

Acute myeloid leukemia

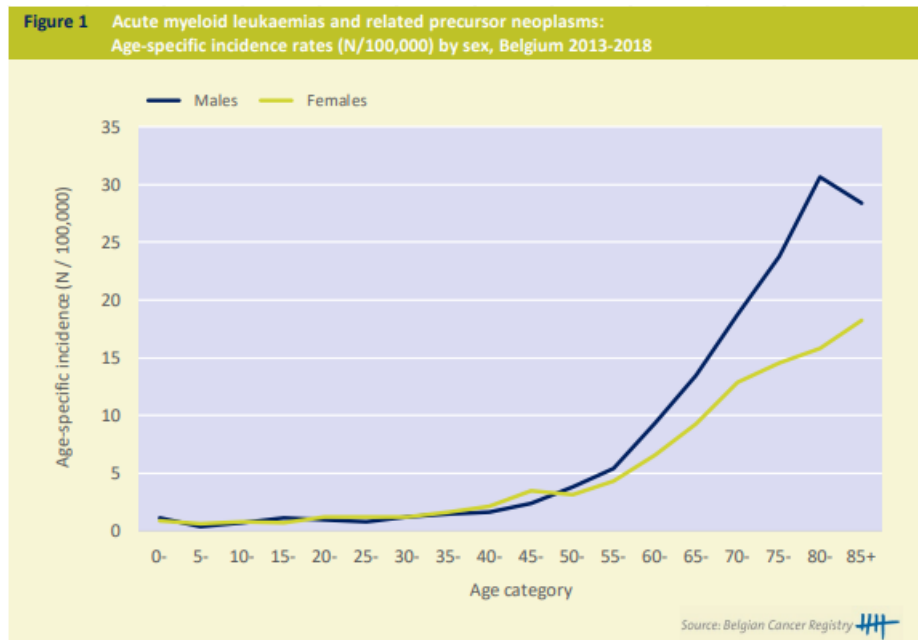
the molecular pathogenesis

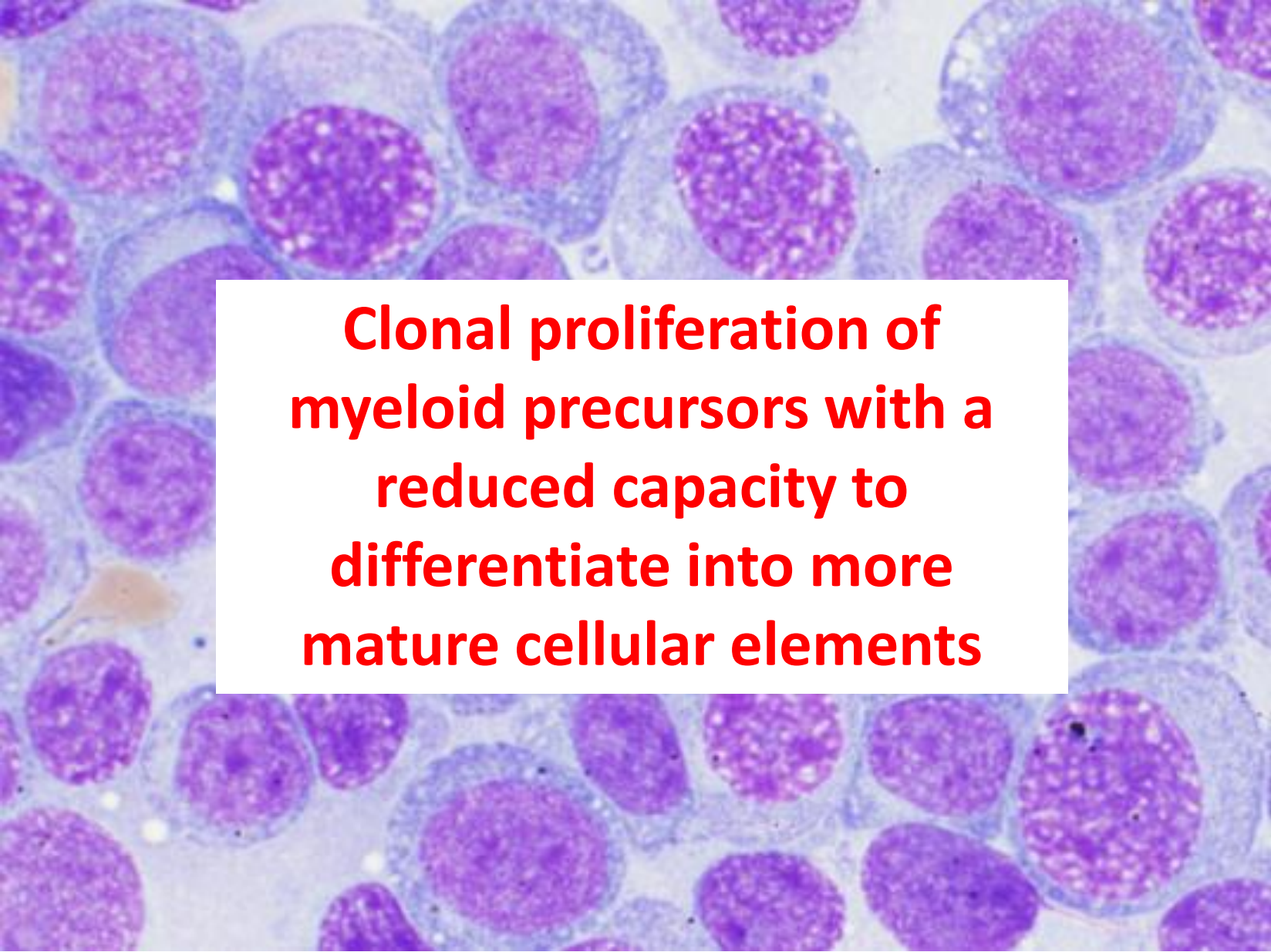
Pr Violaine Havelange, MD, PhD

Department of hematology

Acute myeloid leukemia (AML)

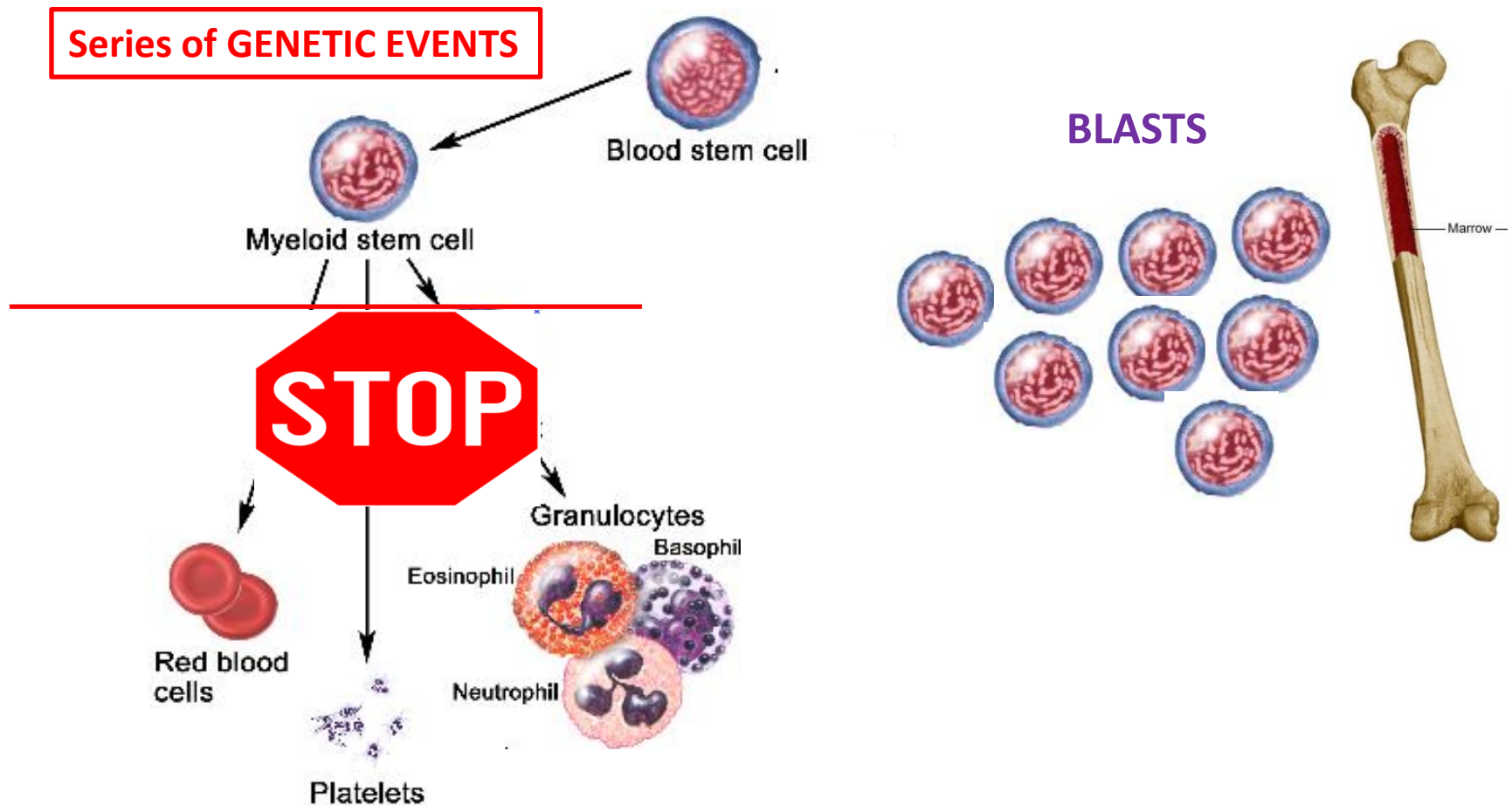
- Incidence : 3-5 cases/100.000/year
- 80% of acute leukemias in adults
- Median age : 65 years



A microscopic image showing a dense population of myeloid precursor cells. The cells are characterized by large, round nuclei with a high nuclear-to-cytoplasmic ratio and prominent nucleoli. The cytoplasm is scant and pale. The overall appearance is that of a clonal proliferation of immature cells.

**Clonal proliferation of
myeloid precursors with a
reduced capacity to
differentiate into more
mature cellular elements**

PHYSIOPATHOLOGY



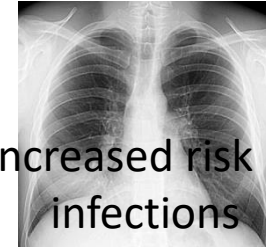
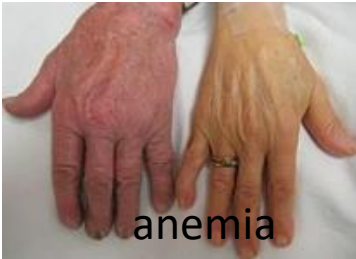
Accumulation of leukemic blasts or immature forms in BM, PB, other tissues

+

Reduction in the production of normal red blood cells, platelets, granulocytes

CLINICAL SYMPTOMS

- complications of pancytopenia



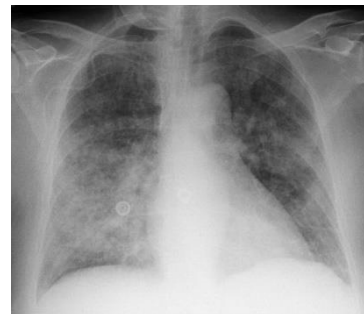
- Extramedullary locations

skin, CNS, oropharynx, organomegaly, joints, myeloid sarcomas



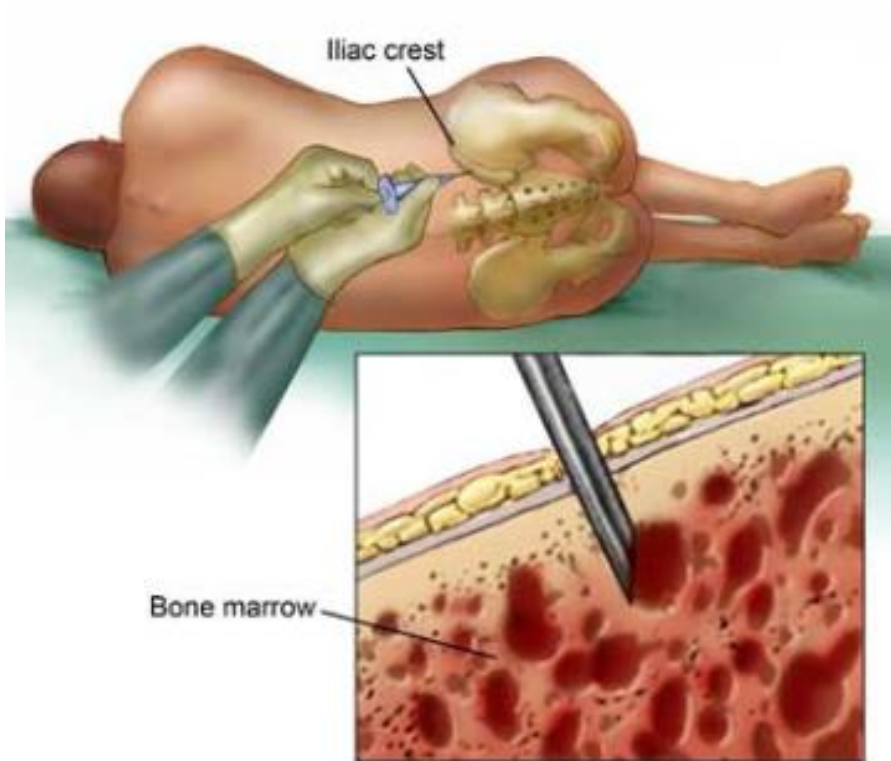
- Symptoms of leukostasis if extremely high white blood cell counts

