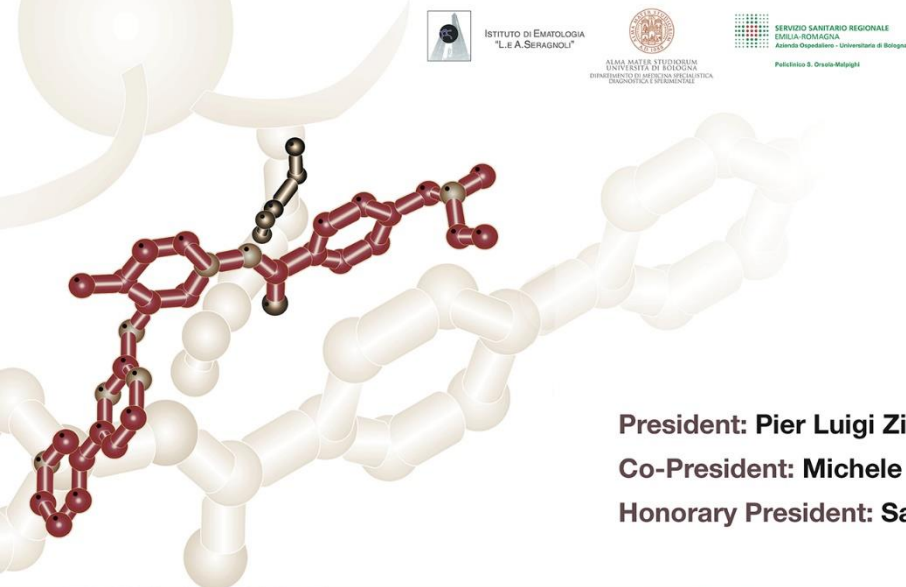




New Drugs in Hematology

President: Pier Luigi Zinzani
Co-President: Michele Cavo
Honorary President: Sante Tura

Bologna,
Royal Hotel Carlton
October 1-3, 2018

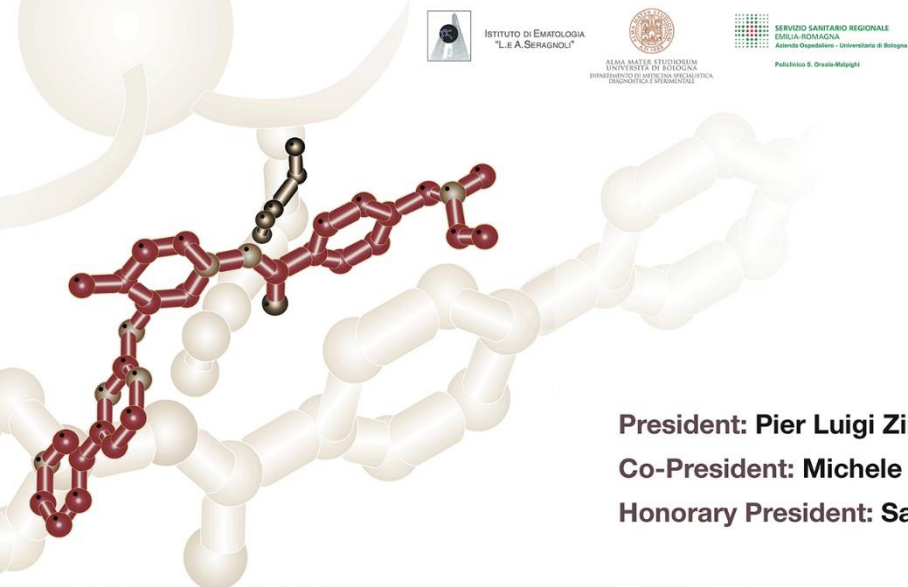
BOLOGNA, ROYAL HOTEL CARLTON

State-of-the-art: from genomic knowledge to targeted therapy in leukemias



Lars Bullinger
Charité University Medicine
Berlin





ISTITUTO DI EMATOLOGIA
"L. e A. SERAGNOLI"



ALMA MATER STUDIORUM
UNIVERSITY OF BOLOGNA
DIPARTIMENTO DI SCIENZE FARMACOLOGICHE,
INGEGNERIA E INFORMATICA



SERVIZIO SANITARIO REGIONALE
EMILIA ROMAGNA
Azienda Ospedaliera - Università di Bologna

Policlinico S. Orsola-Malpighi

New Drugs in Hematology

Bologna,
Royal Hotel Carlton
October 1-3, 2018

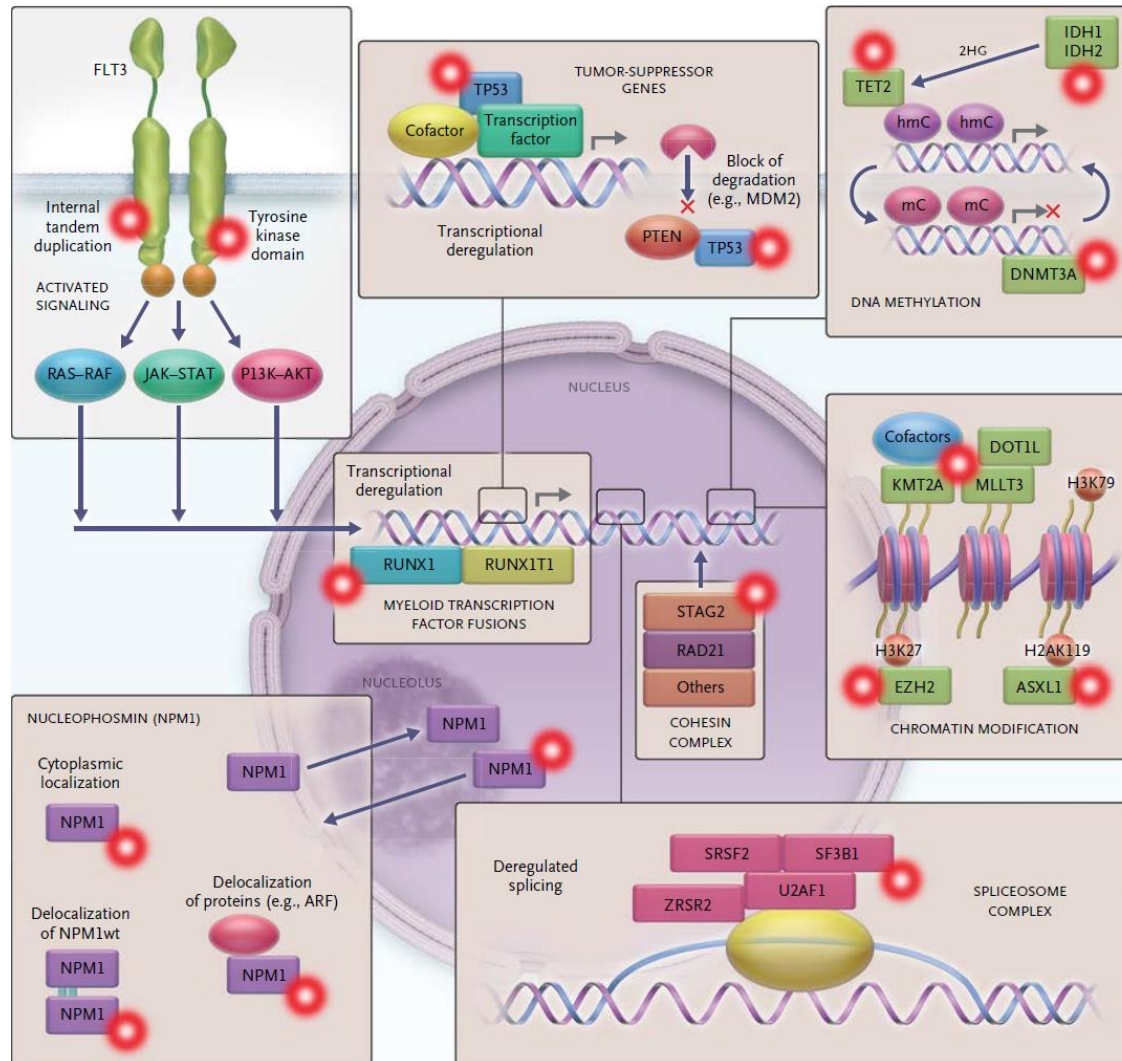
President: Pier Luigi Zinzani
Co-President: Michele Cavo
Honorary President: Sante Tura

BOLOGNA, ROYAL HOTEL CARLTON

Disclosures of NAME SURNAME

Company name	Research support	Employee	Consultant	Stockholder	Speakers bureau	Advisory board	Other
Amgen					x		x
Bayer Oncology	x				x		
Bristol-Myers Squibb					x	x	
Jazz Pharmaceuticals					x	x	
Novartis			x		x	x	
Pfizer					x		
Sanofi	x				x		

Genomic landscape of de novo AML



Commonly mutated functional gene categories:

