

3rd edition

Unmet challenges in high risk hematological malignancies: from bedside to clinical practice

Turin, September 21-22, 2023

Starhotels Majestic

Scientific board:

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Unmet challenges in high risk hematological malignancies: from bedside to clinical practice

High-risk cytogenetic AML

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Disclosures of Pau Montesinos

Company name	Research support	Employee	Consultant	Stockholder	Speakers bureau	Advisory board	Other
Abbvie	x		x		x	x	
Jazz pharma	x		x		x	x	
Daiichi Sankyo	x		x		x	x	
BMS	x		x		x	x	
Pfizer	x		x		x	x	

Diagnosis and management of AML in adults: 2017 ELN recommendations from an international expert panel

Favourable

- t(8;21)(q22;q22.1); *RUNX1-RUNX1T1*
- inv(16)(p13.1q22) or t(16;16)(p13.1;q22); *CBFB-MYH11*
- **Mutated *NPM1* without *FLT3*-ITD or with *FLT3*-ITD^{low}**
- Biallelic mutated *CEBPA*

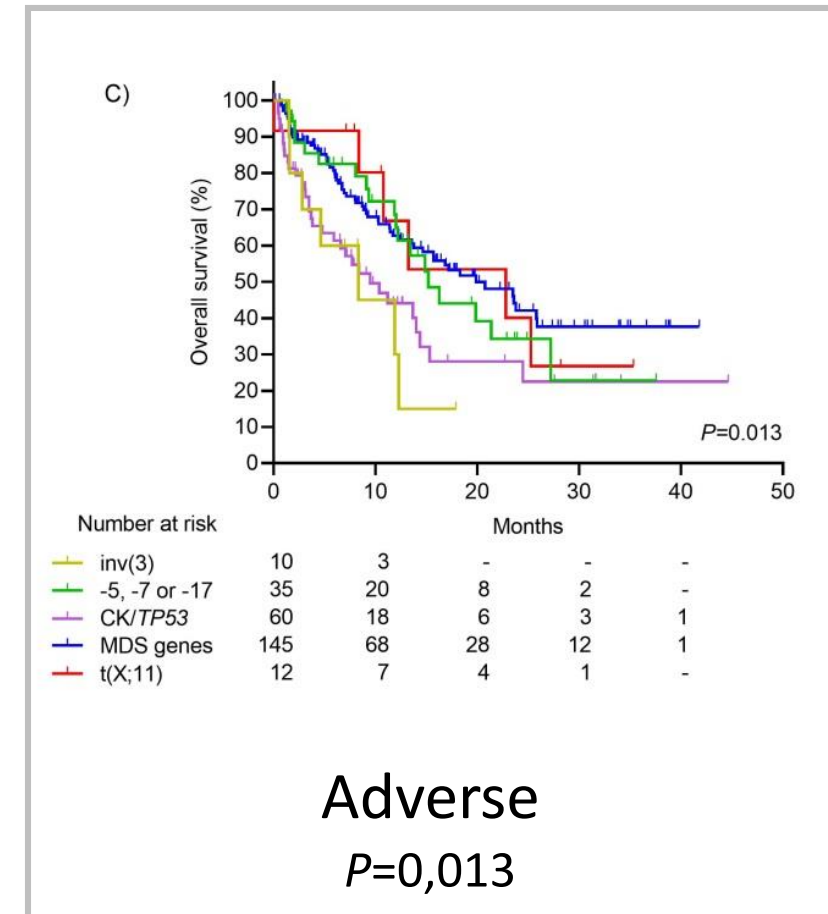
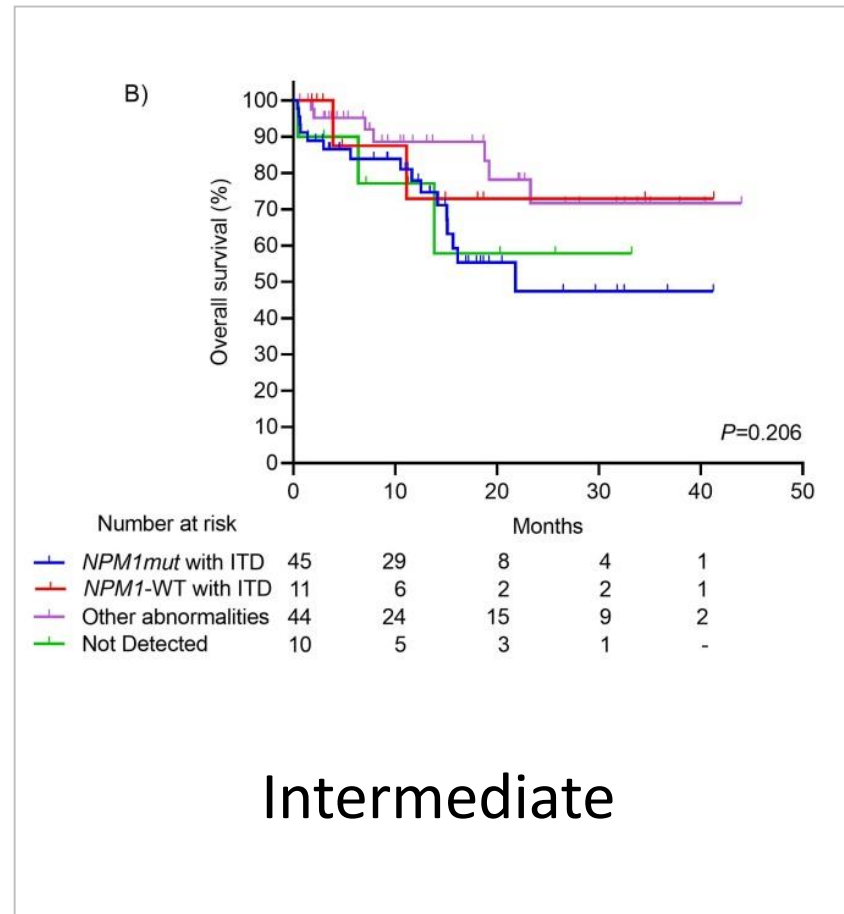
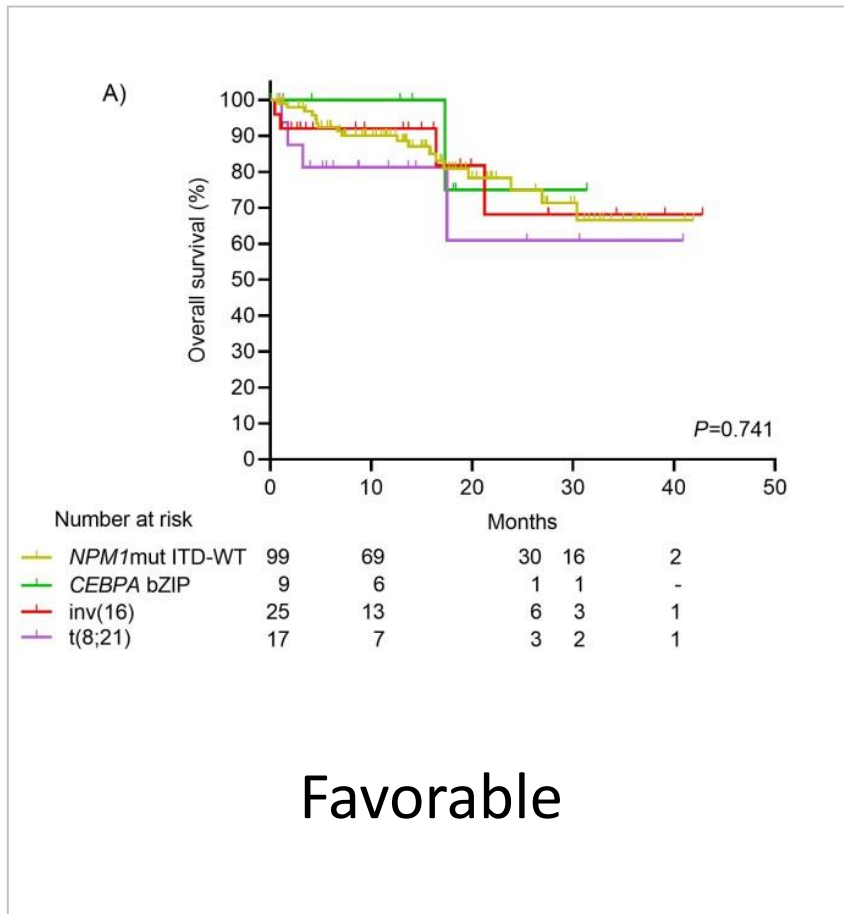
Intermediate

- **Mutated *NPM1* and *FLT3*-ITD^{high}**
- **Wild-type *NPM1* without *FLT3*-ITD or with *FLT3*-ITD^{low}** (without adverse-risk genetic lesions)
- t(9;11)(p21.3;q23.3); *MLL3-KMT2A*
- Cytogenetic abnormalities not classified as favourable or adverse

