

1. HAMBURGER **AML**-SYMPOSIUM

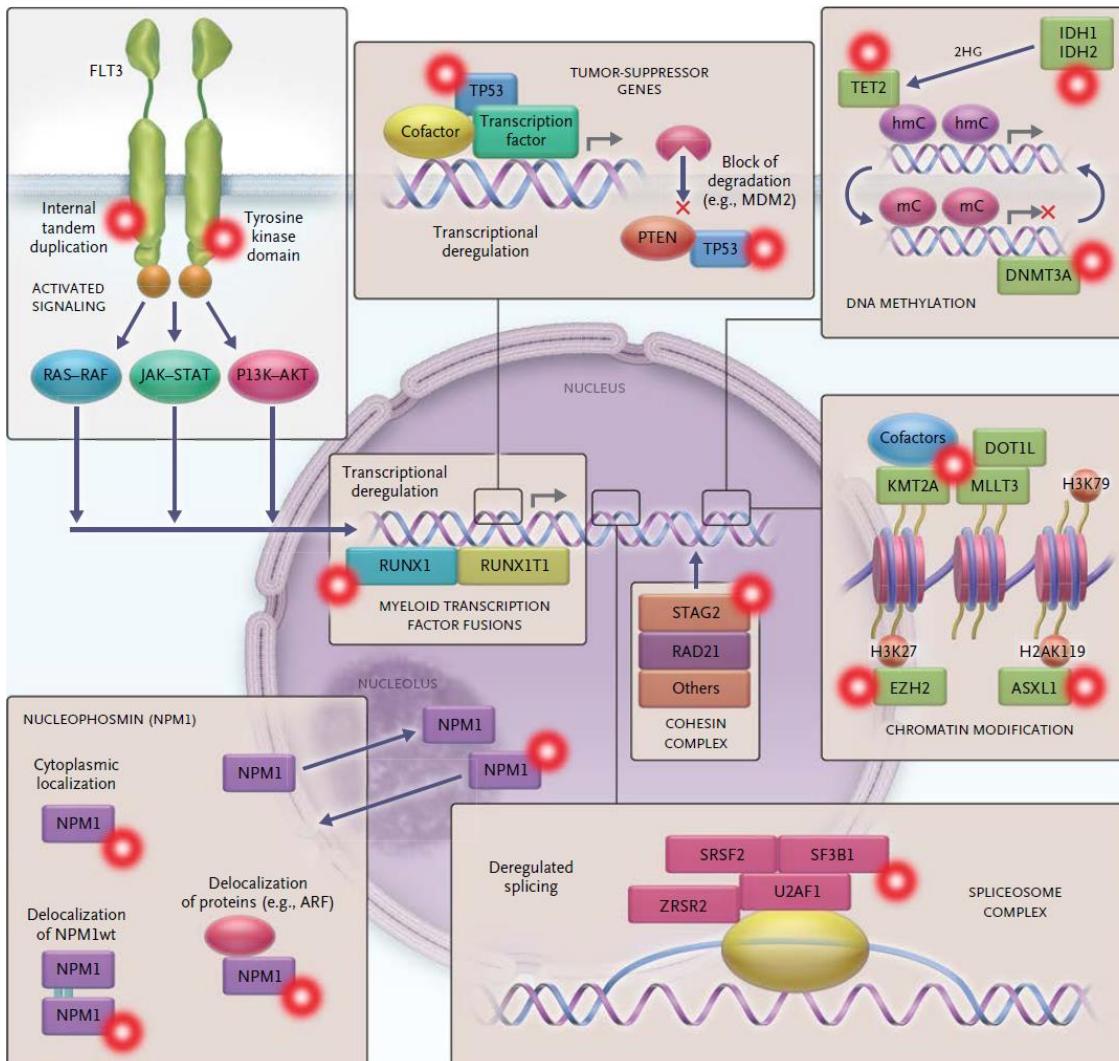
Mittwoch, 27.02.2019

AML- Aktuelles in der First-line

Lars Bullinger
Charité University Medicine
Berlin



Genomic landscape of de novo AML



Commonly mutated functional gene categories:

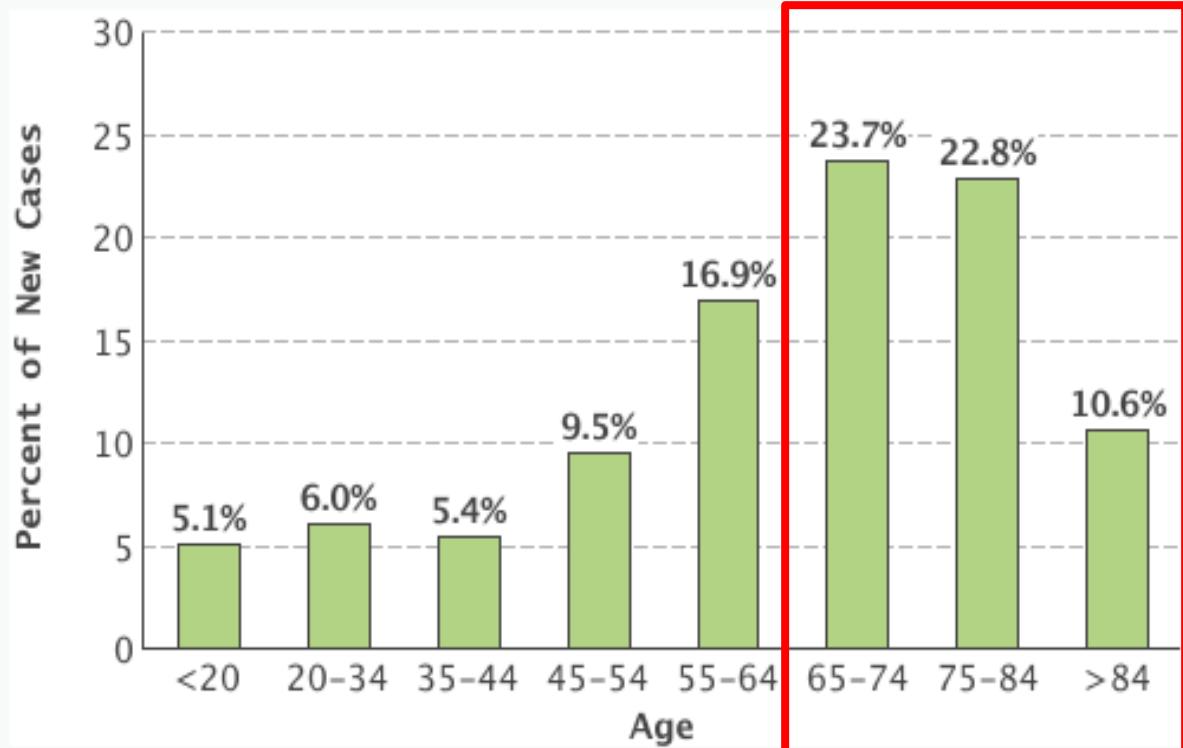
- (1) signaling genes
- (2) transcription factors
- (3) NPM1
- (4) spliceosome complex
- (5) Cohesion complex
- (6) chromatin modification
- (7) DNA methylation
- (8) tumor-suppressors

2017 European LeukemiaNet Guidelines

Risk Category	Genetic Lesion
Favorable	t(8;21)(q22;q22); <i>RUNX1-RUNX1T1</i> inv(16)(p13.1q22); <i>CBFB-MYH11</i> Mutated <i>NPM1</i> without <i>FLT3-ITD</i> or <i>FLT3-ITD</i> ^{low} Biallelic mutated <i>CEBPA</i>
Intermediate	Mutated <i>NPM1</i> and <i>FLT3-ITD</i> ^{high} Wild type <i>NPM1</i> without <i>FLT3-ITD</i> 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 (≥ 3), monosomal karyotype Wild type <i>NPM1</i> and <i>FLT3-ITD</i> ^{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