fever, lung, CNS, heart

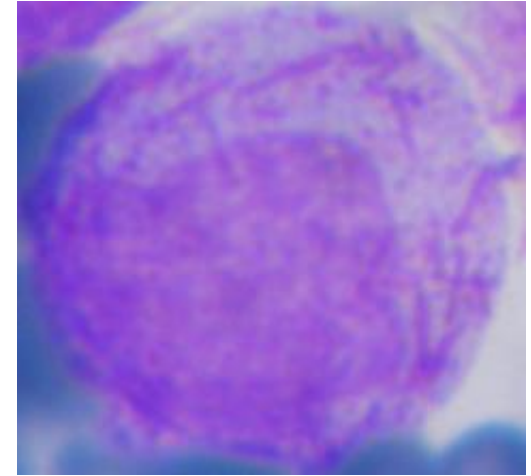
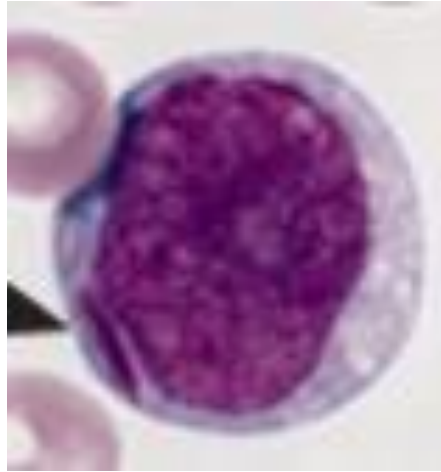


DIAGNOSIS

Bone marrow aspirate/biopsy



MORPHOLOGY



staining with Wright Giemsa

blasts

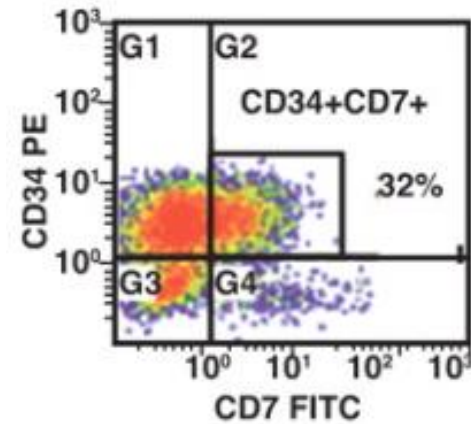
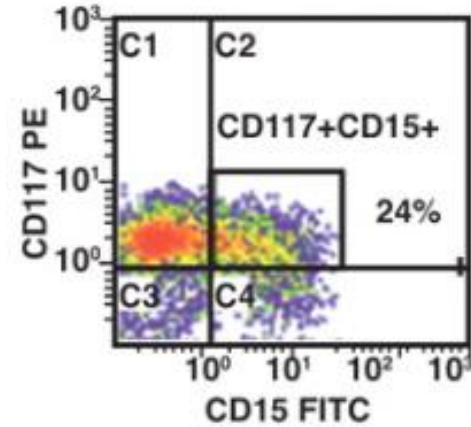
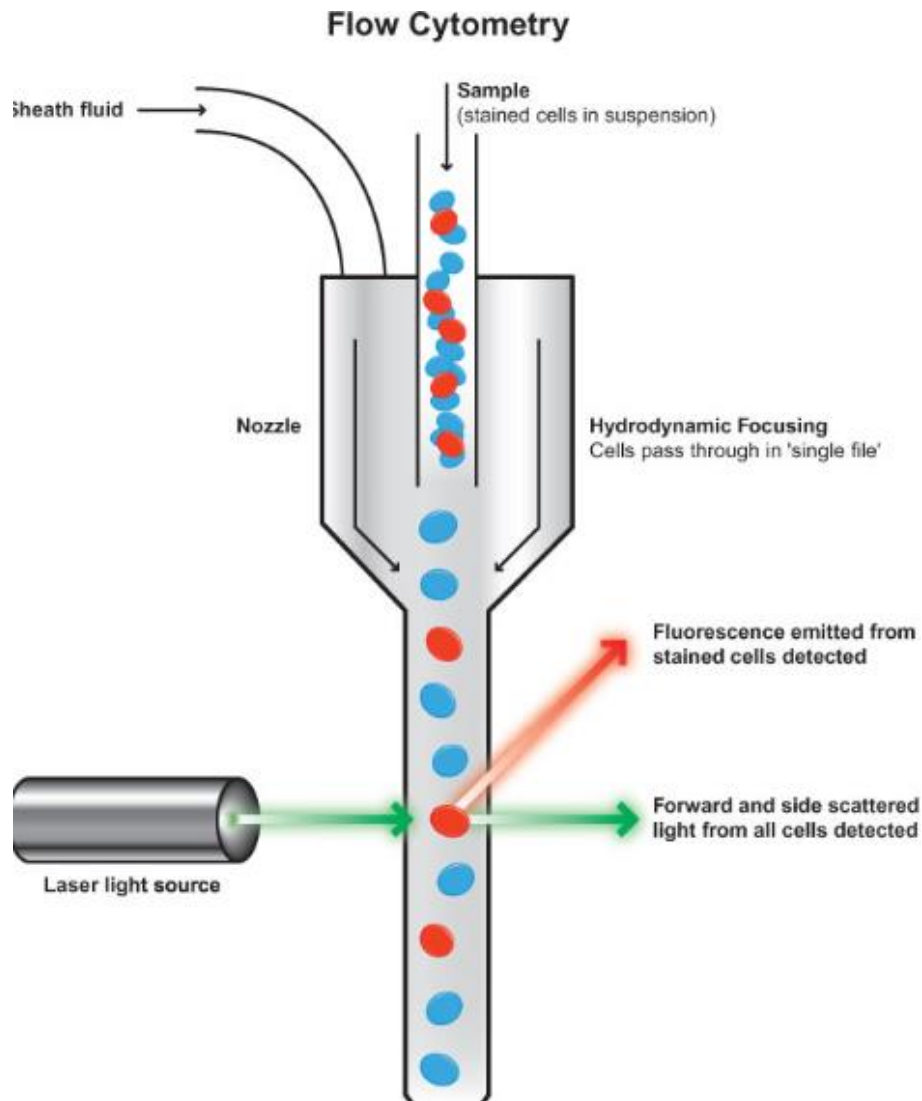
> 20%

immature cells with large nuclei, with prominent nucleoli
pale blue cytoplasm

'auer rod' = pathognomonic of myeloblasts

Cytochemical studies : + sudan black B,
myeloperoxidase or esterase

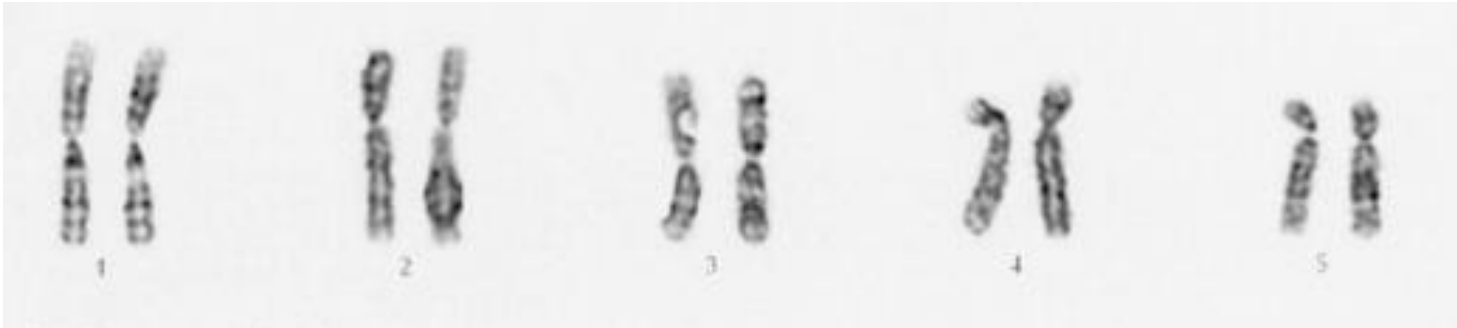
IMMUNOPHENOTYPING



CD34+
HLA-DR +
CD117 +
CD13 +
CD33 +

CYTOGENETICS (karyotype and FISH)

recurrent cytogenetic abnormality in 55% of AML patients



Screening for gene rearrangements§

PML-RARA, CBFB-MYH11, RUNX1-RUNX1T1, BCR-ABL1, other fusion genes
(if available)



t(15;17) in AML M3

(Acute Promyelocytic Leukemia)

MOLECULAR TESTINGS

Fusion transcripts : AML1/ETO; t(8;21)

PML/RARA; t(15;17)

CBFB/MYH11; inv(16)

Tandem internal duplication of *FLT3*

Internal duplication of *KMT2A*

Mutation of *CEBPa*

MOLECULAR TESTINGS



NGS Next Generation Sequencing

ASXL1 (exon 13)

CEBPA (exon 1)

DNMT3A (exon 8-23)

FLT3 (exon 14, exon 15, exon 20-codon 835)

IDH1 (exon 4-hotspot)

IDH2 (exon 4-hotspot)

KIT (exon 8, exon 10, exon 17)

NPM1 (exon 11-codon 288)

RUNX1 (exon 2-9)

TET2 (exon 3, exon 9-11)

TP53 (exon 2-11)

WT1 (exon 7, exon 9)

prognostic

diagnostic/prognostic

diagnostic/prognostic

prognostic/treatment

prognostic/treatment

prognostic/ treatment

prognostic/ treatment

diagnostic/prognostic

diagnostic/prognostic

diagnostic/prognostic

prognostic/ treatment

prognostic

The 2016 revision to the World Health Organization classification of myeloid neoplasms and acute leukemia

Daniel A. Arber,¹ Attilio Orazi,² Robert Hasserjian,³ Jürgen Thiele,⁴ Michael J. Borowitz,⁵ Michelle M. Le Beau,⁶ Clara D. Bloomfield,⁷ Mario Cazzola,⁸ and James W. Vardiman⁹

Acute myeloid leukemia (AML) and related neoplasms

AML with recurrent genetic abnormalities

AML with t(8;21)(q22;q22.1);*RUNX1-RUNX1T1*

AML with inv(16)(p13.1q22) or t(16;16)(p13.1;q22);*CBFB-MYH11*

APL with *PML-RARA*

AML with t(9;11)(p21.3;q23.3);*MLL3-KMT2A*

AML with t(6;9)(p23;q34.1);*DEK-NUP214*

AML with inv(3)(q21.3q26.2) or t(3;3)(q21.3;q26.2); *GATA2, MECOM*

AML (megakaryoblastic) with t(1;22)(p13.3;q13.3);*RBM15-MKL1*

Provisional entity: AML with *BCR-ABL1*

AML with mutated *NPM1*

AML with biallelic mutations of *CEBPA*

Provisional entity: AML with mutated *RUNX1*

AML with myelodysplasia-related changes

Therapy-related myeloid neoplasms

AML, NOS

AML with minimal differentiation

AML without maturation

AML with maturation

Acute myelomonocytic leukemia

Acute monoblastic/monocytic leukemia

Pure erythroid leukemia

Acute megakaryoblastic leukemia

Acute basophilic leukemia

Acute panmyelosis with myelofibrosis

Myeloid sarcoma

Myeloid proliferations related to Down syndrome

Transient abnormal myelopoiesis (TAM)

