



EHA-GBMTA-AHA  
Hematology Tutorial:  
**Diagnostic work-up in acute  
myeloid leukemia**

Session: Acute Myeloid  
Leukemia

20<sup>th</sup> October 2024, Margarita Guenova



# Disclosure

## Prof. Margarita Guenova, MD, PhD

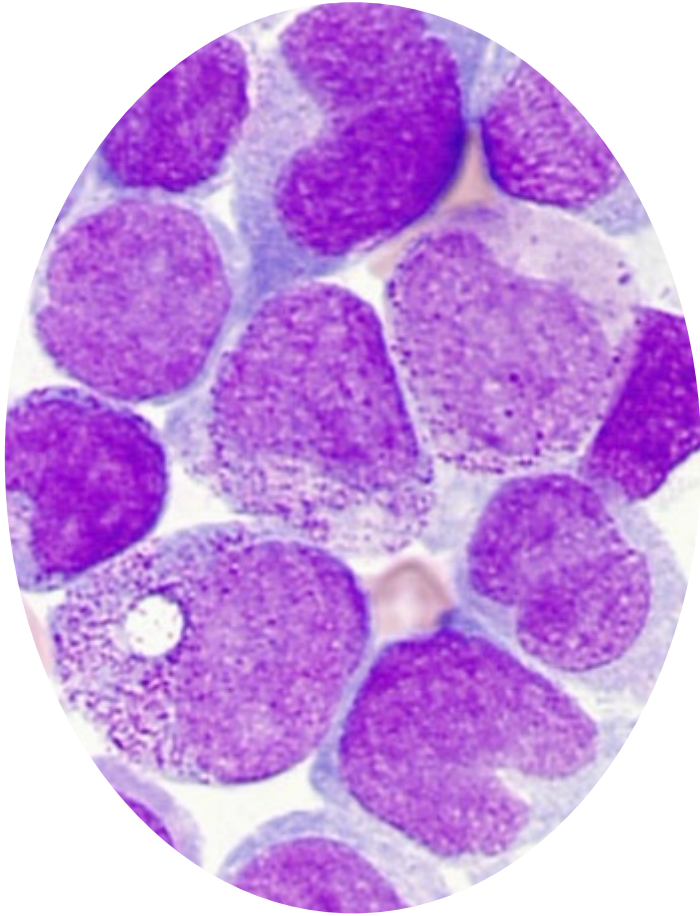
Company	Relationship
Novartis	Speakers' Bureau
AstraZeneca	Speakers' Bureau, Scientific advisory board
Abbvie	Speakers' Bureau
Swixx	Speakers' Bureau, Scientific advisory board
SOBI	Speakers' Bureau, Scientific advisory board

# Learning objectives

## **After attending this presentation, you will be able to:**

1. Understand which tests need to be performed for the diagnosis of acute myeloid leukemia.
2. Recognize how morphology supplemented by immunophenotyping can provide clues to specific cytogenetic/molecular anomalies and the diagnosis of specific AML classification categories.
3. Discuss current classification systems.

# Acute myeloid leukemia



Acute myeloid leukemia (AML) is a rapidly progressing myeloid **neoplasm** characterized by the clonal expansion of immature myeloid-derived cells, known as **myeloid blasts**, in the peripheral blood and bone marrow.

This expansion results in ineffective erythropoiesis and megakaryopoiesis, clinically manifesting as relatively **rapid bone marrow failure** compared to chronic and indolent leukemias. This leads to inadequate production of red blood cells and platelets.

# Classifications of AML

**FAB 1976**

**WHO 2001 HAEM3**

**WHO 2008 HAEM4**

**WHO 2016 HAEM4R**

**WHO 2022 HAEM5**

**ICC 2022**

A story starting with 200 AL cases, 7 hematologists, 8 months of correspondence and 2 days in Paris.

**Acute myeloid leukaemia with defining genetic abnormalities**

Acute promyelocytic leukaemia with PML::RARA fusion		
Acute myeloid leukaemia with RUNX1::RUNX1T1 fusion	Acute promyelocytic leukemia with t(15;17)(q24.1;q21.2)/PML::RARA	≥ 10%
Acute myeloid leukaemia with CBFB::MYH11 fusion	APL with other RARA rearrangements*	≥ 10%
Acute myeloid leukaemia with KMT2A rearrangement	AML with t(8;21)(q22;q22.1)/RUNX1::RUNX1T1	≥ 10%
	AML with inv(16)(p13.1q22) or t(16;16)(p13.1;q22)/CBFB::MYH11	≥ 10%
	AML with t(9;11)(p21.3;q23.3)/MLLT3::KMT2A	≥ 10%
	AML with other KMT2A rearrangements†	≥ 10%
Acute myeloid leukaemia with DEK::NUP214 fusion	AML with t(6;9)(p22.3;q34.1)/DEK::NUP214	≥ 10%
	AML with inv(3)or t(3;3)(q21.3;q26.2)/GATA2; MECOM(EVI1)	≥ 10%
Acute myeloid leukaemia with MECOM rearrangement	AML with other MECOM rearrangements‡	≥ 10%
	AML with t(9;22)(q34.1;q11.2)/BCR::ABL1§	≥ 20%
	AML with mutated NPM1	≥ 10%
Acute myeloid leukaemia with BCR::ABL1 fusion	AML with in-frame bZIP CEBPA mutations	≥ 10%
Acute myeloid leukaemia with NPM1 mutation	AML with myelodysplasia-related cytogenetic abnormalities	≥ 10%*
Acute myeloid leukaemia with CEBPA mutation	MDS/AML (10-19%) / AML (≥ 20%)	≥ 10%*
Acute myeloid leukaemia, myelodysplasia-related	AML (≥ 20%) and MDS/AML (10-19%) with myelodysplasia-related gene mutations	≥ 10%*
	AML (≥ 20%) and MDS/AML (10-19%) with mutated TP53†	≥ 10%*
Acute myeloid leukaemia with RBM15::MRTFA fusion	AML with other rare recurring translocations	≥ 10%
Acute myeloid leukaemia with NUP98 rearrangement		
AML with other defined genetic alterations		

Therapy-related\*

- prior chemotherapy, radiotherapy, immune interventions

Progressing from MDS

- MDS should be confirmed by standard diagnostics

Progressing from MDS/MPN (specify)

- MDS/MPN should be confirmed by standard diagnostics

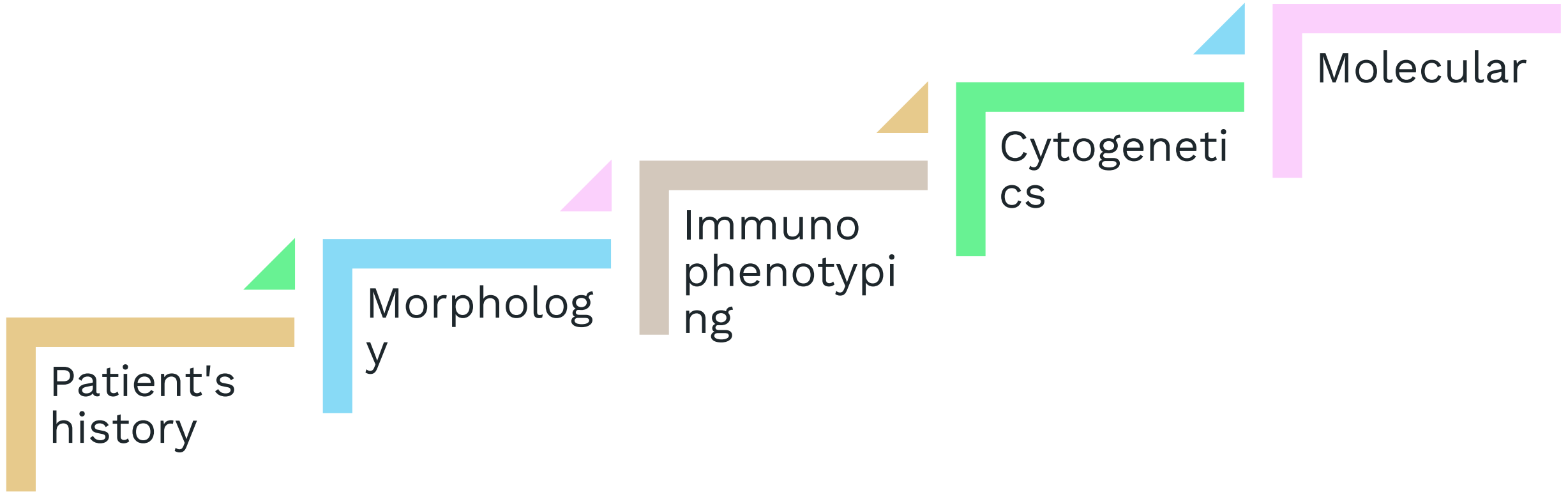
Germline predisposition

**Acute myeloid leukaemia, defined by differentiation**

**AML not otherwise specified (NOS) 10-19% (MDS/AML (AML))**

Acute myeloid leukaemia with minimal differentiation	MDS/AML, NOS	10-19%
Acute myeloid leukaemia without maturation	AML, NOS	≥ 20%

# Stairway to diagnosis



# 01

## Medical

### Demographics and medical history

- prior exposure to toxic agents
- prior malignancy
- therapy for prior malignancy

### Detailed family history

- potential germline predisposition

### Patient bleeding history

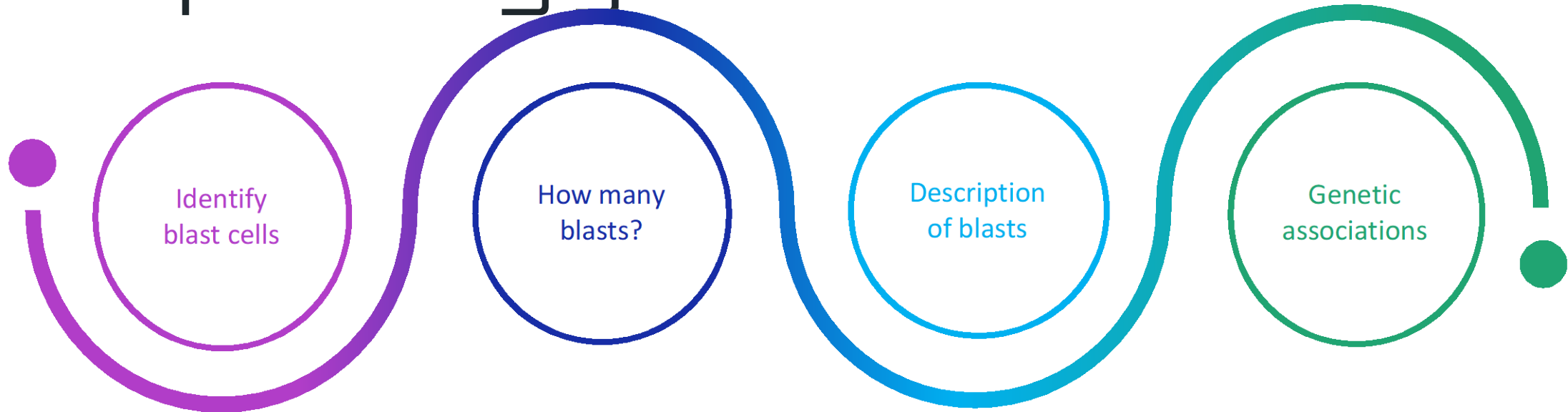
### Analysis of comorbidities





# 02

## Morphology



### MILESTONE 1.

Identification of myeloid blast-equivalents.  
Differentiation of myeloid from lymphoid blasts.

### MILESTONE 2.

Quantification of blast equivalents in bone marrow and peripheral blood

### MILESTONE 3.

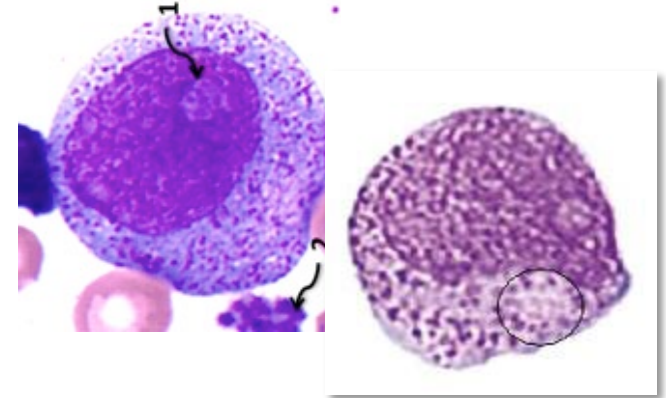
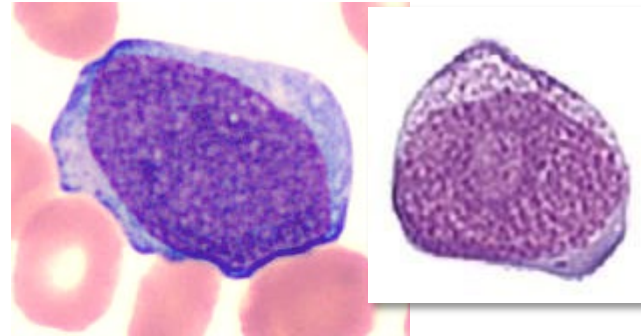
Description of blast morphology and concomitant hematopoiesis

### MILESTONE 4.

Morphological features pointing to specific genetic aberrations/nosological entities

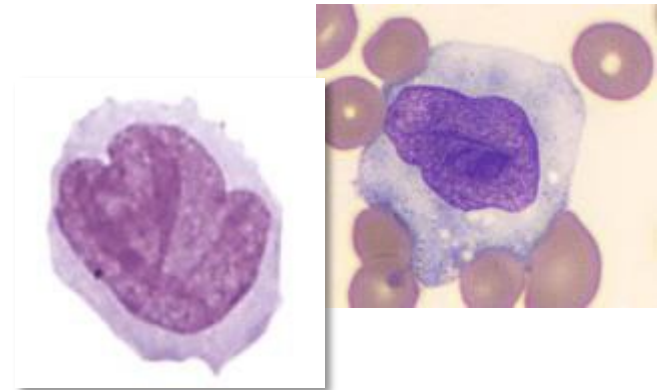
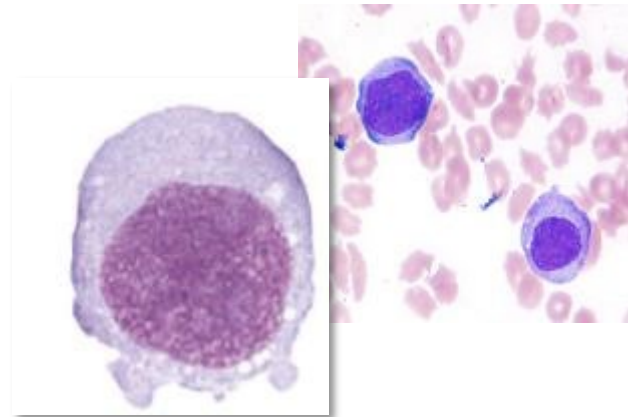
# Blast equivalents in AML

## Myeloblast & Promyelocyte



Mufti, G. J. et al. *Haematologica* 2008;93:1712-1717;  
Palmer L et al, *Int Journal Lab Hematology* 2015; 37:287-303

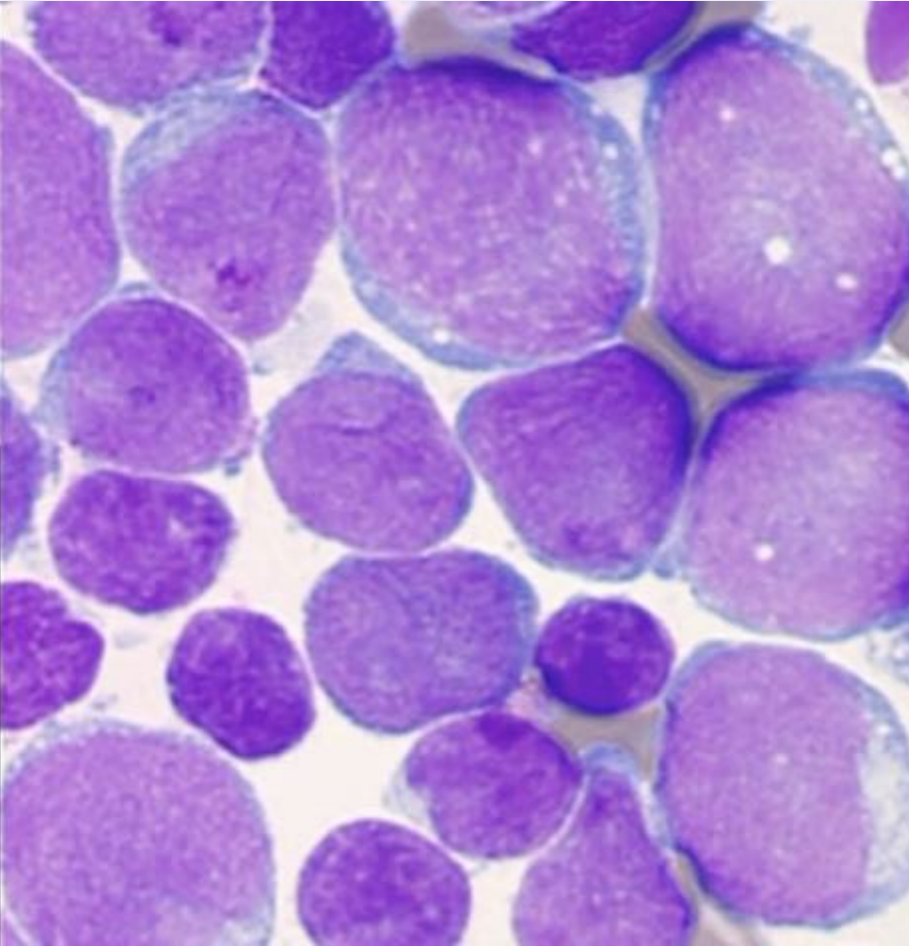
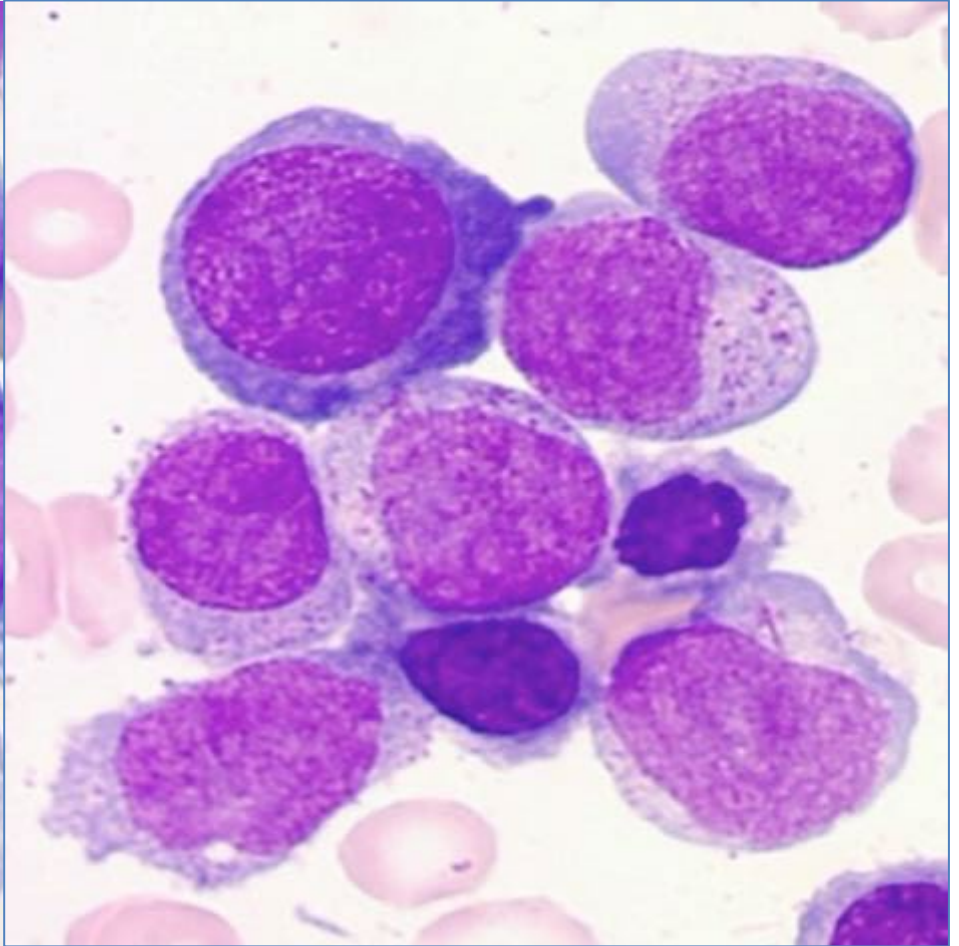
## Monoblast & Promonocyte



Goasguen et al, Morphological evaluation of monocytes and their precursors. *Haematologica*. 2009 Jul;94(7):994-7.