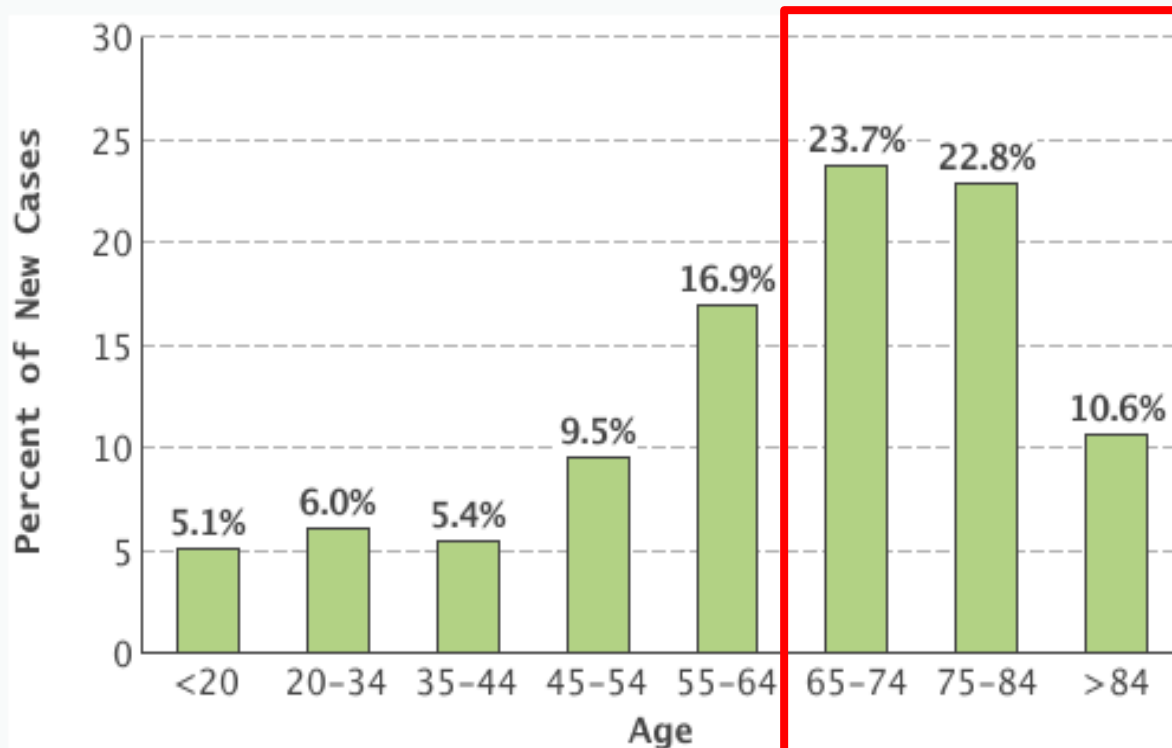
- (1) signaling genes
- (2) transcription factors
- (3) NPM1
- (4) spliceosome complex
- (5) Cohesion complex
- (6) chromatin modification
- (7) DNA methylation
- (8) tumor-suppressors

2017 ELN recommendations

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</i>-ITD or with <i>FLT3</i>-ITD^{low}† Biallelic mutated <i>CEBPA</i>
Intermediate	Mutated <i>NPM1</i> and <i>FLT3</i>-ITD^{high}† Wild-type <i>NPM1</i> without <i>FLT3</i>-ITD or with <i>FLT3</i>-ITD^{low}† (without adverse-risk genetic lesions) t(9;11)(p21.3;q23.3); <i>MLLT3-KMT2A</i>‡ 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,§ monosomal karyotypell Wild-type <i>NPM1</i> and <i>FLT3</i>-ITD^{high}† Mutated <i>RUNX1</i>¶ Mutated <i>ASXL1</i>¶ Mutated <i>TP53</i>#

AML incidence increases with age

Percent of New Cases by Age Group: Acute Myeloid Leukemia



Acute myeloid leukemia is most frequently diagnosed among people aged 65–74.

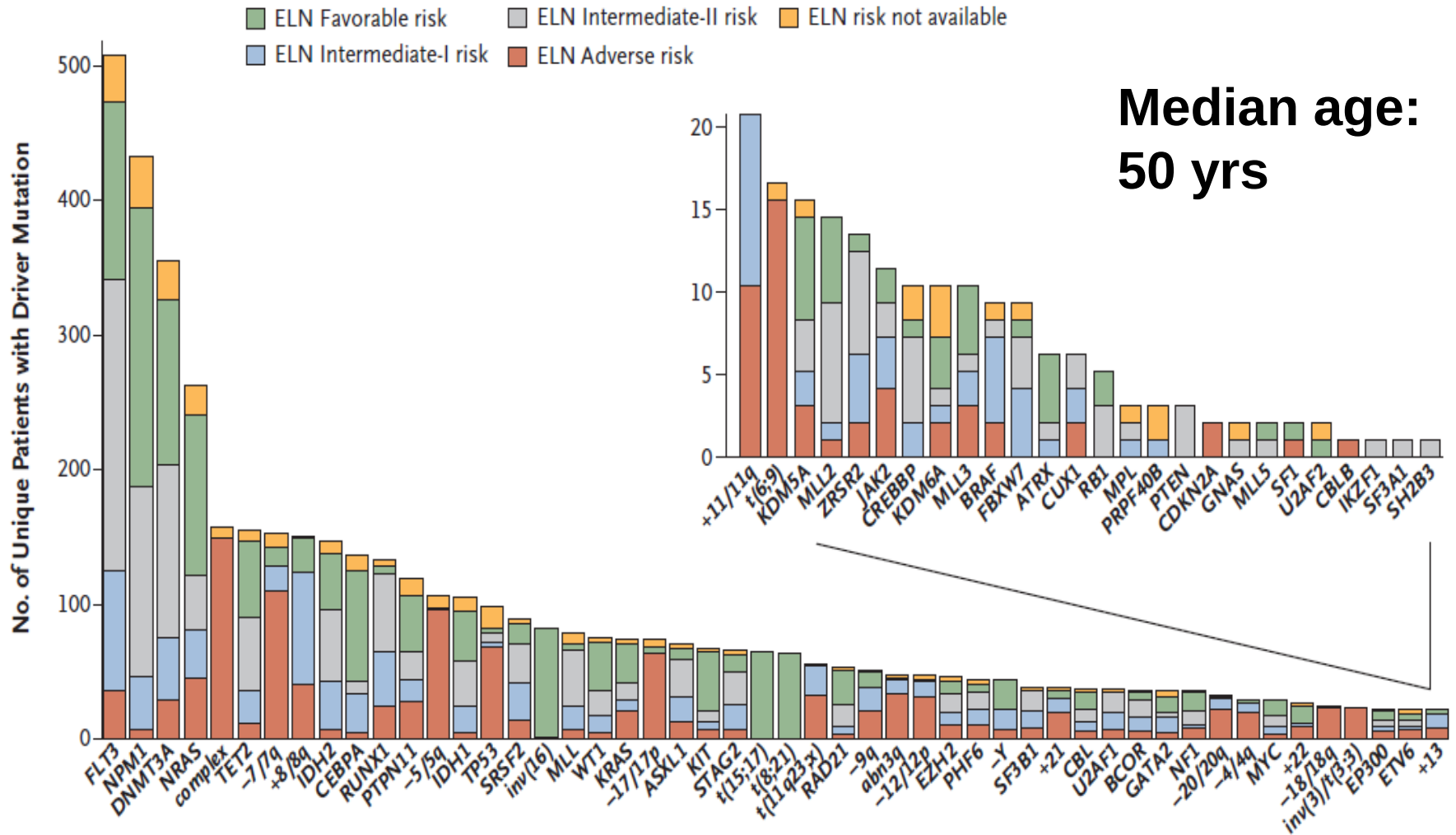
Median Age
At Diagnosis

68

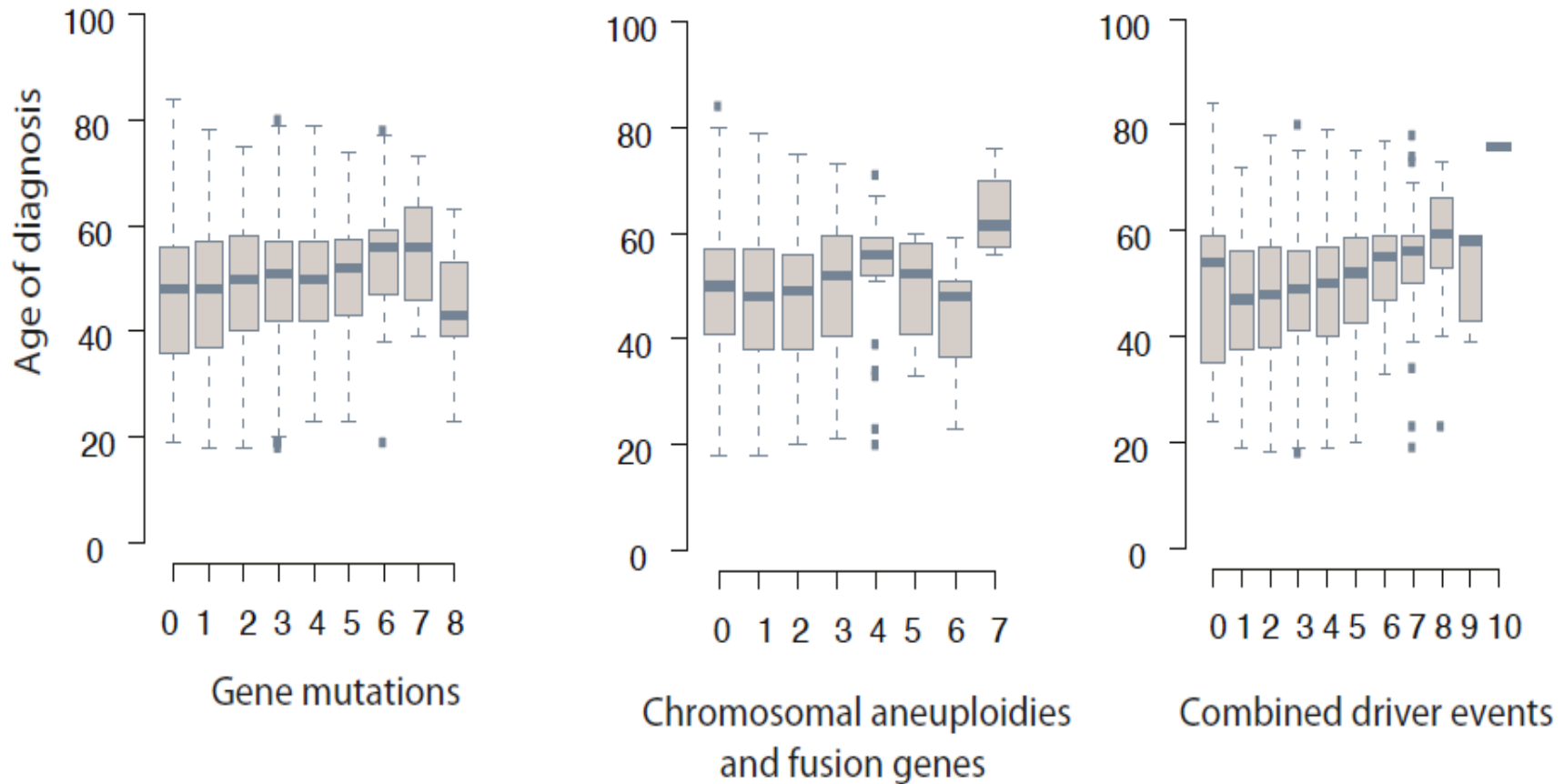
SEER 18 2010–2014, All Races, Both Sexes