Myeloid leukemia associated with Down syndrome

DIAGNOSTIC

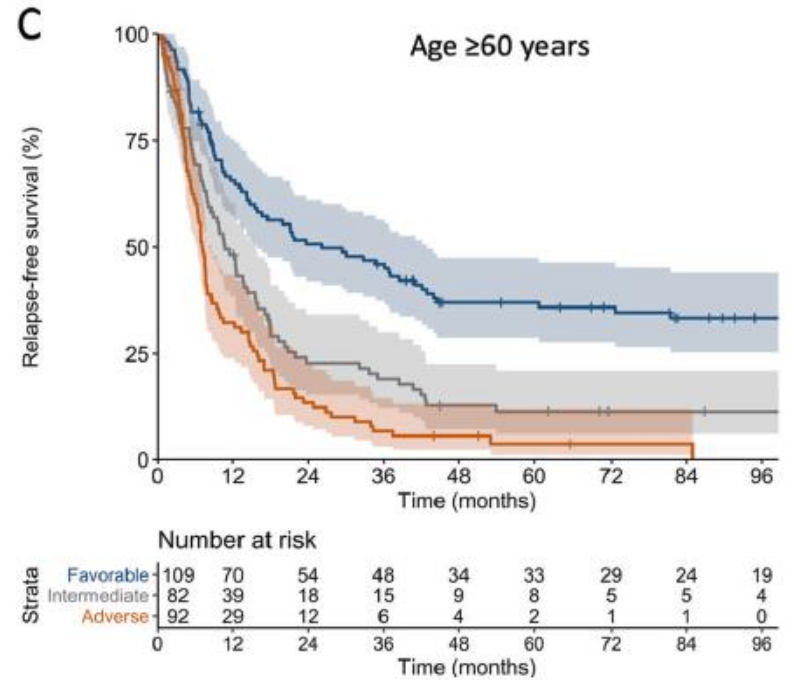
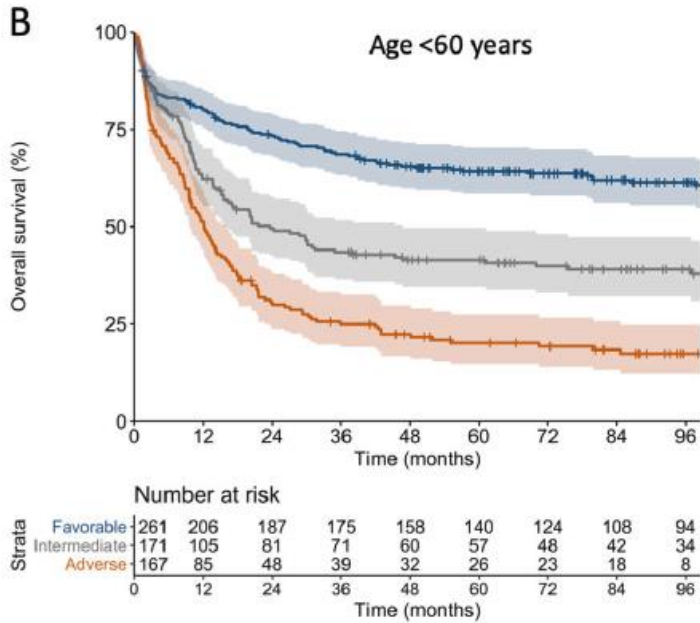
Diagnosis and Management of AML in Adults: 2017 ELN Recommendations from an International Expert Panel

PROGNOSIS - TREATMENT

Table 5. 2017 European LeukemiaNet risk stratification by genetics^a

Risk Category ^b	Genetic Abnormality
Favorable	t(8;21)(q22;q22.1); <i>RUNX1-RUNX1T1</i> inv(16)(p13.1q22) or t(16;16)(p13.1;q22); <i>CBFB-MYH11</i> Mutated <i>NPM1</i> without <i>FLT3</i> -ITD or with <i>FLT3</i> -ITD ^{low(c)} Biallelic mutated <i>CEBPA</i>
Intermediate	Mutated <i>NPM1</i> and <i>FLT3</i> -ITD ^{high(c)} Wild type <i>NPM1</i> without <i>FLT3</i> -ITD or with <i>FLT3</i> -ITD ^{low(c)} (w/o adverse-risk genetic lesions) t(9;11)(p21.3;q23.3); <i>MLLT3-KMT2A</i> ^d Cytogenetic abnormalities not classified as favorable or adverse
Adverse	t(6;9)(p23;q34.1); <i>DEK-NUP214</i> t(v;11q23.3); <i>KMT2A</i> rearranged t(9;22)(q34.1;q11.2); <i>BCR-ABL1</i> inv(3)(q21.3q26.2) or t(3;3)(q21.3;q26.2); <i>GATA2,MECOM(EVI1)</i> -5 or del(5q); -7; -17/abn(17p) Complex karyotype, ^e monosomal karyotype ^f Wild type <i>NPM1</i> and <i>FLT3</i> -ITD ^{high(c)} Mutated <i>RUNX1</i> ^g Mutated <i>ASXL1</i> ^g Mutated <i>TP53</i> ^h

PROGNOSIS



To understand the molecular pathogenesis of AML



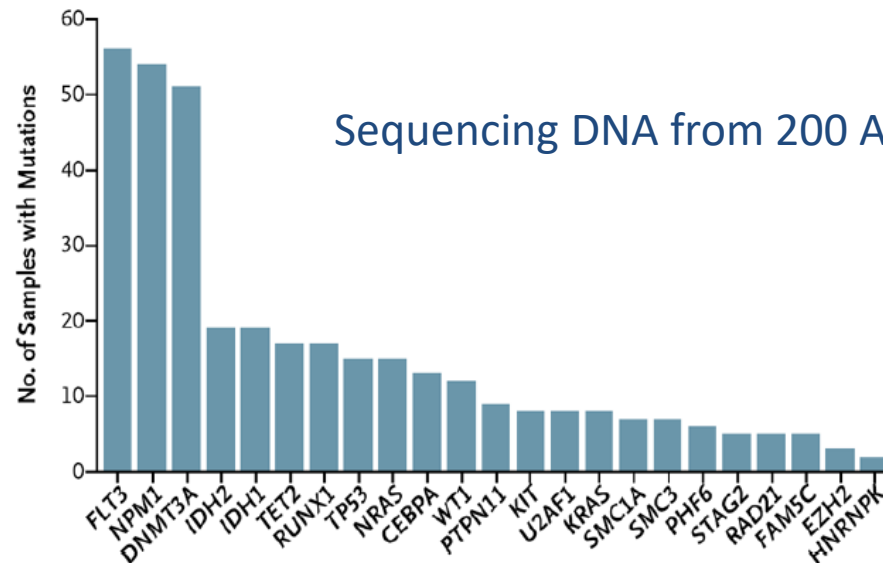
Larges sequencing studies -> genetic heterogeneity
molecular pathogenesis of AML

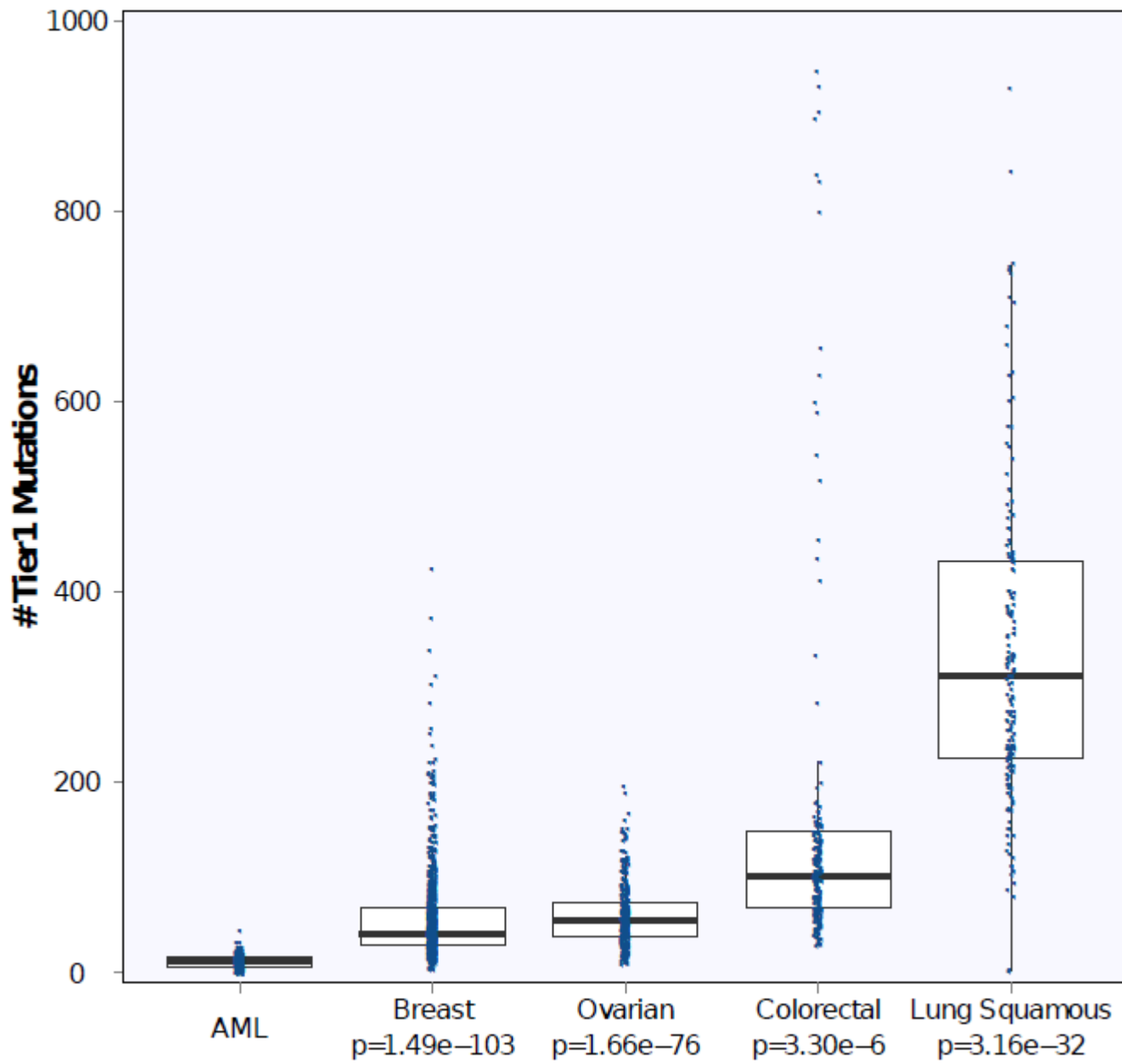
Fewer mutations in AML genome ...

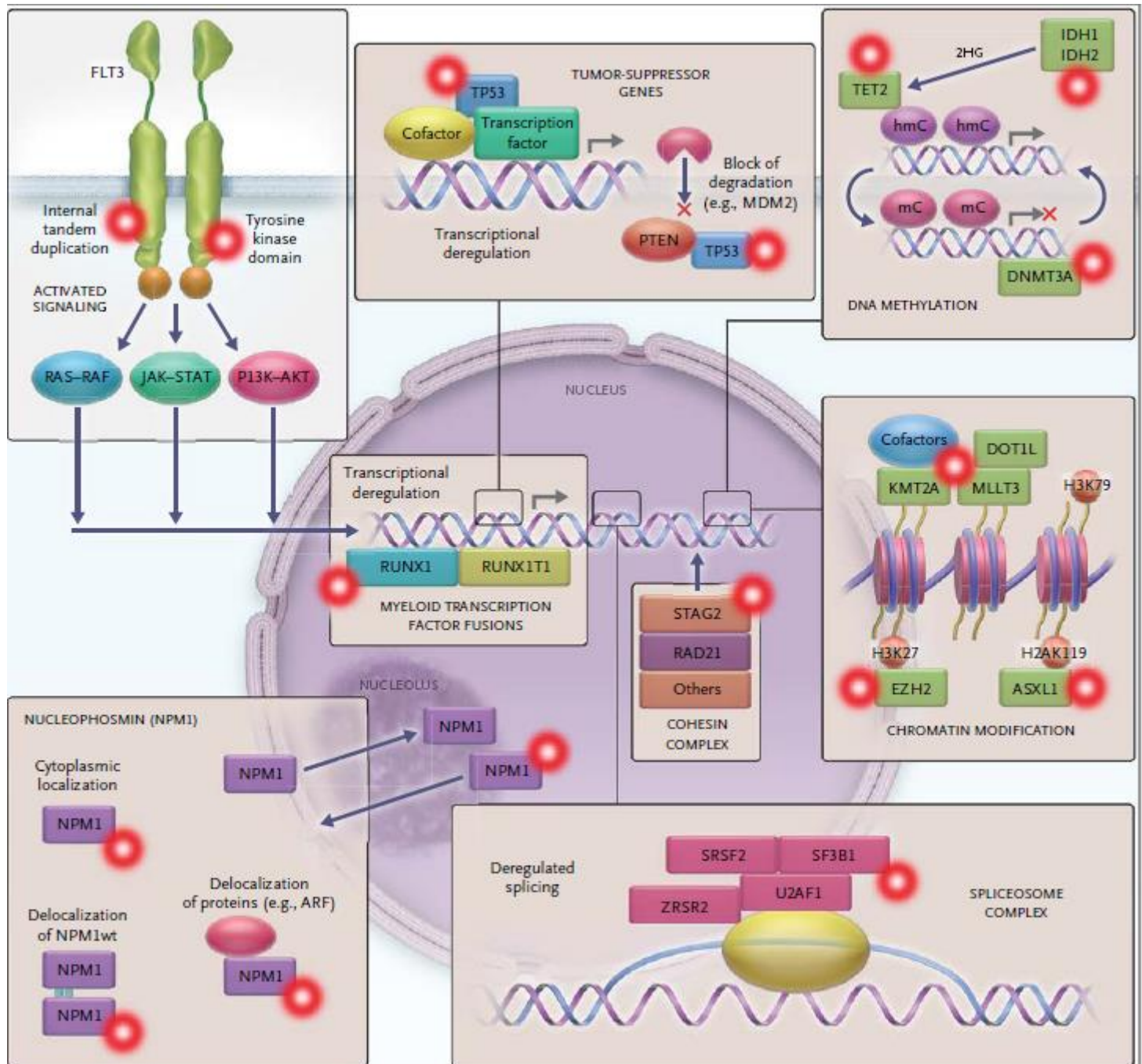
+/- 13 mutations per patient – 5 in genes recurrently mutated in AML