Arber et al The 2016 revision to the WHO classification of myeloid neoplasms and acute leukemia. *Blood*. **2016**;127(20)  
Khoury et al, The 5th edition of the WHO of Haematolymphoid Tumours: Myeloid and Histiocytic/Dendritic Neoplasms. *Leukemia*. **2022**;36(7)  
Arber et al. ICC of Myeloid Neoplasms and Acute Leukemias: integrating morphologic, clinical, and genomic data. *Blood*. **2022**; 140(11)

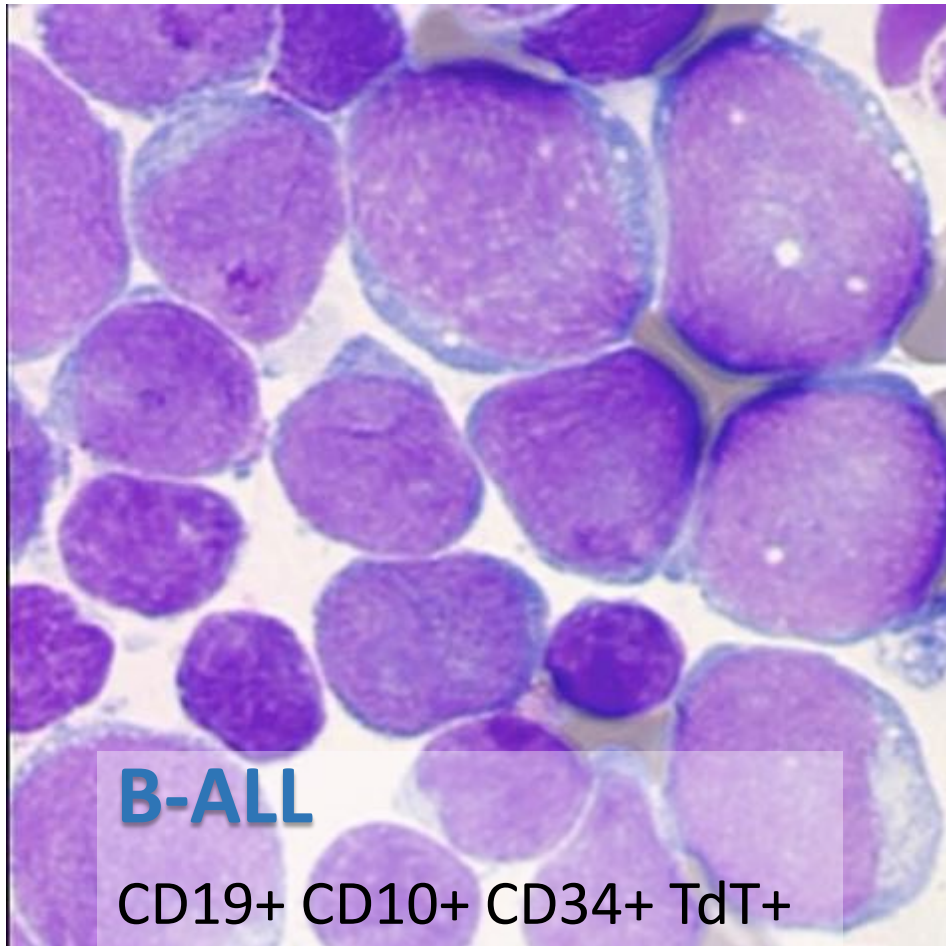
# Myeloblasts vs Lymphoblasts

	Lymphoblasts	Myeloblasts
Heterogeneity		
Cell size		
Nucleus		
Chromatin		
Nucleoli		
Cytoplasm		
Granulations		
Auer rods	Никога	Понякога, вкл. снопове-МЗ
Vacuoles	Понякога	Понякога, особено моноцитните

# Not always easy to decide

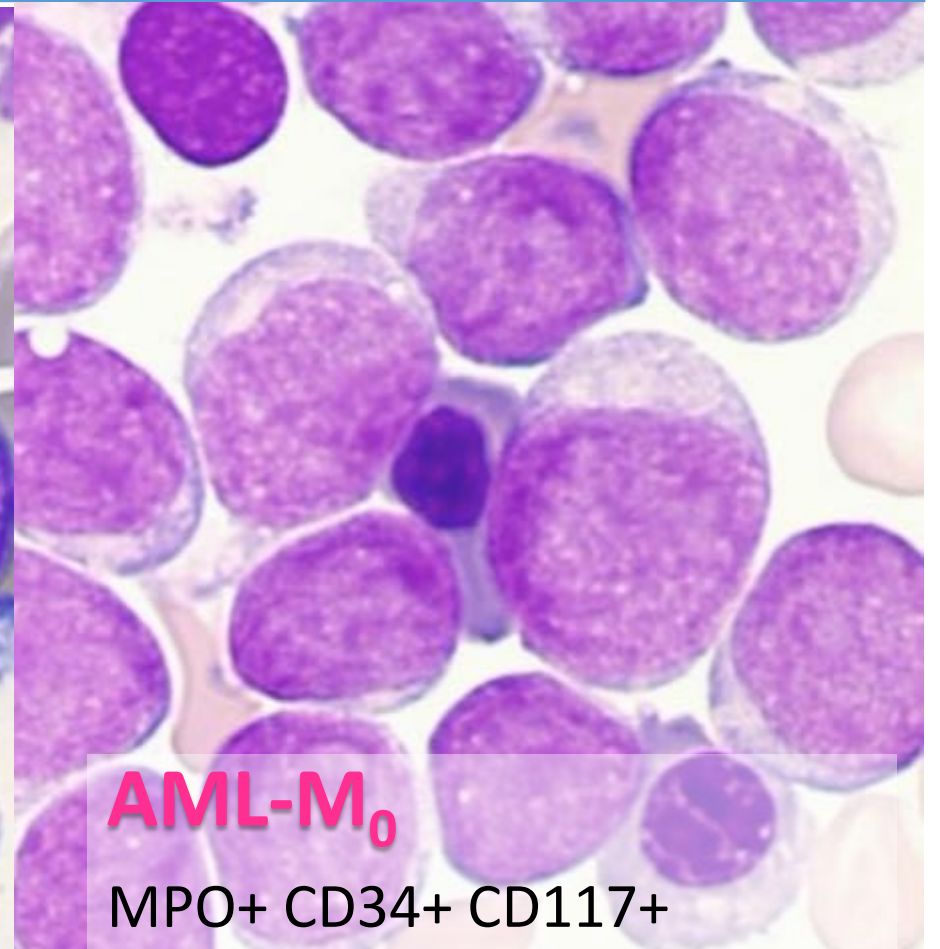
**Lymphoblasts**

**Myeloblasts**



**B-ALL**

CD19+ CD10+ CD34+ TdT+

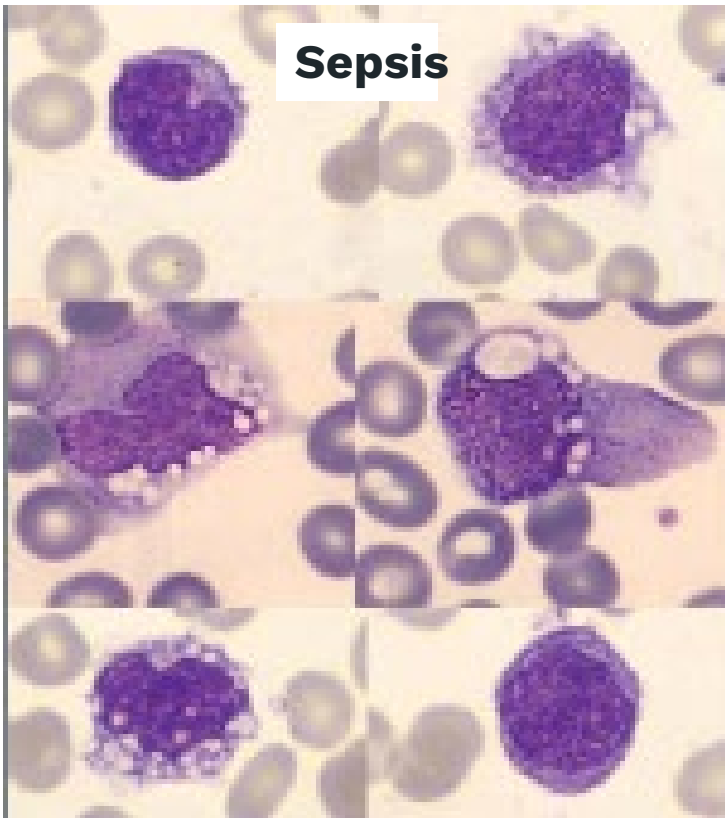


**AML-M<sub>0</sub>**

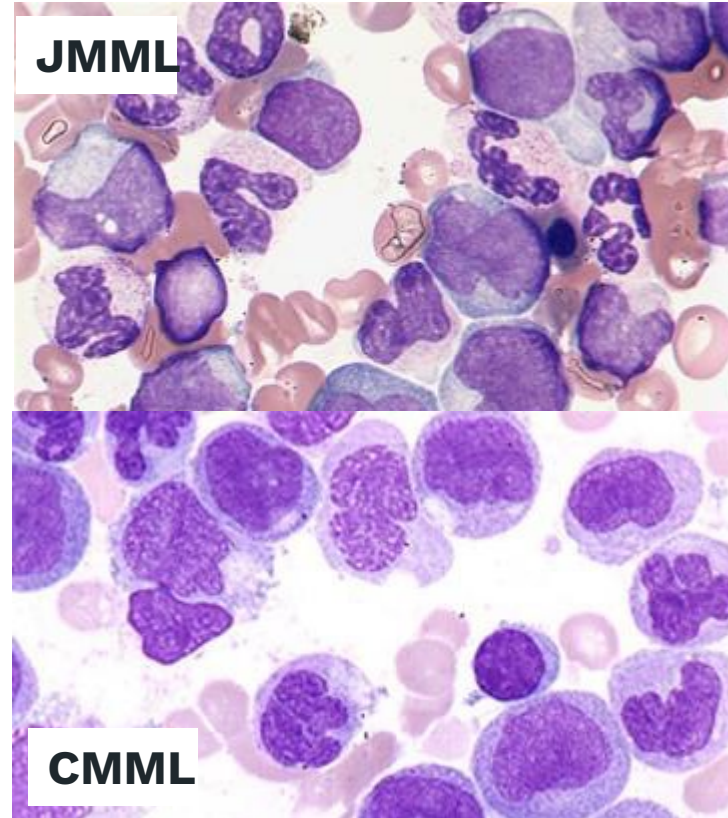
MPO+ CD34+ CD117+

# The monocytic challenge

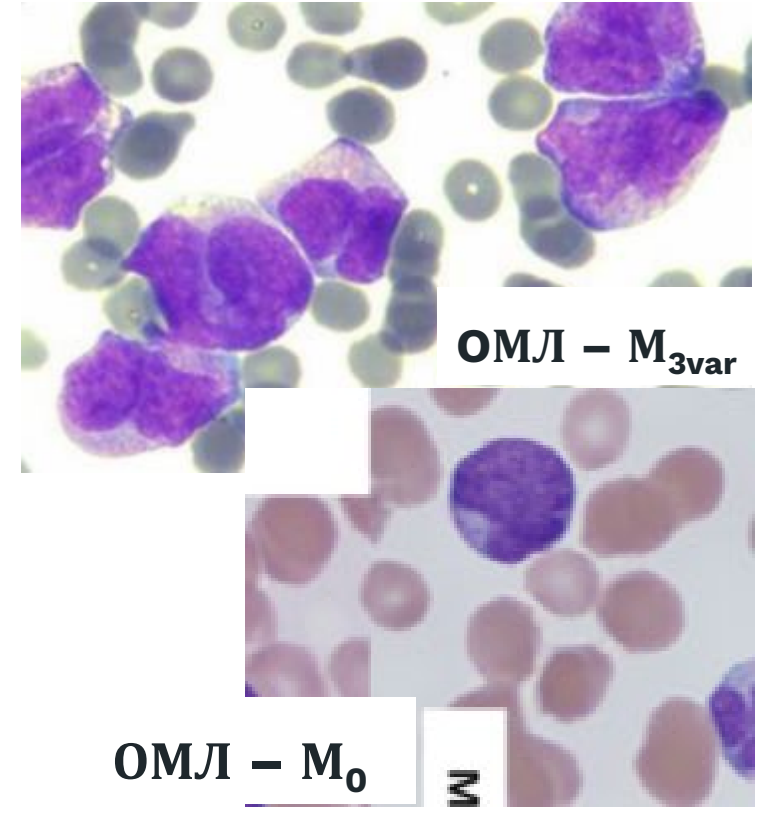
## AMoL vs reactive



## Acute vs Chronic

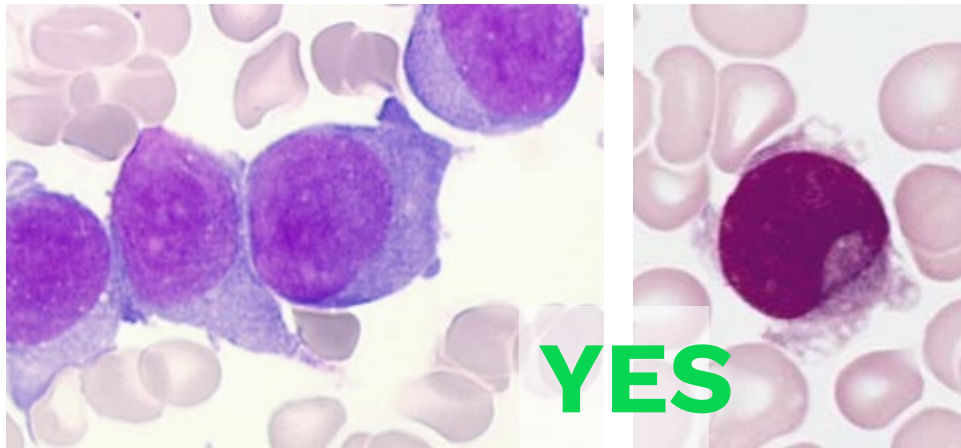


## AMoL vs other AML

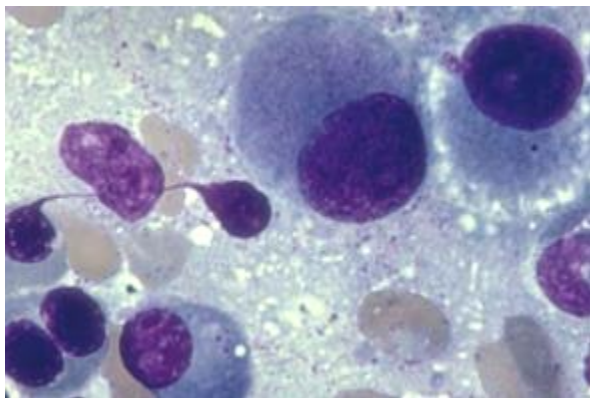


# Blast equivalents in specific AML

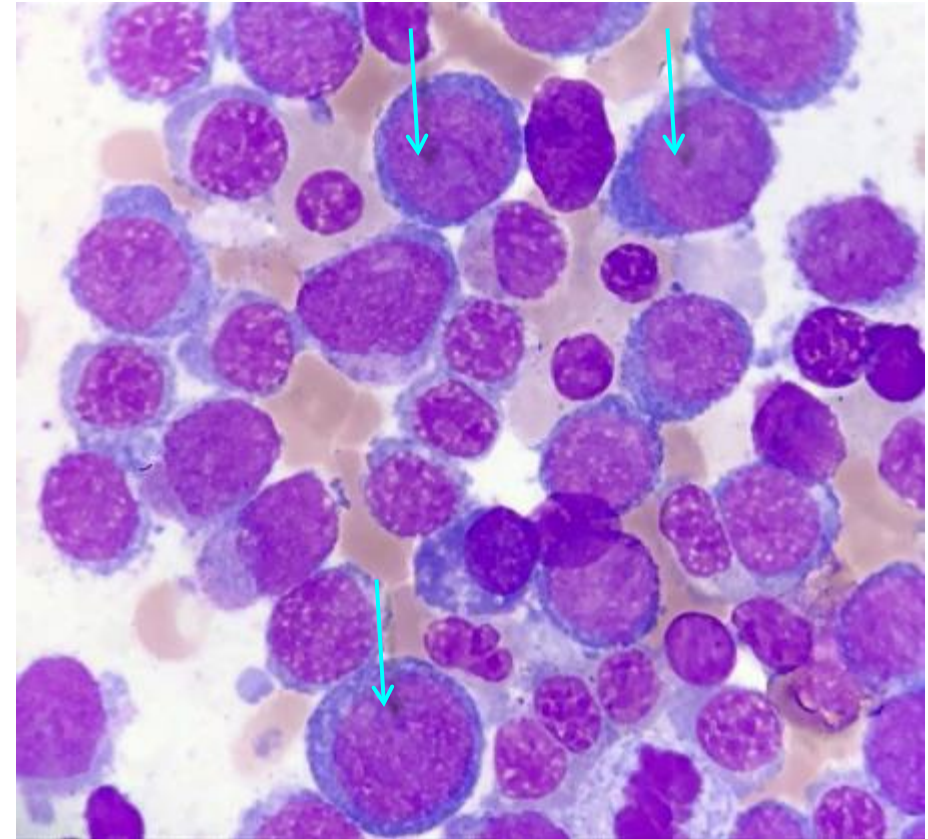
Megakaryoblasts  $\geq 20\%$



**No**  
microMe



Erythroblasts  $\geq 80\%$   
Proerythroblasts  $\geq 30\%$



ASH Image bank

A close-up photograph of a person's hand adjusting five wooden blocks on a yellow surface. The blocks are arranged in a row and spell out the word 'QUANTITY'. The first three blocks are 'Q', 'U', and 'A'. The fourth block is split vertically, with 'LI' on the left side and 'NTI' on the right side. The fifth block is also split vertically, with 'TY' on the left side and 'TY' on the right side. The hand is positioned above the blocks, with fingers resting on the top of the fourth and fifth blocks, as if they are being moved or aligned. The background is a plain, light-colored wall.

