

AML: classification, biology and prognosis

Dimitri Breems, MD, PhD

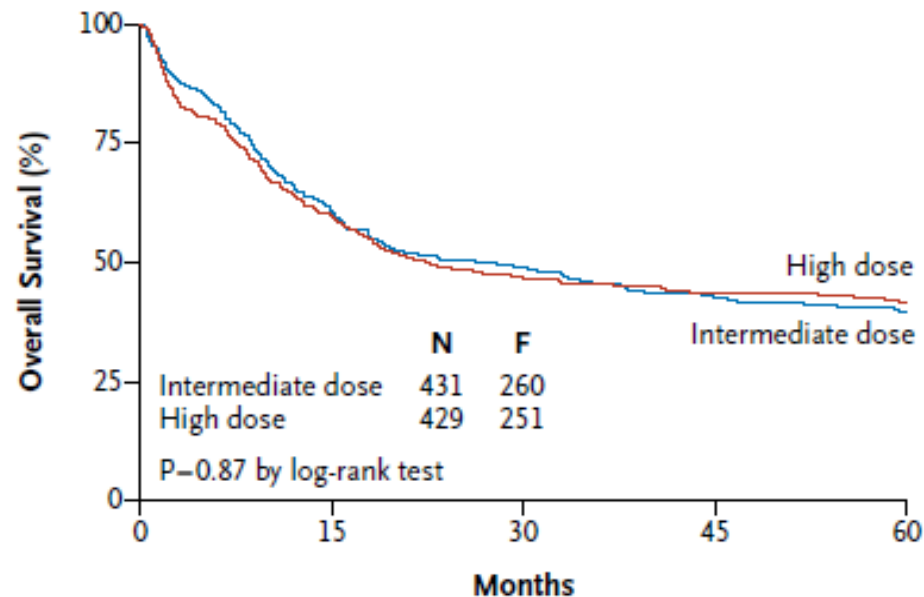
Internist-Hematoloog

Ziekenhuis Netwerk Antwerpen

Acute myeloid leukemia

- Clonal expansion of undifferentiated myeloid precursors
- Impaired hematopoiesis and bone marrow failure
- Heterogeneous response to treatment and prognosis

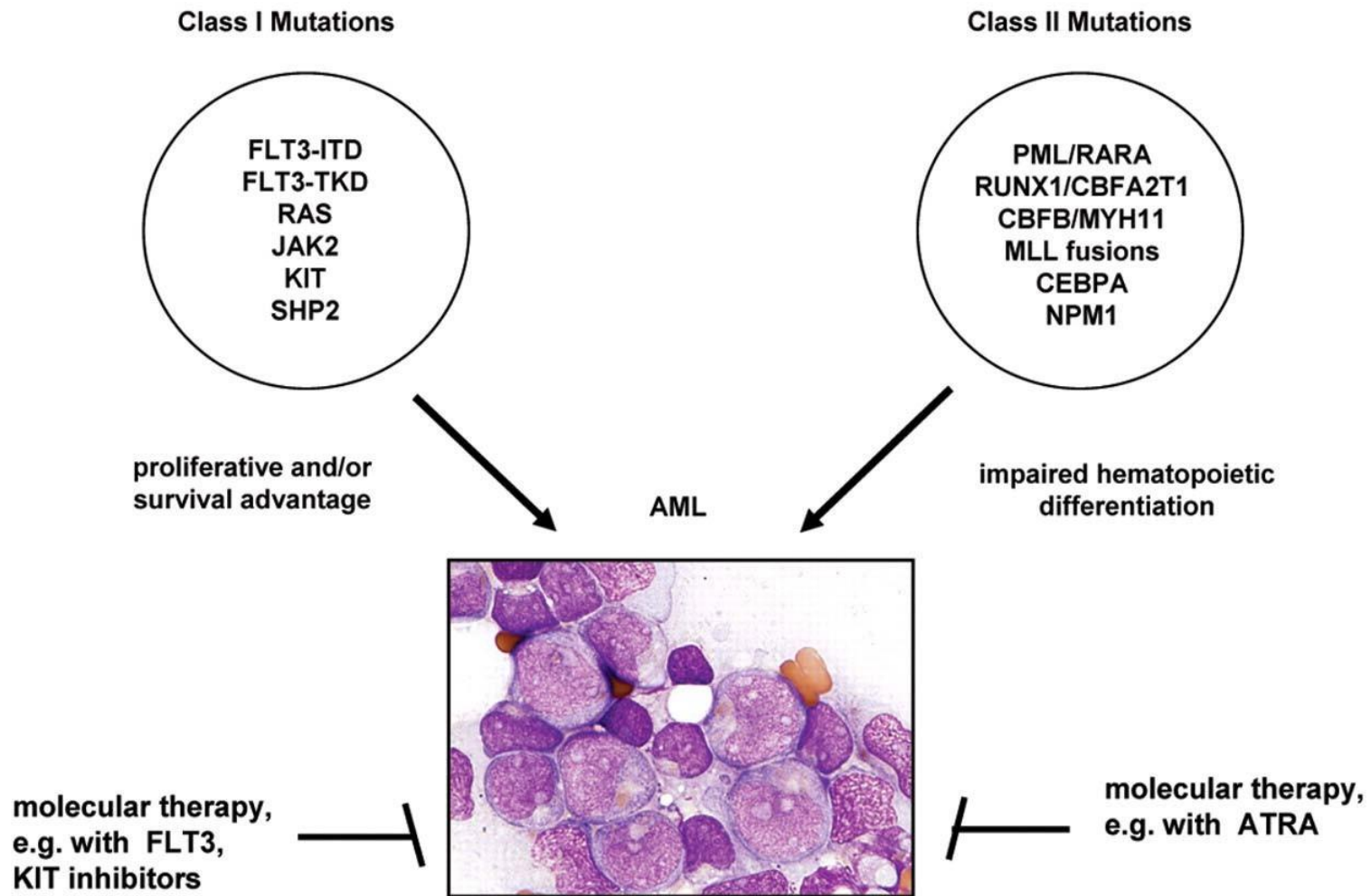
A



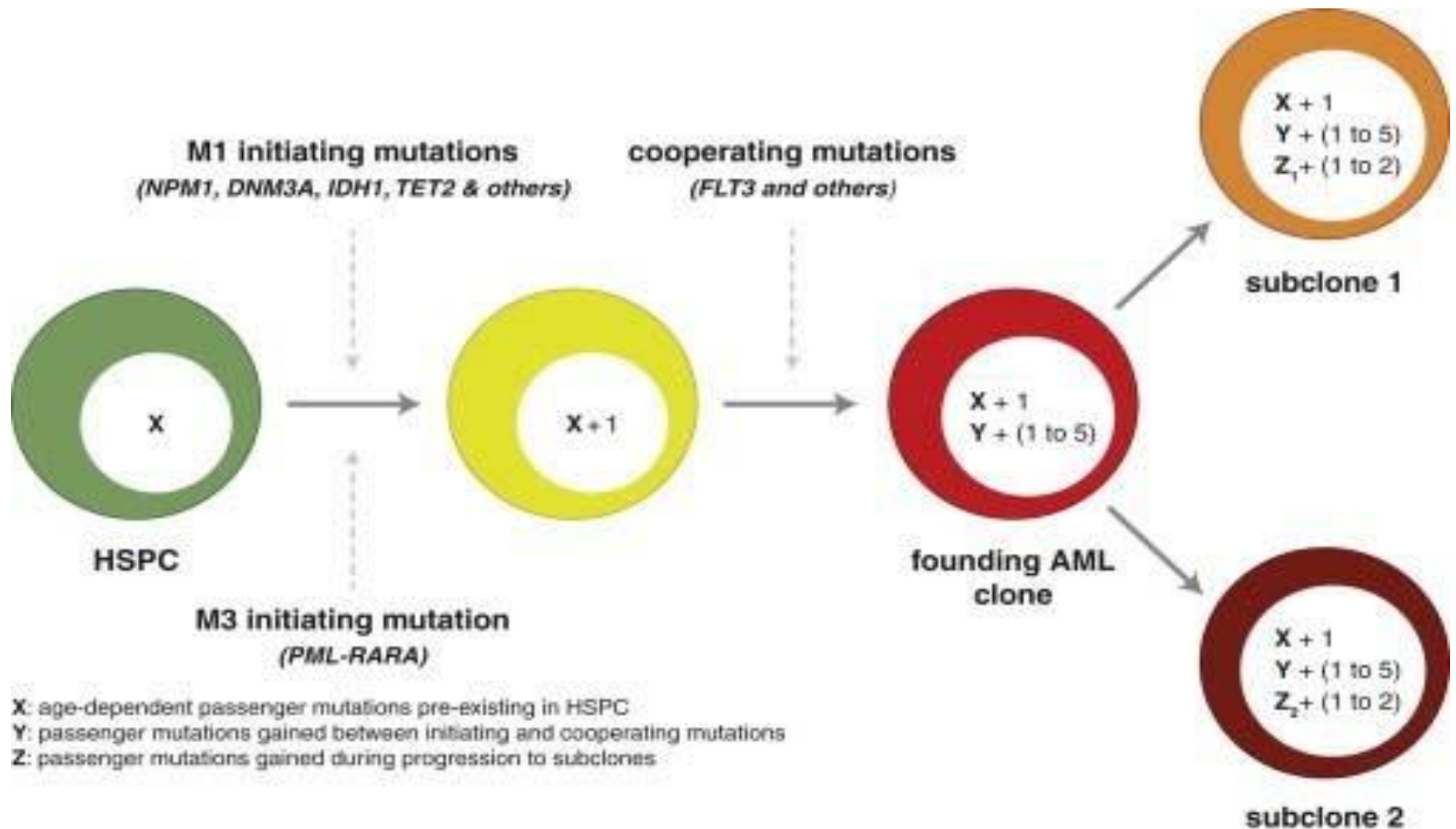
No. at Risk

Intermediate dose	431	259	206	167	109
High dose	429	254	196	174	123

Two cooperating classes of mutations in AML



Evolution of mutations in AML



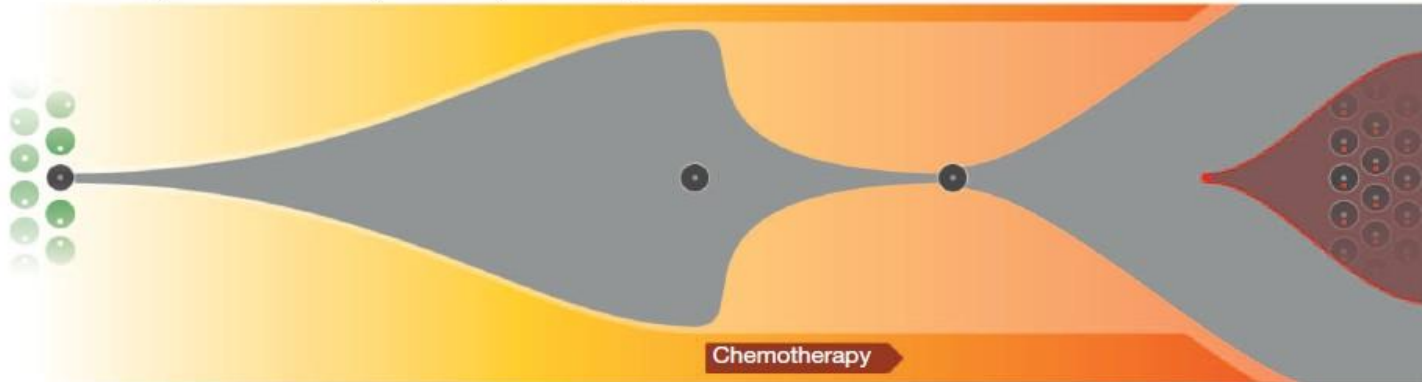
Patterns of relapse in AML

Cell type: ● Normal ● AML

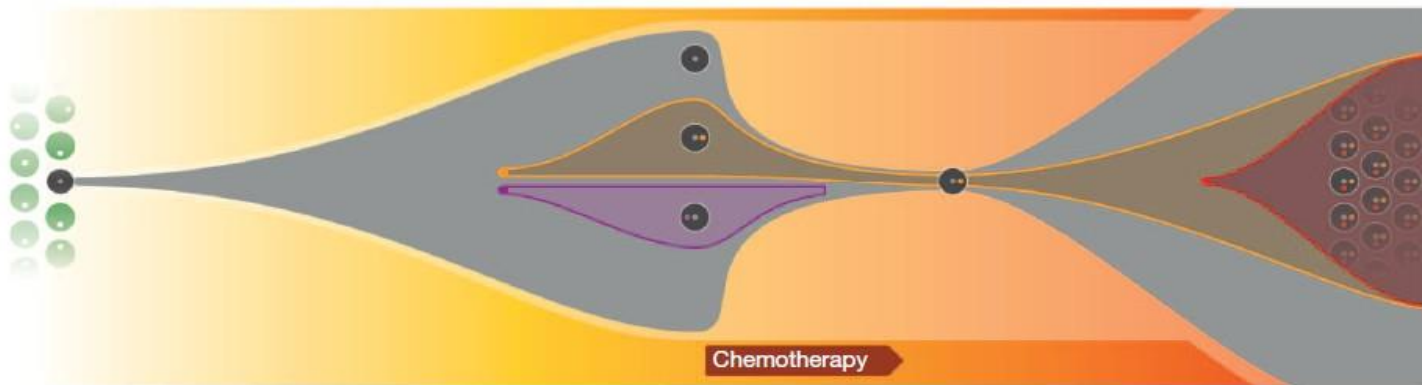
Mutations: ● Founding (cluster 1) ● Relapse enriched (cluster 3) ● Relapse specific (cluster 5) ☆ P
● Primary specific (cluster 2) ● Relapse enriched (cluster 4) ○ Random mutations in HSCs

b

Model 1 (UPNs 400220, 573988, 804168)