>50%

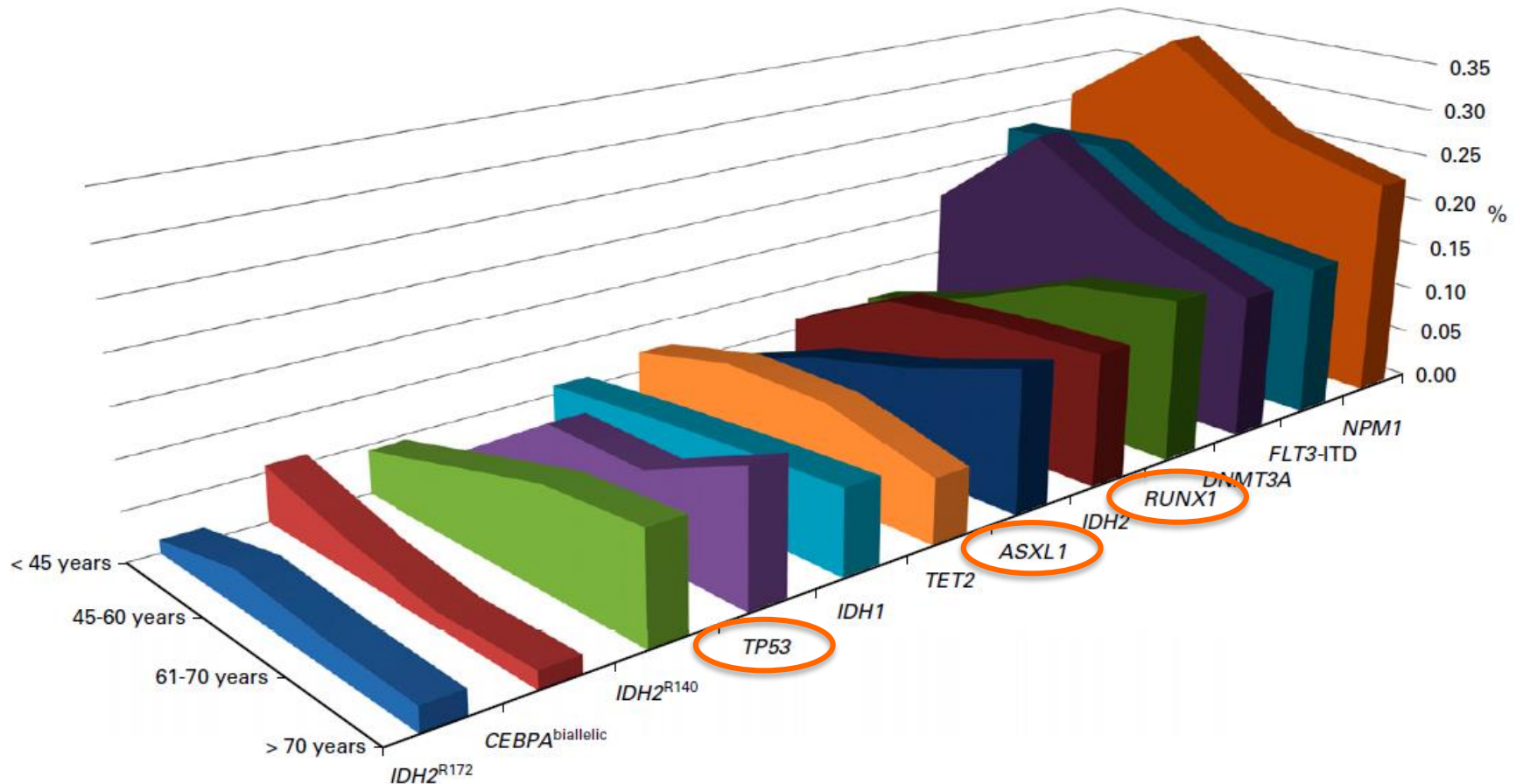
Genomic landscape of adult AML



Number of driver mutations increases with age



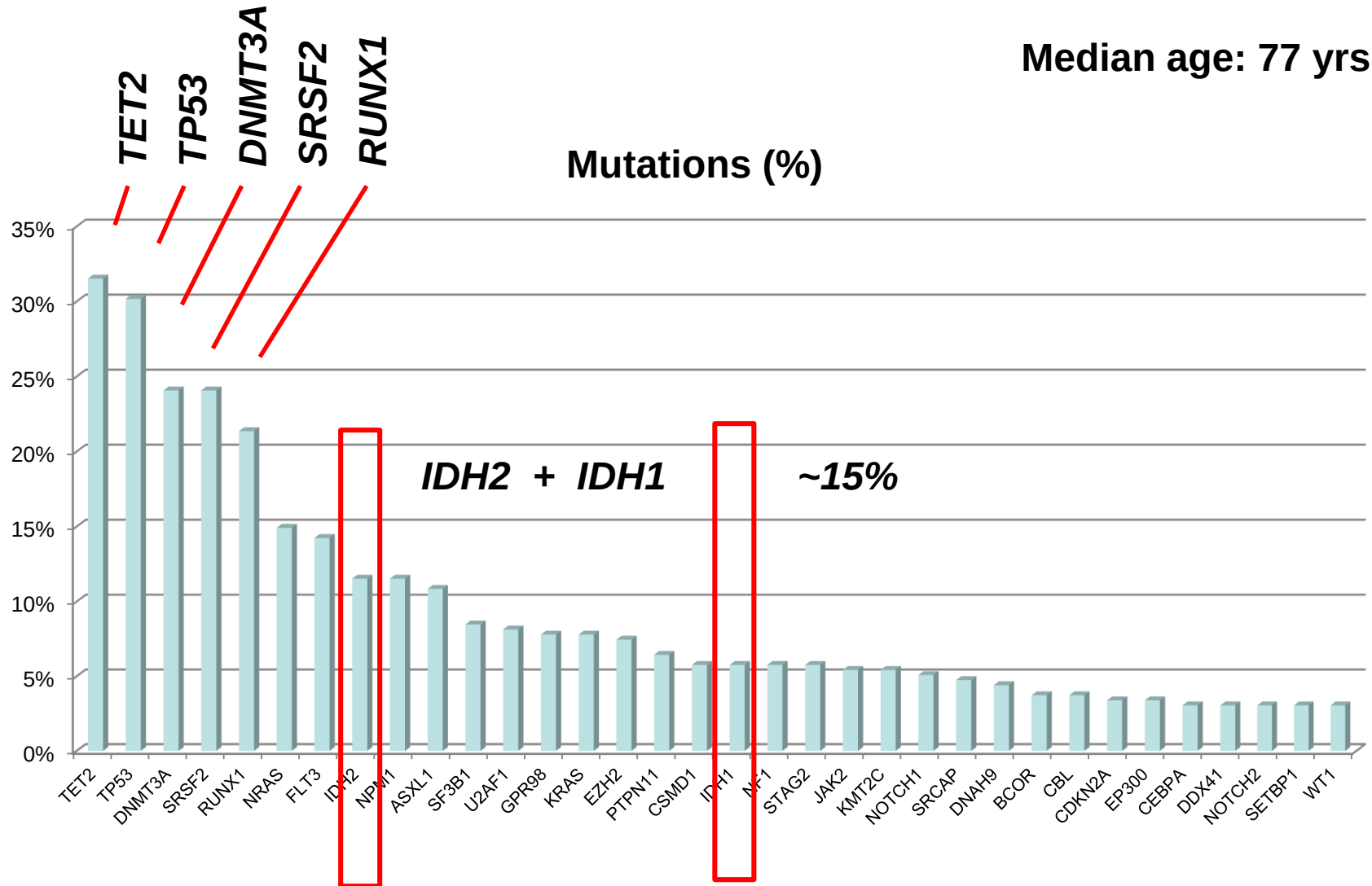
Age-related frequency of gene mutations



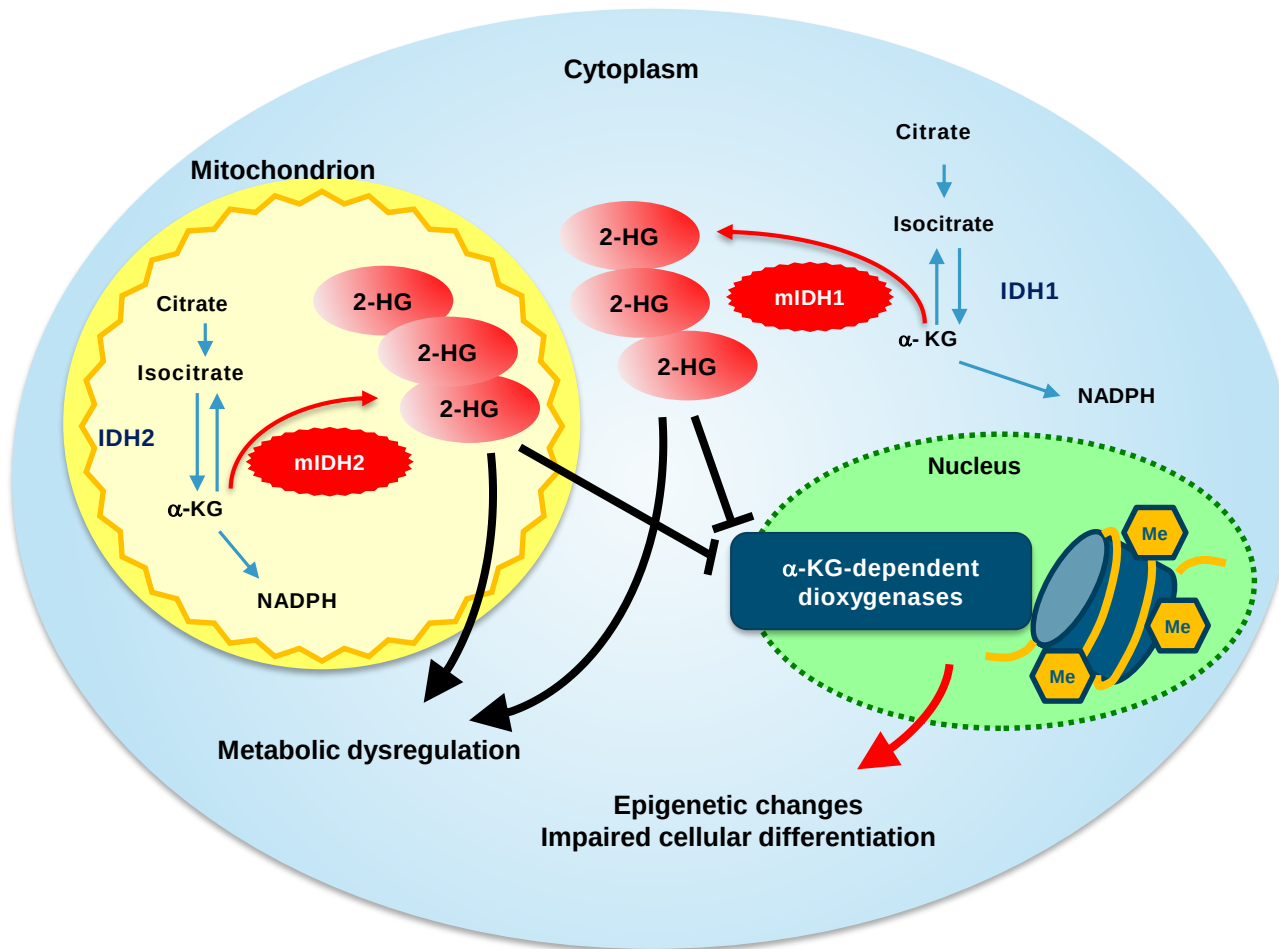
Analysis based on 10,622 AML patients from the AMLSG data base