**Q U A L I T Y**  
**NTI TY**

# How many blasts are needed for AML?



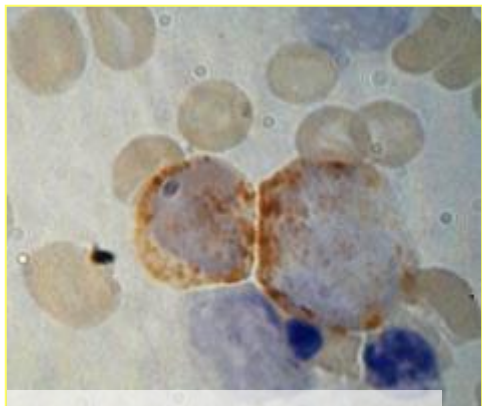
<b>FAB, 1976</b>		<b>≥ 30%</b>
<b>WHO, 2001-17</b>	AML with recurrent genetic aberrations All other AMLs	NA ≥20%
<b>WHO, 2022</b>	AML with defining genetic abnormalities AML defined by differentiation, AML-MR	NA ≥20%
<b>ICC, 2022</b>	AML with defining genetic abnormalities	≥10%
	MDS/AML with TP53 <sup>m</sup>	10-19%
	with myelodysplasia-related cytogenetic abnormalities	10-19%
	with myelodysplasia-related mutations	10-19%
	Not otherwise specified (NOS)	≥20%
	AML with TP53 <sup>m</sup>	≥20%
	with myelodysplasia-related cytogenetic abnormalities	≥20%
with myelodysplasia-related mutations	≥20%	
Not otherwise specified (NOS)	≥20%	
AML with t(9;22)(q34.1;q11.2)/BCR::ABL1		



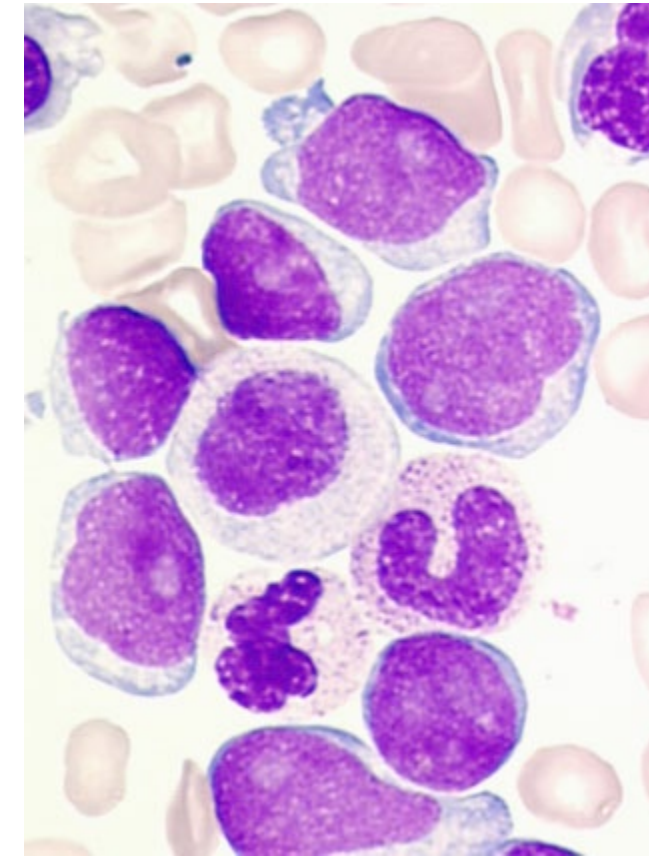
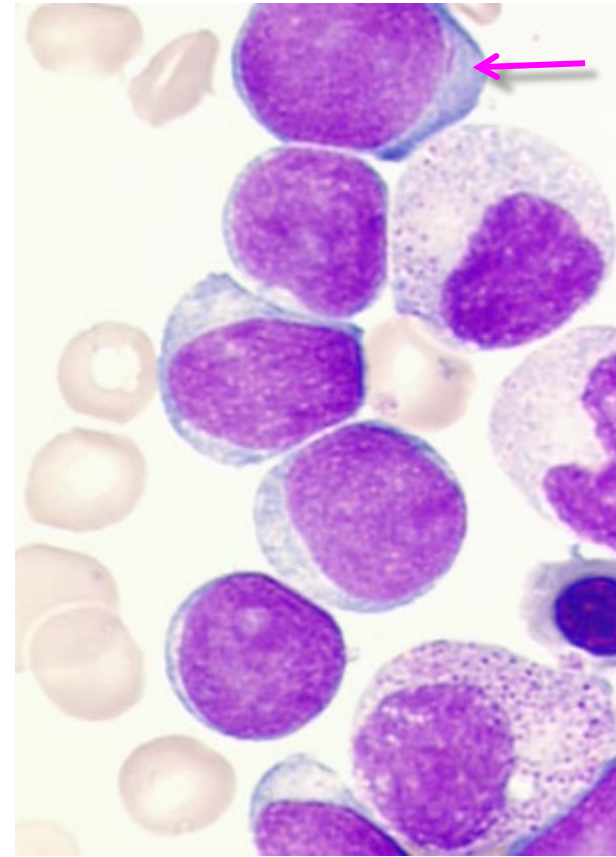
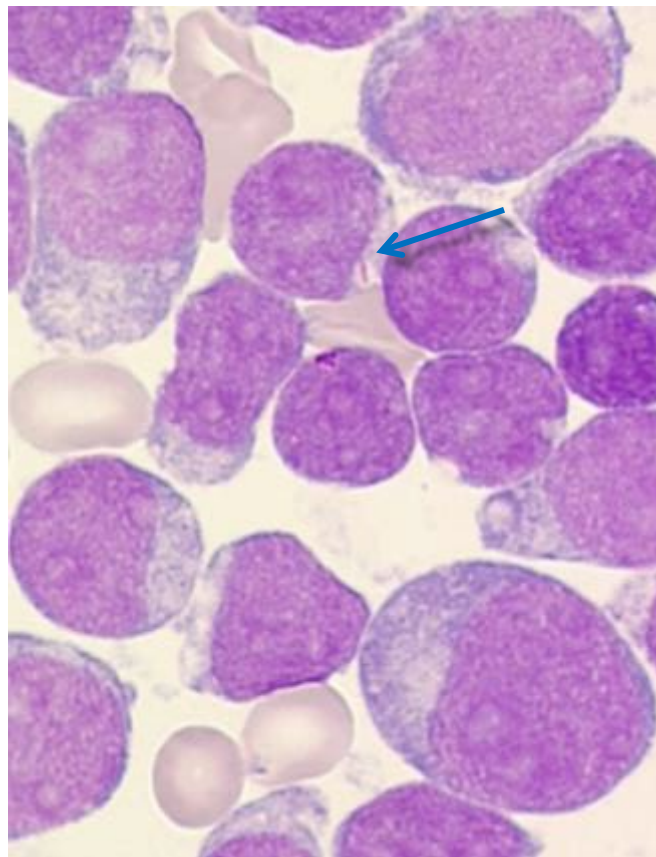
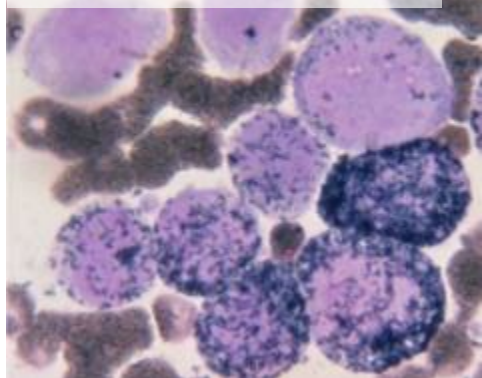
# AML without maturation **vs** with maturation

**M1:** < 10% maturing cells of Gr lineage

**M2:** ≥ 10% maturing cells of Gr lineage  
< 20% monocytoid cells

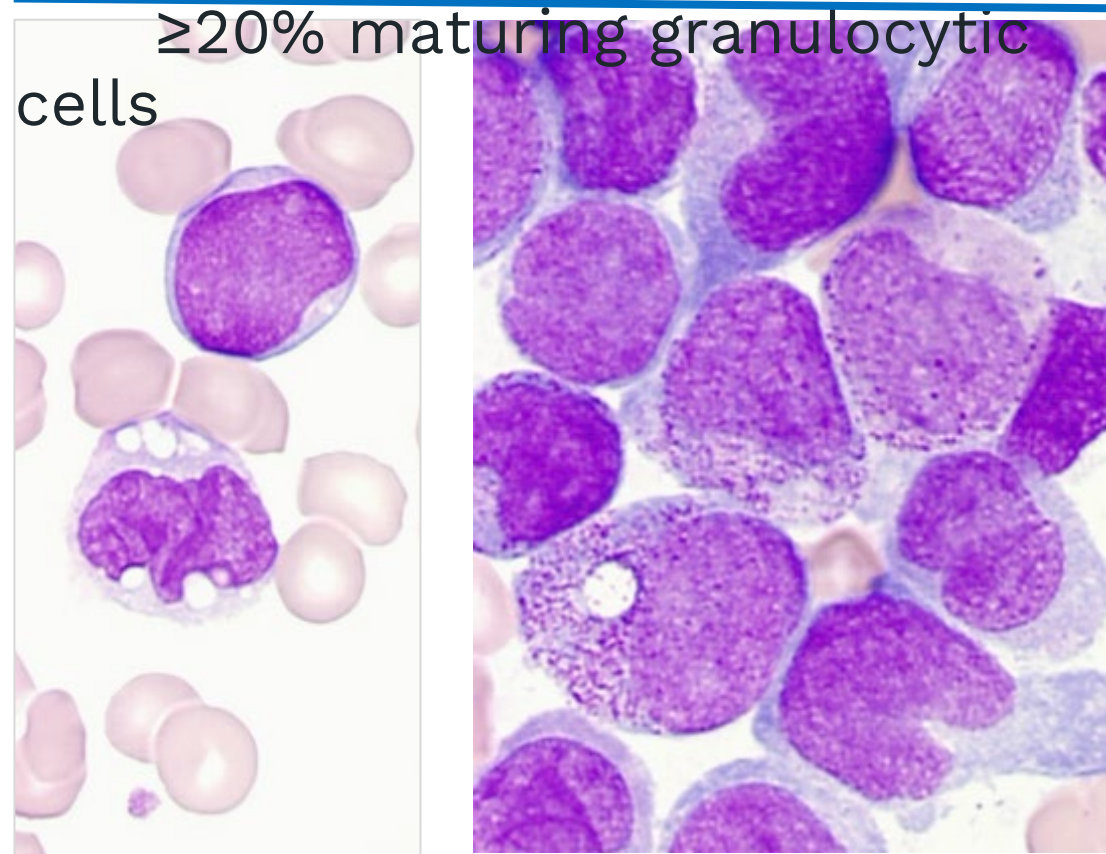


≥3% MPO /SBB

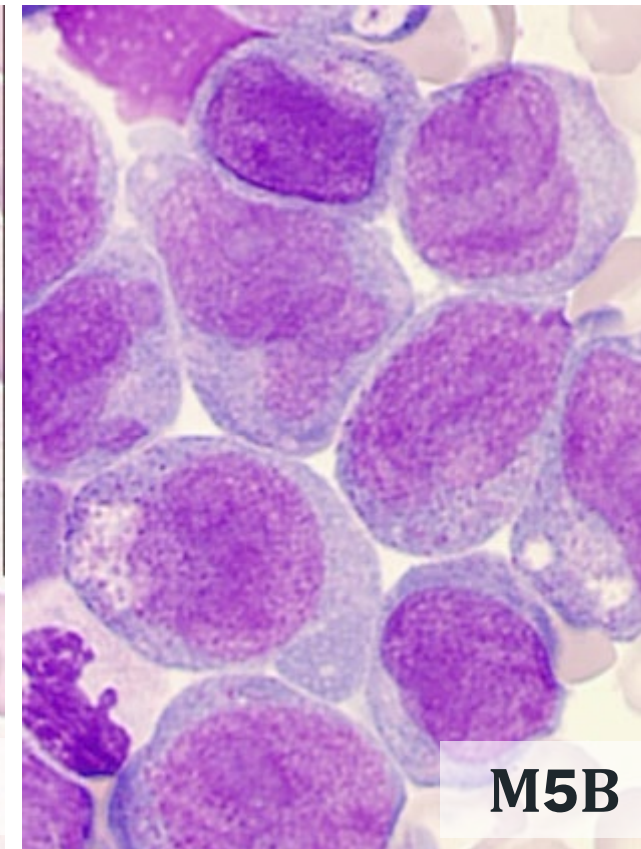
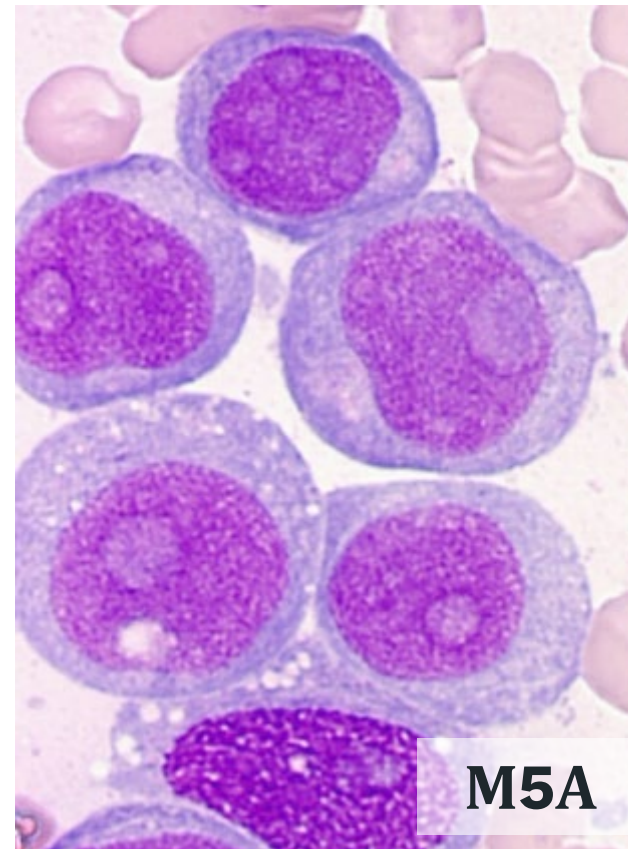


# AML myelomonocytic **vs** monocytic

**M4:**  $\geq 20\%$  monocytes and Mo precursors

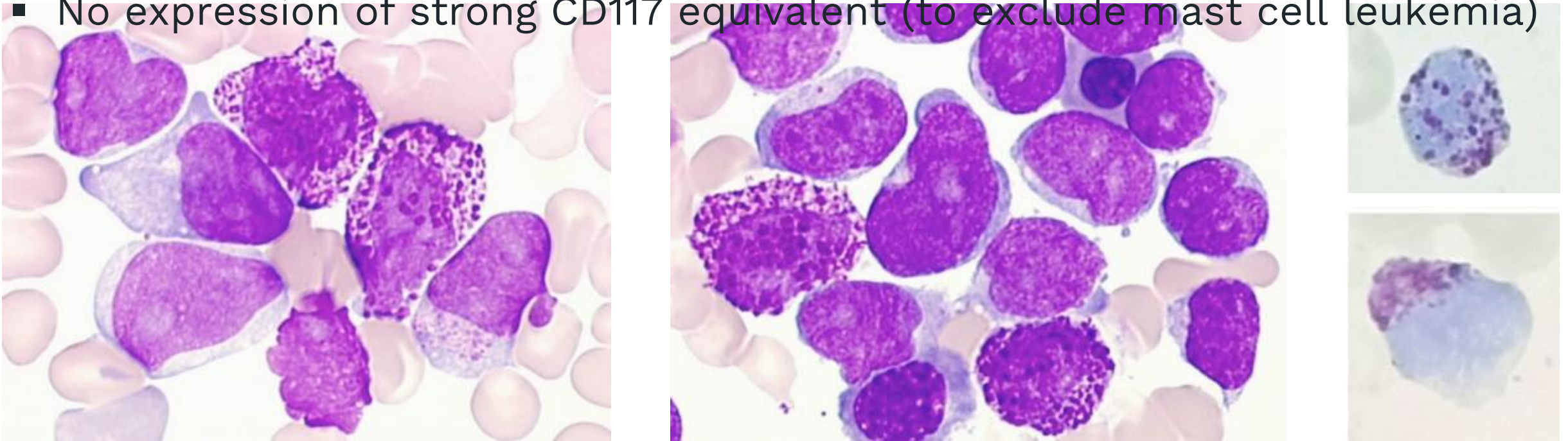


**M5:**  $\geq 80\%$  monocytes and Mo precursors  
 $< 20\%$  maturing granulocytic cells



# Acute basophilic leukemia

- Blasts & immature/mature basophils with metachromasia on toluidine blue staining
- Blasts are negative for cytochemical MPO, SBB, and NSE
- No expression of strong CD117 equivalent (to exclude mast cell leukemia)