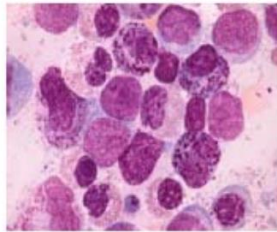


Model 2 (UPNs 426980, 452198, 758168, 869586, 933124)

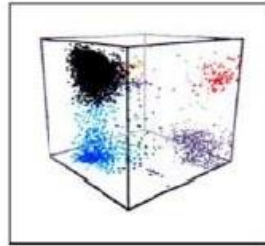


Modern diagnosis of AML

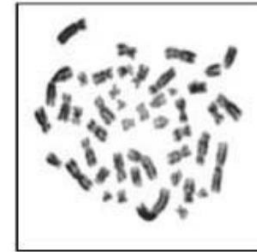
Morphology



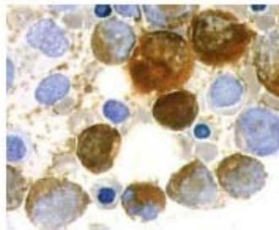
Immunophenotyping



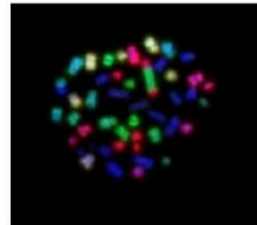
Cytogenetics



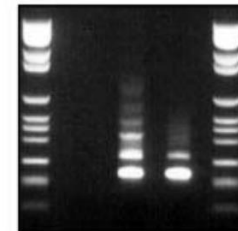
Cytochemistry



FISH



Molecular Biology



FAB classification of AML (morphology)

FAB classification of acute myeloblastic leukaemia

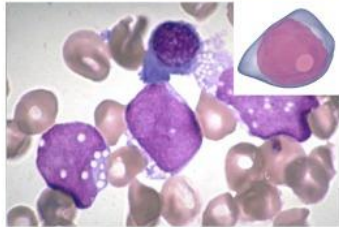


Photo courtesy of: Acute myeloid leukemia pathophysiology, 2012

M0 Acute myeloblastic leukaemia with minimal differentiation

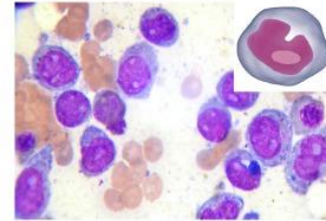
Morphology:

Can resemble LLA-L2 blasts. Medium-sized blasts, rounded nucleus, fine chromatin, basophilic non-granular cytoplasm, prominent nucleoli.

Immunophenotype

- CD13 +
- CD33 +
- CD11b +
- CD11c +
- CD14 +
- CD15 +

FAB classification of acute myeloblastic leukaemia



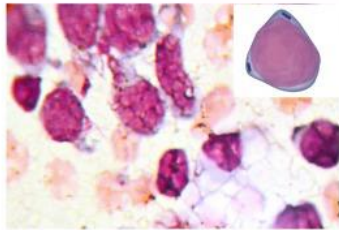
M4 Acute myelomonocytic leukaemia

Morphology:

Large blasts, moderate nucleocytoplasm (n:c) ratio and variable basophilia. The nucleus may be rounded, kidney-shaped or irregular. Nucleoli are usually prominent.

Immunophenotype

- CD13 +
- CD15 +
- CD33 +
- CD11b +
- CD11c +
- CD14 +
- CD64 +
- CD4 +



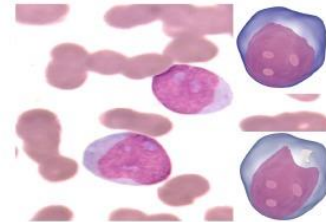
M1 Acute myeloblastic leukaemia without maturation

Morphology:

Medium-sized blasts with high nucleocytoplasm (n:c) ratio, rounded nuclei with immature, dispersed chromatin with one or more prominent nucleoli. Blasts can show fine azurophilic granulation or isolated Auer rods in the cytoplasm in 5% to 10% of cases

Immunophenotype

- MPO +
- CD13 +
- CD33 +
- CD117 +
- CD34 +/-



M5 Acute monoblastic leukaemia

M5a acute monoblastic leukaemia:

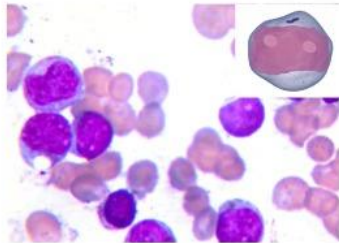
Large blasts with rounded nucleus and dispersed, immature chromatin (1-3 nucleoli) and moderately large and intensely basophilic cytoplasm. The cytoplasm may show some Auer rods and/or prolongations and granulations.

M5b acute monoblastic leukaemia

Promonocytes have a rounded or kidney-shaped nucleus with a less basophilic cytoplasm that is more highly granulated than monoblasts and contains some vacuoles. A finding of erythrophagocytosis together with monocytic blasts suggests a t(8;16) translocation.

Immunophenotype

- CD14 +
- CD68 +
- CD4 +
- CD11c +
- HLA-DR +
- CD64 +



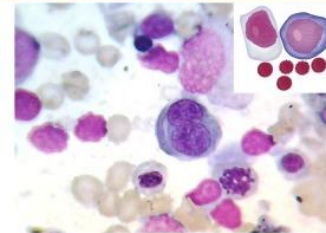
M2 Acute myeloblastic leukaemia with maturation

Morphology:

Small to medium-sized blasts with high nucleocytoplasm (n:c) ratio and rounded nuclei sometimes located in a corner of the cytoplasm. The nucleus shows dispersed, immature chromatin with one or more nucleoli. The cytoplasm is basophilic and can contain traces of primary azurophilic granulation or isolated Auer rods.

Immunophenotype

- MPO +
- CD34 +/-
- CD13 +
- CD15 +
- HLA-DR +/-
- Sudan black +
- CD117 +/-



M6 Acute erythroid leukaemia

M6a erythroid leukaemia with proliferation of mixed blasts: Over 50% erythroid precursors and around 30% myeloblasts.

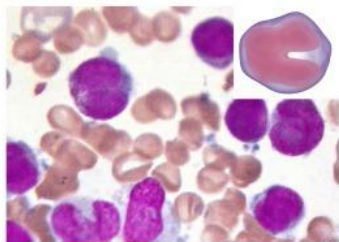
Morphology of erythrocytes in peripheral blood is greatly changed, with schistocytes, "pincer" or mushroom-shaped cells, and spiculated echinocyte and acanthocyte cells.

M6b pure erythroid leukaemia:

Erythroids make up 80% of bone marrow cells, with less than 3% myeloid cells. Erythrocytes in peripheral blood consist of macrocytes, basophilic stippling, Howell-Jolly bodies or Cabot rings.

Immunophenotype

- CD13 +
- CD33 +
- CD15 +
- Glycophorin A +
- Glycophorin C +



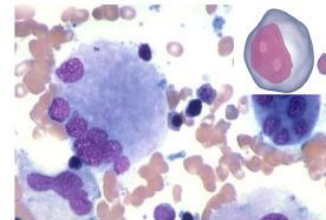
M3 Promyelocytic leukaemia

Morphology:

Abundant, intensely azurophilic granulation. The nucleus is usually monocytic in appearance (reniform) and is either irregular or bilobed with a deep cleft. Scarcely basophilic cytoplasm due to the proliferation of azurophilic granulation. Some atypical promyelocytes also contain elongated or splinter-shaped crystalline cytoplasmic inclusions specific to this type of leukaemia. These usually form clumps, but differ from Auer rods in that they show a tubular substructure on electronic microscopy.

Immunophenotype

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



M7 Acute megakaryocytic leukaemia

Morphology:

Highly immature, polymorphic blasts. The nucleus is eccentric with dispersed, reticulated chromatin and 1-3 prominent nucleoli. The cytoplasm is non-granular, basophilic, and very similar in appearance to platelets, with pseudopods or granulations. Micromegakaryocytes and fragments of megakarioblasts are seen in peripheral blood (giant platelets, some highly degranulated).