Age distribution: <45 yrs, n=2,228; 45-60 yrs, n=3,392; 61-70 yrs, 2,517; >70 yrs, n=2,485

Mutational landscape in AML ≥ 70 yrs (n=295)



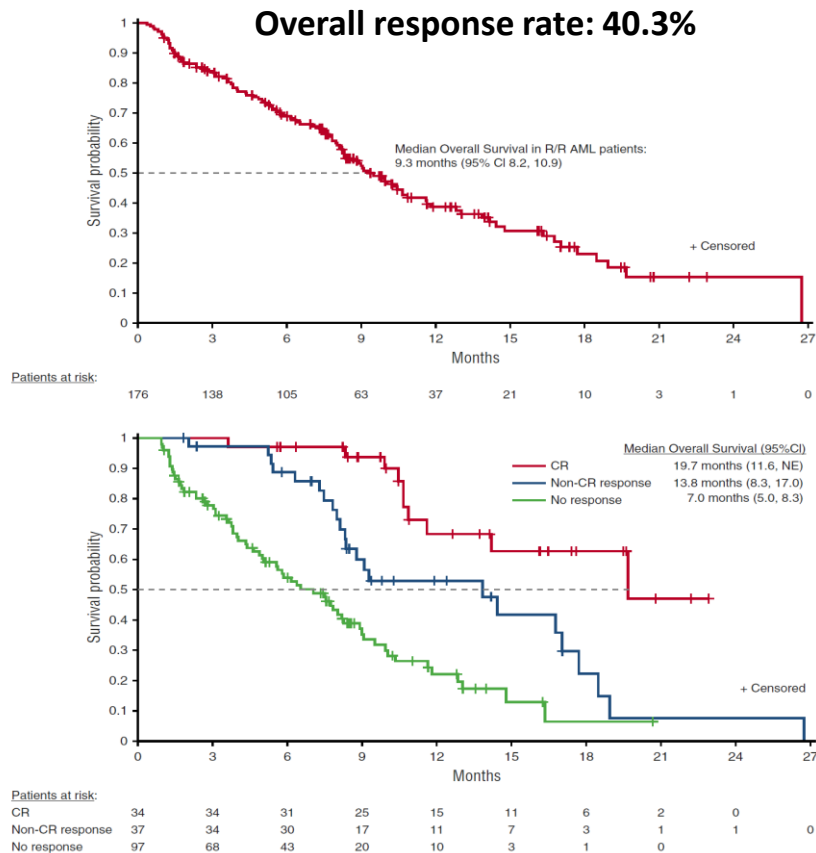
IDH1 and *IDH2* - therapeutic target structure



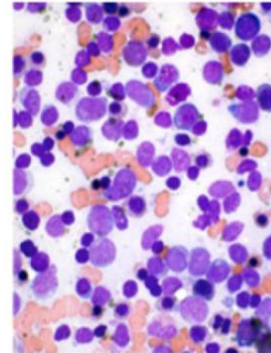
2-HG, 2-hydroxyglutarate; mIDH, mutant IDH

Enasidenib (AG-221)

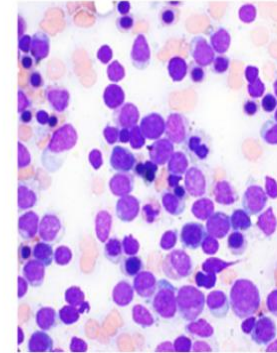
in *IDH2*^{mut} relapsed or refractory AML



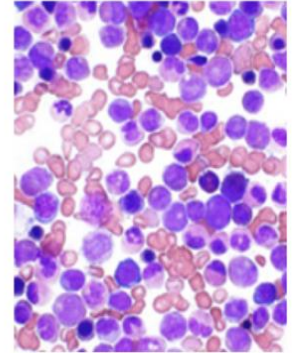
Screening
37% BM blasts



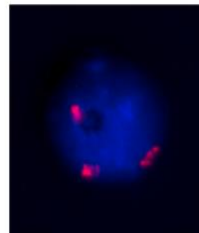
Cycle 1 Day 15
Evidence of cellular differentiation



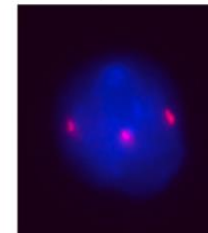
Cycle 3 Day 1
4% BM blasts



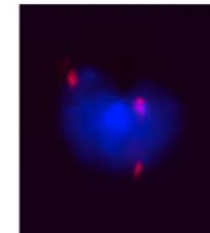
Blasts



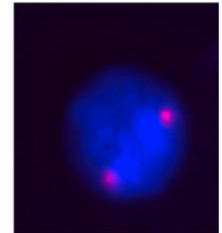
Promyelocytes



Mature Granulocytes



Lymphocytes

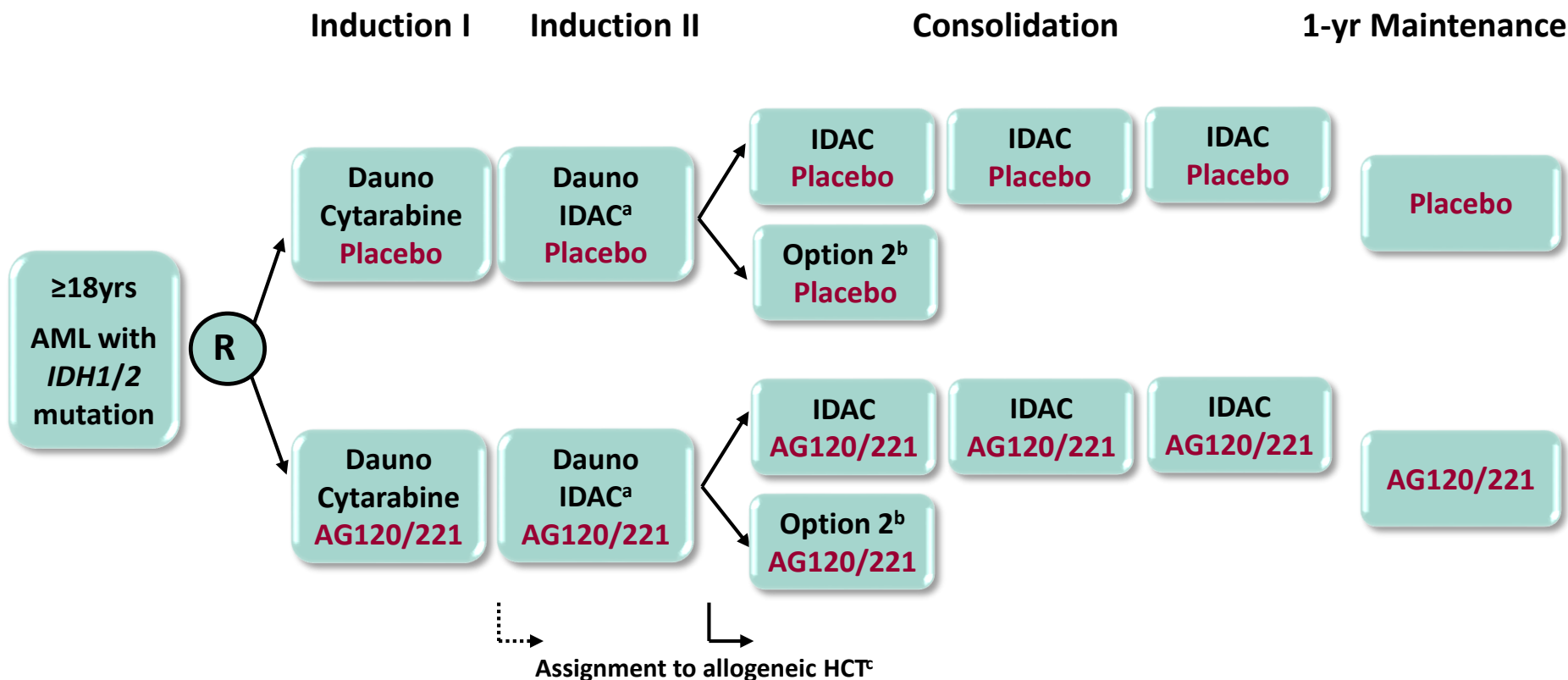


Ivosidenib (AG-120) and Enasidenib (AG-221) clinical development program

	Phase I/II	Phase III
≥2 nd r/r AML		Phase III: AML-004 (IDENTIFY) Enasidenib vs. CCR N=280
Frontline ineligible for intensive chemotherapy	Phase I/II AML-005 Azacitidine + ivosdenib Azacitidine +/- enasidenib N=175	Phase III: AG120-C-009 (AGILE) Azacitidine +/- ivosidenib N=392
Frontline eligible for intensive chemotherapy	Phase I: AG-221-120-C-001 Ivosidenib/enasidenib + intensive Cx N=90	HOVON 150 / AMLSG 29-18 Ivosidenib/enasidenib + intensive Cx N=~800



