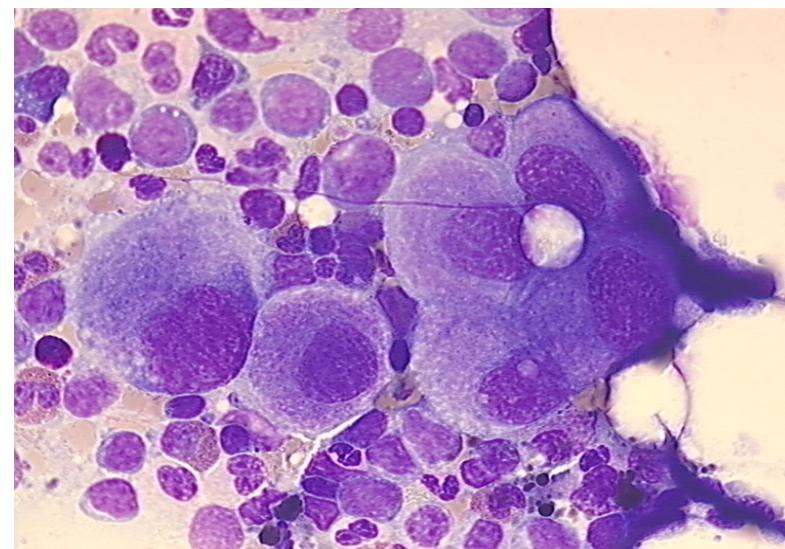


# Le mielodisplasie oggi: inquadramento dell'argomento



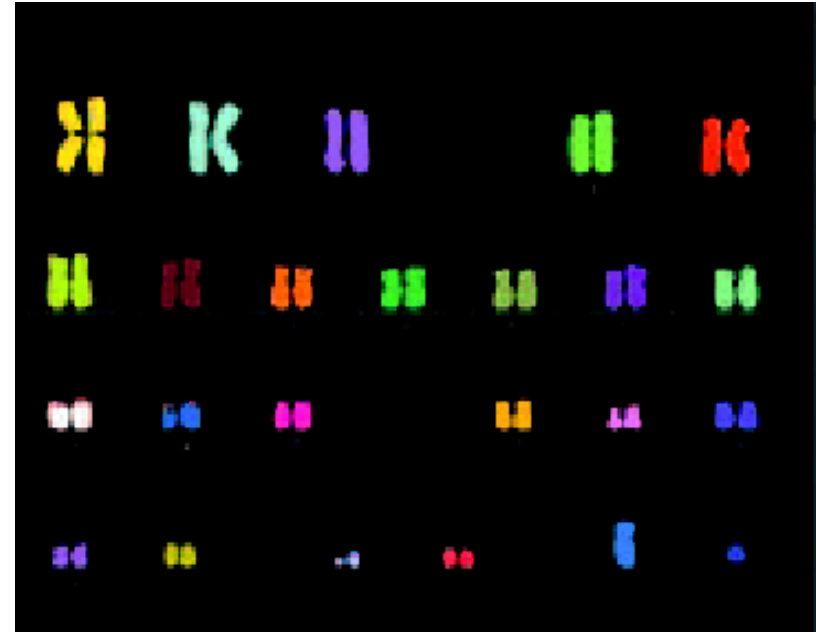
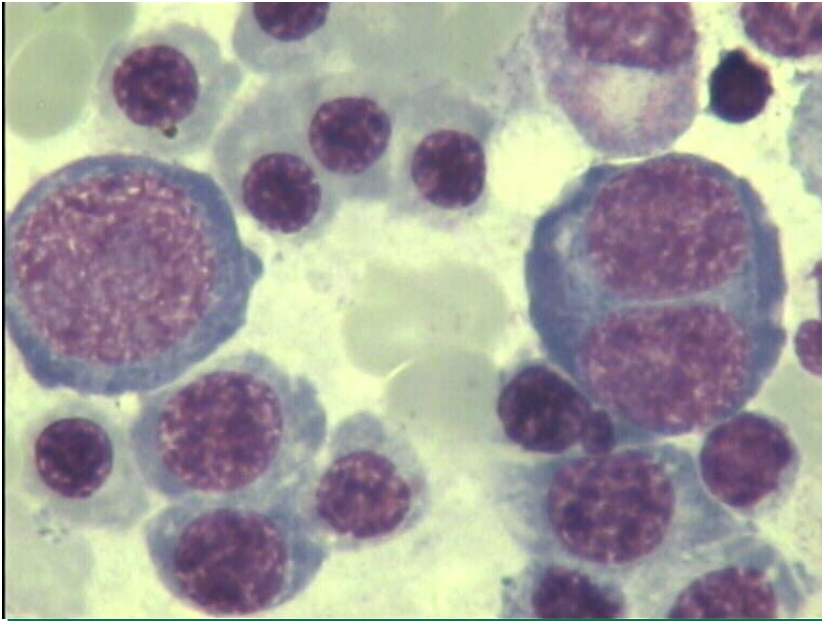
Valeria Santini

MDS UNIT

Ematologia, Università di Firenze



# Myelodysplastic syndromes are a constellation of diseases with difficult diagnosis



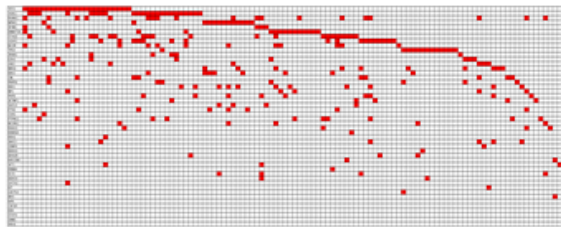
**An accurate diagnosis is the basis for successful prognostic stratification (and treatment) of MDS**

**Criteria: presence and number of dysplastic lineages , percentage of bone marrow blasts, cytogenetic abnormalities**

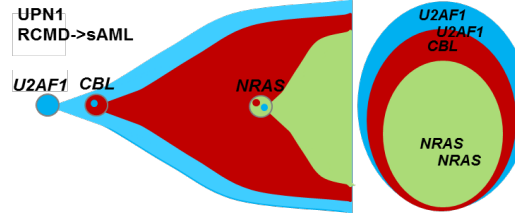
# MDS MOLECULAR PATHOGENESIS

## Somatic discovery

## Germ line discovery



## Clonal hierarchy



## Clinical applications

- Targeted deep NSG panels
- Diagnosis
  - Prognosis
  - MRD

## Somatic diversity

➤ mutations

➤ chromosomal defects

➤ Germline variants

➤ Epigenetic defects

**MOLECULAR DIVERSITY**

➤ Intra-tumor heterogeneity (clonal architecture)

Courtesy J Maciewiesky

**How to evaluate MDS clinically?**  
**how to determine prognosis?**

---



# New classification of cytogenetic risk

Very good	Good	Intermediate	Poor	Very poor
<p><u>Isolated:</u> del(11q) -Y</p>	<p>Normal <u>Isolated:</u> der(1;7) del(5q) del(12p) del(20q)</p>	<p><u>Isolated:</u> 7q- +8 i(17p) +21 +19 Other single</p>	<p><u>Isolated:</u> der(3)(q21q26) -7</p>	<p><u>Complex</u> &gt;3 anomalies</p>
	<p>Double with 5q-</p>	<p>Other double</p>	<p><u>Complex</u> 3 anomalies</p>	
			<p>Double with -7/7q-</p>	

# International prognostic scoring system (IPSS-R) variables and weighted scores

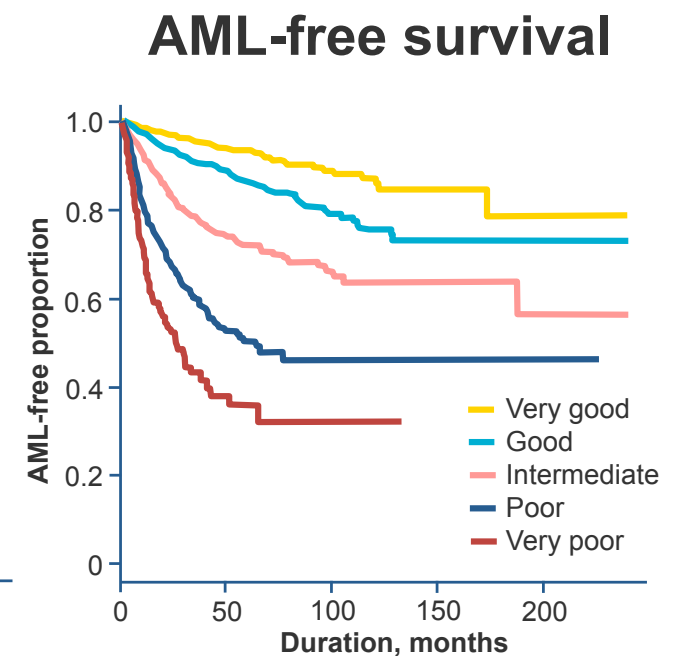
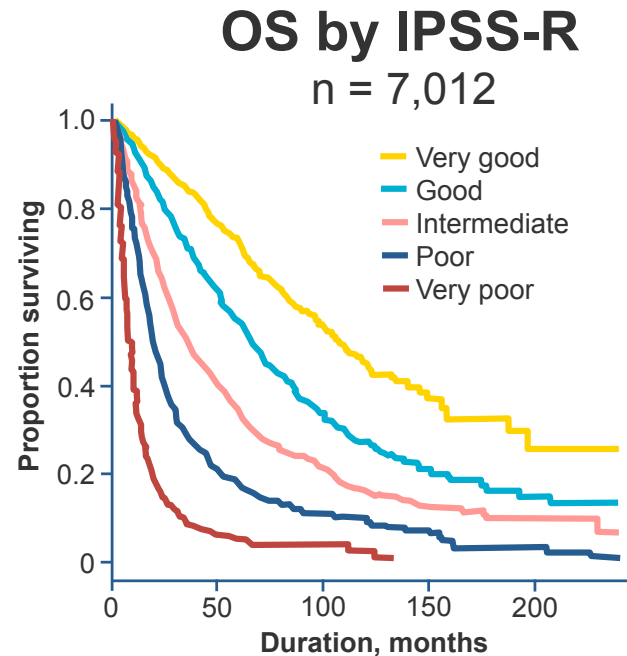
	<b>Very good</b>	<b>Good</b>	<b>Intermediate</b>	<b>Poor</b>	<b>Very poor</b>
<b>Cytogenetics Score</b>	0	1	2	3	4
<b>BM blasts, % Score</b>	≤ 2 0	> 2–< 5 1	5–10 2	> 10 3	
<b>Hb, g/dL Score</b>	≥ 10 0	8–9.9 1	< 8 1.5		
<b>ANC, x 10<sup>9</sup>/L Score</b>	≥ 0.8 0	< 0.8 0.5			
<b>Platelets, x 10<sup>9</sup>/L Score</b>	≥ 100 0	50–99 0.5	< 50 1		

\* Regression analysis for survival and AML evolution.  
ANC, absolute neutrophil count; BM bone marrow.

# IPSS-R: prognostic scores and risk groups

\* Values for 70-year-old patient (for consideration of age: [age in years - 70] x 0.04, add result to sum of other variables). Age, PS, ferritin, and LDH were significant additive features for OS but not for AML transformation.

Risk category	Score
Very low	≤ 1.5
Low	> 1.5–3
Intermediate	> 3–4.5
High	> 4.5–6
Very high	> 6

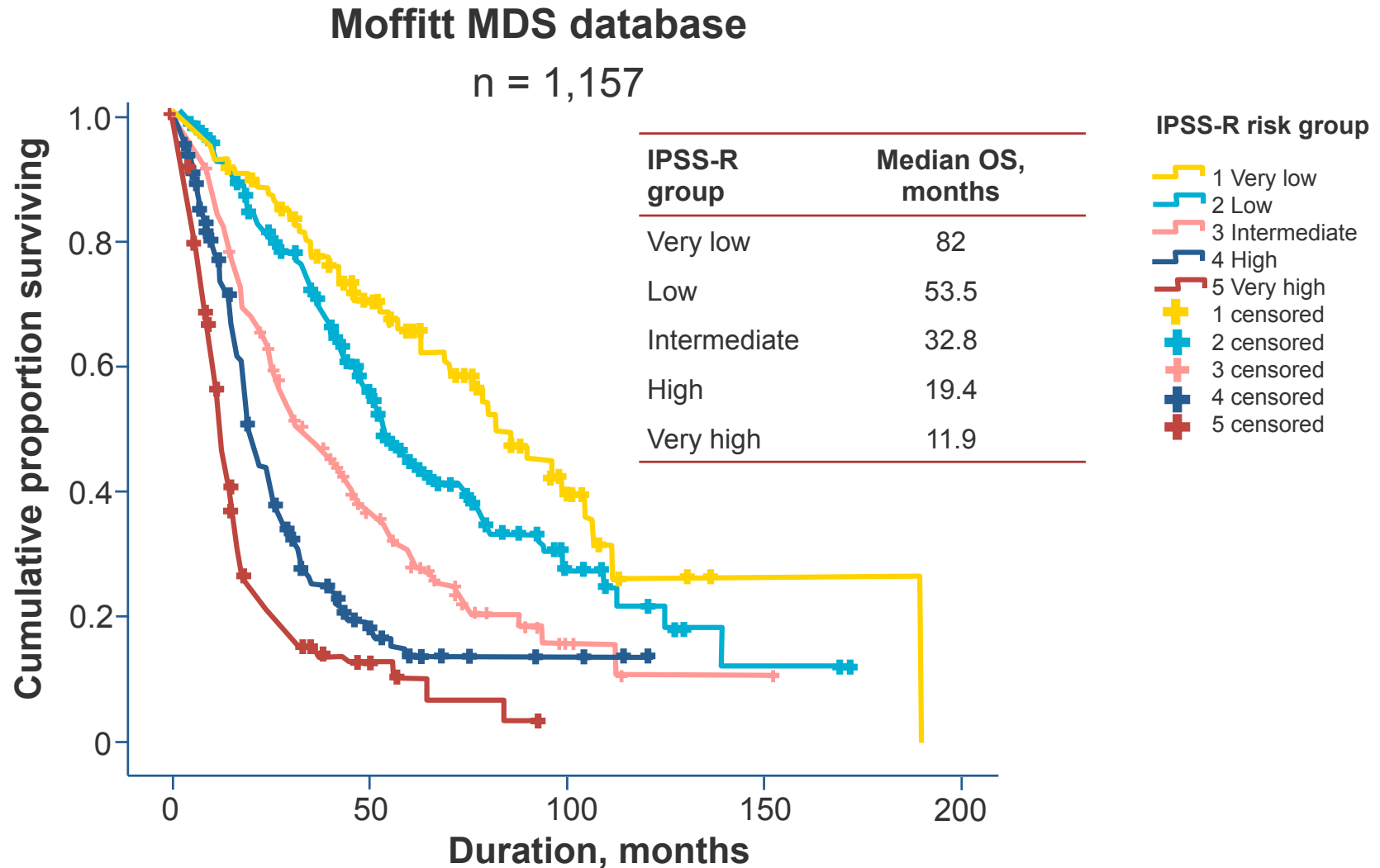


	Very low	Low	Intermediate	High	Very high
Median OS, years	8.8	5.3	3.0	1.6	0.8
AML 25%, years	NR	10.8	3.2	1.4	0.73

NR, not reached.

Greenberg PL, et al. Blood. 2012;120:2454-65 and updated data.