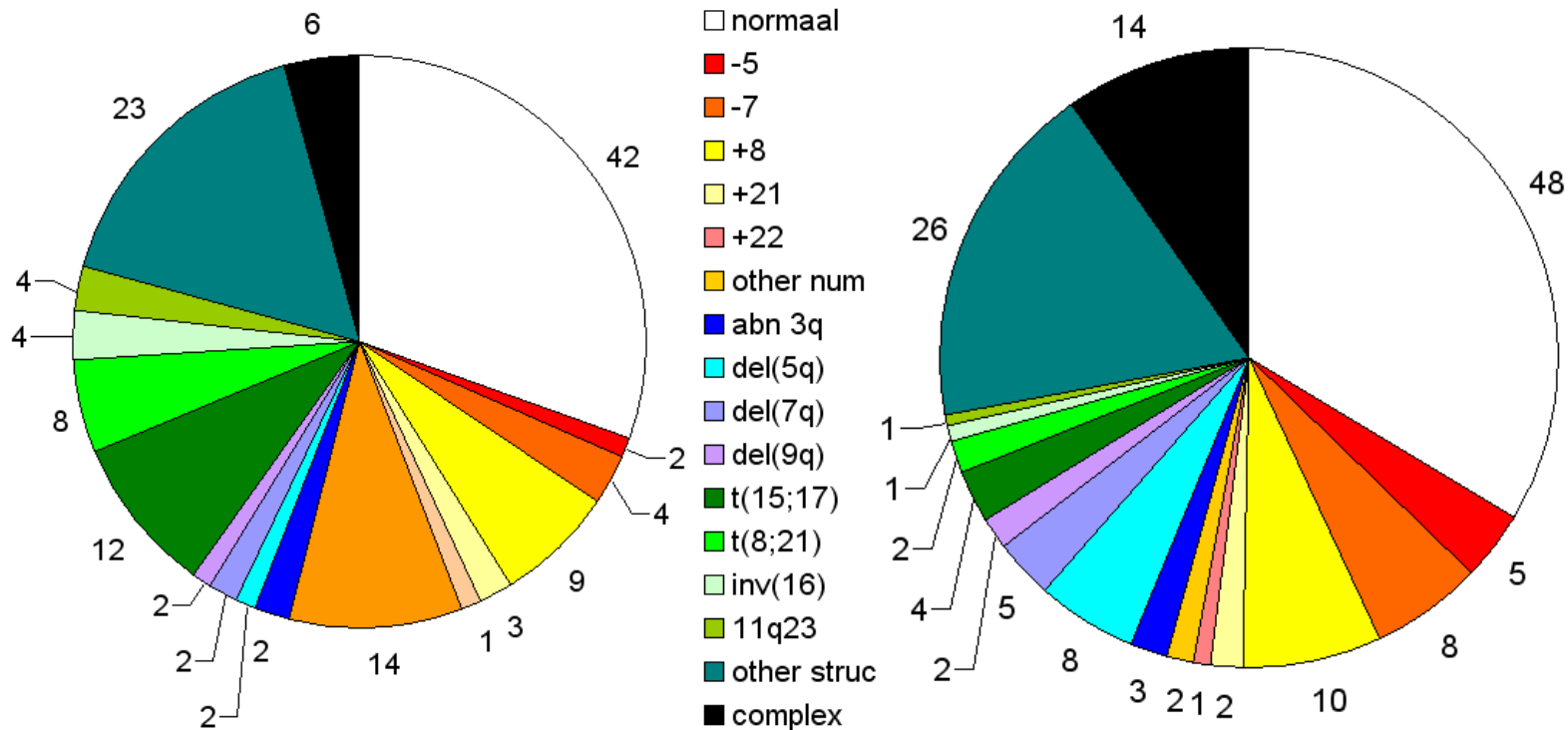
Immunophenotype

- CD41 +
- CD61 +
- CD42 +
- CD13 +
- CD33 +
- CD34 +

Markers for the diagnosis of AML and MPAL

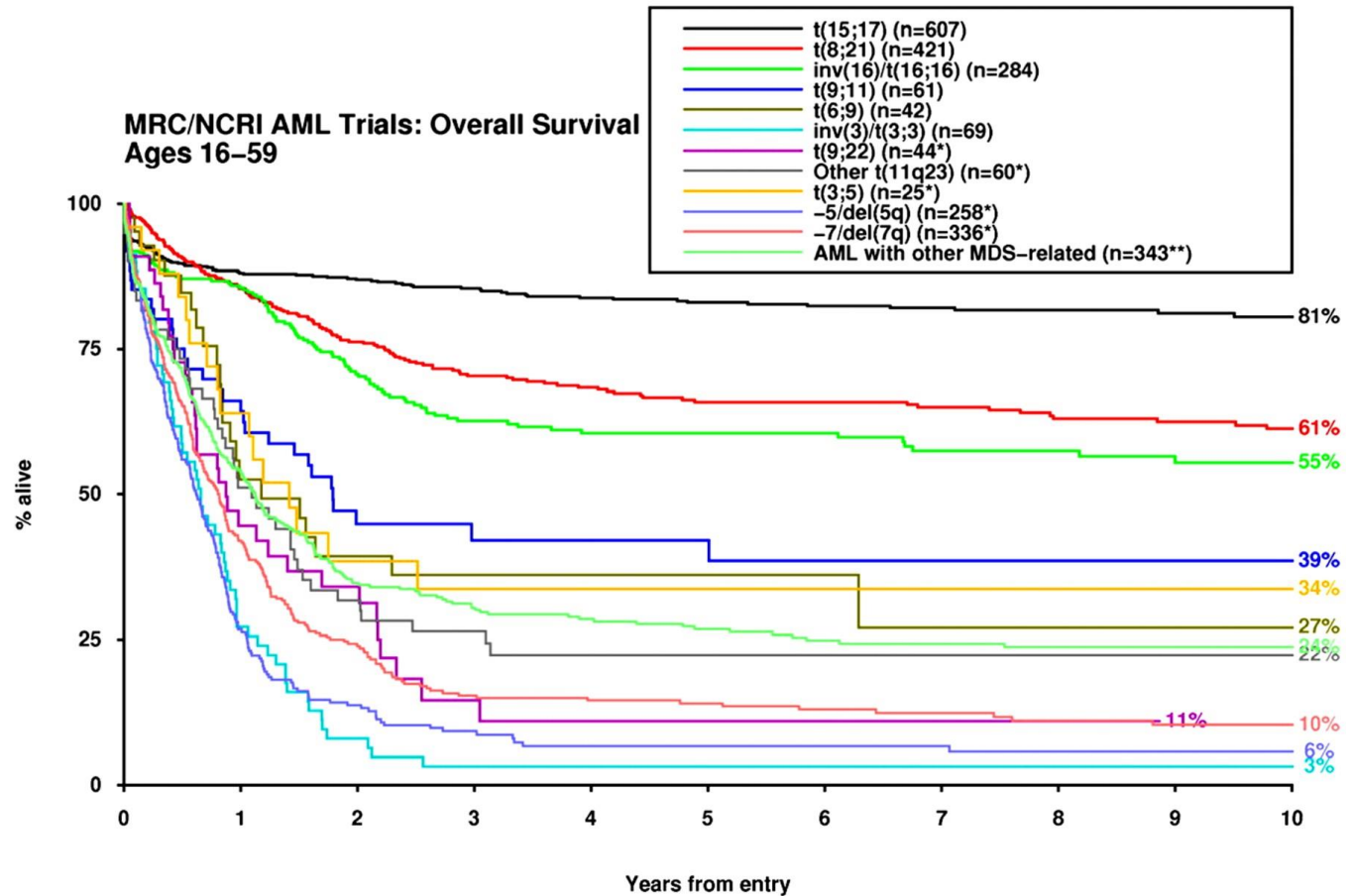
Expression of cell-surface and cytoplasmic markers	
Diagnosis of AML*	
Precursors [†]	CD34, CD117, CD33, CD13, HLA-DR
Granulocytic markers [‡]	CD65, cytoplasmic MPO
Monocytic markers [§]	CD14, CD36, CD64
Megakaryocytic markers	CD41 (glycoprotein IIb/IIIa), CD61 (glycoprotein IIIa)
Erythroid markers	CD235a (glycophorin A), CD36
Diagnosis of MPAL[¶]	
Myeloid lineage	MPO (flow cytometry, immunohistochemistry, or cytochemistry) or monocytic differentiation (at least 2 of the following: nonspecific esterase cytochemistry, CD11c, CD14, CD64, lysozyme)
T-lineage	Strong [#] cytoplasmic CD3 (with antibodies to CD3 ε chain) or surface CD3
B-lineage ^{**}	Strong [#] CD19 with at least 1 of the following strongly expressed: cytoplasmic CD79a, cCD22, or CD10 or weak CD19 with at least 2 of the following strongly expressed: CD79a, cCD22, or CD10

Cytogenetic distribution of AML



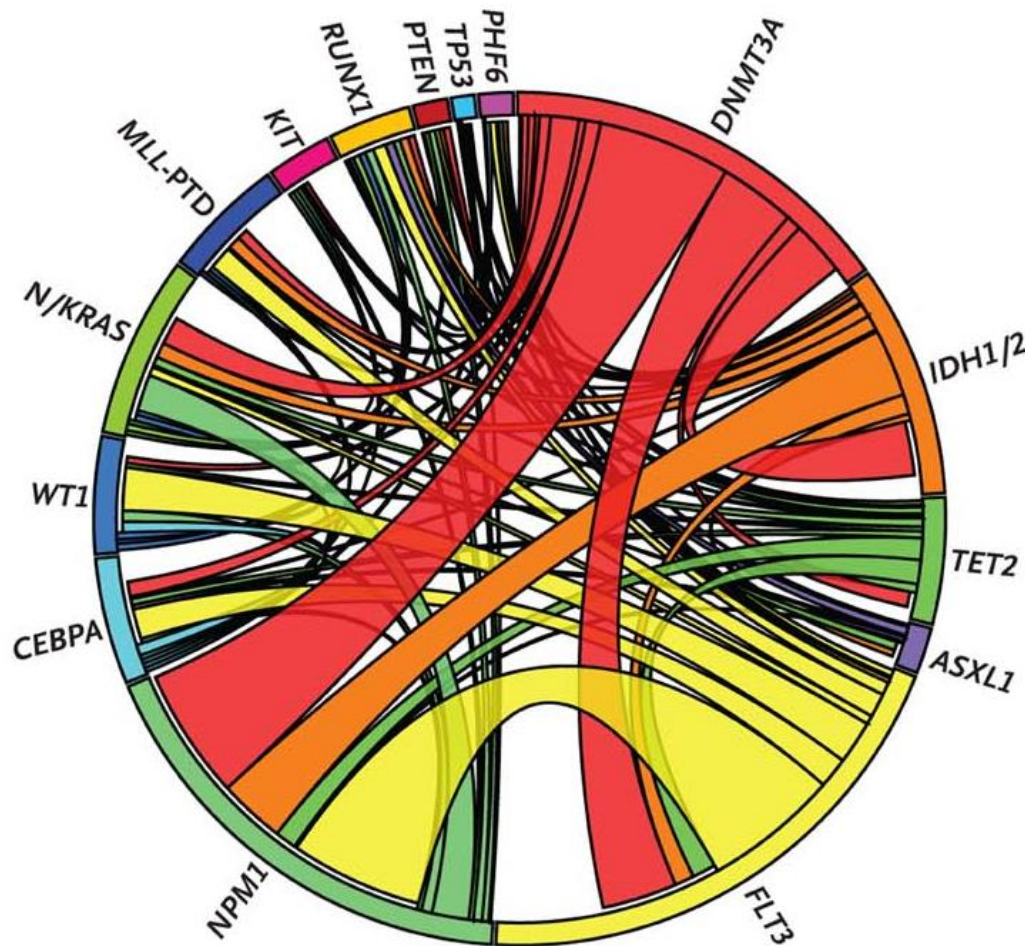
Based on Grimwade et al, Blood 1998;
Grimwade et al, Blood, 2001

Impact of specific genetic aberrations on survival in AML



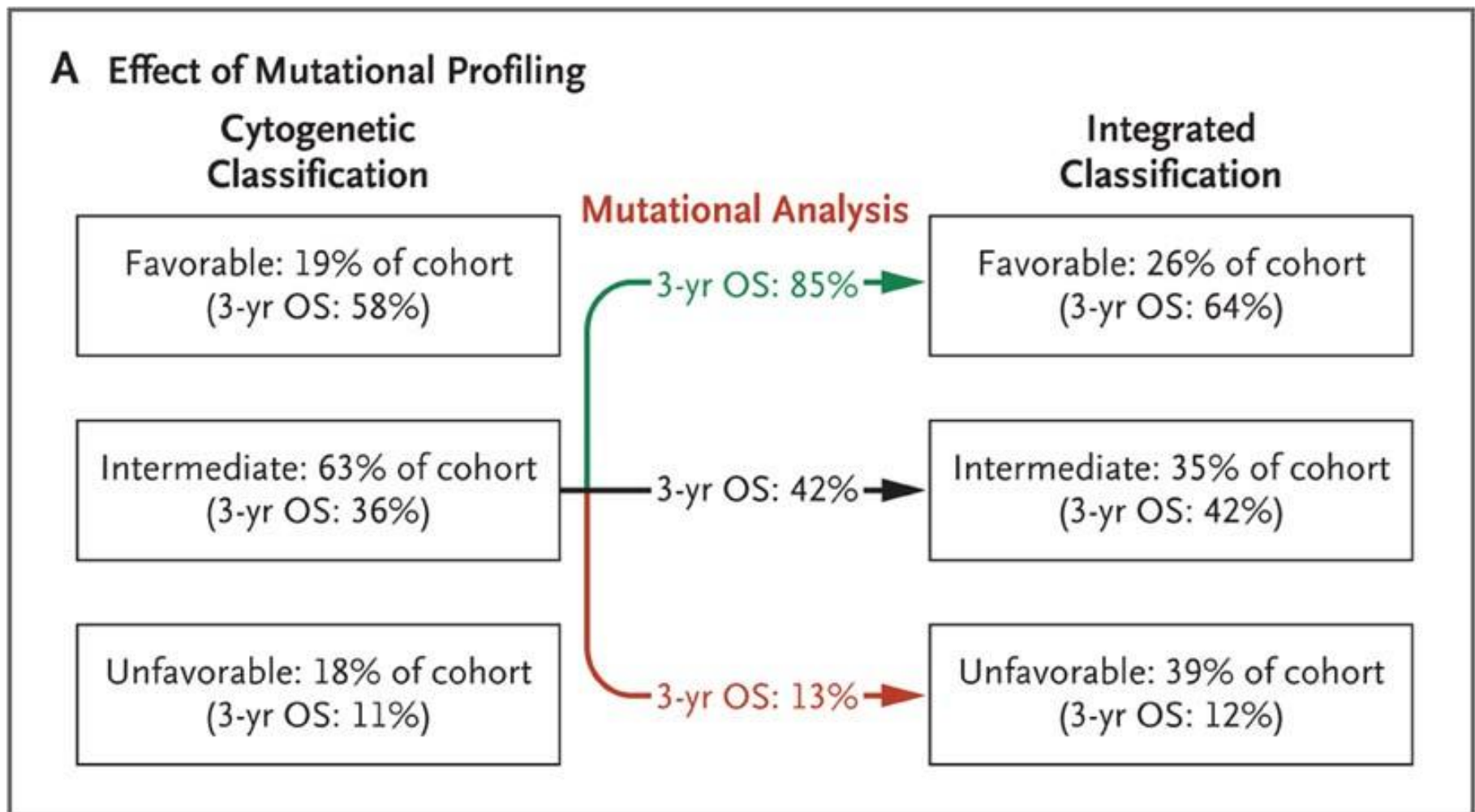
Mutational complexity of AML

A Total Cohort



Gene	Overall Frequency (%)
FLT3 (ITD, TKD)	37 (30, 7)
NPM1	29
DNMT3A	23
NRAS	10
CEBPA	9
TET2	8
WT1	8
IDH2	8
IDH1	7
KIT	6
RUNX1	5
MLL-PTD	5
ASXL1	3
PHF6	3
KRAS	2
PTEN	2
TP53	2
HRAS	0
EZH2	0

Comprehensive mutational profiling for risk stratification and clinical management of AML.