AG-120/AG-221 vs placebo + chemotherapy for *IDH1*^{mut}/*IDH2*^{mut} AML – AMLSG 29-18



Patients in CR/CRi after two cycles of induction proceed to AMLSG/HOVON-specific consolidation therapy; assignment to allogeneic hematopoietic cell transplantation (HCT) according to the local institutional or cooperative group prognostic algorithm; HCT can be performed at any time point following one induction cycle

^a IDAC, intermediate-dose cytarabine; age-adapted dosing

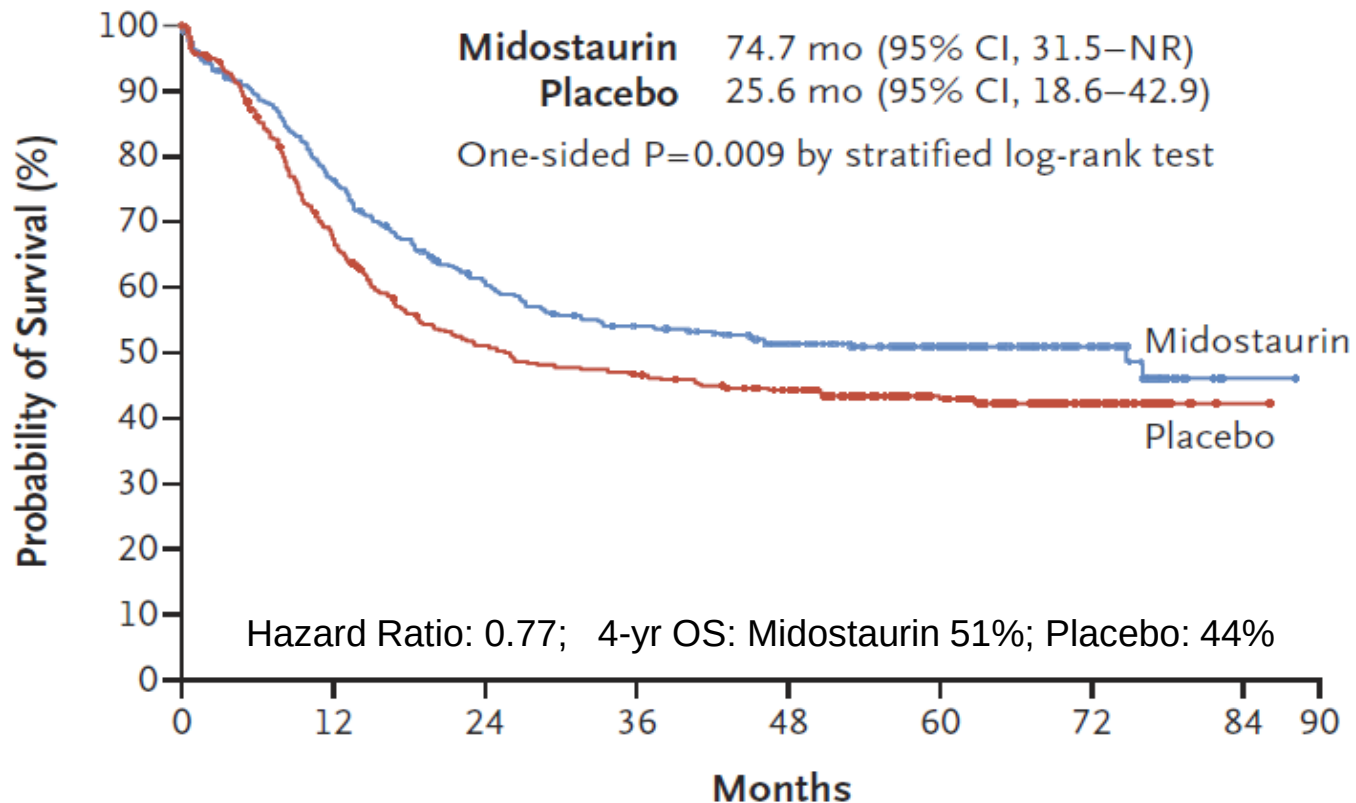
^b HOVON consolidation: autologous HCT; or mitoxantrone / etoposide

^c Assignment based on patient- and disease-related factors

Expected start Q3/2018



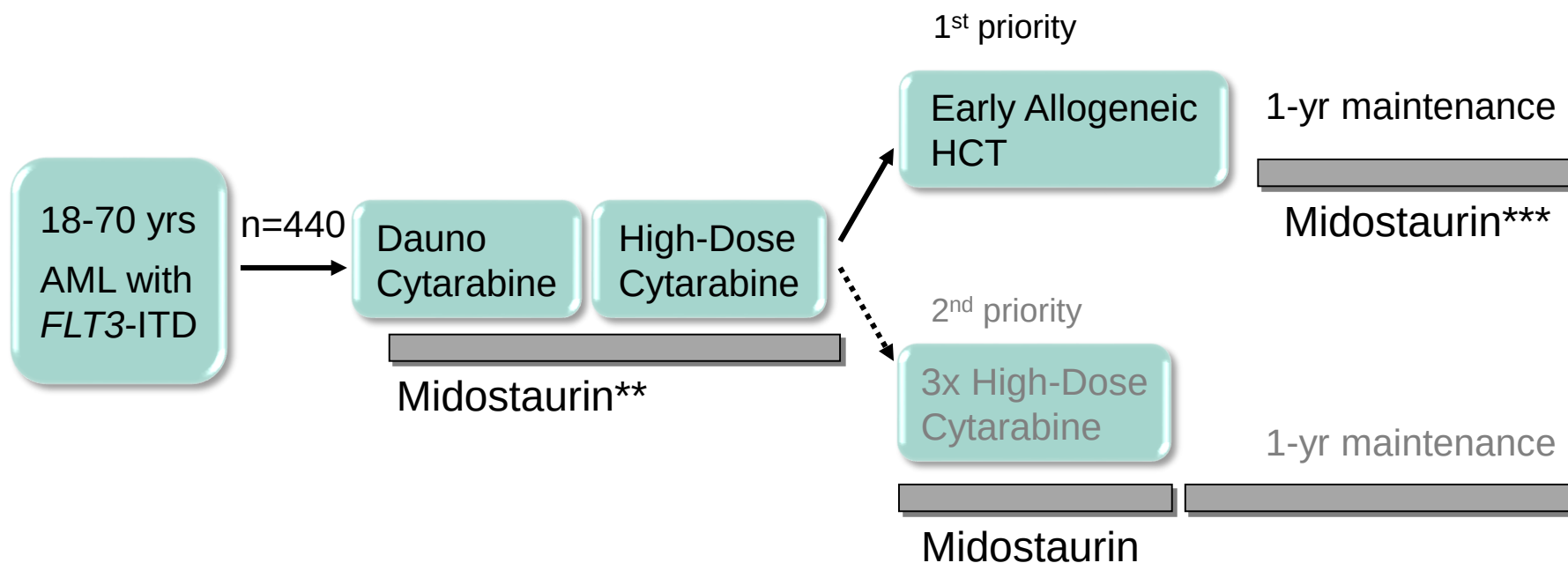
AML with *FLT3* mutation – midostaurin plus chemotherapy (RATIFY)



No. at Risk

Midostaurin	360	269	208	181	151	97	37	1
Placebo	357	221	163	147	129	80	30	1

Midostaurin plus chemotherapy for AML with *FLT3*-ITD – AMLSG 16-10



* Adult patients 18 – 70 years

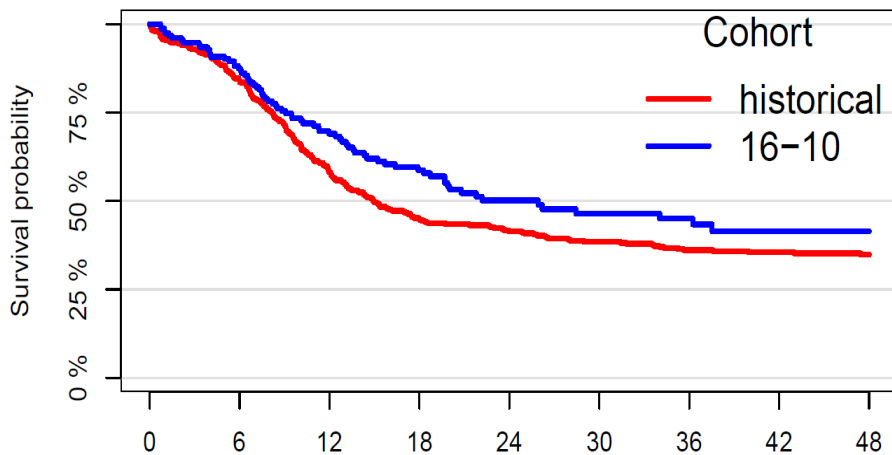
** Continuous dosing of midostaurin (start on day 8; except days of chemotherapy)

*** Midostaurin given also after allogeneic HCT (start d+30)

ClinicalTrials.gov: NCT01477606 (active)