# Critical point for sequential therapy: Is the IPSS-R valid for treated patients?



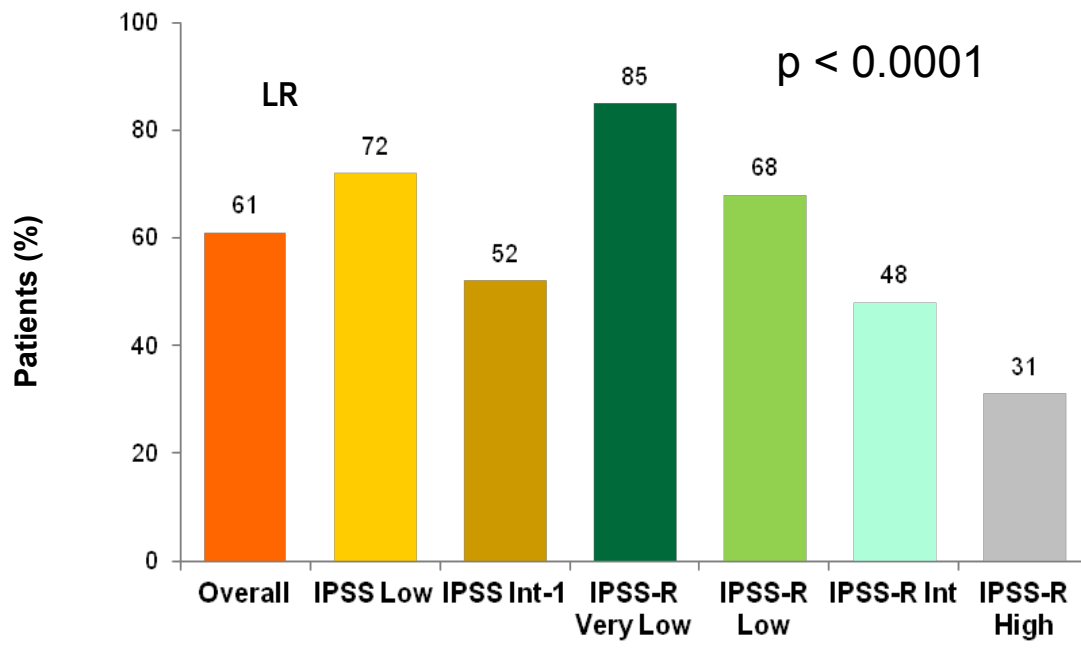
# IPSS-R, sEPO levels, ferritin but no specific mutation predict response to ESAs

Factor	Value	Score	Value	Score
Transfusion requirement*	<2 U/month	0	≥2 U/month	1
Serum EPO*	<500 U/L	0	≥500 U/L	1

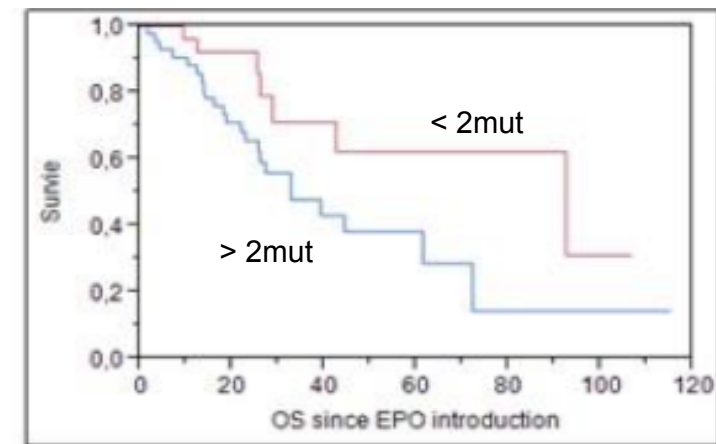
**serum Ferritin** associated with EPO response

Predicted response  
 Score = 0: 74%  
 Score = 1: 23%  
 Score = 2: 7%

Hellström-Lindberg E et al. Br J Haematol. 1997;99(2):344-51.



Number of mutations predicts OS after ESAs (79 pts-)



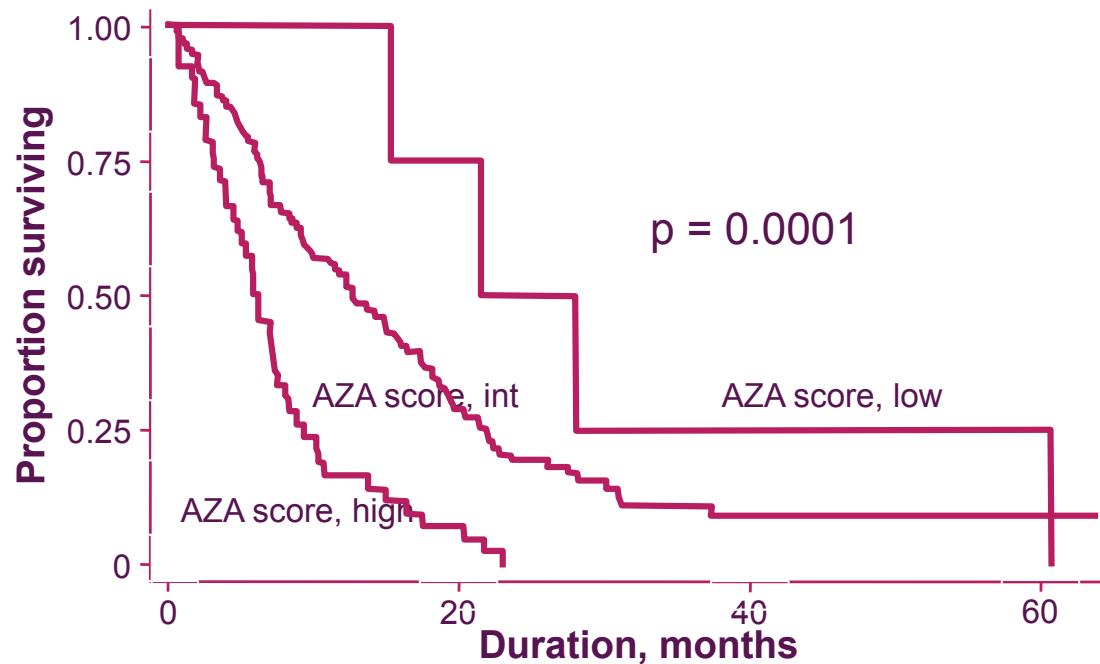
P=0.04



# Clinical and IPSS-R heterogeneity: OS in IPSS-R very high-risk group according to French AZA scoring system

## IPSS-R very high-risk MDS

## French AZA scoring system



Risk factor	Score
ECOG performance status $\geq 2$	1
Intermediate-risk cytogenetics	1
Poor-risk cytogenetics	2
Transfusion dependence $\geq 4$ U/8 wks	1
Peripheral blood blasts present	1

Ades L, et al. Blood. 2012;120:abstract 422 and data presented at ASH 2012.

**Is IPSS-R enough?**

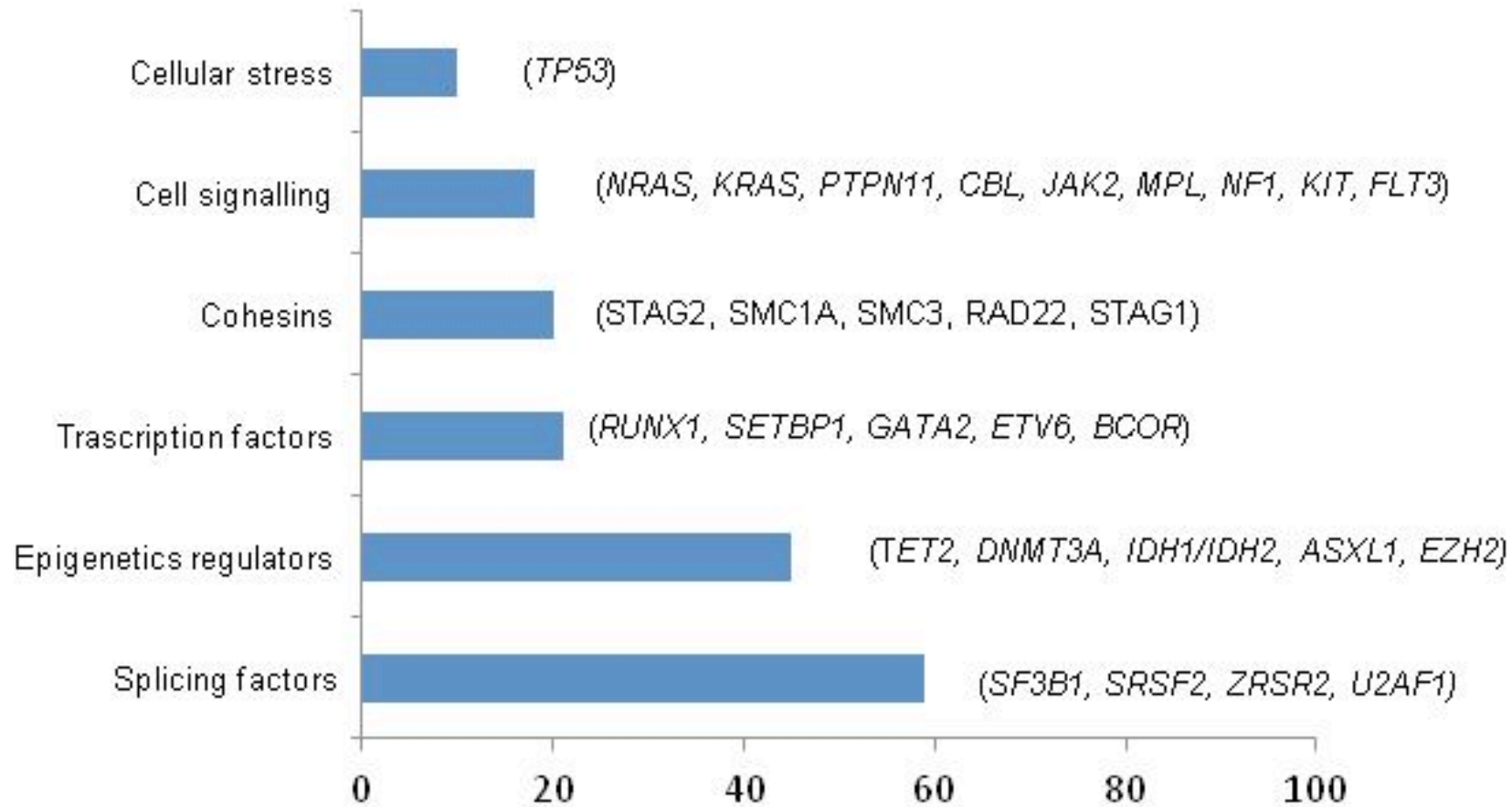
**Molecular variables:  
mutations and DNA methylation**

---

# **Molecular variables: somatic mutations**

- **IPSS-R does not consider somatic mutations**
  - **Somatic mutations are present in nearly 90% of MDS**
  - **Several mutated genes have prognostic significance independent of the IPSS-R**
  - **How to weigh prognostic mutations in clinical practice remains unclear**
-