23 genes recurrently mutated - and 237 genes mutated in ≥ 2 patients

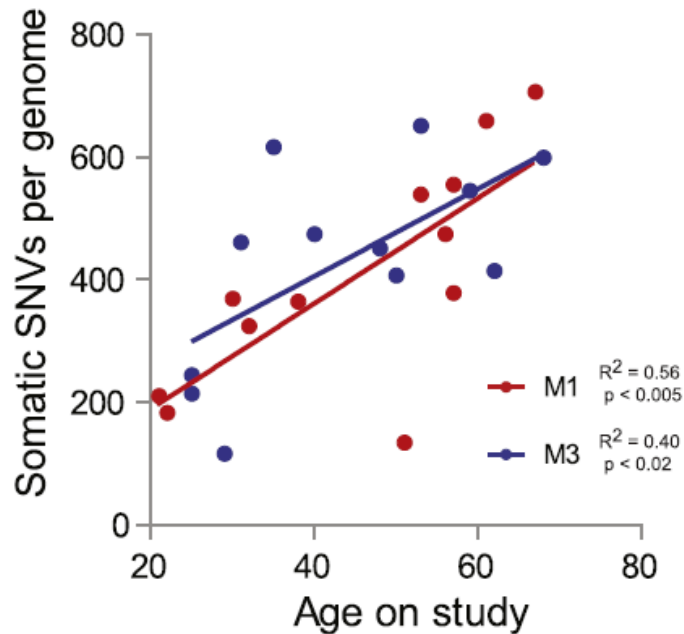
B Significantly Mutated Genes







Sequencing DNA of BM/skin from 12 AML M3 - t(15;17) /12 AML M1 normal KT



- 100s of MUTATIONS/ patient
- total number increases with AGE
- +/- in all AML cells
- widely distributed in the genome
- similar numbers in M3 and M1
- very few are RECURRENT

Most of the mutations in founding clone

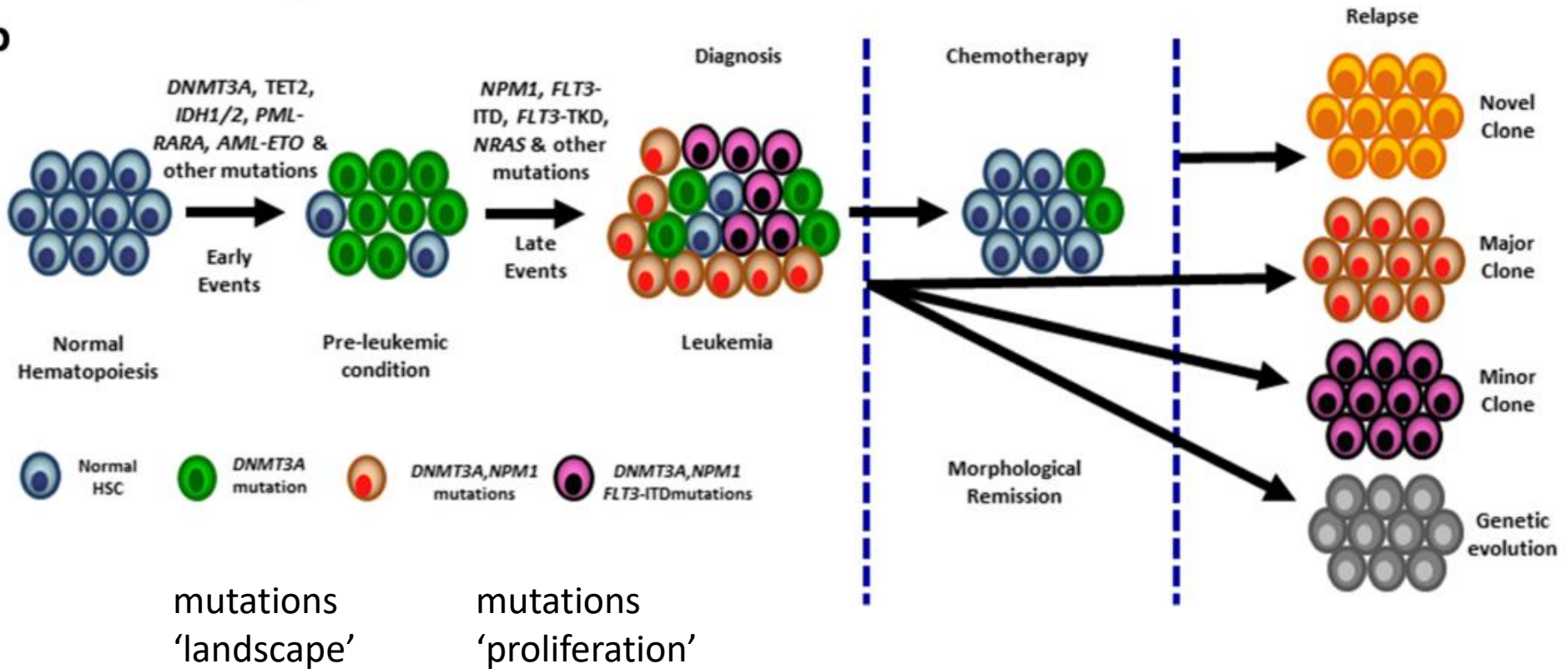
PASSENGER mutations : random events preexisted in HSC – lacking functional consequences

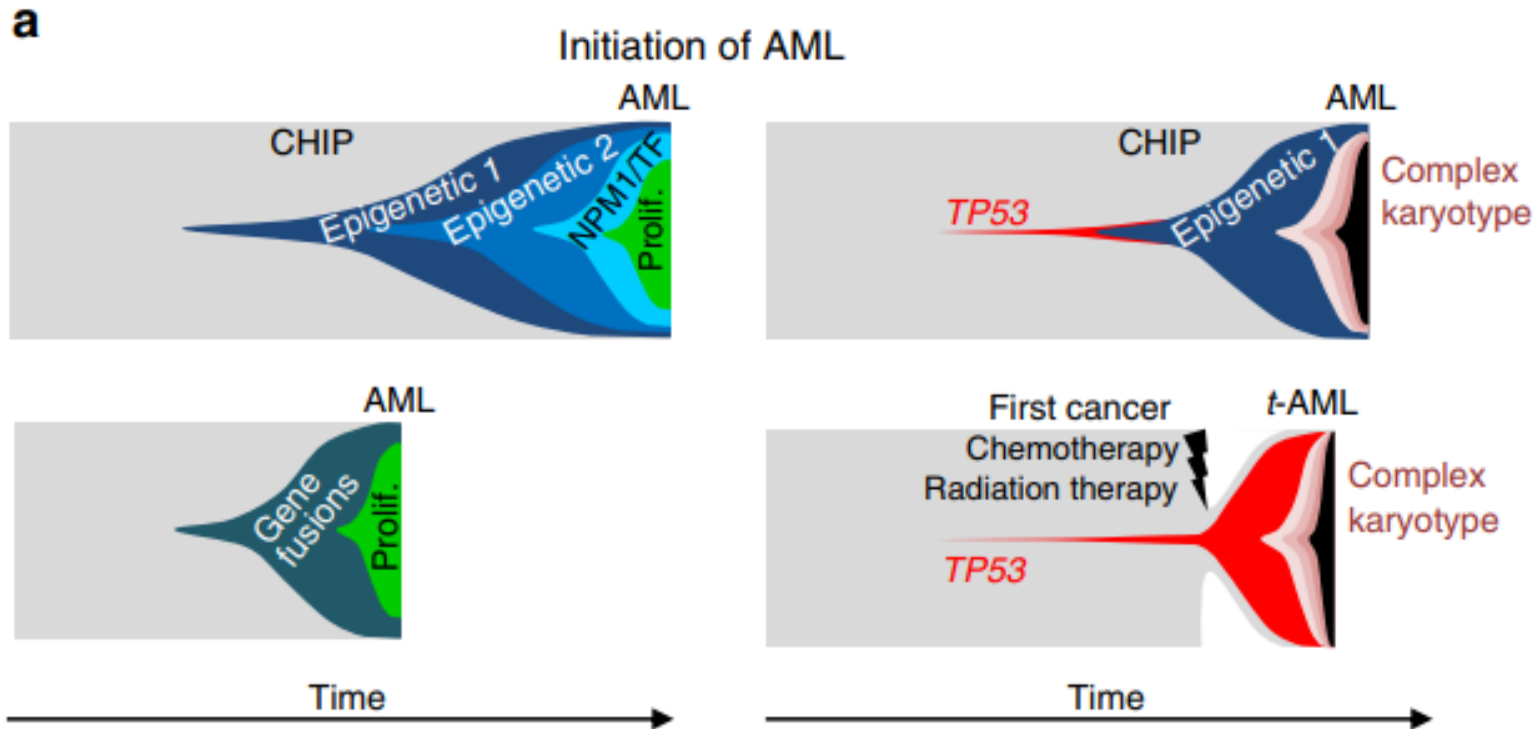
Acquisition of the **DRIVER mutation** (cancer initiating mutation) -> **growth advantage**

AML = multistep clonal evolutionary process

RELAPSE ?

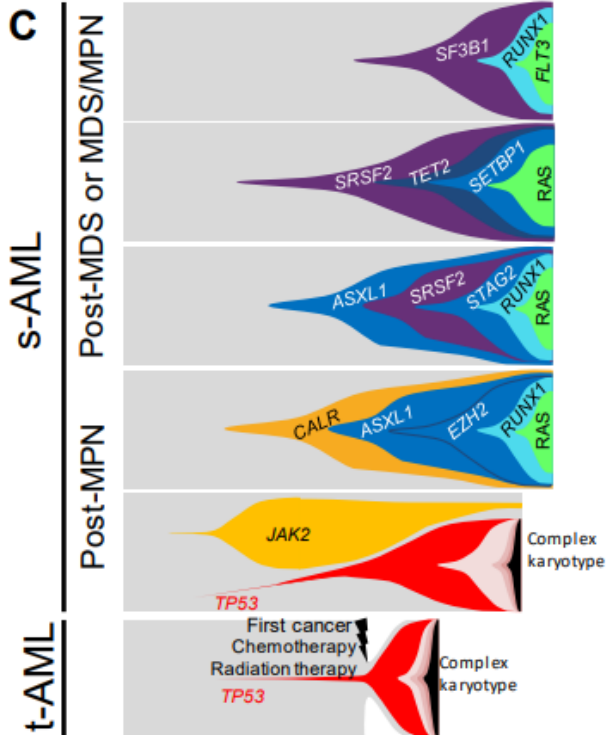
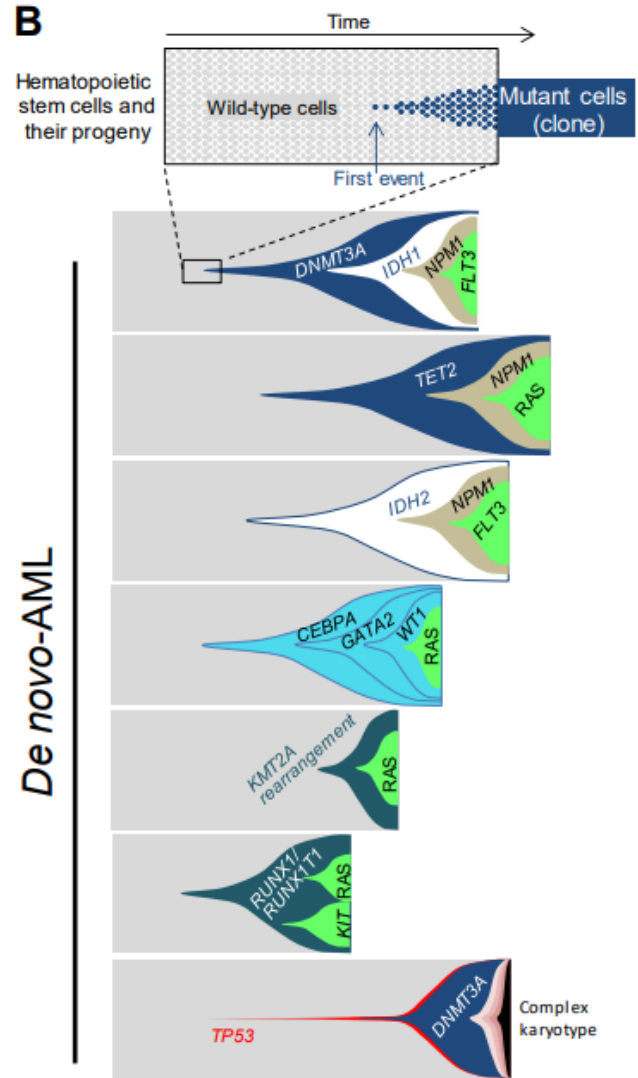
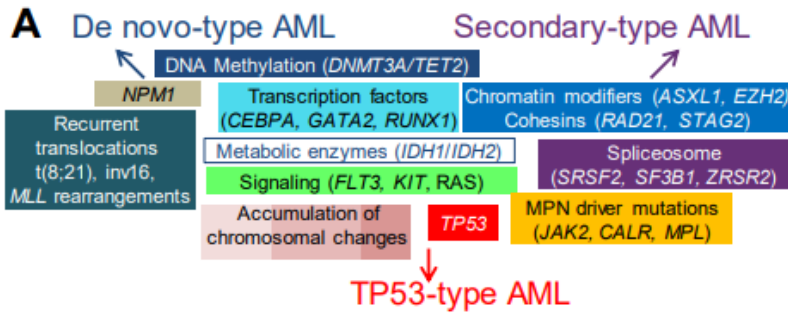
b