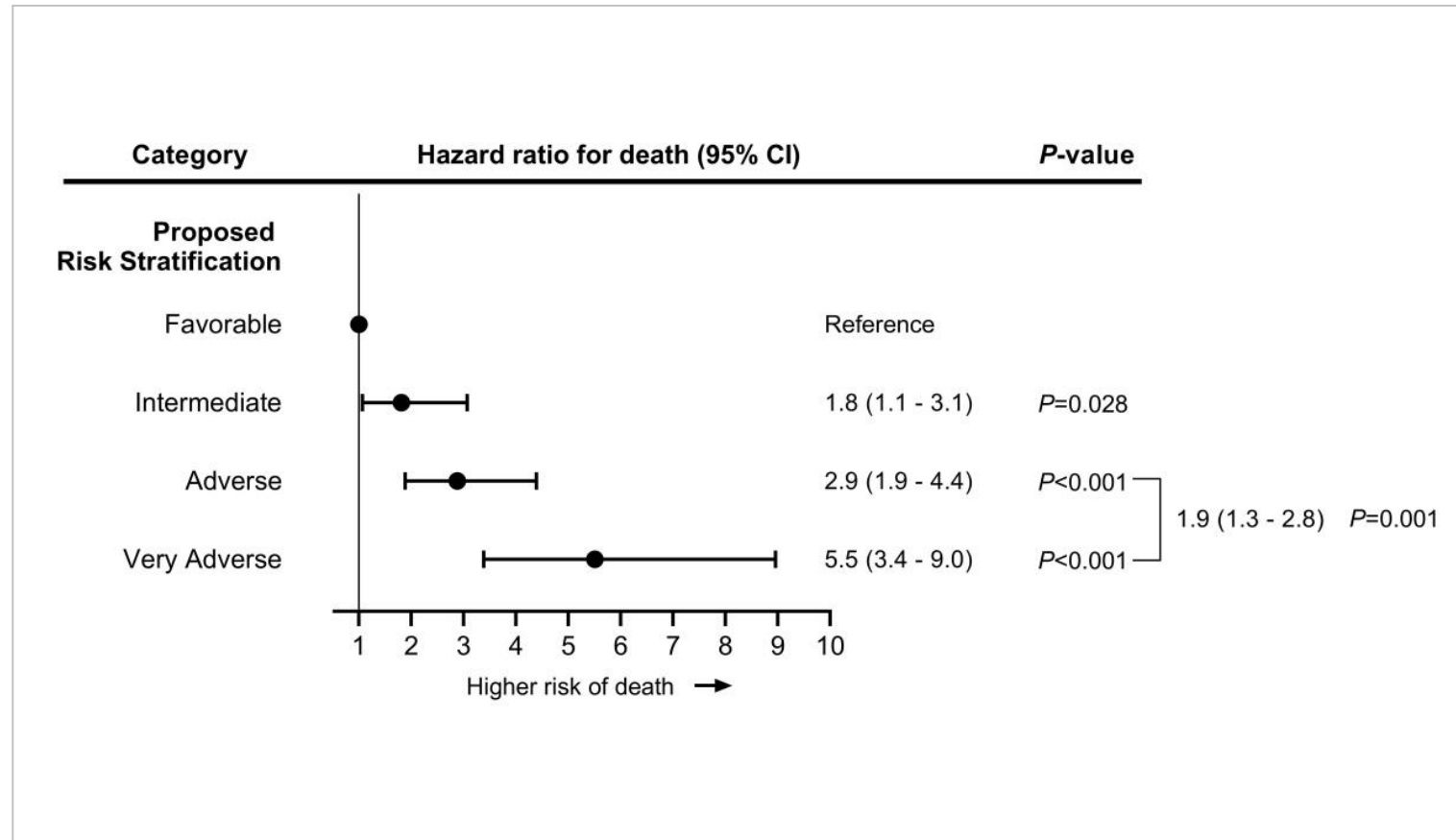
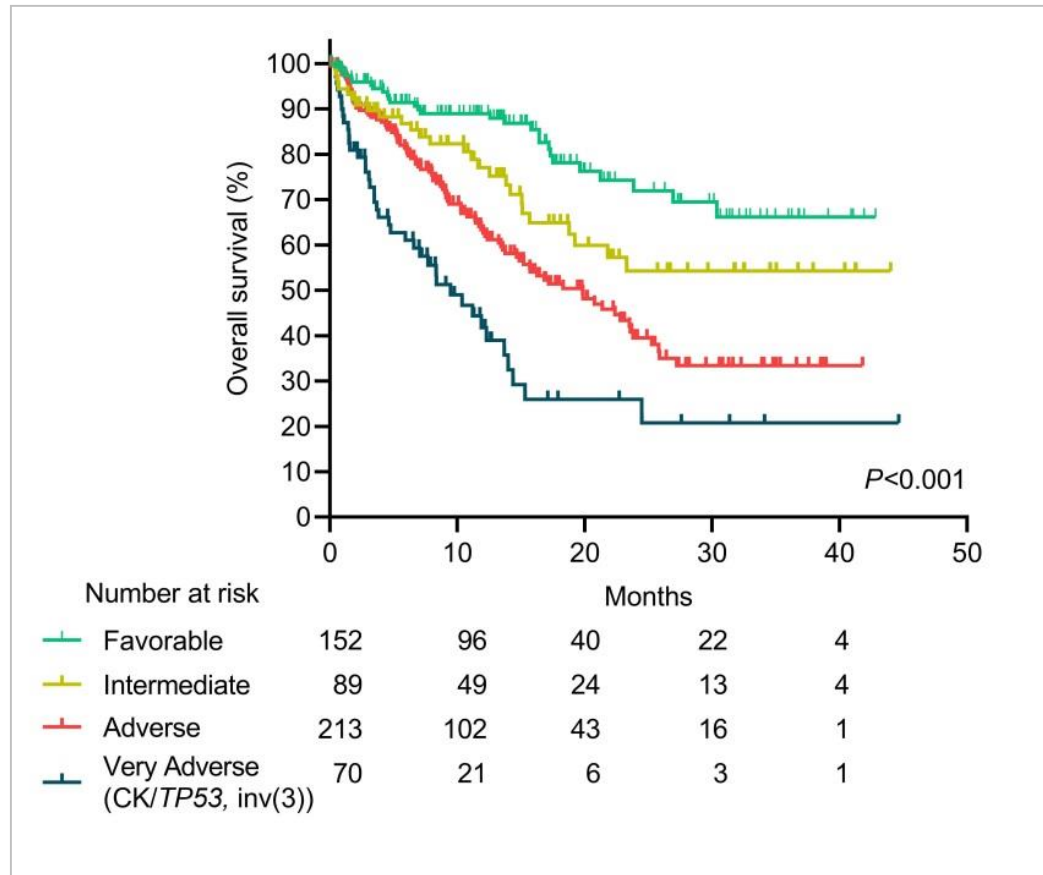
Adverse

- t(6;9)(p23;q34.1); *DEK-NUP214*
- t(v;11q23.3); *KMT2A* rearranged
- t(9;22)(q34.1;q11.2); *BCR-ABL1*
- inv(3)(q21.3q26.2) or t(3;3)(q21.3;q26.2); *GATA2,MECOM(EVI1)*
- -5 or del(5q); -7; -17/abn(17p)
- Complex karyotype, monosomal karyotype
- **Wild-type *NPM1* and *FLT3*-ITD^{high}**
- **Mutated *RUNX1*¶**
- **Mutated *ASXL1*¶**
- **Mutated *TP53***

European LeukemiaNet 2022. Validation by PETHEMA group



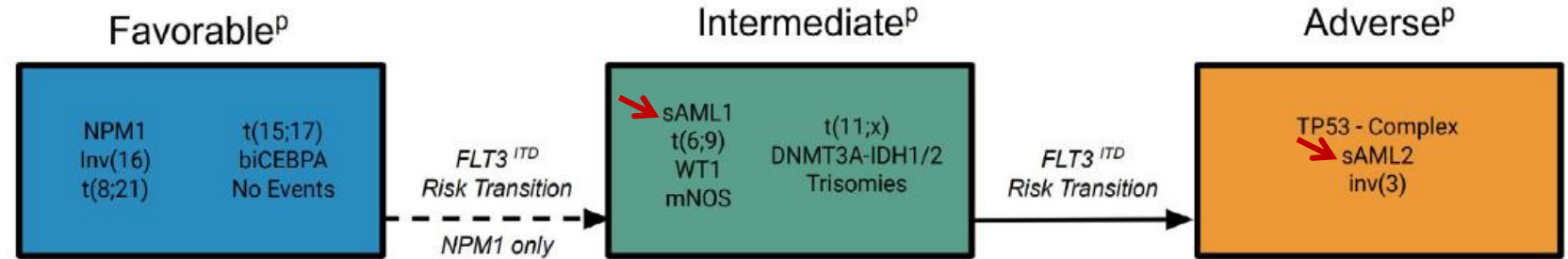
European LeukemiaNet 2022 refinement → Very adverse group



European LeukemiaNet 2022. The issue of MDS-genes

sAML: *SRSF2, SF3B1, U2AF1, ZRSR2, ASXL1, EZH2, BCOR, STAG2, RUNX1, SETBP1*

Tazi *et al.*, Nature
Communications (2022)
13:4622

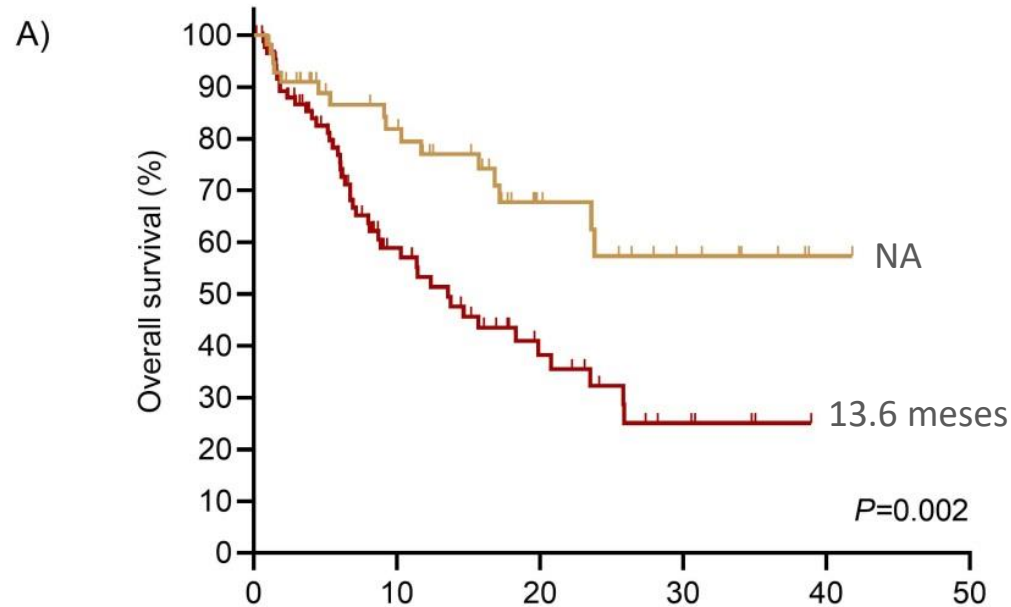


European LeukemiaNet
Döhner H *et al.*,
Blood (2022) 140 (12):
1345–1377.

Risk Category ^b	Genetic Abnormality
Adverse	<ul style="list-style-type: none"> t(6;9)(p23;q34.1)/<i>DEK::NUP214</i> t(v;11q23.3)/<i>KMT2A</i>-rearranged^g t(9;22)(q34.1;q11.2)/<i>BCR::ABL1</i> t(8;16)(p11;p13)/<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,^h monosomal karyotypeⁱ ➔ Mutated <i>ASXL1, BCOR, EZH2, RUNX1, SF3B1, SRSF2, STAG2, U2AF1, or ZRSR2</i>^j Mutated <i>TP53</i>^k

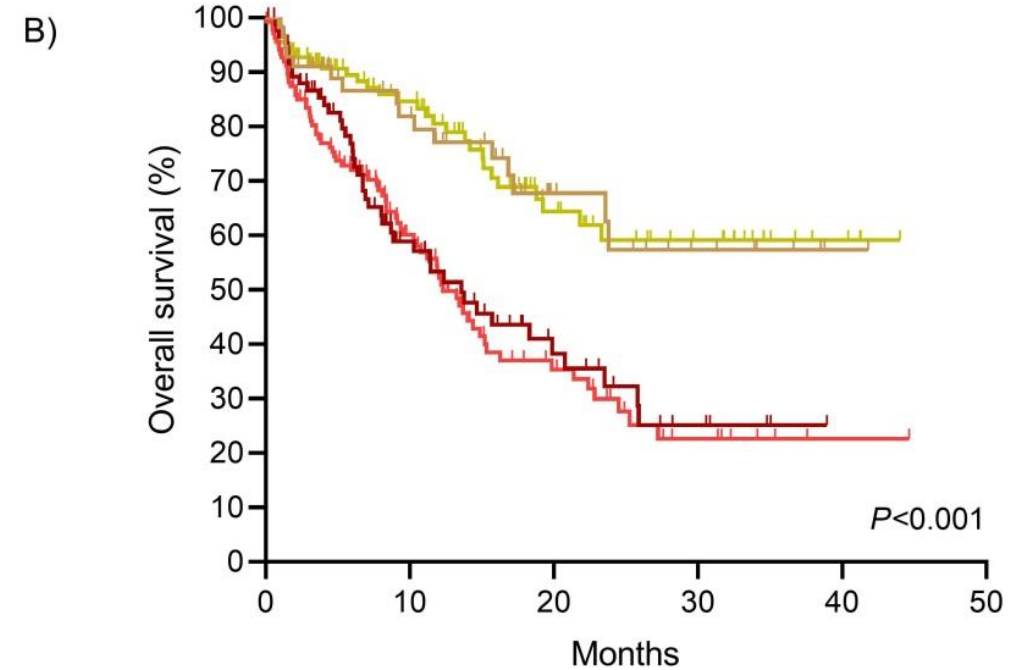
European LeukemiaNet 2022. Validation by PETHEMA group

Genes MDS: *ASXL1*, *BCOR*, *EZH2*, *RUNX1*,
SF3B1, *SRSF2*, *STAG2*, *U2AF1* Y *ZRSR2*



Number at risk

	0	10	20	30	40	50
One mutated MDS gene	57	35	14	7	1	
≥2 mutated MDS genes	88	33	14	5	-	



	0	10	20	30	40	50
Intermediate	111	64	28	16	4	
One mutated MDS gene	57	35	14	7	1	
Adverse	138	55	21	7	1	
≥2 mutated MDS genes	88	33	14	5	-	