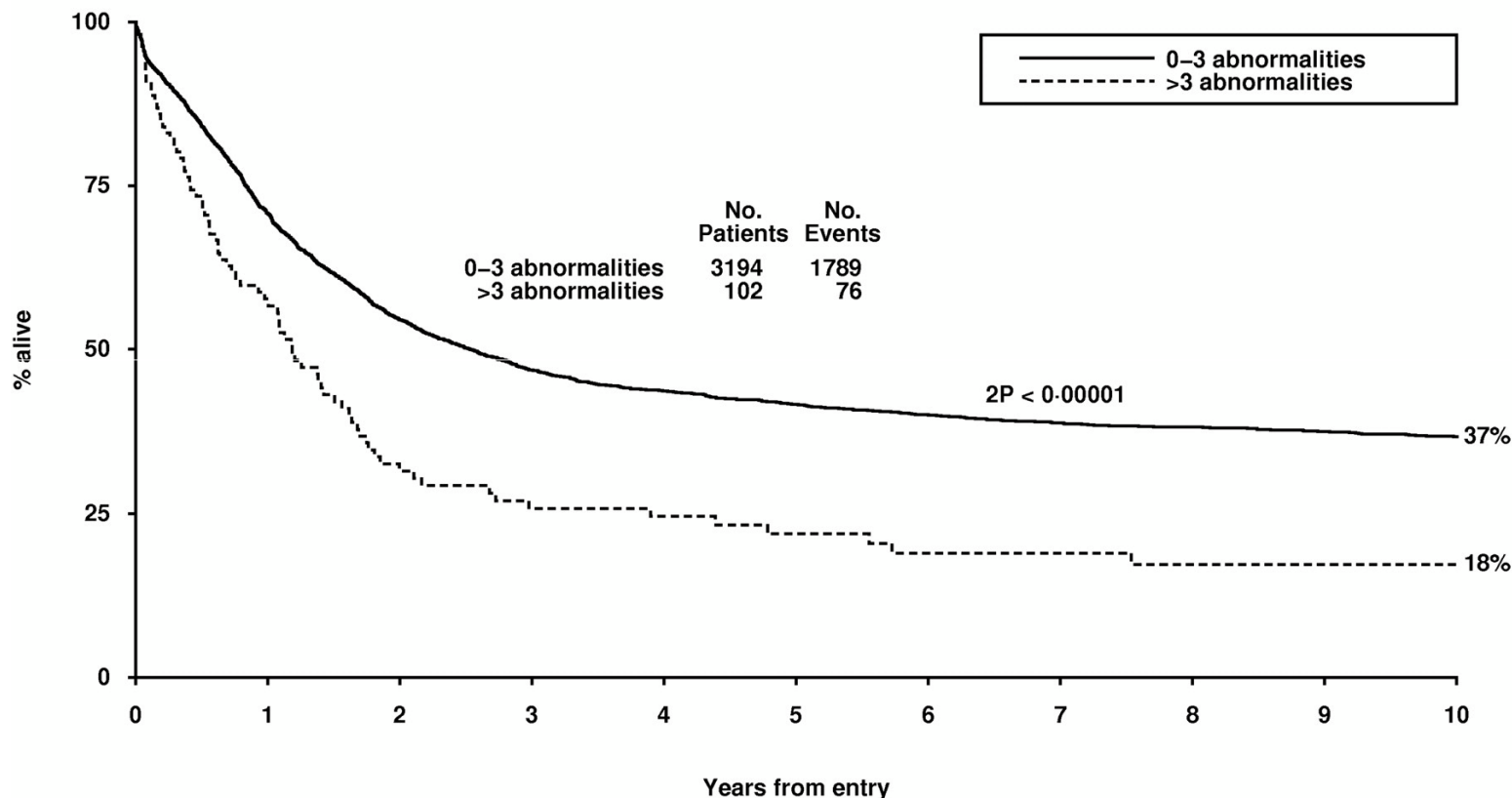


2022 ELN risk genetic stratification

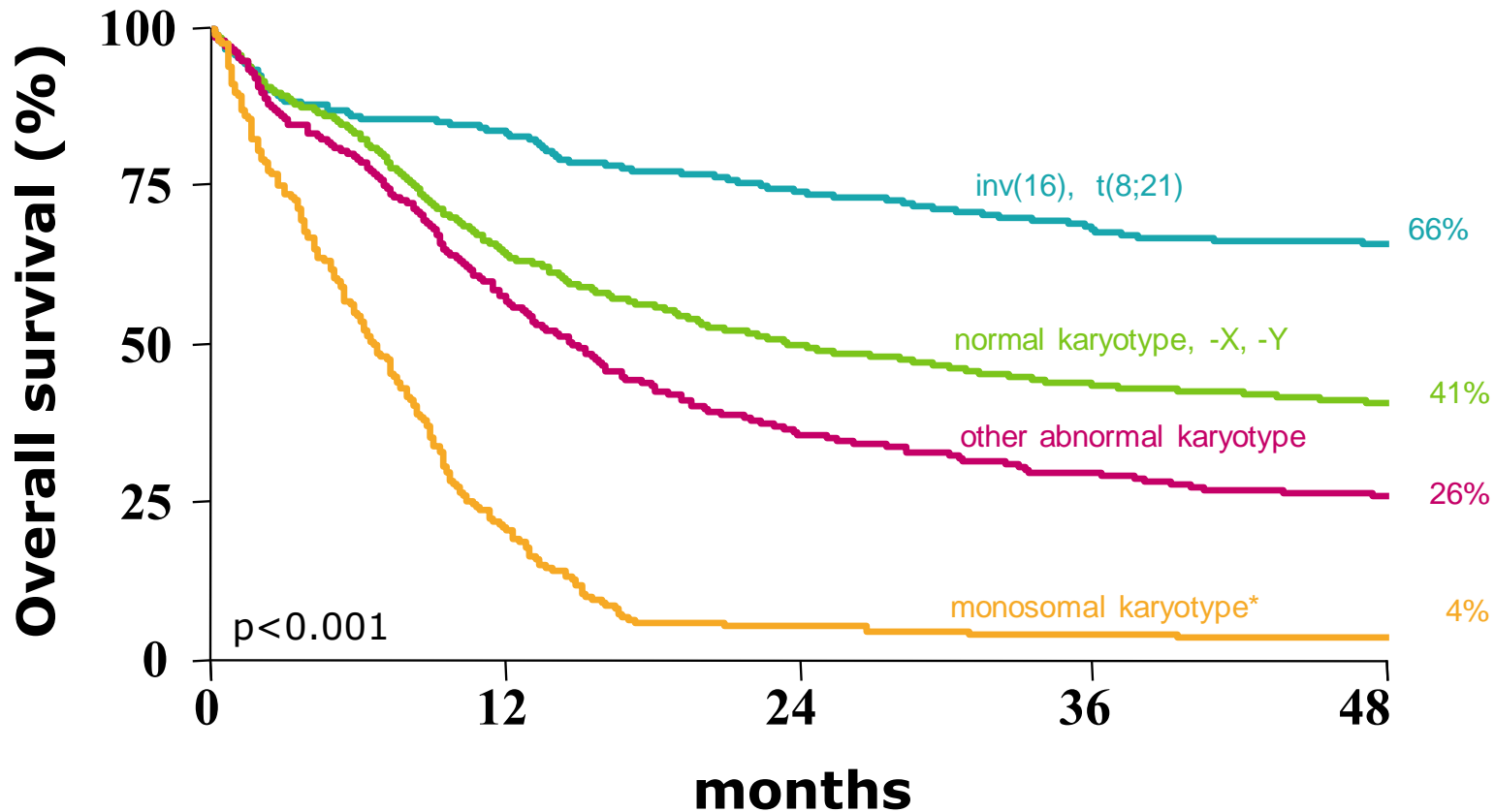
Risk category	Genetic abnormality
Favorable	t(8;21)(q22;q22.1); <i>RUNX1-RUNX1T1</i>
	inv(16)(p13.1q22) or t(16;16)(p13.1;q22); <i>CBFB-MYH11</i>
	Mutated <i>NPM1</i> without <i>FLT3-ITD</i>
	bZIP in-frame mutated <i>CEBPA</i>
Intermediate	Mutated <i>NPM1</i> and <i>FLT3-ITD</i>
	Wild-type <i>NPM1</i> with <i>FLT3-ITD</i> (without adverse-risk genetic lesions)
	t(9;11)(p21.3;q23.3); <i>MLLT3-KMT2A</i>
	Cytogenetic and/or molecular 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>
	t(8;16)(p11.2;p13.3)/ <i>KAT6A-CREBBP</i>
	inv(3)(q21.3q26.2) or t(3;3)(q21.3;q26.2); <i>GATA2,MECOM(EVI1)</i>
	t(3q26.2;v)/ <i>MECOM(EVI1)</i> -rearranged
	-5 or del(5q); -7; -17/abn(17p)
	Complex karyotype, monosomal karyotype
	Mutated <i>ASXL1, BCOR, EZH2, RUNX1, SF3B1, SRSF2, STAG2, U2AF1, and/or ZRSR2</i>
	Mutated <i>TP53</i>

Impact of karyotype complexity on survival for AML patients not belonging to favourable subgroups

MRC/NCRI AML Trials: Overall Survival
Ages 16–59 excluding known prognostic abnormalities



Overall survival in AML patients categorized into favourable, intermediate, adverse and very adverse cytogenetic risk groups



Two or more autosomal monosomy or
1 auto monosomy with structural abn (n=184)
= **monosomal karyotype***

Acute myeloid leukemia

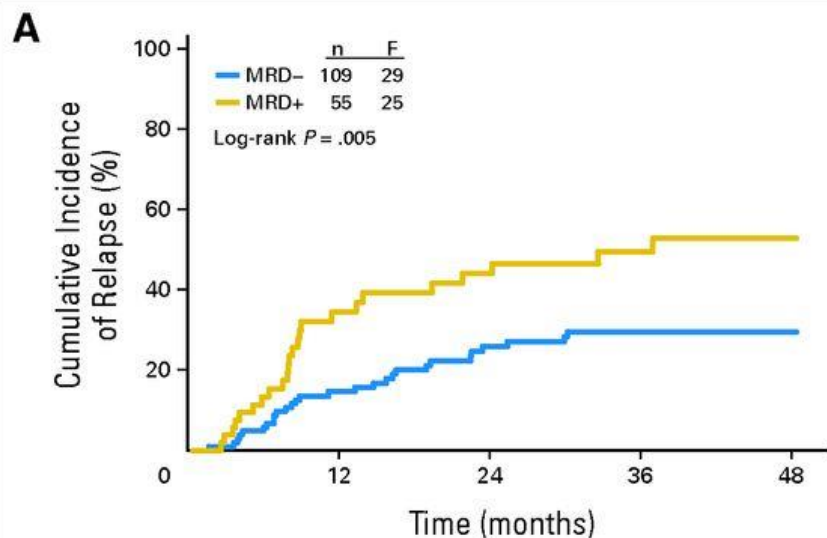
Prognosis according age

Age	Complete remission	Overall survival
18 - 60 years	80%	40% at 5 years
>60 years	65%	28% at 2 years

Prognostic value of minimal residual disease detection in AML with flowcytometry

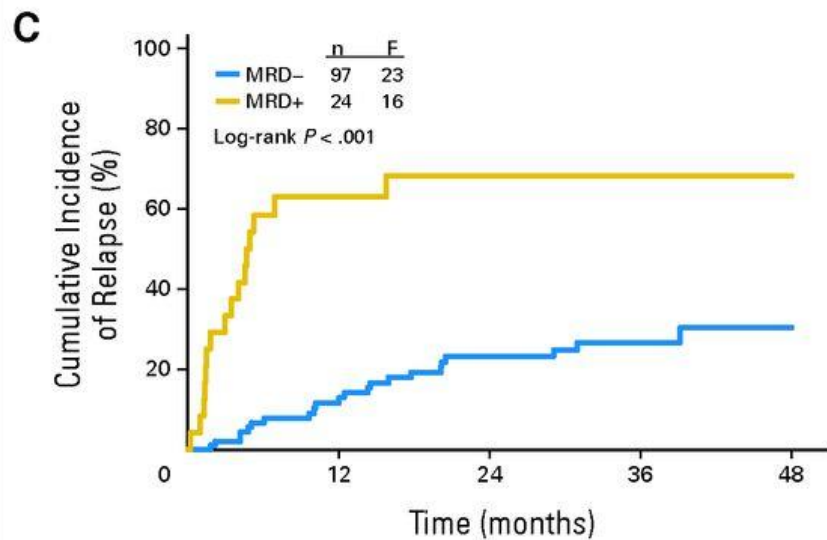
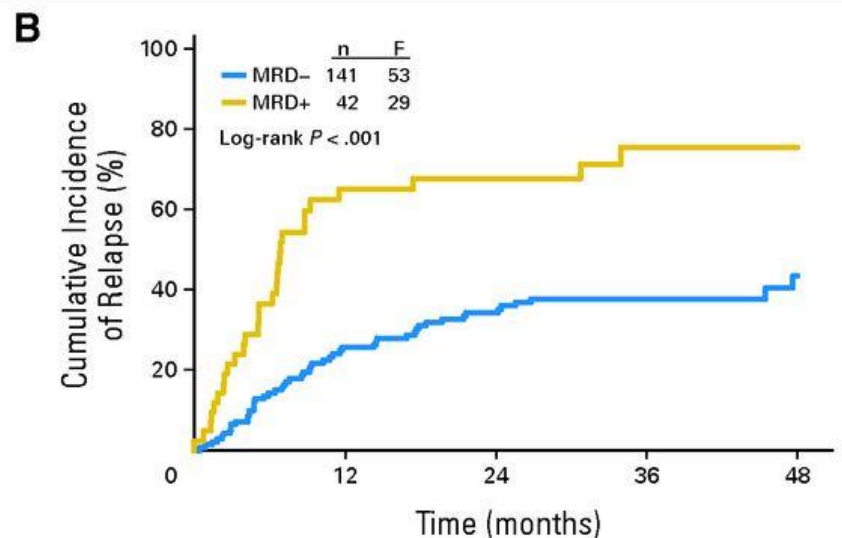
- 517 AML patients, 18-60 years
- 85% of all AMLs:
 - Leukemia-associated phenotype by immunoflow cytometry is determined at diagnosis
 - Minimal residual disease assessment in complete remission:
 - After chemotherapy induction cycle 1
 - After chemotherapy cycle 2
 - After consolidation treatment

Relapse incidence by minimal residual disease



No. at risk

MRD-	109	81	62	45	11
MRD+	55	28	22	15	8



No. at risk

MRD-	97	69	53	24	5
MRD+	24	8	5	3	1

A: After chemotherapy induction cycle 1
 B: After chemotherapy cycle 2
 C: After consolidation treatment