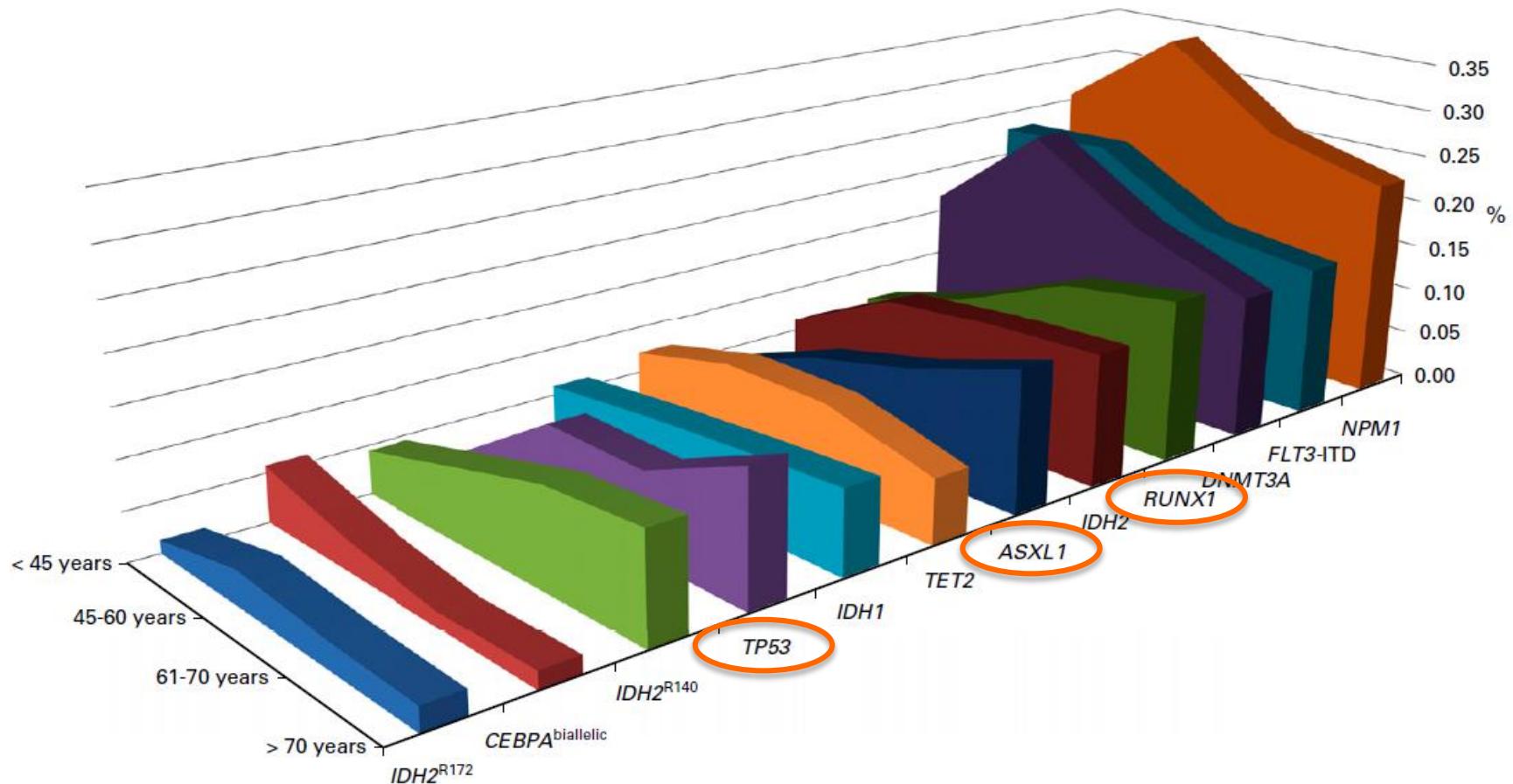


Acute myeloid leukemia
is most frequently
diagnosed among
people aged 65-74.

Median Age
At Diagnosis

68

Age-related frequency of gene mutations



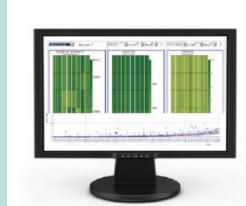
Analysis based on 10,622 AML patients from the AMLSG data base

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

NGS-based routine AML diagnostics

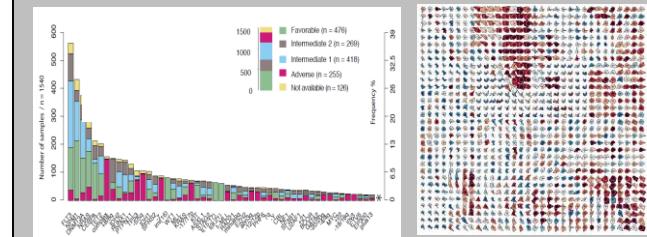
Targeted Re-Sequencing in routine AML diagnostics

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

AMLSG Center

AMLSG BiO Registry

Informed Consent

- Diagnostic work-up
- Documentation of clinical data
- Biobanking

➤ Biosamples (BM/PB) sent via Courier Express

Reference Lab

Genetic Testing

Molecular genetics

- *PML-RARA*
- *RUNX1-RUNX1T1*
- *CBFB-MYH11*
- *MLLT3-KMT2A*
- *NPM1*
- *CEBPA*
- *FLT3*
- *IDH1/2*
- *RUNX1*
- *ASXL1*
- *TP53*

within
24-48 hrs

Cytogenetics

within 1st Rx cycle
within 5-7 days

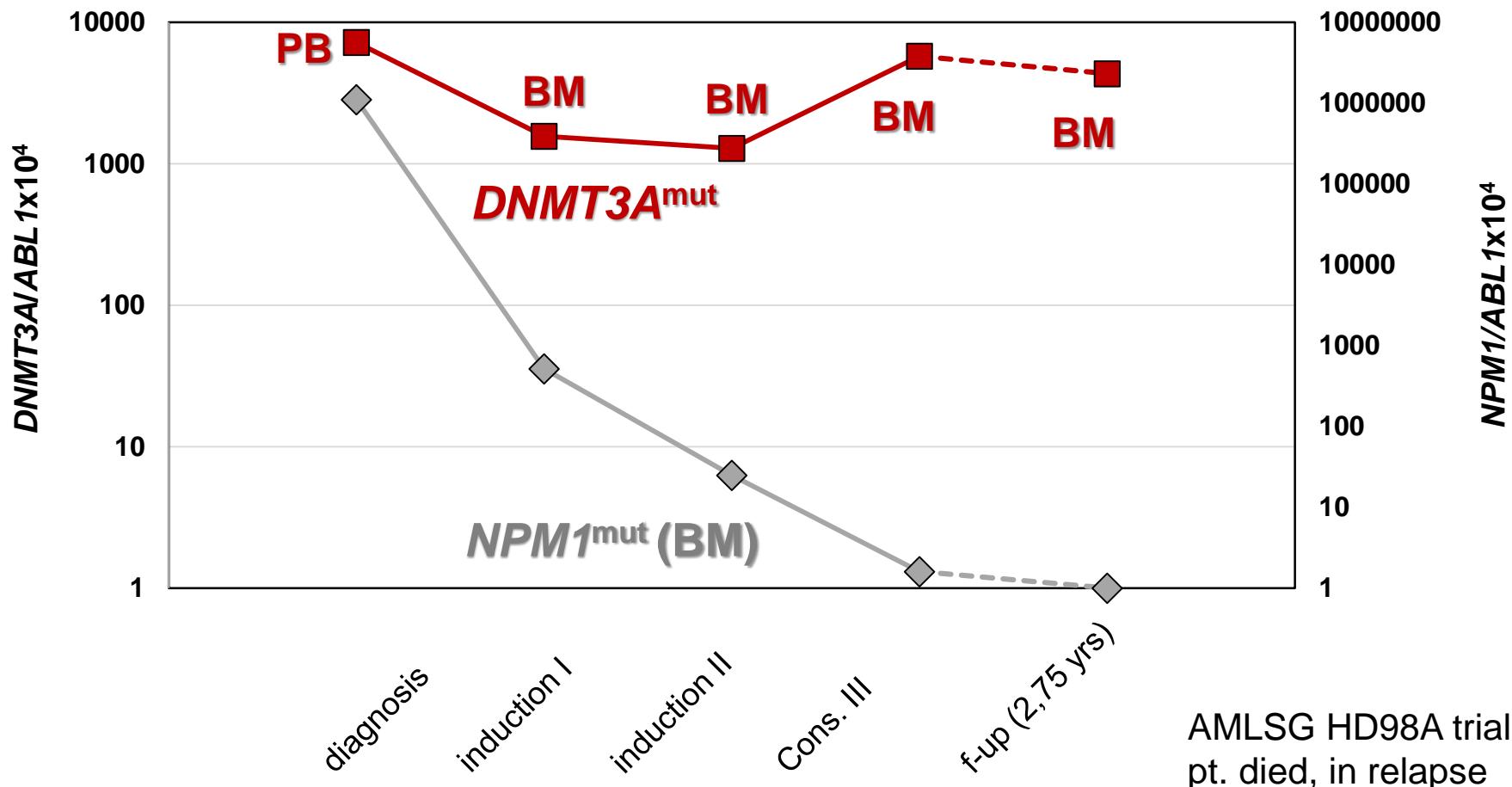
AMLSG Center

Recommendation

APOLLO	+/- ATO-ATRA-Ida
AMLSG 21-13	+/- Dasatinib
AMLSG 19-13	+/- Crenolanib
AMLSG 28-18	Mido vs Gilteritinib
Novartis	+/- Midostaurin
AMLSG 29-18	+/- AG-120/-221
AMLSG 30-18	CPX-351 vs ,3+7'
AMLSG 24-15	AZA + Vosaroxin
Conventional Care	