Use of biomarkers to refine risk-adapted algorithms

“One-size-fits-all” therapy: AML as a single entity

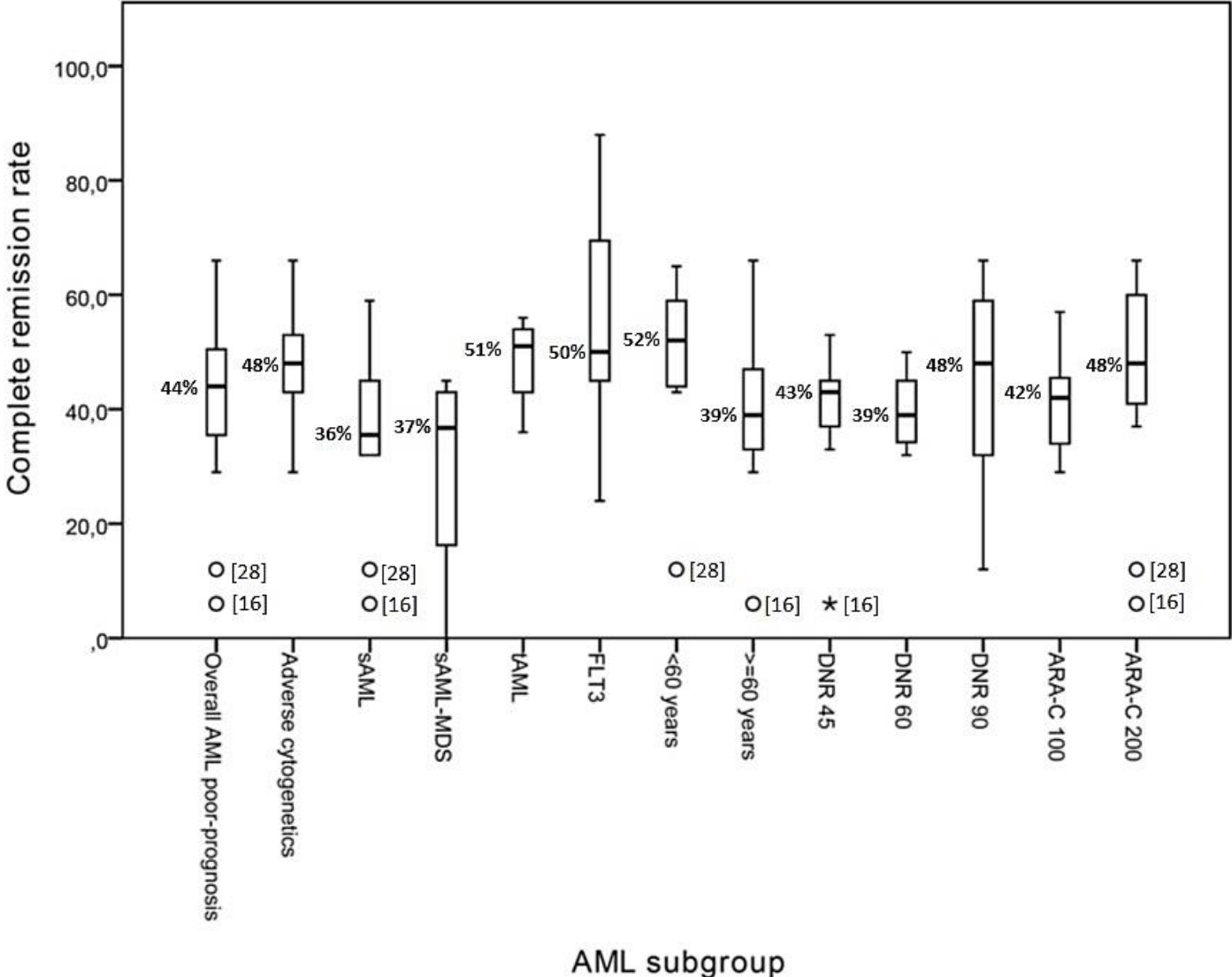


Tailored therapy—Risk-adapted therapy:
Distinct subtypes of AML (prognostic factors)

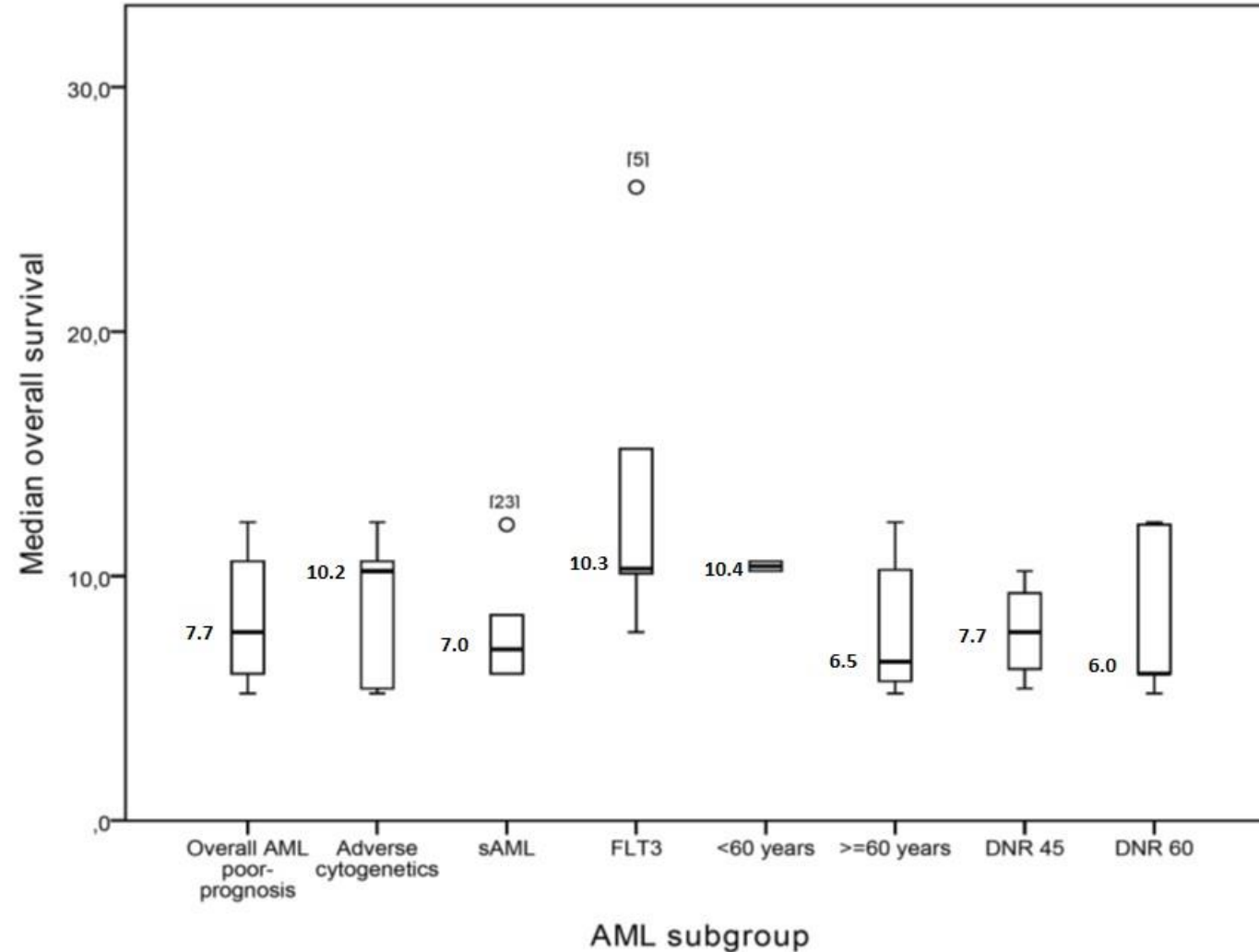


Targeted therapy: Acknowledgment of molecular targets

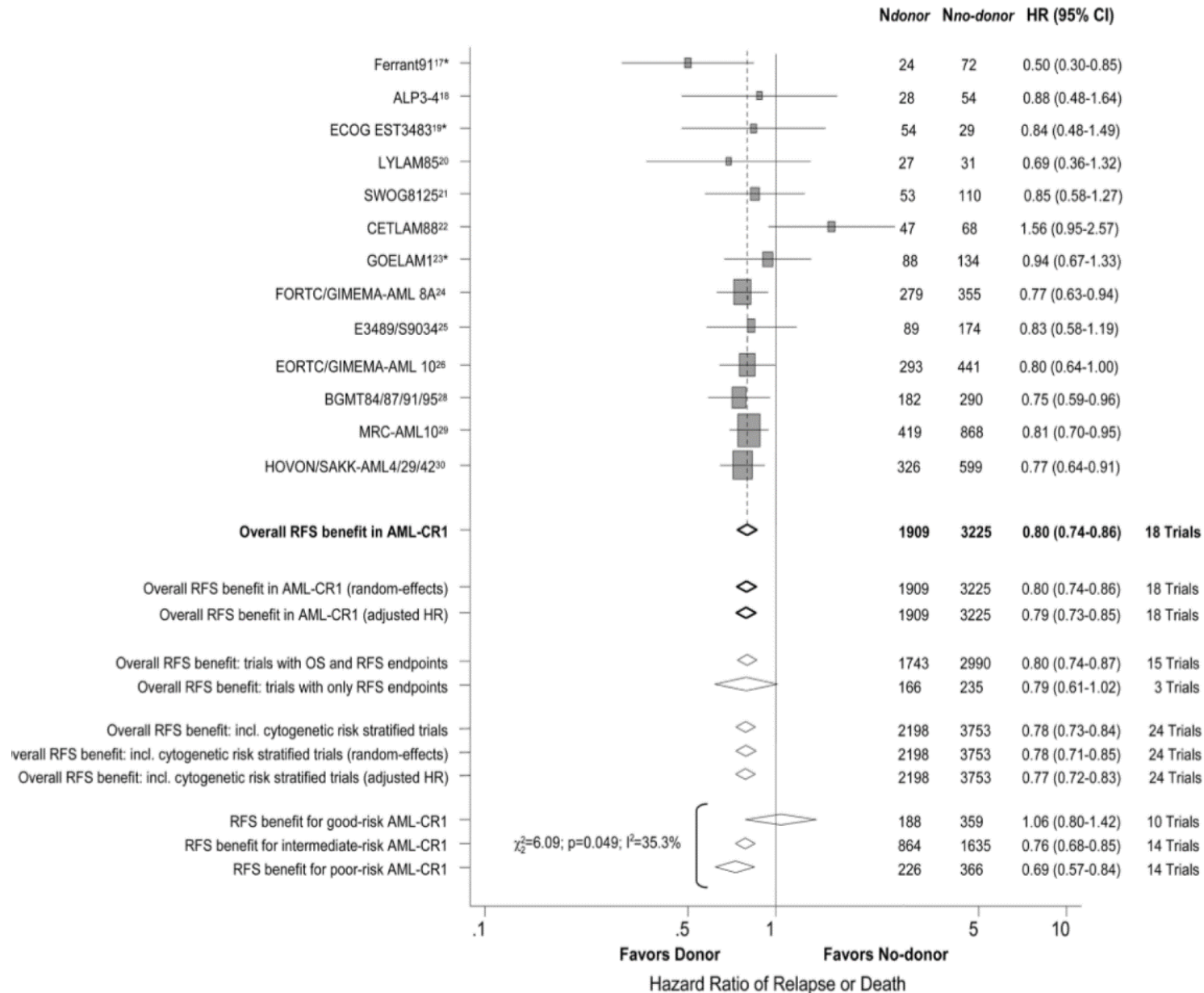
Boxplot diagram of the complete remission (CR) rate of the different subgroups of AML with poor prognosis