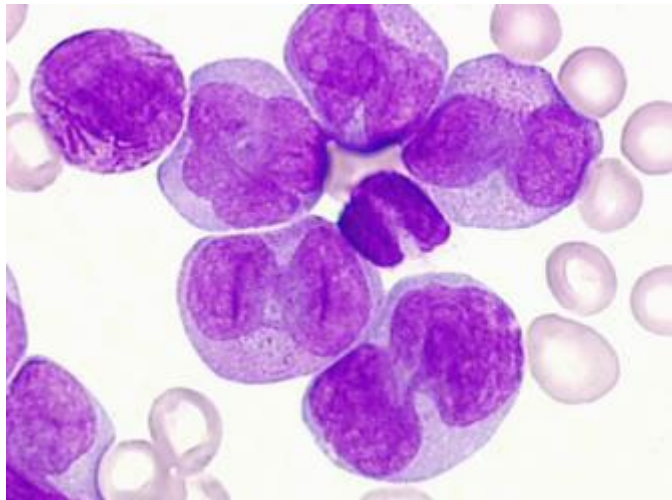
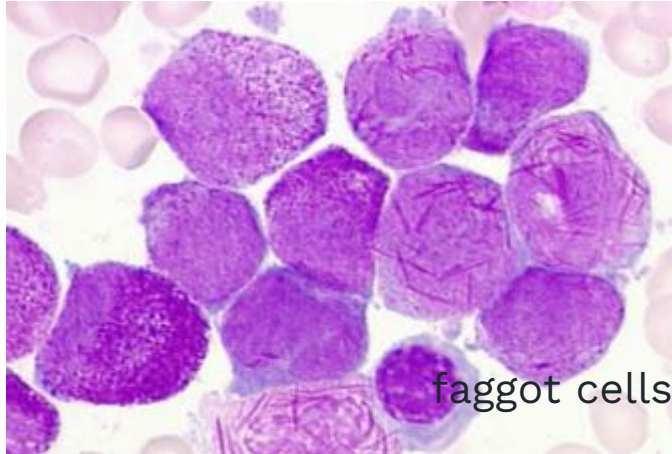
Courtesy Marie-Therese Daniel



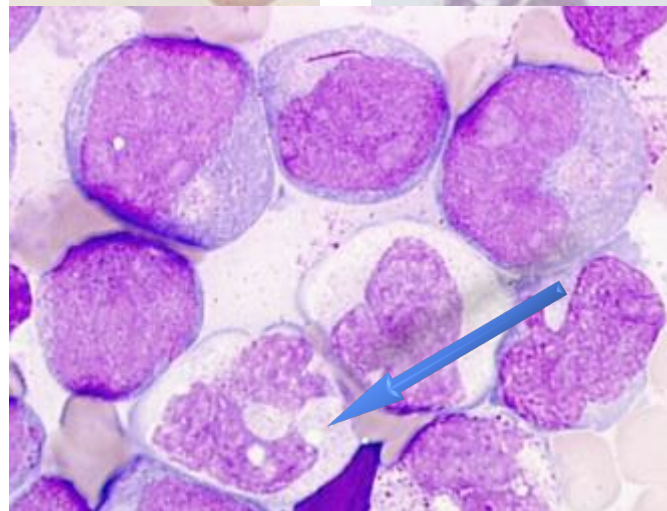
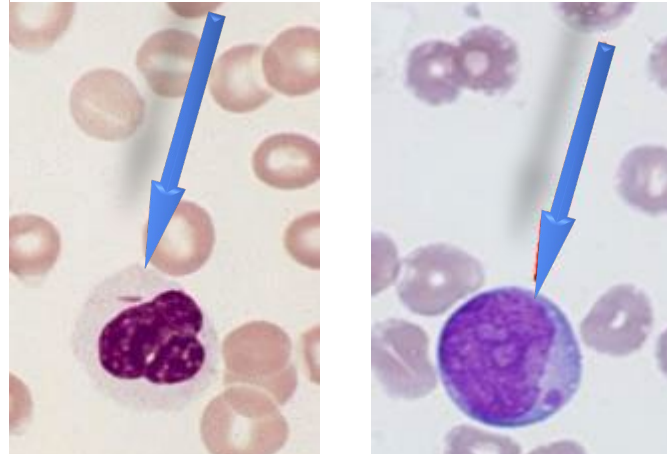
What genetic disorders are behind a certain morphology?

# AML with defining genetic abnormalities

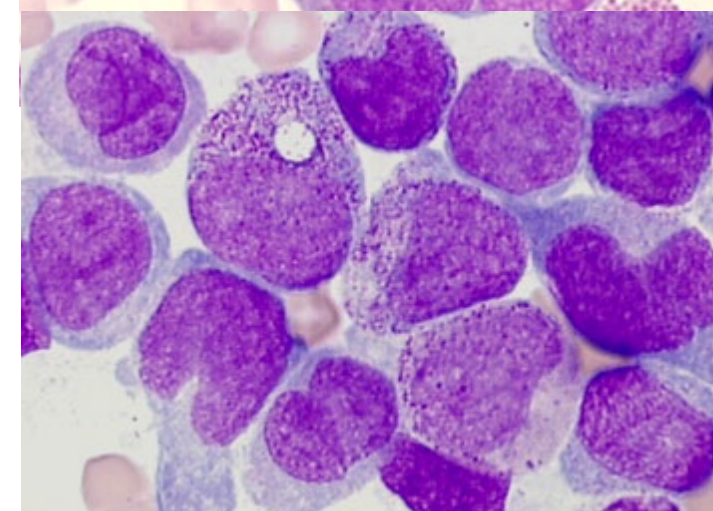
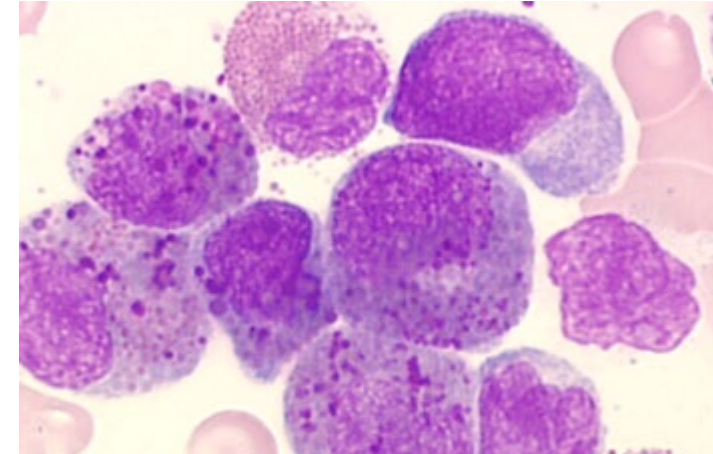
*PML::RARA* fusion



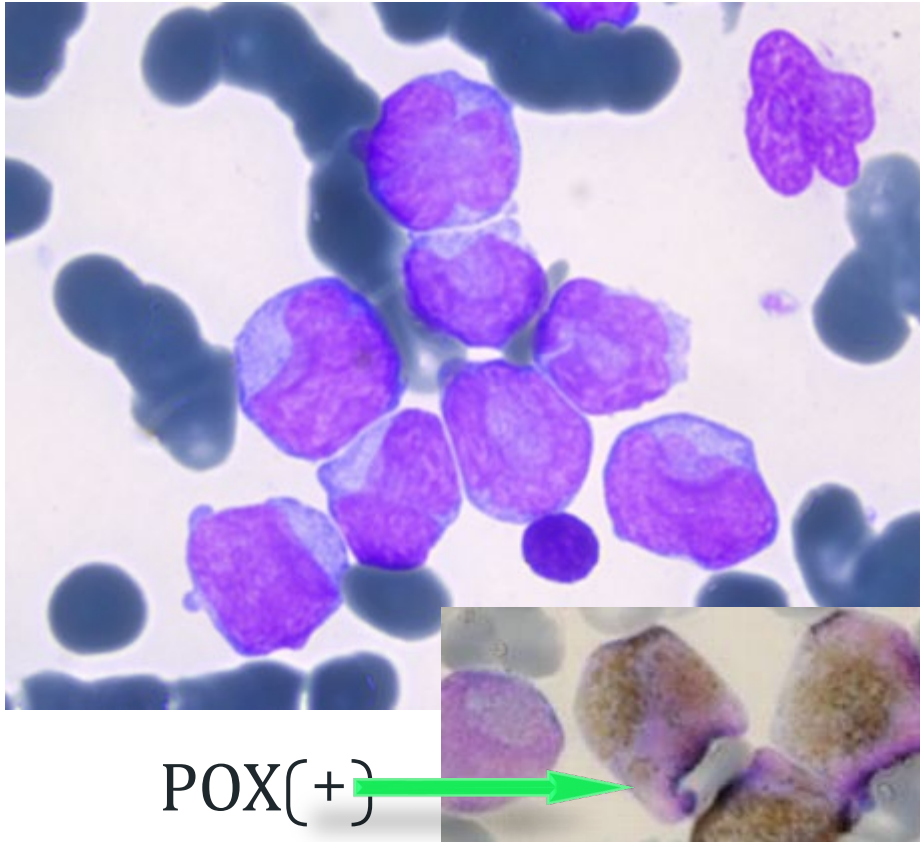
*RUNX1::RUNX1T1*



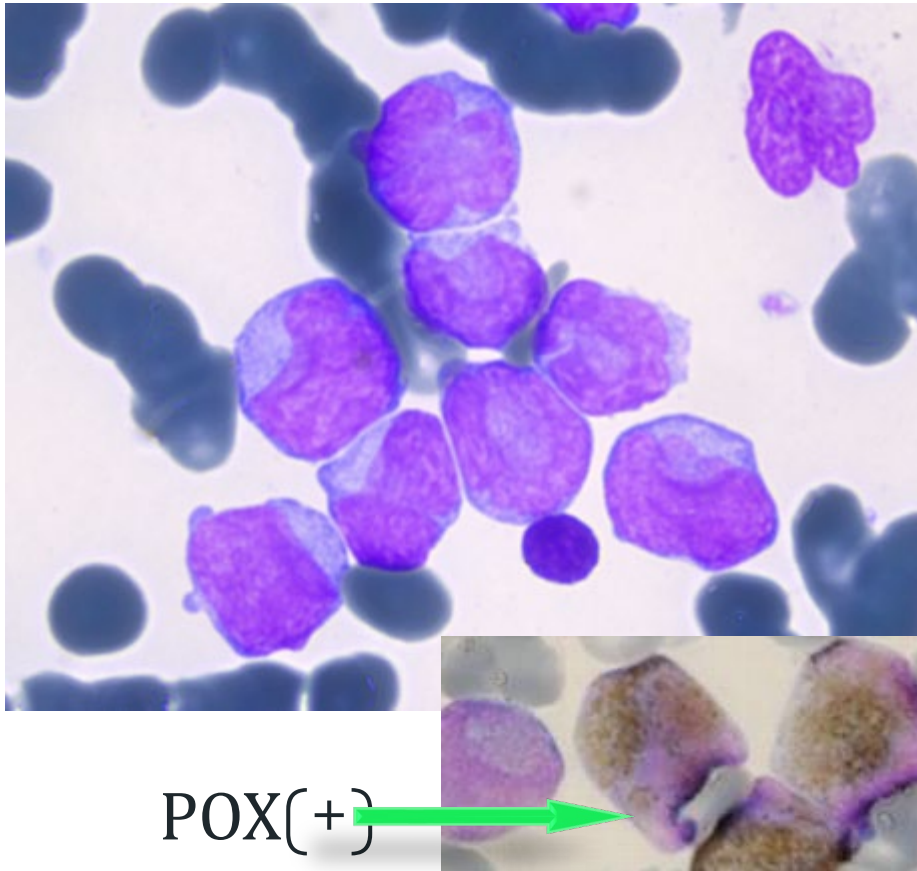
*CBFB::MYH11*



# Cup-like morphology is associated with NPM1<sup>mut</sup> and/or FLT3<sup>mut</sup>

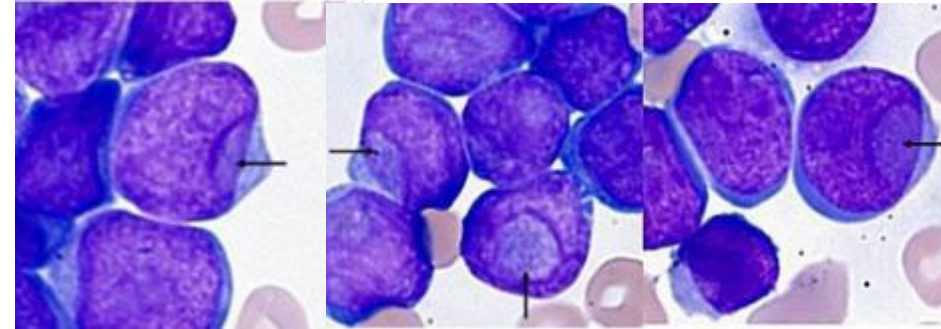


# Cup-like morphology surprise

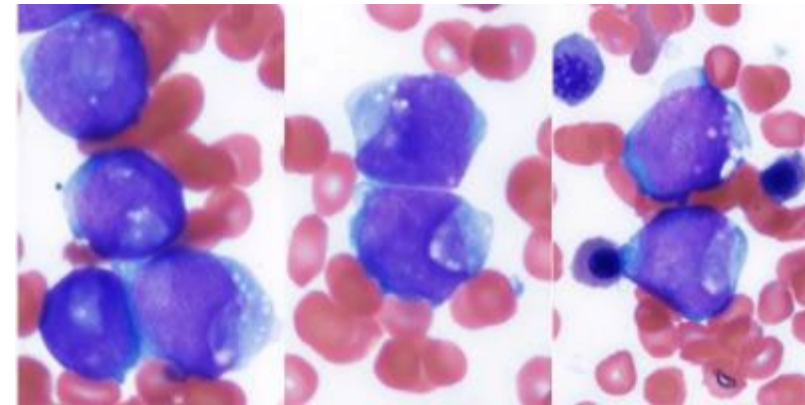


POX(+)

Kroschinsky FP, et al. Cup-like acute myeloid leukemia: new disease or artificial phenomenon? *Haematologica*. 2008; 93: 283; Park BG, et al.. *Ann Hematol*. 2013;92(4):451.



**B-ALL** **Genetics:** t(4;11)(q21;q23) ; KMT2A-AFF1  
**NGS:** KRAS mutation (G13D, VAF 49%)  
Rieu et al, *eJHaem*. 2020;1:589–592.

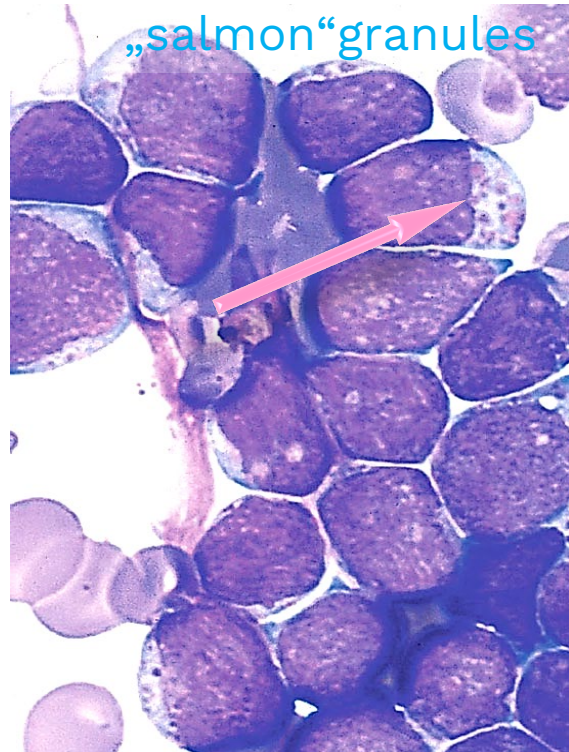


**B-ALL** **Genetics:** 72~80, XXY [5]/XY[12]  
**NGS:** mutations in TP53 and DNMT3A  
Wang et al. *BJH*. 2015;170(5):596.

