KRONOS·BIO

Corporate Presentation

December 2021

KRONOS·BIO

Forward-Looking Statements

This presentation includes certain projections and forward-looking statements as of the date of this presentation provided by Kronos Bio, Inc. (the “Company”). The information in this presentation is current only as of its date and may have changed since that date. These projections and forward-looking statement include, but are not limited to, those regarding the Company’s future financial position, the Company’s strategy, intellectual property matters, the Company’s clinical development plans and timelines, regulatory matters, market size and opportunity and the Company’s estimates regarding expenses capital requirements and needs for additional financing. These projections and forward-looking statements are based on the beliefs of the Company’s management as well as assumptions made and information currently available to the Company. Such statements reflect the current views of the Company with respect to future events and are subject to business, regulatory, economic and competitive risks, uncertainties, contingencies and assumptions about the Company, including, among other things, the development of its business, trends in the industry, the legal and regulatory framework for the industry and future expenditures. These risks and uncertainties are described under the “Risk Factor” heading of the Company’s form 10-Q dated September 30, 2021 and filed with the U.S. Securities and Exchange Commission on November 9, 2021. In light of these risks, uncertainties, contingencies and assumptions, the events or circumstances referred to in the forward-looking statements may not occur. None of the future projections, expectations, estimates or prospects in this presentation should be taken as forecasts or promises nor should they be taken as implying any indication, assurance or guarantee that the assumptions on which such future projections, expectations, estimates or prospects have been prepared are correct or exhaustive or, in the case of the assumptions, fully stated in the presentation. The actual results may vary from the anticipated results and the variations may be material.

This presentation discusses product candidates that are under clinical study and which have not yet been approved for marketing by the U.S. Food and Drug Administration. No representation is made as to the safety or effectiveness of these product candidates for the use for which such product candidates are being studied.

Company Overview

CDK9 Inhibitor KB-0742

- First clinical data released in Q4 2021, showing differentiated half-life
- Data are from stage 1 of ongoing Phase 1/2 study; study is continuing to enroll patients
- KB-0742 was internally discovered, showcasing promise of product engine and translational capabilities

Product Engine

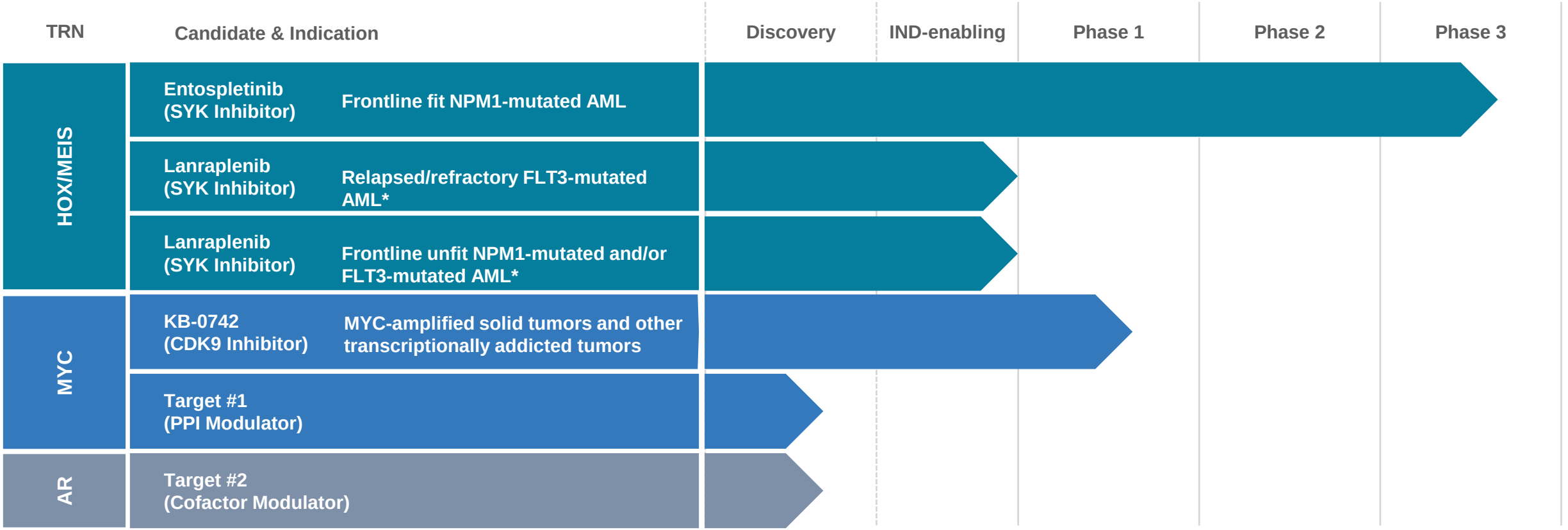
- Two new discovery programs announced in November 2021
- Ability to understand and target the entire TRN
- Capability to map TRNs in a differentiated manner to enable discovery and translation
- SMM platform to enable screening of TRN in transcriptionally dysregulated environment

SYK Inhibitor Portfolio

- Development strategy focuses on maximizing impact to better address patients' needs
  - ENTO: Ongoing Phase 3 AGILITY trial in combination induction regimens as a frontline treatment for patients with AML
  - LANRA: Combination regimens with targeted agents
- Opportunity to potentially address patients with mutations present in more than two-thirds of AML

AML: Acute myeloid leukemia. CDK9: Cyclin Dependent Kinase 9. SMM: Small molecule microarray. SYK: Spleen tyrosine kinase. TF: Transcription factor.
TRN: Transcriptional regulatory network.

Advancing a robust pipeline of targeted oncology programs



*IND filed

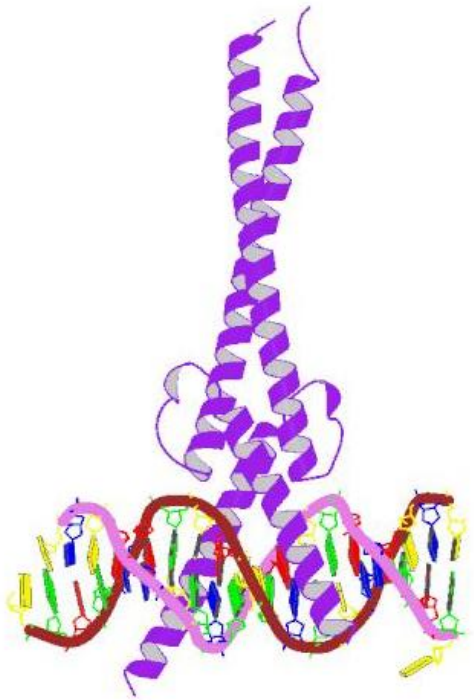
KRONOS·BIO

- Introduction
- **Targeting Oncogenic TRNs**
- Lead Programs
  - SYK
  - CDK9
- The Kronos Bio Opportunity

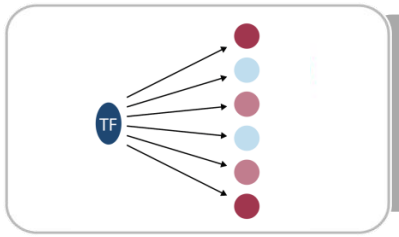
Transcription factors (TFs) are high-value but historically challenging targets

> 500 human TFs
> 50 known oncogenic role

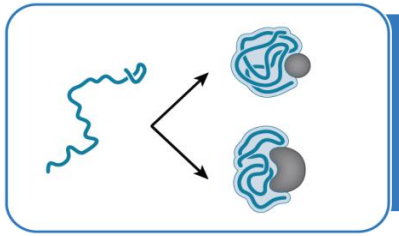
MYC oncogenic TF



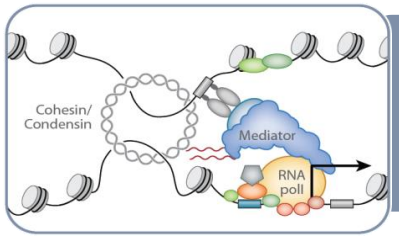
CHALLENGES



Context-dependent **activity**



Context-dependent **structure**

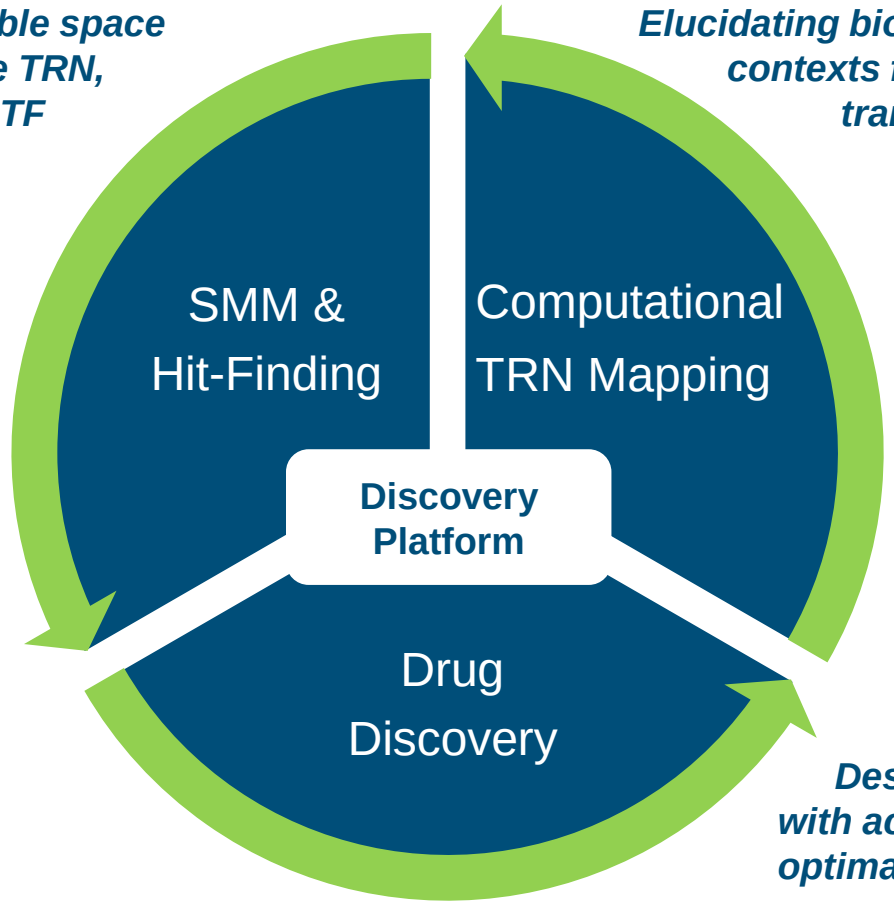


Context-dependent **complexes**

Product engine systematically targets dysregulated transcription factors and associated TRNs

Expanding druggable space by targeting the TRN, not just the TF

Elucidating biological & therapeutic contexts for dysregulated transcription



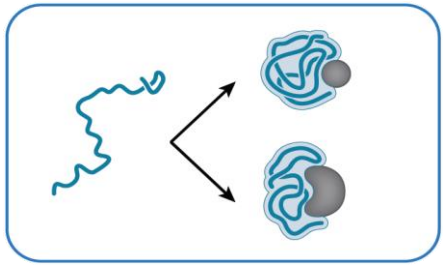
Addressing structural complexities of transcription factors (TFs) & their complexes

Hypothesis driven clinical trials delivering early proof of concept & generating data for iterative discovery

Designing candidates with activity, PK & dosing to optimally drug dysregulated transcription

Map gene expression signatures and critical nodes in oncogenic TRNs

STRUCTURE



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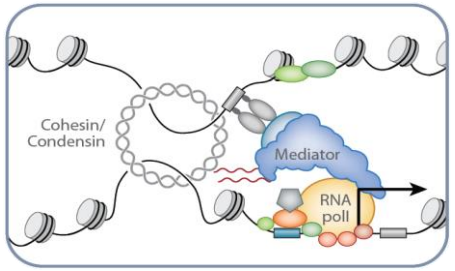
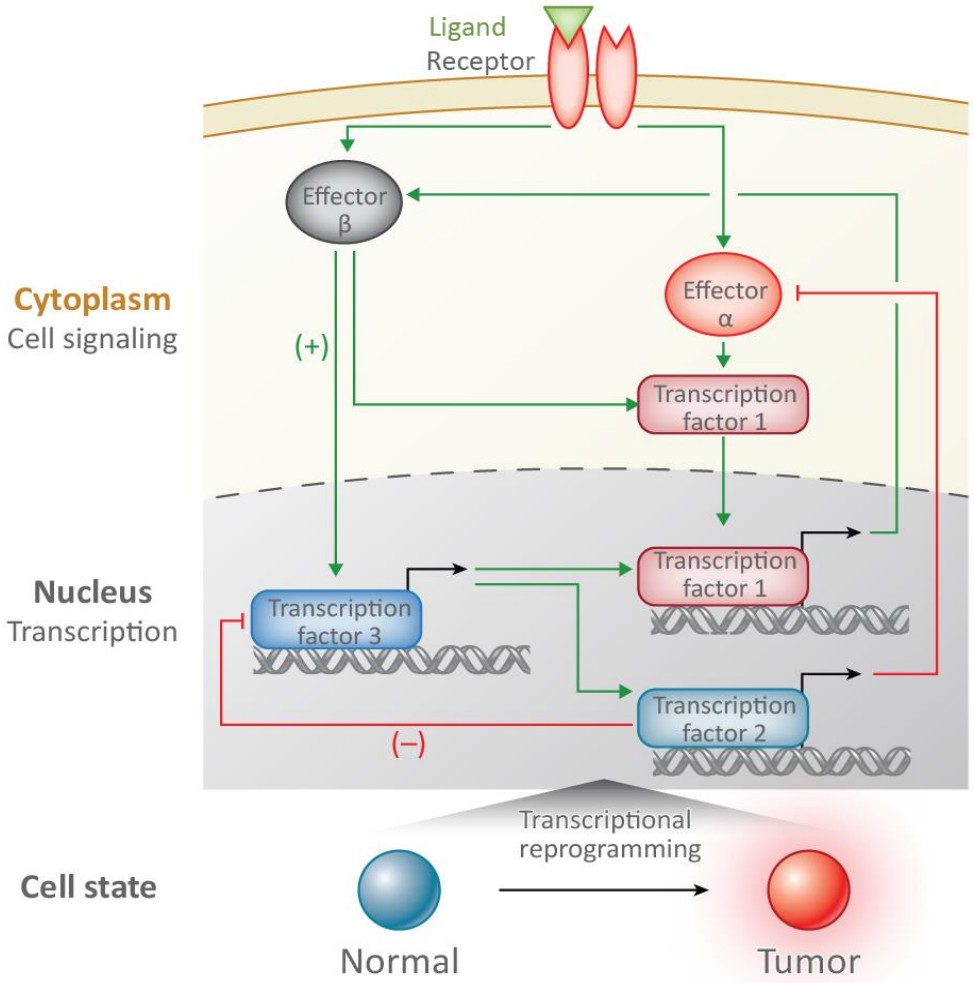
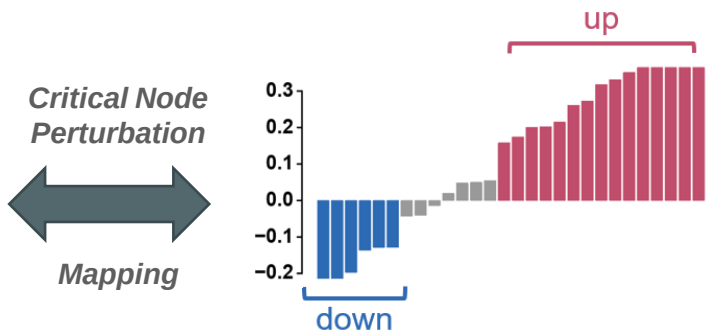




- Identify **context-dependent** transcriptomic effects in relevant cancer lines

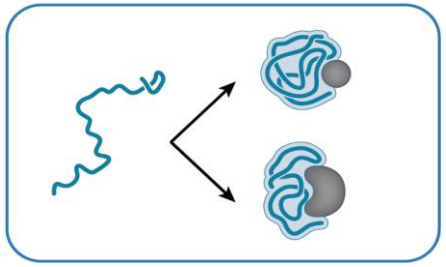


Signature of on-target gene expression response

TF: Transcription factor. TRN: Transcriptional regulatory network.

