutations activate classical and/or alternative NFkB pathway in 45% MMCL and >17% MM tumors



Extrinsic and intrinsic agents to target the NF κ B pathway in MM



Extrinsic activation of NF κ B

BAFF, APRIL > BCMA, TACI, BAFF-R > NF κ B activation

BCMA-Fc
TACI-Ig

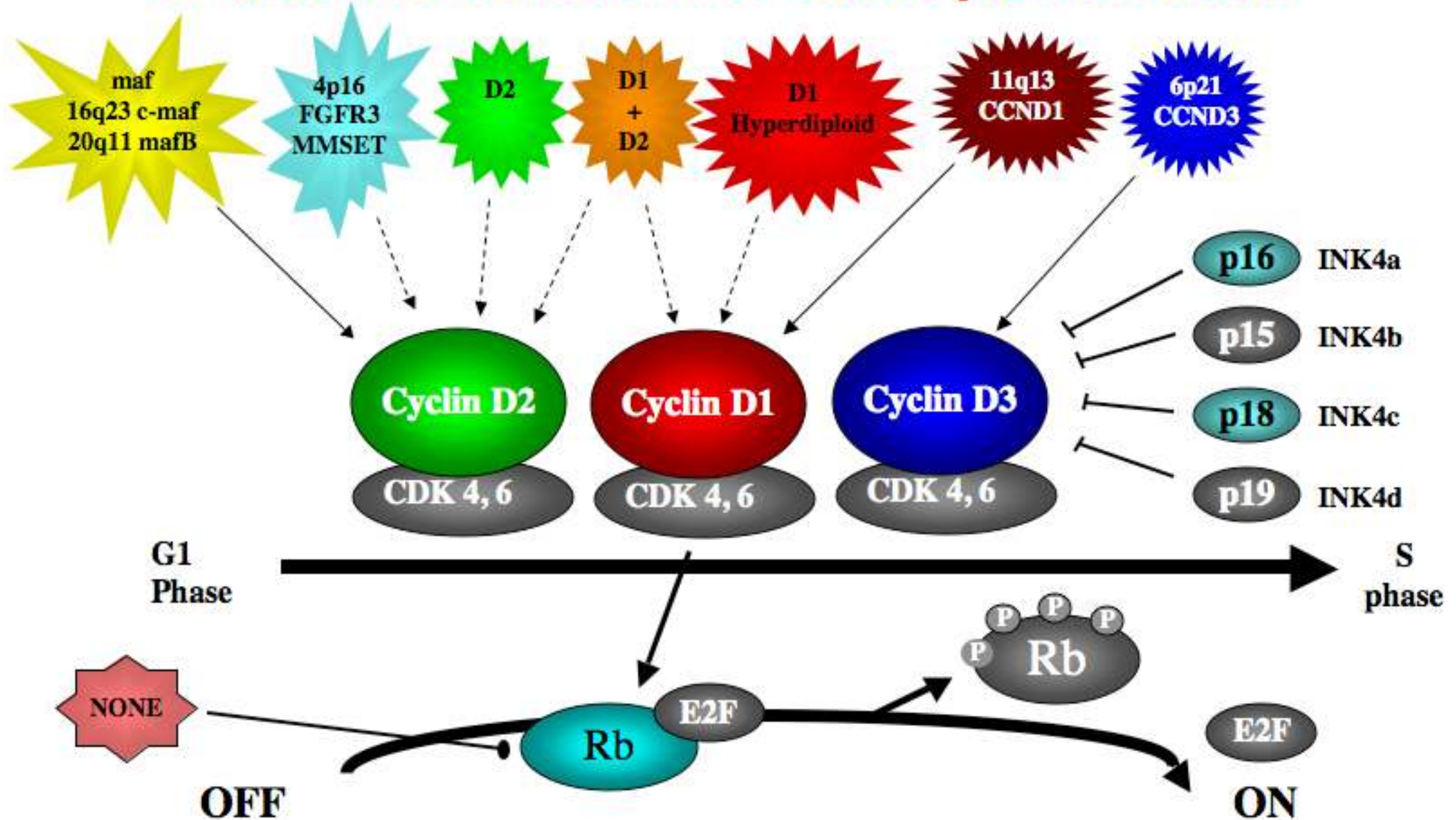
Bortezomib
IKK β inhibitor
NIK inhibitors

The p18INK4C PARADOX:
increased p18 RNA / insensitivity to p18
in most HMCL & proliferative (PI > 2) MM