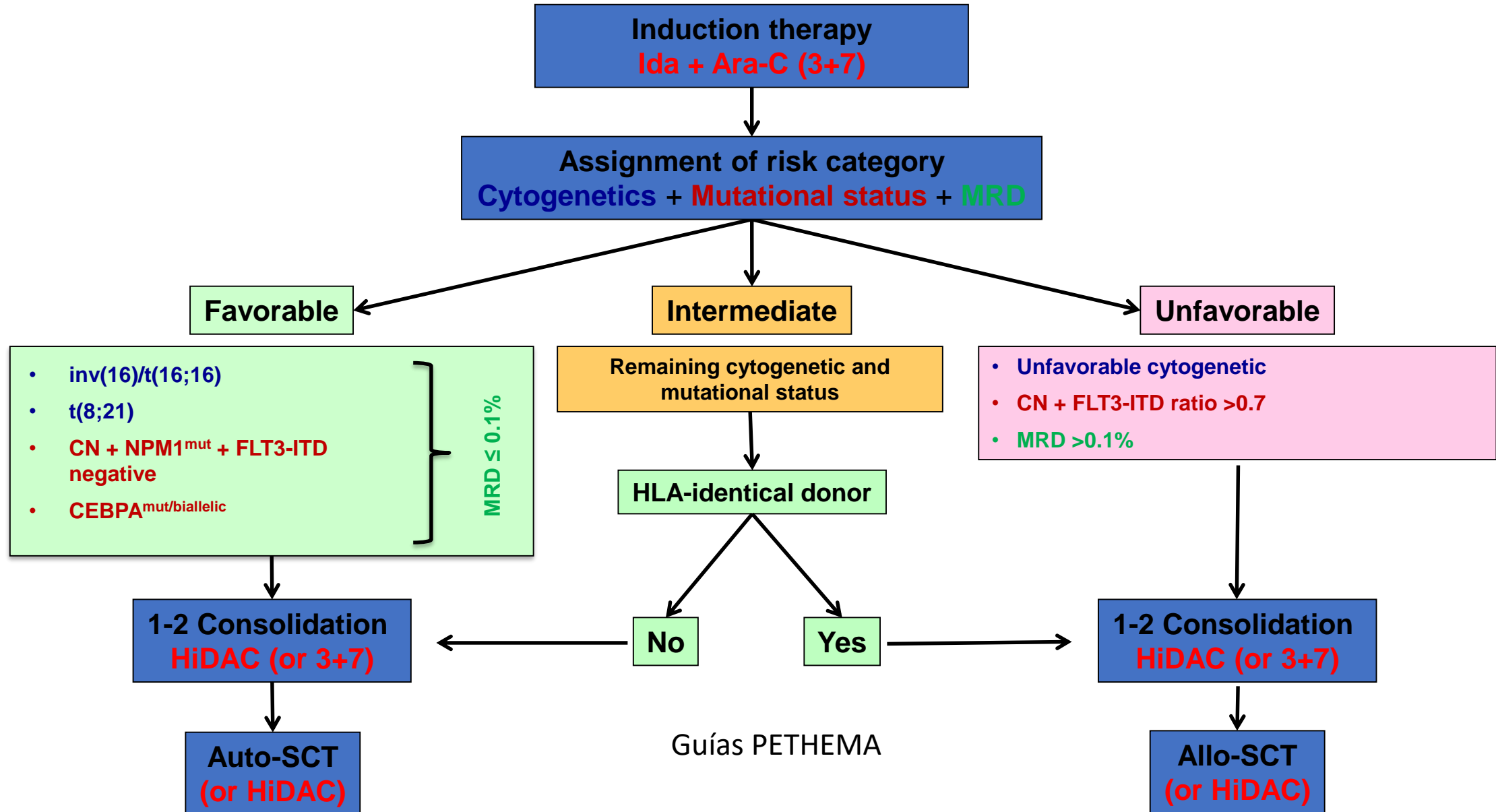
Boxplot diagram of the median overall survival (OS) rate of the different subgroups of AML with poor prognosis



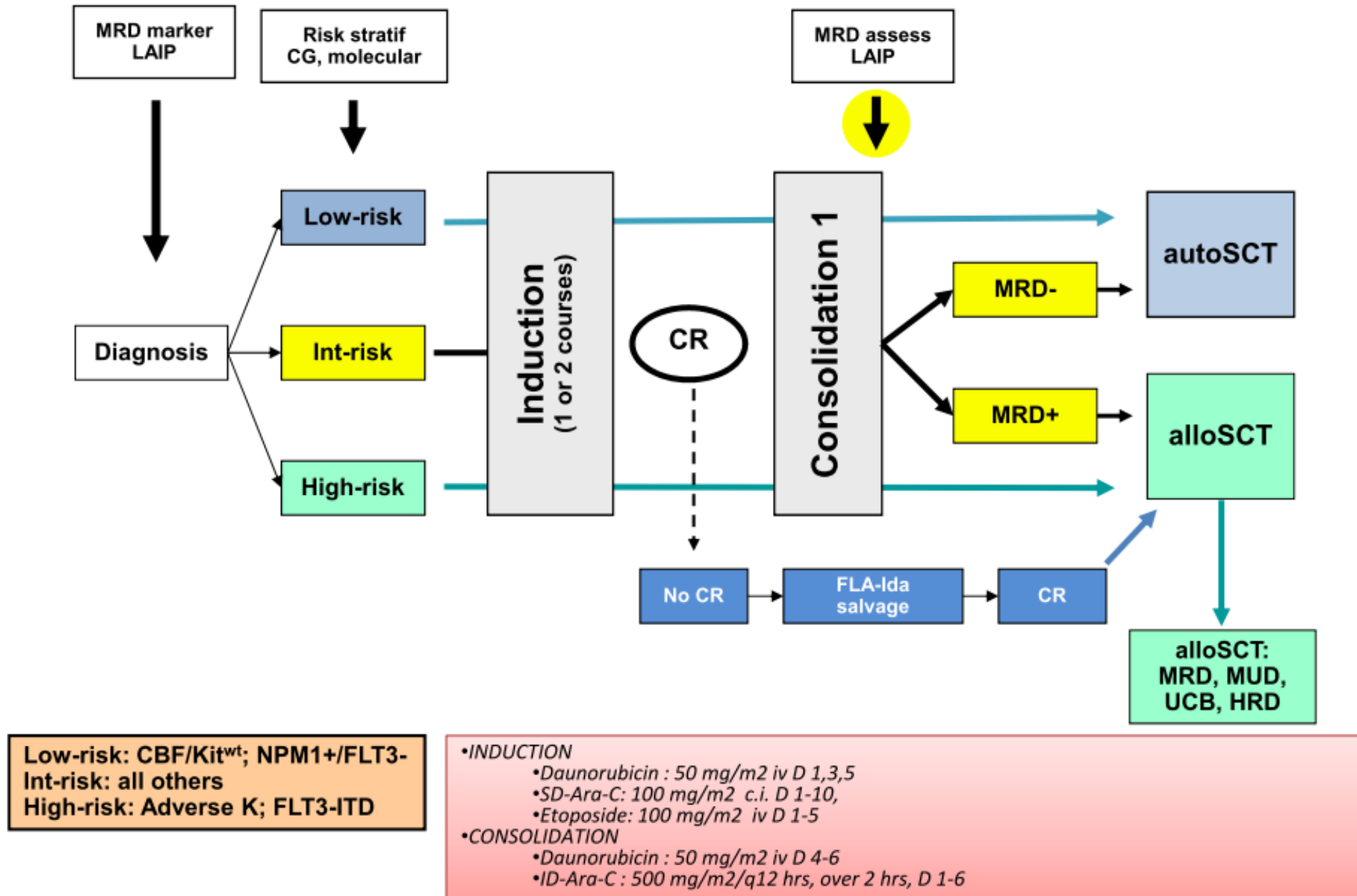
Role of allogeneic stem cell transplantation in acute myeloid leukemia