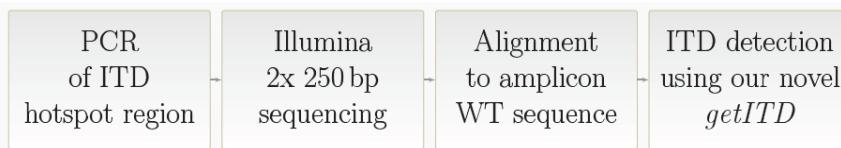


MRD of *DNMT3A*^{mut}-R882H and *NPM1*^{mut}



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

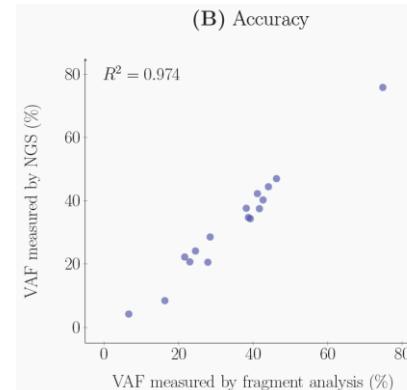
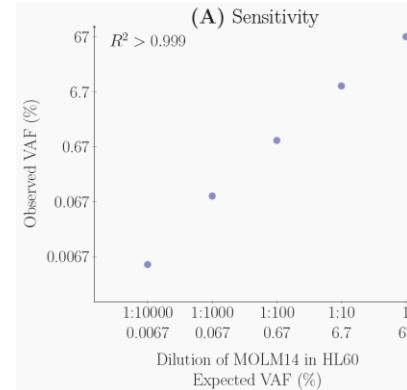
MRD Assay



FLT3-ITD Detektion

MOLM14 →	1 -----AGCAATCTAGGTATGAAAGCCAGCTACAGATGGTACAGGTGACCG	45
	
Reference →	1 gacagagacaatttaggtatgaaaggccagctacagatggtacaggtgaccg	50
	. . .	
46	GCTCCTCAGATAATGAGTACTTCTACGTTGATTCAGAGAATATGAATTG	95
	. . .	
51	gctcctcagataatgagtaacttctacg-----ttg	80
	-----ttg	
96	ATTCAGAGAATATGAATATGATCTCAAATGGGAGTTCCAAGAGAGAAAAT	145
	. . .	
81	atttcagagaatatgaatatgatctcaaatggagtttccaagagaaaaat	130
	. .	
146	TTAGAGTTGGTAAGAATGGAATGTGCCAAATGTTCTGCAGCATTCTT	195
	. .	
131	ttagagttggtaagaatggaatgtgc当地atgtttctgcagcatttctt	180
	atgtttctgcagcatttctt	
196	TTCCATTGAAAATCTTAAAATGCACGTACTCACCATTTGTCTTGCAG	245
	. .	
181	ttccattggaaaatcttaaaatgcacgtactcaccattgtcttgcag	230
	. .	

Test Performance



FLT3-ITD Mutations

⇒ *FLT3-ITD* mutations in approximately 25% of patients

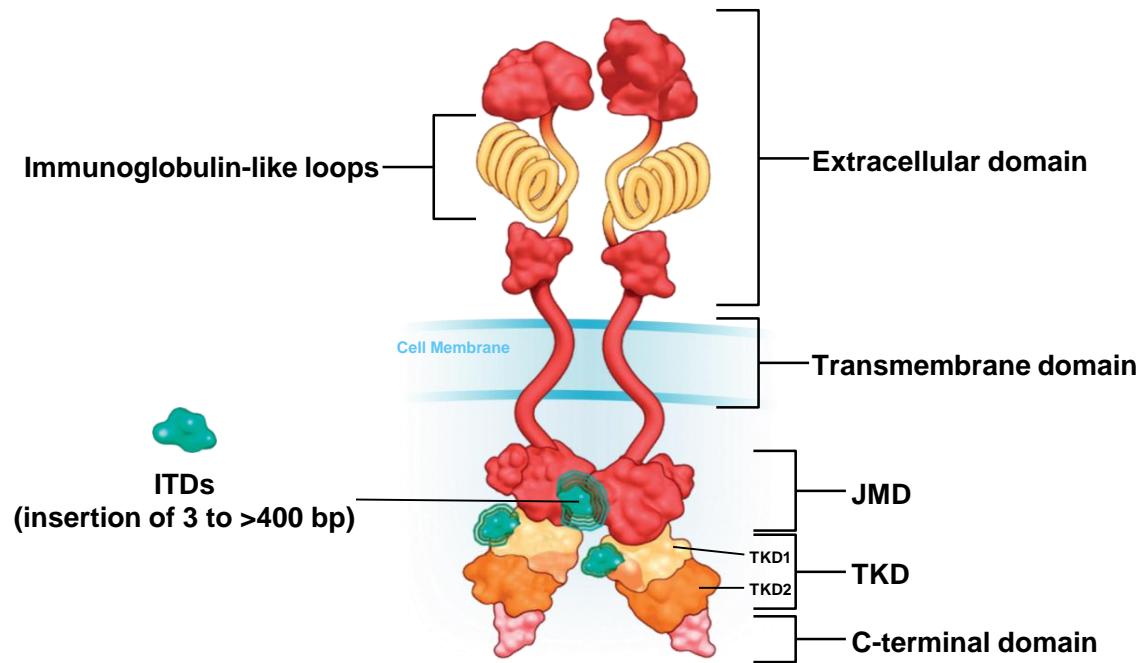


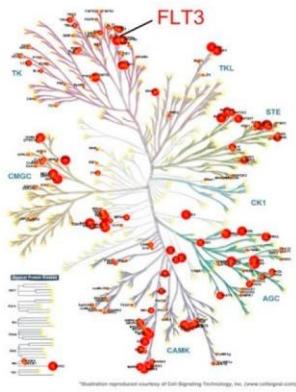
Figure adapted from Taylor & Francis Ltd, <http://www.tandfonline.com>: Patnaik MM. *Leuk Lymph*. 2017;1-14.

⇒ driver mutation associated with high leukemic burden and poor prognosis
(high risk of relapse, decreased response to salvage therapy, short OS)

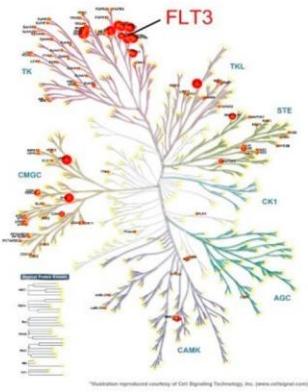
References: 1. Schneider F, et al. *Ann Hematol*. 2012;91(1):9-18. 2. Santos FP, et al. *Cancer*. 2011;117(10):2145-2155. 3. Kainz B, et al. *Hematol J*. 2002;3(6):283-289. 4. Kottardis PD, et al. *Blood*. 2001;98(6):1752-1759. 5. Patel JP, et al. *N Engl J Med*. 2012;366(12):1079-1089. 6. Levis M. *Hematol Am Soc Hematol Educ Program*. 2013;2013:220-226. 7. Ravandi F, et al. *Leuk Res*. 2010;34(6):752-756. 8. Tallman MS. *Hematol Am Soc Hematol Educ Program*. 2005:143-150.