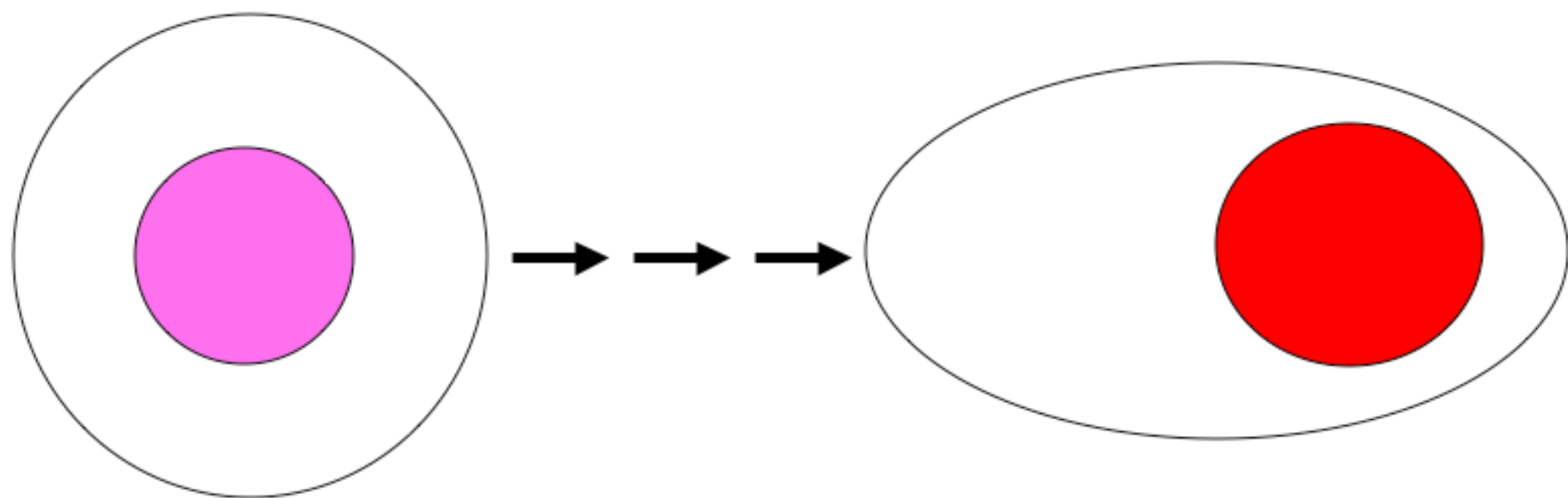
CELLS	PI	% HIGH p18
NL PC	<1	0
HMCL	>2	59
MM	<1	3
	1-2	13
	>2	60

Increased E2F -> increased proliferation and increased p18 RNA

Sequential disruption of the RB pathway is associated with increased proliferation



**Memory B cell that shares clonotype and primary IgH translocation
but not K-RAS mutation is a premalignant precursor
but not a tumor propagating/cancer stem cell**



**Memory B cell
CD138- CD19+
IgH translocation
K-RAS NOT mutated**

**Myeloma tumor cell
CD138+ CD19-
IgH translocation
K-RAS MUTATION**

Bob Kyle



MGUS mostly/?always precedes MM

- Monoclonal Ig is detected at least 2.5 years prior to diagnosis of MM in most patients

Weiss et al: 27/30 patients (90%)

Landgren study: 75 patients (>95%)

- Four (13%) light chain only MM evolved from light chain only MGUS, both detected only by sFLC

Consistent with Dispenzieri et al that there is a similar fraction of light chain only MGUS and MM

K-RAS mutations in 17% of MM, but not detected in MGUS

	No.	N-RAS	K-RAS	N+K-RAS
MGUS	51	0.08	0*	0.06
MM	248	0.14	0.17	0.31

* $P < 10^{-7}$

N-RAS: 21% CYCLIN D1 but only 4% CYCLIN D2 MM

K-RAS: 17% CYCLIN D1 and CYCLIN D2 MM

**? Overlapping but non-identical roles for
K- and N-RAS mutations in MGUS/MM**

Kathy Giusti
MMRF > MMRC



MYC dysregulation during MM pathogenesis

FISH: MYC-Ig rearrangements occur late in pathogenesis

0% MGUS

6% untreated MM

27% advanced MM

50% MM cell line

CGH: MYC locus rearrangements in MM

- Discordant with MYC-Ig rearrangements detected by FISH
MM, 35% in newly diagnosed and 42% in relapsed**
- Prevalence is 16% with t(11;14) but 55% for hyperdiploid**