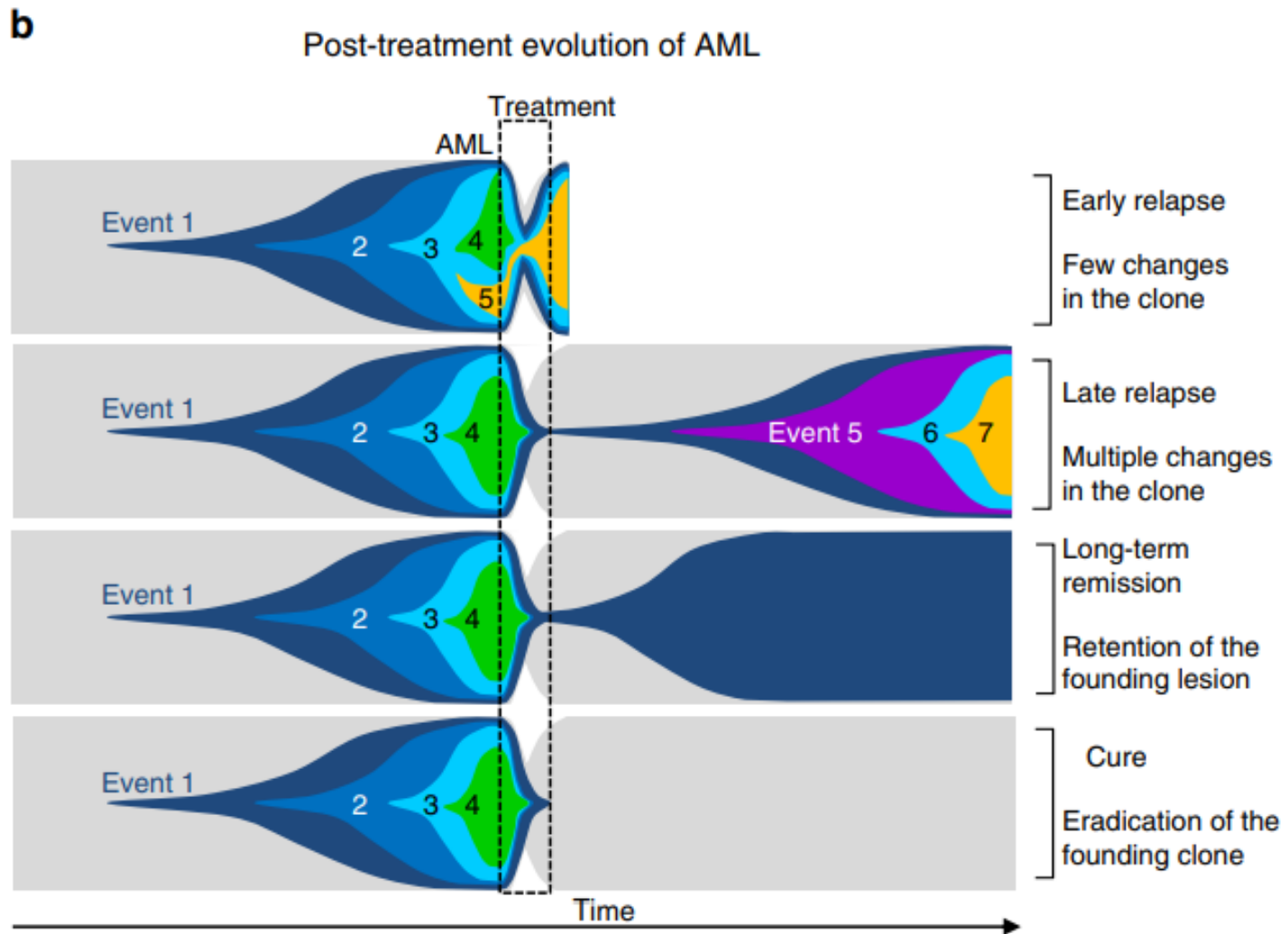


initiating pre-leukaemic lesions

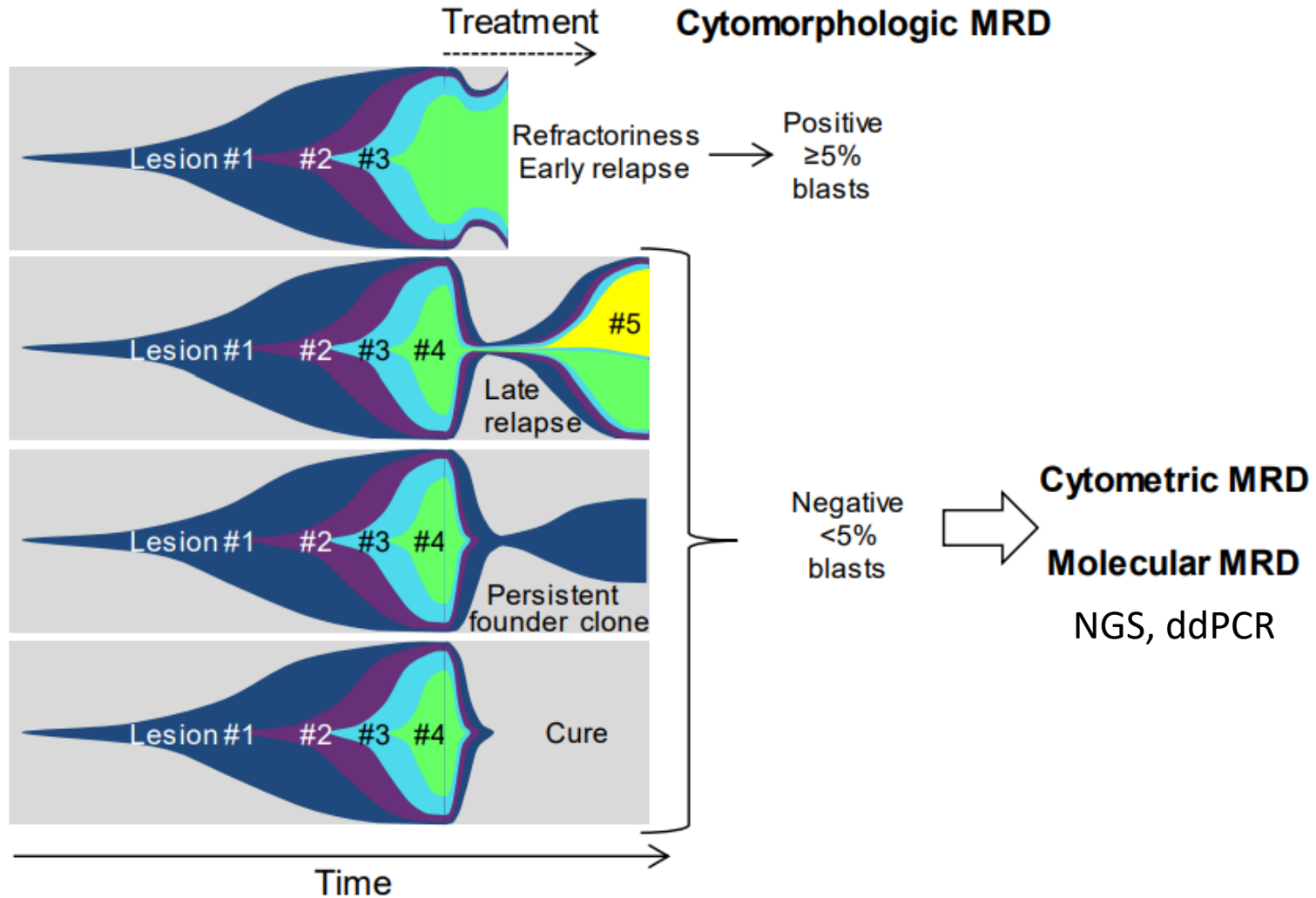
- early occurrence in the clone
- persistence at relapse
- ability to initiate multilineage haematopoietic repopulation and leukaemia *in vivo*

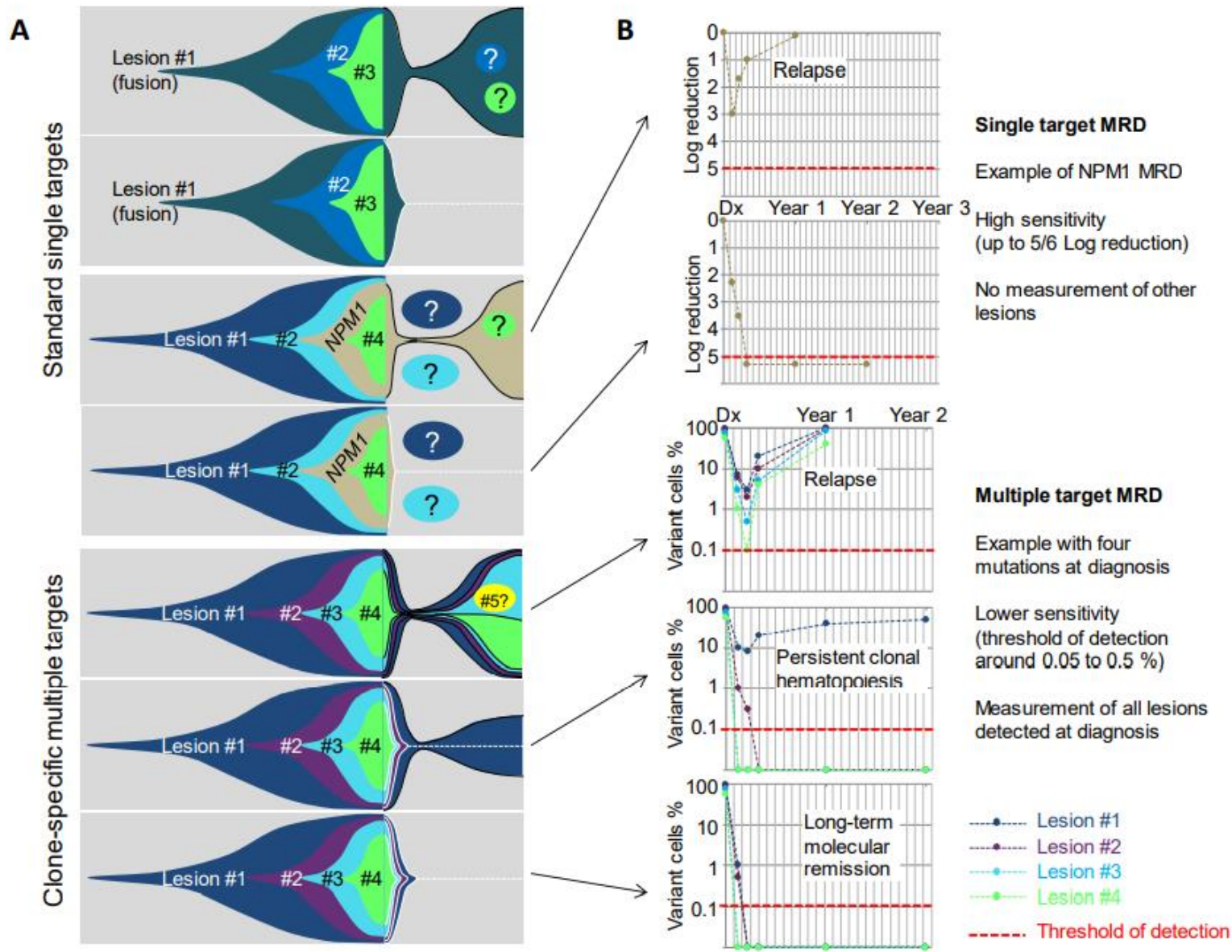


-> therapy : **relapses/MRD/** targeted therapies



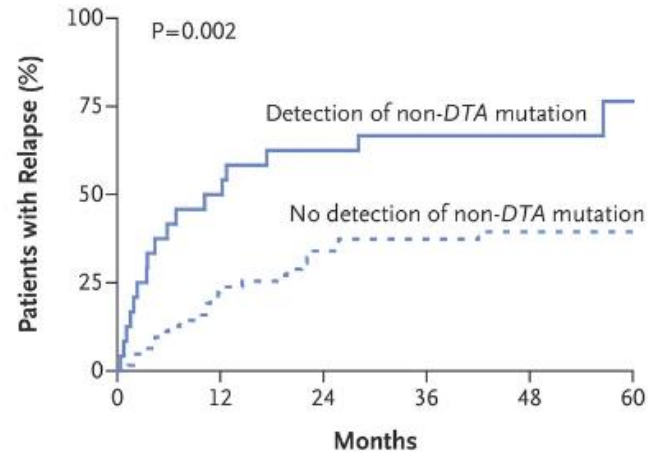
-> therapy : relapses/**MRD**/ targeted therapies