Screen using small molecule microarray (SMM) platform

STRUCTURE



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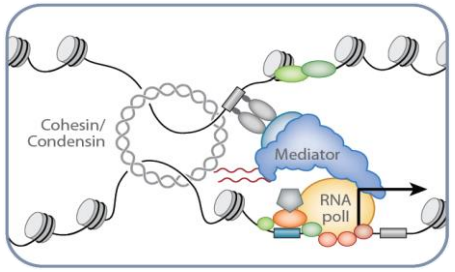
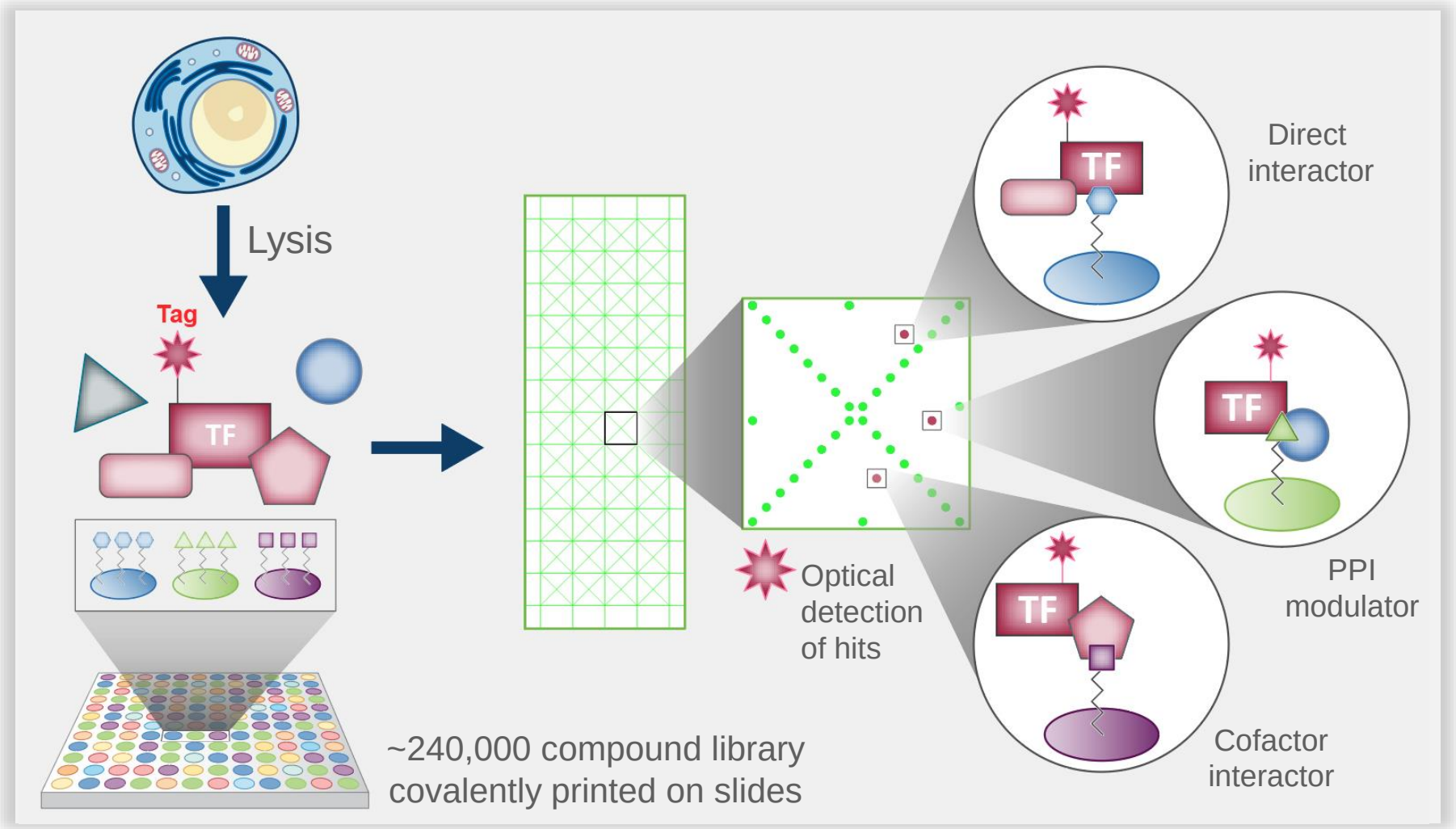
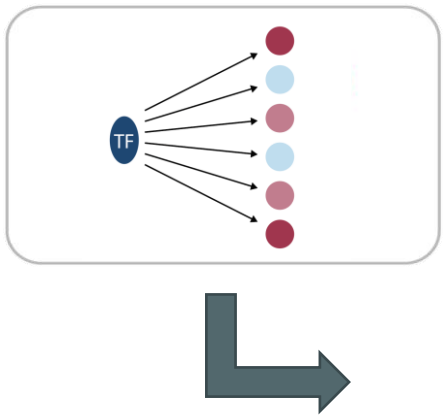




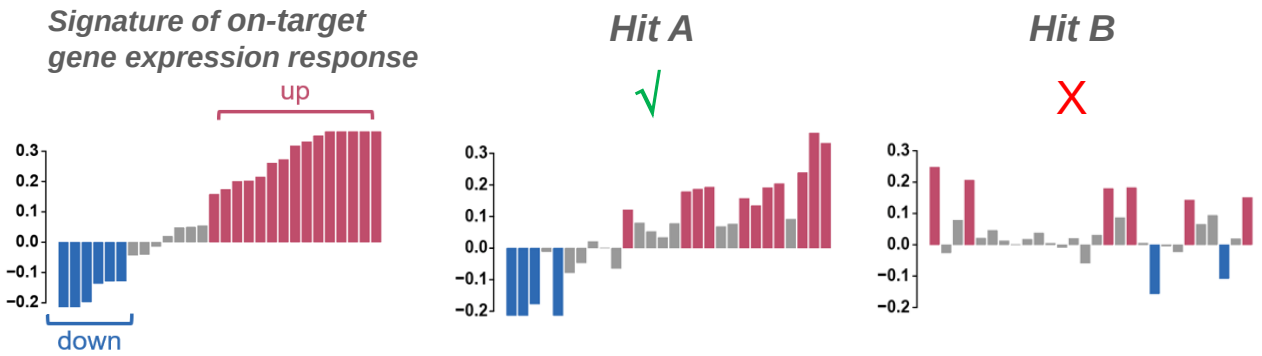
PPI: Protein-protein interaction. TF: Transcription factor. TRN: Transcriptional regulatory network.

Prioritize SMM hits based on selectivity, assessed by TRN gene expression signature

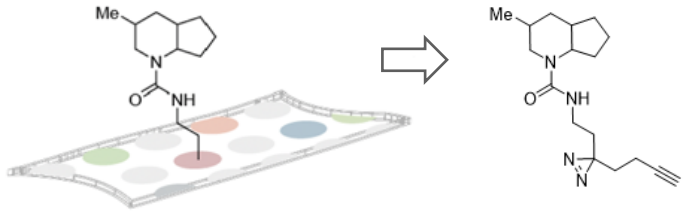
TF ACTIVITY



Hits picked via selective TRN gene expression signature



Chemo-proteomic target deconvolution



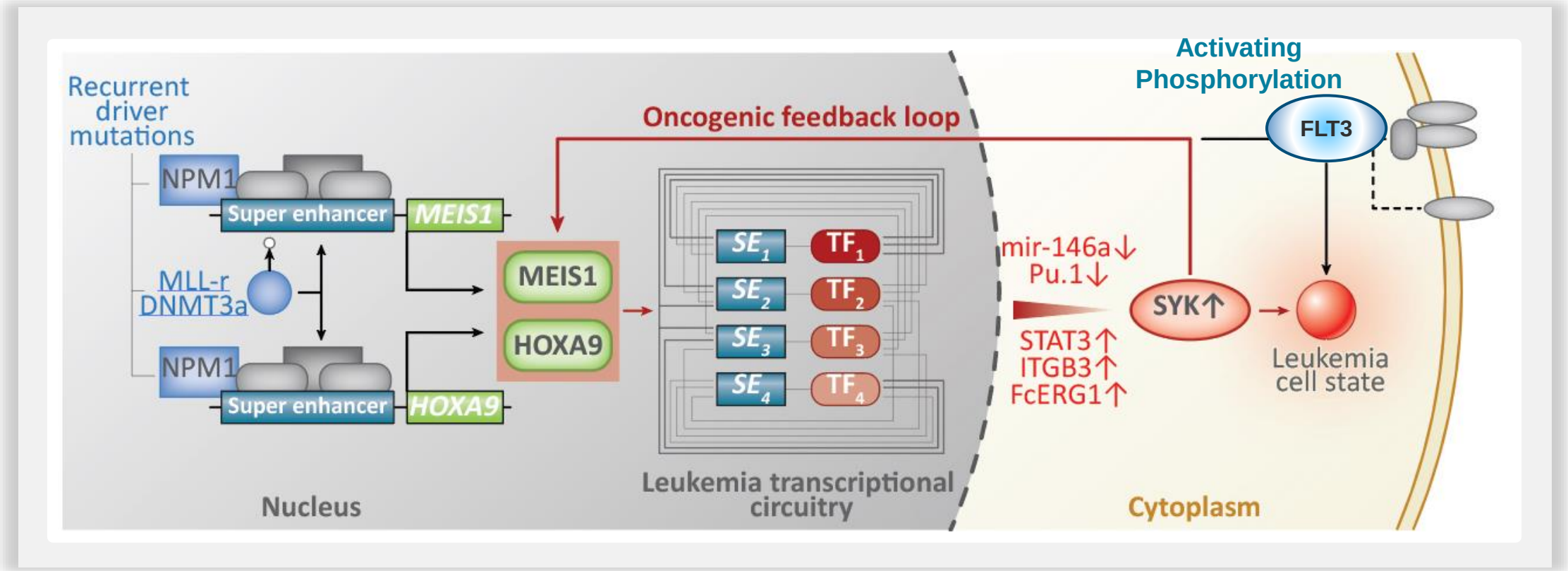
- Identify hits that **selectively** perturb the oncogenic TRN
- Confirm or deconvolute the molecular targets of hits
- Drive hit-to-lead and lead optimization of **transcription factor modulators**

TF: Transcription factor. TRN: Transcriptional regulatory network.

KRONOS·BIO

- Introduction
- Targeting Oncogenic TRNs
- **Lead Programs**
  - **SYK**
  - CDK9
- The Kronos Bio Opportunity

SYK is a critical dependency in NPM1 and FLT3 mutated AML

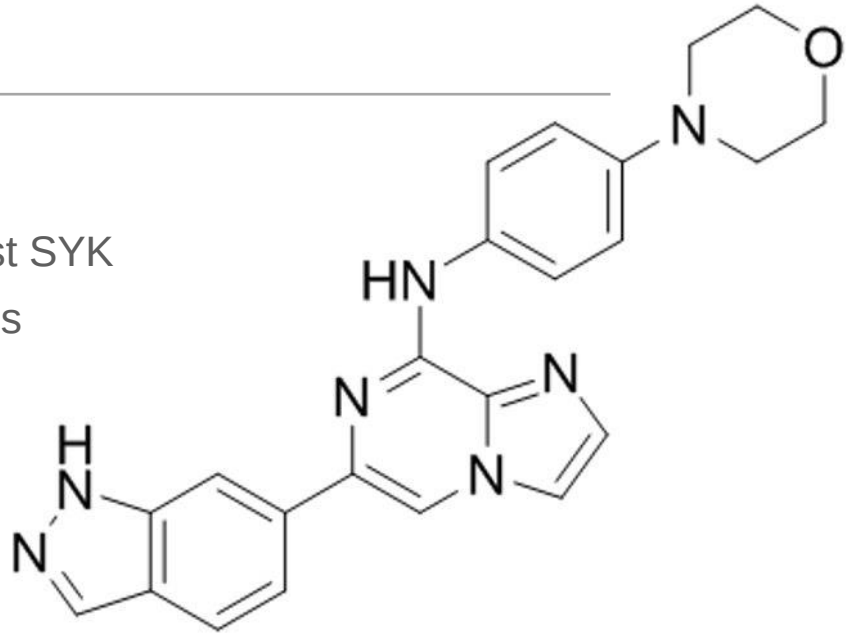


- SYK stabilizes the HOX/MEIS TRN downstream of NPM1 via a positive feedback loop *Mohr et al. 2017. Cancer Cell*
- SYK phosphorylation of FLT3 is required for FLT3 ITD leukemogenesis *Puissant et al. 2014. Cancer Cell*

AML: Acute myeloid leukemia. DNMT3a: DNA Methyltransferase 3 Alpha. FLT3: Fms related tyrosine kinase 3. ITD: Internal tandem duplication. MLL-r: Mixed-lineage leukemia rearrangements. NPM1: Nucleophosmin 1. SYK: Spleen tyrosine kinase. TRN: Transcriptional regulatory network.