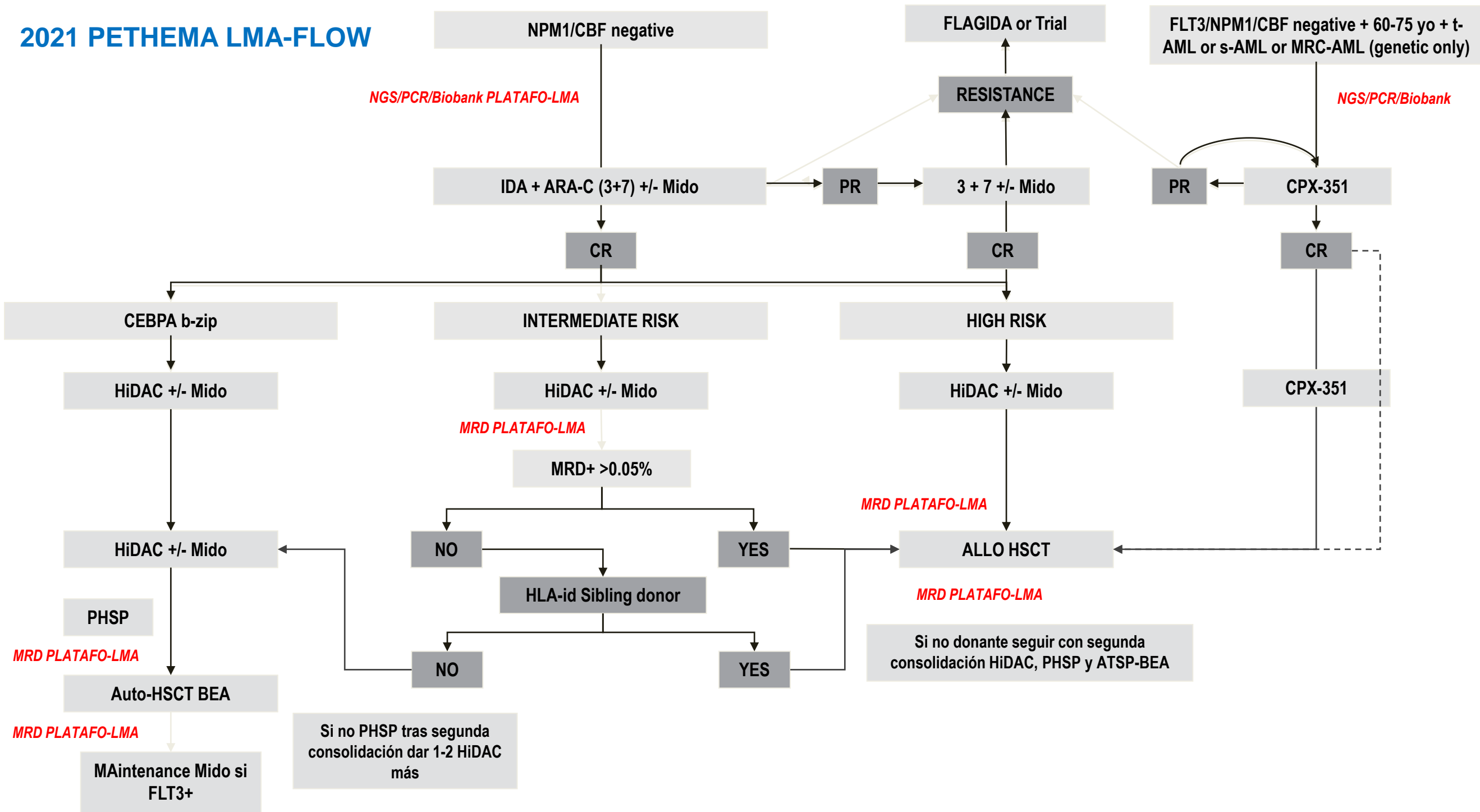
PETHEMA LMA2007/2010 protocol



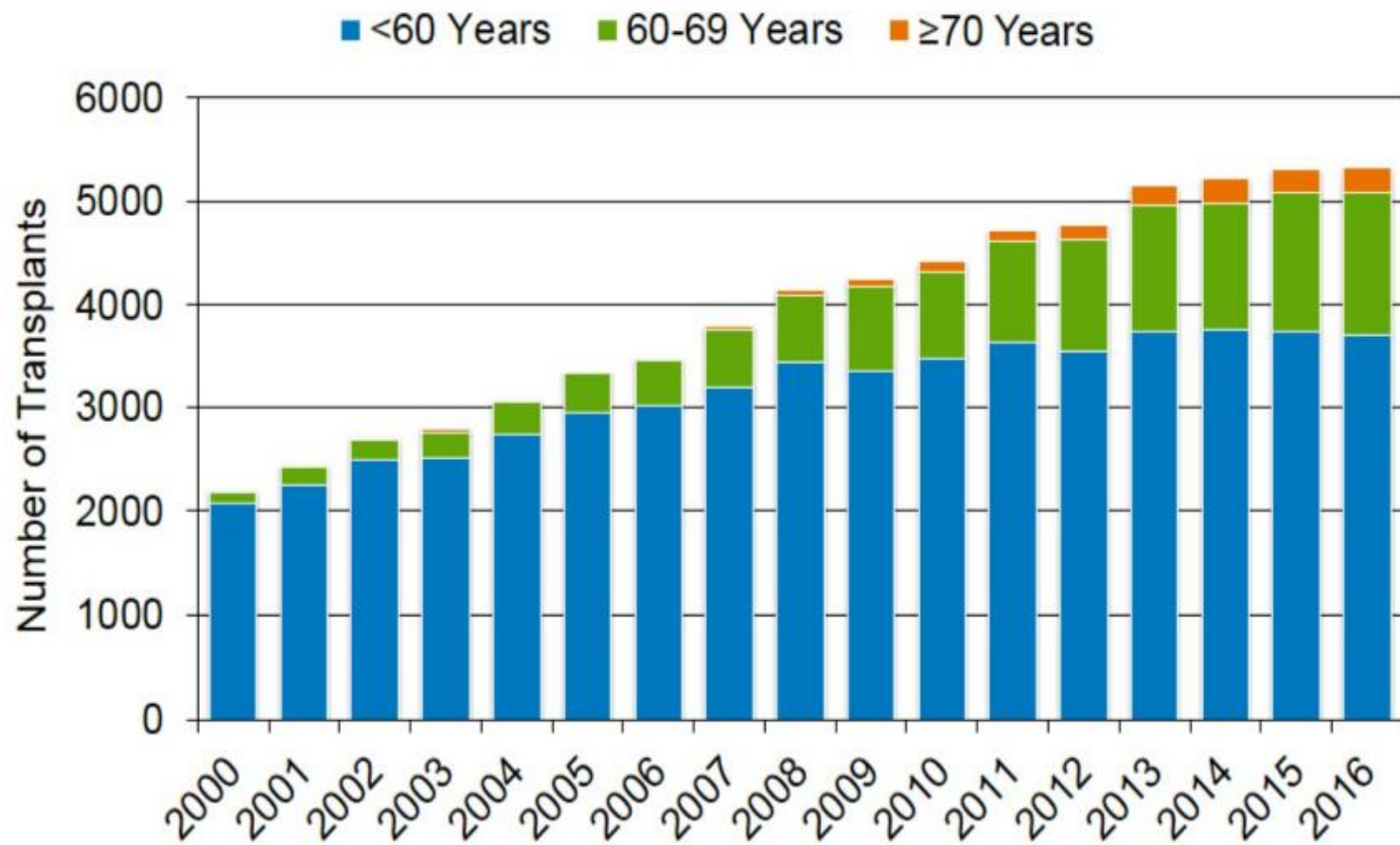
GIMEMA AML1310 trial – Schedule



2021 PETHEMA LMA-FLOW



Trends in allogeneic HCT in the US by recipient age*

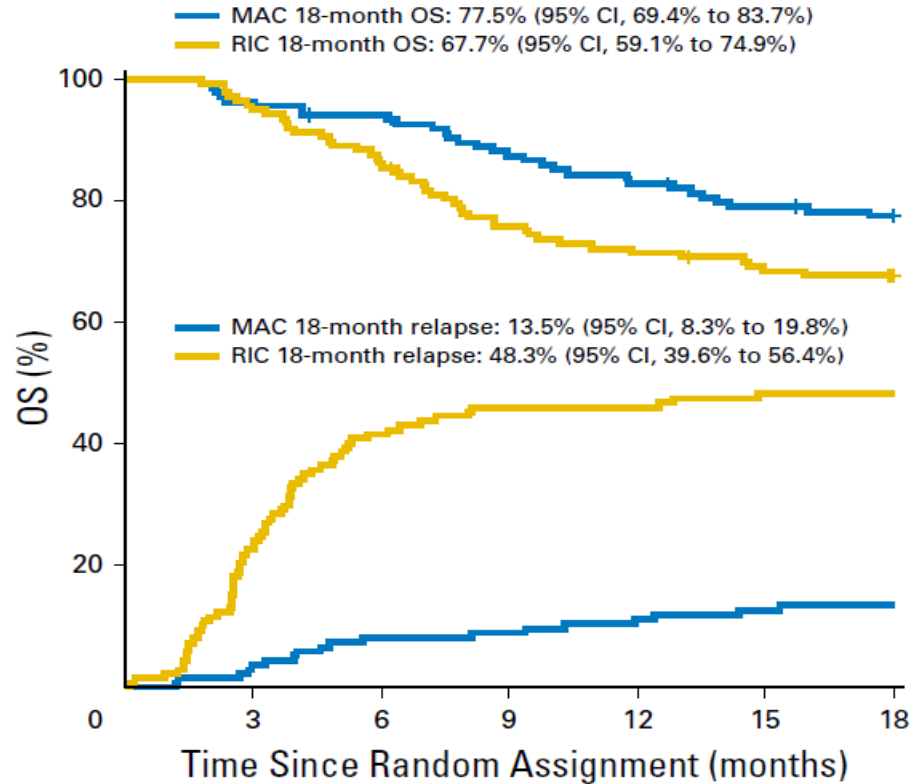


*Transplants for AML, ALL, NHL, Hodgkin Disease, Multiple Myeloma

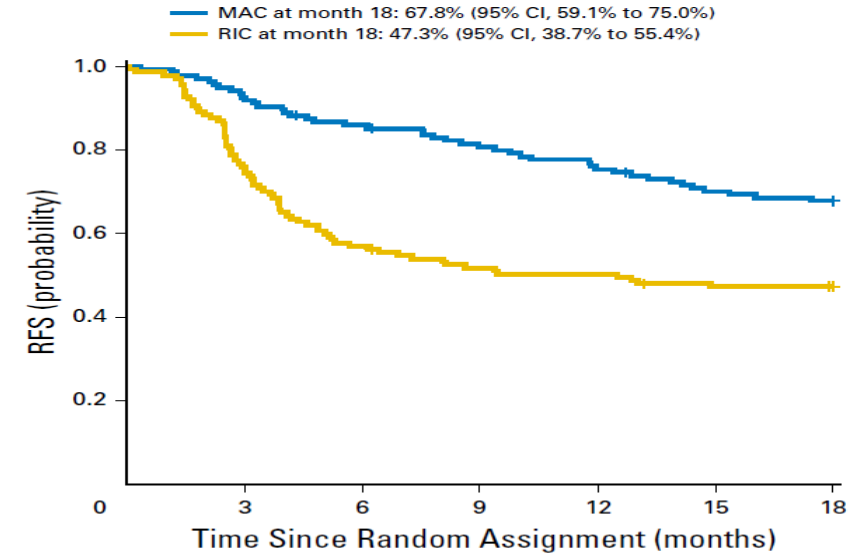
D'Souza A, Fretham C. Current Uses and Outcomes of Hematopoietic Cell Transplantation (HCT): CIBMTR Summary Slides, 2018. Available at <http://www.cibmtr.org>

Randomized trial: RIC vs MAC in AML and MDS patients: Age 18-65 and comorbidity index < 4

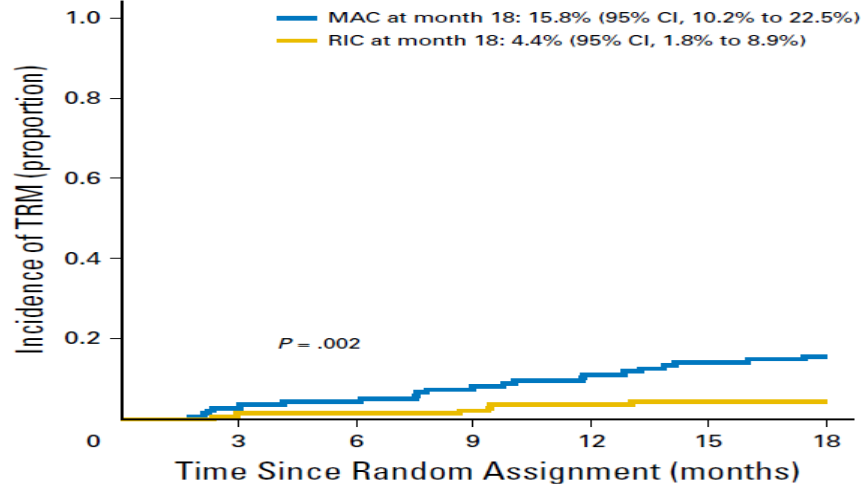
A



MAC OS	135	130	126	116	110	104	101
RIC OS	137	130	118	103	97	92	88
MAC relapse	135	126	117	110	103	96	92
RIC relapse	137	104	78	70	68	63	62