# Recurrent somatic mutations are found in > 80% of MDS cases



# **Somatic mutations in MDS:**

**prognostic value**

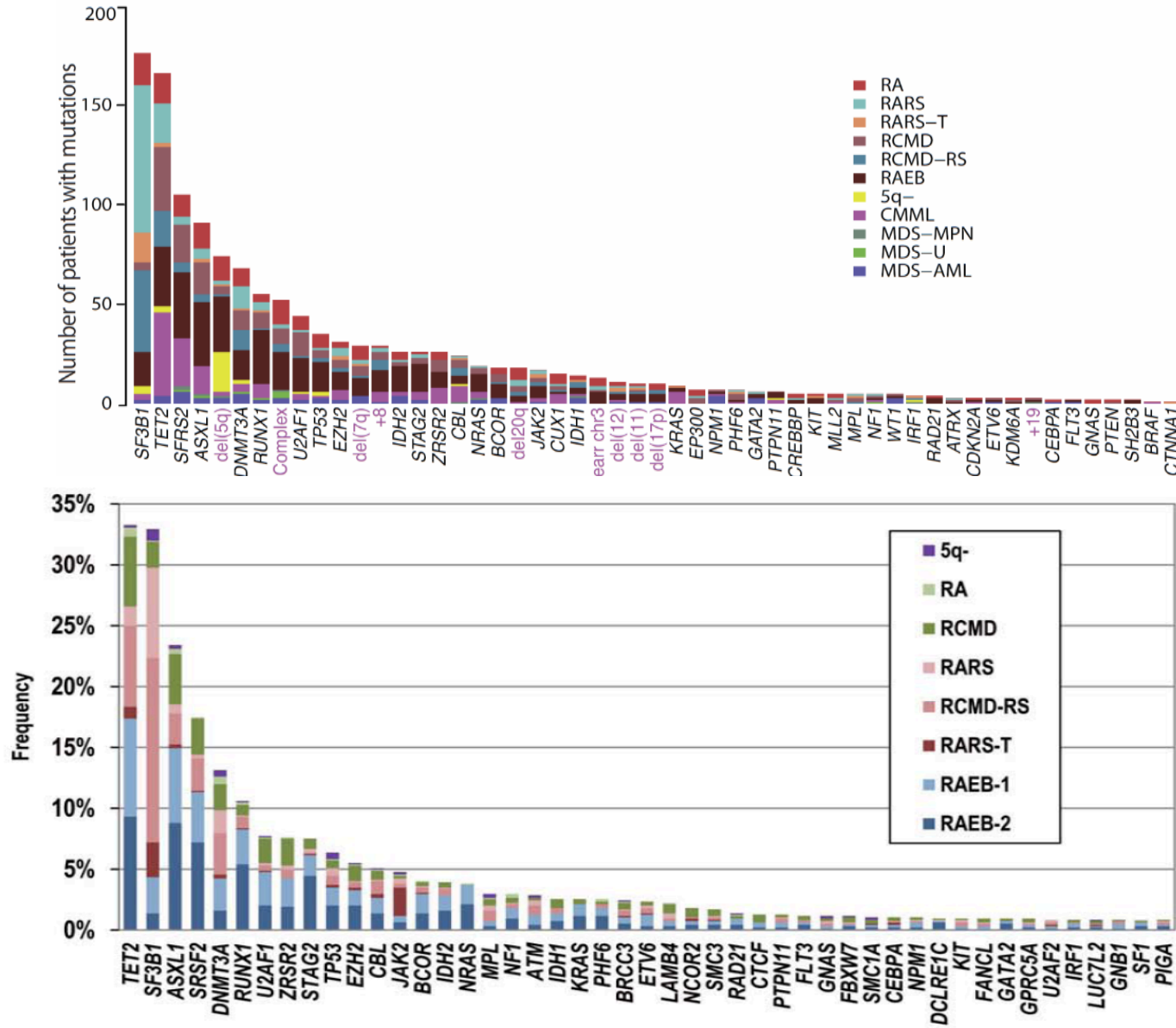
**possible therapeutic target**

**confirm diagnosis (?)**

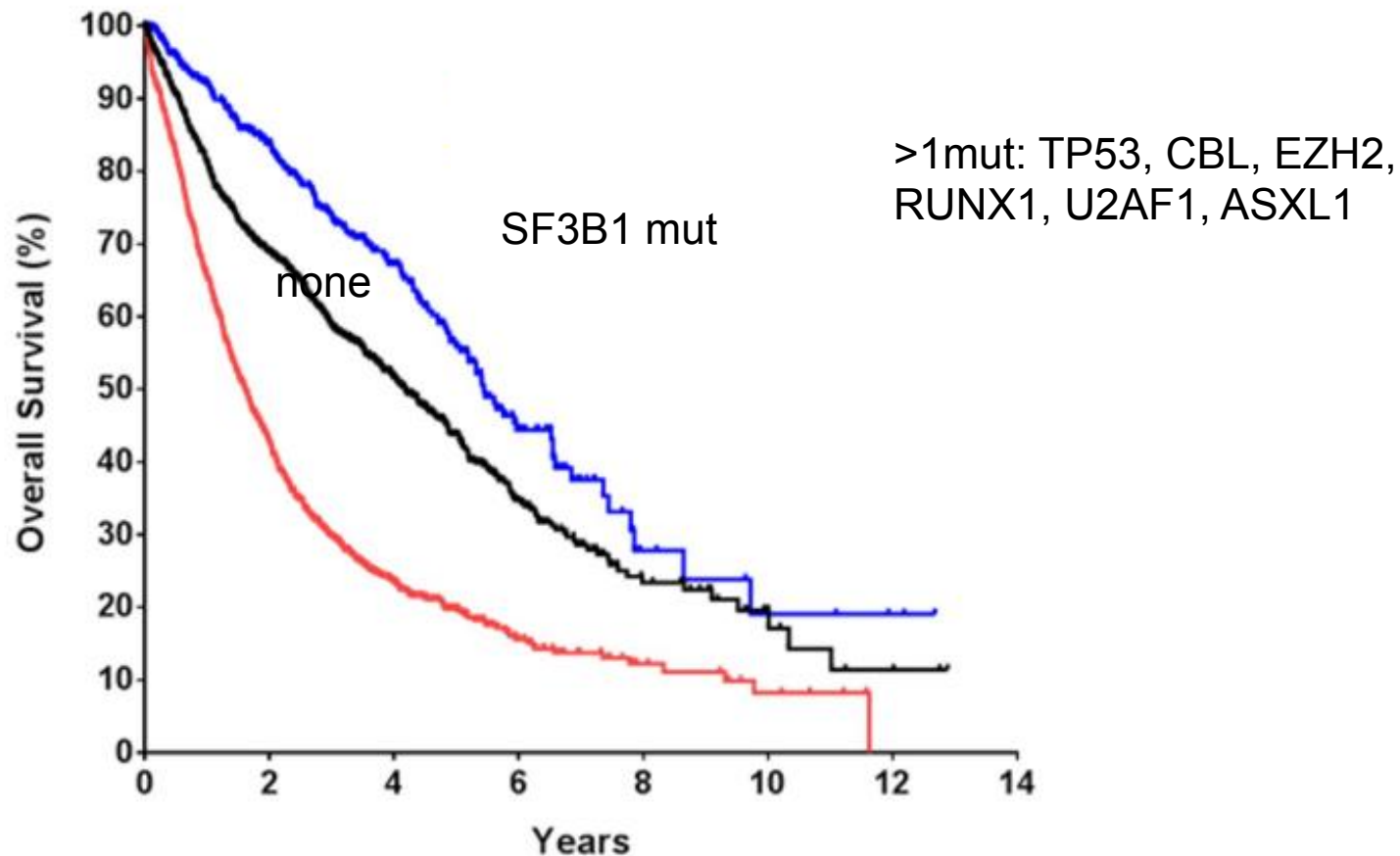
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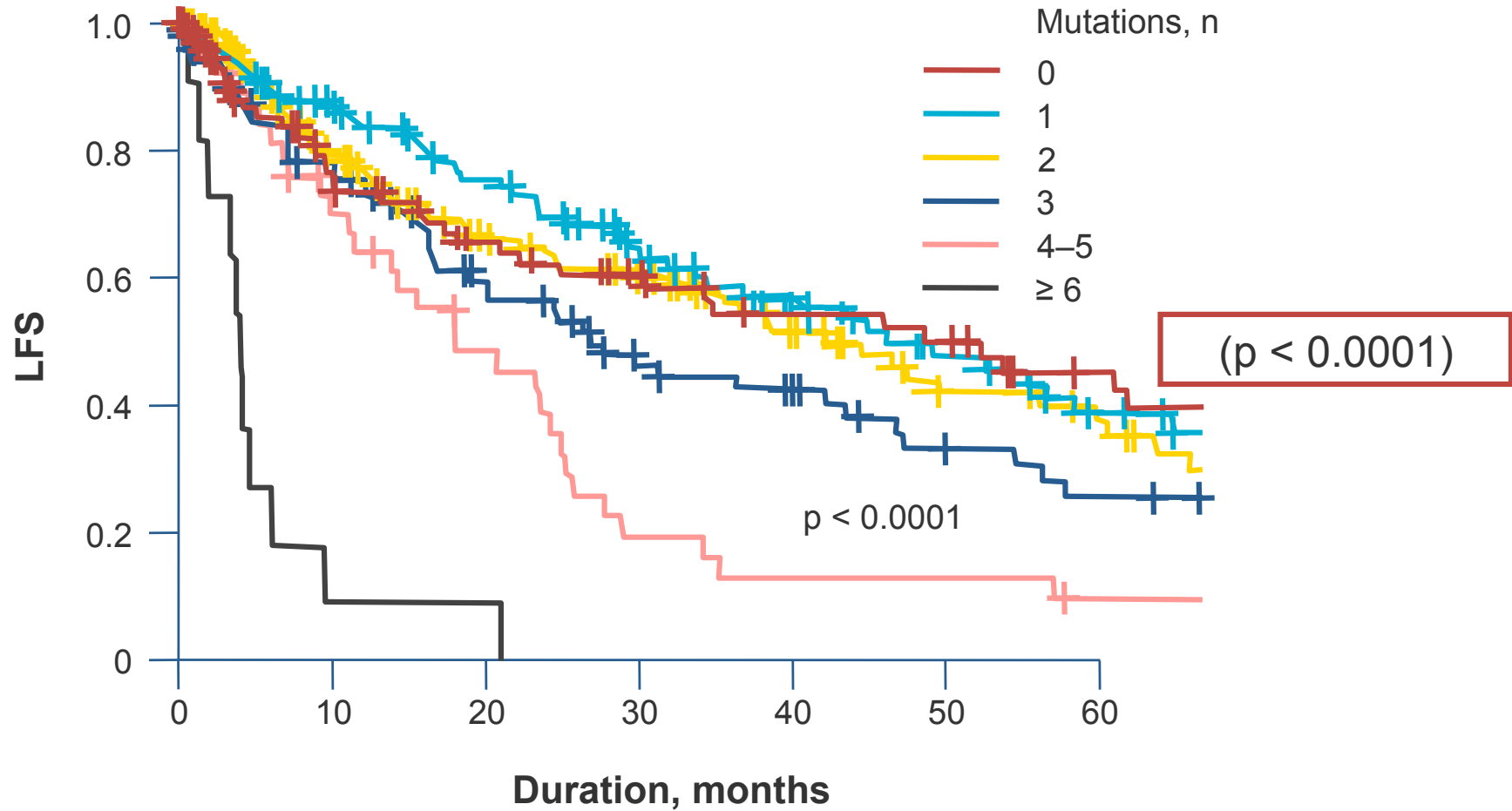
# Somatic Mutations in MDS



# Somatic gene mutations in MDS are independent prognostic indicators

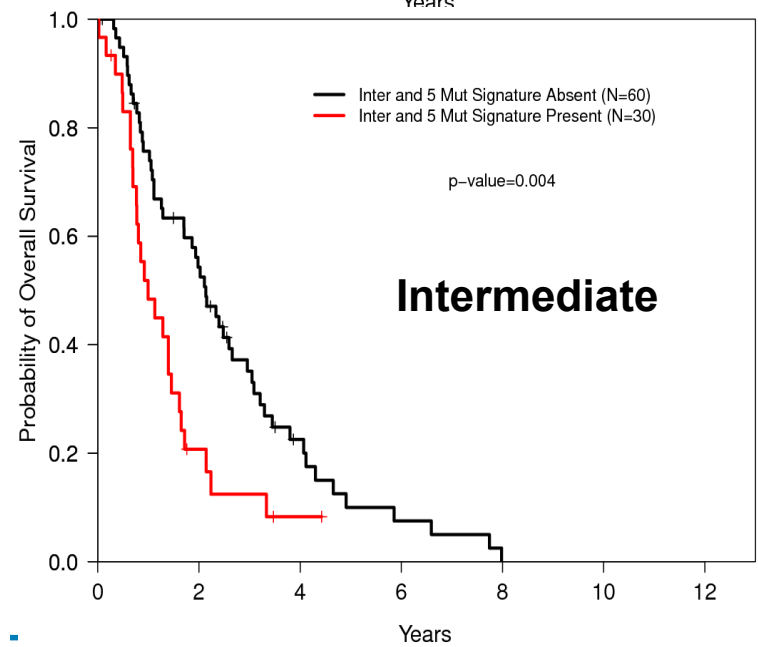
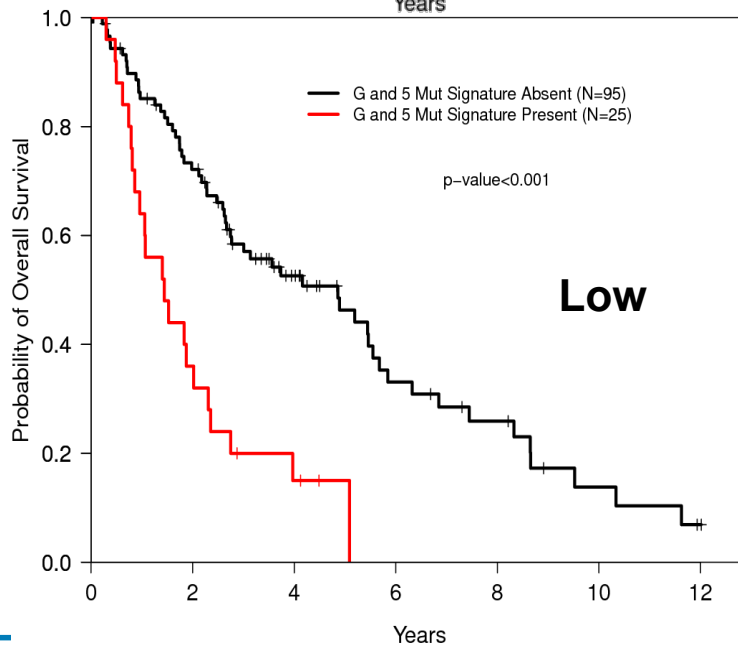
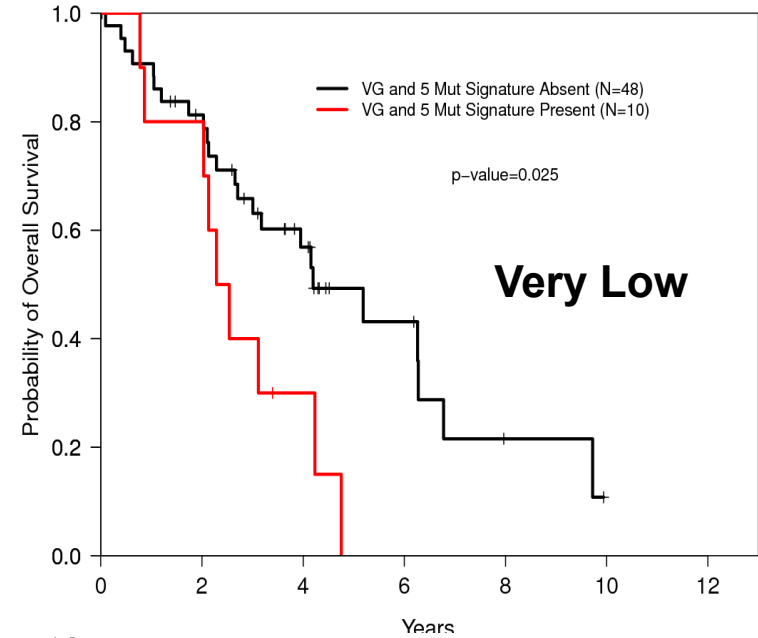
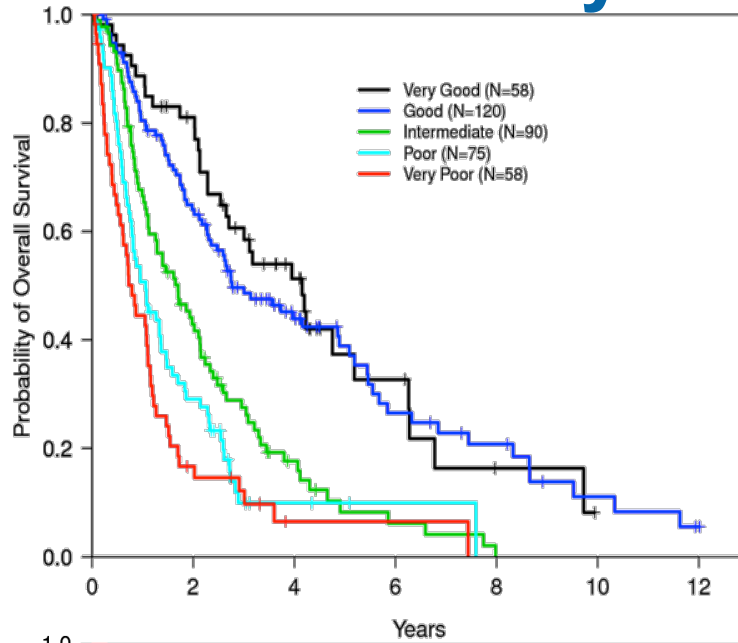


# Leukaemia-free survival in MDS inversely correlates with number of driver mutations



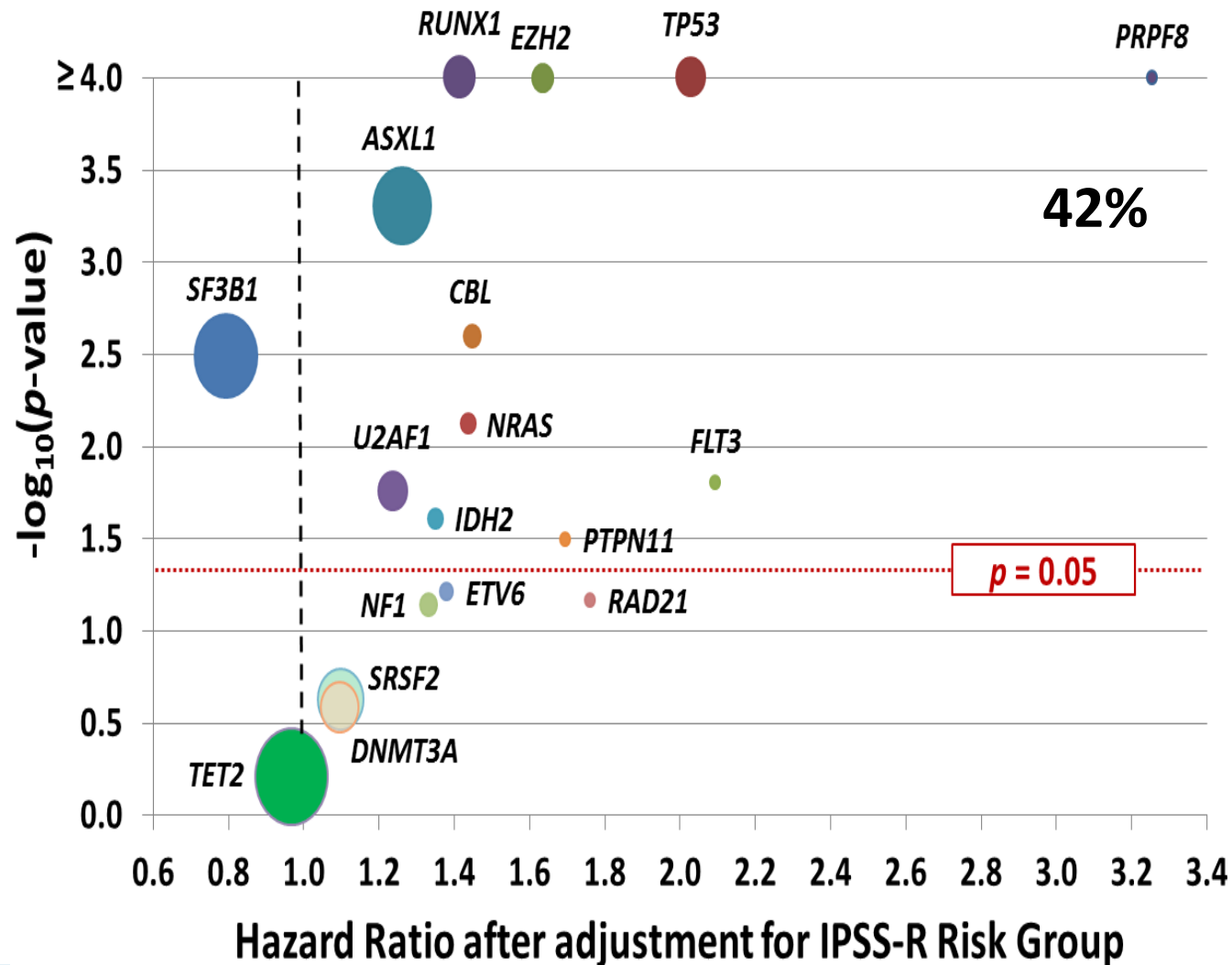
# Impact of Mutations by IPSS-R Group

- TP53
- ETV6
- ASXL1
- EZH2
- RUNX1



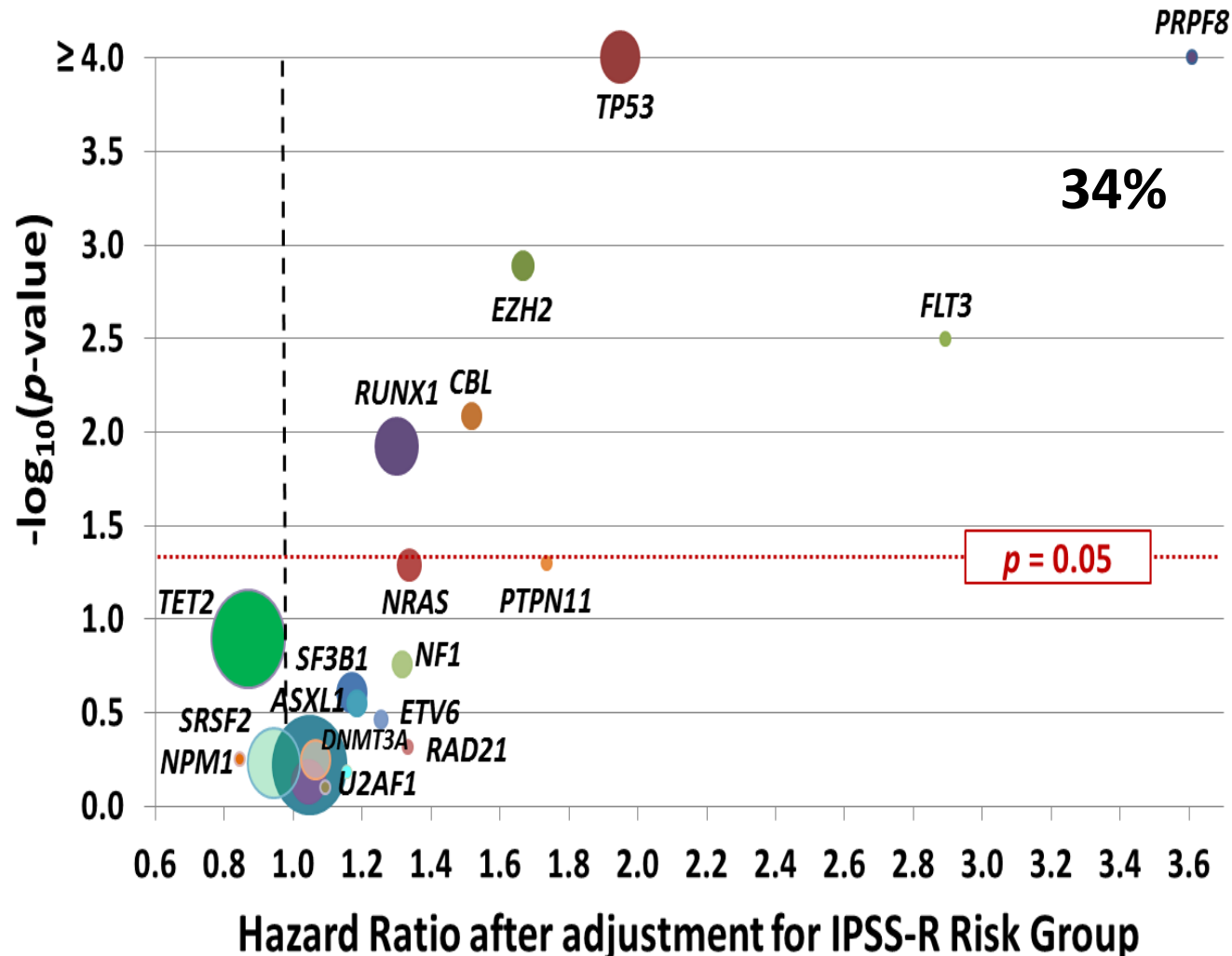
• Bejar R, et al. N Engl J Med. 2011;364:2496-506.