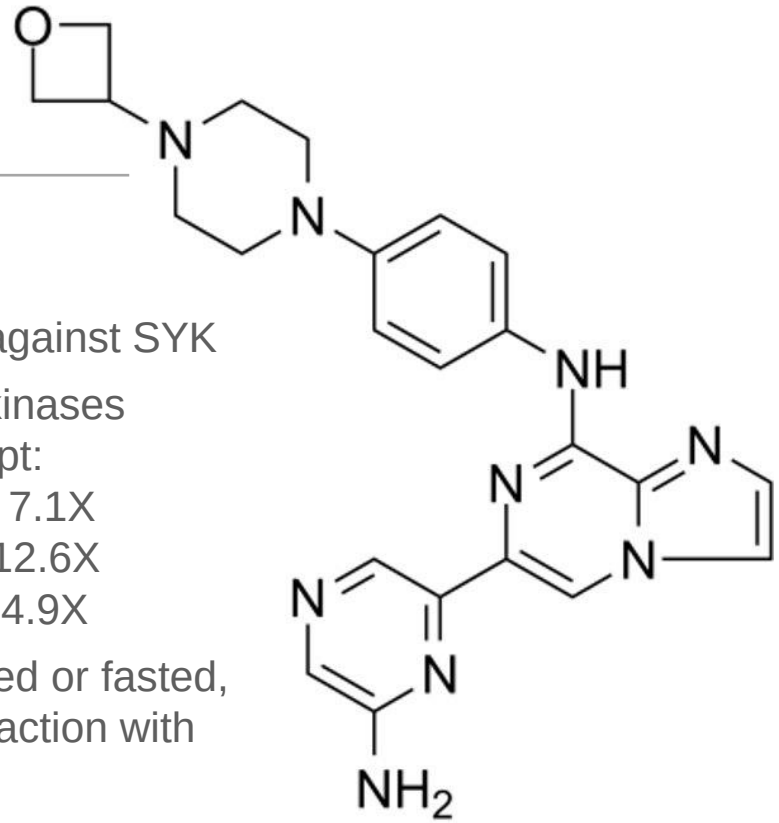
Kronos Bio portfolio includes two potent, selective clinical-stage SYK inhibitors

ENTO



- 8.5 nM IC_{50} against SYK
- >10X on all kinases profiled except:
  - FLT3 = 2.4X
  - JAK2 = 2.0X
  - SRC = 8.2X
- BID dosing, in fasted state, cannot be taken with PPIs
- Clinical data in hematologic malignancies

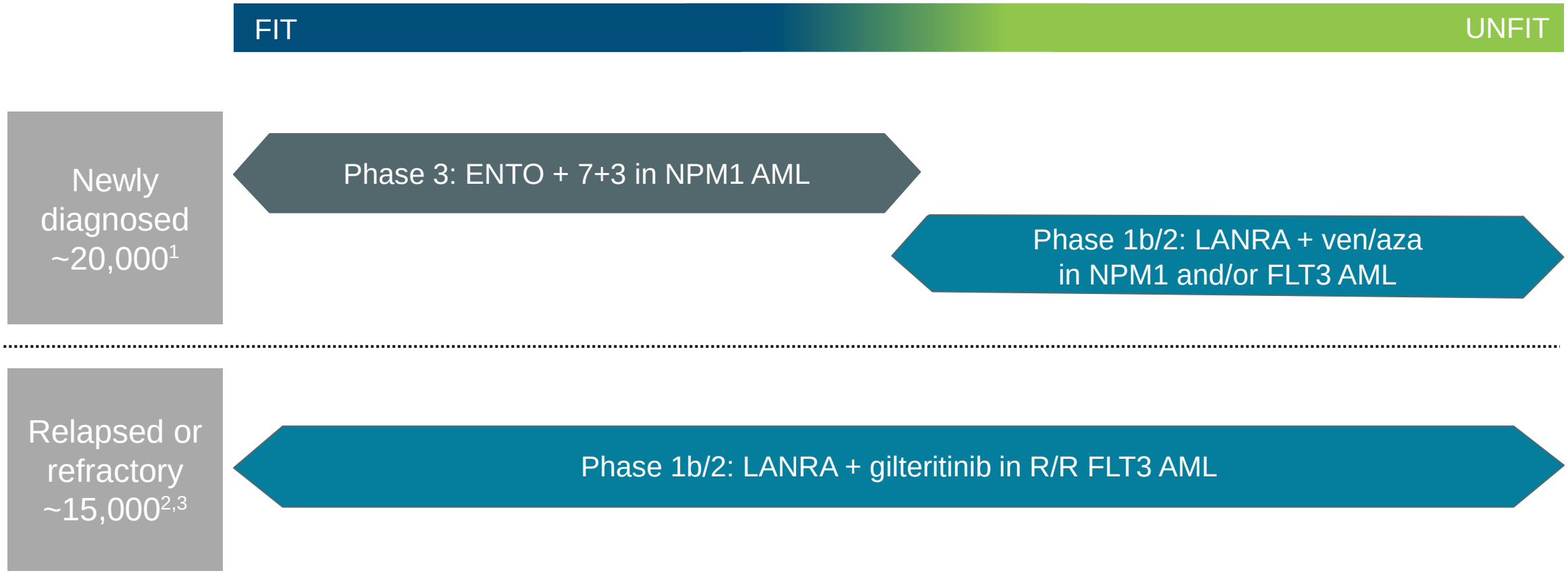
LANRA



- 9.5 nM IC_{50} against SYK
- >15X on all kinases profiled except:
  - Zap70 = 7.1X
  - JAK2 = 12.6X
  - SRC = 14.9X
- QD dosing, fed or fasted, no drug interaction with PPIs
- Clinical data in autoimmune diseases

AML: Acute myeloid leukemia. ENTO: Entospletinib. FLT3: Fms related tyrosine kinase 3. JAK2: Janus Kinase 2. LANRA: Lanraplenib. nM: Nanomolar. PPI: Proton pump inhibitor. SRC: Proto-oncogene tyrosine-protein kinase Src. SYK: Spleen tyrosine kinase. Zap70: Zeta-chain-associated protein kinase 70.

ENTO and LANRA have potential to cover the entire NPM1 newly diagnosed and the R/R FLT3 AML patient populations*



*Investigational products are not approved by the FDA. Clinical trial programs only.
U.S. incidence: 1. SEER U.S. 2020 newly diagnosed AML; 2. Koenig K. et al. (2020); 3. Bose P. et al. (2017).
ENTO: Entospletinib. FLT3: Fms related tyrosine kinase 3. LANRA: Lanraplenib. NPM1: Nucleophosmin 1. R/R: Relapsed/refractory. Ven/aza: Venetoclax/azacitidine.

SYK inhibitor program: Entospletinib

Entospletinib
SYK Inhibitor
HOXA9/MEIS1 AML

Potent and selective SYK inhibitor with ~7 years of clinical data in more than 1,300 patients, including more than 700 patients with a variety of hematologic malignancies

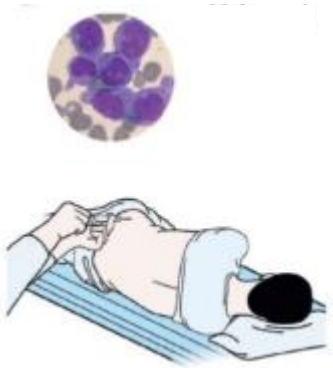
Clinical trials show encouraging activity in patients with HOXA9/MEIS1-high AML (associated with NPM1 and FLT3 mutation and MLL rearrangement)

In development to treat newly diagnosed NPM1-mutated AML patients eligible to receive intensive induction chemotherapy

Registrational Phase 3 trial assessing measurable residual disease negative complete response (MRD negative CR) is ongoing; pivotal data expected in H2 2023

AML: Acute myeloid leukemia. FLT3: Fms related tyrosine kinase 3. MLL: Mixed-lineage leukemia. NPM1: Nucleophosmin 1. SYK: Spleen tyrosine kinase.

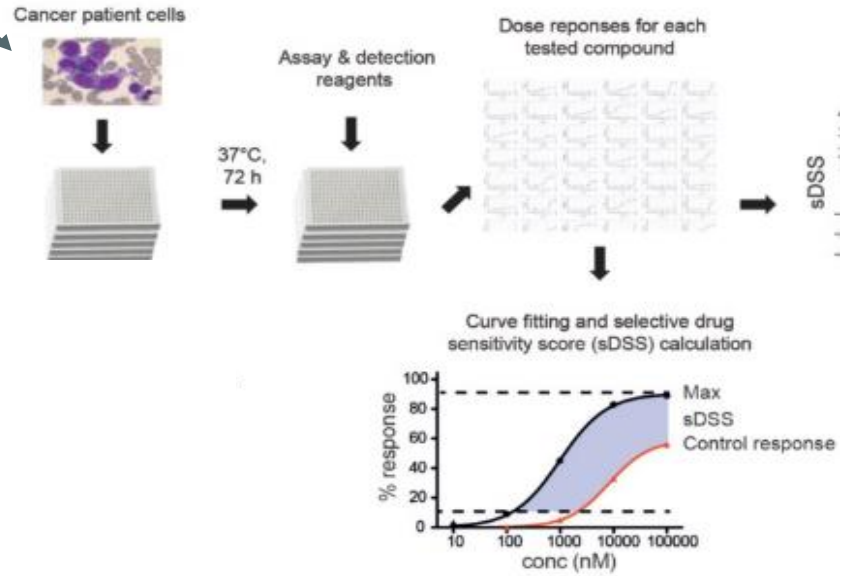
Sensitivity to ENTO correlates strongly with the presence of NPM1 and/or FLT3 mutation in AML patient bone marrow samples

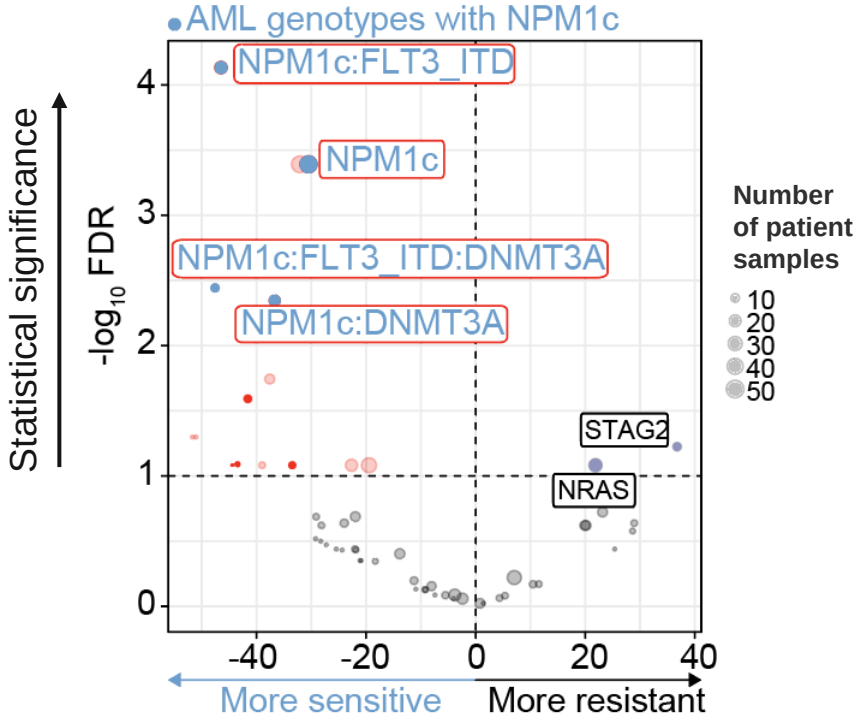


652 bone marrow samples from 572 AML patients

✓ **Mutations**
✓ **Gene expression**

Drug sensitivity screen





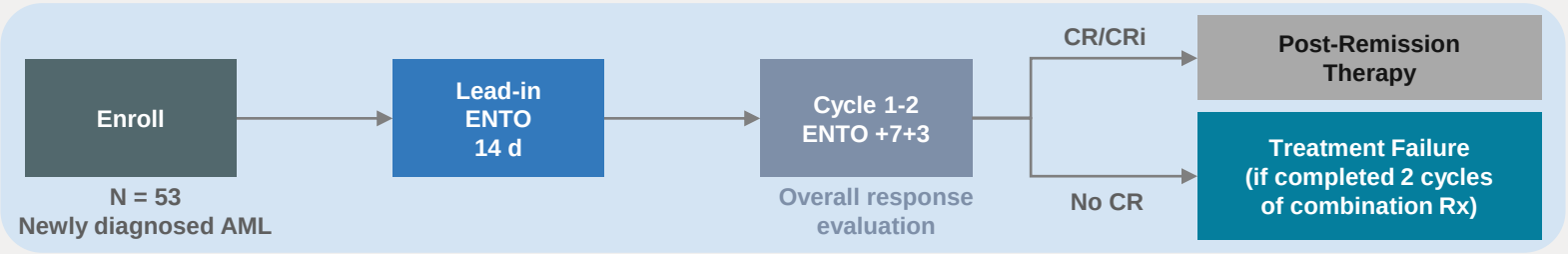
Fold Change in Sensitivity Mutant vs Wild-type

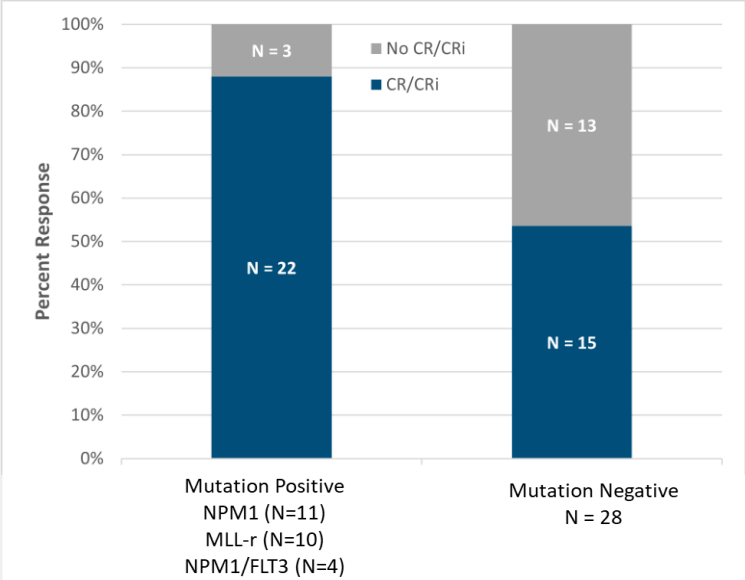
Beat AML acute myeloid leukemia

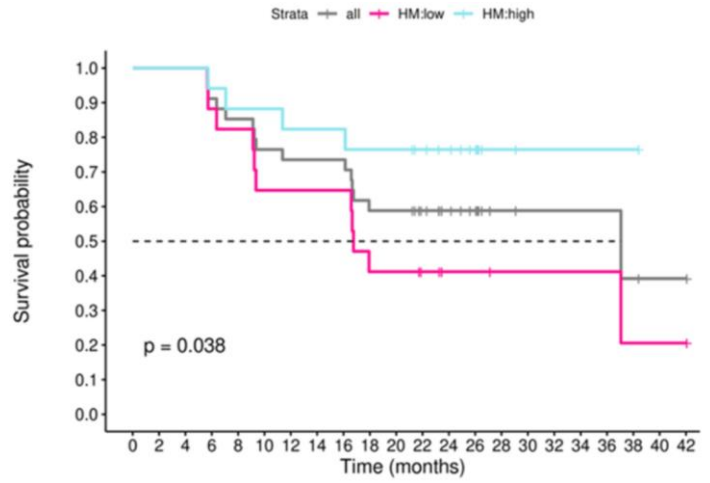
Tyner et al. 2018, Nature 562:526-531.
AML: Acute myeloid leukemia. DNMT3A: DNA methyltransferase 3A. ENTO: Entospletinib. FLT3: Fms related tyrosine kinase 3. ITD: Internal tandem duplication. NPM1: Nucleophosmin 1.
NRAS: Neuroblastoma RAS Viral Oncogene Homolog. STAG2: Stromal Antigen 2.