MYC RNA expression:

MMR > MMNR > MGUS

**HMCL: mono-allelic with MYC locus rearrangement
bi-allelic without rearrangement**

MYC dysregulation occurs both early and late in MM pathogenesis

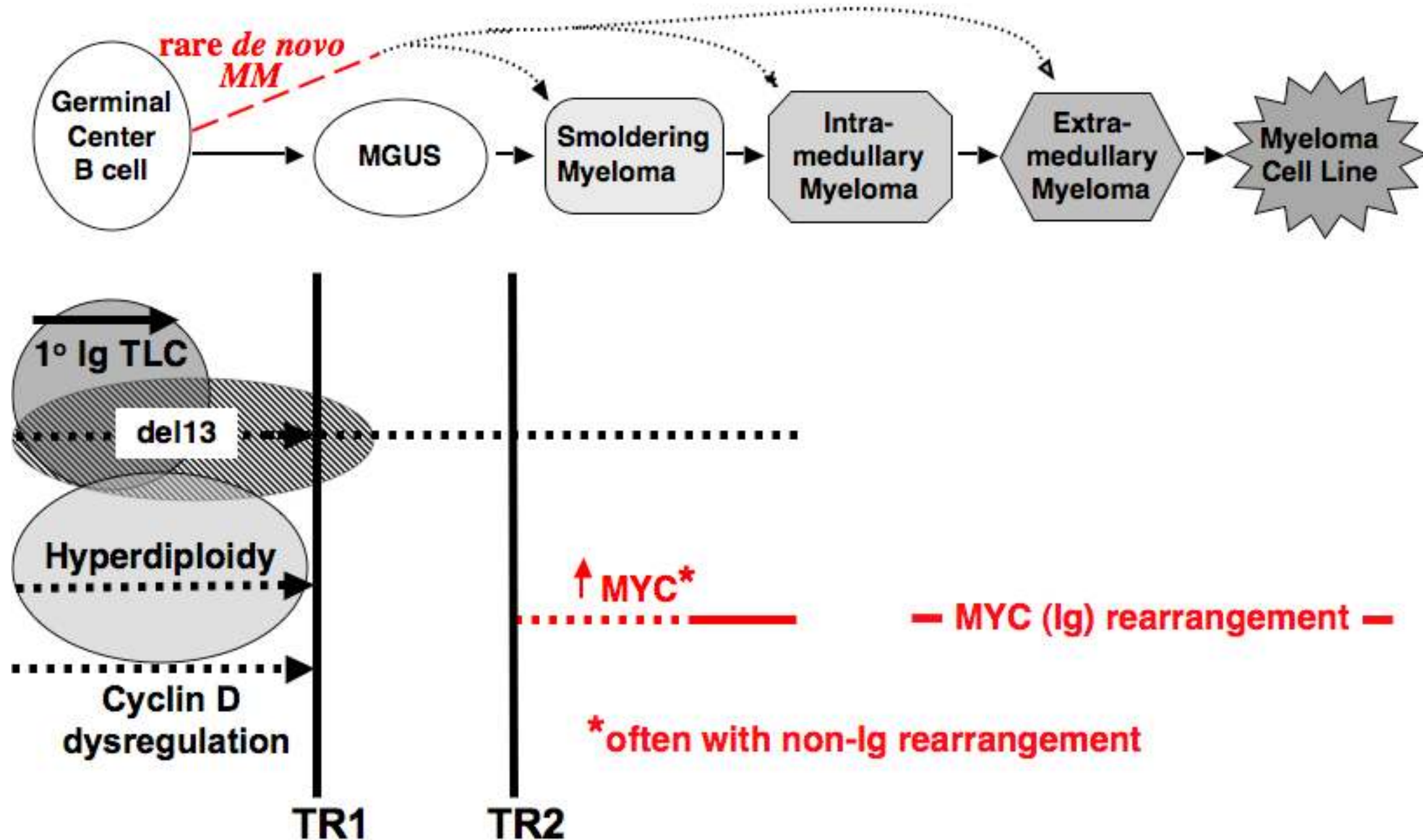
EARLY

- Increased MYC RNA in MM compared to MGUS (?SMM)
- Cryptic rearrangements detected by CGH
- MYC-Ig rearrangements are rare