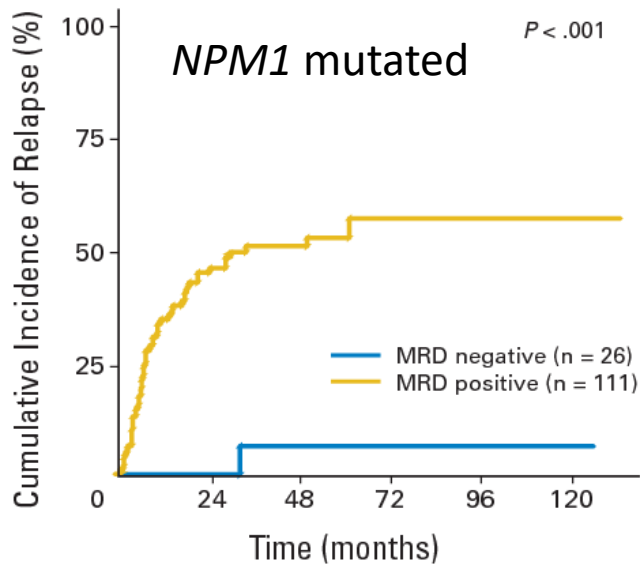
Molecular MRD associated with relapse

A Relapse among Patients with Persistent DTA Mutations



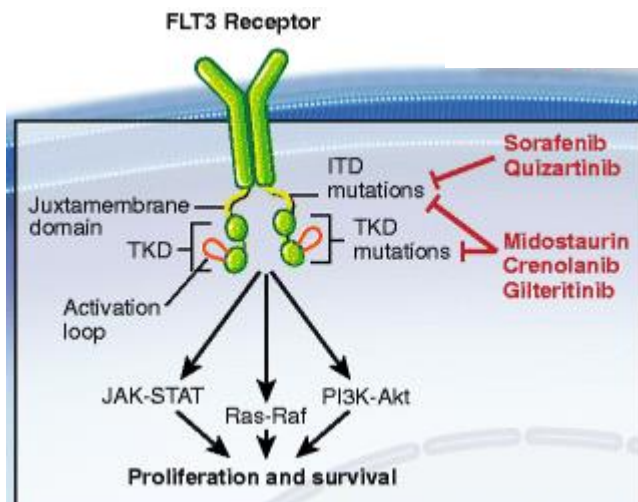
No. at Risk

Detection	24	11	8	5	4	2
No detection	63	45	33	29	22	17

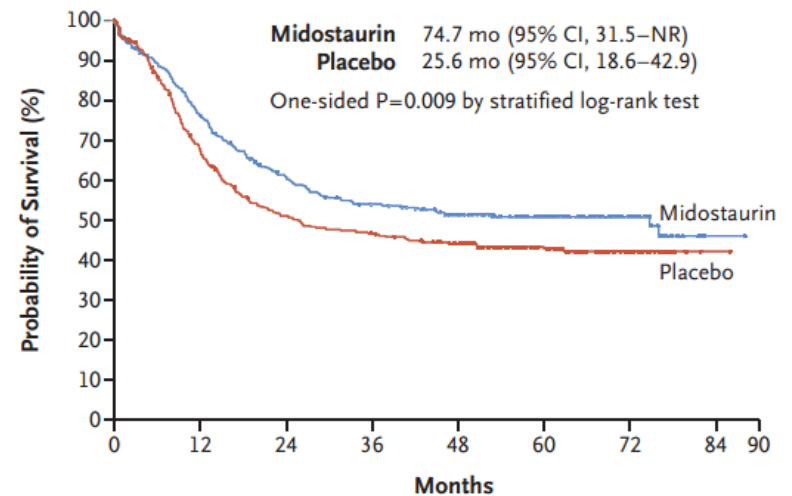


-> therapy : relapses/MRD/ **targeted therapies**

FLT3 inhibitors



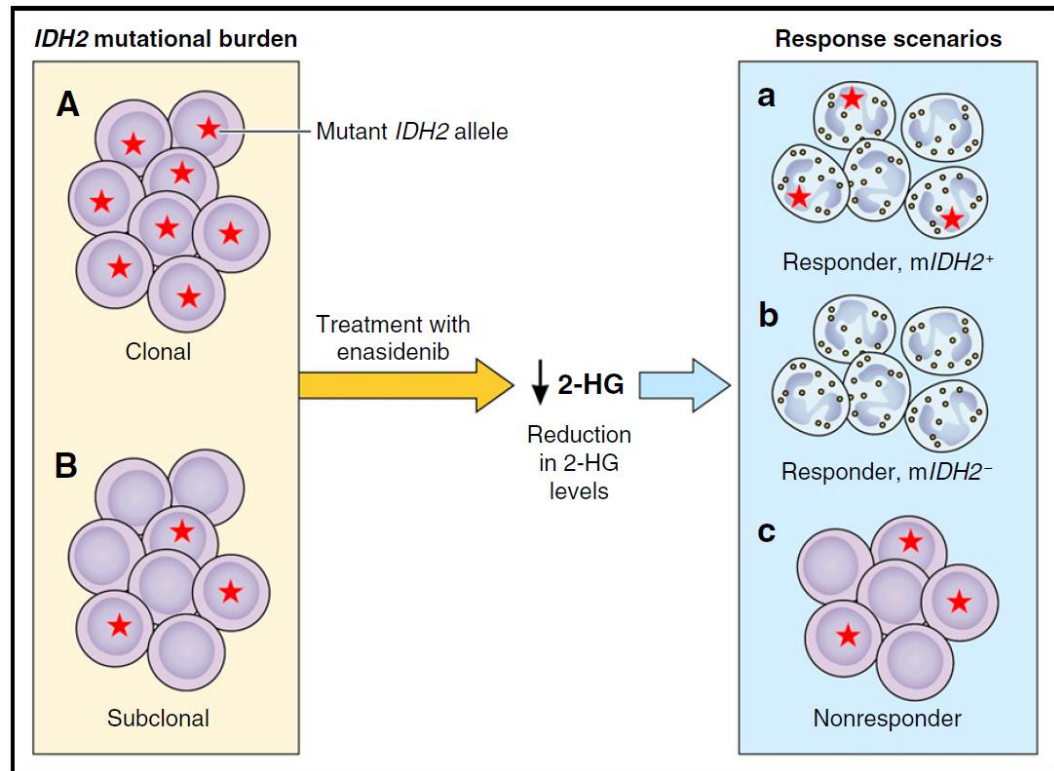
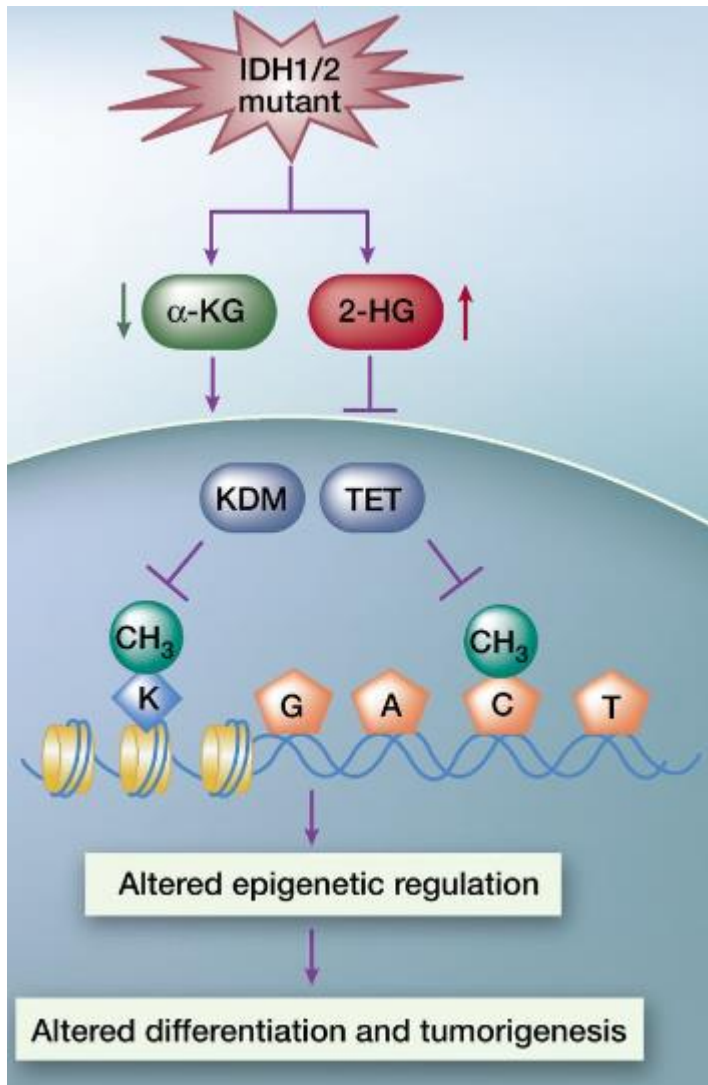
A Median Overall Survival



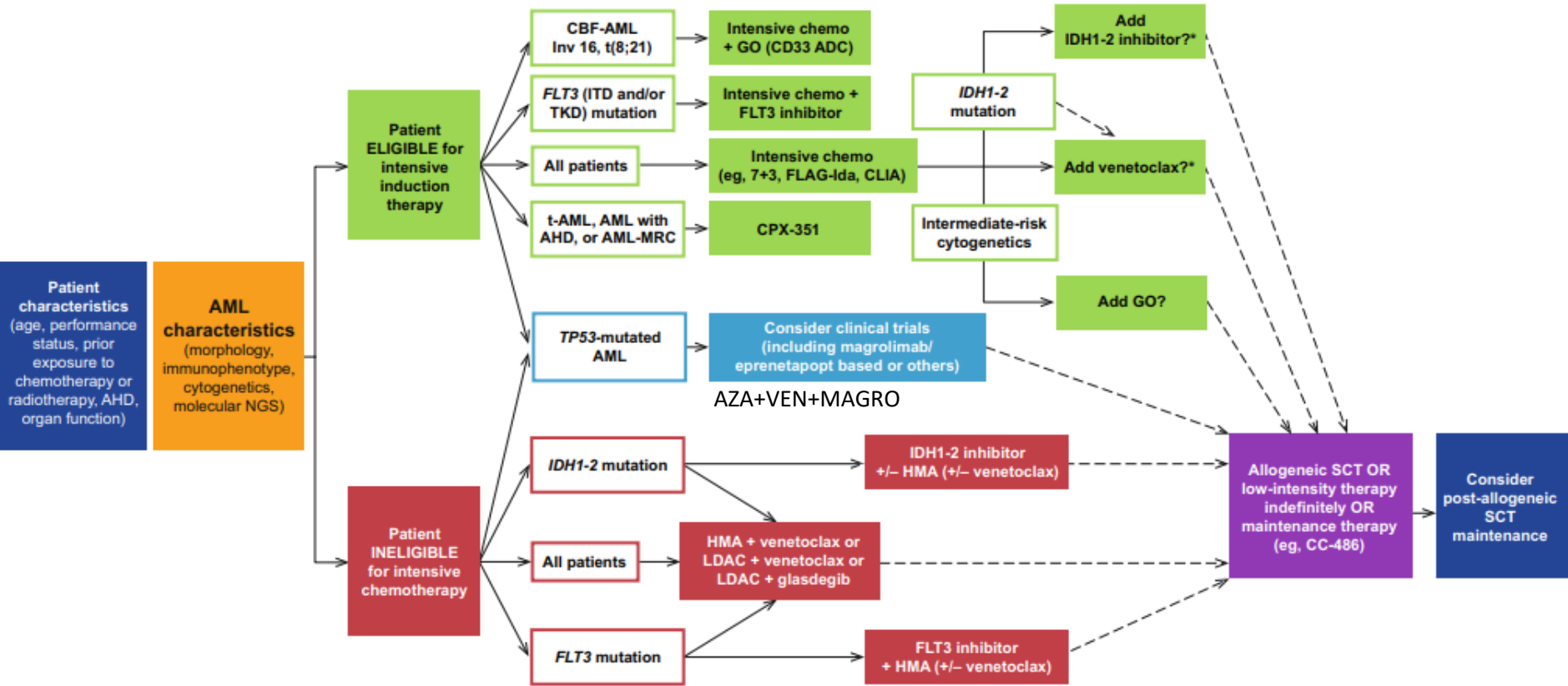
No. at Risk

	0	12	24	36	48	60	72	84	90
Midostaurin	360	269	208	181	151	97	37	1	1
Placebo	357	221	163	147	129	80	30	1	1