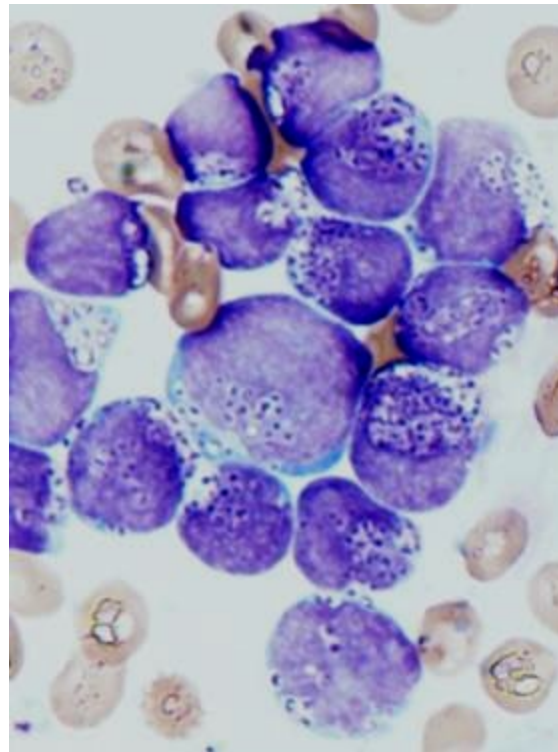
# Other surprises



Granules are not AML®

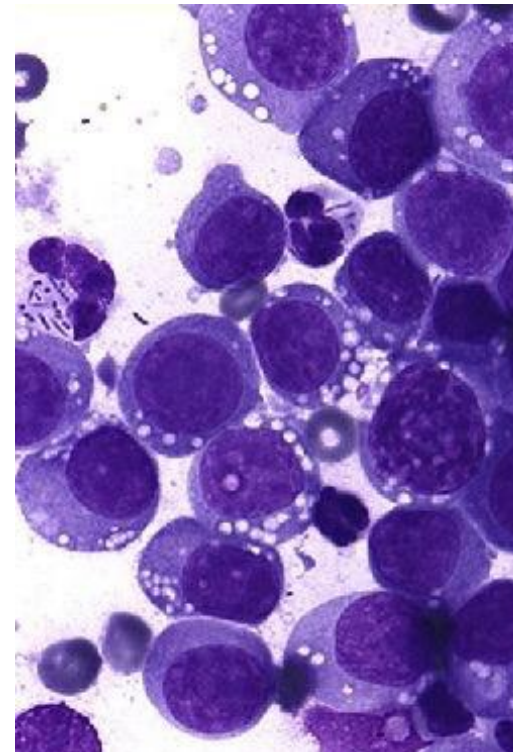


**B-ALL**



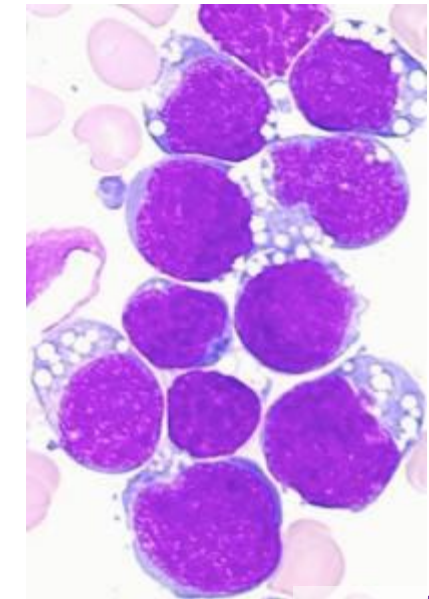
**Ph'(+) B-ALL**

Looks like Burkitt®



**AML-M5**

Lyzozym+; CD56+



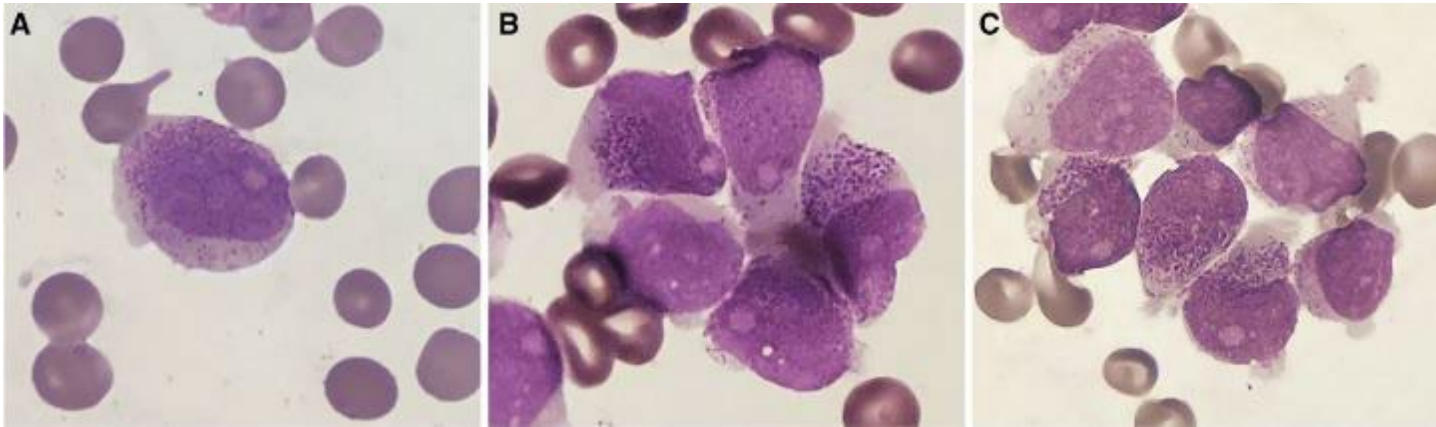
**Burkitt**



# Other misleading images



## Promyelocytic disguise

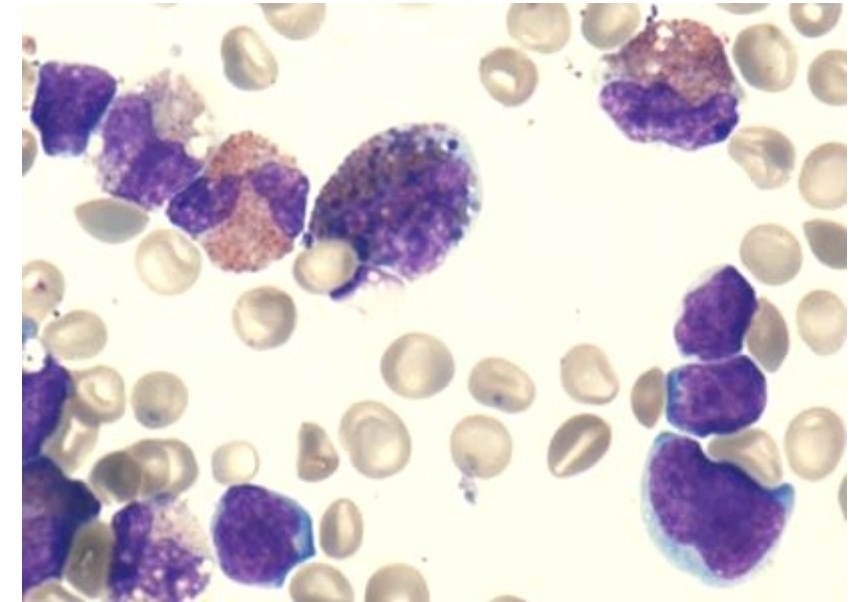


### **B-ALL**

CD19+ CD10+ CD34+ TdT+

Ma Y et al. IJH. 2019;110(6):645-646.

## Eosinophilic clue



### **B-ALL**

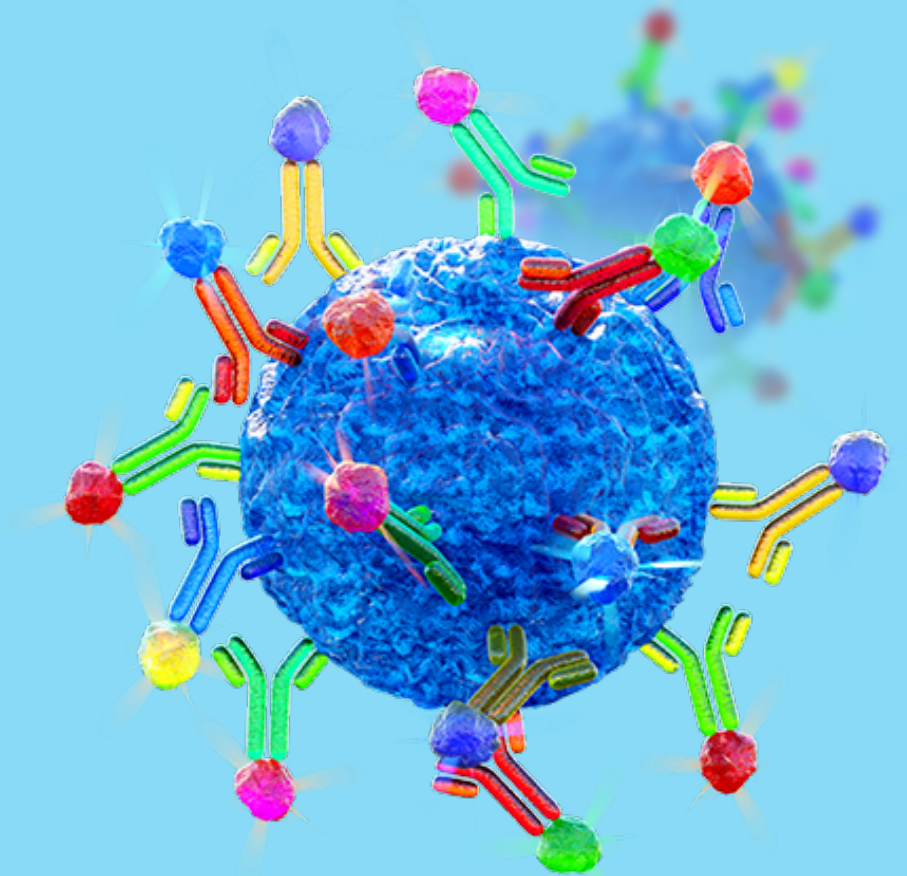
5q33.2 rearrangement

Ma Y, et al. Promyelocyte-like blasts in B-lymphoblastic leukemia of a 67-year-old male patient. Int J Hematol. 2019 Dec;110(6):645-646.

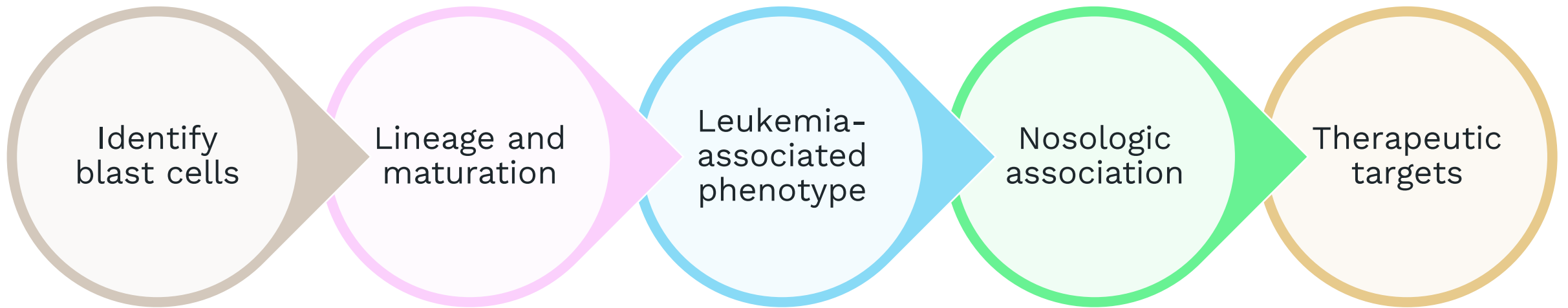
Gujral S et al. B-lymphoblastic leukemia/lymphoma with IGH::IL3 fusion. In: In: WHO Classification of Tumours Editorial Board. Haematolymphoid tumours. Lyon (France): IARC; 2024. . (WHO classification of tumours series, 5th ed.; vol. 11). <https://publications.iarc.who.int/637>.

# 03

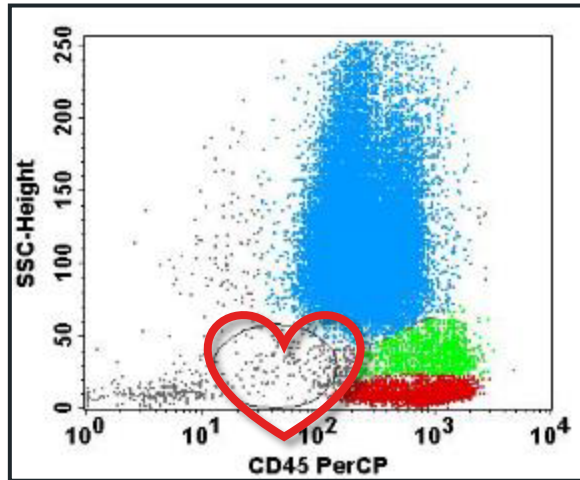
## Immuno phenotyping



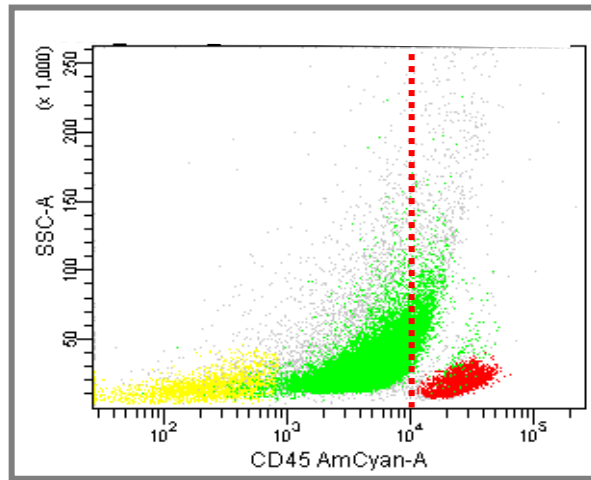
# Immunophenotyping



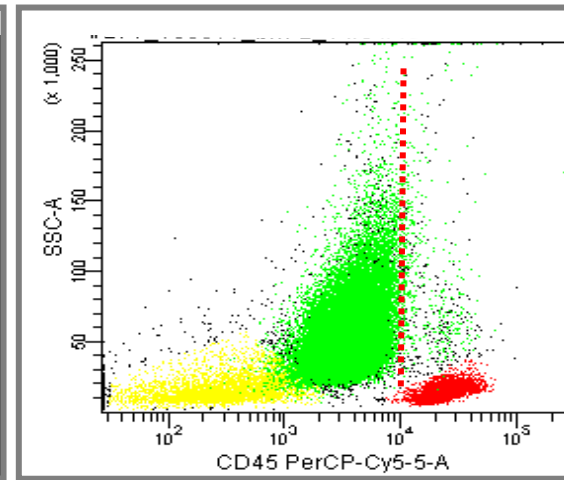
# Identification of blast cells



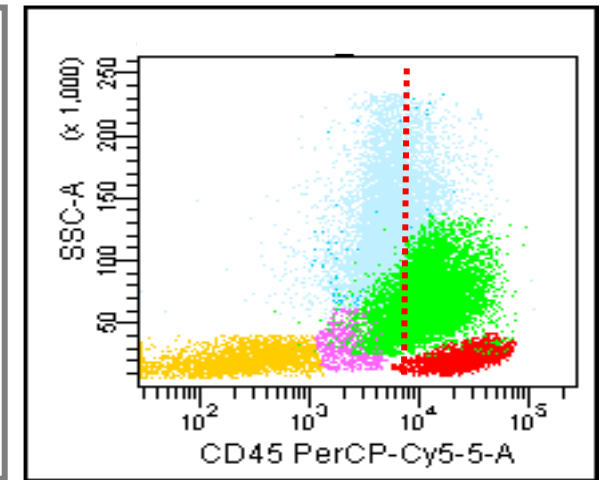
Control



AML without maturation

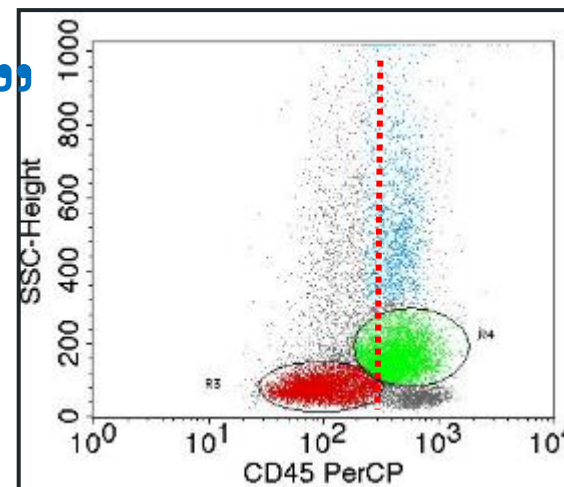


Acute promyelocytic



AML monocytic

“CD45 / SSC gating”



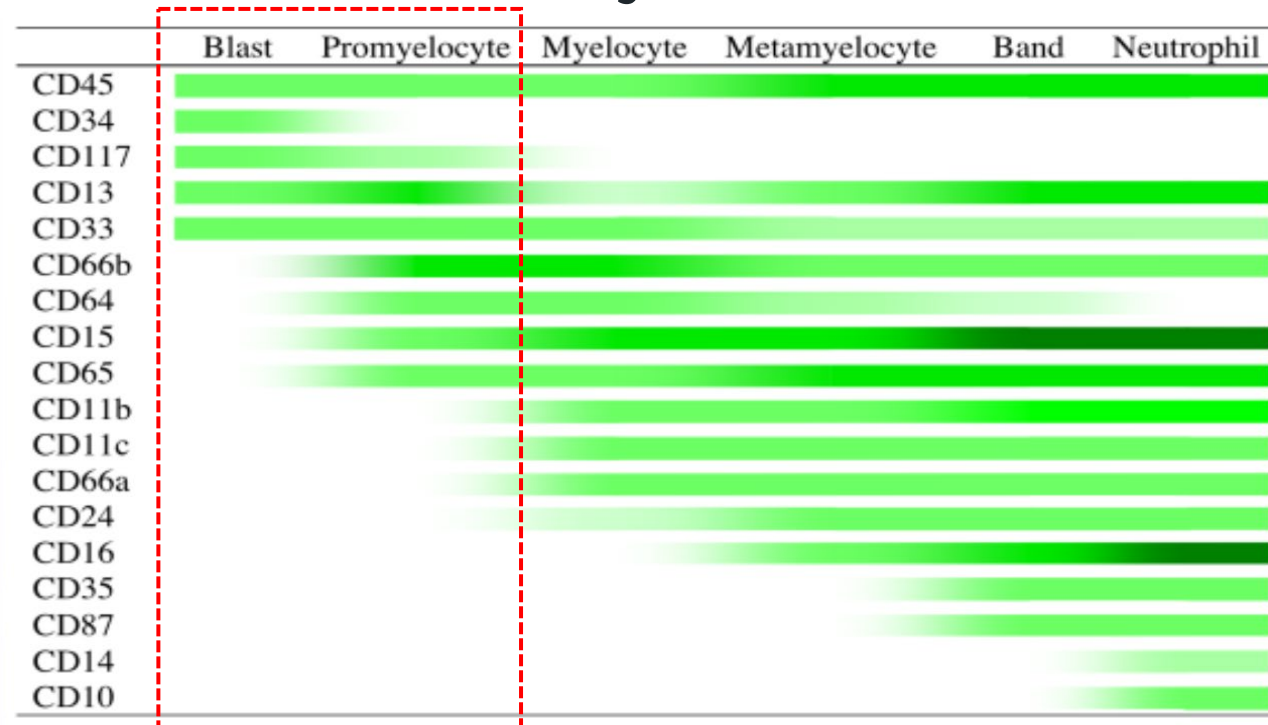
AML myelomonocytic

# Lineage and maturation

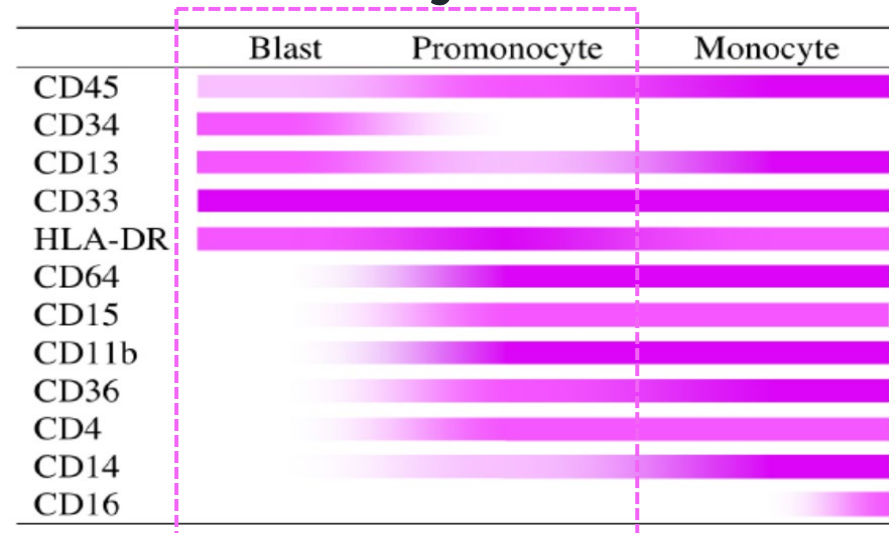
AML diagnosis	Immunophenotypic markers
<b>Precursor markers</b>	CD34, CD117, HLA DR
<b>Myeloid markers</b>	Myeloperoxidase, or CD13, CD33 [ $\geq 2$ ]
<b>Myeloid maturation</b>	CD11b, CD15, CD64, CD65
<b>Monocytic markers</b>	CD14, CD64, CD11c, lysozyme [ $\geq 2$ ], CD36, CD4, CD38,
<b>Megakaryocytic markers</b>	CD41 (glycoprotein IIb/IIIa), CD61 (glycoprotein IIIa), CD42b (glycoprotein Ib)
<b>Erythroid markers</b>	CD235a (glycophorin A), CD71, CD36
<b>Core MRD markers</b>	CD34, CD117, CD45, CD33, CD13, CD56, CD7, HLA-DR If monocytic: CD64, CD11b, CD4 (in addition)