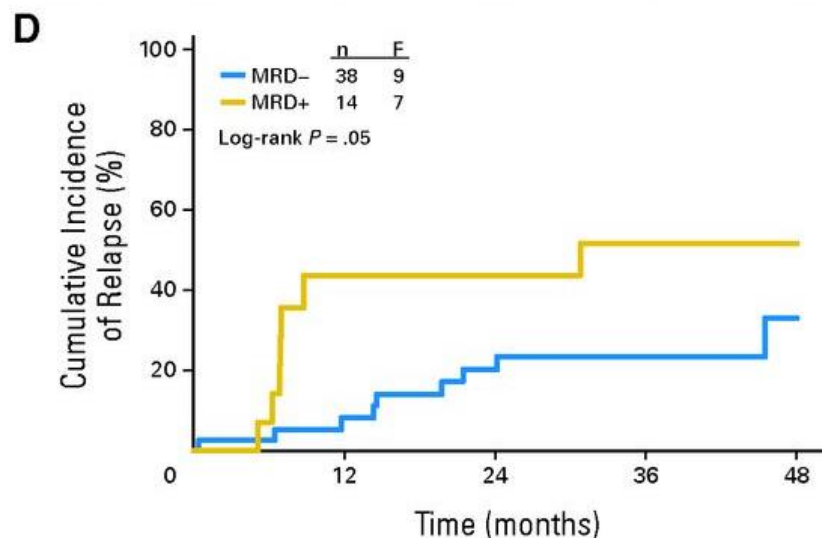
Relapse incidence by minimal residual disease