IDH1,2 inhibitors



Maintenance AZA oral



*Under investigation

To understand the 'preleukemic states'

* CHIP/CHOP

Clonal Hematopoiesis : a population of blood/bone marrow cells that share an acquired mutation

CHIP : Clonal Hematopoiesis of Indeterminate Potential

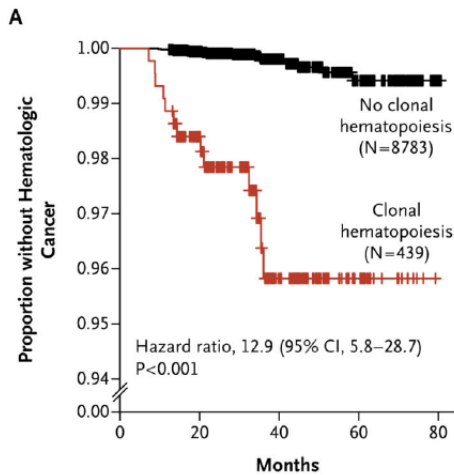
Somatic mutations associated with AML/MDS in healthy subjects

Minimal VAF of 2%

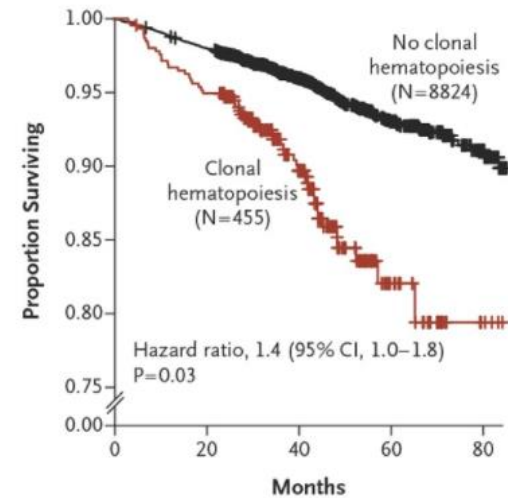
Table 1. Mutations observed in blood of healthy older persons, separated by frequency of detection of variants

Common (>50) variants, n		Less common (10-49) variants, n		Uncommon (5-9) variants, n*	
<i>DNMT3A</i>	403	<i>TP53</i>	33	<i>GNAS</i>	8
<i>TET2</i>	72†	<i>JAK2</i>	31	<i>BRCC3</i>	6
<i>ASXL1</i>	62†	<i>SF3B1</i>	27	<i>CREBBP</i>	6
		<i>GNB1</i>	22	<i>NRAS</i>	6
		<i>CBL</i>	12	<i>RAD21</i>	6
		<i>SRSF2</i>	11	<i>SETDB1</i>	6
		<i>PPM1D</i>	†	<i>U2AF1</i>	5
				<i>SETD2</i>	5

Low risk of transformation to myeloid malignancies

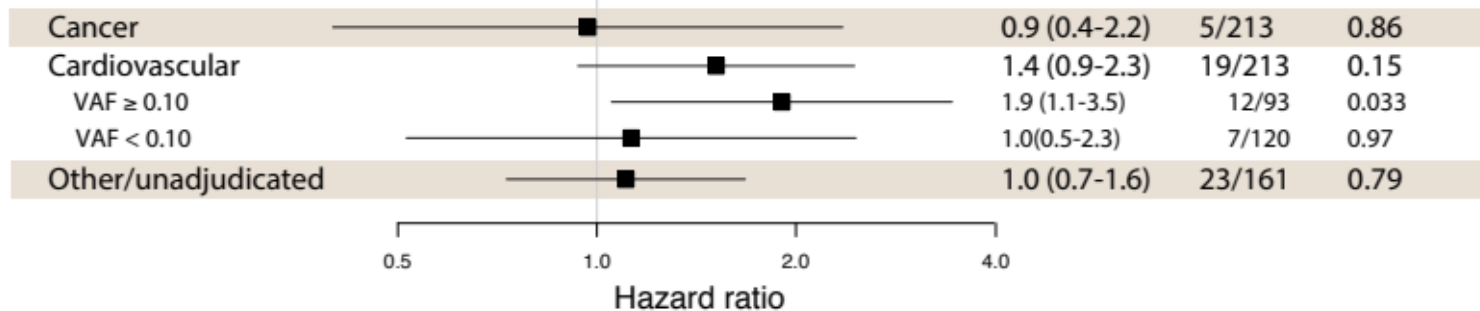


0,5-1% per year



Cause specific mortality

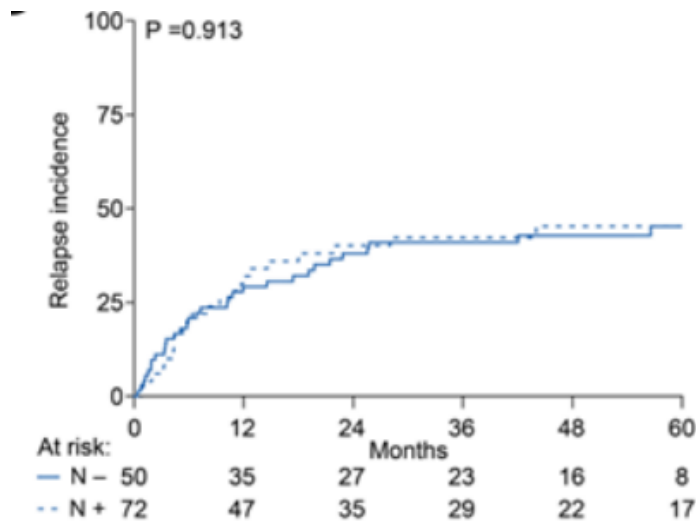
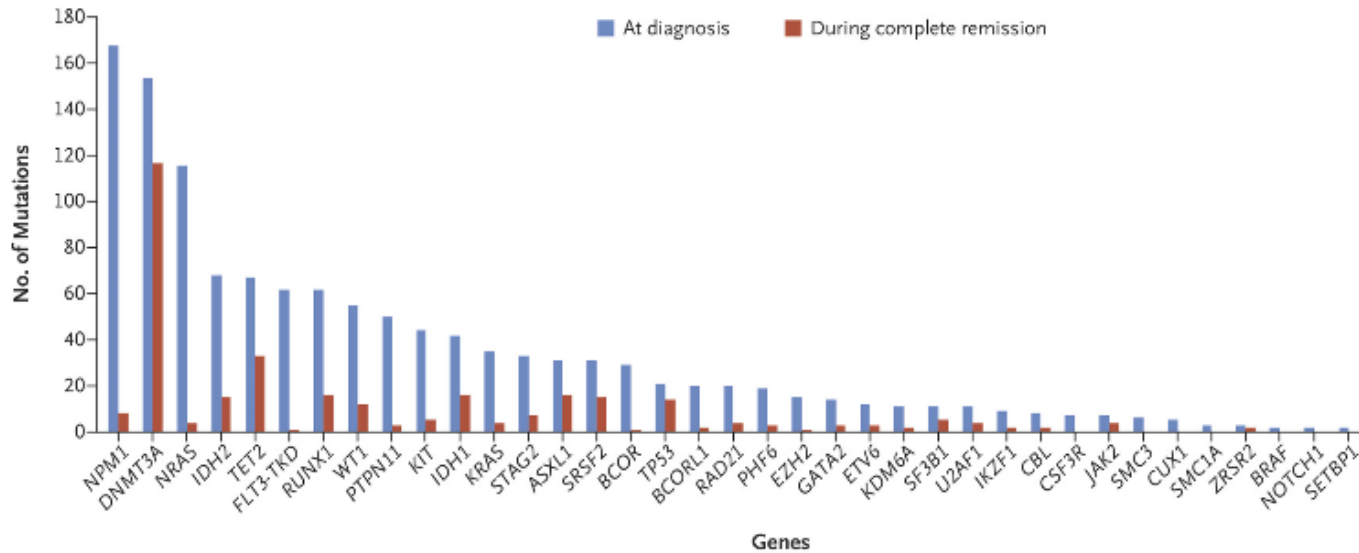
n=4,775



coronary heart disaes, early onset myocardial infarction, heart failure, ischemic stroke

Can persist in AML in remission (DNMT3A, TET2...)

A Detection of Mutations at Diagnosis and during Complete Remission



persistence of DTA mutation was not associated with relapse

CHOP : Clonal Hematopoiesis with Oncogenic Potential

disease related/specific lesion that trigger differentiation and/or proliferation

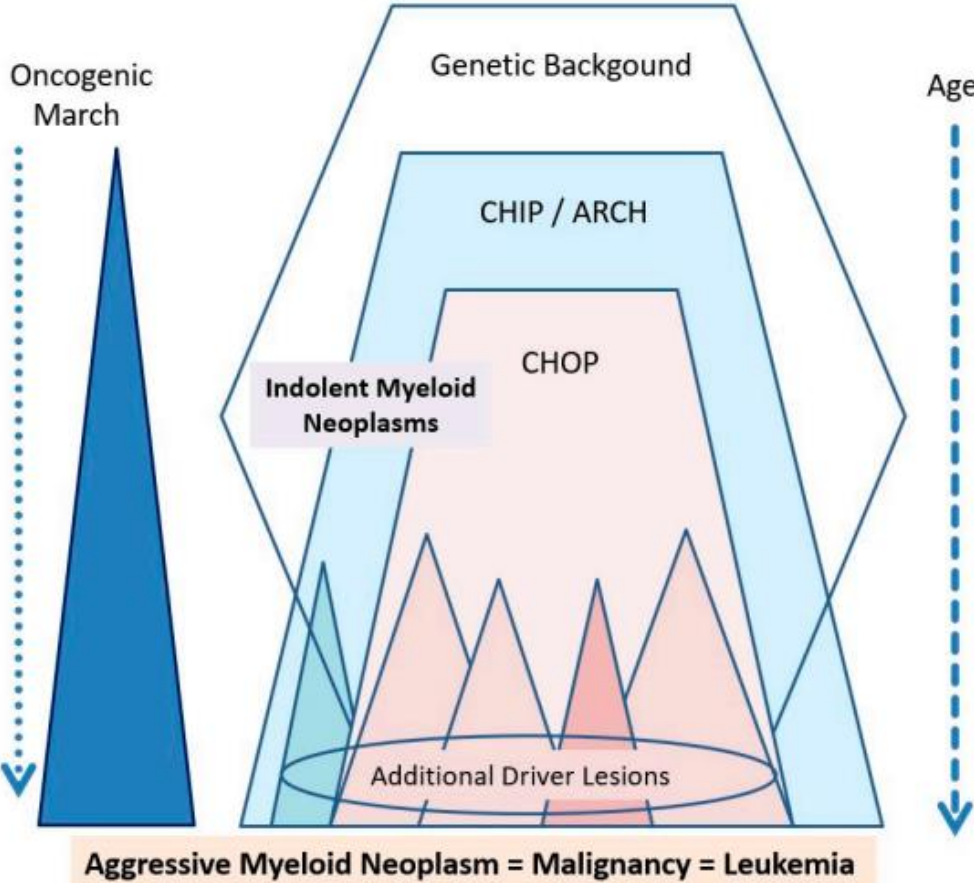
high risk of transformation to myeloid malignancies

indicate adverse risk if persistent in CR ?