ENTO + 7+3 shows preferential activity in frontline AML patients with mutations that drive high HOXA9/MEIS1 expression

PHASE 1b/2 | PHASE 3







HOXA9/MEIS1 (H/M) mRNA measured at baseline in a subset (n=34)

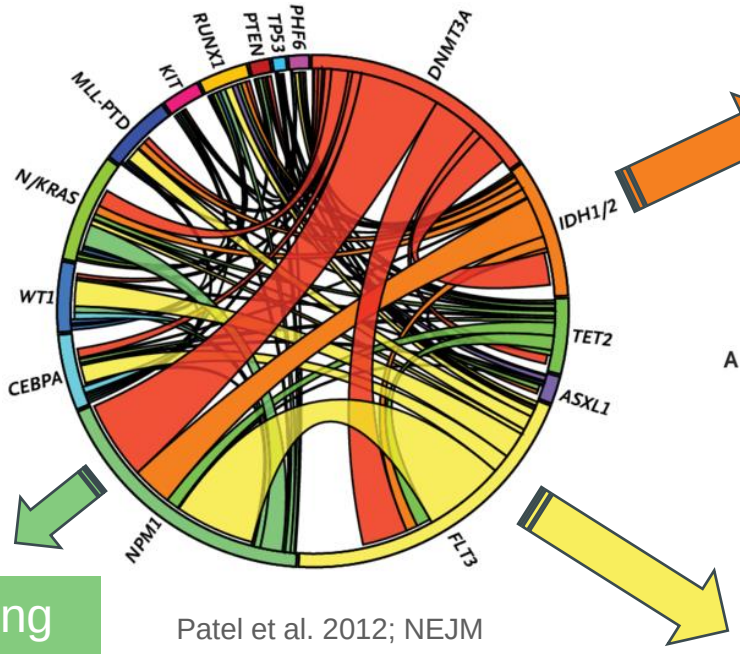
- 3/23 MLL-r patients achieved CR with ENTO monotherapy
- 37/53 (70%) achieved CR/CRi with ENTO + 7+3 induction
- HOX/MEIS high patients achieved superior CR/CRi rate and OS vs HOX/MEIS normal
- ENTO was well tolerated with 7+3 induction

Phase 1b/2 data are consistent with the dependency between SYK and HOX/MEIS high AML subsets

Walker et al, 2020. Clin Cancer Res 26:5852-5859.
AML: Acute myeloid leukemia. CR/CRi: Complete response/complete response with incomplete hematologic recovery. ENTO: Entospletinib. FLT3: Fms related tyrosine kinase 3.
MLL-r: Mixed-lineage leukemia rearrangements. NPM1: Nucleophosmin 1. OS: Overall survival.

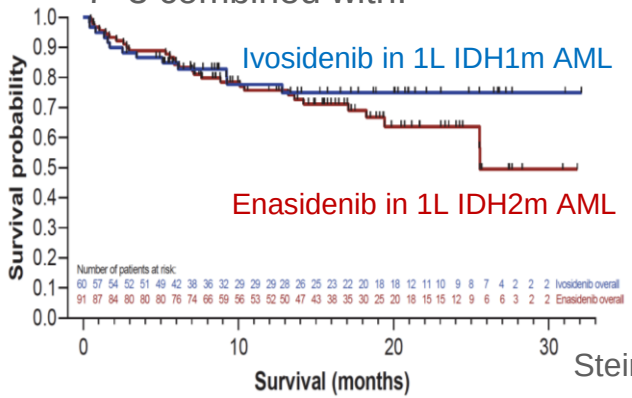
The addition of genetically targeted therapies to intensive induction backbones is leading to improved outcomes

- AML is a heterogeneous disease driven by recurring mutations
- Therapies that target the underlying mutational drivers can extend survival

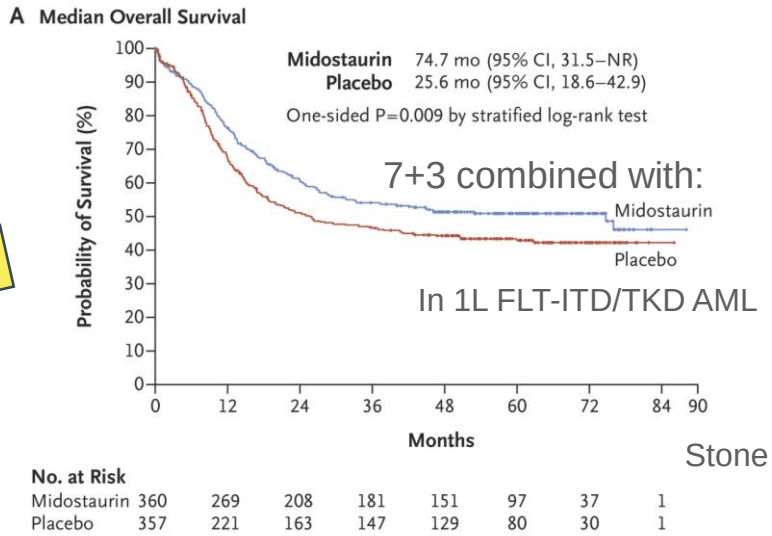


Patel et al. 2012; NEJM

7+3 combined with:



Stein E, et. al Blood 2020

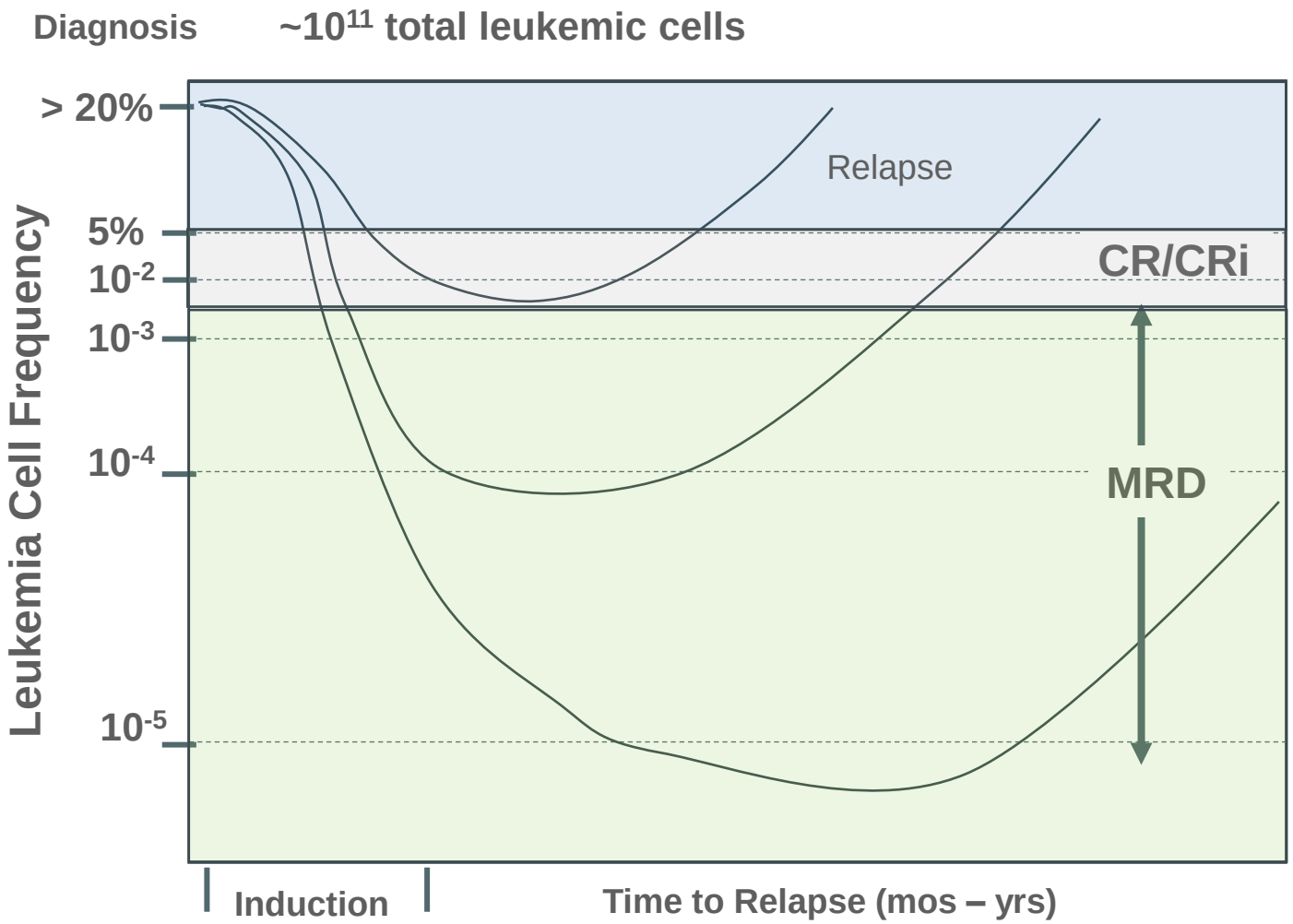


In 1L FLT-ITD/TKD AML

Stone R, et. al, NEJM 2017

Targeted therapies addressing NPM1 mutation or downstream signaling have not been approved

NPM1 mutations are ideal markers for **M**easurable **R**esidual **D**isease



Morphology: applicable to all patients, not very sensitive

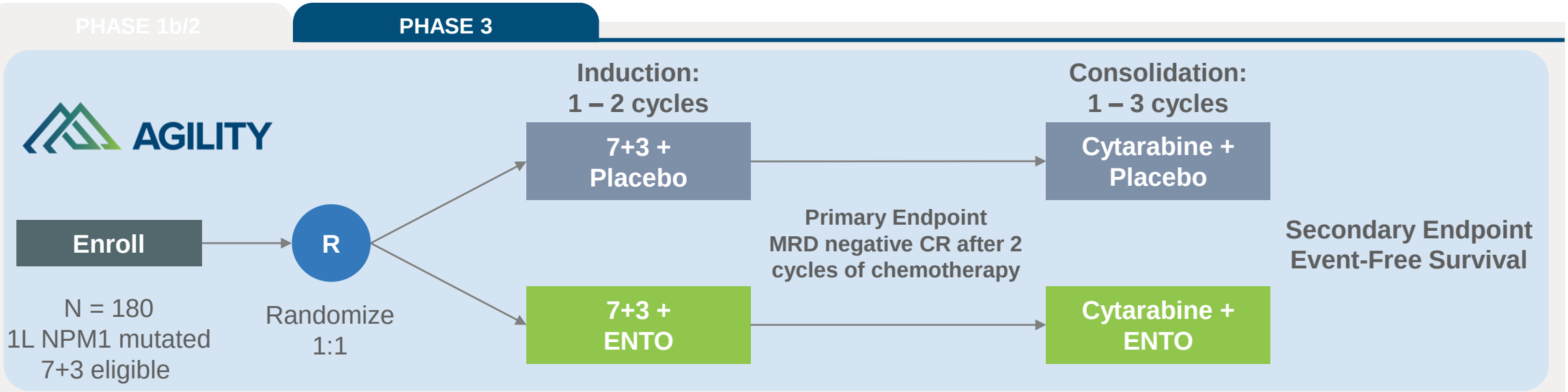
FISH: applicable to patients with clonal cytogenetics, not very sensitive

Multi-parameter Flow Cytometry

Molecular (PCR/NGS): applicable to NPM1 mutations, MLL-r and FLT3 ITD

CR/CRi: Complete response/complete response with incomplete hematologic recovery. FLT3 ITD: Fms related tyrosine kinase 3 with internal tandem duplication. MLL-r: Mixed-lineage leukemia rearrangements. NPM1: Nucleophosmin 1. NGS: Next generation sequencing. PCR: Polymerase chain reaction.

Phase 3 AGILITY trial of entospletinib with intensive induction/ consolidation is treating patients with frontline fit NPM1-mutated AML



- **Patient enrollment based on existing clinical assays for NPM1 mutation**
- **Validate one assay to meet FDA label requirements for CDx in parallel with trial conduct**
- **Primary endpoint of MRD negative CR after two cycles of chemotherapy**

Pivotal data expected in H2 2023

AML: Acute myeloid leukemia. CR: Complete response. CDx: Companion diagnostic. ENTO: Entospletinib. FDA: U.S. Food and Drug Administration. MRD: Measurable residual disease. NPM1: Nucleophosmin 1.