After chemotherapy cycle 2

D: Good risk

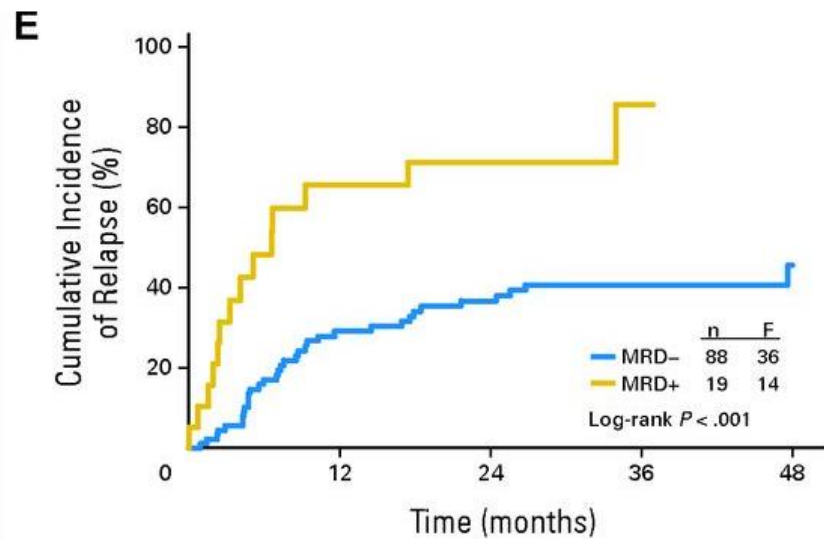
C: Intermediate risk

F: Poor risk



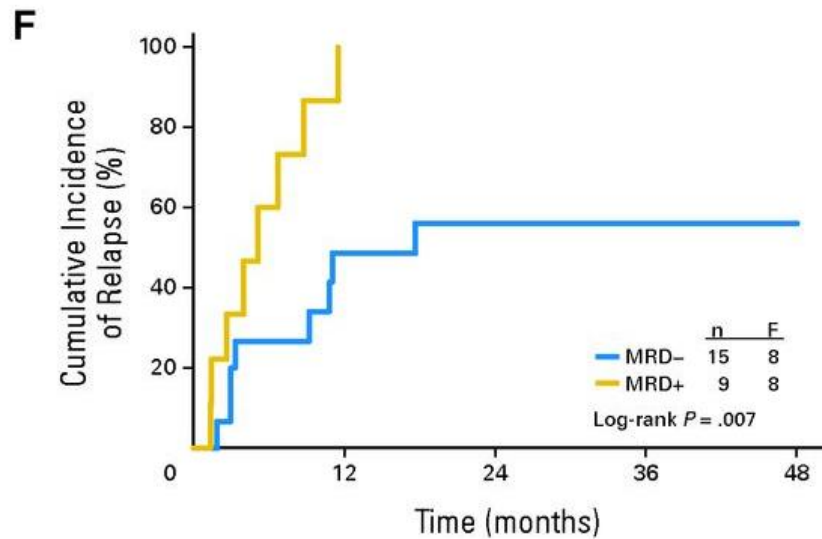
No. at risk

MRD-	38	31	24	18	6
MRD+	14	7	7	5	2



No. at risk

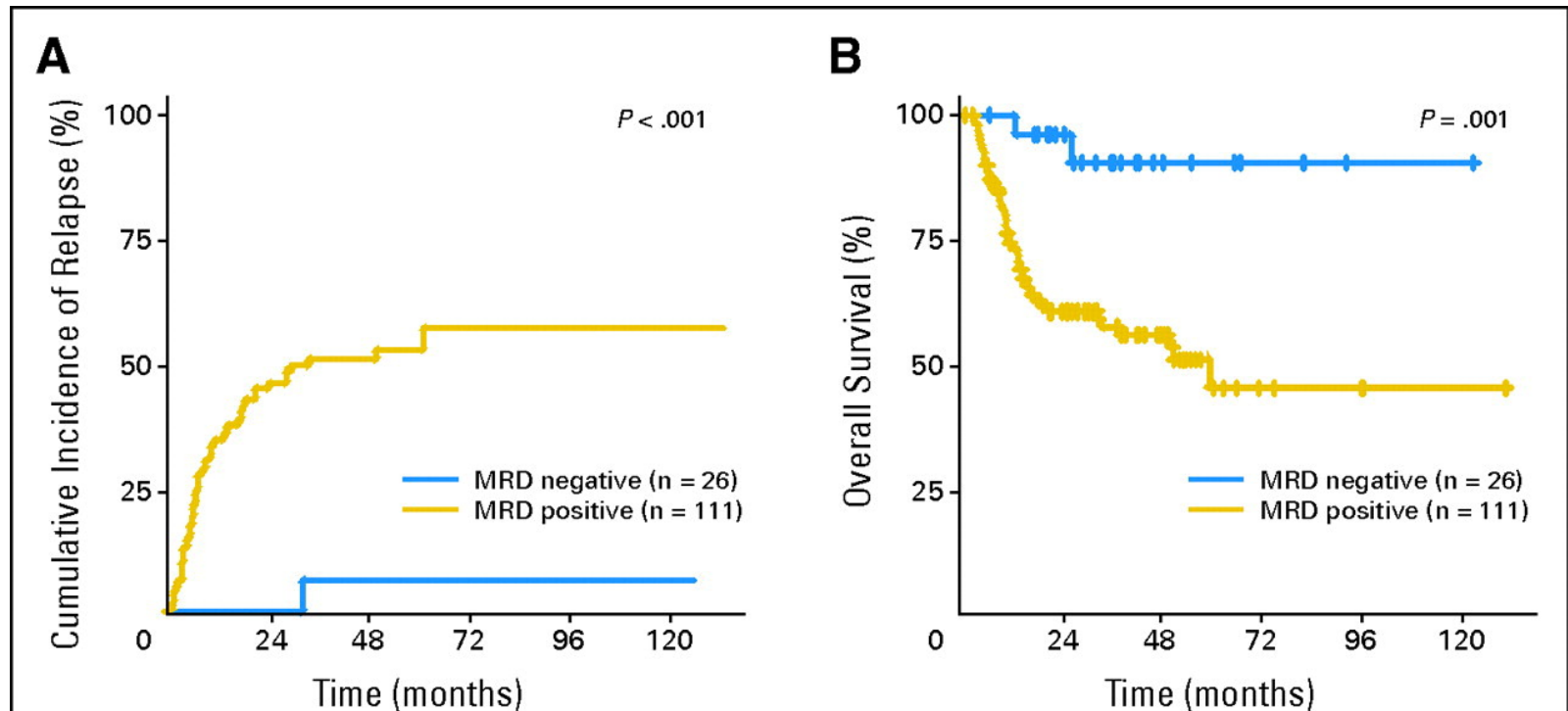
MRD-	88	58	48	36	11
MRD+	19	6	5	1	0



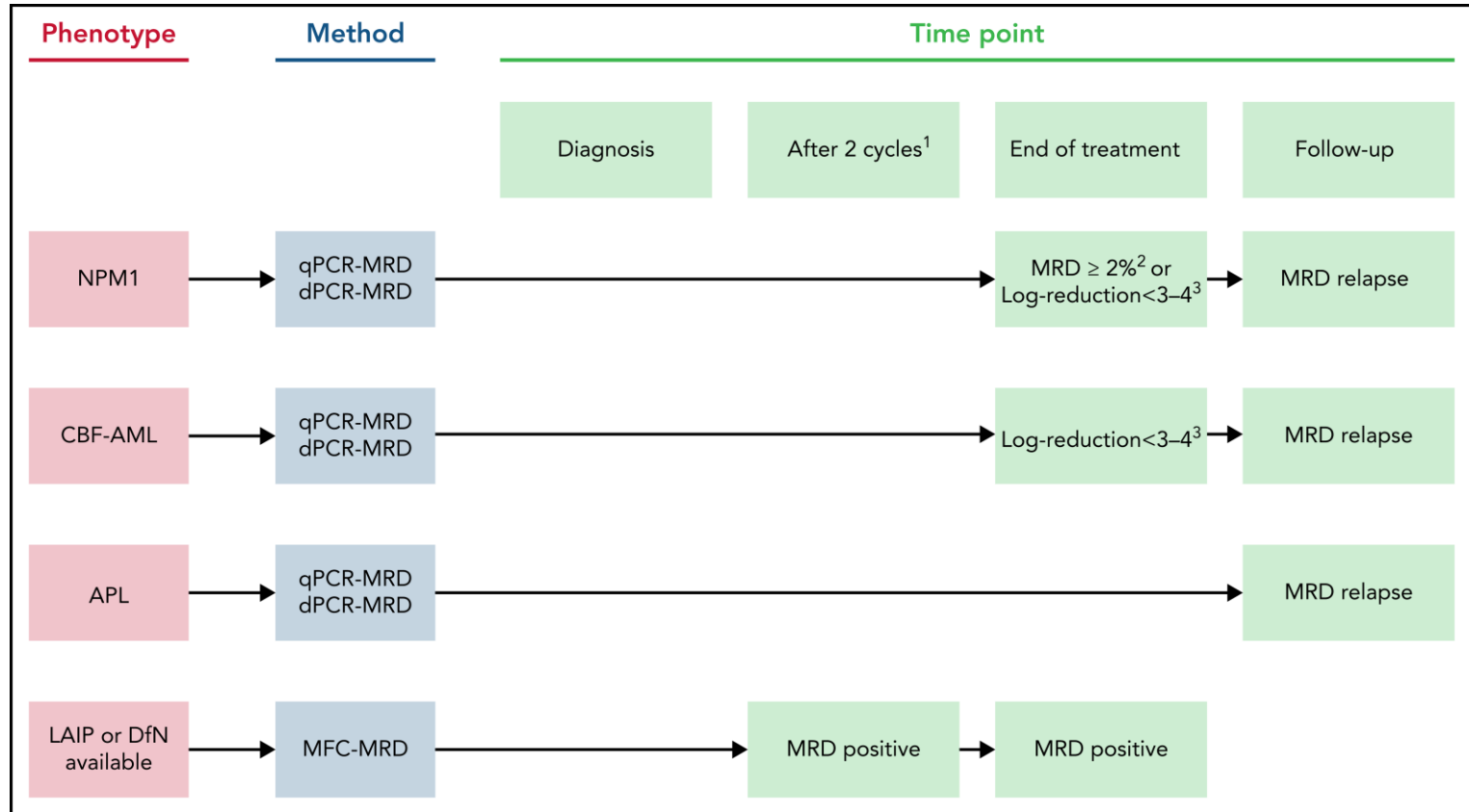
No. at risk

MRD-	15	7	6	3	1
MRD+	9	0	0	0	0

Prognostic value of minimal residual disease detection in NPM1-mutated AML



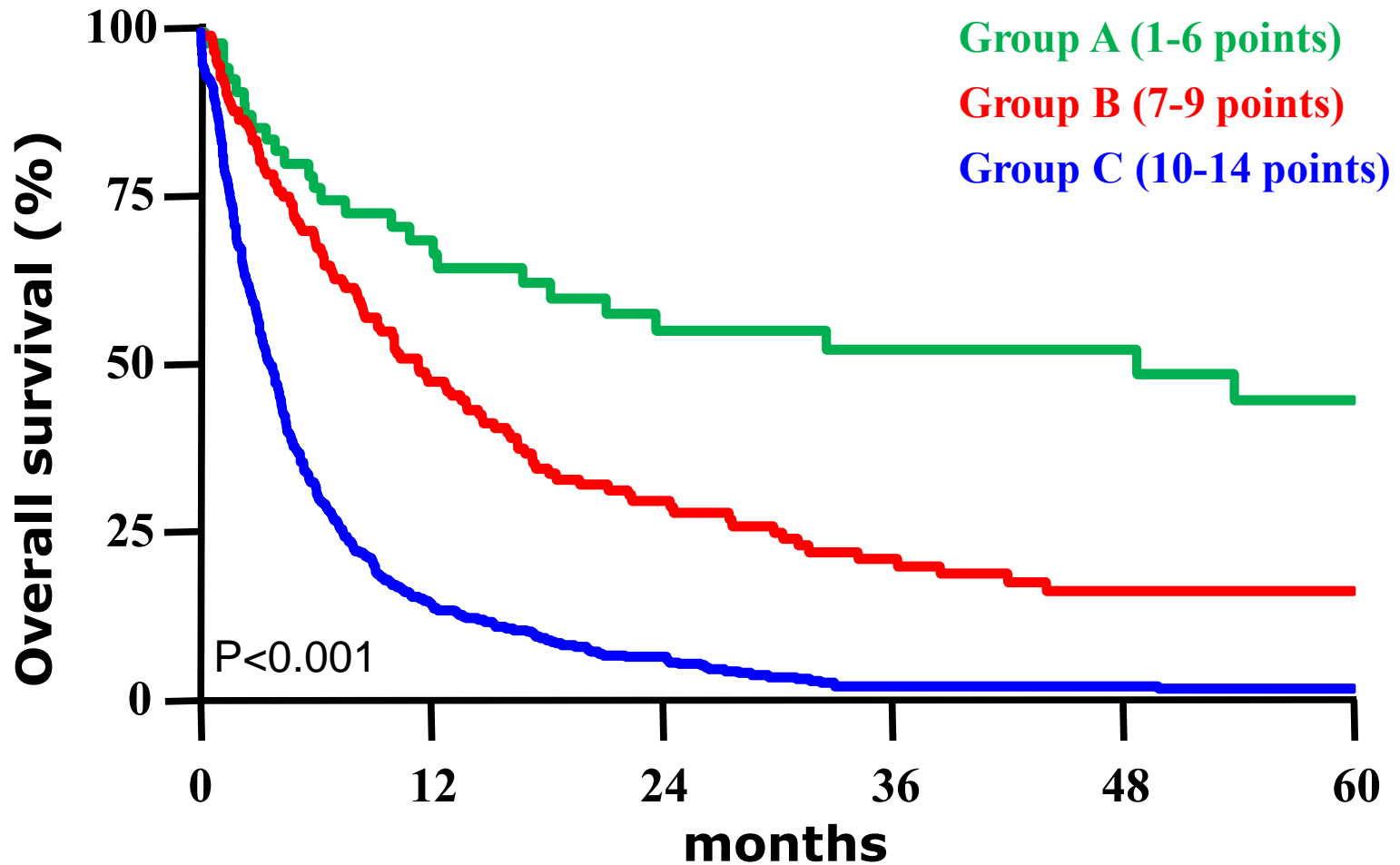
2021 Update on MRD in acute myeloid leukemia: a consensus document from the European LeukemiaNet MRD Working Party



Prognostic score (0 – 14 points) for AML at first relapse

Prognostic factor		Coefficient	Points
Relapse free interval from first CR	>18 months	0	0
	7 to 18 months	0.69	3
	<=6 months	1.28	5
Cytogenetics at diagnosis	t(16;16) or inv(16)	0	0
	t(8;21)	0.68	3
	Other	1.19	5
Age at first relapse	<=35 years	0	0
	36 to 45 years	0.21	1
	>45 years	0.47	2
STC before first relapse	No	0	0
	Yes	0.49	2

Overall survival among patients with AML in first relapse according to prognostic group

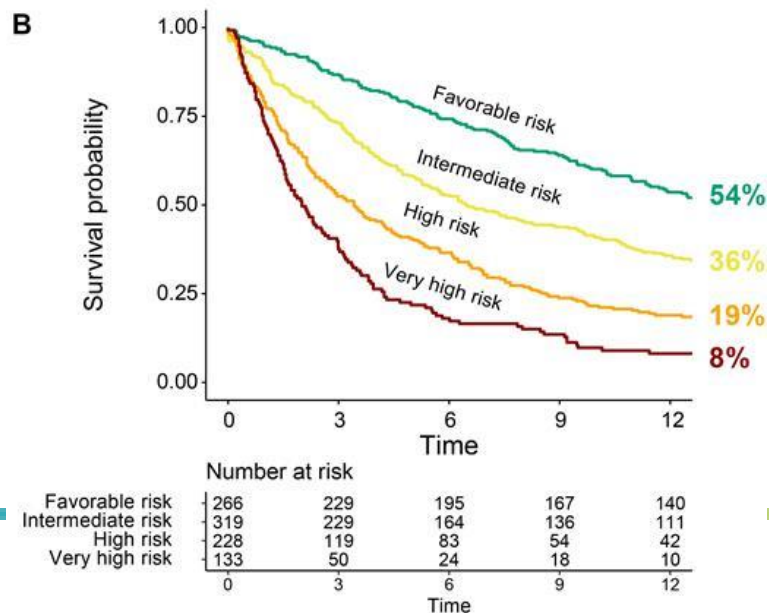


Novel prognostic model for patients with AML in first relapse with improved prognostic accuracy

A

Variable	Points
Clinical data	
Age \geq 60 (years)	2
Relapse free interval \leq 1 (year)	2
WBC \geq 10 ($\times 10^9/L$)	1
Previous allo-SCT	2
Cytogenetic data	
CK/MK	2
No t(16;16) or t(8;21)	3
t(v;11q23)	2
Molecular data	
TP53	2
FLT3-ITD	1

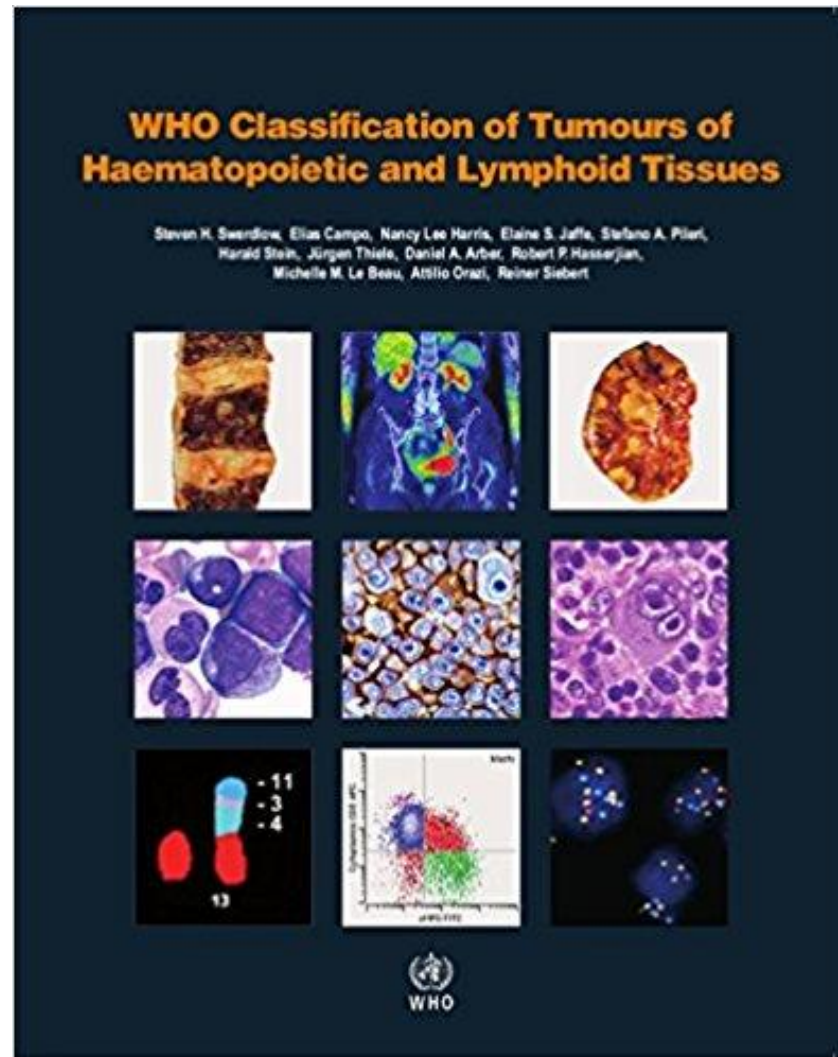
Favorable risk: ≤ 5 points
Intermediate risk: 6-7 points
High risk: 8-9 points
Very high risk: ≥ 10 points



Identification of molecular abnormalities have therapeutic consequences

<u>Abnormality</u>	<u>Treatment option</u>
□ PML-RARA gene fusion	Retenoic acid (ATRA)
□ FLT3 mutations	FLT3-inhibitors
□ IDH1 mutations	IDH1 inhibitors
□ IDH2 mutations	IDH2 inhibitors
□ KMT2A rearrangements	Menin/KMT2A inhibitors
□ NPM1 mutations	Menin/KMT2A inhibitors

WHO classification



Swerdlow et al, Revised 4th Edition, 2017

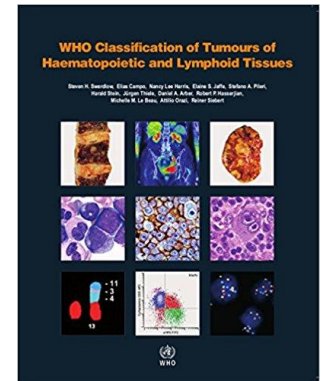
Contents

Chapter 7: Myeloid neoplasma with germline predisposition

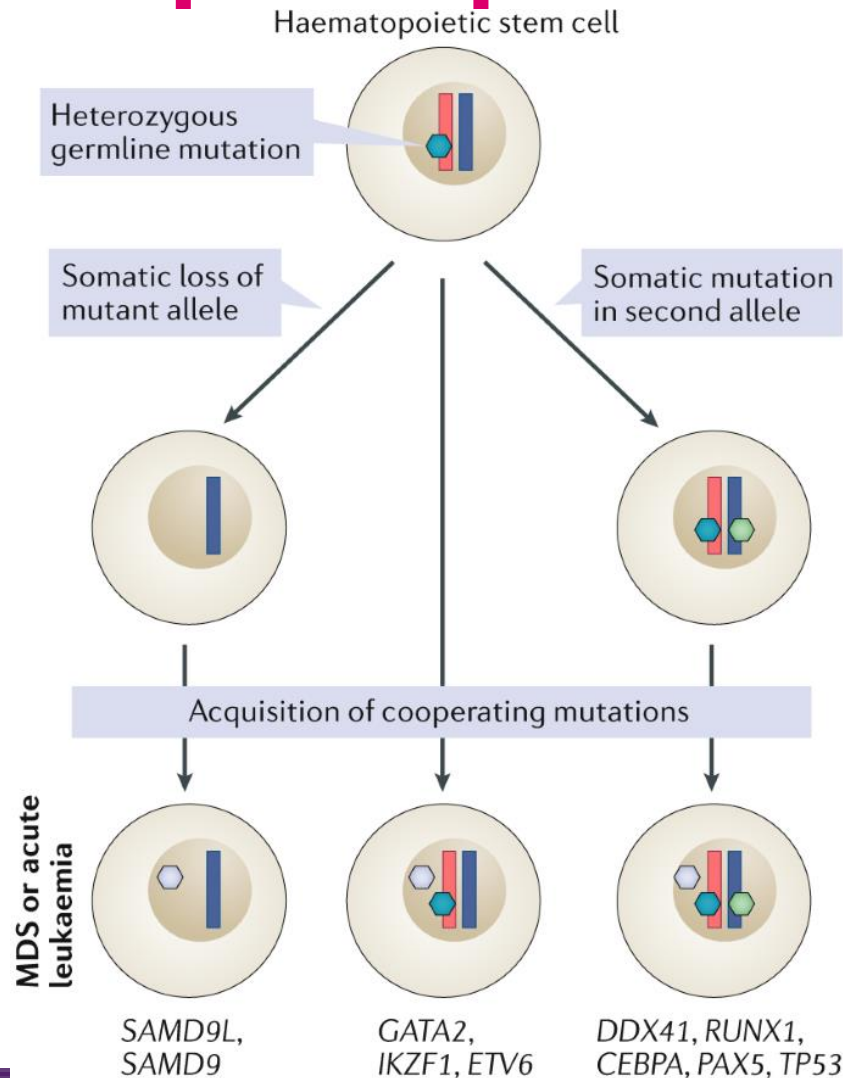
Chapter 8: Acute myeloid leukemia and related precursor neoplasms

Chapter 9: Blastic plasmacytoid dendritic neoplasm

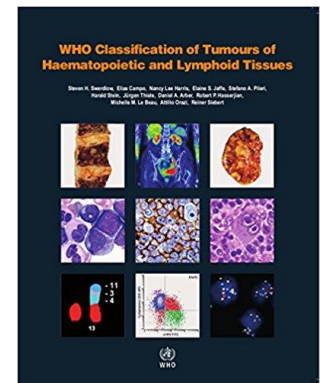
Chapter 10: Acute leukemias of ambiguous lineage
Mixed phenotype acute leukemia (MPAL)



7: Myeloid neoplasms with germline predisposition

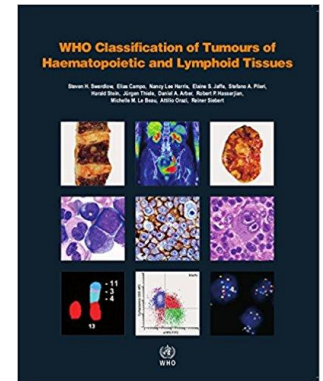


⬢ Germline variant
 ⬢ Mutation in wild-type allele
 ⬢ Cooperating somatic mutation