FLT3 Inhibitors in Clinical Development

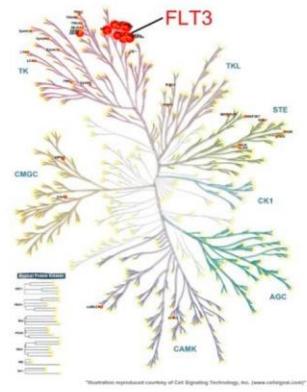
Relative selectivity and potency (IC_{50}) of TKIs against FLT3-ITD



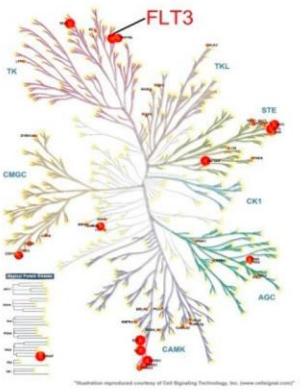
Midostaurin
1000 nM



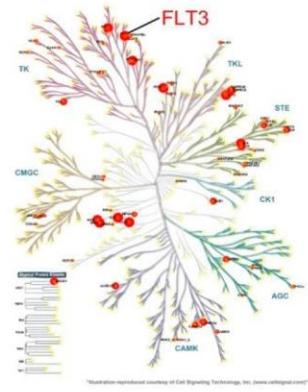
Sorafenib
265 nM



Quizartinib
18 nM



Crenolanib
35 nM

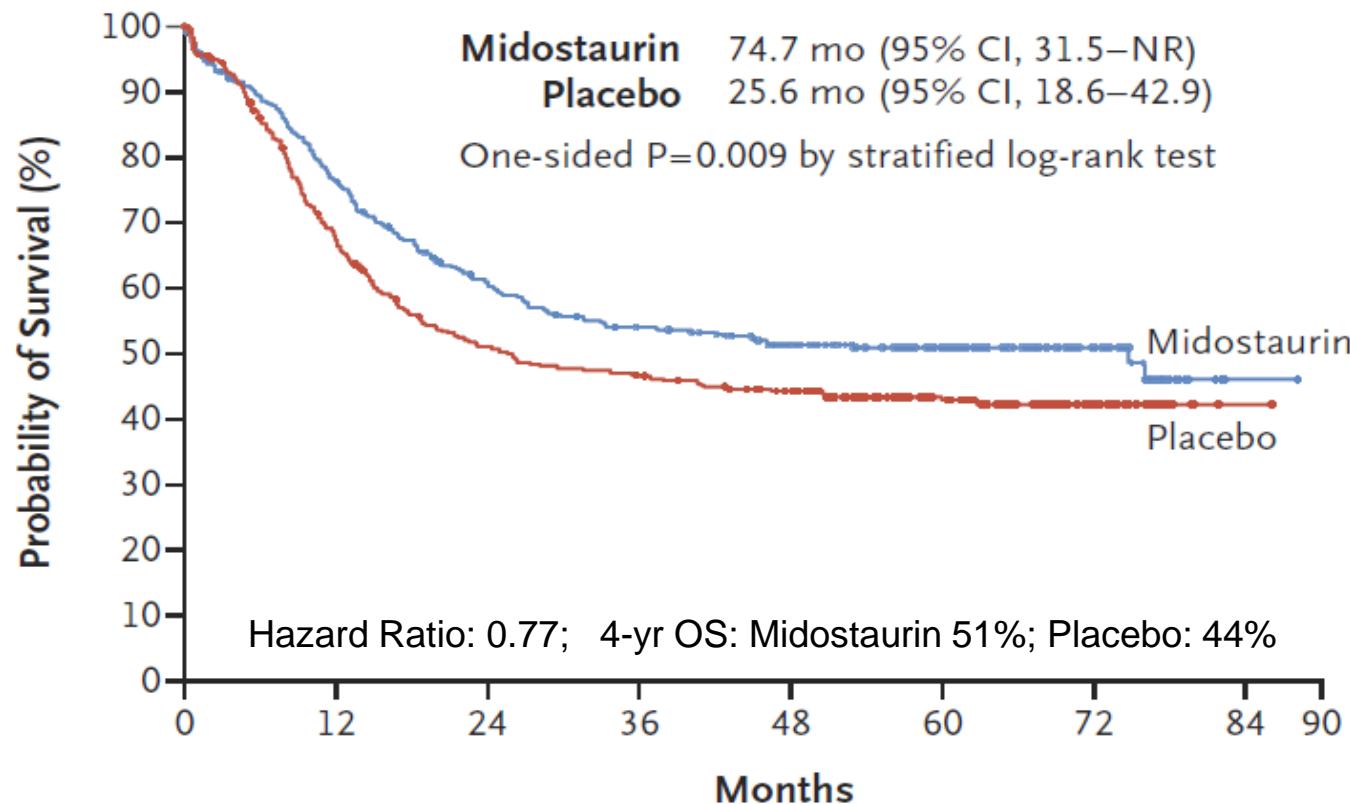


Gilteritinib
0.29 nM

- **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. Staudt D, et al. Int J Mol Sci. 2018;19(10).

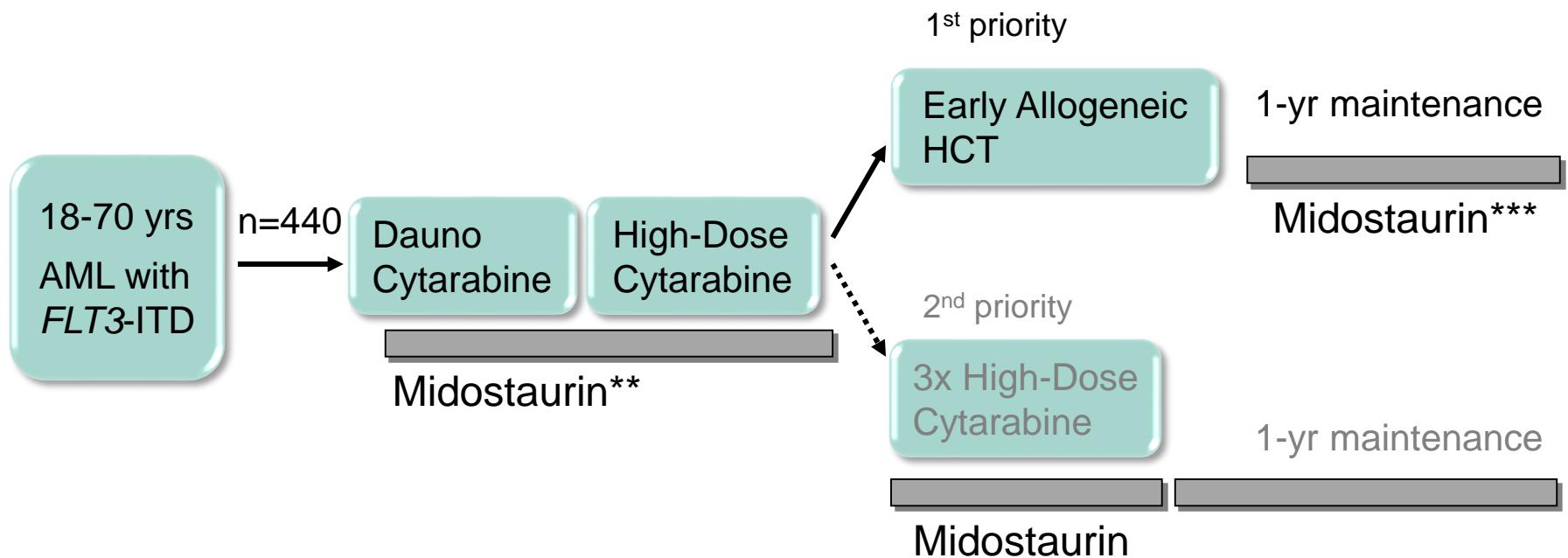
AML with *FLT3* mutation – midostaurin plus chemotherapy (RATIFY)



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

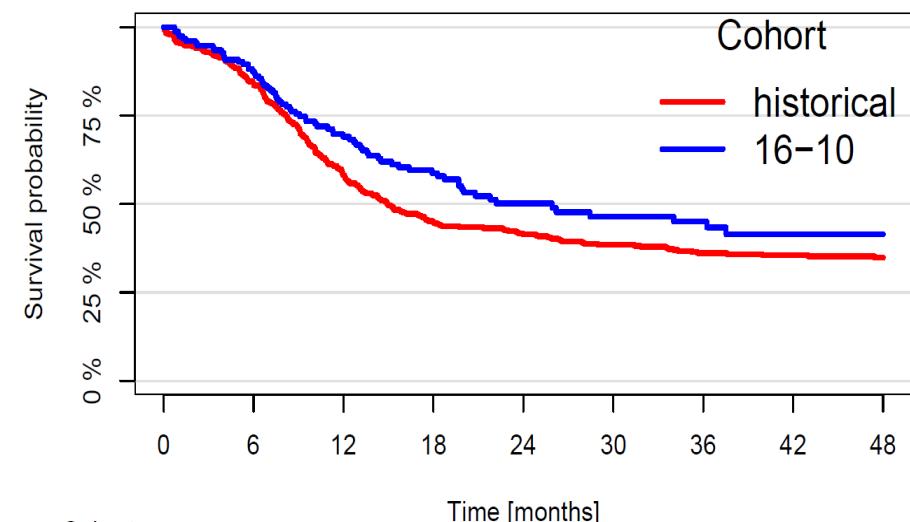
** Continuous dosing of midostaurin (start on day 8; except days of chemotherapy)