SYK inhibitor program: Lanraplenib

Lanraplenib
SYK Inhibitor
HOXA9/MEIS1 AML

Potent and selective SYK inhibitor investigated in more than 250 patients, with clinical data in autoimmune diseases showing favorable PK and safety profile for chronic dosing

Equivalent anti-leukemic activity to ENTO in primary AML bone marrow samples supports investigational combination with FLT3 inhibitor and venetoclax/azacitidine

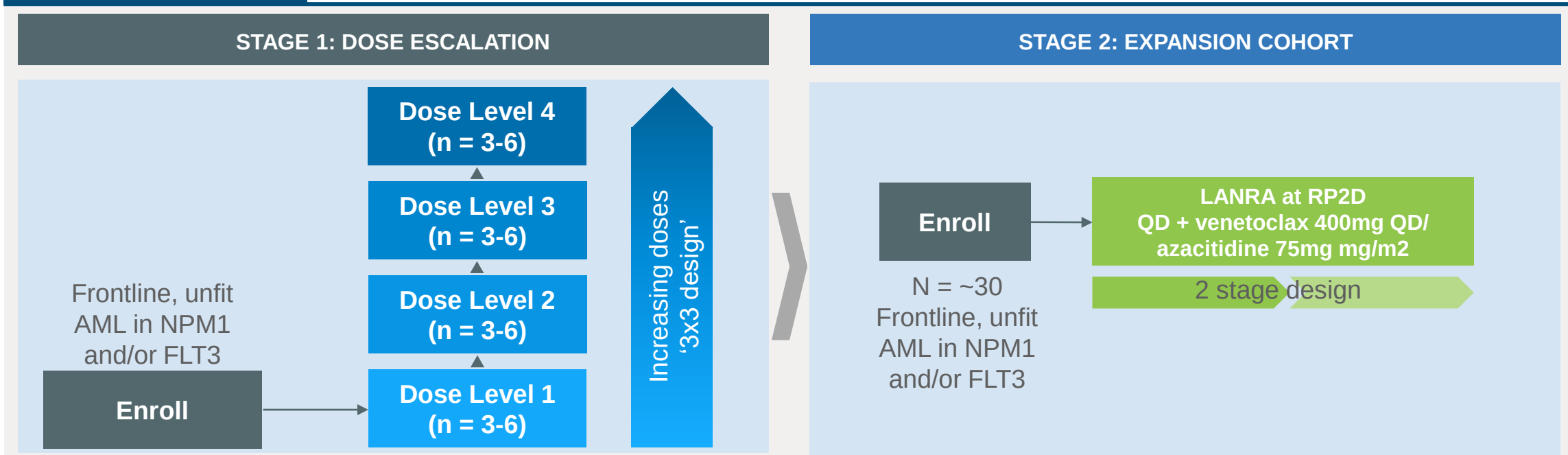
Phase 1b/2 clinical trial in patients with R/R FLT3-mutated AML scheduled to begin in Q1 2022

Phase 1b/2 clinical trial in newly diagnosed NPM1-mutated and/or FLT3-mutated AML patients who are not eligible for intensive induction chemotherapy scheduled to begin in early 2022

AML: Acute myeloid leukemia. FLT3: Fms related tyrosine kinase 3. NPM1: Nucleophosmin 1. R/R: Relapsed/refractory. SYK: Spleen tyrosine kinase.

Phase 1b/2 trial of LANRA + ven/aza in frontline elderly/unfit NPM1 and/or FLT3 AML

PHASE 1b/2



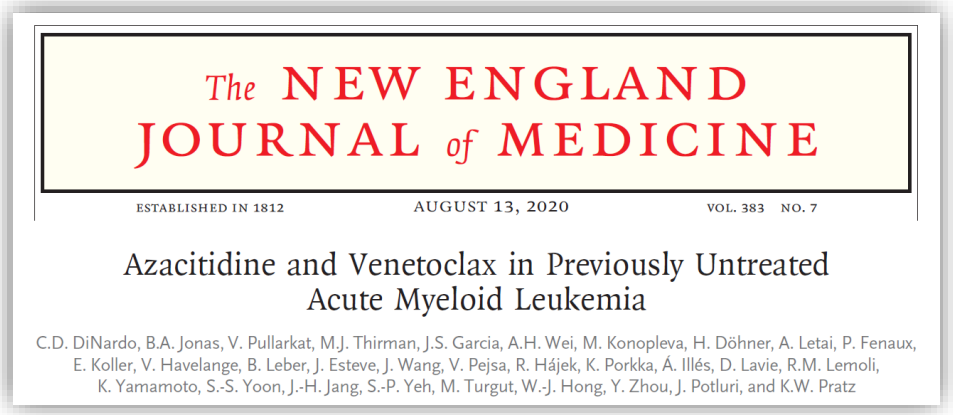
- **Evaluate initial safety, PK, and antileukemic activity in escalating doses of LANRA QD in combination with venetoclax 400 mg QD and azacitidine 75 mg/m2**

- **Further evaluate safety and antileukemic activity**
- **Inform Phase 3 trial design**

LANRA + ven/aza clinical trial initiation expected in early 2022

AML: Acute myeloid leukemia. FLT3: Fms related tyrosine kinase 3. LANRA: lanraplenib. NPM1: Nucleophosmin 1. PK: pharmacokinetics. QD: Quaque die (once a day). RP2D: Recommended Phase 2 dose. R/R: Relapsed/refractory. Ven/aza: Venetoclax/azacitidine.

Other AML opportunities for SYK inhibition: Investigational combination with ven/aza in frontline elderly/unfit patients with NPM1 and/or FLT3 ITD/TKD



The NEW ENGLAND JOURNAL of MEDICINE

ESTABLISHED IN 1812 AUGUST 13, 2020 VOL. 383 NO. 7

Azacitidine and Venetoclax in Previously Untreated Acute Myeloid Leukemia

C.D. DiNardo, B.A. Jonas, V. Pullarkat, M.J. Thirman, J.S. Garcia, A.H. Wei, M. Konopleva, H. Döhner, A. Letai, P. Fenaux, E. Koller, V. Havelange, B. Leber, J. Esteve, J. Wang, V. Pejsa, R. Hájek, K. Porkka, Á. Illés, D. Lavie, R.M. Lemoli, K. Yamamoto, S.-S. Yoon, J.-H. Jang, S.-P. Yeh, M. Turgut, W.-J. Hong, Y. Zhou, J. Potluri, and K.W. Pratz

VIALE-A Trial (ven/aza approval)

- N = 433
- > 18 yo AND ineligible for 7+3 based on:
  - ✓ Age ≥ 75 yo OR
  - ✓ Unfit by Ferrara criteria
- Enrolled at 134 sites/27 mos = 0.12 p/s/m

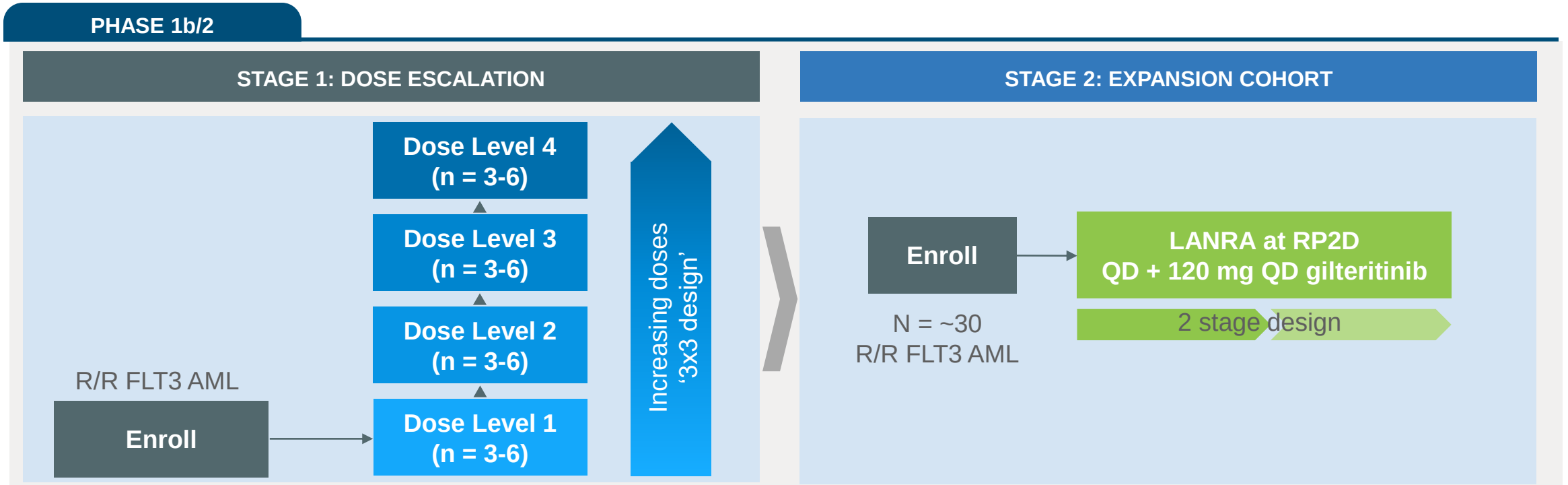
Endpoint	aza/placebo	ven/aza
CR	17.9%	36.7%
mOS	9.6 mo	14.7 mo

All subjects OS HR 0.66; CR+CRi 66.4%
NPM1 mut OS HR 0.73; CR+CRi 66.7%

NPM1 mutants had the same outcome as overall population in VIALE-A trial

AML: Acute myeloid leukemia. CR/CRi: Complete response/complete response with incomplete hematologic recovery. FLT3: Fms related tyrosine kinase 3. HR: Hazard ratio. ITD: Internal tandem duplication. mOS: Median overall survival. NPM1: Nucleophosmin 1. OS: Overall survival. p/s/m: Patients/site/month. SYK: Spleen tyrosine kinase. TKD: Tyrosine kinase domain. Ven/aza: Venetoclax/azacitidine.

Phase 1b/2 trial of LANRA + gilteritinib in relapsed/refractory FLT3 AML



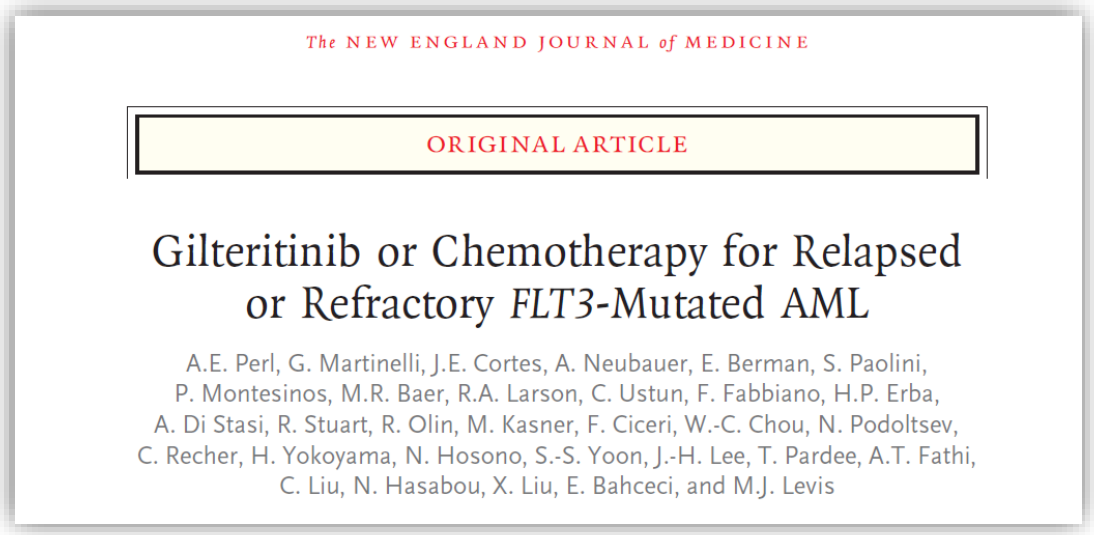
- Evaluate initial safety, PK, and antileukemic activity (cCR rate) in escalating doses of LANRA QD in combination with gilteritinib 120 mg QD

- Further evaluate safety and antileukemic activity (cCR rate and DoR)
- Inform Phase 3 trial design

LANRA + gilteritinib clinical trial initiation expected in Q1 2022

AML: Acute myeloid leukemia. cCR: Complete clinical response. DoR: Duration of response. FLT3: Fms related tyrosine kinase 3. LANRA: Lanraplenib. PK: pharmacokinetics. QD: Quaque die (once a day). RP2D: Recommended Phase 2 dose. R/R: Relapsed/refractory.

Other AML opportunities for SYK inhibition: Investigational combination with gilteritinib in R/R patients with FLT3 ITD/TKD



The NEW ENGLAND JOURNAL of MEDICINE

ORIGINAL ARTICLE

Gilteritinib or Chemotherapy for Relapsed or Refractory *FLT3*-Mutated AML

A.E. Perl, G. Martinelli, J.E. Cortes, A. Neubauer, E. Berman, S. Paolini, P. Montesinos, M.R. Baer, R.A. Larson, C. Ustun, F. Fabbiano, H.P. Erba, A. Di Stasi, R. Stuart, R. Olin, M. Kasner, F. Ciceri, W.-C. Chou, N. Podoltsev, C. Recher, H. Yokoyama, N. Hosono, S.-S. Yoon, J.-H. Lee, T. Pardee, A.T. Fathi, C. Liu, N. Hasabou, X. Liu, E. Bahceci, and M.J. Levis

ADMIRAL Trial (gilteritinib approval)

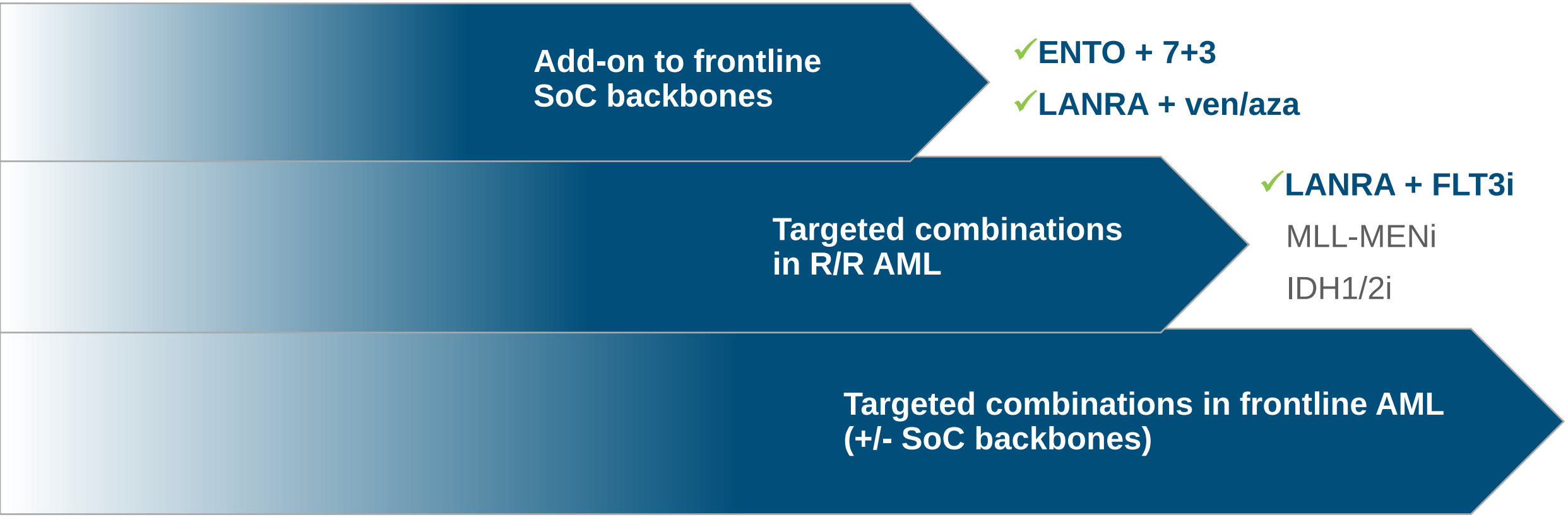
- N = 371
- > 18 yo refractory to 1-2 cycles of 7+3 or relapsed after CR with 7+3 AND
- FLT3 ITD/TKD
- Enrolled at 107 sites/28 mo = 0.12 p/s/m

Endpoint	Chemo (N = 124)	Gilteritinib (N = 247)
CR	10.5%	21.1%
mOS*	5.6 mo	9.3 mo (HR 0.64)
mEFS	0.7 mo	2.8 mo (HR 0.79)

*Prior midostaurin (N = 37) OS HR = 0.70

Perl et al, 2019. NEJM 381:381:1728-1740.
AML: Acute myeloid leukemia. CR: Complete response. FLT3: Fms related tyrosine kinase 3. HR: Hazard ratio. ITD: Internal tandem duplication. mEFS: Median event-free survival. mOS: Median overall survival. R/R: Relapsed/refractory. SYK: Spleen tyrosine kinase. TKD: Tyrosine kinase domain.