# Normal immunophenotypic patterns

## Granulocytic



## Monocytic



## WHO – HAEM5

### Acute myeloid leukaemia with defining genetic abnormalities

- Acute promyelocytic leukaemia with PML::RARA fusion
- Acute myeloid leukaemia with RUNX1::RUNX1T1 fusion
- Acute myeloid leukaemia with CFBF::MYH11 fusion
- Acute myeloid leukaemia with KMT2A rearrangement
- Acute myeloid leukaemia with DEK::NUP214 fusion
- Acute myeloid leukaemia with MECOM rearrangement
- Acute myeloid leukaemia with BCR::ABL1 fusion
- Acute myeloid leukaemia with NPM1 mutation
- Acute myeloid leukaemia with CEBPA mutation
- Acute myeloid leukaemia, myelodysplasia-related
- Acute myeloid leukaemia with RBM15::MRTFA fusion
- Acute myeloid leukaemia with NUP98 rearrangement
- AML with other defined genetic alterations

### Acute myeloid leukaemia, defined by differentiation

#### Acute myeloid leukaemia with minimal differentiation

Acute myeloid leukaemia without maturation

Acute myeloid leukaemia with maturation

Acute basophilic leukaemia

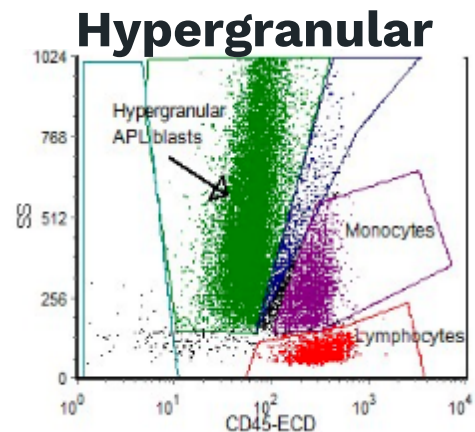
Acute myelomonocytic leukaemia

# Required for diagnosis

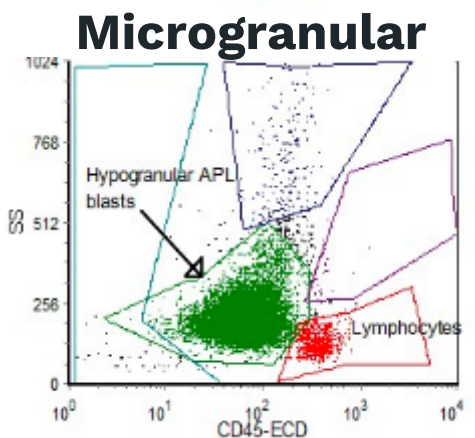
## Some entities require phenotype for diagnosis

- **AML with minimal differentiation:**  
≥ 2 CD13, CD33, CD117
- **Acute erythroid leukemia:**  
CD235, CD71, CD36
- **Acute megakaryoblastic leukemia:**  
CD41, CD42, CD61
- **Differential diagnosis:**  
MPAL – My/T; My/B

# Or quick guide to diagnosis: APL PML::RARA



**SSC<sup>high</sup> 100%** - CD117, MPO, CD33



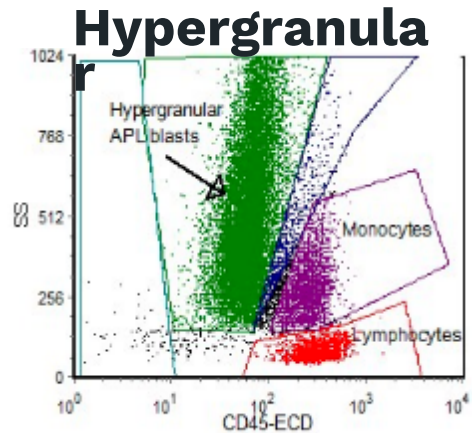
**SSC<sup>low</sup> 0%** - HLA DR

	Hyper granular	Micro granular
CD2	23%	90%
CD3	2%	75%
CD4	0%	0%



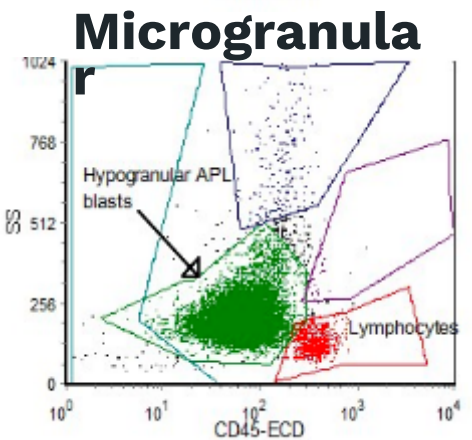
# Or quick guide to diagnosis:

APL PML::RARA



**SSC<sup>high</sup> 100%** - CD117, MPO, CD33

CD117, MPO(+)

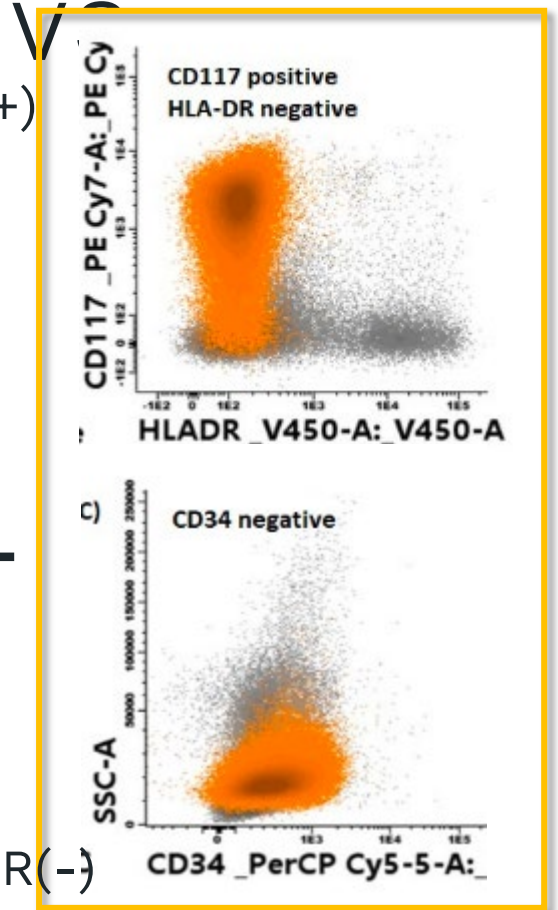


**SSC<sup>low</sup> 0%** - HLA DR

	Hyper granular	Micro granular
CD2	23%	90%
CD3	2%	75%

**APL-like NPM1<sup>mut</sup> AML**

CD34, HLA DR(-)



# Aberrant phenotypes (LAP)

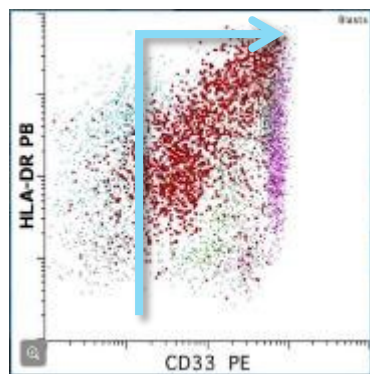
Abnormal expression intensity  $\uparrow\downarrow\emptyset$

Asynchronous "mature" + "immature"

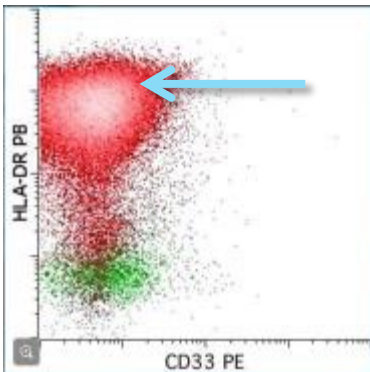
Homogeneous instead of variable expression

Mixed lineage expression

normal

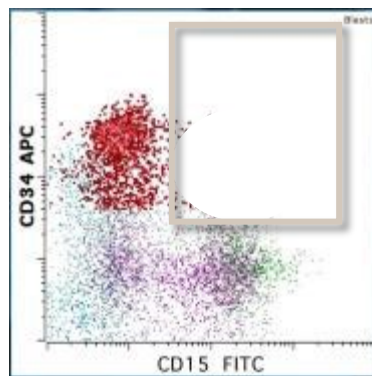


AML

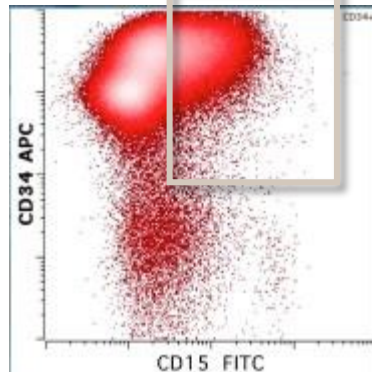


CD33(-)

normal

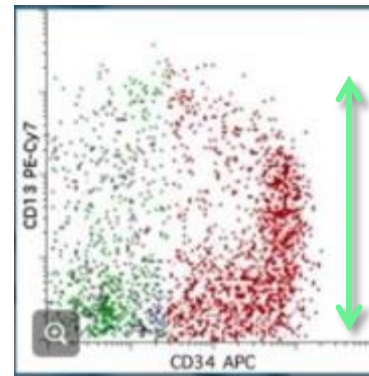


AML

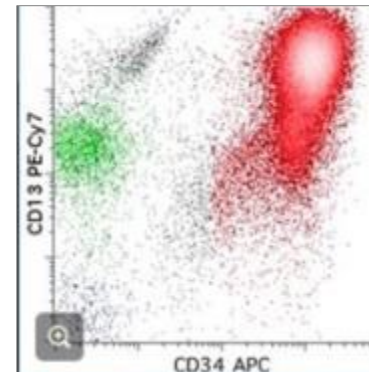


CD34(+)CD15(+)