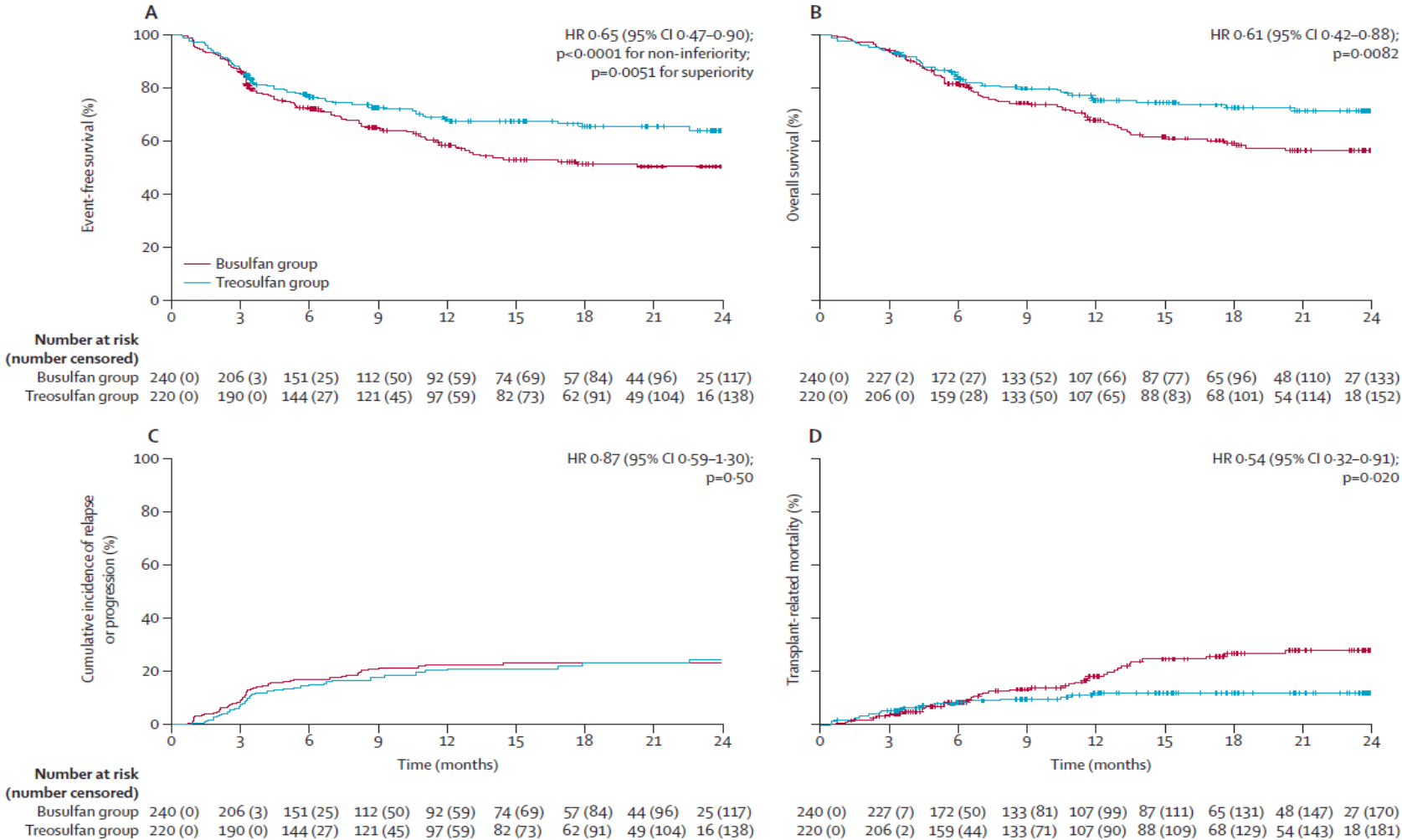


No. at risk							
MAC	135	125	115	107	100	92	89
RIC	137	104	78	70	68	63	62



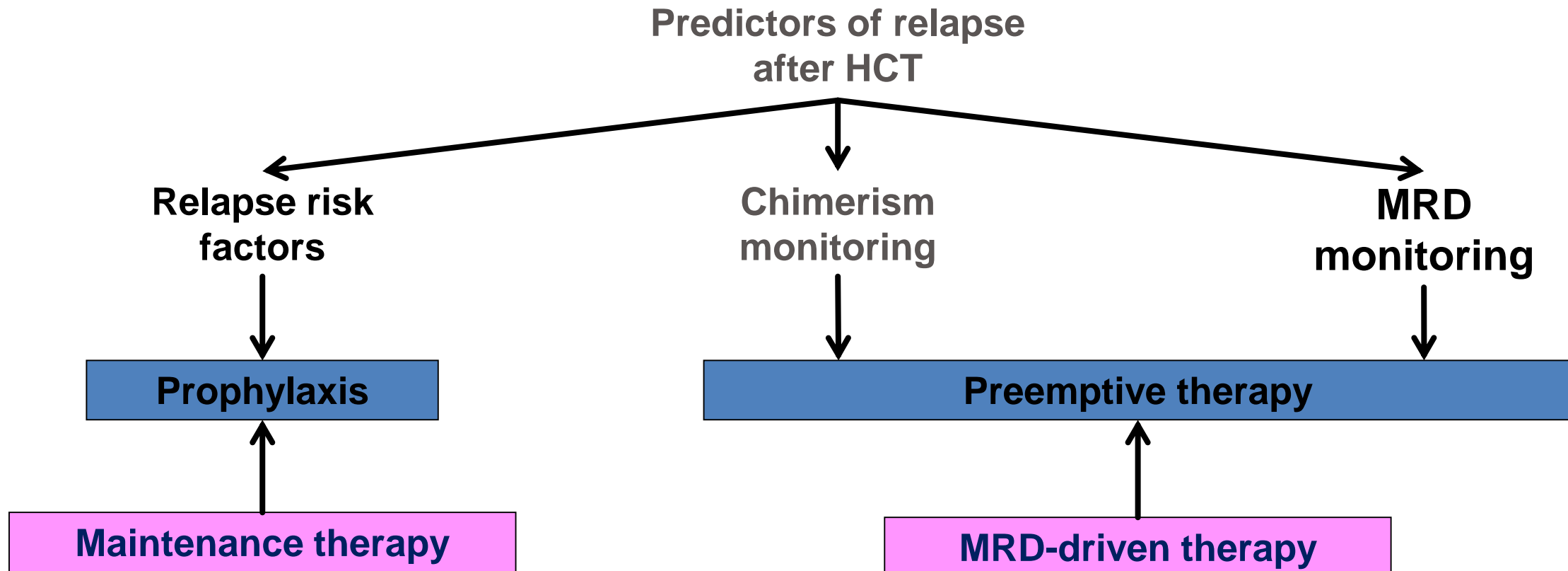
No. at risk							
MAC	135	126	117	110	103	96	0
RIC	137	104	78	70	68	63	0

Randomized trial: Treosulfan or busulfan plus fludarabine as RIC before allo-HSCT for older patients with AML or MDS



Strategies to control relapse in AML

Maintenance vs. preemptive therapy



Phase 3 trial of 10-day decitabine versus 7+3 followed by transplantation in fit AML patients aged ≥ 60 years: HRQoL

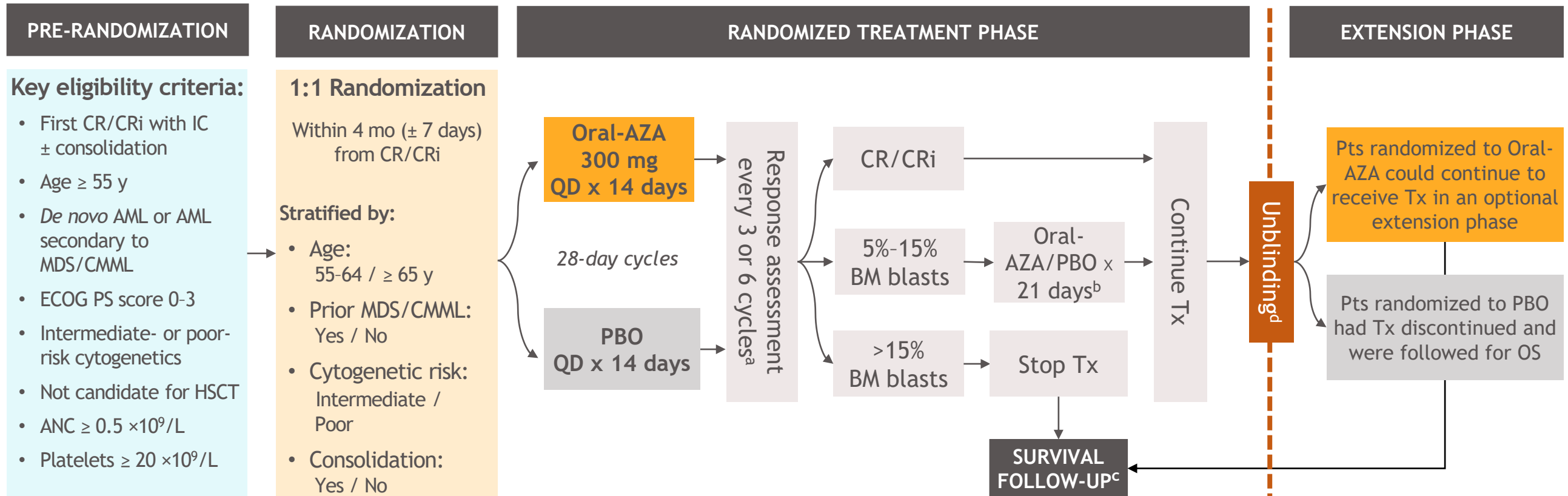
Study design	International, open-label, Phase 3 randomized controlled trial comparing 10-day decitabine followed by HSCT versus intensive chemotherapy (7+3) followed by HSCT*
Eligibility	Age ≥ 60 years; newly diagnosed AML (de novo or secondary); eligible for induction chemotherapy; ECOG PS ≤ 2
Enrolment	606 patients (303 per arm); around a third were aged ≥ 70 years
Clinical outcomes	<i>Presented at EHA 2022:</i> Similar survival with decitabine versus 7+3; comparable alloHSCT rates; more favorable safety profile with decitabine ¹
HRQoL	<ul style="list-style-type: none"> Assessed using EORTC QLQ-C30 and its module for older patients (EORTC QLQ-ELD14), specifically based on 5 <i>a priori</i>-selected primary scales: physical functioning, role functioning, fatigue, pain, and illness burden Assessments were performed at baseline and then short-term (2 months from randomization) and long-term (6 and 12 months) For patients undergoing HSCT, HRQoL was assessed prior to the procedure and at day 100 after transplant QoL deterioration was defined as any of the following: death; progression; or clinically meaningful deterioration from baseline in at least one of the primary HRQoL scales

*Decitabine was administered for 10 days consecutively in cycle 1 (20 mg/m²), 10 or 5 days in subsequent cycles (depending on bone marrow blast clearance at day 28); intensive chemotherapy was daunorubicin 60 mg/m² x 3 days, cytarabine 200 mg/m² x 7 days, followed by 1–3 additional chemotherapy cycles.
 AML, acute myeloid leukemia; ECOG PS, Eastern Cooperative Oncology Group performance status; EHA, European Hematology Association; EORTC, European Organisation for Research and Treatment of Cancer; HRQoL, health-related QoL; HSCT, hematopoietic stem cell transplant; QLQ, QoL questionnaire; QoL, quality of life.

1. Lübbert M et al. *HemaSphere* 2022;6:26–27.

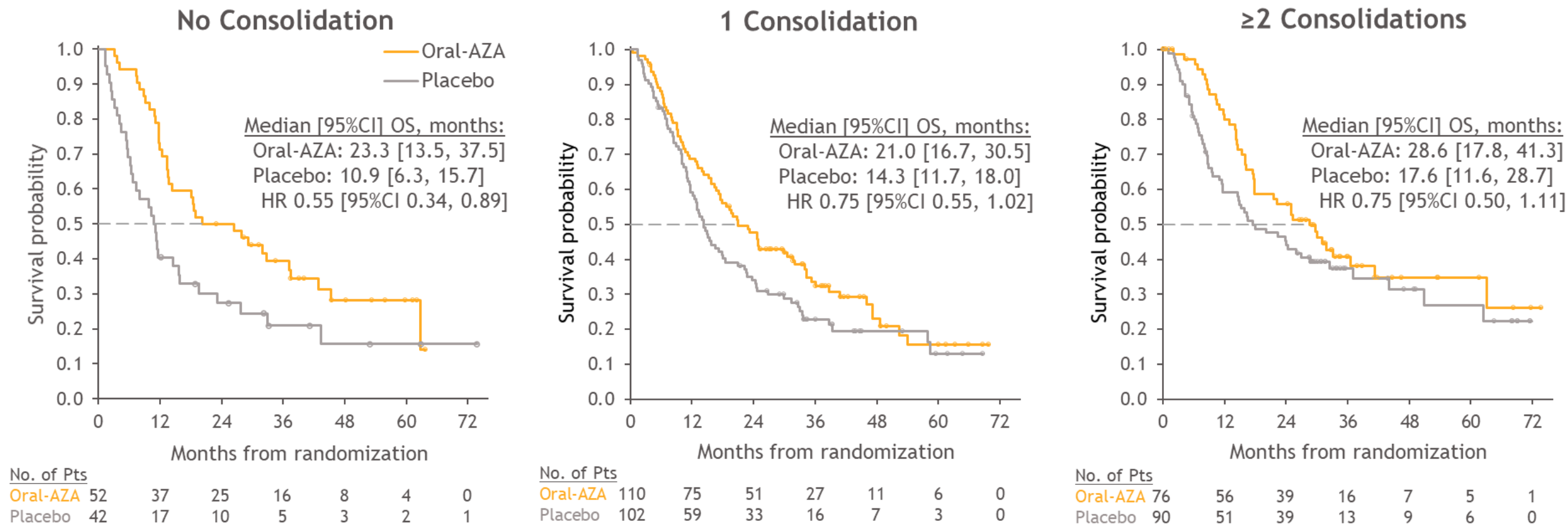
QUAZAR AML-001: Study design and key eligibility criteria

International, multicenter, PBO-controlled, double-blind, randomized, phase 3 trial



QUAZAR: Overall survival by number of consolidations

- OS was also prolonged with Oral-AZA within each consolidation cohort
- Median OS ranged from 21.0–28.6 months in the Oral-AZA arm and 10.9–17.6 months in the placebo arm



OS estimates were derived using Kaplan-Meier methods and compared for Oral-AZA vs. placebo using log-rank test. Hazard ratios (HRs) and 95% CIs were generated using a stratified Cox proportional hazards model.