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

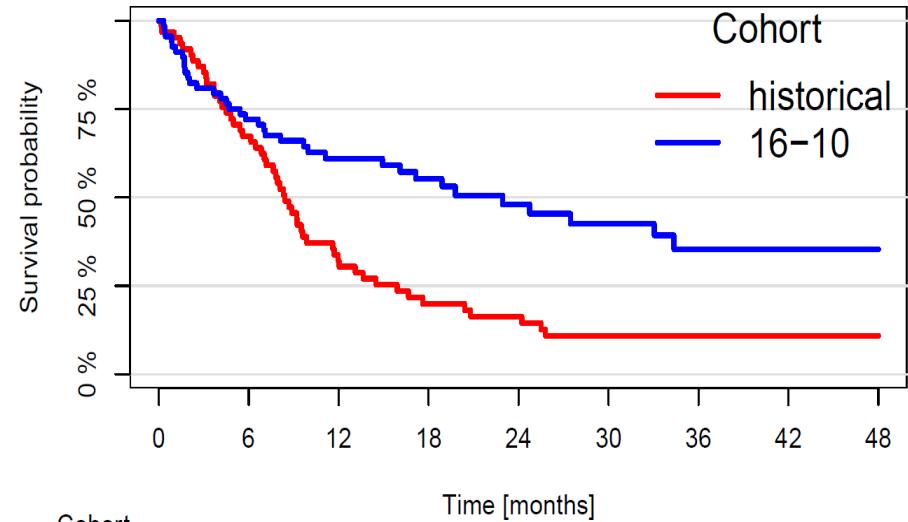
ClinicalTrials.gov: NCT01477606 (active)

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

Age 18-60 years



Age 60-70 years

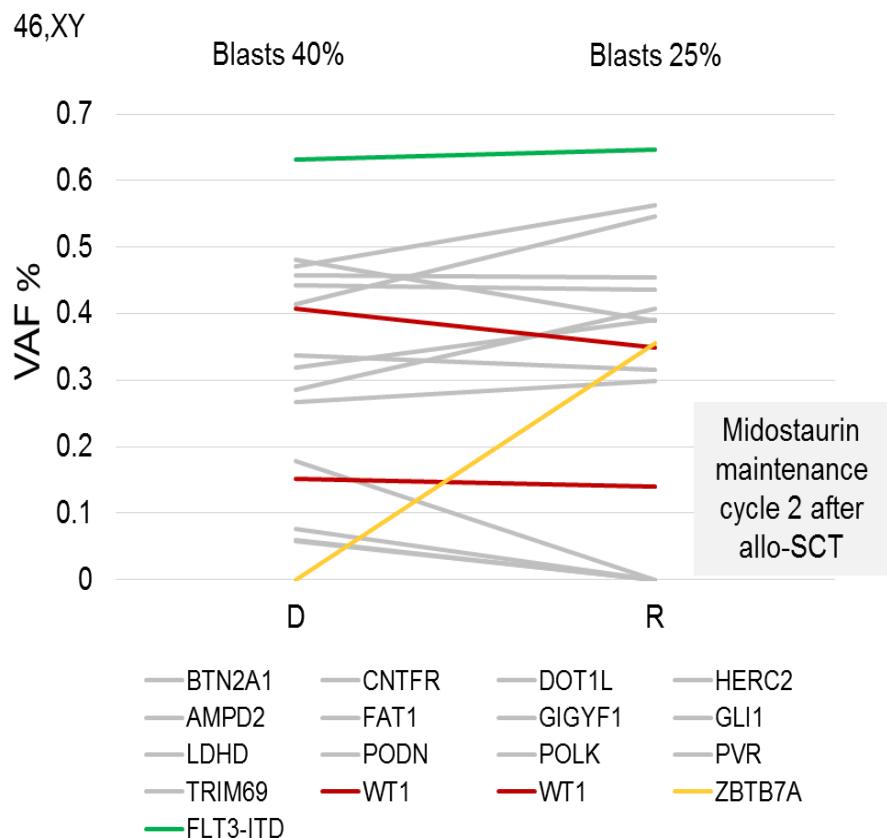
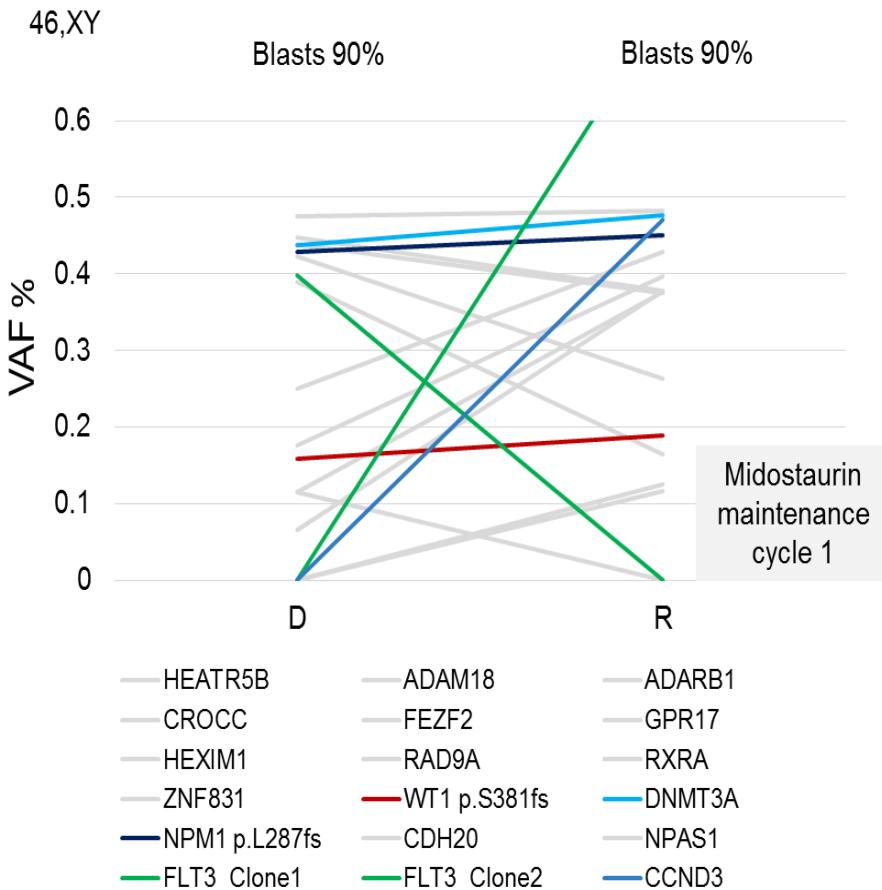


HR = 0.70 (CI95% 0.535, 0.920)

HR = 0.49 (CI95% 0.316, 0.753)

Resistance to FLT3 inhibition

Patterns of clonal evolution – persistence of FLT3 at relapse

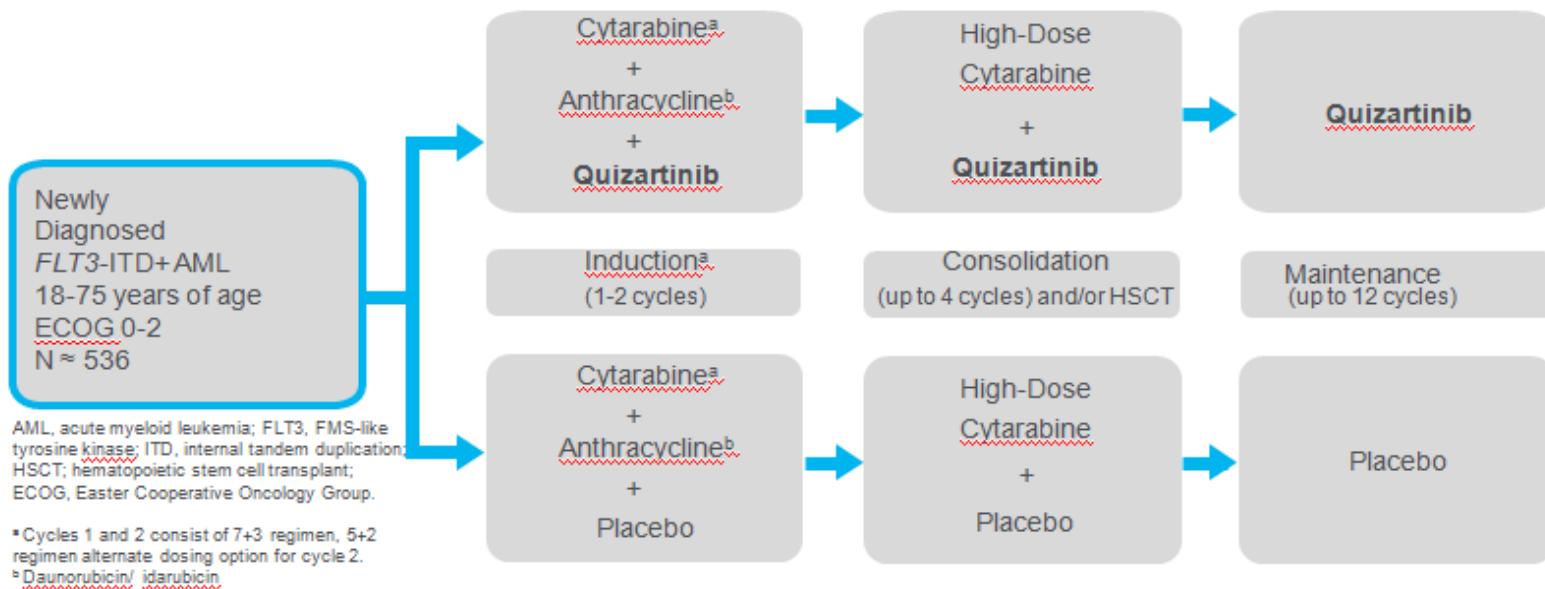


BM = Bone Marrow; D = Diagnosis; R = Relapse; VAF = Variant Allele Frequency

Ongoing: QuANTUM-FIRST - Phase 3 Trial in Newly Diagnosed *FLT3*-ITD Mutated AML

Quizartinib Advancement into the Next Generation of Trials for Unmet Needs in AML