AMLSG 16-10 vs historical control - Propensity Score Weighting Analysis*

Age 18-60 years

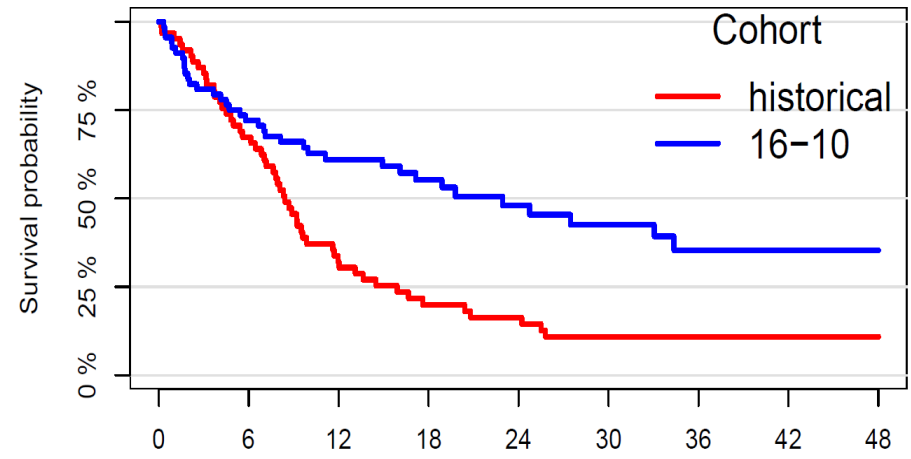


Time [months]

Cohort									
historical:	353	296	203	155	141	131	121	111	97
16-10:	155	131	92	67	46	36	28	12	4

HR = 0.70 (CI95% 0.535, 0.920)

Age 60-70 years



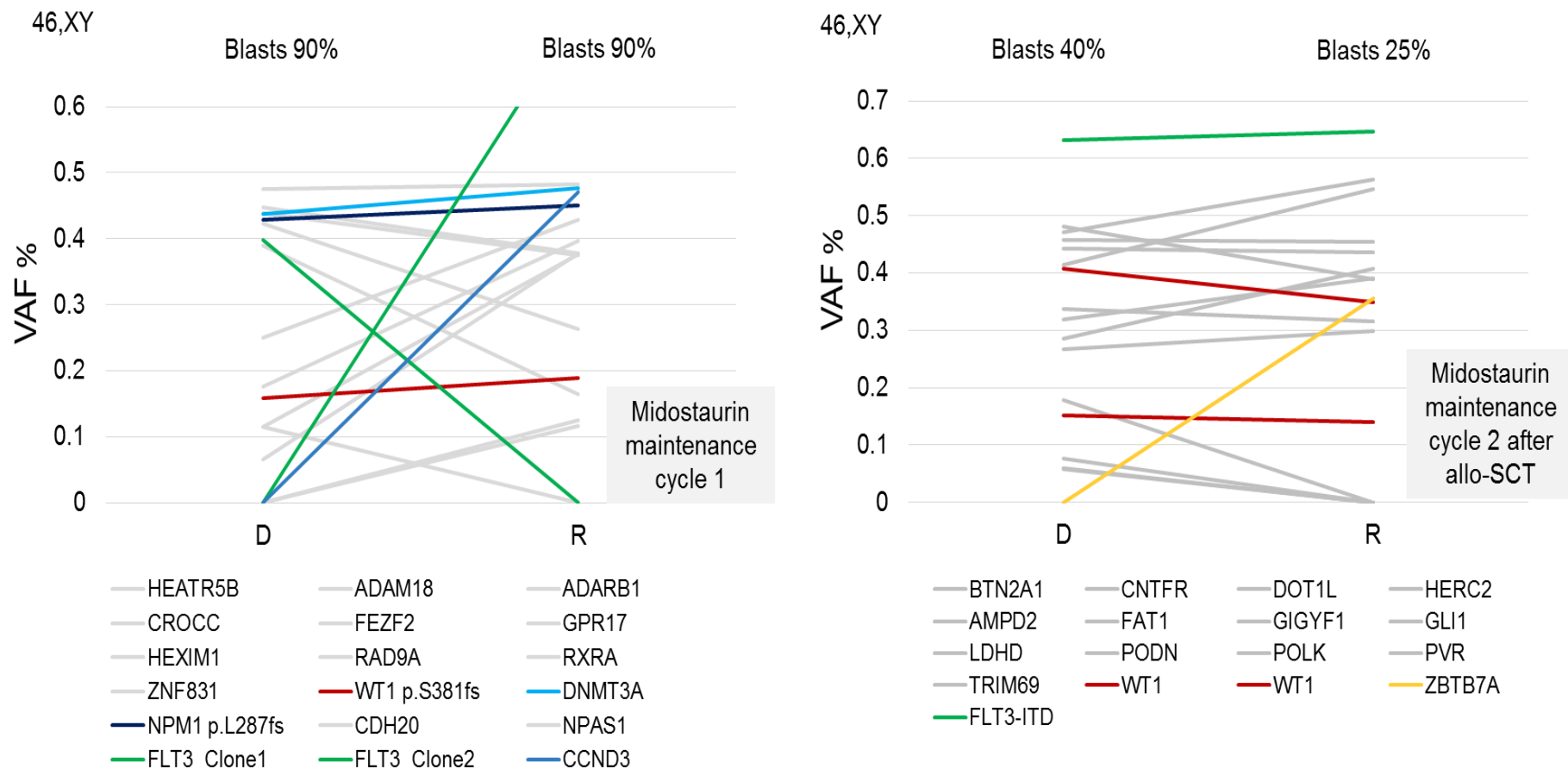
Time [months]

Cohort									
historical:	62	41	19	11	9	5	5	5	5
16-10:	68	48	34	27	18	14	8	6	4

HR = 0.49 (CI95% 0.316, 0.753)

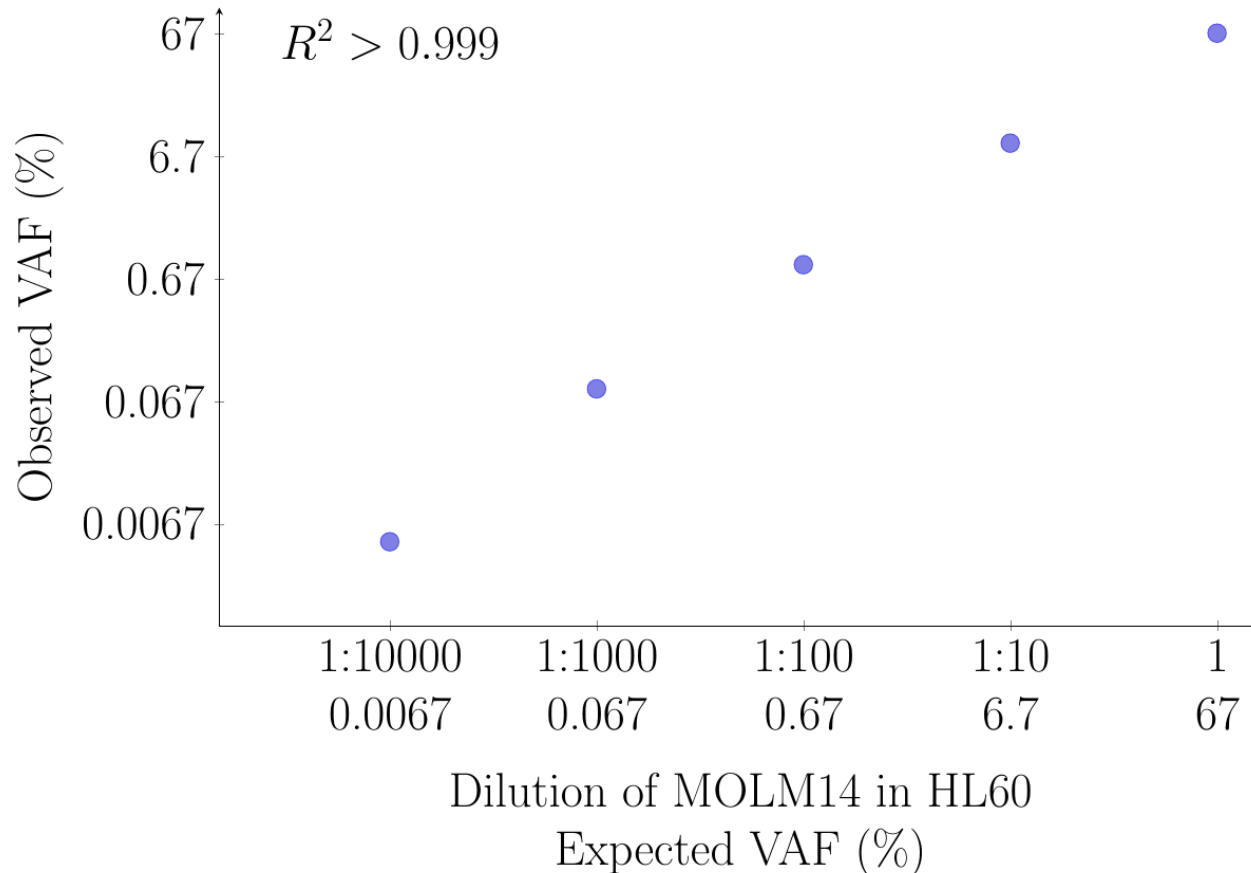
Resistance to FLT3 inhibition

Patterns of clonal evolution – persistence of FLT3 at relapse



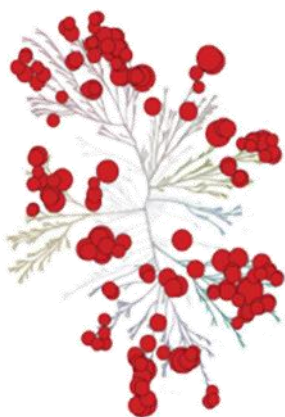
BM = Bone Marrow D = Diagnosis; R = Relapse; VAF = Variant Allele Frequency

Next-Generation-Sequencing based MRD monitoring in *FLT3*-ITD AML

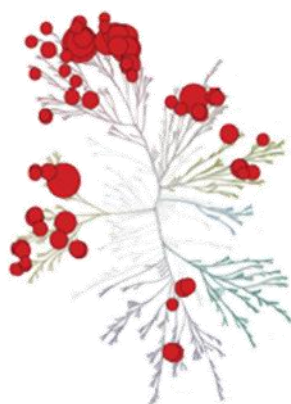


FLT3 Inhibitors in Clinical Development

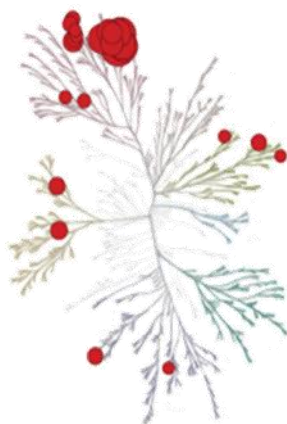
Relative selectivity and potency (IC_{50}) of TKIs against FLT3-ITD