normal

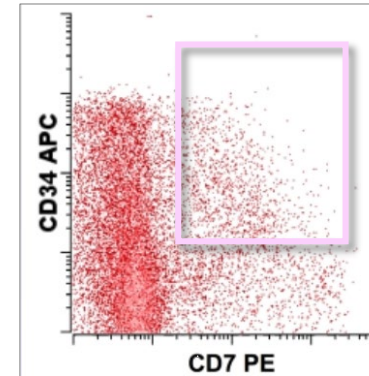


AML

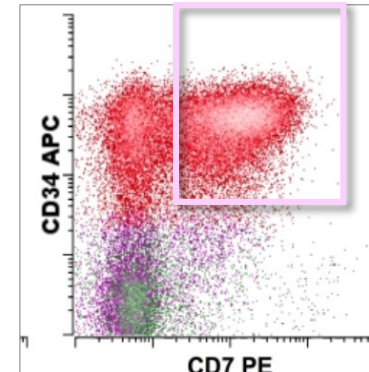


CD34(+)bright

normal

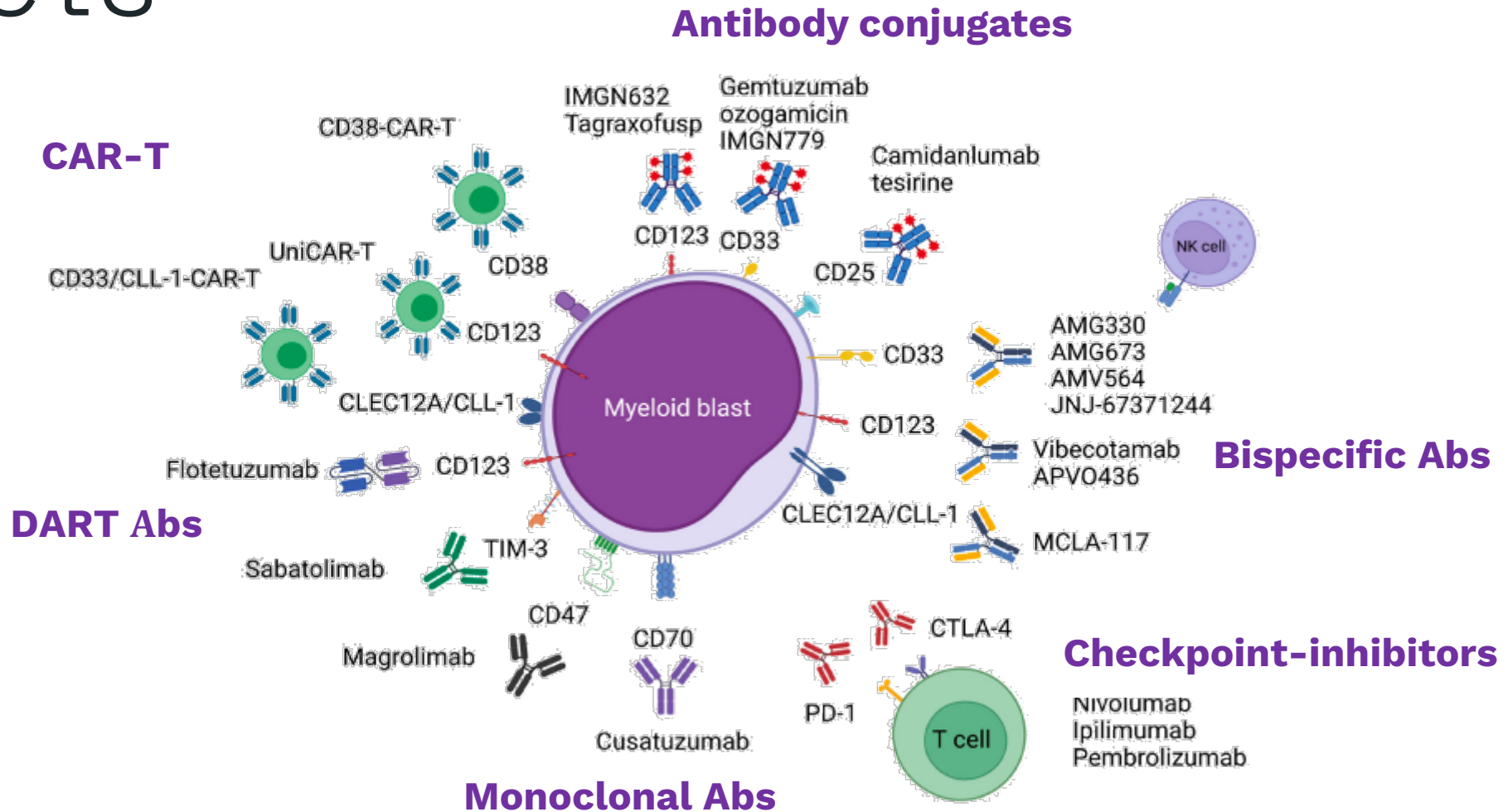


AML



CD7(+) My blasts

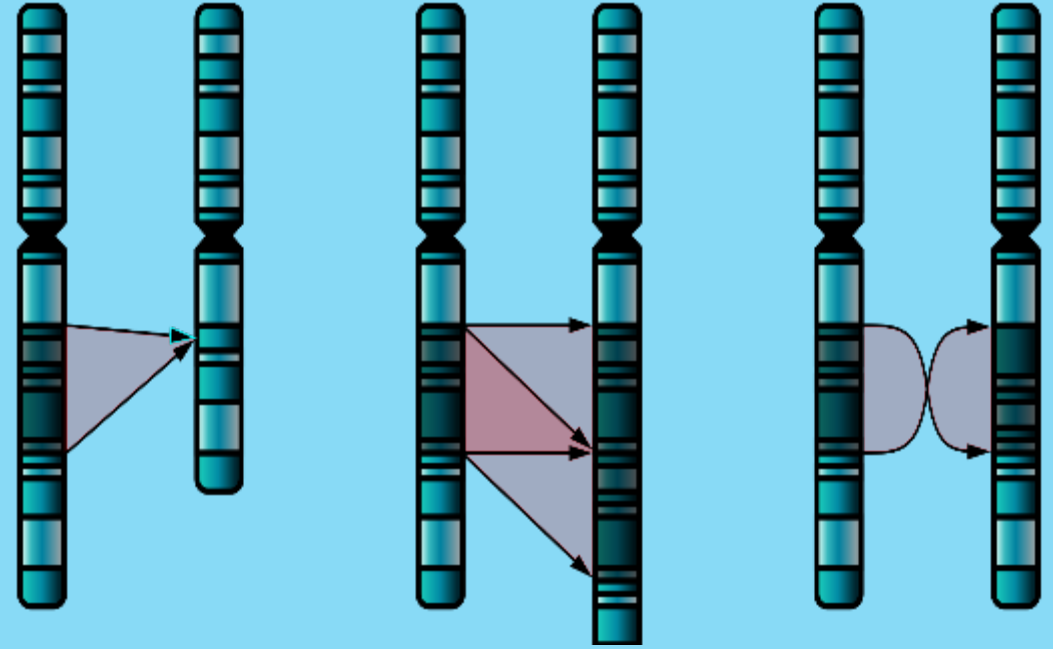
# Identification of therapeutic targets



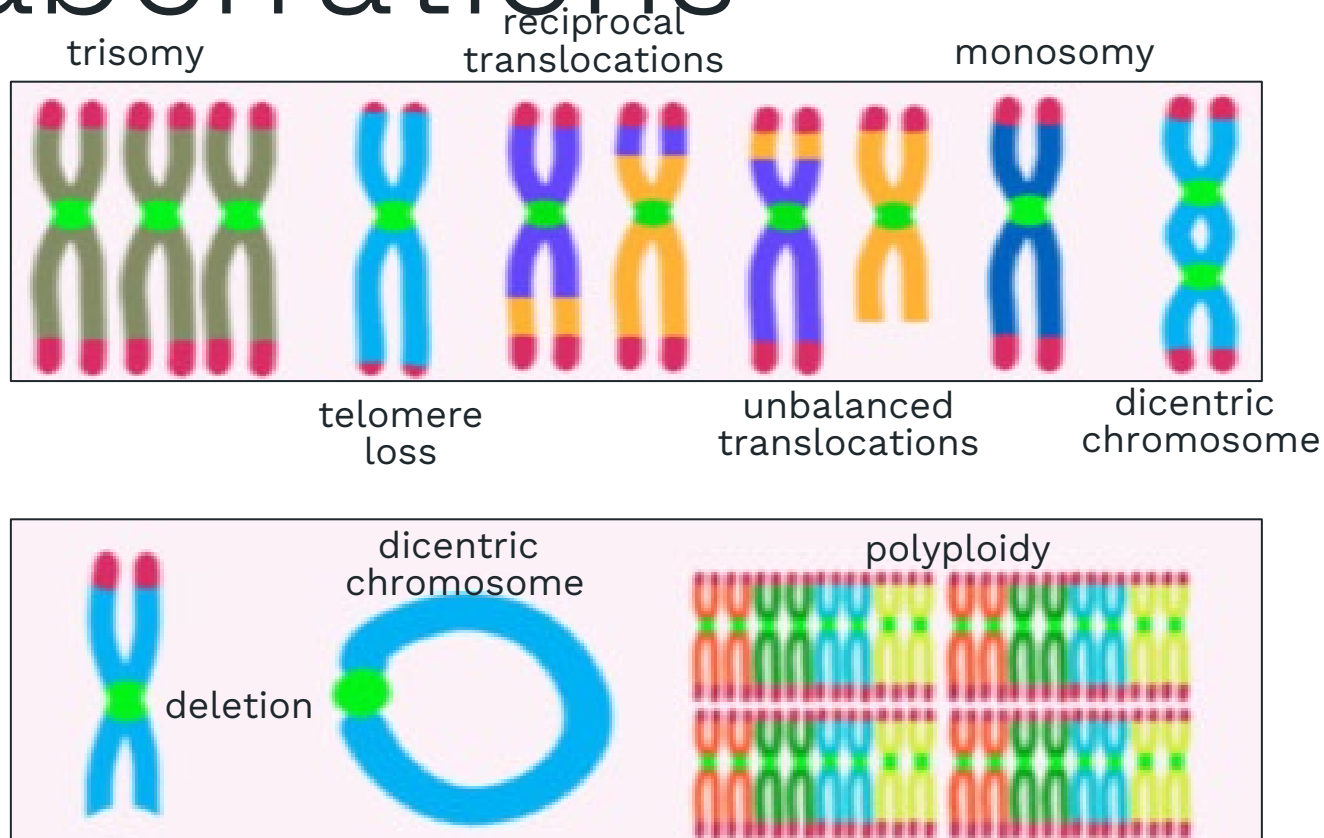
# 04

## Cytogenetics

- Detection of chromosomal aberrations
- Classification of AML entities
- Risk stratification



# Detection of chromosomal aberrations



## Complex karyotype:

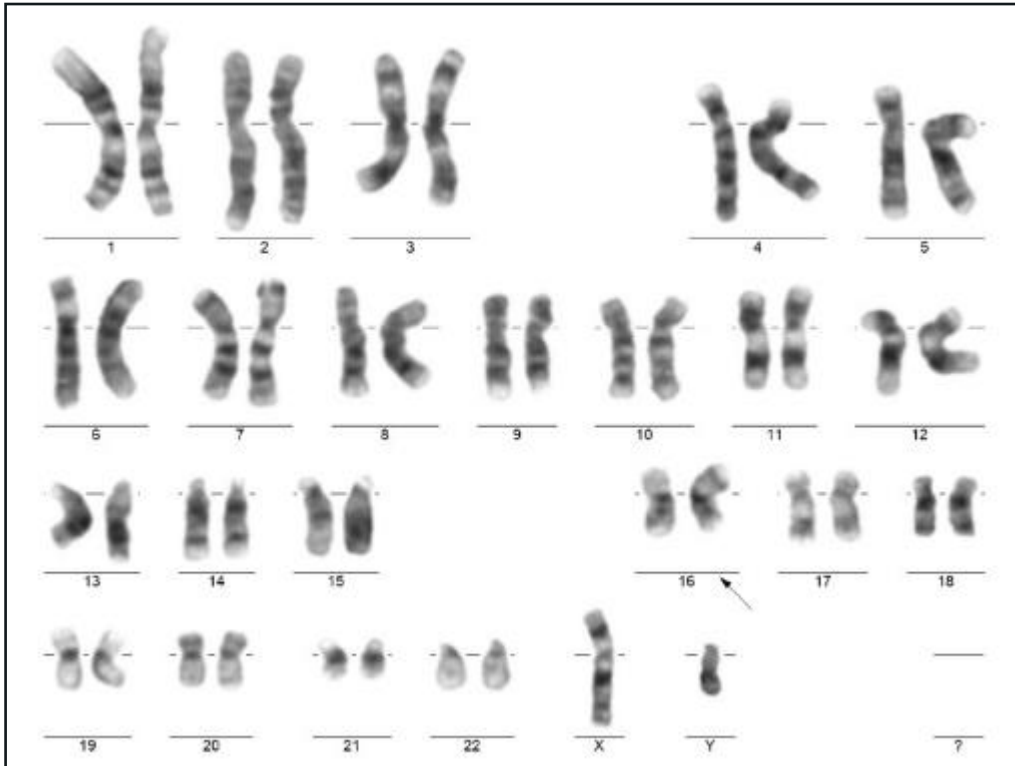
- presence of  $\geq 3$  different chromosomal aberrations in the same clone.

## Monosomal karyotype:

- presence of  $\geq 2$  autosomal monosomies  
or
- presence of 1 autosomal monosomy in combination with at least 1 structural aberration

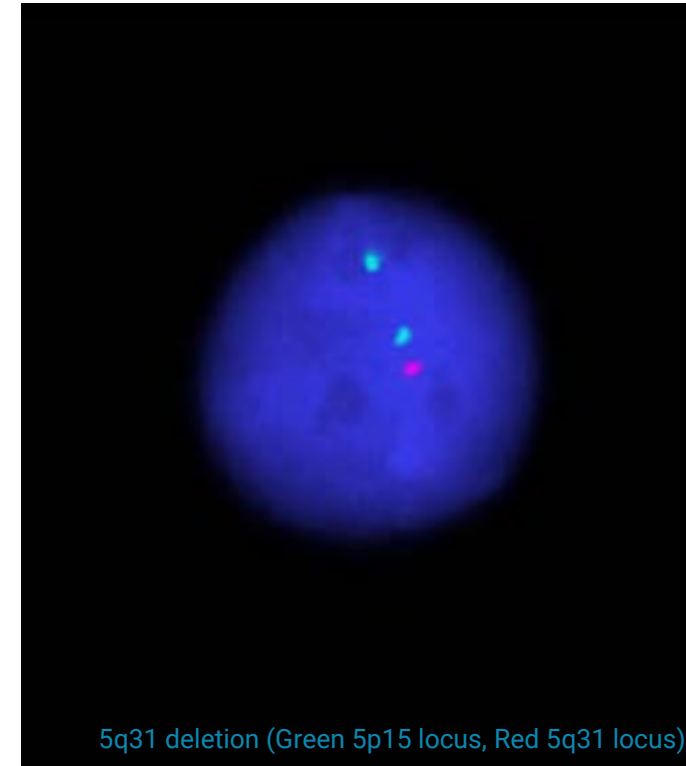
# Technical aspects

## Conventional cytogenetics



Courtesy prof. G.Balatzenko

## Fluorescence in situ hybridization



Within 5-7 days<sup>1</sup>

# Genetic abnormalities define

entity

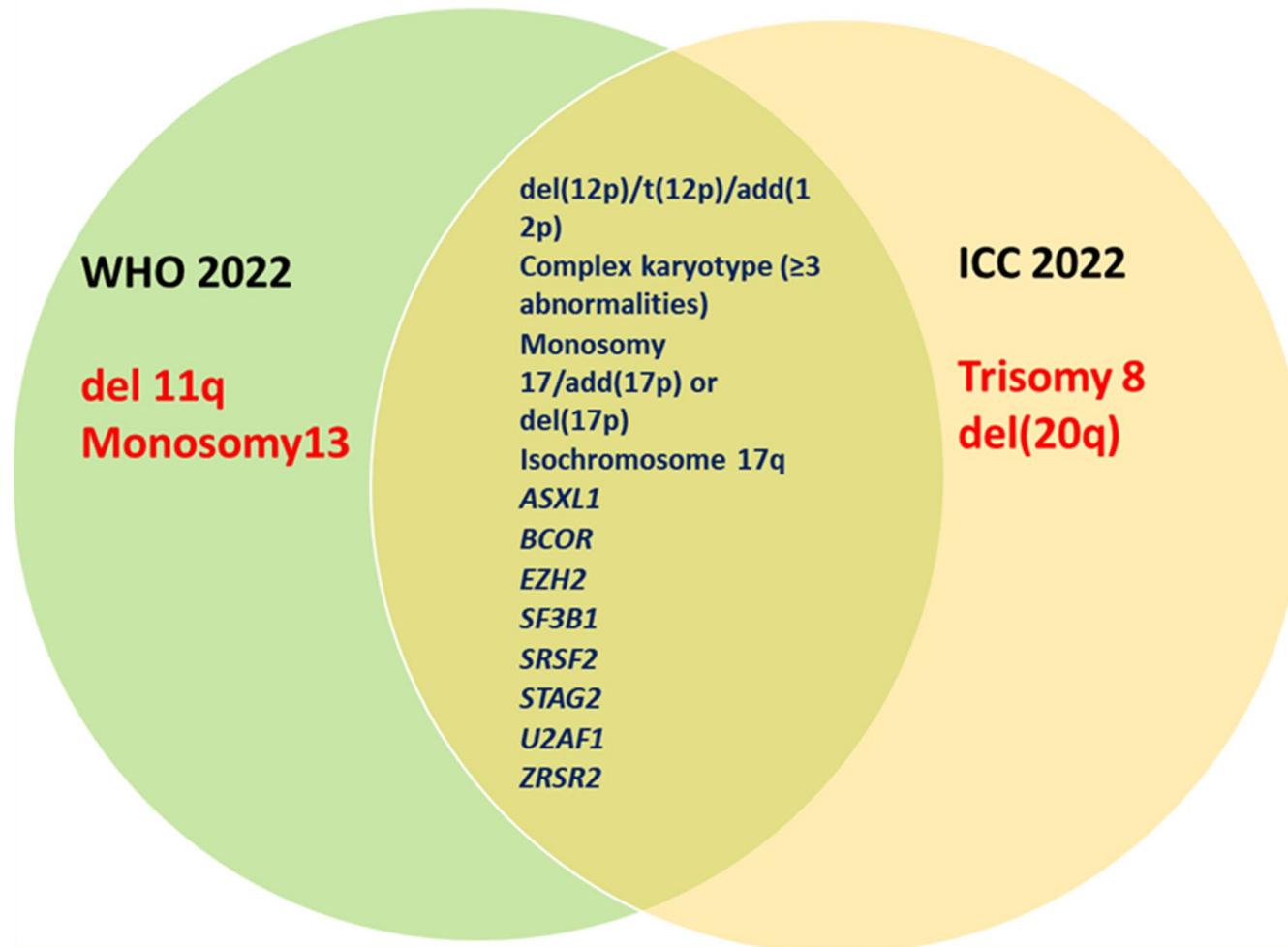
WHO – HAEM5	ICC	Minimal panel
<b>Acute myeloid leukaemia with defining genetic abnormalities</b>		
Acute promyelocytic leukaemia with <b>PML::RARA</b> fusion	Acute promyelocytic leukemia with <b>t(15;17)(q24.1;q21.2)/PML::RARA</b>	PML::RARA, CBFB::MYH11, RUNX1::RUNX1T1, KMT2A rearrangements, BCR::ABL1
Acute myeloid leukaemia with <b>RUNX1::RUNX1T1</b> fusion	APL with other RARA rearrangements*	
Acute myeloid leukaemia with <b>CBFB::MYH11</b> fusion	AML with <b>t(8;21)(q22;q22.1)/RUNX1::RUNX1T1</b>	
Acute myeloid leukaemia with <b>KMT2A</b> rearrangement	AML with <b>inv(16)(p13.1q22) or t(16;16)(p13.1;q22)/CBFB::MYH11</b>	
Acute myeloid leukaemia with <b>DEK::NUP214</b> fusion	AML with <b>t(9;11)(p21.3;q23.3)/MLLT3::KMT2A</b>	
Acute myeloid leukaemia with <b>MECOM</b> rearrangement	AML with other KMT2A rearrangements	
Acute myeloid leukaemia with <b>BCR::ABL1</b> fusion	AML with <b>t(6;9)(p22.3;q34.1)/DEK::NUP214</b>	
Acute myeloid leukaemia with <b>NPM1 mutation</b>	AML with <b>inv(3) or t(3;3)(q21.3;q26.2)/GATA2; MECOM</b>	
Acute myeloid leukaemia with <b>CEBPA mutation</b>	AML with other MECOM rearrangements	
Acute myeloid leukaemia, myelodysplasia-related	AML with <b>t(9;22)(q34.1;q11.2)/BCR::ABL1</b>	
Acute myeloid leukaemia with <b>RBM15::MRTFA</b> fusion	AML with mutated <b>NPM1</b>	
Acute myeloid leukaemia with NUP98 rearrangement	AML with in-frame <b>bZIP CEBPA</b> mutations ≥ 10%	
AML with other defined genetic alterations	AML with <b>myelodysplasia-related cytogenetic abnormalities</b>	
	MDS/AML (10-19%) / AML (≥ 20%)	
	AML (≥ 20%) and MDS/AML (10-19%) with <b>myelodysplasia-related gene mutations</b>	
	AML (≥ 20%) and MDS/AML (10-19%) with <b>mutated TP53</b>	
	AML with other rare recurring translocations	

Döhner et al, Diagnosis and management of AML in adults: 2022 recommendations from an international expert panel on behalf of the ELN. Blood. 2022;140(12):1345-1377

39 Arber et al. ICC of Myeloid Neoplasms and Acute Leukemias: integrating morphologic, clinical, and genomic data. Blood. 2022; 140(11)

WHO Classification of Tumours Editorial Board. Haematolymphoid tumours. Lyon (France): IARC; 2024.

# AML, myelodysplasia-related



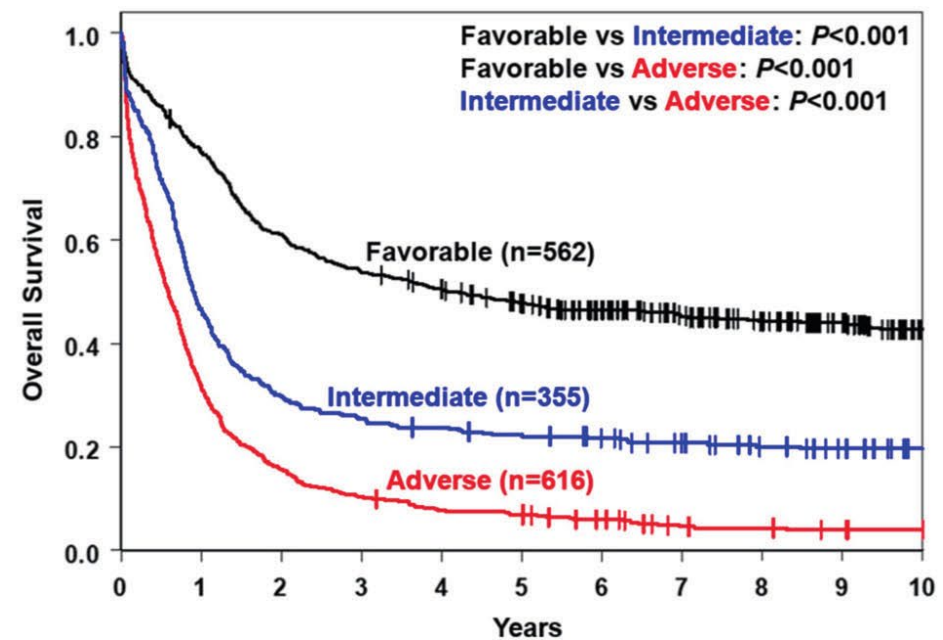
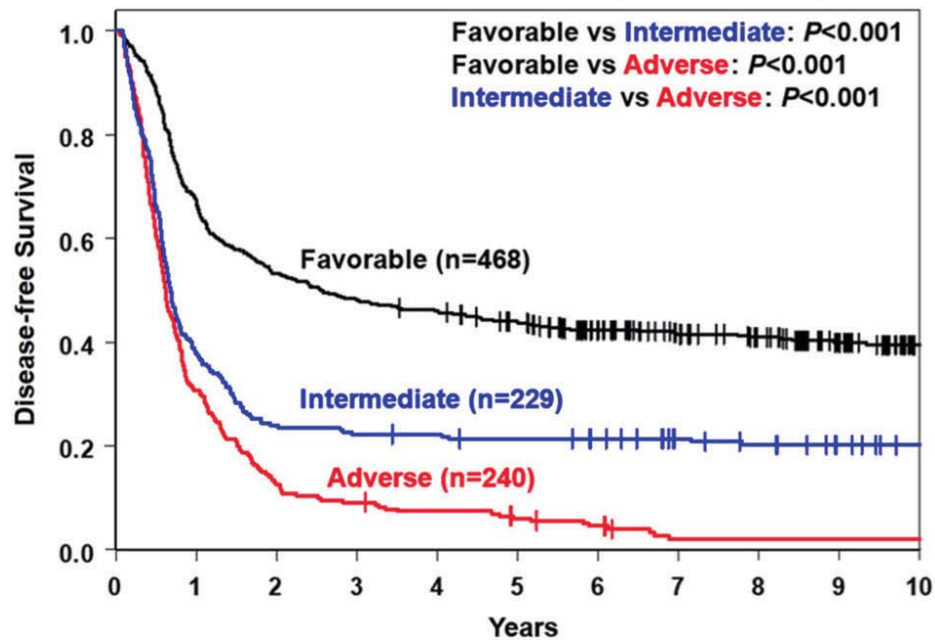