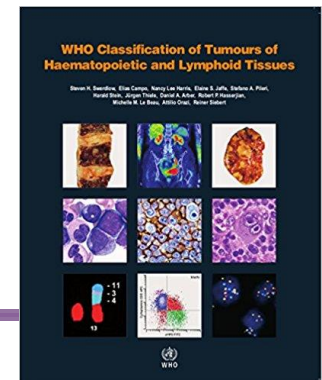
8: Acute myeloid leukemia and related precursor neoplasms

- AML with recurrent genetic abnormalities
- AML with myelodysplasia-related changes
- Therapy-related myeloid neoplasms
- AML not otherwise specified
- Myeloid sarcoma
- Myeloid proliferations associated with Down syndrome



AML with recurrent genetic abnormalities

- AML with t(8;21)(q22;q22); *RUNX1-RUNX1T1*
- AML with inv(16)(p13.1;1q22) or t(16;16)(p13.1;q22); *CBFB-MYH11*
- Acute promyelocytic leukemia with *PML-RARA* FAB M3
- AML with t(9;11)(p21.3;q23.3); *KMT2A-MLLT3*
- 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 (=EVI1)*
- AML (megakaryoblastic) with t(1;22)(p13.3;q13.1); *RBM15-MKL1*
- AML with *BCR-ABL1*
- AML with with gene mutations
 - AML with mutated *NPM1*
 - AML with biallelic mutation of *CEBPA*
 - AML with mutated *RUNX1*



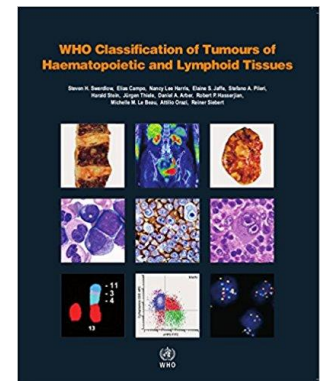
AML, myelodysplasia-related

- $\geq 20\%$ blasts in PB or BM
- AND one of the following:
 - History of MDS or MDS/MPN
 - Defining cytogenetic abnormalities
 - Multilineage dysplasia: dysplasia in $\geq 50\%$ of cells in ≥ 2 myeloid lineages
- AND absence of both prior cytotoxic therapy for unrelated disease and aforementioned recurring genetic abnormalities



Therapy-related myeloid neoplasms

- ❑ t-AML, t-MDS or t-MDS/MPN
- ❑ Excluded: progression from MPN or evolution of primary MDS or MDS/MPN to AML (secondary AML)
- ❑ Cytotoxic agents implicated in therapy-related myeloid neoplasms
 - ❑ Alkylating agents
 - ❑ Ionizing radiation therapy
 - ❑ Topoisomerase II inhibitors
 - ❑ Others



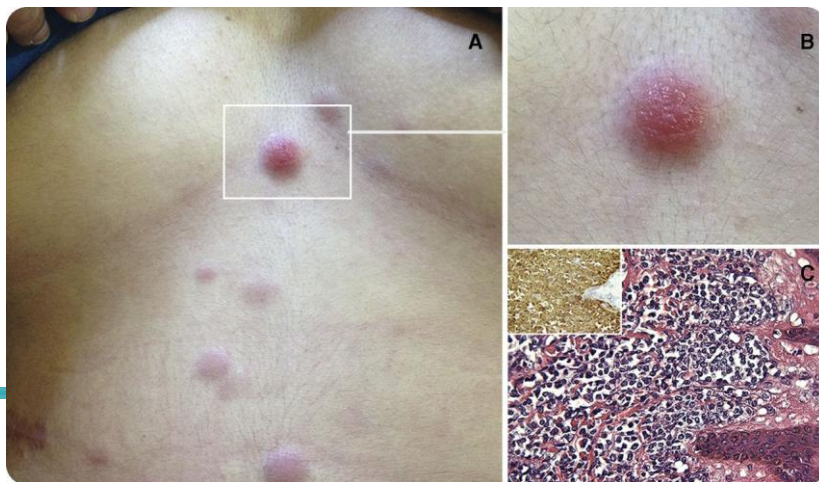
AML not other specified

- AML with minimal differentiation FAB M0
 - MPO negative, CD13+, CD117+, CD33+ (60%)
- AML without maturation FAB M1
 - >90% blasts of NEC
- AML with maturation FAB M2
- Acute myelomonocytic leukemia FAB M4
- Acute monoblastic/monocytic leukemia FAB M5a/b
- Acute erythroid leukemia FAB M6
- Acute megakaryoblastic leukemia FAB M7
- Acute basophilic leukemia
- Acute panmyelosis with myelofibrosis



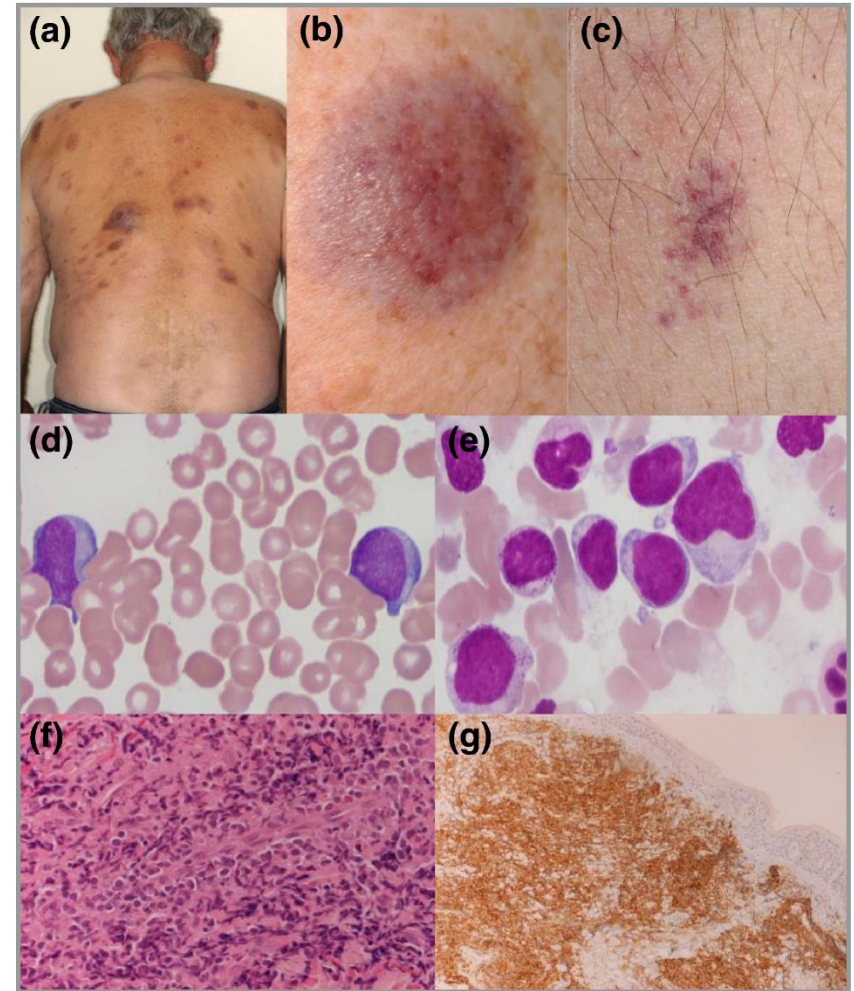
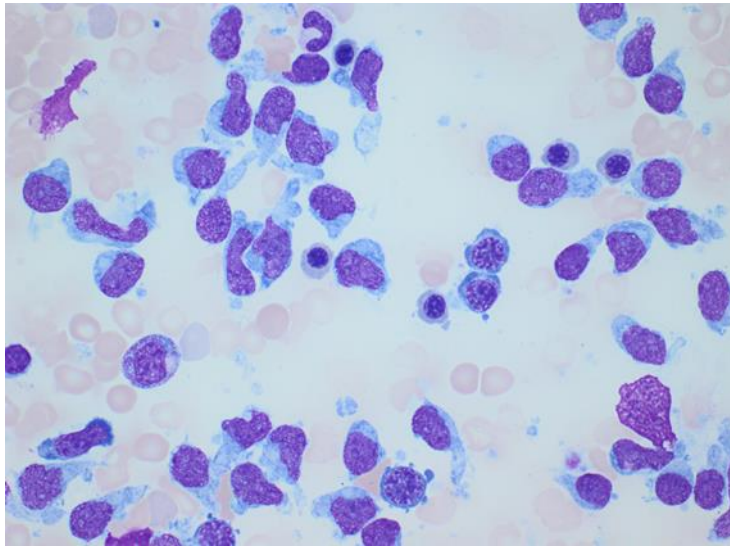
Myeloid sarcoma

- ❑ Tumor mass consisting of myeloid blasts with or without maturation
- ❑ Occurring in other anatomical site than bone marrow
- ❑ Not: Infiltration of any site of the body by myeloid blasts in a patient with AML
- ❑ Localization, any site, most frequent:
 - ❑ Skin, lymph nodes, GI tract, bone, soft tissue, testes

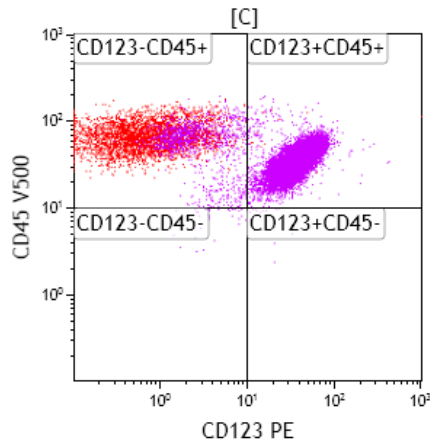
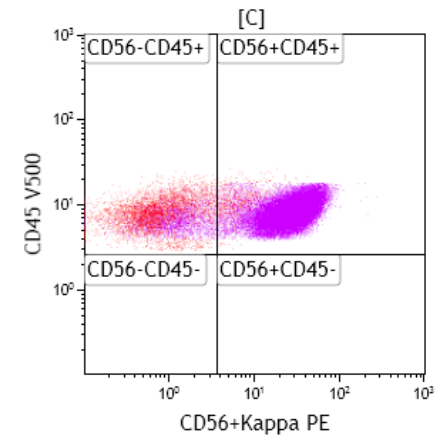
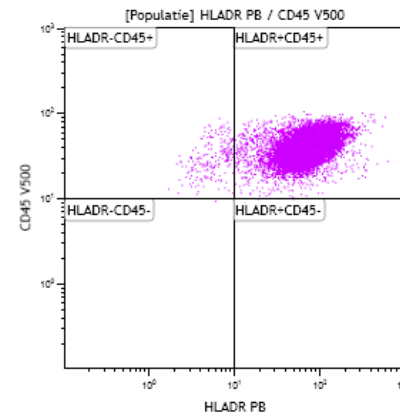
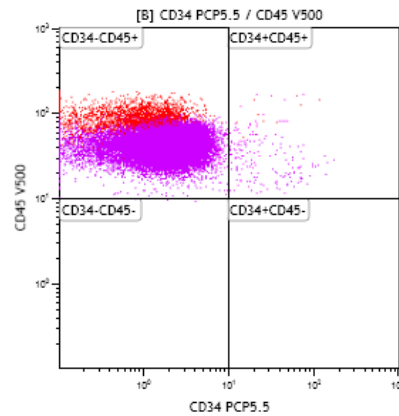
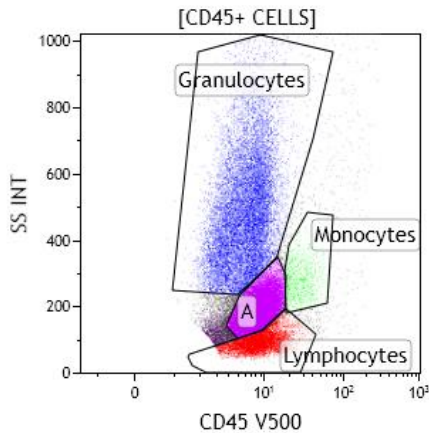


9: Blastic plasmacytoid dendritic neoplasm (BPDCN)

- Aggressive tumor derived from precursors of plasmacytoid dendritic cells
- High frequency of cutaneous and bone marrow involvement and leukemic dissemination



9: Blastic plasmacytoid dendritic neoplasm (BPDCN)

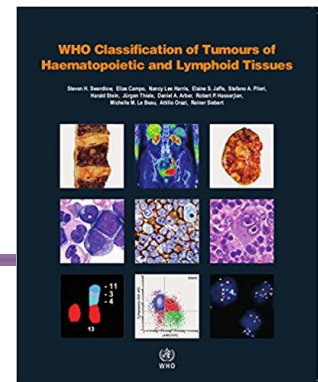


Populatie A

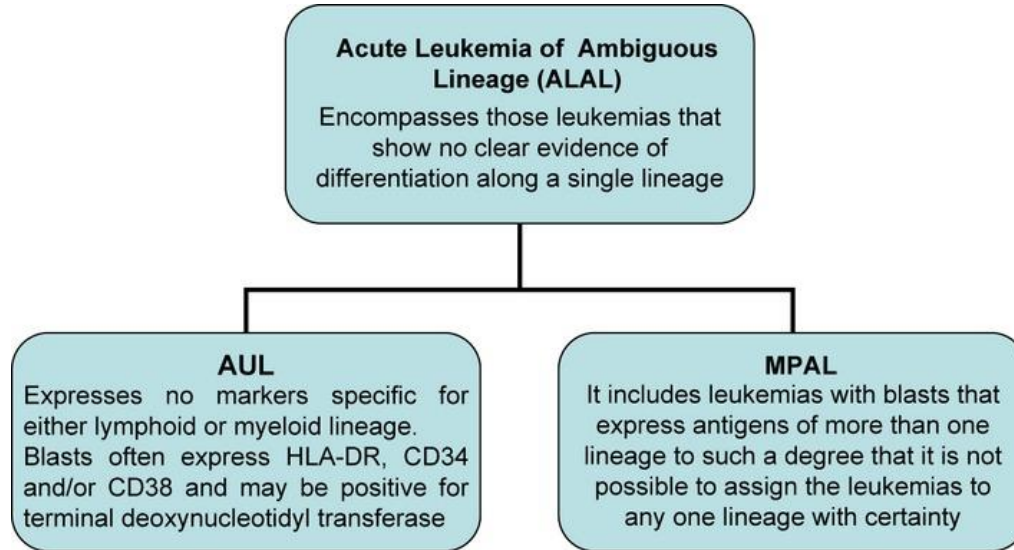
CD45+ HLADR+ **CD56+ CD4+(LD) CD123+**

CD34- CD19- CD3- cytCD3- cytCD79a- cytTdT-

cytMPO-



10: Acute leukemias of ambiguous lineage



Requirements for assigning more than one lineage to a single blast population
Myeloid lineage Myeloperoxidase or Monocytic differentiation (at least 2 of the following: NSE, CD11c, CD14, CD64, lysozyme)
B lineage Strong CD19 with at least 1 of the following strongly expressed: CD79a, cytoplasmic CD22, CD10 or Weak CD19 with at least 1 of the following strongly expressed: CD79a, cytoplasmic CD22, CD10
T lineage Cytoplasmic CD3 or surface CD3



But, Summer 2022...