A Phase 3, Randomized, Double-Blind, Placebo-controlled Study of Quizartinib (AC220) Administered in Combination With Induction and Consolidation Chemotherapy, and Administered as Maintenance Therapy in Subjects 18 to 75 Years Old With Newly Diagnosed ***FLT3*-ITD (+) Acute Myeloid Leukemia**



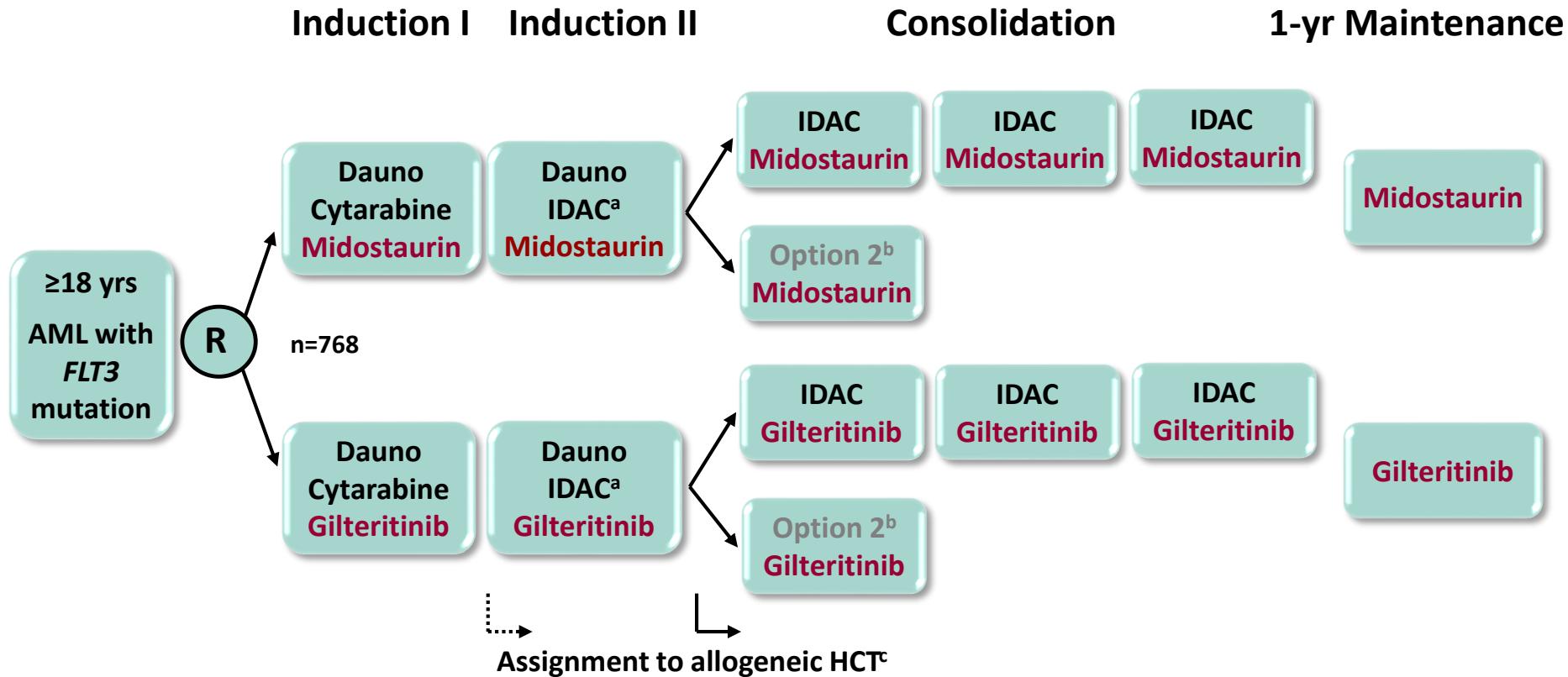
Primary Endpoint: Event-free Survival (EFS)

Secondary Endpoints:

- Overall Survival (OS)
- Complete Remission (CR)
- Composite Complete Remission (CRc)
- CR with no evidence of minimal residual disease (MRD)

Location: North America, Europe, Asia/Other Regions | **ClinicalTrials.gov Identifier:** NCT02668653

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

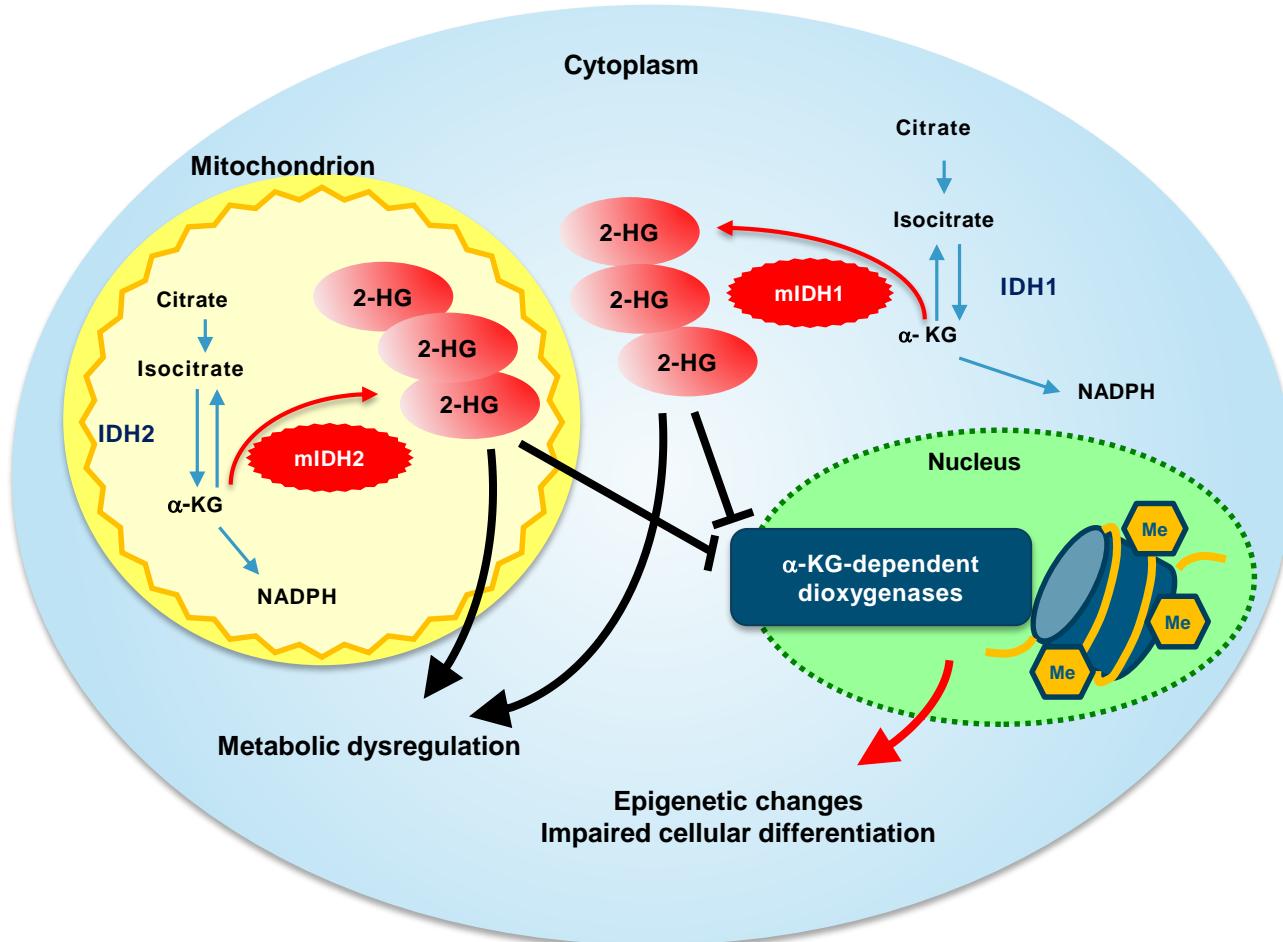
^b HOVON consolidation: autologous HCT; or mitoxantrone / etoposide