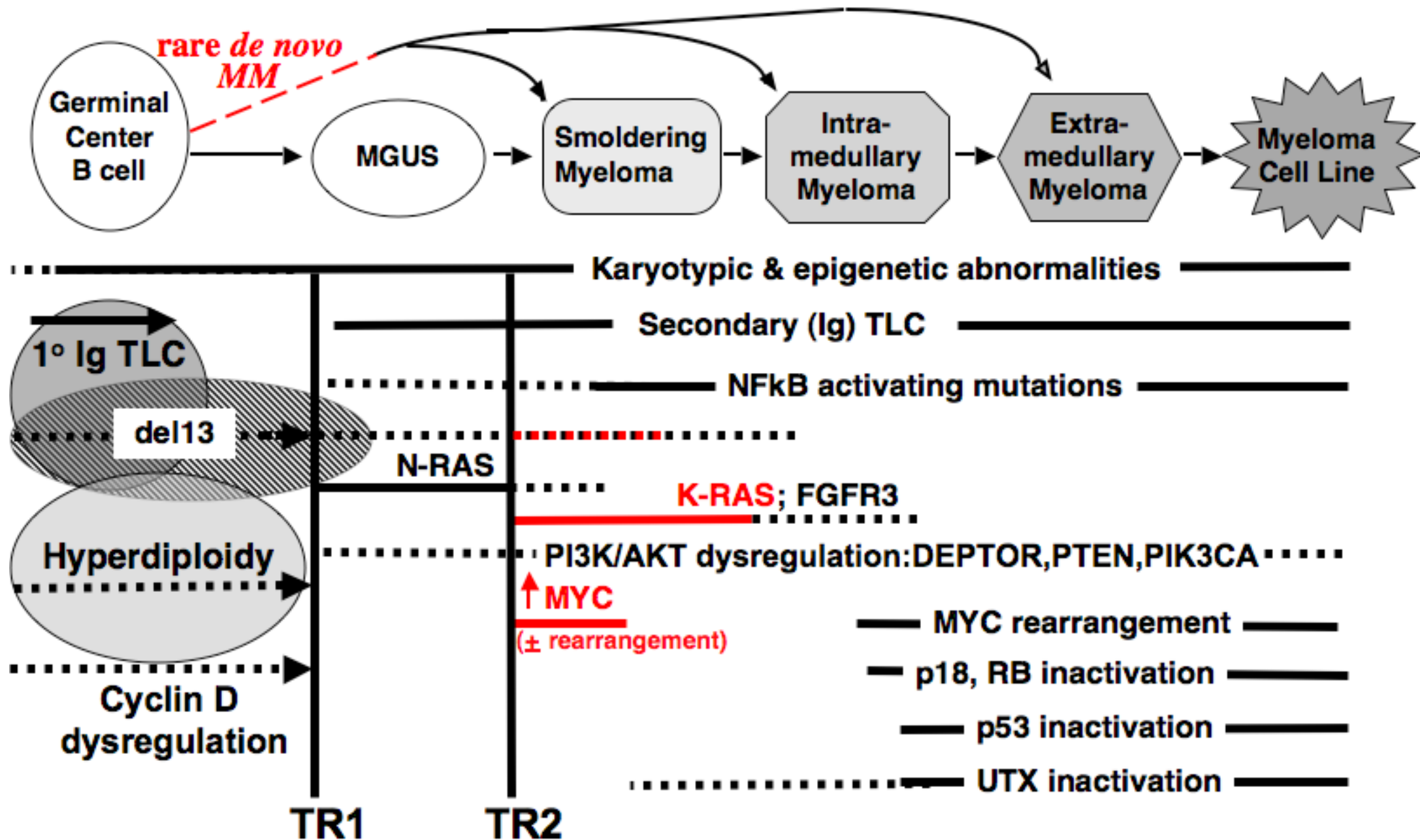
LATE

- MYC rearrangements often involve juxtaposition of MYC near an Ig locus (IgH>IgL>IgK)
- Associated with increased prevalence of p53 mutations
- Associated with increased proliferation and stromal cell independence, i.e., extramedullary

MYC dysregulation: 2 stages of MM pathogenesis



Molecular pathogenesis of MM



Kuehl lab

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Yulia Demchenko
Oleg Glebov
Gina Kim

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* No longer there