The 5th edition of the WHO classification of haematolymphoid tumors: Myeloid and histiocytic dendritic neoplasm

Khoury et al. *Leukemia* 2022 Jul; Jul;36(7):1703-1719.


International Consensus Classification of myeloid neoplasms and acute leukemias: integrating morphologic, clinical and genomic data

Arber et al. *Blood* 2022 Sep 15;140(11):1200-1228.



The 5th edition of the WHO classification of haematolymphoid tumors: Myeloid and histiocytic dendritic neoplasm

Khoury et al. Leukemia 2022 Jul; Jul;36(7):1703-1719.

- AML with **defining** genetic abnormalities
 - AML with myelodysplasia-related changes
 - Therapy-related myeloid neoplasms
 - AML **defined by differentiation**
 - Myeloid sarcoma
 - Myeloid proliferations associated with Down syndrome
- 

AML with recurrent genetic abnormalities, no blast cutoff

- Acute promyelocytic leukemia with *PML-RARA* fusion
- AML with *RUNX1-RUNX1T1* fusion
- AML *CBFB-MYH11* fusion
- AML with *DEK-NUP214* fusion
- AML with *RBM15-MRTFA* fusion
- AML with *BCR-ABL1* fusion, $\geq 20\%$ blasts
- AML with *KMT2A* rearrangement
- AML with *MECOM* rearrangement
- AML with *NUP98* rearrangement
- AML with *NPM1* mutation
- AML with *CEBPA* mutation, $\geq 20\%$ blasts
- AML with other defined genetic alterations
- AML myelodysplasia-related, $\geq 20\%$ blasts, updated definition

AML, myelodysplasia-related

- $\geq 20\%$ blasts in PB or BM
- AND one of the following:
 - History of MDS or MDS/MPN
 - Defining cytogenetic abnormalities
 - Complex karyotype: 3 or more chromosomal abnormalities
 - Unbalanced abnormalities: -7, del(7q), del(5q), i(17q), -13, del(13q), del(11q), del(12p), t(12p) or del(17p)
 - Loss of 5q, 7q, 12p or 17p due to unbalanced translocation
 - Defining somatic mutations
 - ASXL1, BCOR, EZH2, SF3B1, SRSF2, STAG2, U2AF1, ZSRF2
- AND absence of both prior cytotoxic therapy for unrelated disease and aforementioned recurring genetic abnormalities

Therapy-related myeloid neoplasms

t-AML, t-MDS or t-MDS/MPN

Excluded: progression from MPN or evolution of primary MDS or MDS/MPN to AML (secondary AML)

Cytotoxic agents implicated in therapy-related myeloid neoplasms

- Alkylating agents

- Ionizing radiation therapy

- Topoisomerase II inhibitors

- Others

AML defined by differentiation

- AML with minimal differentiation FAB M0
 - MPO negative, CD13+, CD117+, CD33+ (60%)
- AML without maturation FAB M1
 - >90% blasts of NEC
- AML with maturation FAB M2
- Acute myelomonocytic leukemia FAB M4
- Acute monoblastic/monocytic leukemia FAB M5a/b
- Acute erythroid leukemia FAB M6
- Acute megakaryoblastic leukemia FAB M7
- Acute basophilic leukemia

International Consensus Classification of myeloid neoplasms and acute leukemias: integrating morphologic, clinical and genomic data

Arber et al. Blood 2022 Sep 15;140(11):1200-1228.

- MDS/AML (previously MDS-EB2, 10-19% blasts)
- More genetically defined integrated classification
 - AML with recurrent genetic abnormalities
 - AML with myelodysplasia-related changes
 - ~~Therapy related myeloid neoplasms~~
 - AML not otherwise specified
 - Myeloid sarcoma
- Myeloid proliferations associated with Down syndrome

Diagnostic qualifiers that should be used following a specific MDS, AML (or MDS/AML) diagnosis

Therapy-related <ul style="list-style-type: none">• prior chemotherapy, radiotherapy, immune interventions
Progressing from MDS <ul style="list-style-type: none">• MDS should be confirmed by standard diagnostics
Progressing from MDS/MPN (specify) <ul style="list-style-type: none">• MDS/MPN should be confirmed by standard diagnostics
Germline predisposition

Classification of AML with % blasts (1)

- Acute promyelocytic leukemia with t(15;17)(q24.1;q21.2); *PML-RARA* $\geq 10\%$
- APL with other *RARA* rearrangements $\geq 10\%$
- AML with t(8;21)(q22;q22); *RUNX1-RUNX1T1* $\geq 10\%$
- AML with inv(16)(p13.1;q22) or t(16;16)(p13.1;q22); *CBFB-MYH11* $\geq 10\%$
- AML with t(9;11)(p21.3;q23.3); *KMT2A-MLLT3* $\geq 10\%$
- AML with other *KMT2A* rearrangements $\geq 10\%$
- AML with t(6;9)(p23;q34.1); *DEK-NUP214* $\geq 10\%$
- AML with inv(3)(q21.3q26.2) or t(3;3)(q21.3;q26.2); *GATA2;MECOM(EVI1)* $\geq 10\%$
- AML with other *MECOM* rearrangements $\geq 10\%$
- AML with other rare recurring translocations (supplemental table) $\geq 10\%$
- AML with t(9;22)(q34.1;q11.2); *BCR-ABL1* $\geq 20\%$
- AML with mutated *NPM1* $\geq 10\%$
- AML with in-frame bZIP *CEBPA* mutations $\geq 10\%$
- AML and MDS/AML with mutated *TP53* (MDS/AML 10-19 blasts, AML $\geq 20\%$)

Classification of AML (2)

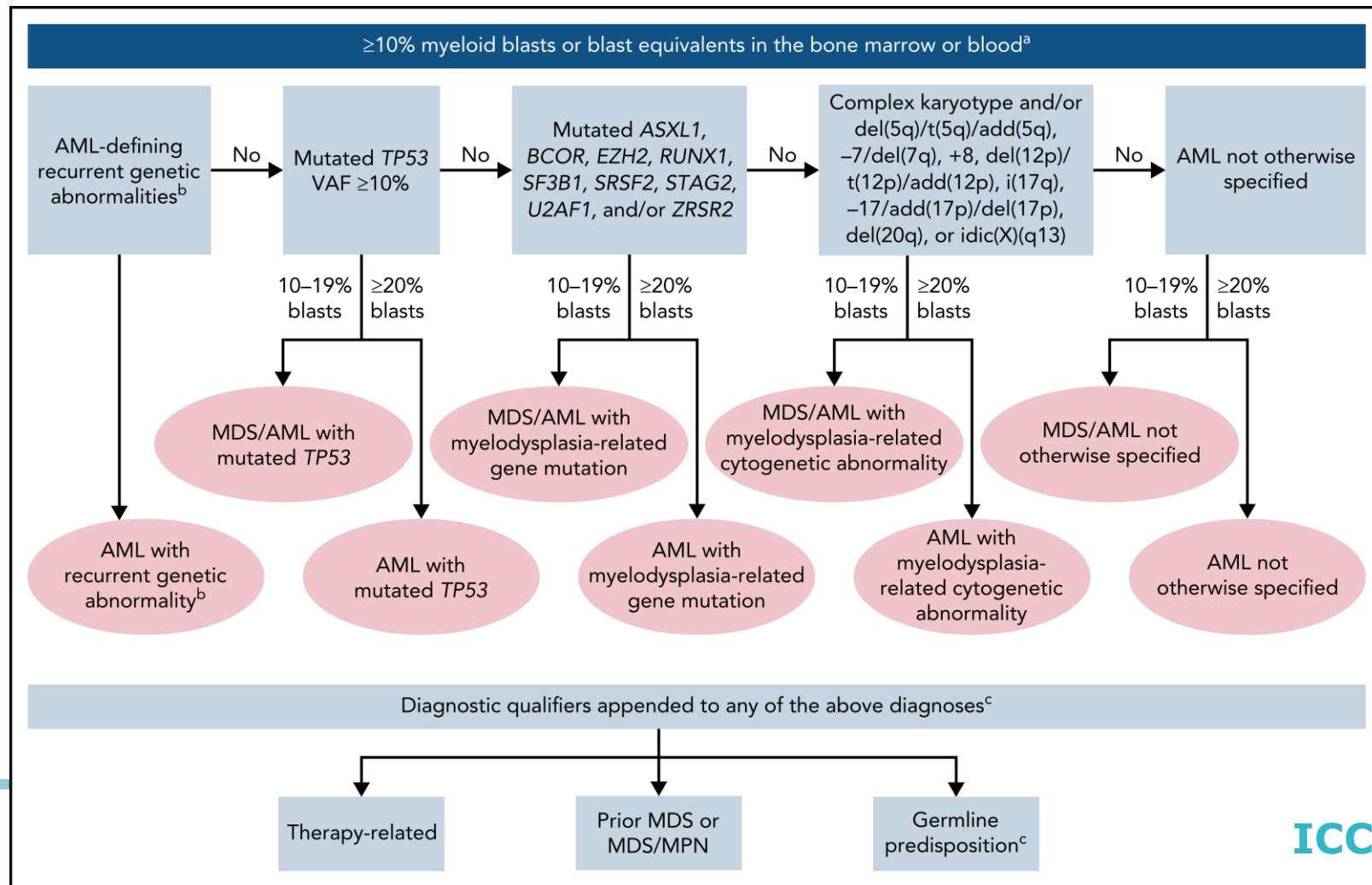
- **Supplemental Table: AML with other rare recurring translocations**
- AML with t(1;3)(p36.3;q21.3)/PRDM16::RPN1
- AML with t(3;5)(q25.3;q35.1)/NPM1::MLF1
- AML with t(8;16)(p11.2;p13.3)/KAT6A::CREBBP
- AML (megakaryoblastic) with t(1;22)(p13.3;q13.1)/RBM15::~~MKL1~~MRTF1
- AML with t(5;11)(q35.2;p15.4/ NUP98::NSD1
- AML with t(11;12)(p15.4;p13.3)/NUP98::KMD5A
- AML with NUP98 and other partners
- AML with t(7;12)(q36.3;p13.2)/ETV6::MNX1
- AML with t(10;11)(p12.3;q14.2)/PICALM::MLLT10
- AML with t(16;21)(p11.2;q22.2)/FUS::ERG
- AML with t(16;21)(q24.3;q22.1)/RUNX1::CBFA2T3
- AML with inv(16)(p13.3q24.3)/CBFA2T3::GLIS2

Classification of AML with % blasts (3)

- AML and MDS/AML with myelodysplasia-related gene mutations (MDS/AML 10-19 blasts, AML \geq 20%) Defined by mutations in ASXL1, BCOR, EZH2, RUNX1, SF3B1, SRSF2, STAG2, U2AF1 or ZSRF2
- AML with myelodysplasia-related cytogenetic abnormalities (MDS/AML 10-19 blasts, AML \geq 20%) Defined by detecting a complex karyotype (\geq 3 unrelated clonal chromosomal abnormalities in the absence of other class-defining recurring genetic abnormalities), del(5q)/t(5q)/add(5q), -7/del(7q), +8, del(12p)/t(12p)/add(12p), i(17q), -17/add(17p) or del(17p), del(20q), and/or idic(X)(q13) clonal abnormalities
- AML not otherwise specified (NOS) (MDS/AML 10-19 blasts, AML \geq 20%)
- Myeoid sarcoma

Diagnosis and management of AML in adults: 2022 recommendations from an international expert panel on behalf of the European LeukemiaNet

Döhner et al. Blood 2022 Sep 22;140(12):1345-1377



Literature AML

Diagnosis and management of AML in adults: 2022
recommendations from an international expert panel on behalf
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