# IPSS-R Adjusted Hazard Ratios for Mutated Genes

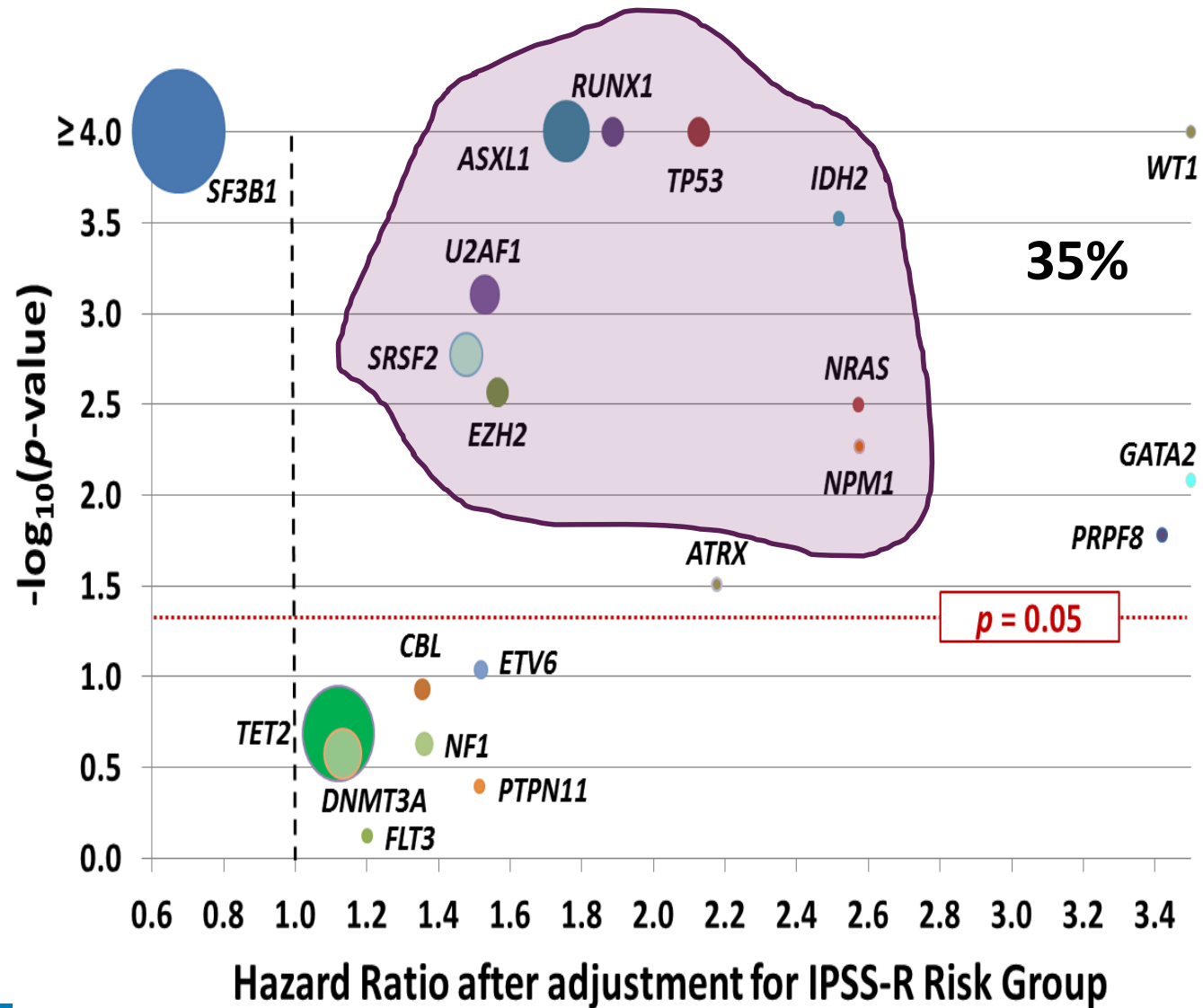




# Division by Blast Proportion (5-30%)

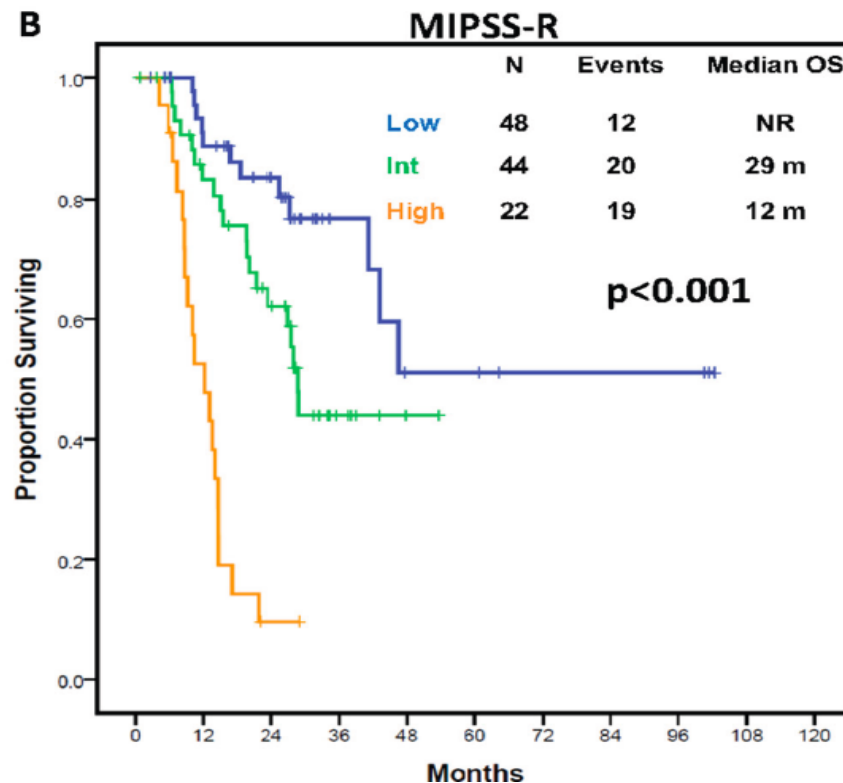
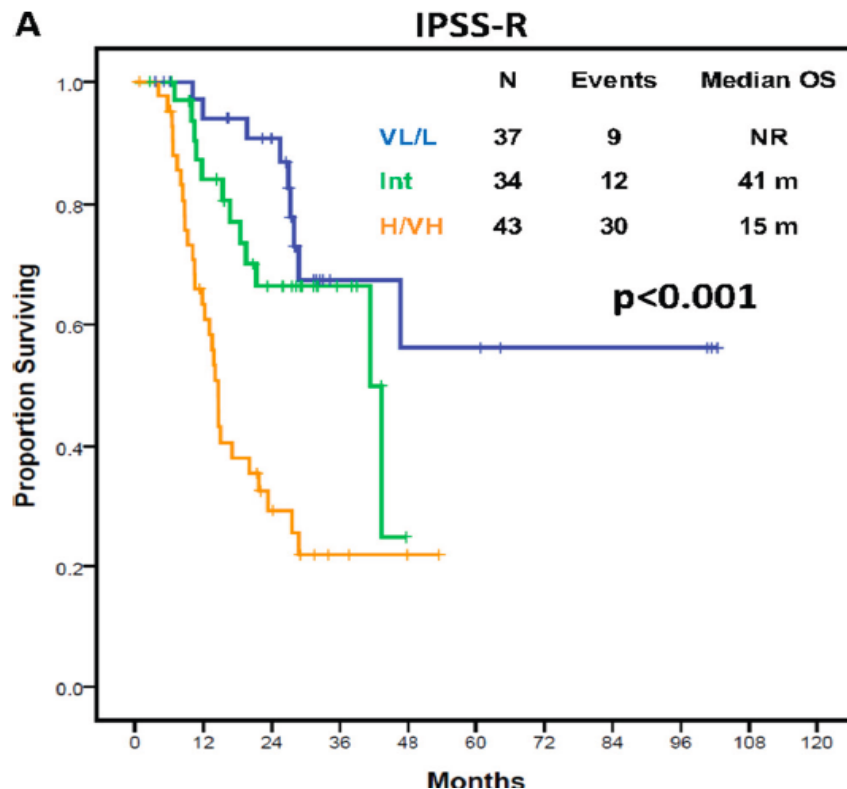


# Division by Blast Proportion (<5%)

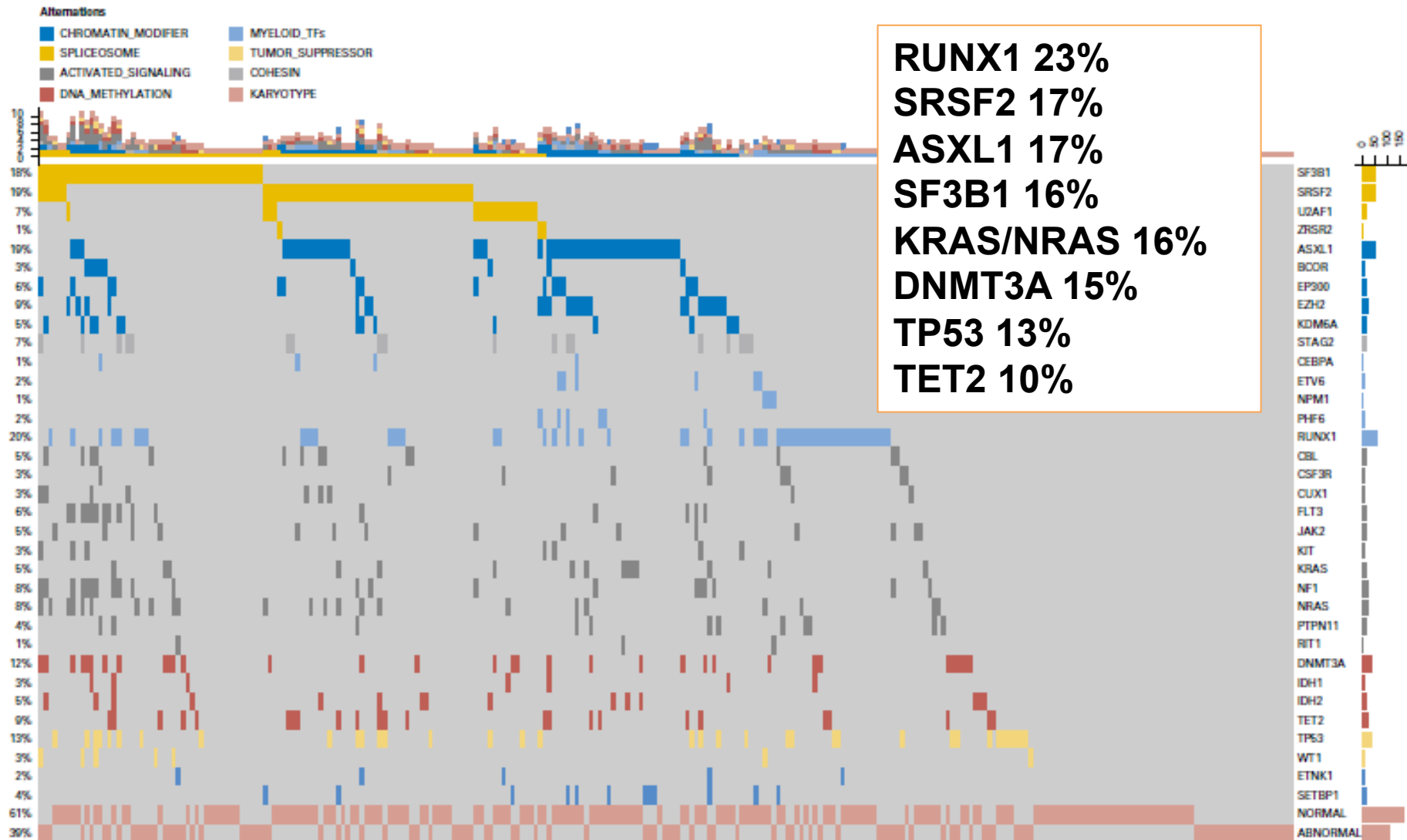


# IPSS-R integrated model with molecular variables (83 pts)

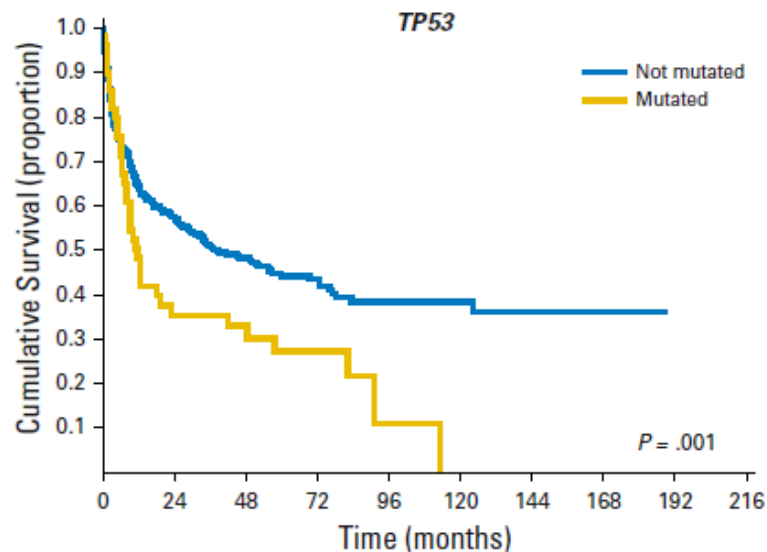
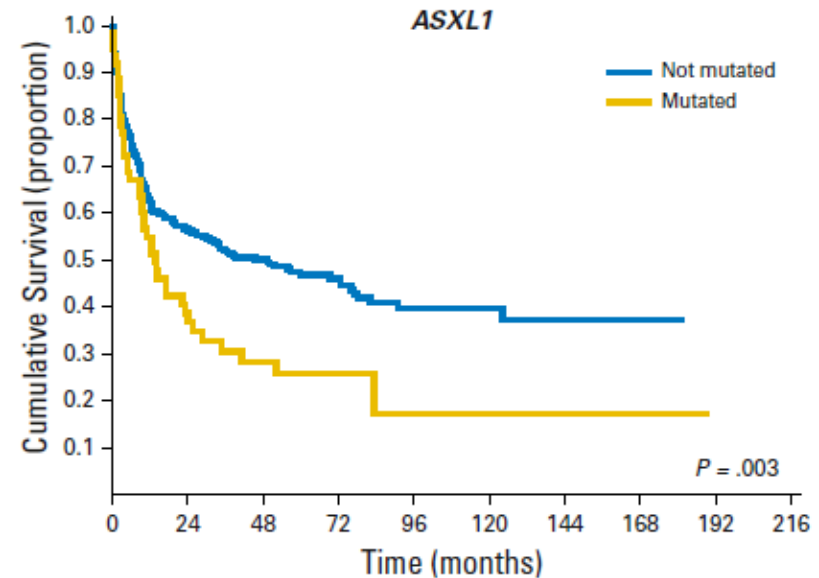
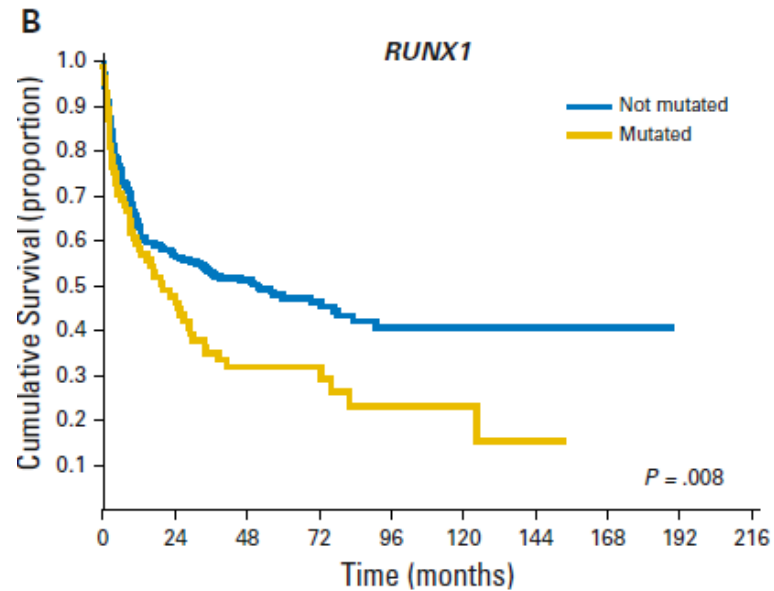
Variable	Hazard Ratio	95% CI	p value	Score
IPSS-R				
Intermediate	1.45	0.56–3.77	0.45	0.5
High/Very high	4.66	2.01–10.84	< 0.001	1.5
TP53	3.12	1.3–7.49	0.011	1
Mutations 3 or more	2.51	1.32–4.76	0.005	1