Strategy to maximize the potential of SYK inhibitors in genetically defined subsets of AML



AML: Acute myeloid leukemia. FLT3i: Fms related tyrosine kinase 3 inhibitor. IDH1/2i: Isocitrate Dehydrogenase (NADP(+)) 1 or 2 inhibitor. MLL-MENi: Mixed-lineage leukemia-Menin inhibitor. R/R: Relapsed or refractory. SoC: Standard of care. SYK: Spleen tyrosine kinase. Ven/aza: Venetoclax/azacitidine.

KRONOS·BIO

- Introduction
- Targeting Oncogenic TRNs
- **Lead Programs**
  - SYK
  - **CDK9**
- The Kronos Bio Opportunity

CDK9 Inhibitor Program: KB-0742

KB-0742
CDK9 Inhibitor
Solid Tumors

- **CDK9 is a global regulator of transcription and a critical node in multiple oncogenic TRNs**
- **KB-0742 originated from proprietary SMM screen**
- **Differentiated selectivity profile, oral bioavailability and other attractive pharmacologic properties**
- **Demonstrated dependence on CDK9 in MYC amplified tumors**
- **Dose escalation stage of Phase 1/2 clinical trial underway**

CDK9: Cyclin-dependent kinase 9. SMM: Small molecule microarray. TF: Transcription factor. TRN: Transcriptional regulatory network.

Interim KB-0742 data summary from ongoing dose escalation

- **Pharmacokinetic profile:** Long-half life and accumulation support approach to defining a therapeutic window for CDK9
- **Pharmacodynamic results:** Evidence of target engagement as measured by proprietary target engagement assays developed and prospectively validated at Kronos Bio
- **Safety:** Consistent with what is typically seen among heavily pretreated patients with advanced cancer in Phase 1 studies; we are continuing to enroll the trial.
- **Dosing schedule:** Data support current 3 day on/4 day off dosing schedule

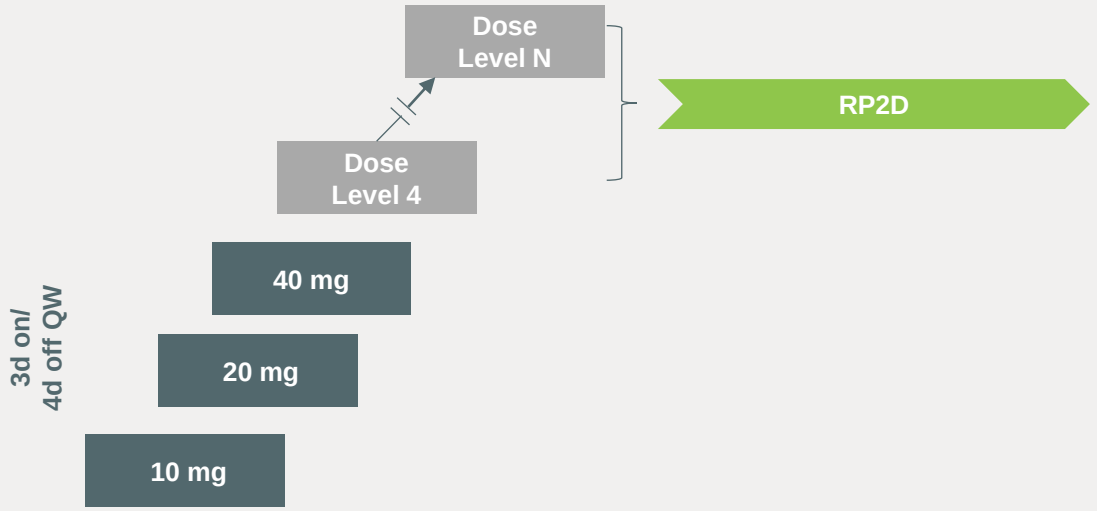
Background: Study included mixed population of heavily pre-treated patients with solid tumors not selected for MYC amplification or other response biomarkers.

Positive data support KB-0742's differentiated profile

Ongoing KB-0742 Phase 1/2 trial includes two stages

PHASE 1/2

STAGE 1: DOSE ESCALATION



- Relapsed/refractory solid tumor population **not selected for MYC amplification**
- Understand safety, PK and PD **in PBMC**
- Refine dosing schedule to maximize therapeutic window

STAGE 2: EXPANSION COHORTS

Cohort A: MYC-Dependent Solid Tumors

NSCLC, SCLC, TNBC, Gastric/Gastroesophageal
N=40

Cohort B: Other Transcriptionally Addicted Tumors

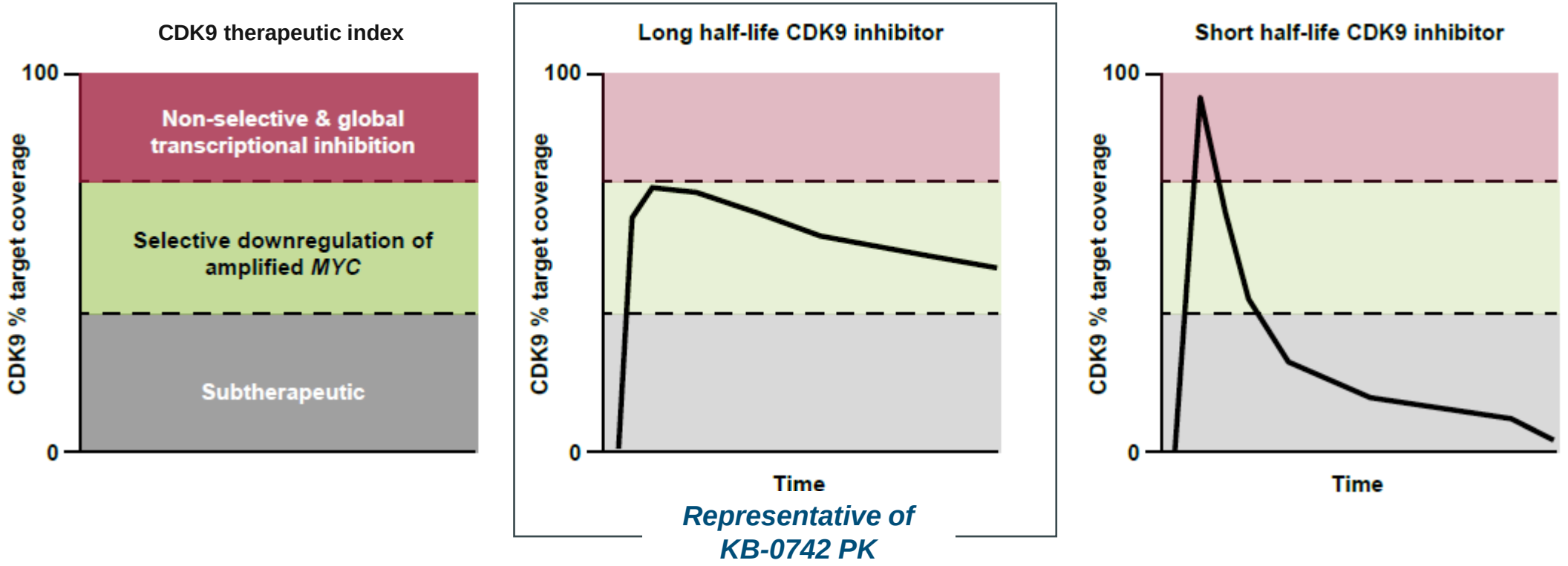
Sarcoma, Chordoma
N=30

Path to Registrational Trial

- **Biomarker selected** patients most likely to benefit from CDK9 inhibition
- Confirm safety and PD **in tumor tissue**
- Anti-tumor activity in specific tumor types

NSCLC: Non-small cell lung cancer. PD: Pharmacodynamics. PK: Pharmacokinetics. QW: Weekly. SCLC: Small cell lung cancer. TNBC: Triple-negative breast cancer. PBMC: Peripheral Blood Mononuclear Cells. RS2D: recommended stage 2 dose

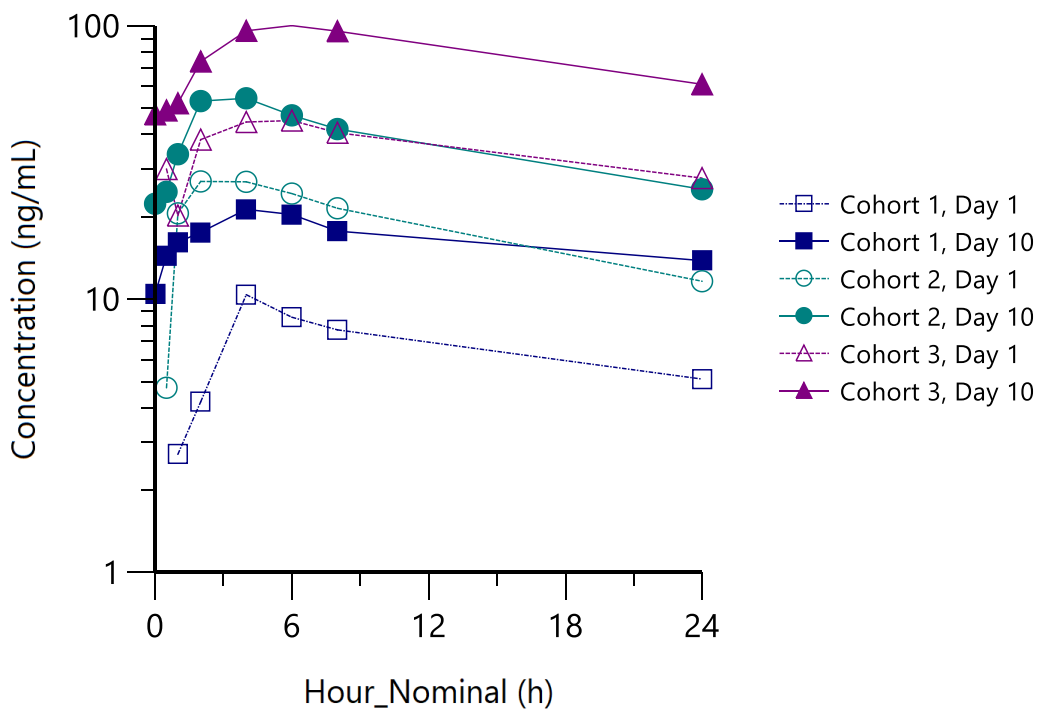
A long plasma half-life provides a differentiated opportunity to establish a therapeutic window for CDK9 inhibition



Representative of KB-0742 PK

KB-0742 has plasma half-life of ~24 hours

CLINICAL PK



TAKEAWAYS

- Preliminary PK analysis indicates that KB-0742 exhibited a dose-proportional increase in plasma exposure from 10 to 40 mg
- The t_{max} and half-life appeared independent of dose and time
- KB-0742 plasma half-life is approximately 24 hours, leading to accumulation ratios (AUC Day 10/AUC Day 1) of 2.1 to 2.5.

This PK profile suggests KB-0742 has the potential to achieve target engagement without reaching excessive and potentially toxic peak concentrations.