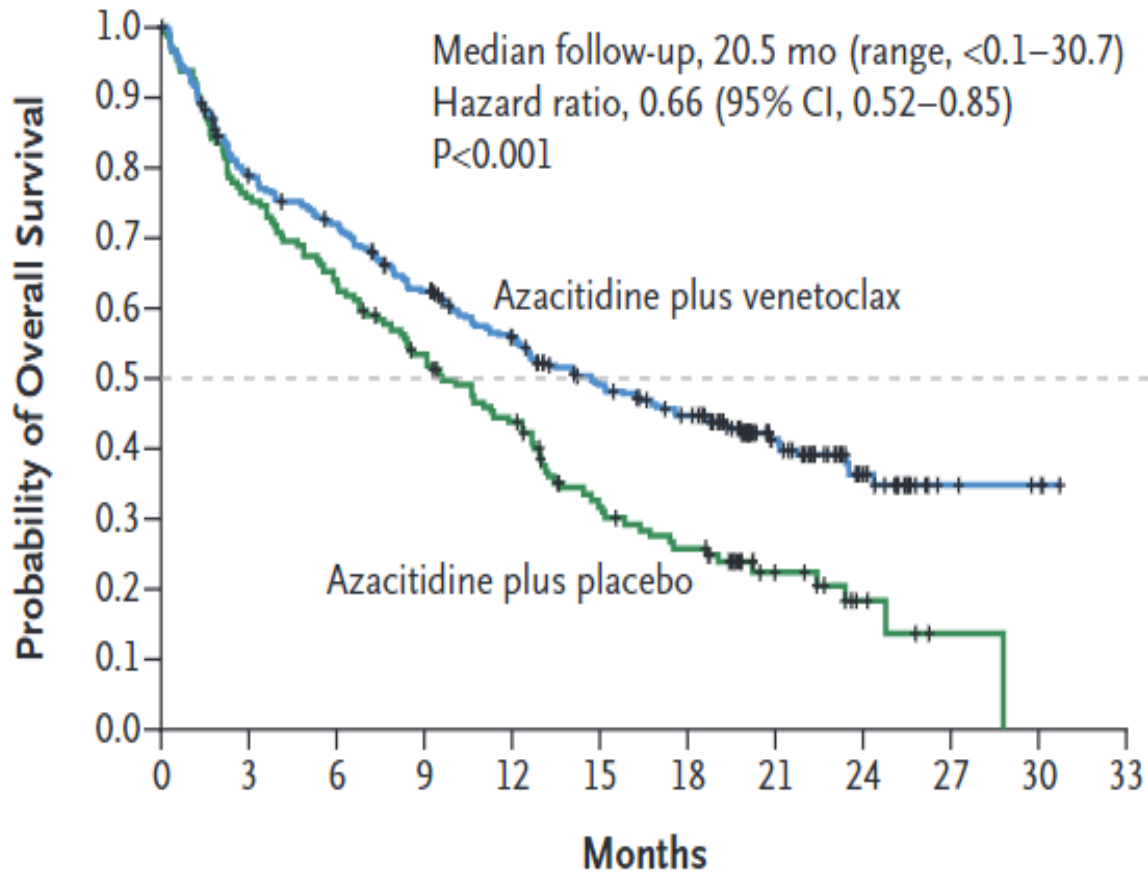
95%CI, 95% confidence interval; AZA, azacitidine; HR, hazard ratio; No., number; OS, overall survival; pts, patients.

Results of VIALE-A : Azacitidine +/- Venetoclax

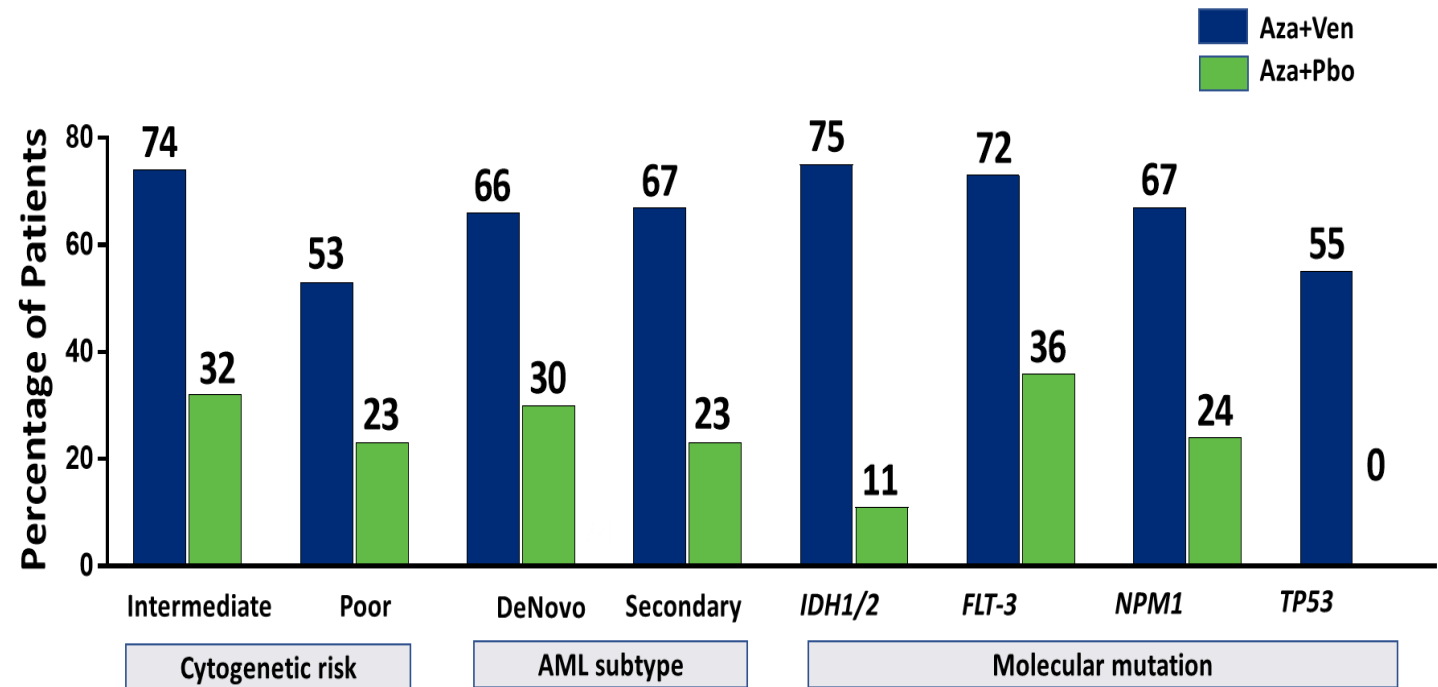
Significant OS improvement with azacitidine + venetoclax

CR rate: 36.7% vs 17.9% ($P < .001$)

CR/CRi rate: 66.4% vs 28.3% ($P < .001$)

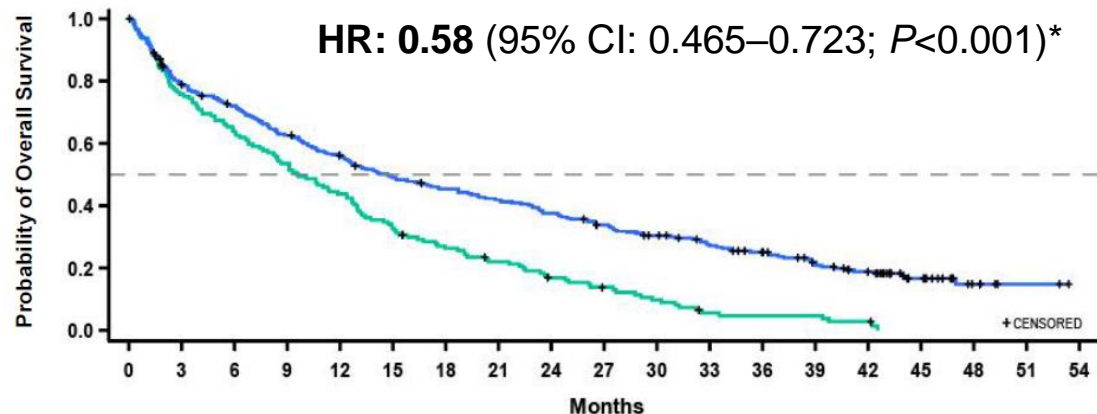


Improved responses occurred *independent* of high risk genomics



Long-term follow-up from VIALE-A: Overall survival

All patients (median follow up: 43.2 months)

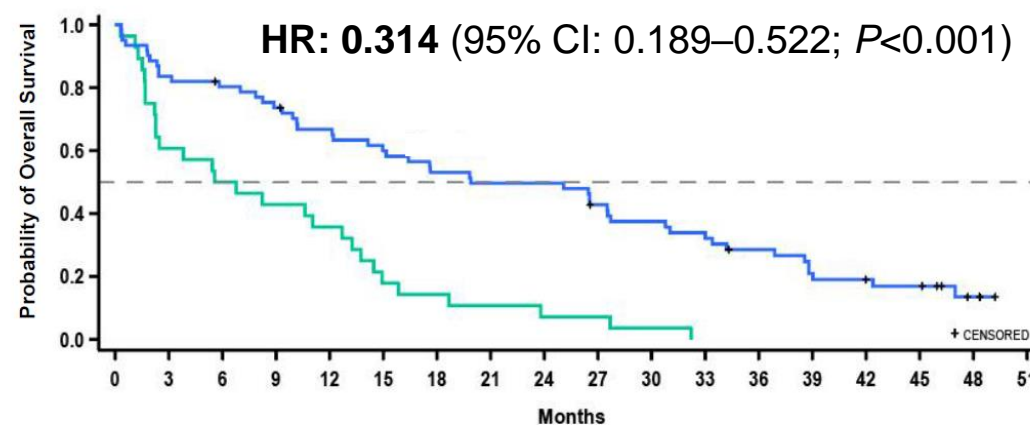


Patients at Risk

	0	3	6	9	12	15	18	21	24	27	30	33	36	39	42	45	48	51	54
Ven+Aza	286	220	199	173	153	133	122	113	101	89	78	67	57	45	34	18	6	2	0
Pbo+Aza	145	109	92	77	63	47	37	30	22	17	12	6	5	5	3	0	0	0	0

	Events / patients (%)	Median OS, months (95% CI)
Ven + aza	222/286 (77.6)	14.7 (12.1–18.7)
Pbo + aza	138/145 (95.2)	9.8 (7.4–12.7)

Patients with *IDH1/2* mutations



Patients at Risk

	0	3	6	9	12	15	18	21	24	27	30	33	36	39	42	45	48	51
Ven+Aza	61	51	48	44	39	35	31	29	29	24	21	19	15	11	9	8	3	0
Pbo+Aza	28	17	14	12	10	5	4	3	2	2	1	0	0	0	0	0	0	0

	Events / patients (%)	Median OS, months (95% CI)
Ven + aza	49/61 (80.3)	19.9 (12.2–27.7)
Pbo + aza	28/28 (100)	6.2 (2.3–12.7)

*Compared with HR of 0.66 at 75% OS analysis.

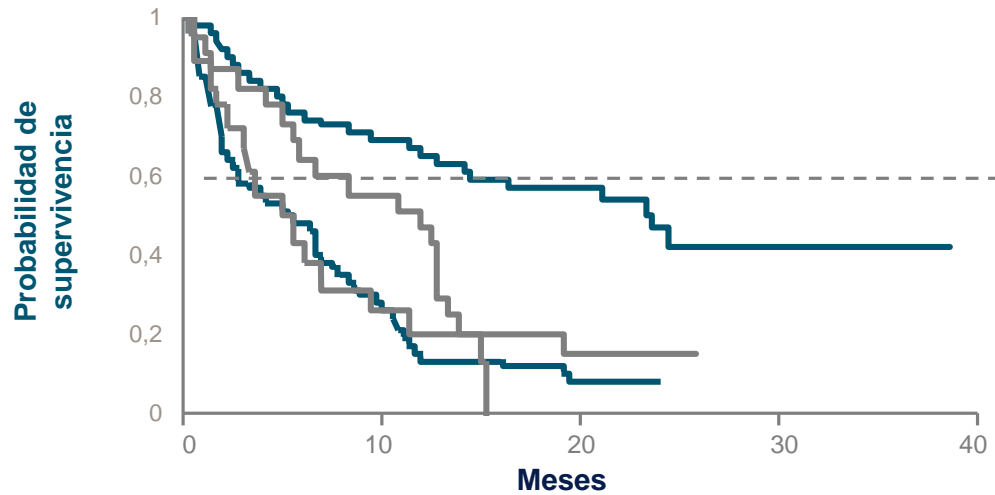
Aza, azacitidine; CI, confidence interval; HR, hazard ratio; IDH, isocitrate dehydrogenase; OS, overall survival; pbo, placebo; ven, venetoclax.