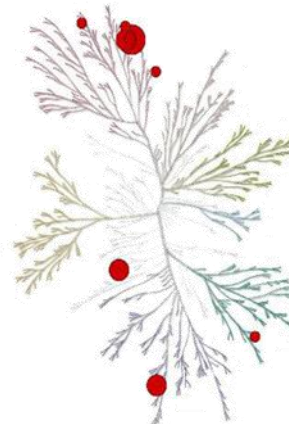
Midostaurin
1000 nM



Sorafenib
265 nM



Quizartinib
18 nM



Crenolanib
35 nM

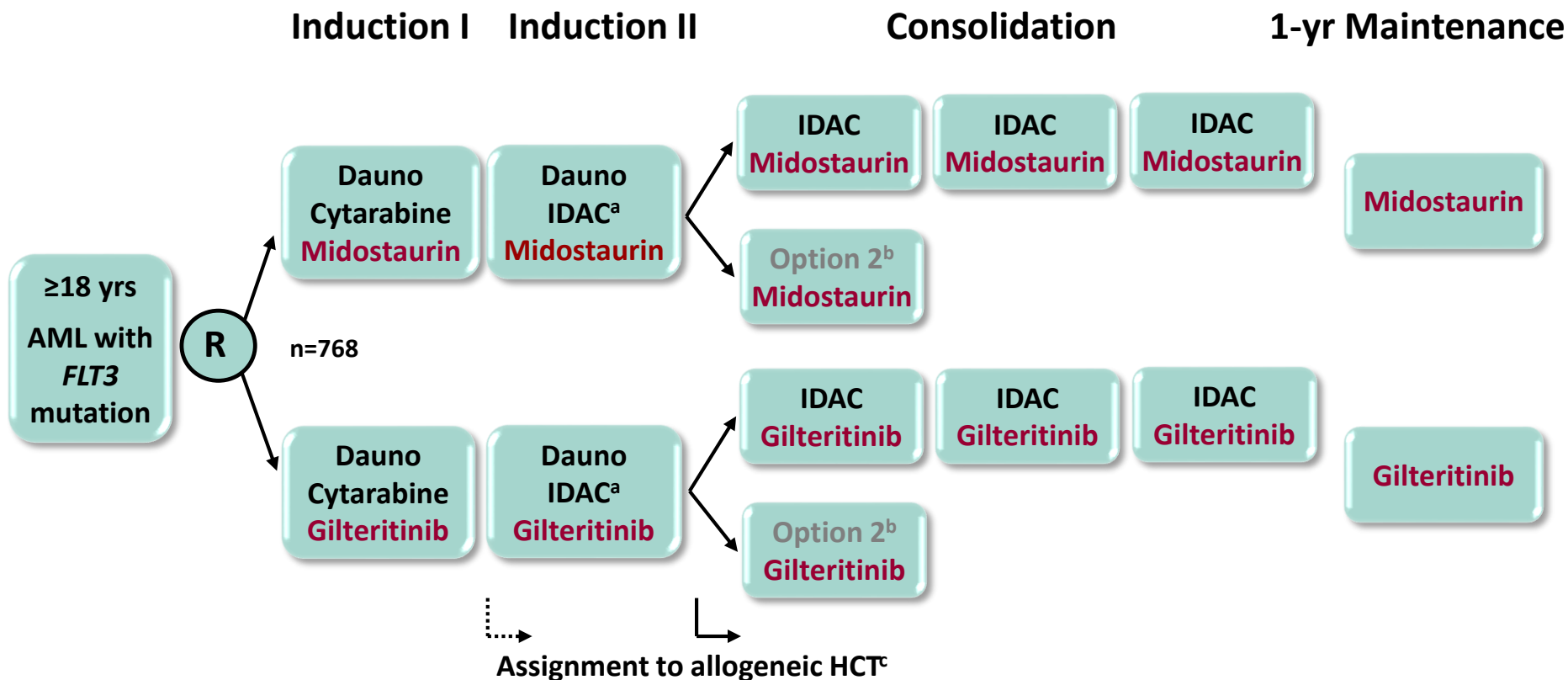
Kinase	IC_{50} (nmol/L)
FLT3	0.29
LTK	0.25
ALK	0.42
AXL	0.70
TRKA	1.1
RET	1.8
ROS	1.5
MER	2.9
c-KIT	230

Gilteritinib
0.29 nM

- 1st generation TKIs non-selective; less favorable safety profile; when used as single agent, only transient blast reductions observed
- 2nd generation TKIs (quizartinib [AC220], crenolanib, gilteritinib [ASP2215]) more selective and more potent

Galanis A, et al. Cancer Res. 2012;72:3660 (abstract); Karaman MW, et al. Nature Biotechnology. 2008;26(1):127-132; Zarrinkar PP, et al. Blood. 2009;114(14):2984-2992.

Midostaurin vs Gilteritinib + chemotherapy for *FLT3*^{mut} AML – AMLSG 28-18



Patients in CR/CRi after two cycles of induction proceed to AMLSG/HOVON-specific consolidation therapy; assignment to allogeneic hematopoietic cell transplantation (HCT) according to the local institutional or cooperative group prognostic algorithm; HCT can be performed at any time point following one induction cycle

- ^a IDAC, intermediate-dose cytarabine; age-adapted dosing
- ^b HOVON consolidation: autologous HCT; or mitoxantrone / etoposide
- ^c Assignment based on patient- and disease-related factors

NGS-based routine AML diagnostics

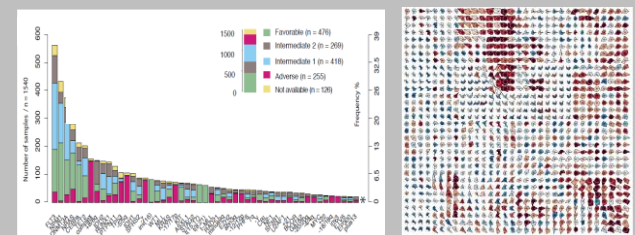
Targeted Re-Sequencing in routine AML diagnostics

e.g. with the aid of Illumina
sequencing technology
(MiSeq)
=> „Myeloid Panel“



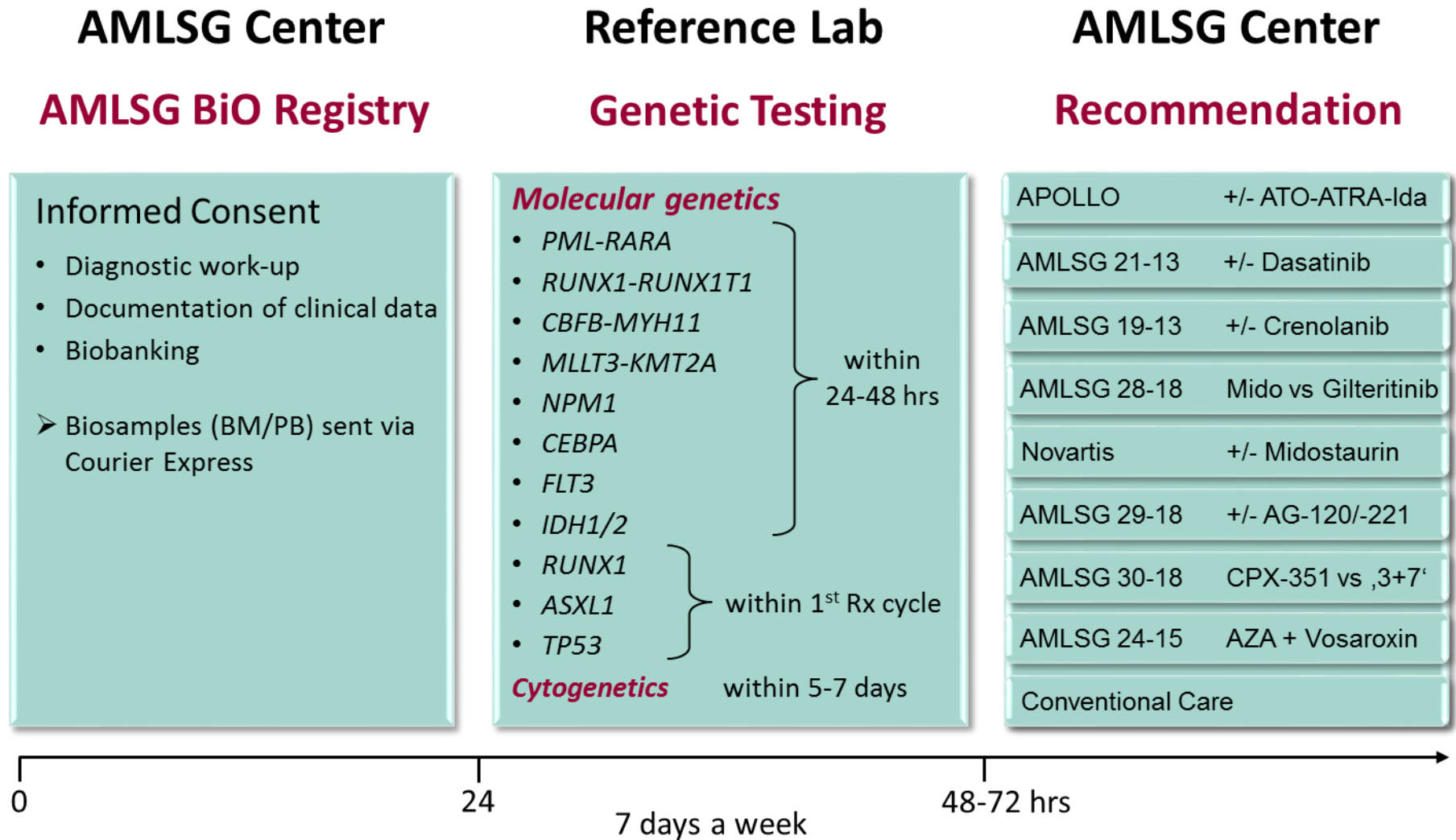
Building up databases => Linking genetic and clinical information („Knowledge Databases“)

Continuous process
(data sets from older pts,
targeted therapies, etc.)