# Mutation patterns observed in MDS treated with allo-HSCT



# Relationship between type of oncogenic mutations and overall survival of MDS receiving allo-HSCT

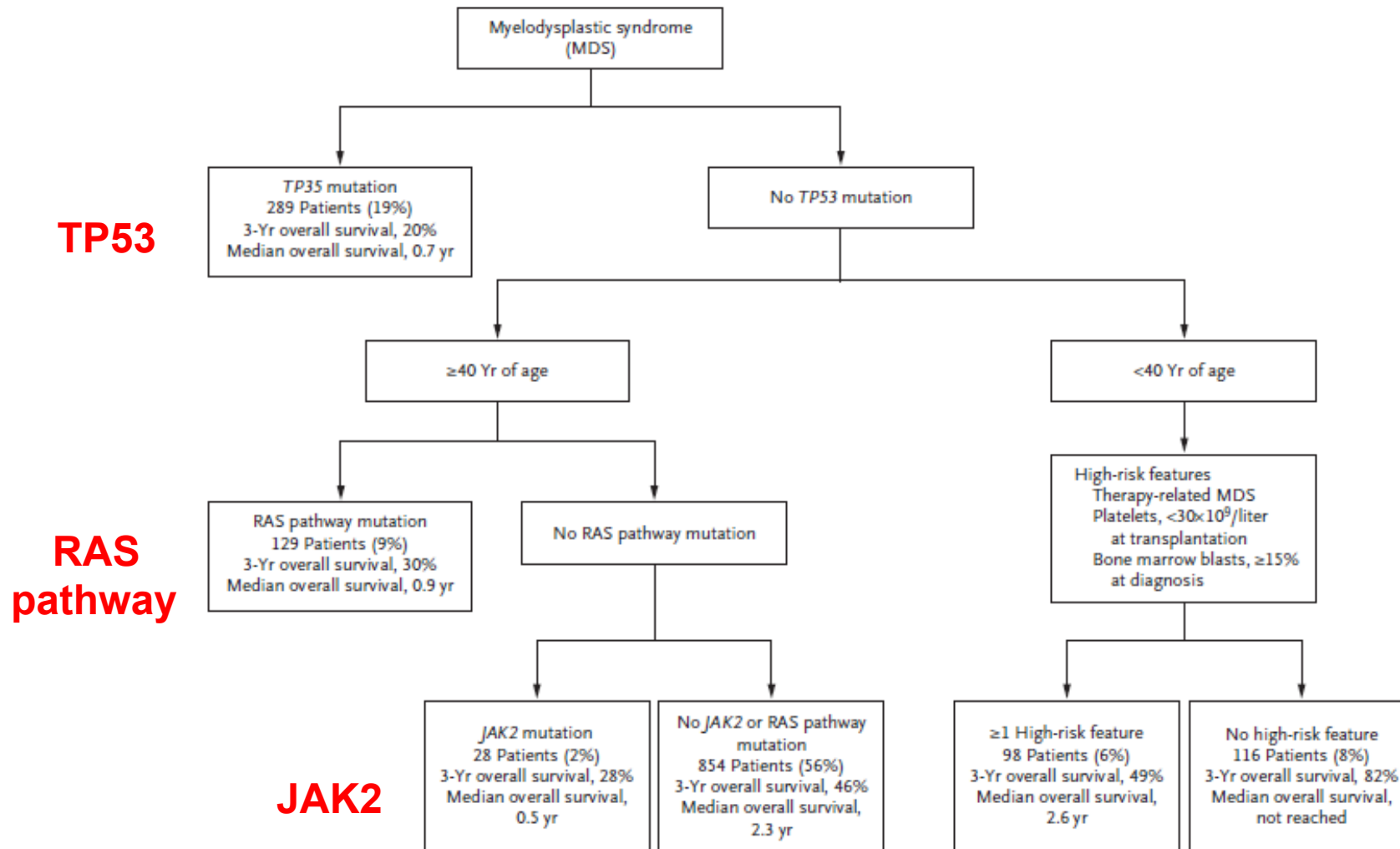


Multivariable analysis				
MDS patients	Probability of relapse		Overall Survival	
Variable	HR	P	HR	P
ASXL1	1.89	.003	1.72	.008
RUNX1	1.67	.02	1.59	.035
TP53	1.90	.019	1.82	.022

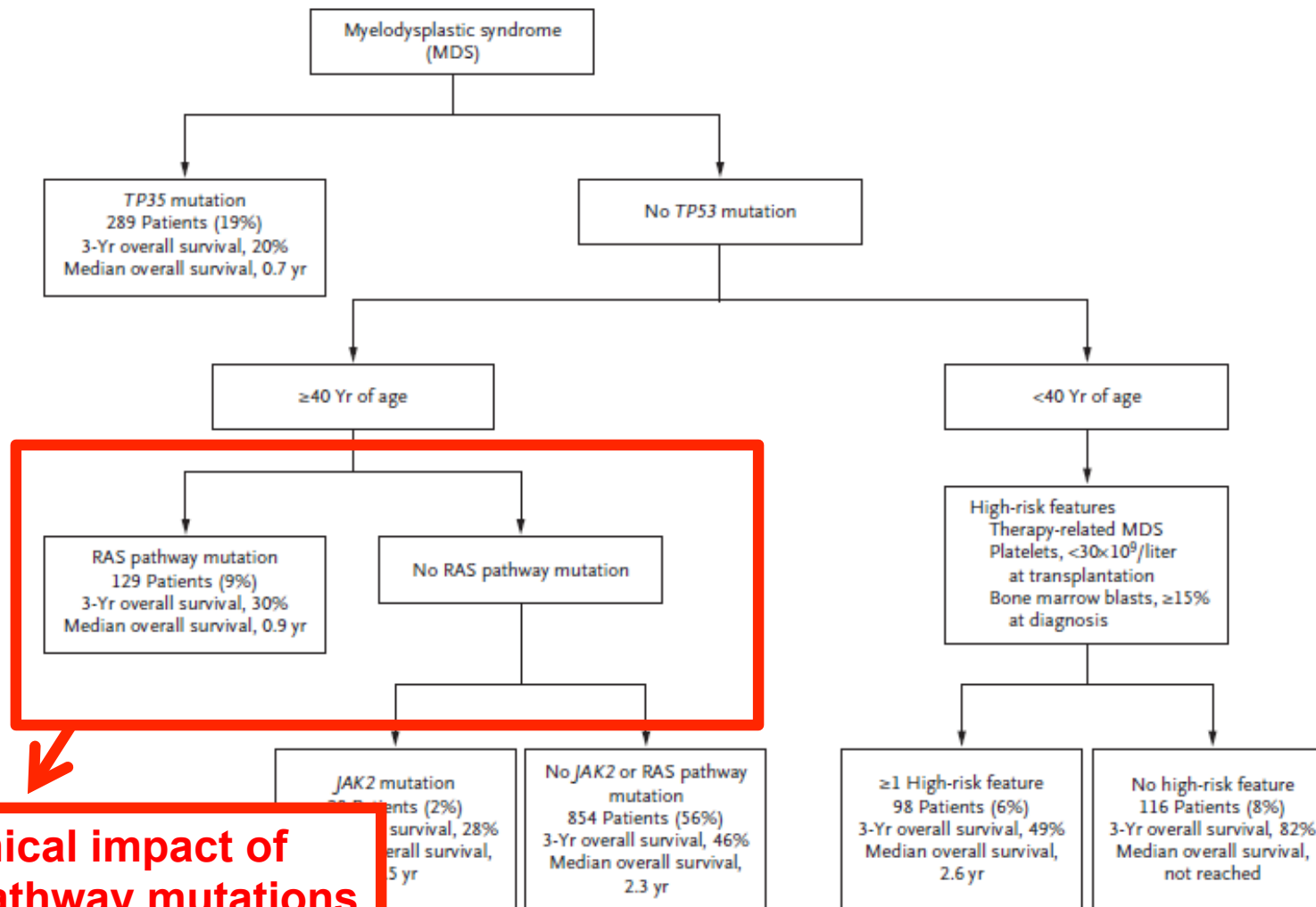


# Prognostic Mutations in Myelodysplastic Syndrome patients treated with HSCT.

## TP53 mutations are the strongest predictor



# Prognostic Mutations in Myelodysplastic Syndrome patients treated with HSCT

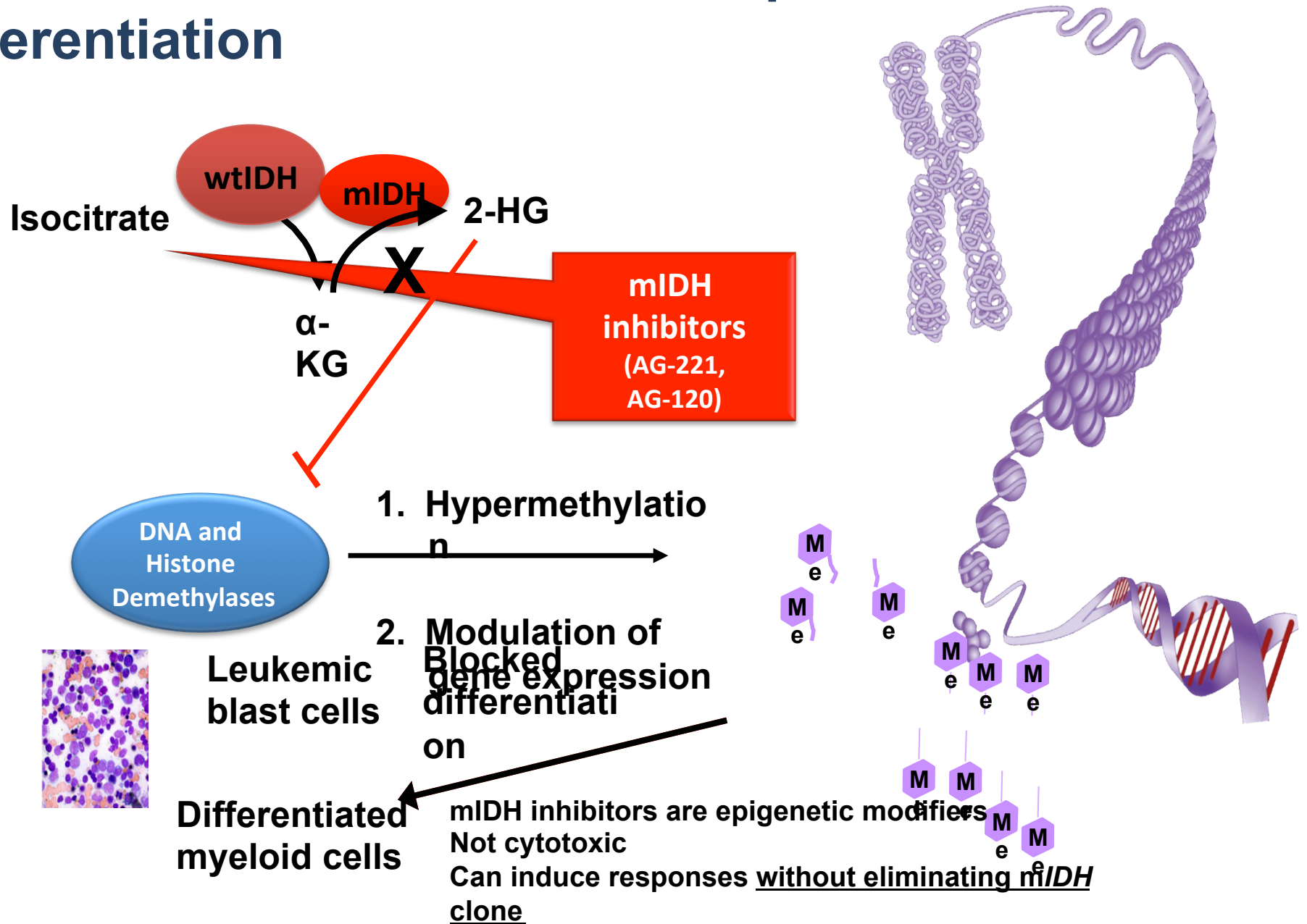


**Clinical impact of RAS pathway mutations limited to MDS/MPN**

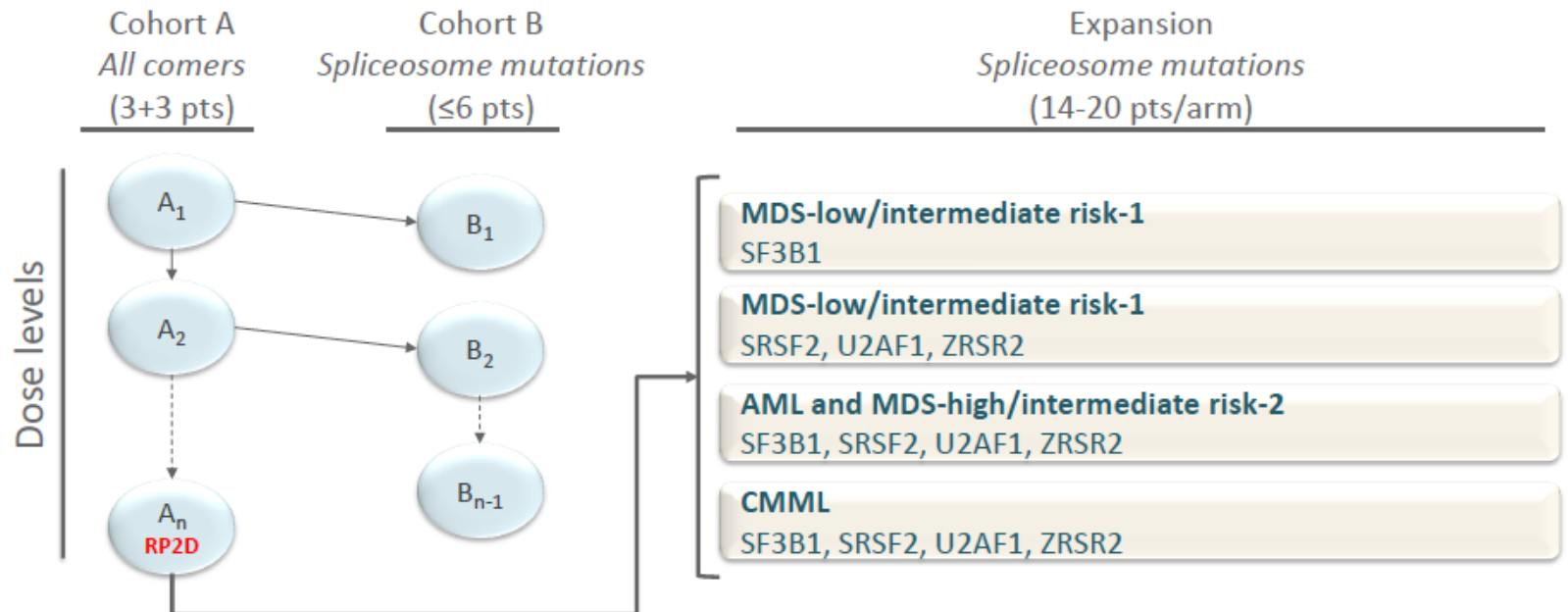
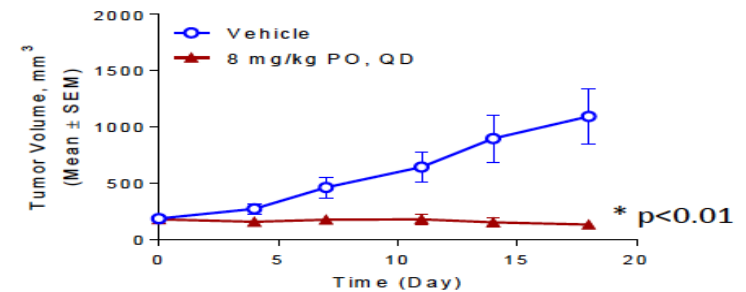
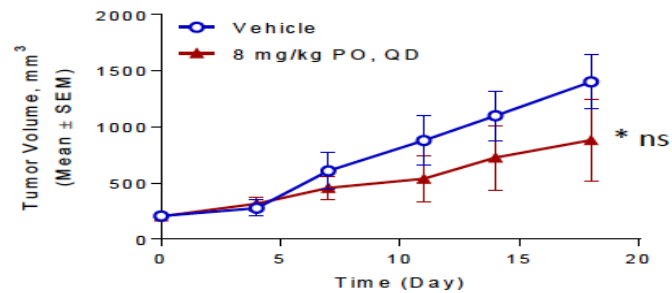
# **Somatic mutations in MDS: possible therapeutic target**