Real life results of HMA+VEN in high-risk Genetic AML

Reference	n	genetics	schedule	Response	Response %	mOS
Winters 2019 - Single center (USA) ¹	5	TP53+	AZA+VEN	CR/CRi	40	NA
Grenet ASH 2021 - Multicentric (USA) ²	57	TP53+	HMA+VEN	CR/CRi	48	6.4
Johnson EHA 2022 - Single center (USA) ³	ND (103*)	TP53+	HMA+VEN	CR/CRi	32	NA
Venugopal 2022 A - Single center (USA) ⁴	53	TP53+	HMA+VEN LDAC+VEN	CR/CRi	56	6.4
Daver 2023 - Multicenter (USA) ⁵	94	TP53+ or 17p deletion	HMA+VEN	NA	NA	7.6
Winters 2019 - Single center (USA) ¹	10	Unfavorable cytogenetic	AZA+VEN	CR/CRi	60	NA
De Bellis 2022 - Multicentric (Italy) ⁷	23	Adverse karyotype	HMA+VEN	CR/CRi	61	10.5
Johnson EHA 2022 - Single center (USA) ³	ND (103*)	Adverse karyotype	HMA+VEN	CR/CRi	49	NA
Lam EHA 2022 - Single center (UK) ⁸	5	Adverse risk	AZA+VEN	CR/CRi	65	NA
Gherson 2023 - Multicentric (USA) ⁹	136	Adverse ELN	HMA+VEN	NA	NA	7.9
Grenet ASH 2021 - Multicentric (USA) ²	162	Adverse ELN	HMA+VEN	CR/CRi	52	9.7
Kale ASH 2022 - Single center (USA) ¹⁰	ND (28*)	Adverse ELN	HMA+VEN	NA	NA	11.7
Vachhani 2022 - Multicenter (USA) ¹¹	65	Adverse ELN	HMA+VEN	CRc	45	NA

OS in TP53 AML in phase 3 RCT (VIALE-A & CPX351)

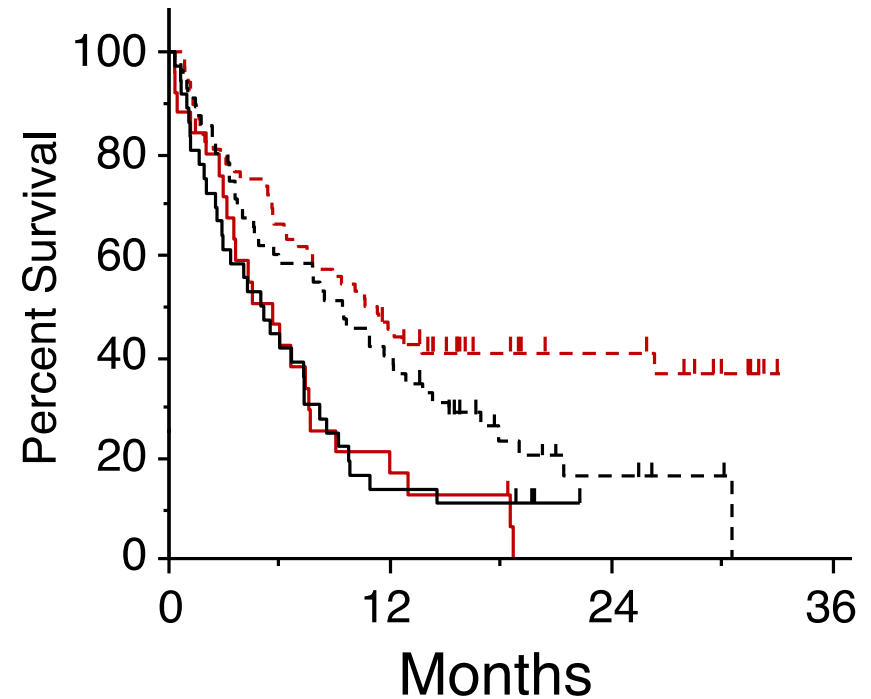
VENAZA



—	VEN+AZA, TP53 wt	50	34	24	1	0
—	VEN+AZA, TP53 mut	54	13	3	0	0
—	AZA, TP53 wt	22	12	2	0	0
—	AZA, TP53 mut	18	4	0	0	0

	mOS, months (IC 95%)
VEN+AZA TP53 wt:	23,43 (11,93 - NR)
VEN+AZA TP53 mut:	5,17 (2,17 - 6,83)
AZA TP53 wt:	11,29 (4,9 - 12,78)
AZA TP53 mut:	4,90 (2,14 - 9,30)

7+3 / CPX-351



—+—	CPX-351, mutation present	—+—	CPX-351, no mutation
—+—	7+3, mutation present	—+—	7+3, no mutation

OS in TP53 AML (MDACC USA)

Table: Median overall survival (95% CI) and adjusted hazard ratio by allo-SCT status

Allo-SCT status	Overall (N=370)	Cohort A Ven+HMA (N=94)	Cohort B Intensive Chemo (N=135)	Cohort C HMA only (N=141)
No, n (%)	340 (92)	89 (95)	114 (84)	137 (97)
Deceased, yes, n (%)	279 (82)	65 (73)	89 (78)	125 (91)
Median OS, mos (95% CI)	7.0 (6.0, 7.8)	7.2 (5.7, 8.4)	7.3 (6.5, 9.8)	5.7 (4.2, 7.0)
Yes, n (%)	30 (8)	5 (5)	21 (16)	4 (3)
Deceased, yes, n (%)	15 (50)	1 (20)	12 (57)	2 (50)
Median OS, mos (95% CI)	33.7 (13.0, 44.1)	NA (10.7, NA)	28.9 (12.8, 36.5)	45.5 (44.1, 46.9)
Allo-SCT (yes vs no)*		aHR (95% CI)		P-value
In overall model (Cohort A, B, and C)		0.4 (0.2, 0.6)		<0.001

*Adjusted in Cox model for baseline covariates including age at baseline, time to 1L start, number of comorbidities, TP53m/cytogenetic risk level, 17p del status, bone marrow blast percentage at baseline, secondary AML, therapy-related AML, and healthcare practice type. 1L, initial therapy; aHR, adjusted hazard ratio; allo-SCT, allogeneic stem cell transplantation; AML, acute myeloid leukemia; CI, confidence interval; HMA, hypomethylating agents; mos, months; NA, not applicable; OS, overall survival; Ven, venetoclax.

Magrolimab + Aza in Patients With MDS and AML: Response in Patients With TP53 Mutation

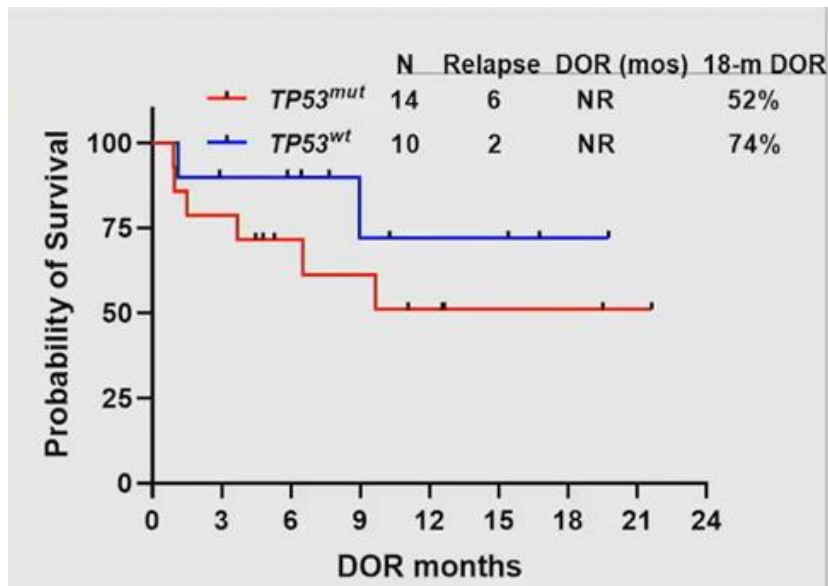
Outcome	MDS TP53 Mutant (n = 12)	AML TP53 Mutant (n = 4)
ORR, n (%)	9 (75)	3 (75)
CR, n (%)	5 (42)	2 (50)
CRi/marrow CR, n (%)	4 (33)	1 (25)
Complete cytogenetic response, n/N (%)*	4/8 (50)	3/3 (100)
MRD negativity in responders, n/N (%)	4/9 (44)	0
Median DoR, mos	NR (0.03+ to 15.1)	NR (0.03+ to 5.2+)
6-mo survival probability, %	91	100
Median follow-up, mos (range)	8.8 (1.9 to 16.9)	7 (4.2 to 12.2)

*Responders with cytogenetic abnormalities at baseline.

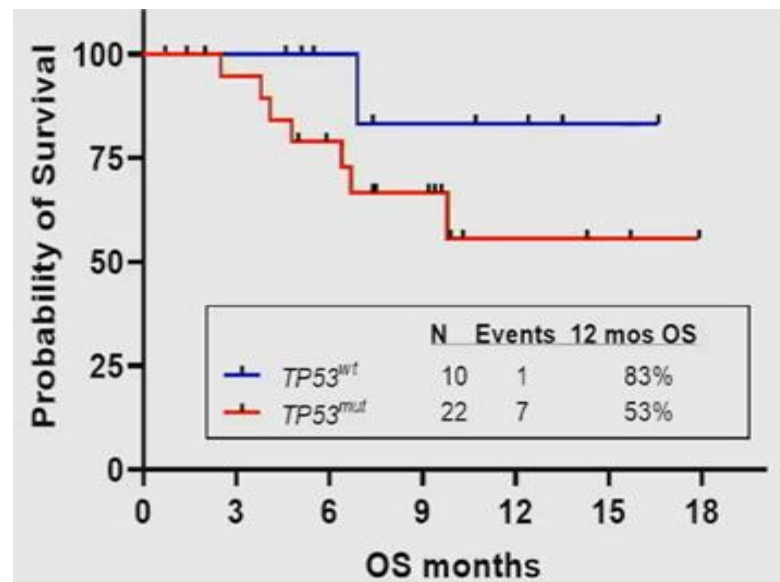
Phase 1/2 study of azacitidine with venetoclax and magrolimab: Frontline response and survival

- **Frontline cohort, N=43** (n=33 de novo AML; n=10 secondary AML)
 - Median age: 70 years, 37% female; 91% had adverse ELN 2017 risk stratification; 65% had adverse cytogenetics*
 - $TP53^{mut}$: n=27 (63%); $TP53^{WT}$: n=16 (37%)
- **Response rates:**
 - CR: n=21/43 (49%); CR+CRi: n=31/43 (72%)
 - MRD-negative best response: n=16/28 (67%)[†]

DOR (frontline de novo patients, n=33):[‡]



OS (frontline de novo patients, n=33):[‡]



Frontline secondary AML (n=10):

- Median DOR
 - $TP53^{mut}$: 5.9 months
 - $TP53^{WT}$: 2.2 months
- Median OS
 - $TP53^{mut}$: 7.6 months
 - $TP53^{WT}$: 9.6 months

*Per ELN 2017. [†]Among CR/CRi patients with longitudinally MRD-evaluable samples. [‡]Median follow-up 14.5 months.
 AML, acute myeloid leukemia; CR, complete remission; CRi, CR with incomplete count recovery; DOR, duration of response; ELN, European LeukemiaNet; MRD, minimal residual disease; mut, mutated; NR, not reached; OS, overall survival; WT, wild type.

Menin-KMT2A Pathway Represents a Foundational Target for Ziftomenib

- *NPM1*-m and *KMT2A*-r drive overexpression of *HOXA9/MEIS1* genes, critical for transformation to AML
- *KMT2A*(MLL) sits upstream from major AML targets (ie, *FLT3*, *IDH1/2*, *DNMT3A*)
- *KMT2A*(MLL)-dependent genes contribute to therapeutic resistance and relapse to current SOC
- Menin inhibition down regulates *HOXA9/MEIS1*, leading to differentiation of leukemic blasts