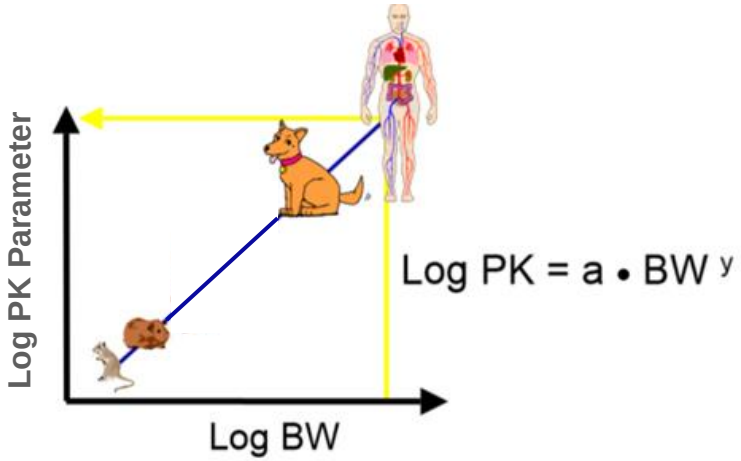
KB-0742 selectivity and projected PK provide advantages for safely inhibiting CDK9 in patients

Highly selective

	KB-0742
CDK9	IC_{50} = 6 nM
CDK13	62x
* CDK2	66x
CDK12	98x
CDK18	>200x
CDK3	>200x
* CDK7	>200x
CDK16	>200x
CDK5	>200x
CDK17	>200x
* CDK1	>200x
* CDK4	>200x
* CDK6	>200x
CDK14	>200x
CDK8	>200x
CDK19	>200x

Avoids off-target toxicity from cell cycle CDKs*

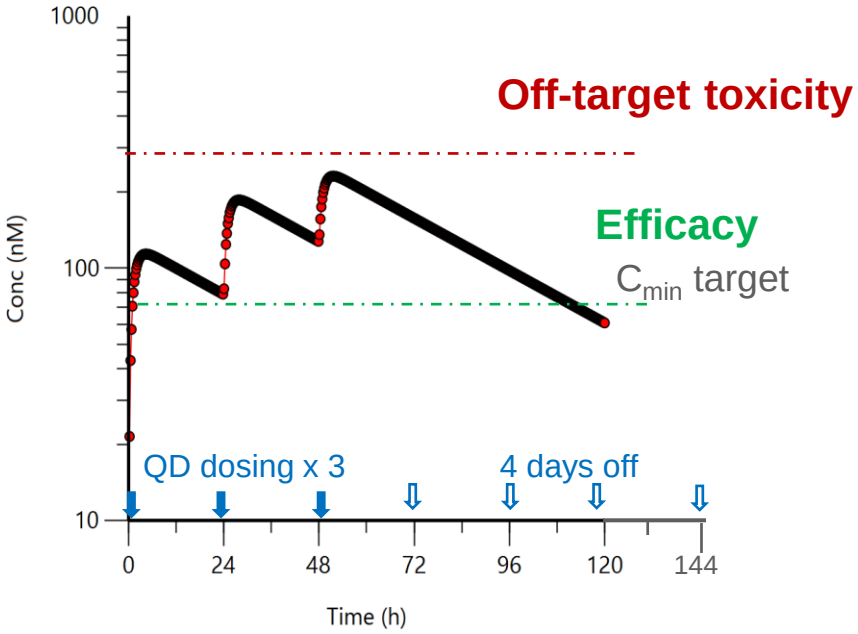
Favorable PK properties in preclinical models



- ✓ Projected human %F = 75%
- ✓ Stable in microsome/hepatocyte preps
- ✓ Low projected clearance
- ✓ Moderate-high volume of distribution

Projected long human plasma half-life

Simulated human PK based on projected half-life



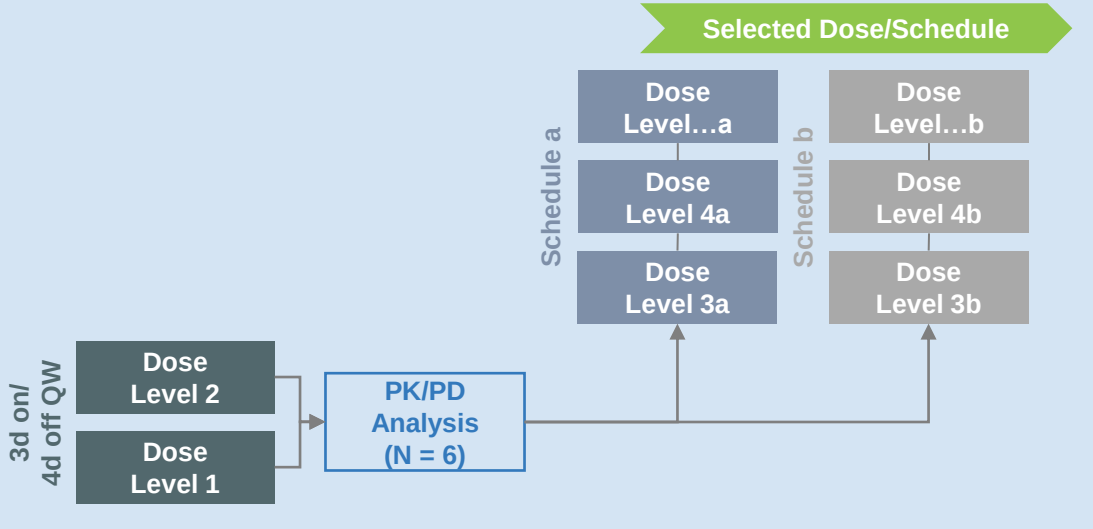
Achieves desired time above threshold while avoiding high C_{max}

BW: Body weight. CDK: Cyclin-dependent kinase. nM: Nanomolar. PK: pharmacokinetics. QD: Quaque die (once a day).

Ongoing KB-0742 Phase 1/2 trial includes two stages

PHASE 1/2

STAGE 1: DOSE ESCALATION



- Understand safety and PK/PD relationship
- Refine dosing schedule to maximize therapeutic window

STAGE 2: EXPANSION COHORTS

Cohort A: MYC-Dependent Solid Tumors

NSCLC, SCLC, TNBC, Gastric/Gastroesophageal

Cohort B: Other Transcriptionally Addicted Tumors

Sarcoma, Chordoma

Path to Registrational Trial

- Confirm safety and PD response in patient populations enriched for MYC amplification
- Inform Phase 2/3 trial design

Initial safety, PK and PD data from dose escalation cohorts expected in Q4 2021

NSCLC: Non-small cell lung cancer. PD: Pharmacodynamics. PK: Pharmacokinetics. QW: Weekly. SCLC: Small cell lung cancer. TNBC: Triple-negative breast cancer.

KRONOS·BIO

- Introduction
- Targeting Oncogenic TRNs
- Lead Programs
  - SYK
  - CDK9
- **The Kronos Bio Opportunity**

Strong financial profile

~$398M

cash, cash equivalents and investments

(unaudited, as Sept. 30, 2021)

Cash runway at least into

2024

~55M

shares outstanding

Multiple potential value catalysts

Program	2021	2022	2023	H1 2024
Clinical Programs				
ENTO *SYK Inhibitor* Frontline fit NPM1mt AML (registrational study)	Initiated Phase 3		Pivotal data readout	
LANRA *SYK Inhibitor* R/R FLT3mt AML		Initiate Phase 1b/2; Initial safety, PK and PD data	Clinical PoC data	
LANRA *SYK Inhibitor* Frontline unfit NPM1mt AML and/or FLT3mt AML		Initiate Phase 1b/2	Initial safety, PK and PD data	Clinical PoC data
KB-0742 *CDK9 Inhibitor* MYC-amplified and transcriptionally addicted tumors	Positive interim	Efficacy signal from expansion cohorts		

Discovery: Additional programs associated with MYC, AR, MYRB, IRF4 and other TRNs, with IND anticipated in 2023

AML: Acute myeloid leukemia. AR: Androgen receptor. CDK9: Cyclin Dependent Kinase 9. ENTO: Entospletinib. FLT3: Fms related tyrosine kinase 3. IND: Investigational new drug application. LANRA: Lanraplenib. NPM1: Nucleophosmin 1. PD: pharmacodynamics. PK: pharmacokinetics. PoC: Proof of concept. RP2D: Recommended phase 2 dose. R/R: Relapsed/refractory. SYK: Spleen tyrosine kinase.

~~IM~~POSSIBLE.
~~UN~~DRUGGABLE.
~~UN~~ACHIEVABLE.

Kronos Bio Investment Highlights

- Pioneering a new approach to target a potentially large market opportunity – dysregulated transcription factors and their associated TRNs
- SYK inhibitor program with potential to address patients with mutations present in more than 2/3 of AML
- Highly differentiated CDK9 program targeting MYC-amplified tumors
- Proprietary product engine to drive accelerated expansion of product candidates focused on high-value targets
- Highly experienced management team with more than 25 therapeutic product approvals

Dedicated to Transforming Patient Outcomes in Cancer by Targeting Dysregulated Transcription

AML: Acute myeloid leukemia. CDK9: Cyclin-dependent kinase 9. SYK: Spleen tyrosine kinase. TRN: Transcriptional regulatory network.

Demonstrated leadership advancing transformative therapies

Leadership Team

Norbert Bischofberger, Ph.D.
President and Chief Executive Officer

Barbara Kosacz
Chief Operating Officer and General Counsel

Jorge DiMartino, M.D., Ph.D.
Chief Medical Officer and Executive Vice President, Clinical Development

Yasir Al-Wakeel, BM BCh
Chief Financial Officer and Head of Corporate Development

Christopher Dinsmore, Ph.D.
Chief Scientific Officer

Board of Directors

Arie Belldegrun, M.D., FACS
Co-Founder and Chair

Norbert Bischofberger, Ph.D.
President and Chief Executive Officer

Roshawn Blunt
1798 LLC

Marianne De Backer, Ph.D., MBA
Bayer AG

Joshua Kazam
Co-Founder, Two River

Elena Ridloff
Stealth Startup

Otello Stampacchia, Ph.D.
Omega Funds

David Tanen
Two River

Taiyin Yang, Ph.D.
Gilead Sciences

Efforts guided by scientific advisory board comprised of leading KOLs

Owen Witte, M.D.
Scientific Advisory Board Chairman
UCLA

Myles Brown, M.D.
Dana-Farber Cancer Institute
Brigham and Women's Hospital
Harvard Medical School

David Chang, M.D., Ph.D.
President, Chief Executive Officer and Co-Founder of Allogene Therapeutics

Robert Eisenman, Ph.D.
Fred Hutchinson Cancer Research Center
University of Washington School of Medicine

Angela Koehler, Ph.D.
Scientific Founder
Associate Professor, Koch Institute for Integrative Cancer Research (MIT)

Roger D. Kornberg, Ph.D.
Winzer Professor in Medicine, Stanford University School of Medicine
Nobel Laureate 2006

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APPENDIX

Transcription factors (TFs) are high-value but historically challenging targets

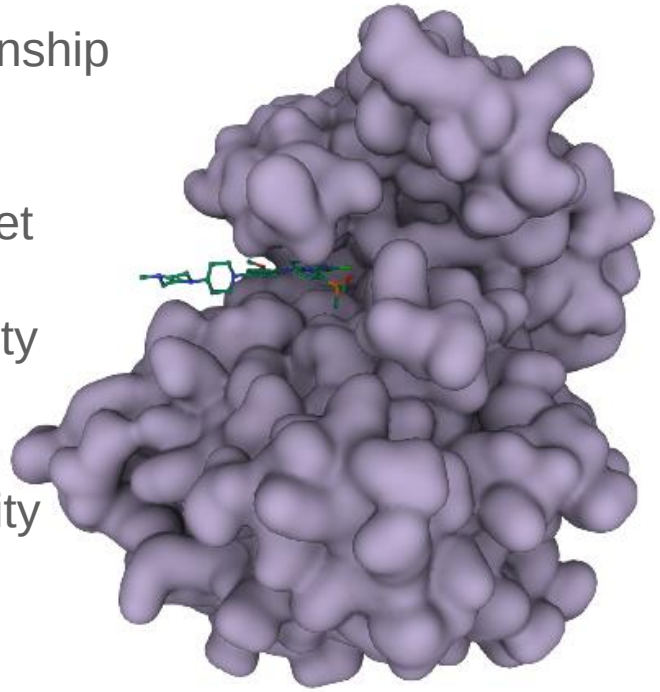
Anaplastic lymphoma kinase (ALK)
classic druggable protein

Structure/function relationship established

Ligandable binding pocket

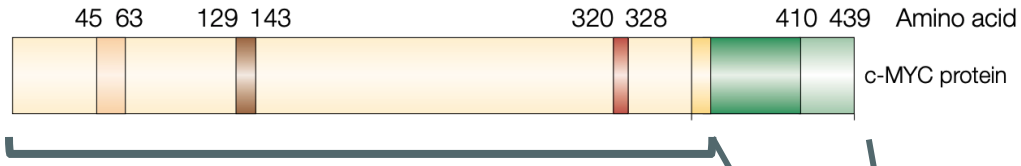
Established *in vitro* activity assays

Ability to assess selectivity (e.g., across kinases)



PDB 6MX8

MYC



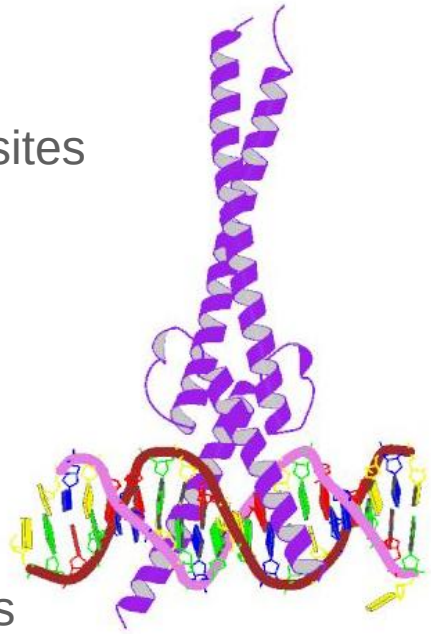
80% of MYC protein is intrinsically disordered

Acts by recruiting numerous cofactors to genomic binding sites

No active site

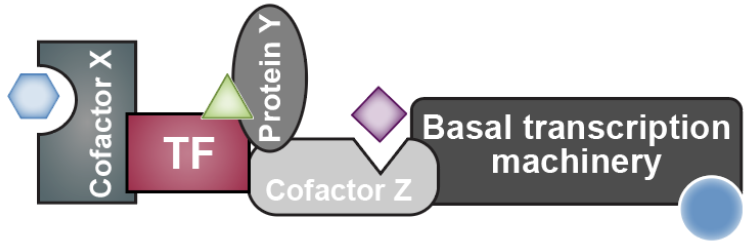
No *in vitro* activity assays

Cellular assays confounded by difficulty distinguishing MYC-specific vs. global effects