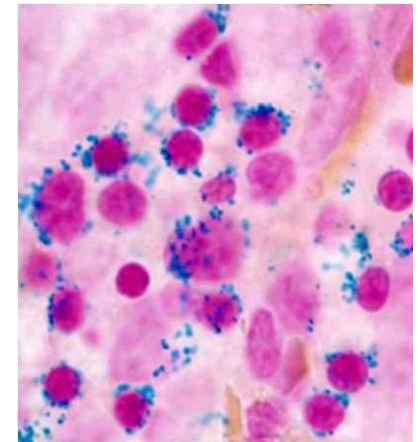
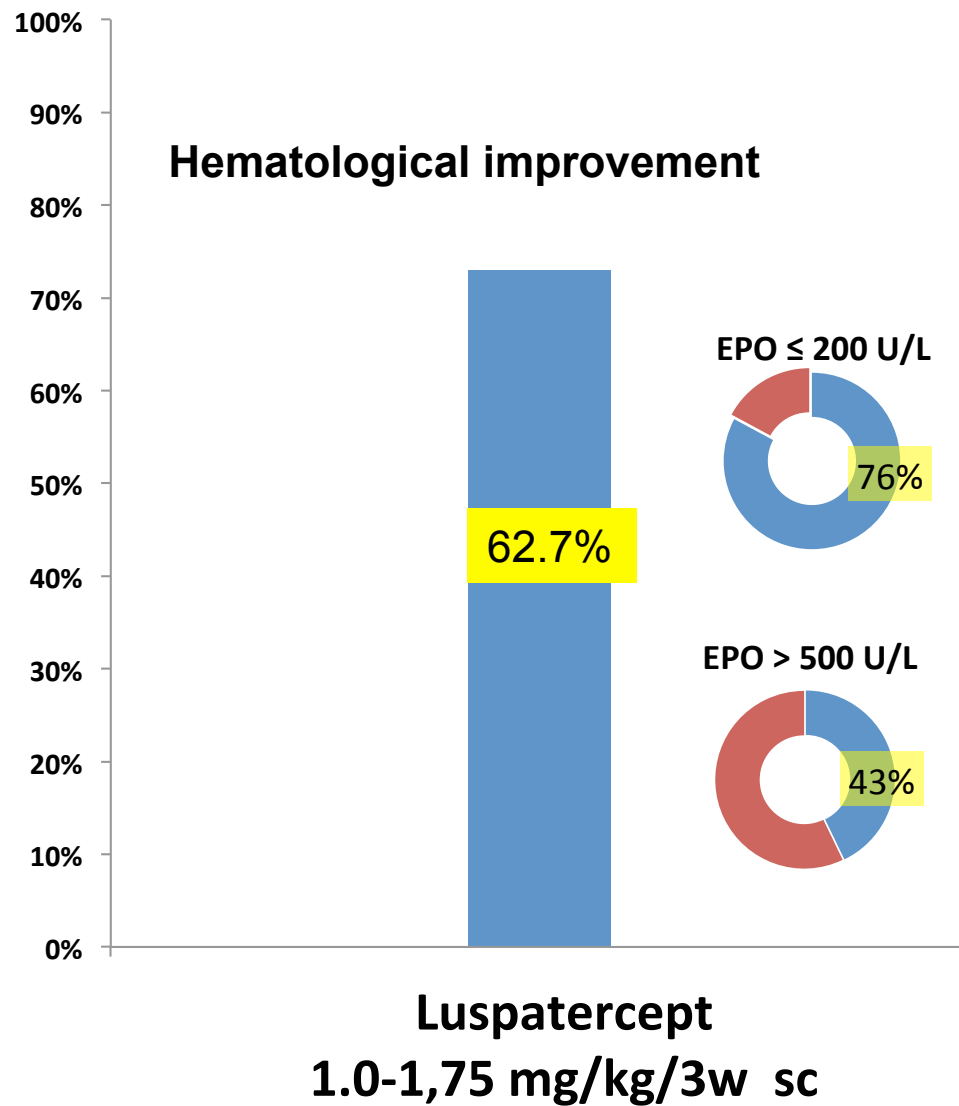
# Mutant IDH1/2 (5-10% in MDS) inhibitors reduce production of 2-HG and promote cellular differentiation



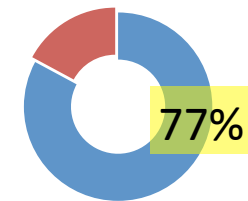
# Preclinical and clinical studies of oral H3B-8800 for MDS carrying mutations in spliceosome genes



# SF3B1 mutation is a possible predictor of response to TGFbeta-pathway inhibition in LR-MDS pts



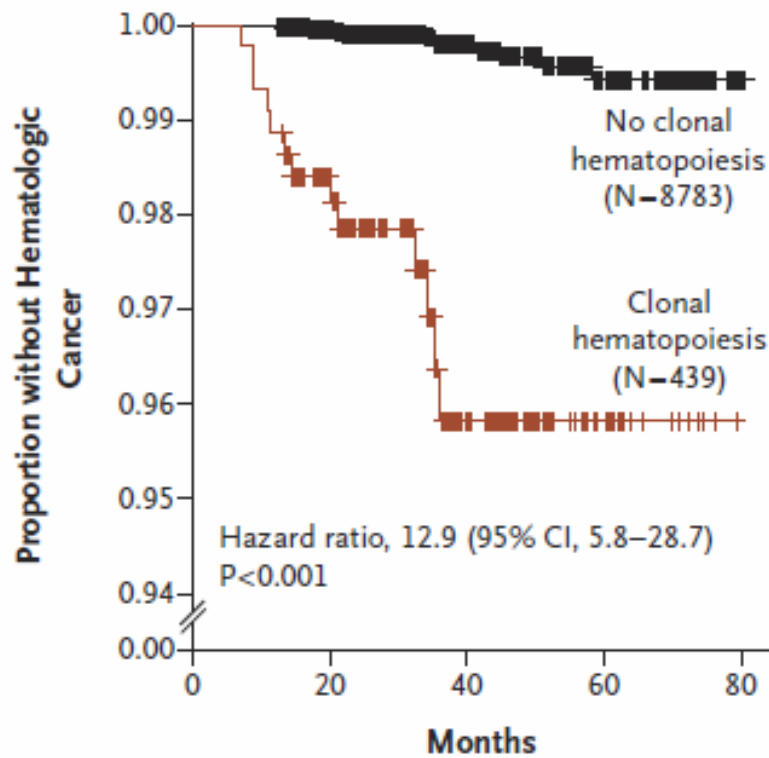
**SF3B1 mut**



ORIGINAL ARTICLE

## Clonal Hematopoiesis and Blood-Cancer Risk Inferred from Blood DNA Sequence

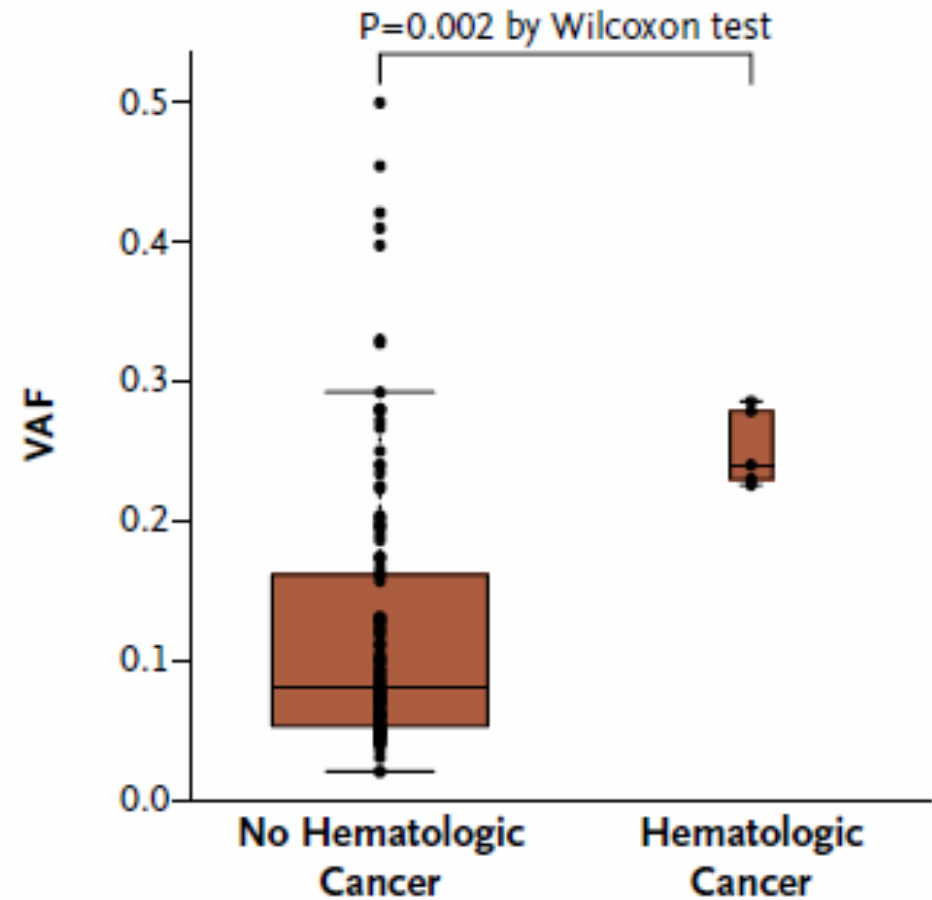
Giulio Genovese, Ph.D., Anna K. Kähler, Ph.D., Robert E. Handsaker, B.S.,



ORIGINAL ARTICLE

## Age-Related Clonal Hematopoiesis Associated with Adverse Outcomes

Siddhartha Jaiswal, M.D., Ph.D., Pierre Fontanillas, Ph.D., Jason Flannick, Ph.D.,



**Inherited predisposition to  
myelodysplastic syndromes and  
other haematological malignancies**

---



# WHO 2016 classification of myeloid neoplasms with germ line predisposition

**Myeloid neoplasms with germ line predisposition without a preexisting disorder or organ dysfunction**

AML with germ line *CEBPA* mutation

Myeloid neoplasms with germ line *DDX41* mutation\*

**Myeloid neoplasms with germ line predisposition and preexisting platelet disorders**

Myeloid neoplasms with germ line *RUNX1* mutation\*

Myeloid neoplasms with germ line *ANKRD26* mutation\*

Myeloid neoplasms with germ line *ETV6* mutation\*

**Myeloid neoplasms with germ line predisposition and other organ dysfunction**

Myeloid neoplasms with germ line *GATA2* mutation

Myeloid neoplasms associated with BM failure syndromes

Myeloid neoplasms associated with telomere biology disorders

JMML associated with neurofibromatosis, Noonan syndrome or

Noonan syndrome-like disorders

Myeloid neoplasms associated with Down syndrome\*

---

\*Lymphoid neoplasms also reported.

**Inherited predisposition to  
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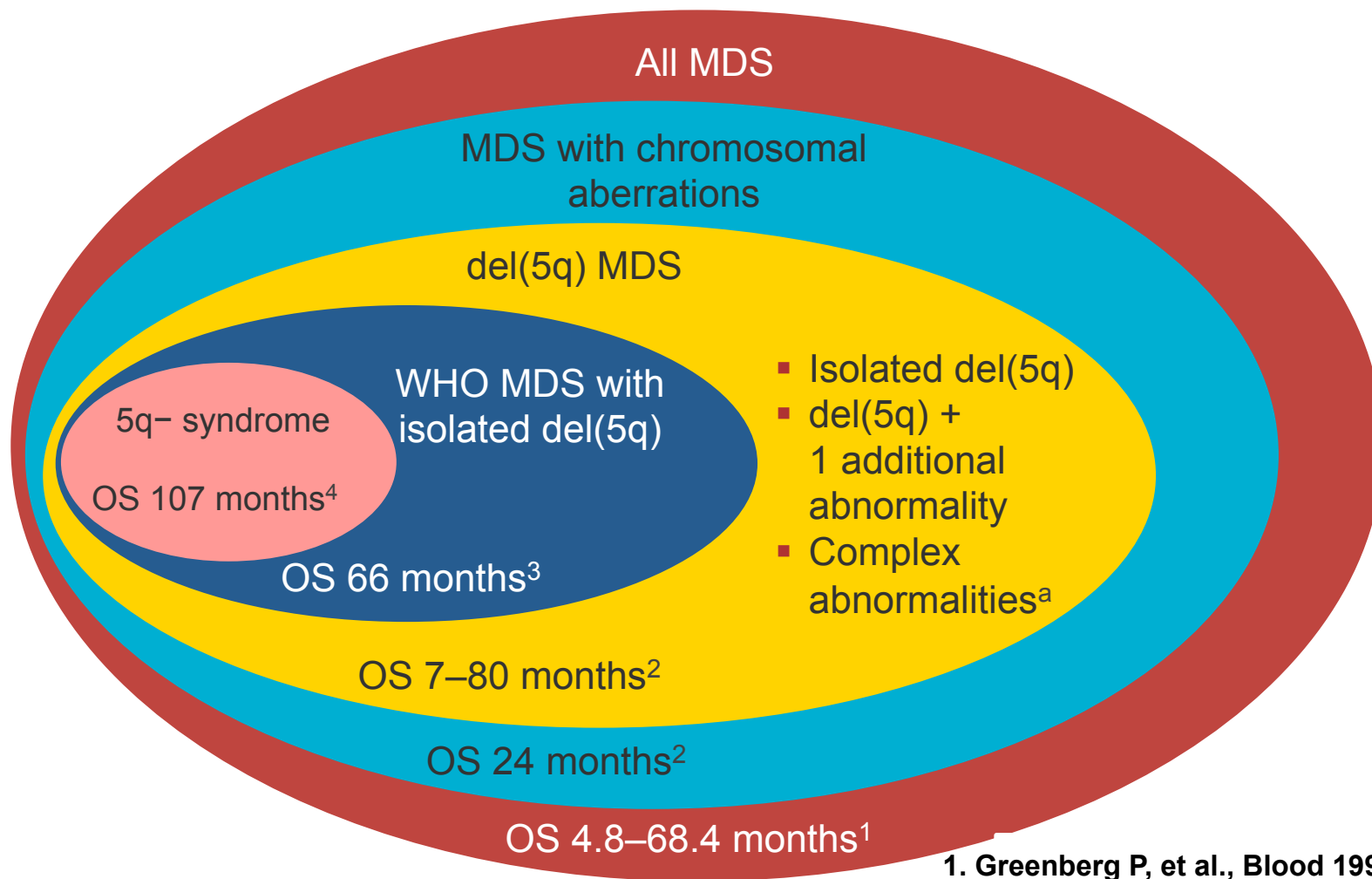
Myeloid neoplasms associated with Down syndrome\*

---

\*Lymphoid neoplasms also reported.