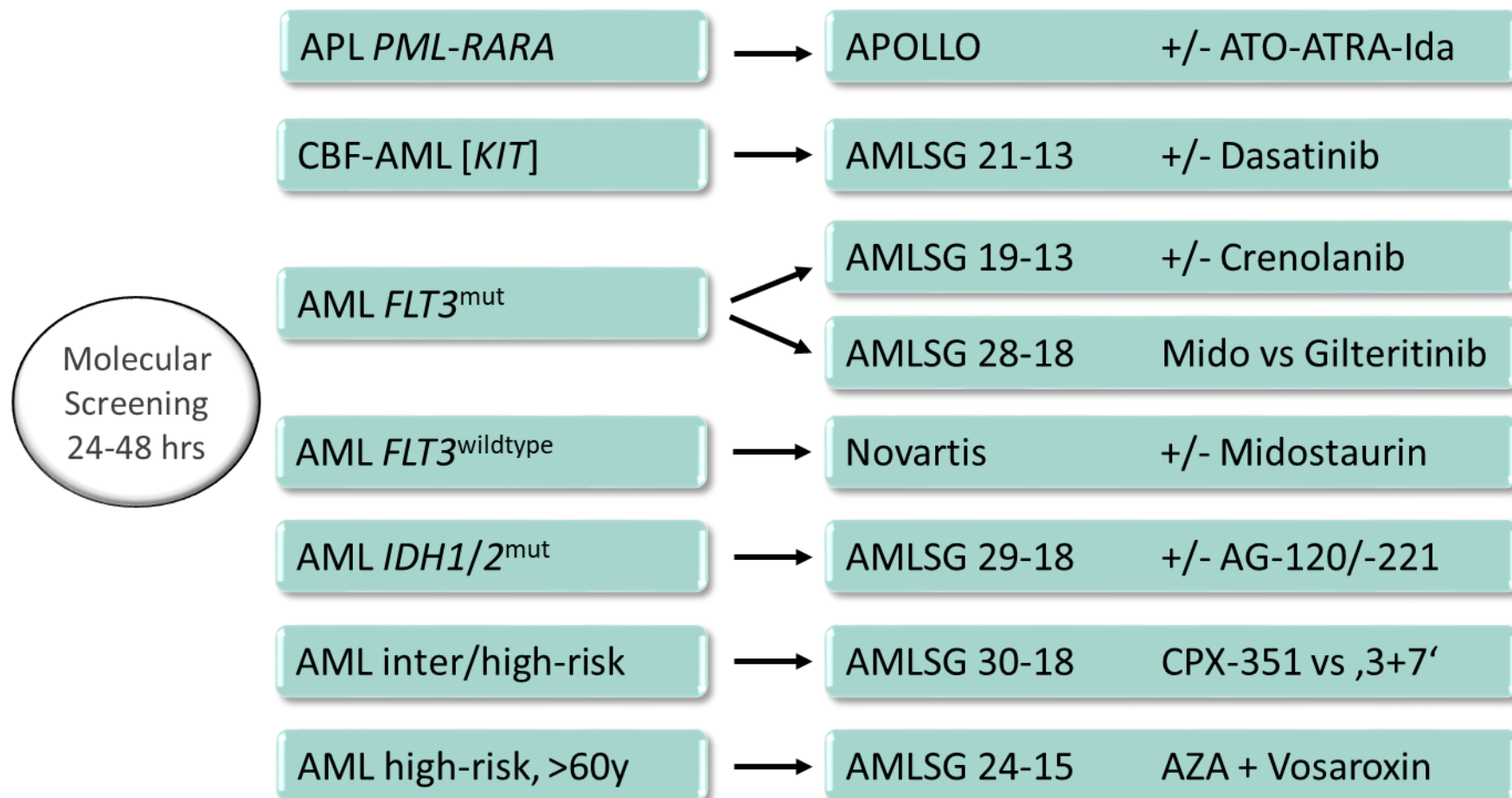
**Individualized
risk prediction and
therapeutic decision making**

Translation into the clinic

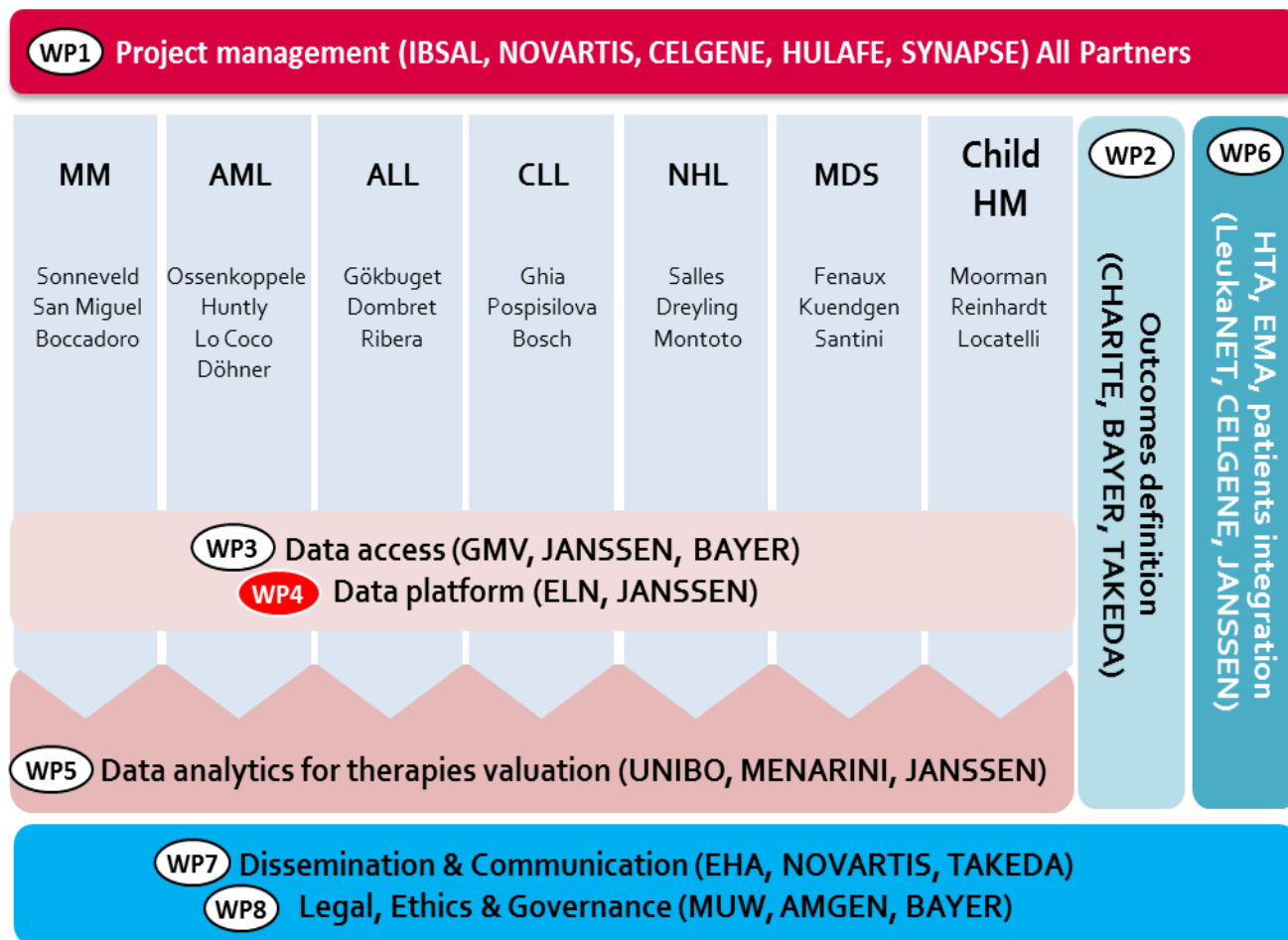


Genetics guided AML therapy

⇒ AMLSG 2018 portfolio – intensive therapy



Big Data for Better Outcomes program



HARMONY

**Healthcare Alliance
for Resourceful
Medicines Offensive
against Neoplasms in
Hematology**



efpia

imi innovative medicines initiative

Precision medicine in AML: hype or hope?

- We have entered a new era in leukemia genomics
- Currently, cytogenetics and *NPM1*, *CEBPA*, *FLT3*, *RUNX1*, *ASXL1* and *TP53* mutational screening are standard of care (ELN)
 - ⇒ *Targeted gene panel testing*
- Explosion of knowledge starts to be translated into therapeutic benefit
 - ⇒ *Building up large knowledge data bases*
 - ⇒ *Novel compounds at the horizon hold promise to enter the clinic*
- Major challenge: identification of predictive biomarkers that help selecting the appropriate therapy for an individual patient
 - ⇒ *Integrate biosampling, companion studies*
- **Enter your patients, younger or older, on a clinical trial!**

K. Döhner
V. Gaidzik
J. Krönke
F. Kuchenbauer
P. Paschka
F. Rücker
F. Stegelmann
H. Döhner
Ulm



T. Blätte
A. Dolnik
M. Hoyos
S. Lux
E. Sträng

F. Damm
J. Westermann
Berlin

F. Buchholz
C. Thiede
Dresden
H. Serve
Frankfurt
A. Ganser
M. Heuser
B. Schlegelberger
Hannover

S. Fröhling
P. Lichter
C. Müller-Tidow
C. Scholl
A. Trumpp
Heidelberg

A. Eggert
U. Keilholz
Berlin

G. Martinelli
Bologna
S. Armstrong
B. Ebert
Boston
P. Campbell
B. Huntly
Cambridge

J. Downing
Memphis
E. Papaemmanuil
New York
P. Valk
Rotterdam
J. Hernandez
Salamanca



STUDY
AML
GROUP