Screen

SMM campaigns against a TRN can generate multiple programs



Example of progression within Hit Discovery

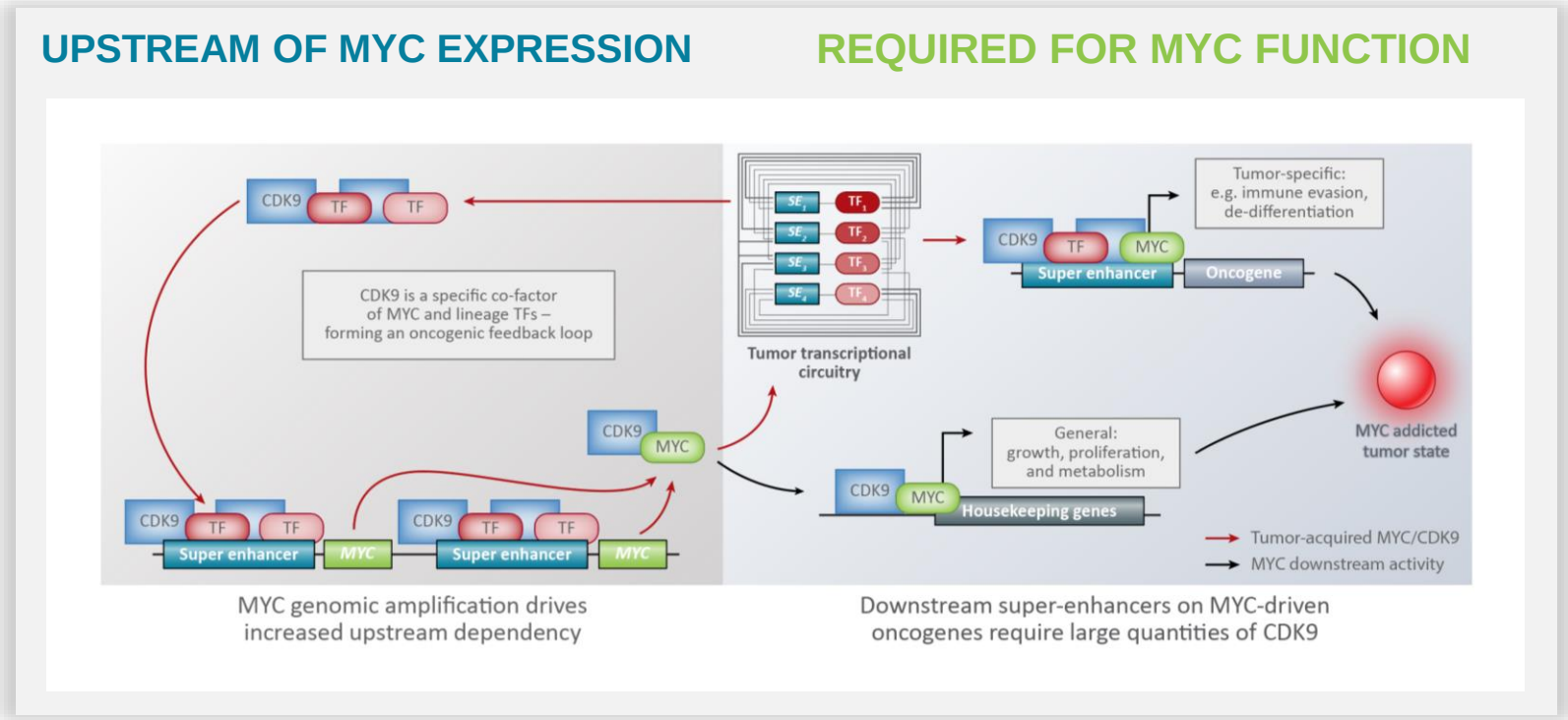
TRN mapping, screen & assay design → **Screen complete, Hits characterization** → **Hit functional validation & target definition** → **Graduate to Hit to Lead**

Mapping TF TRN in multiple tumor contexts → TF SMM screen → Hits prioritized by selectivity and potency

- TF cofactor X → Lead program 1
- TF : protein Y interaction → Lead program 2
- Off target (basal)

SMM: Small molecule microarray. TF: Transcription factor. TRN: Transcriptional regulatory network.

CDK9 is a global transcription elongation factor and an essential co-factor for the MYC TRN

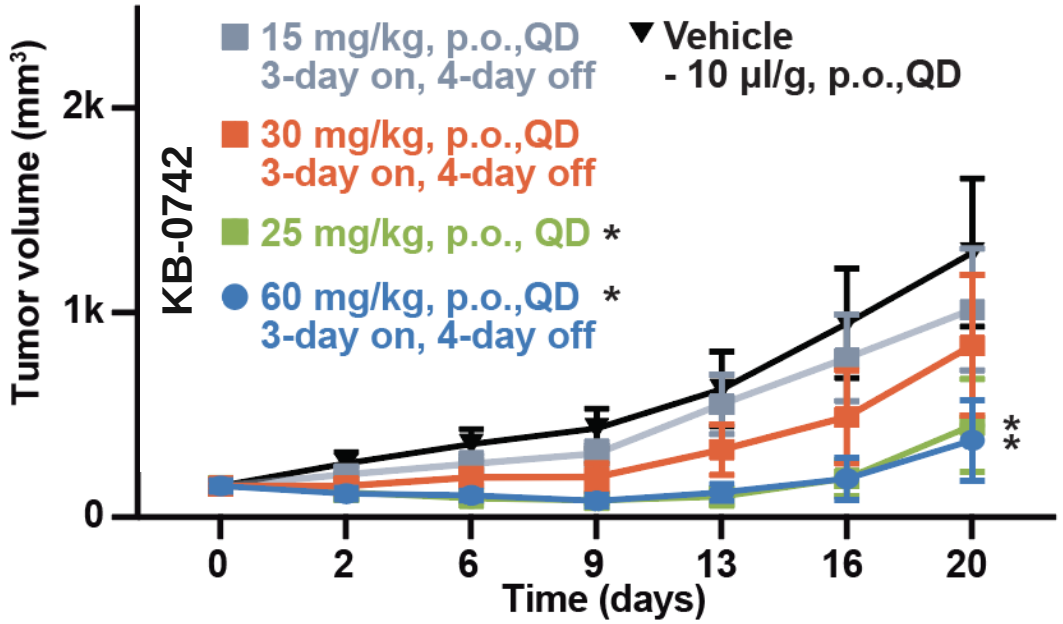


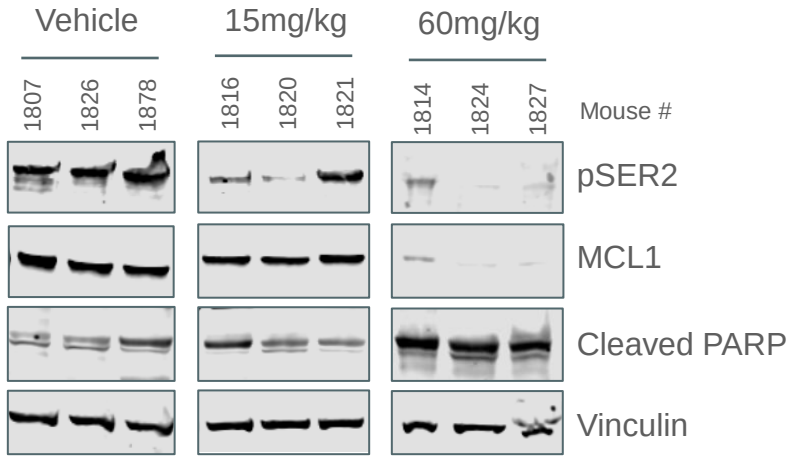
- CDK9 phosphorylates RNA pol II, allowing transcription to proceed
- MYC requires CDK9 to maintain its own mRNA expression
- MYC requires CDK9 to drive expression of its target genes
- Tumors that are addicted to MYC have heightened sensitivity to CDK9 inhibition
- Intermittent, partial inhibition of CDK9 can be active without causing unacceptable toxicity

CDK9 is an attractive target in transcriptionally addicted cancers, and specifically MYC-amplified solid tumors, due to its essential role in transcriptional elongation

CDK9: Cyclin-dependent kinase 9. TF: Transcription factor. TRN: Transcriptional regulatory network.

Intermittent dosing is as efficacious as continuous dosing in a MYC-driven AML xenograft model

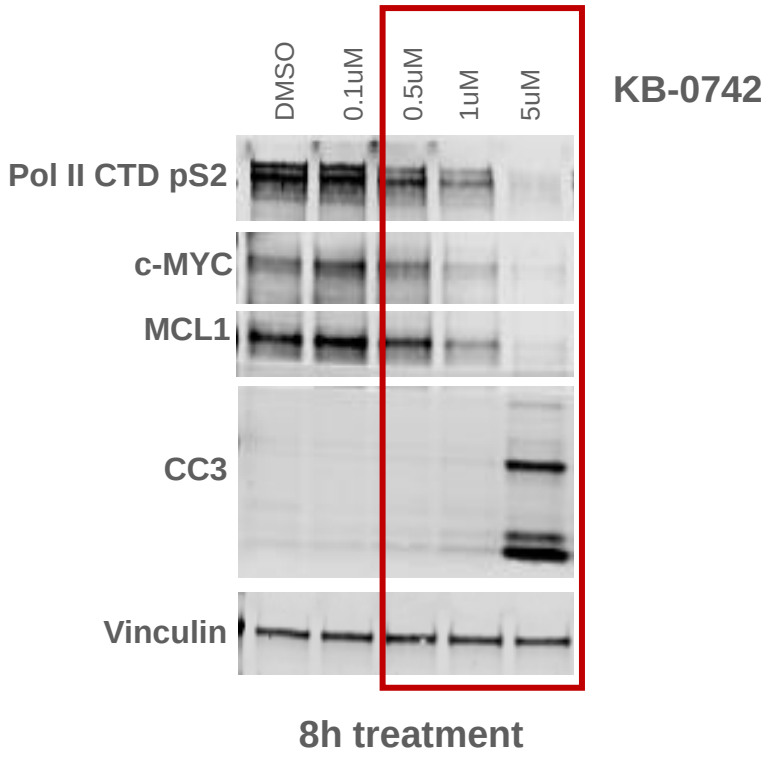




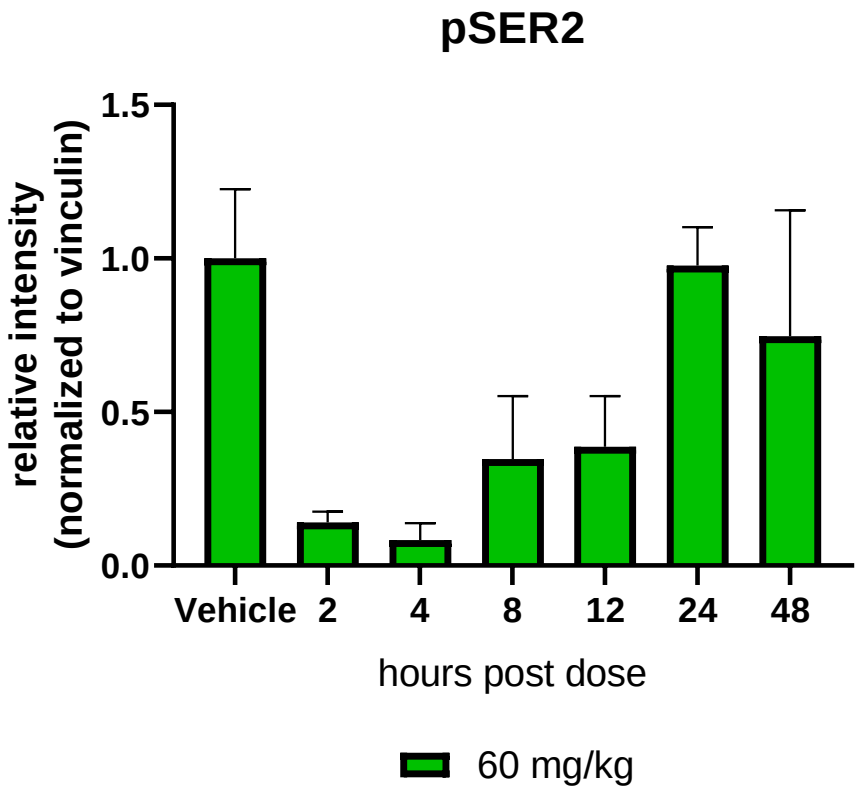
AML: Acute myeloid leukemia. QD: Quaque die (once a day).

Efficacious dosing of KB-0742 results in >50% target engagement for at least 12 hours

MV4-11 cells (*in vitro*)



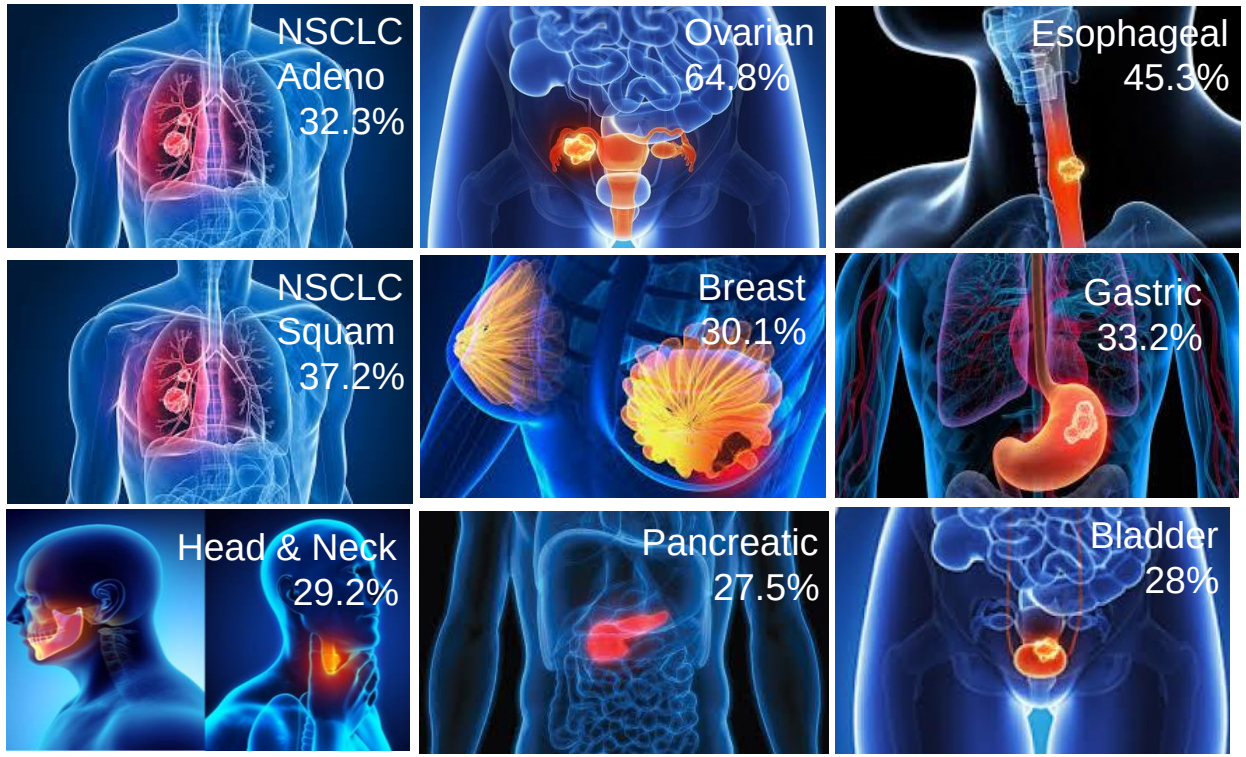
MV4-11 tumors (*in vivo*)



DMSO: Control. pSER2: Phosphoserine 2.

MYC amplification can be used to select cancer patients who may be more likely to respond to KB-0742

- Detected by tumor DNA sequencing
- Found in ~30% of tumors in the TCGA dataset
- Reported out by commercially available tumor sequencing platforms (e.g., Foundation Medicine, Tempus) in clinical use
- Correlates well with MYC mRNA and protein expression



Percentage of tumors in the TCGA dataset with copy number gains of MYC.
Schaub et al, 2018. Cell Systems 6:282-300.

TCGA: The Cancer Genome Atlas.

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