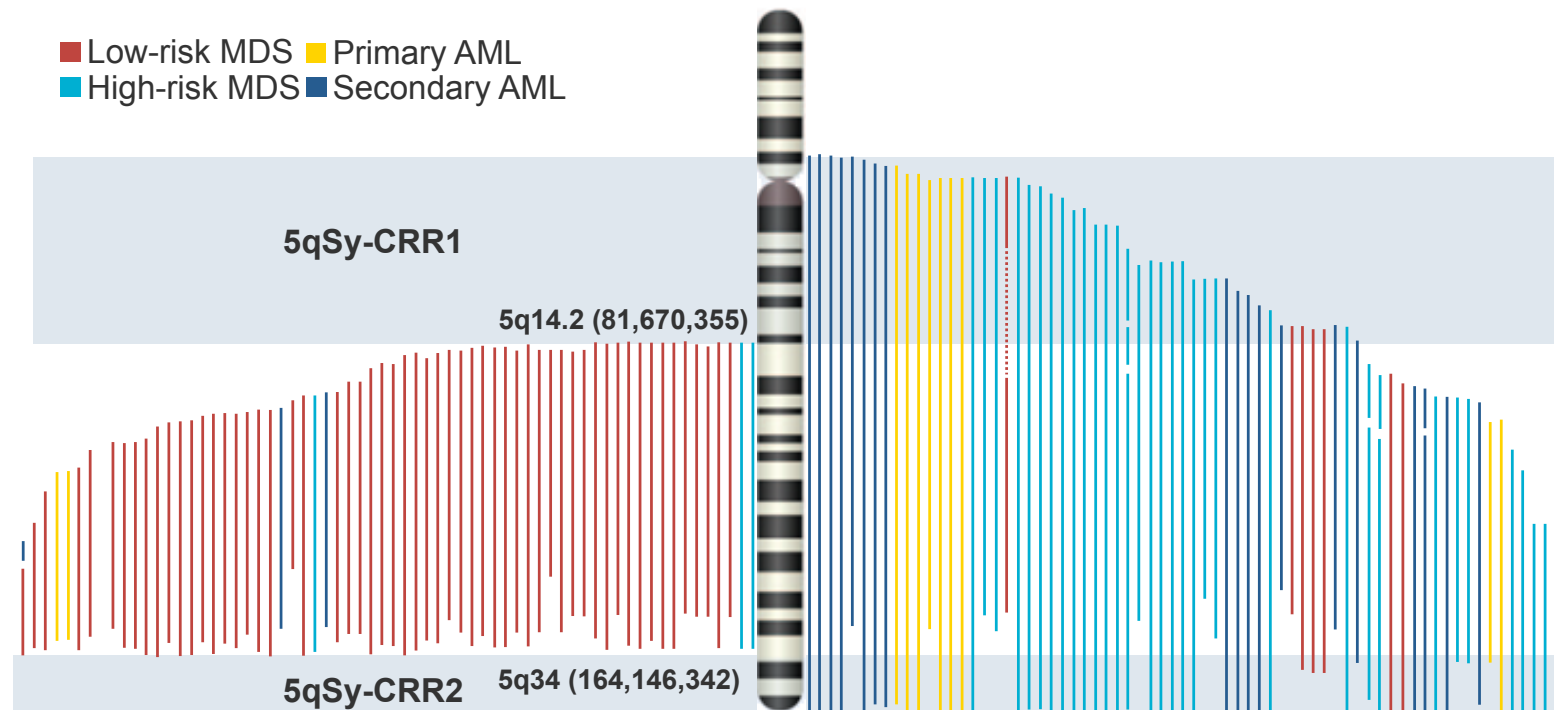
- **Patient with de novo MDS at a younger age (< 50yrs)**
- **Patient with MDS and familial history of AML**
- **Patient with MDS and peculiar extra hematological symptoms:**
  1. **Perform an accurate family and personal history**
  2. **Search for signs and symptoms of congenital syndromes**
  3. **Perform mutational analysis for genes involved in inherited predisposition**
  4. **Select accurately HSCT donor (completely avoid related matched donor?)** Slow engraftment, donor derived leukemia
  5. **Familial genetic counseling ( anticipation of onset through generations)**

# del(5q) MDS is not always 5q- syndrome



1. Greenberg P, et al., Blood 1997;89:2079–88
2. Haase D, et al., Blood 2007;110:4385–95
3. Mallo M, et al., Leukemia 2011;25:110–2
4. Giagounidis A, et al., Hematology 2004;9:271–7

# CRR vs CDRs in del(5q) MDS: impact on prognosis



- In patients who had intact CRRs vs those who had lesions that occurred in the CRRs
  - OS was longer (32 vs 14 months;  $p = 0.04$ )
  - baseline platelet count was higher ( $171$  vs  $84 \times 10^5/\mu\text{L}$ ;  $p \leq 0.001$ )
- Less AML progression occurred in patients with smaller lesions than in those with lesions involving the distal ends of 5q ( $p = 0.002$ )

# TP53 mutations in MDS and their impact on patient outcomes

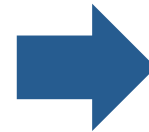
Retrospective analysis of the incidence and prognostic impact of TP53 mutations in patients with del(5q) by using next-generation sequencing

## Patient characteristics (n = 318)

- Median age, years (range): **65 (17–72)**
- IPSS risk, n (%)
  - Low: **71 (24)**
  - Int-1: **101 (32)**
  - Int-2: **58 (18)**
  - High: **29 (9)**
- 40 patients (12%) received BM transplantation, intensive chemotherapy, azacitidine, or lenalidomide

Multivariate analysis:<sup>b</sup> TP53 mutational status was the strongest predictor for OS and PFS (p < 0.0001 for both)

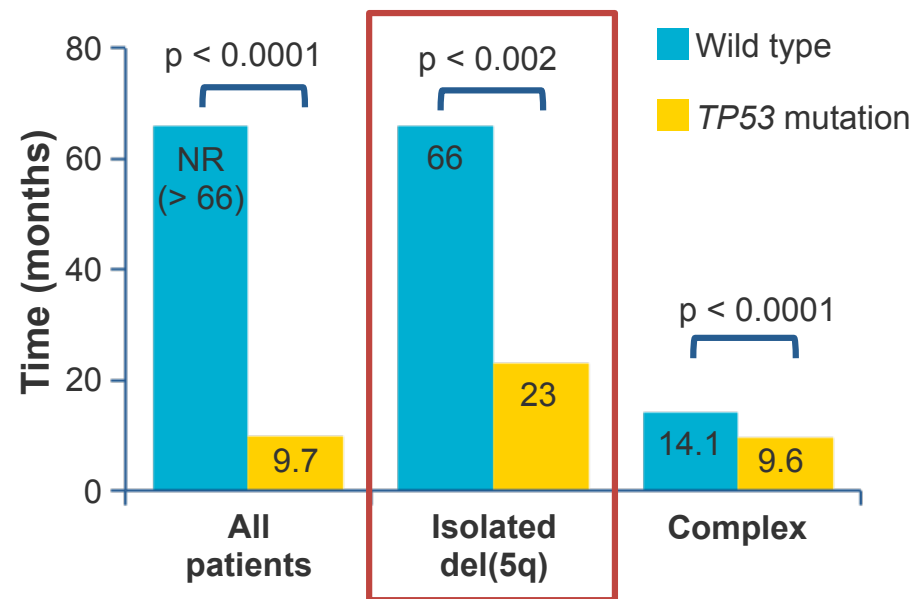
**TP53 mutations are an independent prognostic marker in patients with del(5q) MDS**



## TP53 mutational status

- Patients with mutation, n (%): **30 (9.4)**
- Median clone size, % (range): **42 (2.5–93)**

## OS by TP53 mutational status<sup>a</sup>



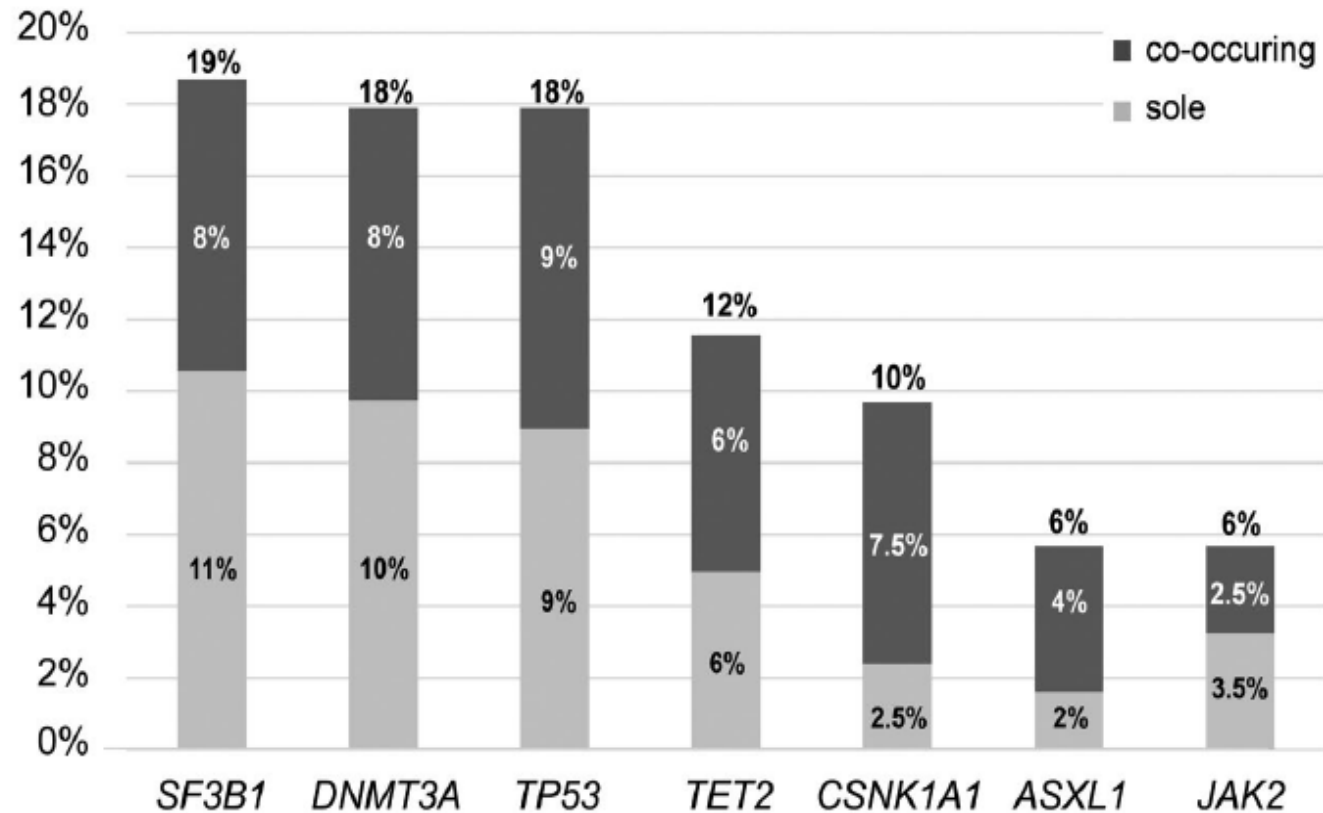
<sup>a</sup> Survival analysis was censored at treatment date.

<sup>b</sup> Co-variables: age; sex; WHO subtype; IPSS risk; ± mutations.

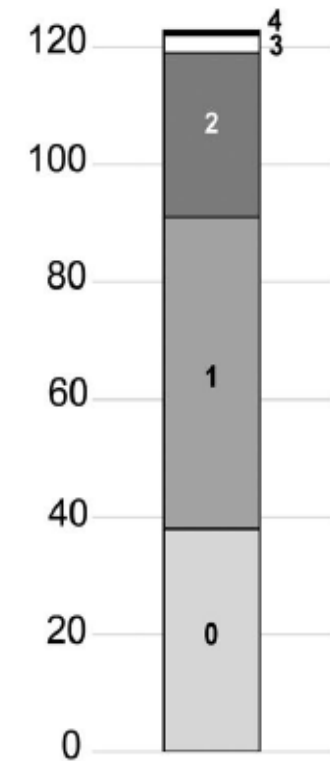
IPSS, International Prognostic Scoring System; PFS, progression-free survival.