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

Expected start: Q2 / 2019

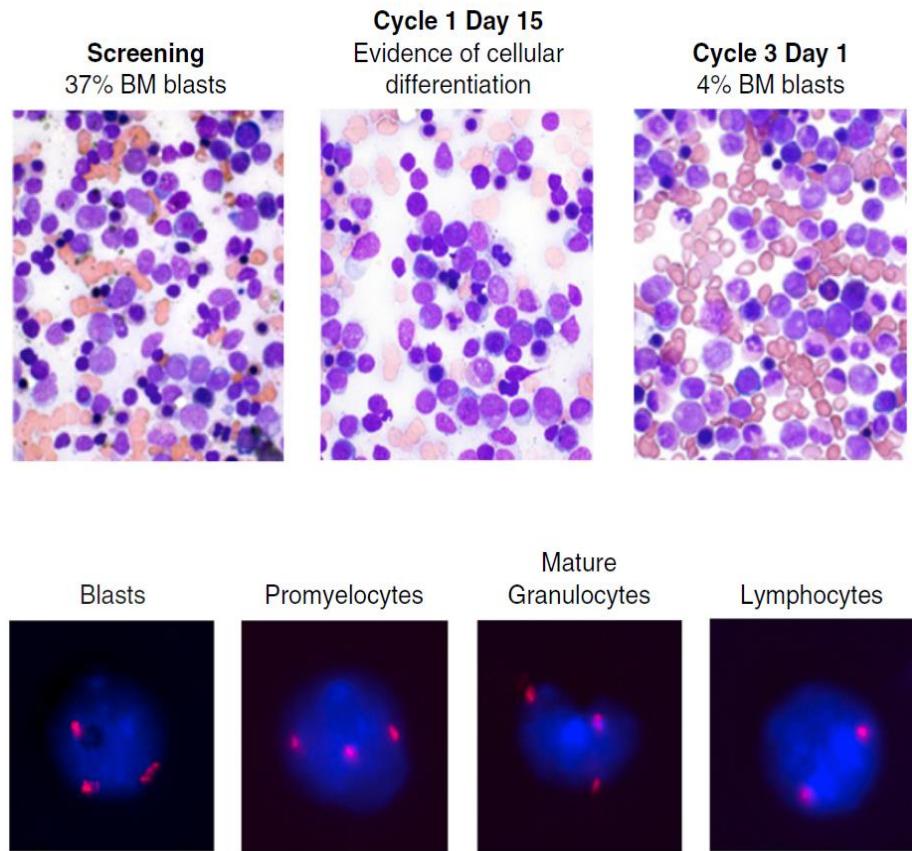
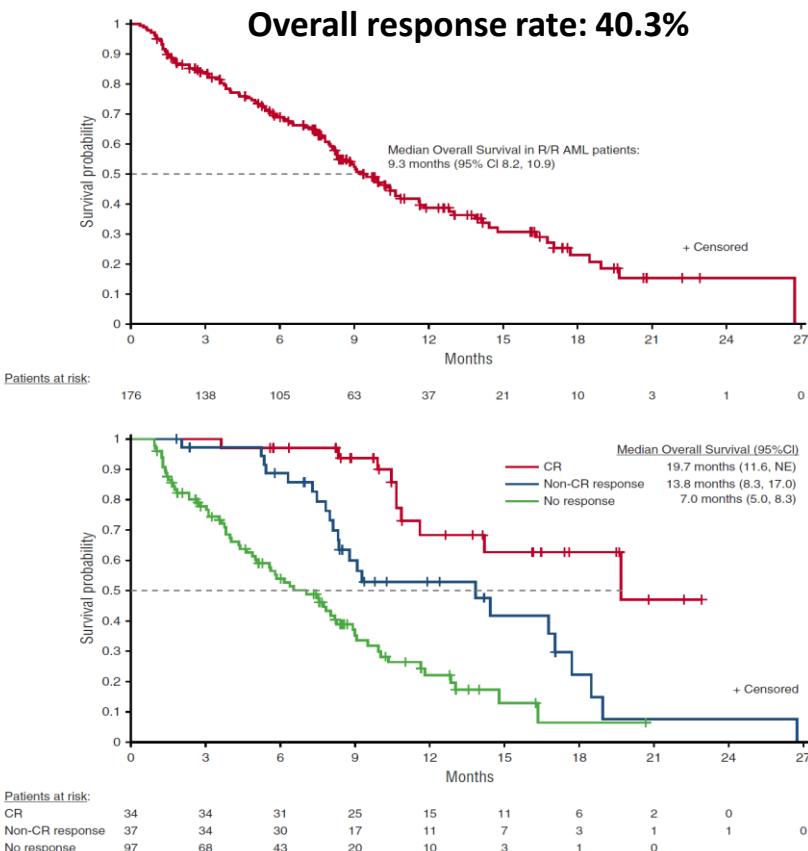


IDH1 and *IDH2* - therapeutic target structure



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

Enasidenib (AG-221) in *IDH2*^{mut} relapsed or refractory AML

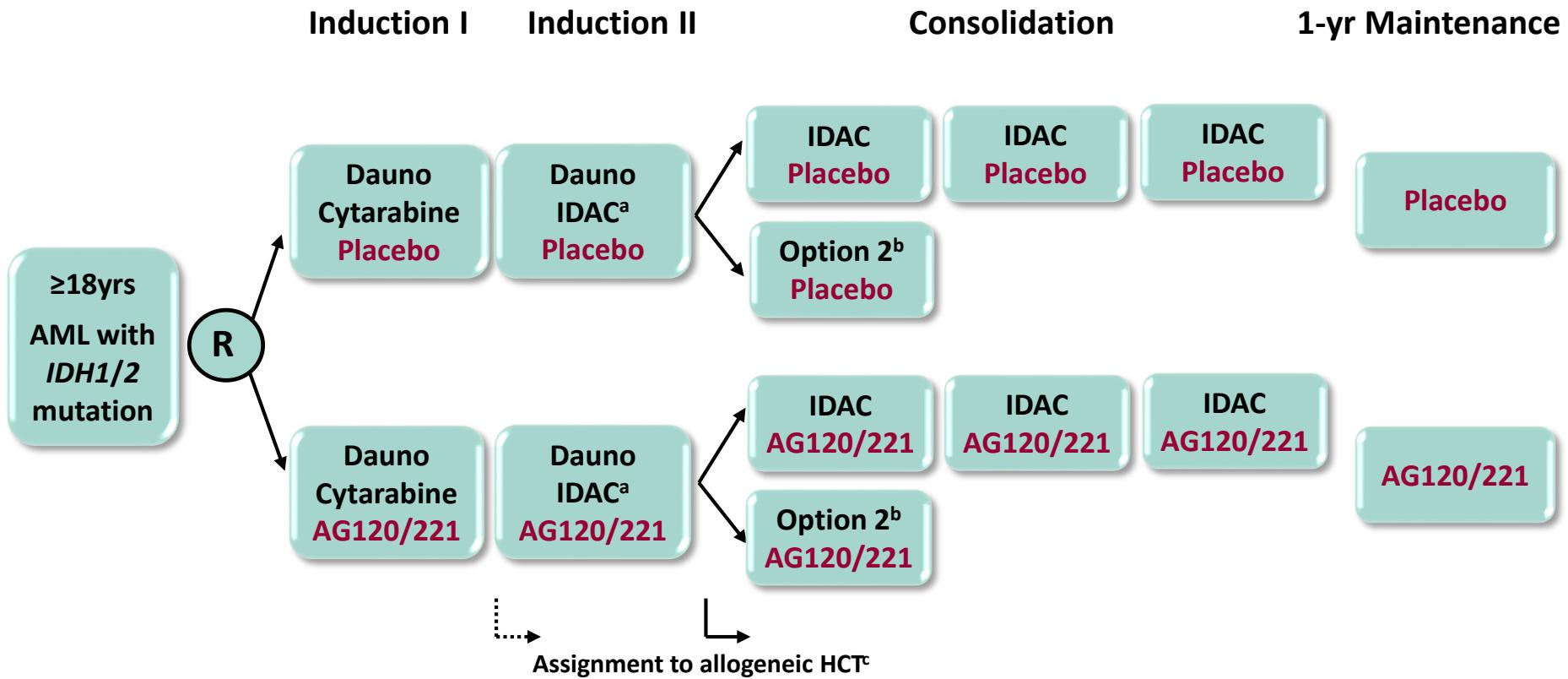


Ivosidenib (AG-120) and Enasidenib (AG-221) clinical development program

	Phase I/II	Phase III
≥2 nd r/r AML		Phase III: AML-004 (IDHENTIFY) Enasidenib vs. CCR N=280
Frontline ineligible for intensive chemotherapy	Phase I/II AML-005 Azacitidine + ivosidenib 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