# Risk classification by genetics

FL M2022

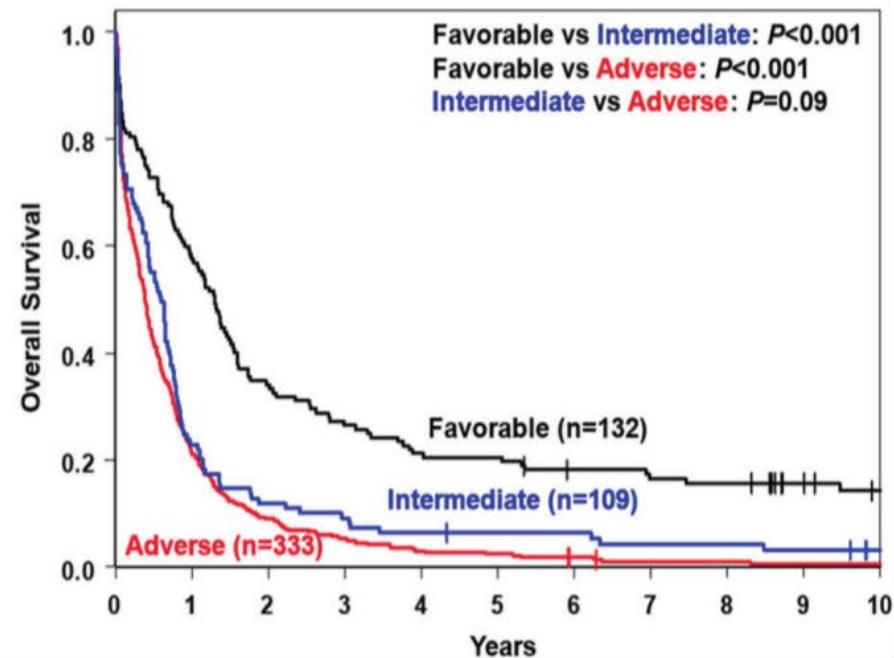
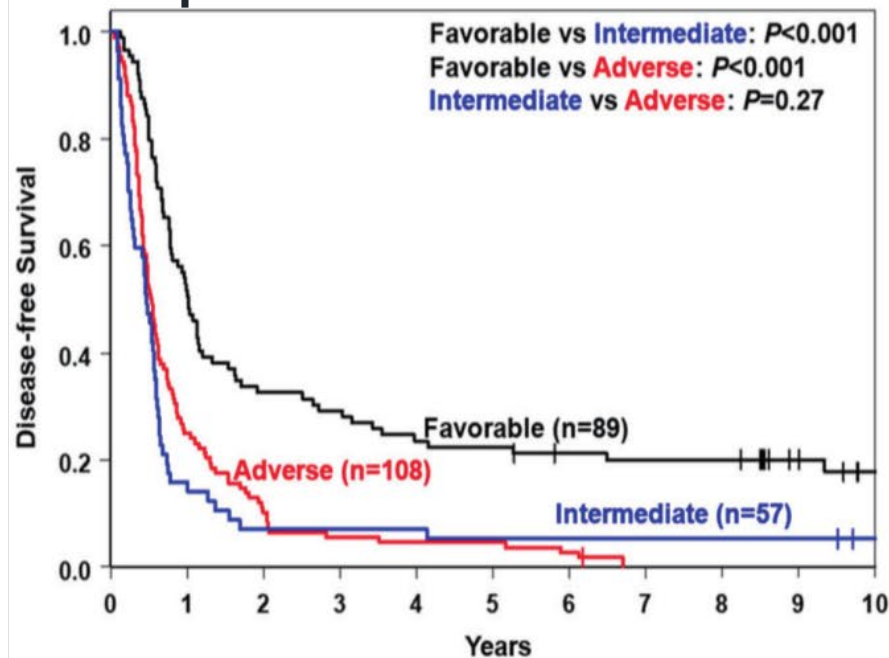
Risk category	Genetic abnormality
<b>Favorable</b>	<ul style="list-style-type: none"><li>• t(8;21)(q22;q22.1)/RUNX1::RUNX1T1</li><li>• inv(16)(p13.1q22) or t(16;16)(p13.1;q22)/ CFBF::MYH11</li><li>• Mutated NPM1 without FLT3-ITD</li><li>• bZIP in-frame mutated CEBPAk</li></ul>
<b>Intermediate</b>	<ul style="list-style-type: none"><li>• Mutated NPM1†,§ with FLT3-ITD</li><li>• Wild-type NPM1 with FLT3-ITD (without adverse-risk genetic lesions)</li><li>• t(9;11)(p21.3;q23.3)/MLLT3::KMT2A</li><li>• Cytogenetic and/or molecular abnormalities not classified as favorable or adverse</li></ul>
<b>Adverse</b>	<ul style="list-style-type: none"><li>• t(6;9)(p23.3;q34.1)/DEK::NUP214</li><li>• t(v;11q23.3)/KMT2A-rearranged</li><li>• t(9;22)(q34.1;q11.2)/BCR::ABL1</li><li>• t(8;16)(p11.2;p13.3)/KAT6A::CREBBP</li><li>• inv(3)(q21.3q26.2) or t(3;3)(q21.3;q26.2)/GATA2, MECOM(EVI1)</li><li>• t(3q26.2;v)/MECOM(EVI1)-rearranged</li><li>• 25 or del(5q); 27; 217/abn(17p)</li><li>• Complex karyotype, monosomal karyotype</li><li>• Mutated ASXL1, BCOR, EZH2, RUNX1, SF3B1, SRSF2, STAG2, U2AF1, and/or ZRSR2</li><li>• Mutated TP53a</li></ul>

# Outcome prediction by ELN<sup>2022</sup> genetic-risk classification



n=1637 adults with AML, treated with cytarabine/anthracycline regimens

# Suboptimal for elderly and for adults receiving less-intensive therapies



de novo AML patients,  
aged  $\geq 60$  years

# Genetic risk classification ELN<sup>2024</sup> for adults receiving less-intensive therapies

Risk category	Genetic abnormality
<b>Favorable</b>	<ul style="list-style-type: none"> <li>• Mutated <i>NPM1</i> (<i>FLT3</i>-ITD<sup>neg</sup>, <i>NRAS</i><sup>wt</sup>, <i>KRAS</i><sup>wt</sup>, <i>TP53</i><sup>wt</sup>)</li> <li>• Mutated <i>IDH2</i> (<i>FLT3</i>-ITD<sup>neg</sup>, <i>NRAS</i><sup>wt</sup>, <i>KRAS</i><sup>wt</sup>, <i>TP53</i><sup>wt</sup>)</li> <li>• Mutated <i>IDH1</i><sup>b</sup> (<i>TP53</i><sup>wt</sup>)</li> <li>• Mutated <i>DDX41</i><sup>c</sup></li> <li>• Other cytogenetic and/or molecular abnormalities<sup>d</sup> (<i>FLT3</i>-ITD<sup>neg</sup>, <i>NRAS</i><sup>wt</sup>, <i>KRAS</i><sup>wt</sup>, <i>TP53</i><sup>wt</sup>)</li> </ul>
<b>Intermediate</b>	<ul style="list-style-type: none"> <li>• Other cytogenetic and molecular abnormalities<sup>d</sup> (<i>FLT3</i>-ITD<sup>pos</sup> and/or <i>NRAS</i><sup>mut</sup> and/or <i>KRAS</i><sup>mut</sup>; <i>TP53</i><sup>wt</sup>)</li> </ul>
<b>Adverse</b>	<ul style="list-style-type: none"> <li>• Mutated <i>TP53</i></li> </ul>

# 05

## Molecular testing

should screen for all the genetic abnormalities that:

- define disease
- define risk categories
- that are needed for targeted treatment modalities



<https://pixabay.com/photos/dna-genetics-mutation-gene-science-6560897/>

# Molecular testing at AML diagnosis

## AML-associated gene fusions

- *t(15;17)(q24.1;q21.2)/PML::RARA*
- *t(8;21)(q22;q22.1)/RUNX1::RUNX1T1*
- *inv(16)(p13.1q22)* or  
*t(16;16)(p13.1;q22)/CBFB::MYH11*
- *t(9;11)(p21.3;q23.3)/MLLT3::KMT2A*
- *t(6;9)(p22.3;q34.1)/DEK::NUP214*
- *inv(3)* or *t(3;3)(q21.3;q26.2)/GATA2;*  
*MECOM(EVI1)*
- *t(9;22)(q34.1;q11.2)/BCR::ABL1*

**Detectable by RNA based PCR**

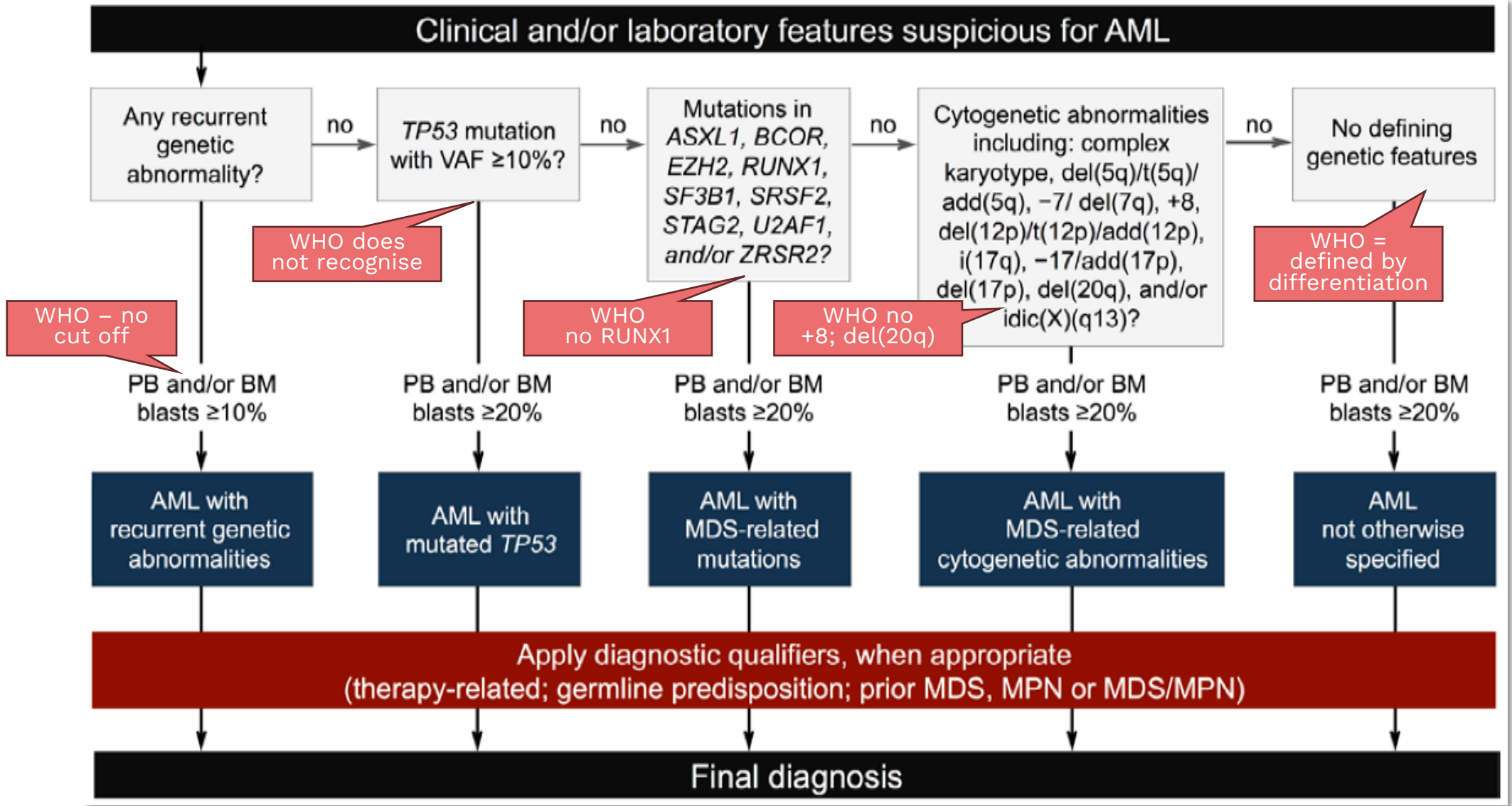
## AML-associated gene mutations

- *FLT3-ITD/ FLT3-TKD, IDH1, IDH2*
- *NPM1*
- *CEBPA, DDX41, TP53; ASXL1, BCOR, EZH2, RUNX1, SF3B1, SRSF2, STAG2, U2AF1, ZRSR2*
- Additional genes recommended to test at Dg: *ANKRD26, BCORL1, BRAF, CBL, CSF3R, DNMT3A, ETV6, GATA2, JAK2, KIT, KRAS, NRAS, NF1, PHF6, PPM1D, PTPN11, RAD21, SETBP1, TET2, WT1*

**Detectable by DNA based PCR or NGS**

# Molecular markers guiding AML

	Target	Frequency	Selected agent
<b>AML with defining genetic abnormalities</b>	<i>PML::RARA</i>	1-25%	All-Trans Retinoic Acid(ATRA), Arsenic Trioxide (ATO)
	<i>RUNX1::RUNX1T1</i>	1-5%	Anti-CD33 ADC (Gemtuzumab ozogamicin)
	<i>CBFB::MYH11</i>	1-5%	Anti-CD33 ADC (Gemtuzumab ozogamicin)
	<i>KMT2A rearranged</i>	1-3%	Menin inhibitors (not approved)
	<i>BCR::ABL1</i>	1%	Imatinib
	<i>NPM1 mutation</i>	15-30%	Anti-CD33 ADC (Gemtuzumab ozogamicin)
	<i>Myelodysplasia relat</i>	10-50%	CPX-351, Venetoclax
<b>Signaling molecules</b>	<i>FLT3 mutation</i>	15-30%	Midostaurin, Gilteritinib, Quizartinib
<b>Epigenetic modifiers</b>	<i>IDH1 mutation</i>	6-8%	Ivosidenib, Olutasidenib
	<i>IDH2 mutation</i>	10-15%	Enasidenib
<b>Tumor suppressor</b>	<i>TP53</i>	5-25%	Nothing approved so far!



Pizzi et al. What's New in the Classification, Diagnosis and Therapy of Myeloid Leukemias. Hemato 4.2 (2023): 112-134.; Döhner et al, Diagnosis and management of AML in adults: 2022 recommendations from an international expert panel on behalf of the ELN. Blood. 2022; 140(12):1345-1377; WHO Classification of Tumours Editorial Board. Haematolymphoid tumours. Lyon (France): IARC; 2024.



# In conclusion

- AML is a complex and diverse disease characterized by a wide range of clinical manifestations, morphological and immunophenotypic characteristics, as well as chromosomal and genomic abnormalities.
- The assessment of morphology and immunophenotyping can provide valuable insights into the potential cytogenetic aberrancies present in certain AML cases. Utilizing both modalities together allows for a highly accurate diagnosis and can highlight the necessity for prompt, targeted treatment even before cytogenetic or molecular confirmation is available (e.g., in cases of acute promyelocytic leukemia, APL).

# In conclusion

- Genetic evaluation forms the foundation of contemporary classifications and risk stratification in AML. Karyotyping, FISH for cases where karyotyping is not feasible, and molecular testing should be conducted for every AML patient, regardless of their age.
- The rapid growth in our understanding of AML genomics has driven a paradigm shift in classification systems, moving from morphology-based to integrated genomic diagnosis. This has enabled better risk stratification and paved the way for personalized therapy in AML.
- The importance of multidisciplinary diagnostics in a holistic approach to treating patients with AML is crucial for achieving enduring therapeutic success.



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Svetlana Angelova  
Inna Ivanova  
Siana Ivanova

### Hematology Clinic

Martin Donchev  
Emil Alexov  
Penka Ganeva  
Janitza Davidkova

# Reading list:

1. Arber DA, et al. International Consensus Classification of Myeloid Neoplasms and Acute Leukemias: integrating morphologic, clinical, and genomic data. *Blood*. 2022 Sep 15;140(11):1200-1228.
2. Bain BJ, Béné MC. Morphological and Immunophenotypic Clues to the WHO Categories of Acute Myeloid Leukaemia. *Acta Haematol*. 2019;141(4):232-244.
3. Bullinger L, Döhner K, Döhner H. Genomics of Acute Myeloid Leukemia Diagnosis and Pathways. *J Clin Oncol*. 2017 Mar 20;35(9):934-946.
4. Döhner H, et al. Diagnosis and management of AML in adults: 2022 recommendations from an international expert panel on behalf of the ELN. *Blood*. 2022;140(12):1345-1377.
5. Falini B, Martelli MP. Comparison of the International Consensus and 5th WHO edition classifications of adult myelodysplastic syndromes and acute myeloid leukemia. *Am J Hematol*. 2023 Mar;98(3):481-492.
6. Kayser S, Levis MJ. The clinical impact of the molecular landscape of acute myeloid leukemia. *Haematologica*. 2023 Feb 1;108(2):308-320.
7. Khoury JD, et al. The 5th edition of the World Health Organization Classification of Haematolymphoid Tumours: Myeloid and Histiocytic/Dendritic Neoplasms. *Leukemia*. 2022;36(7):1703-1719.
8. Lucas F, Hergott CB. Advances in Acute Myeloid Leukemia Classification, Prognostication and Monitoring by Flow Cytometry. *Clin Lab Med*. 2023 Sep;43(3):377-398.
9. Narayanan D, Weinberg OK. How I investigate acute myeloid leukemia. *Int J Lab Hematol*. 2020 Feb;42(1):3-15.
10. Saft L. The role of flow cytometry in the classification of myeloid disorders. *Pathologie (Heidelb)*. 2023 Dec;44(Suppl 3):164-175.
11. WHO Classification of Tumours Editorial Board. Haematolymphoid tumours. Lyon (France): International Agency for Research on Cancer; 2024. (WHO classification of tumours series, 5th ed.; vol. 11). <https://publications.iarc.who.int/637>