Table 3. Somatic mutations producing clonal hematopoiesis of oncogenic potential (CHOP).

Mutation	Effects of the Mutant on Clonal Cells			Affected
	Differentiation	Proliferation	Oncogenesis	Myeloid Neoplasm
<i>BCR-ABL1</i> _{p210}	+	+	+*	Ph+ CML
<i>JAK2</i> V617F	+	+/-	-	MPN
<i>CALR</i> mutations	+	+/-	-	MPN
<i>MPL</i> mutations	++	+/-	-	
<i>KIT</i> D816V	++	+/-	-	ISM and AdvSM
<i>FIP1L1-PDGFR</i> A	+	+/-	-	CEL, MPN-eo
<i>RUNX1- RUNX1T1</i>	+/-	++	+	AML
<i>CBFβ-MYH11</i>	+/-	++	+	AML
<i>FLT3 ITD</i> mutations	+/-	+	+/-	AML
<i>NPM1</i> mutations	-	++	+/-	AML
<i>KRAS, HRAS</i> mutations	-	++	+	AML
<i>TP53</i> mutations	-	+	+	MPN, CMML, AML

Model of progression



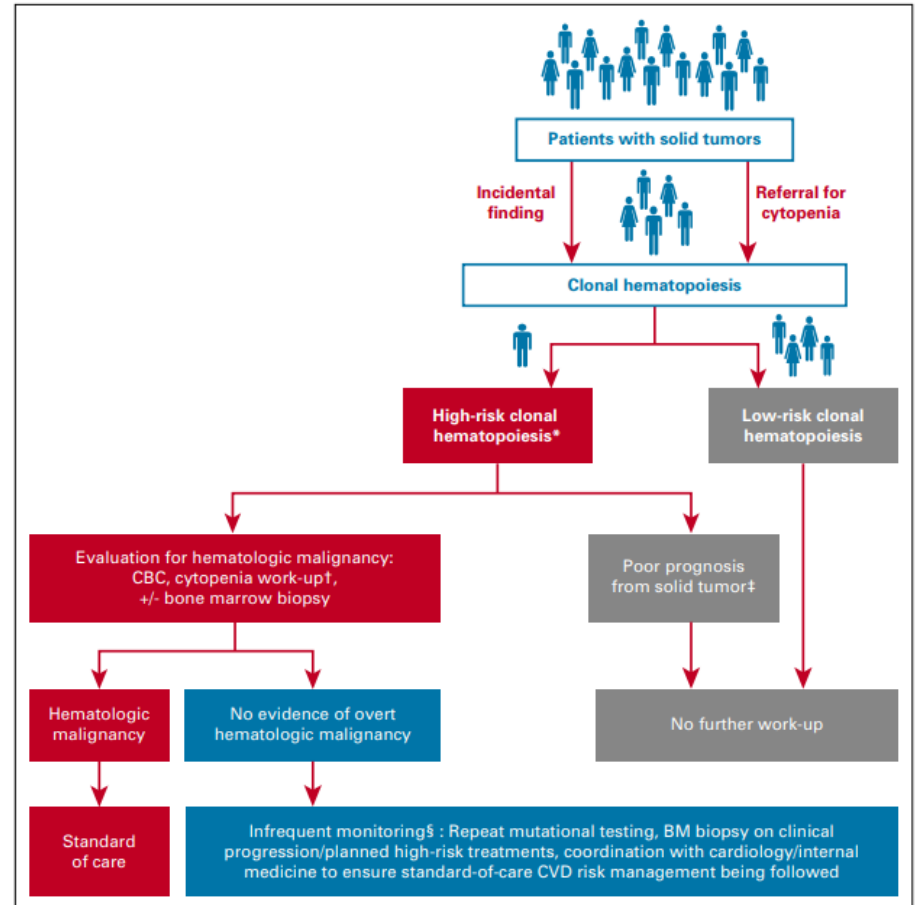
How to manage CHIP ? CHOP ?

Blood count 1x/6 months

Bone marrow exam if cytopenia

Repeat NGS to follow clonal burden evolution ?

Cardiovascular follow-up



* Germlines mutations

Table 17. Classification of myeloid neoplasms with germ line predisposition

Myeloid neoplasm classification

Myeloid neoplasms with germ line predisposition without a preexisting disorder or organ dysfunction

AML with germ line *CEBPA* mutation

Myeloid neoplasms with germ line *DDX41* mutation*

Myeloid neoplasms with germ line predisposition and preexisting platelet disorders

Myeloid neoplasms with germ line *RUNX1* mutation*

Myeloid neoplasms with germ line *ANKRD26* mutation*

Myeloid neoplasms with germ line *ETV6* mutation*

Myeloid neoplasms with germ line predisposition and other organ dysfunction

Myeloid neoplasms with germ line *GATA2* mutation

Myeloid neoplasms associated with BM failure syndromes (anémie de Fanconi, Shwachman-Diamond, ...)

Myeloid neoplasms associated with telomere biology disorders

JMML associated with neurofibromatosis, Noonan syndrome or

Noonan syndrome-like disorders

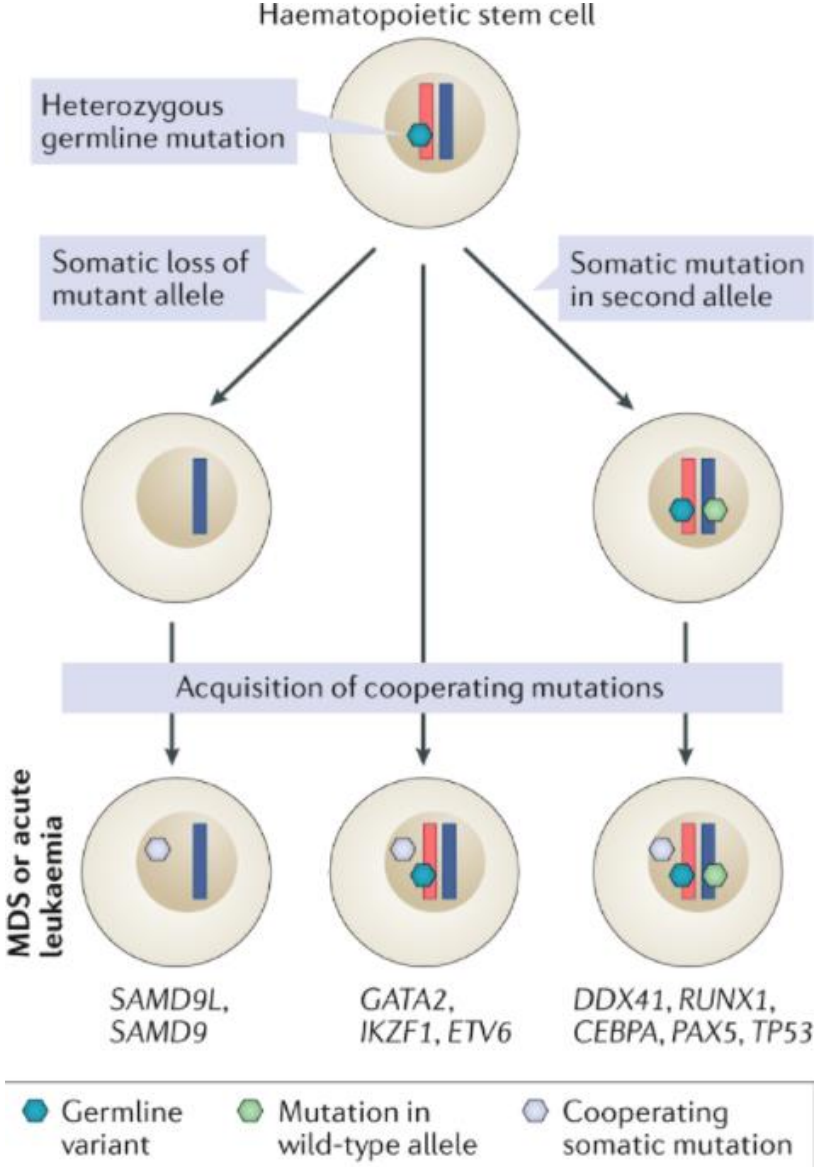
Myeloid neoplasms associated with Down syndrome*

*Lymphoid neoplasms also reported.

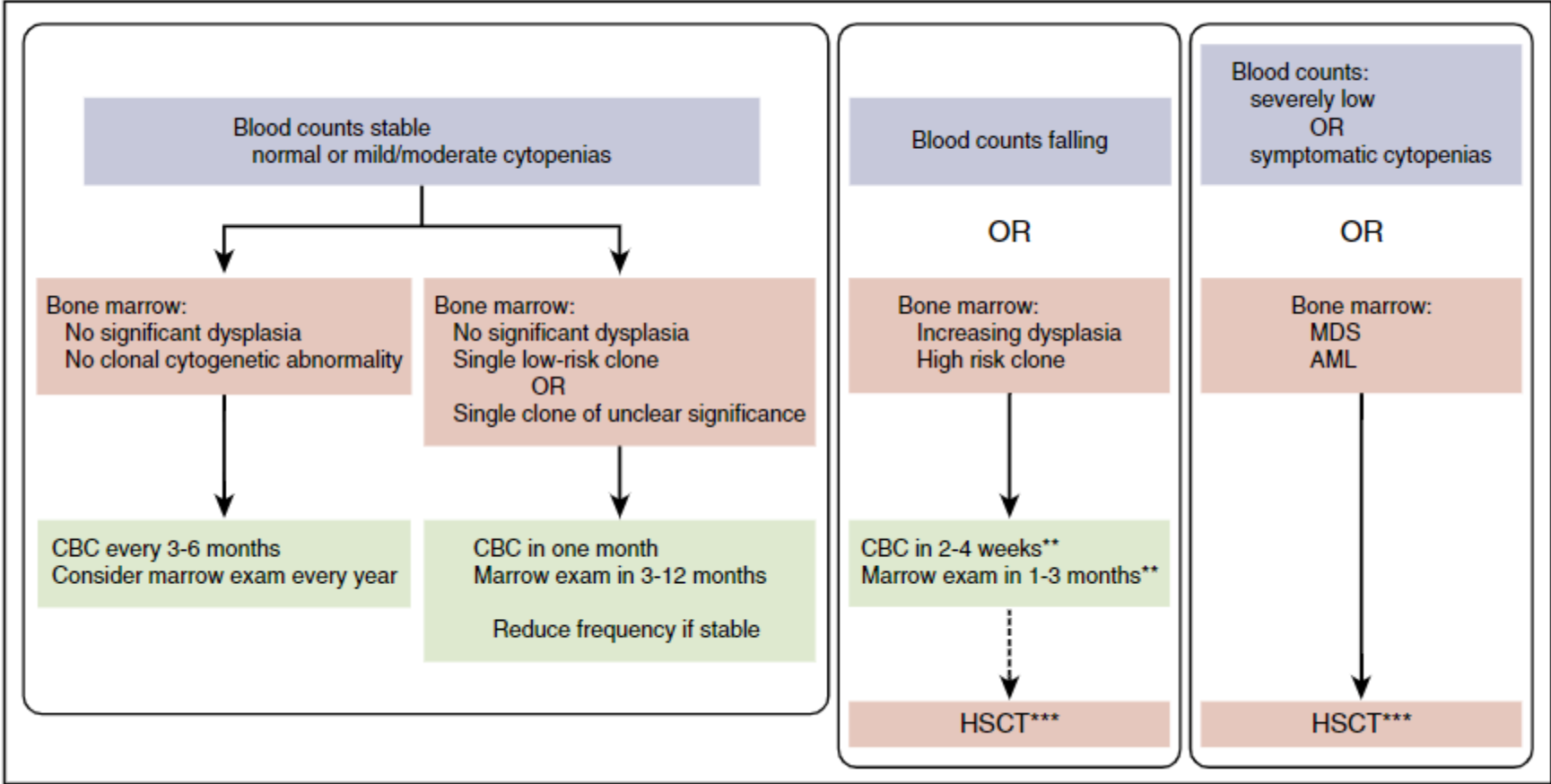
Polymorphismes (KMT5B, HLA, RAVR2, AK4)

! only a minority will represent suspicious anamnesis

Model of disease progression



How to manage germline predisposition to AML ?



Conclusions



To understand the molecular mechanisms of AML

-> therapy : relapses/MRD/ targeted therapies

To understand the 'preleukemic states'

- * CHIP/CHOP
- * Germlines mutations

A microscopic view of plant tissue cells, likely from an onion skin, stained with a purple dye (likely iodine) and a blue dye (likely methylene blue). The cells are roughly rectangular and arranged in a brick-like pattern. The purple staining highlights the nuclei and other internal organelles, while the blue staining highlights the cell walls. A white rectangular box is superimposed over the center of the image, containing the text "Thank you for your attention" in a bold, red, sans-serif font.

Thank you for your attention