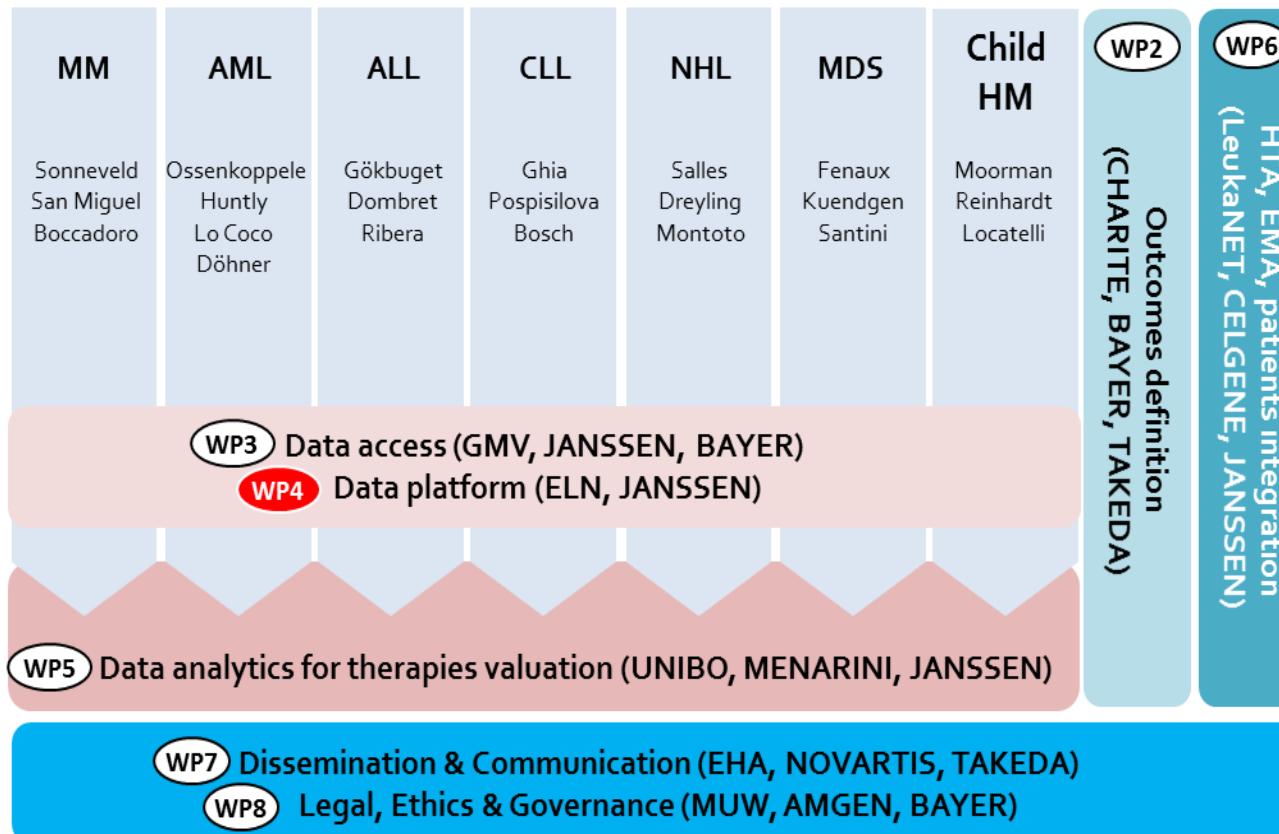
^b HOVON consolidation: autologous HCT; or mitoxantrone / etoposide

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

Expected start Q2 / 2019

Big Data for Better Outcomes program

WP1 Project management (IBSAL, NOVARTIS, CELGENE, HULAFE, SYNAPSE) All Partners



Healthcare Alliance
for Resourceful
Medicines Offensive
against Neoplasms in
Hematology



Precision Medicine – Fiction or Reality?

Charité Season 1: 1880s



Weißes Blut.

„Vorher sehr wenig reihen Blutzellen befand der ungern gebrüste Thell aus denselben farblosen oder weißen Körpern, die auch im normalen Blut vorhanden, nämlich kleinen, nicht ganz regelmäßigen Blutzellmolekülen, größerem, längeren, seitwälligem, kugelförmigem und granulirten Zellen mit einem zentralen, hellleuchtenden oder fleckförmigen oder mit mehreren naßfrischen, distinaten Kernen. Die größeren dieser Zellen hatten ein leicht gelbliches Aussehen. Das Verhältniss zwischen den farbigen und farblosen Blutzellen sollte sich hier ungemein unterscheiden, wie im normalen Blut, indem die farbigen die Regel, die farblosen eine Art von Ausnahme zu bilden schienen. Wenn ich jedoch von weißem Blute spreche, so meine ich in der That ein Blut, in welchem die Proportionen zwischen den rothen und farblosen (in Weise weichen) Blutzellen einen umgekehrten ist, ohne daß eine Besinnung fremderer chemischer oder morphologischer Elemente zu bemerken wäre.“

„Ich würde mich glücklich schämen, der Wissenschaft davorschreiten zu einer neuen und, wie es mir scheint, nicht unumstößlichen Thatsache verschlossen zu haben. —“

Dr. Virchow.

Virchow:
Leukemia diagnosis

Charité Season 2: 1940s



Hirschfeld:
Modern hematology

Charité Season 3: 2010s



Use of Gene-Expression Profiling to Identify Prognostic Subclasses in Adult Acute Myeloid Leukemia

Lars Bullinger, M.D., Konstantina Dühren, M.D., Eric Iaia, Stephan Freling, M.D., Richard F. Schenck, M.D., Robert Tibshirani, Ph.D., Hermann Ottens, M.D., and Jennifer R. Phillips, M.D., Ph.D.

ABSTRACT

In patients with acute myeloid leukemia (AML), the presence or absence of recurrent cytogenetic abnormalities is used to identify the appropriate therapy. However, the current classification system does not fully reflect the molecular heterogeneity of the disease, and its clinical stratification is difficult, especially for patients with intermediate-risk AML with no recurrent cytogenetic abnormalities.

RESULTS
We used complementary DNA microarrays to determine the levels of gene expression in peripheral blood mononuclear cells from 113 patients with AML and 40 patients with normal marrow. We used unsupervised hierarchical clustering analysis to identify molecular subgroups with distinct gene expression signatures. Using a training set of 77 patients with AML, we developed a prognostic model to predict survival. We derived a gene-expression-based clinical outcome predictor, which we then tested using an independent validation group comprising 57 remaining patients.

RESULTS
Our unsupervised analysis identified two molecular subtypes in AML, including two prognostically relevant subgroups in AML with a normal karyotype. Using the supervised learning algorithm, we constructed an optimal 17-gene prognostic predictor, which showed promising performance in an independent validation group (n=61), including the subgroup of patients with AML with a normal karyotype (n=13). This predictor had a hazard ratio of 2.2 for death and a significant independent prognostic factor (odds ratio, 8.8; 95 percent confidence interval, 2.6 to 26; P<0.001).

CONCLUSIONS
The use of gene-expression profiling improves the molecular classification of adult AML.

Bullinger:
Omics based classification

Precision medicine in AML

- 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: identify gene-gene interactions to effectively combine treatment strategies to overcome mechanisms of resistance
 - ⇒ *Integrate biosampling, companion studies*
- **Enter your patients, younger or older, on a clinical trial!**

K. Döhner
S. Cocciardi
V. Gaidzik
J. Krönke
P. Paschka
F. Rücker
L. Schmalbrock
H. Döhner
UlM



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

S. Fröhling
P. Lichter
C. Müller-Tidow
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Berlin

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Memphis

T. Blätte
A. Dolnik
K. Lang
J. Schrezenmeier
E. Sträng

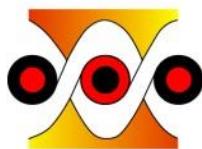
F. Damm
J. Westermann
Berlin

E. Papaemmanuil
New York

P. Valk
Rotterdam

J. Hernandez
Salamanca

S. Ogawa
Tokyo



STUDY
AML
GROUP

Deutsche Krebshilfe
HELPEN. FORSCHEN. INFORMIEREN.
DFG Deutsche Forschungsgemeinschaft

 **SFB 1074**

 Bundesministerium
für Bildung
und Forschung

 TRANSCAN

 imi