# Most frequently mutated genes in MDS with isolated del5q

**A**

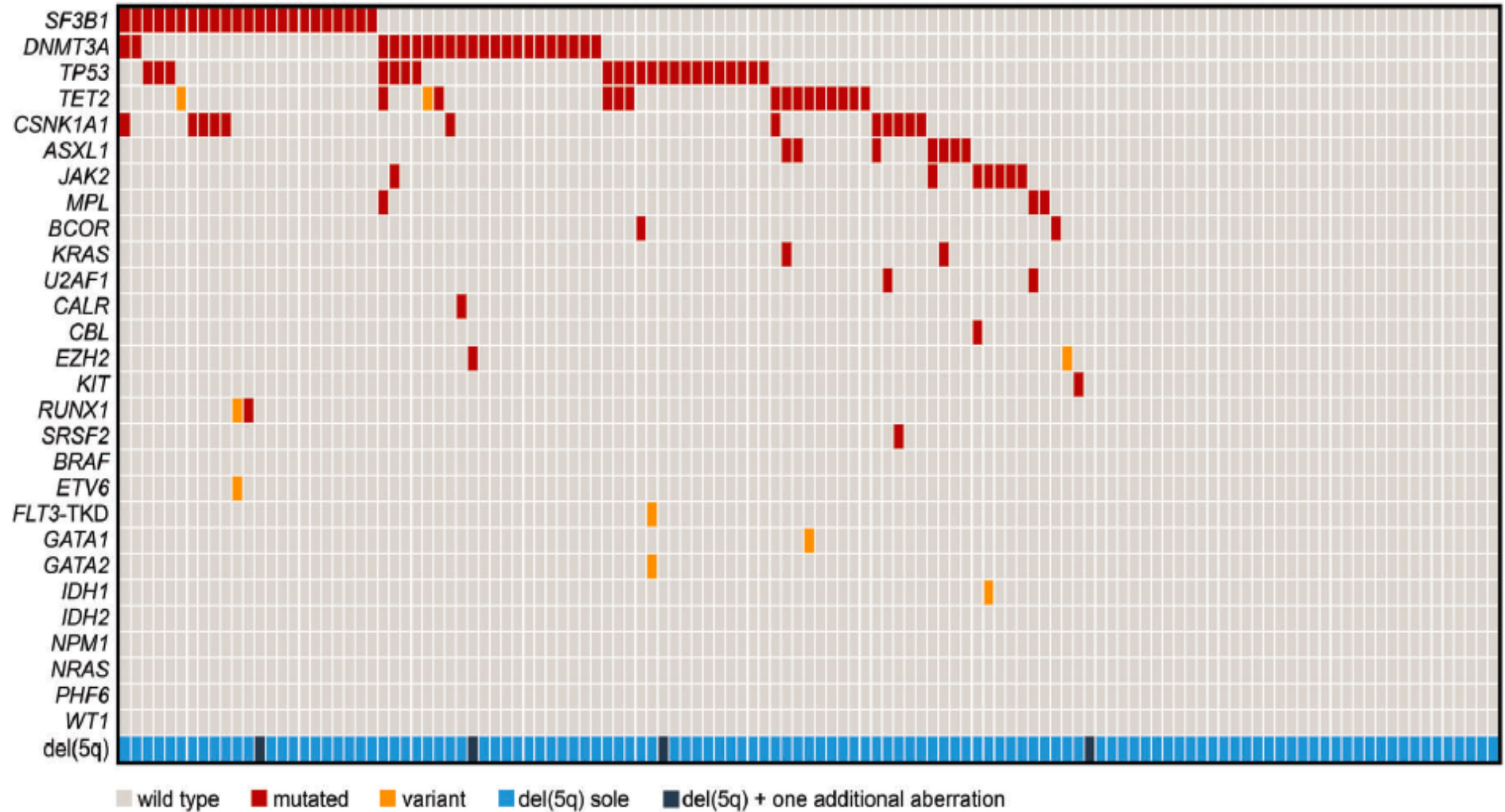


**B**





# Most frequently mutated genes in MDS with isolated del5q

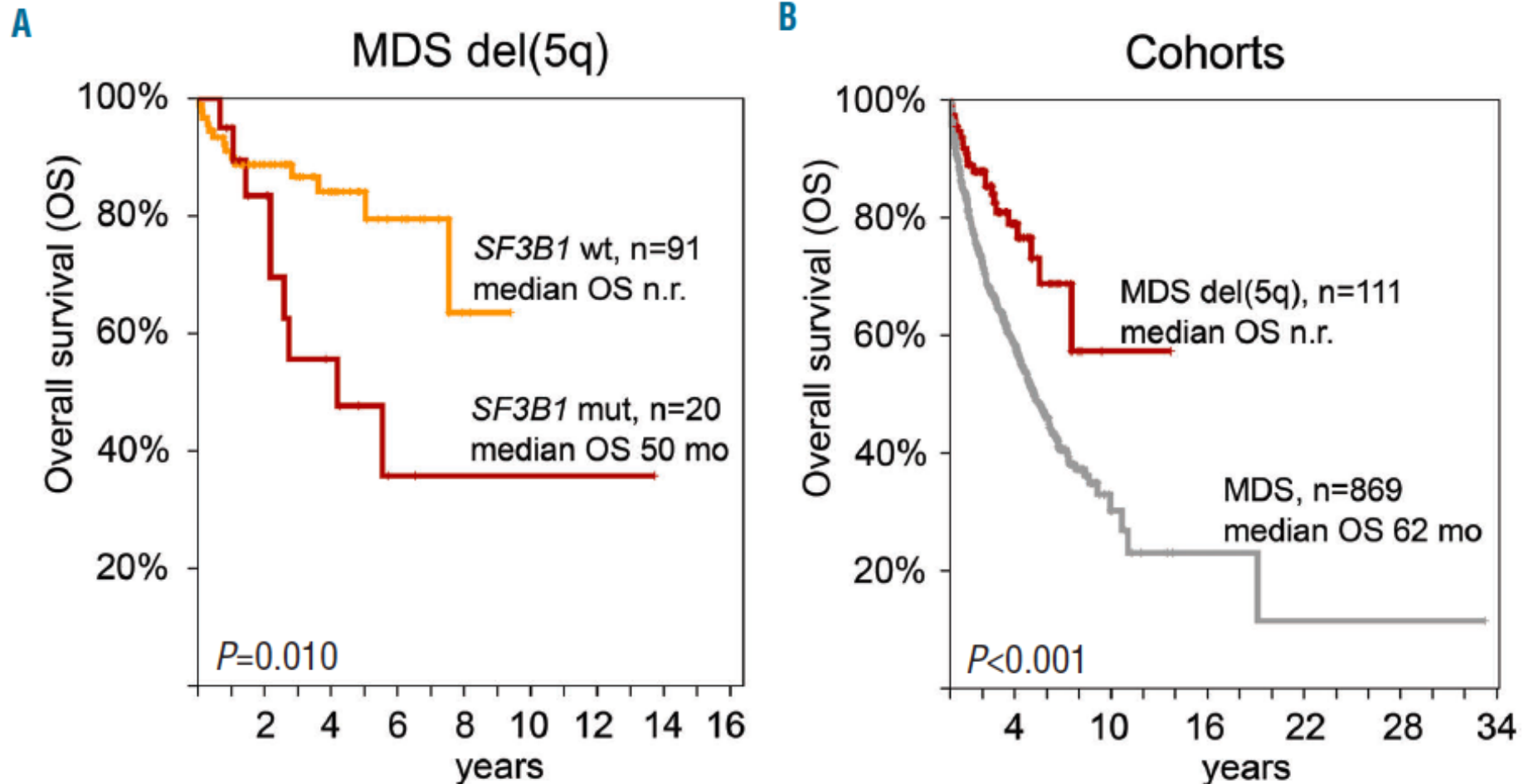


# Most frequently mutated genes in MDS with isolated del5q and comparison with nondel5q MDS

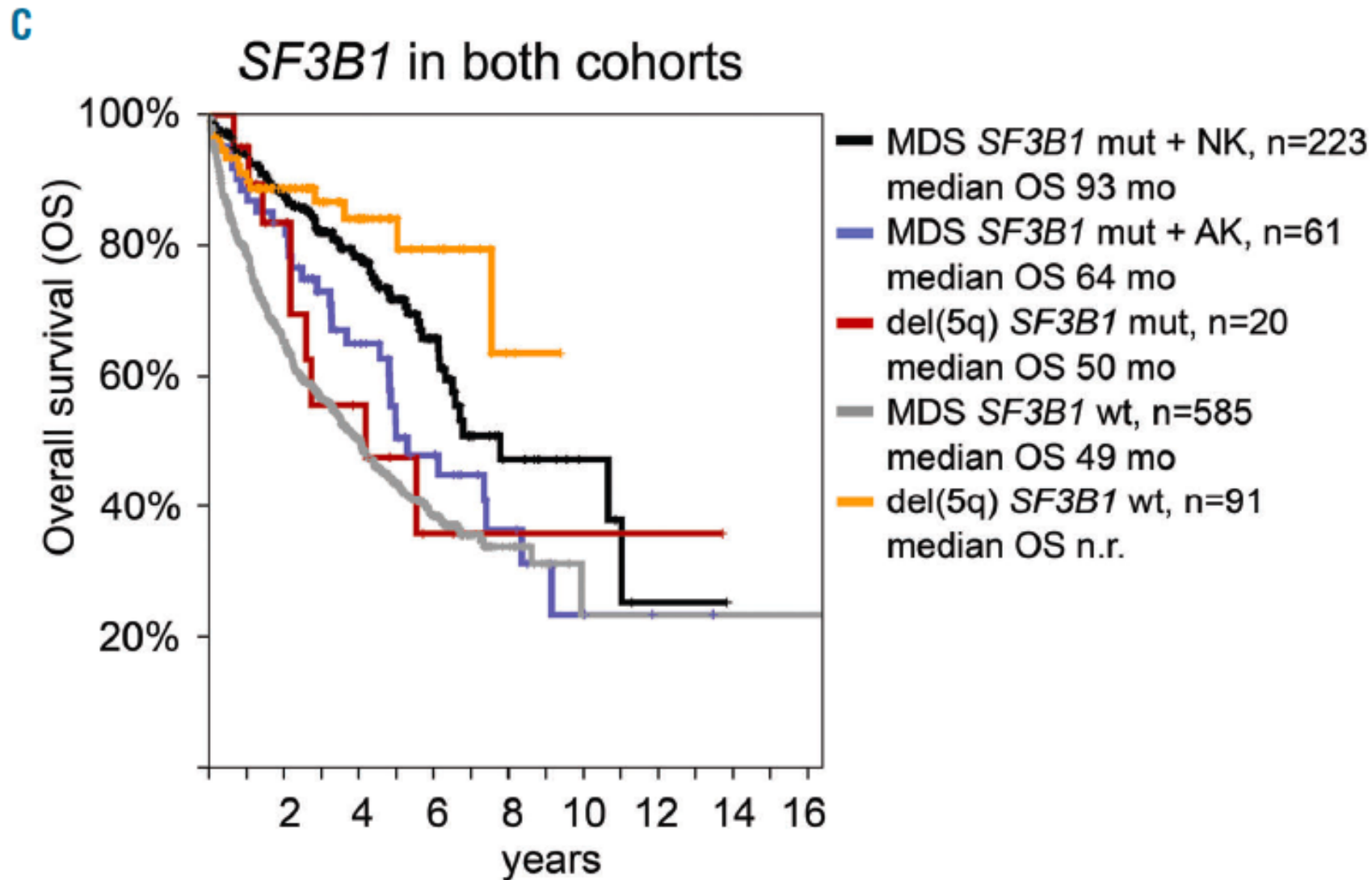
MDS del(5q)	rank	MDS
<i>SF3B1</i>	1	<i>TET2</i>
<i>DNMT3A</i>	2	<i>SF3B1</i>
<i>TP53</i>	3	<i>ASXL1</i>
<i>TET2</i>	4	<i>SRSF2</i>
<i>CSNK1A1</i>	5	<i>DNMT3A</i>
<i>ASXL1</i>	6	<i>RUNX1</i>
<i>JAK2</i>	7	<i>U2AF1</i>
	8	<i>ZRSR2</i>
	9	<i>STAG2</i>
	10	<i>TP53</i>
	11	<i>EZH2</i>
	12	<i>CBL</i>
	13	<i>JAK2</i>
	14	<i>BCOR</i>
	15	<i>IDH2</i>

mutation frequency

# SF3B1 mutations are not a good prognostic factor In MDS with isolated del5q



# SF3B1 mutations are not a good prognostic factor In MDS with isolated del5q



# Somatic mutation evaluation in MDS

1. Help refining diagnosis according to WHO for MDS with RS
2. Indicate possibility of experimental target therapy
3. Prompt to earlier intervention in presence of multiple or prognostically negative mutations
4. Prognostic value in MDS with del5q (TP53 mut)
5. Prognostic value in HSCT
6. No indication to select or exclude from HMA therapy or from HSCT on the basis of mutations

**Somatic mutations in suspect of  
MDS:  
a help in diagnosis?**

---

**Dysplasia can be induced by other causes than MDS**

**Cytopenias without dysplasia may be tricking**

**...**

**and definite diagnosis is often a challenge**

---

**ICUS** idiopathic cytopenia of unknown significance

**IDUS**

idiopathic dysplasia of unknown significance

**CHIP/ARCH**

clonal hemopoiesis of indeterminate potential/ age related clonal hemopoiesis

**CCUS**

clonal cytopenia of unknown significance

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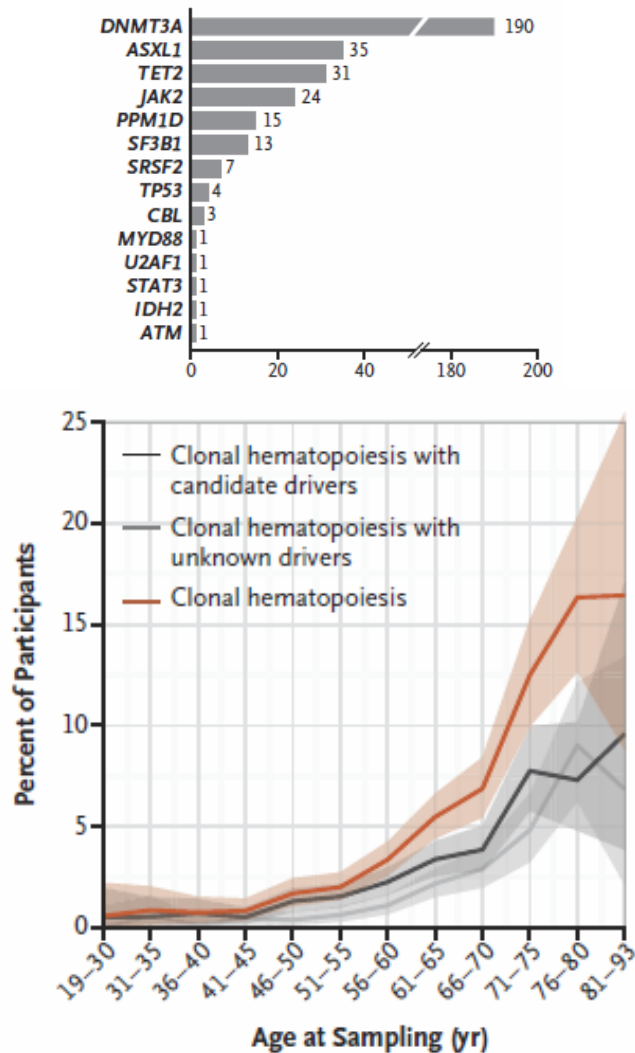


# Clonal hemopoiesis in the era of deep sequencing

ORIGINAL ARTICLE

## Clonal Hematopoiesis and Blood-Cancer Risk Inferred from Blood DNA Sequence

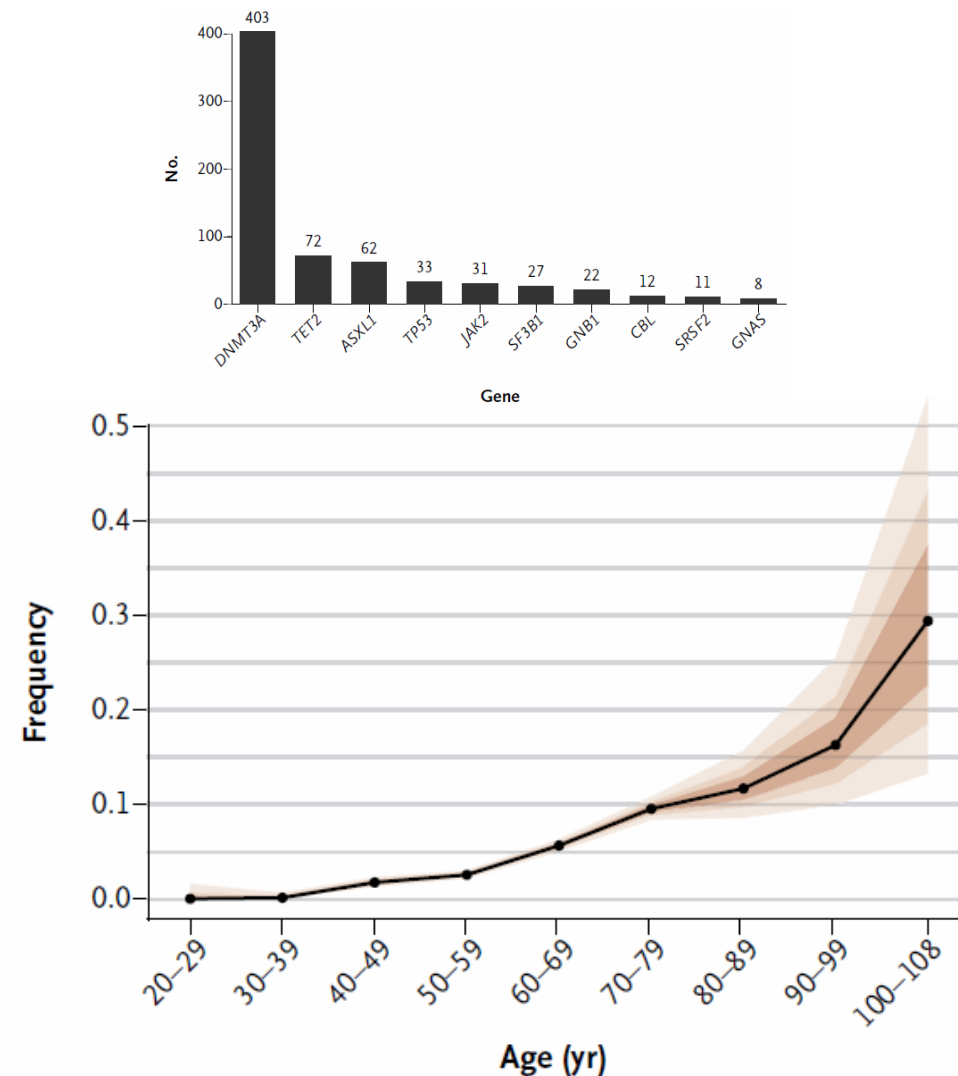
Giulio Genovese, Ph.D., Anna K. Köhler, Ph.D., Robert E. Handsaker, B.S.,



ORIGINAL ARTICLE

## Age-Related Clonal Hematopoiesis Associated with Adverse Outcomes

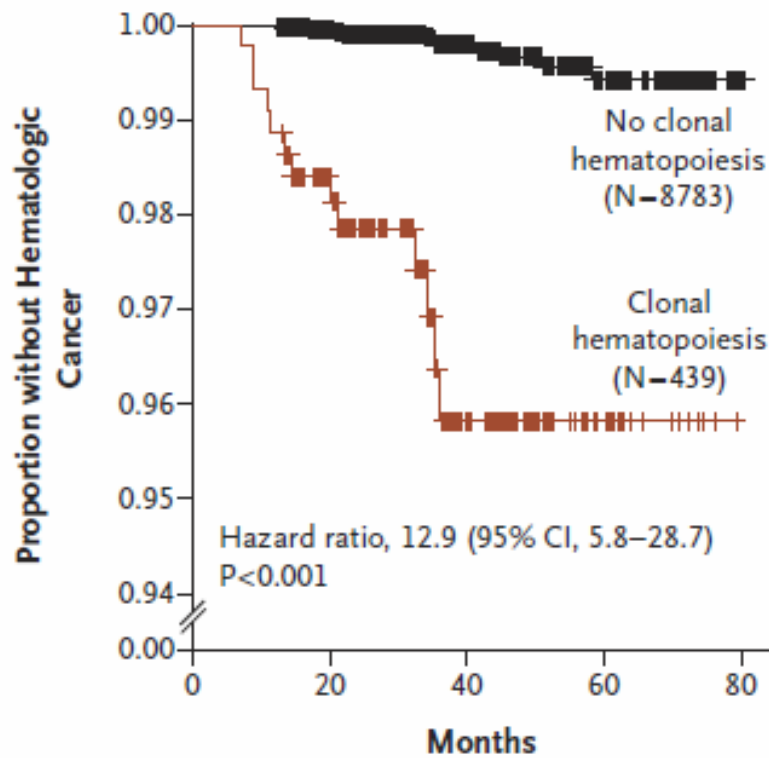
Siddhartha Jaiswal, M.D., Ph.D., Pierre Fontanillas, Ph.D., Jason Flannick, Ph.D.,



ORIGINAL ARTICLE

## Clonal Hematopoiesis and Blood-Cancer Risk Inferred from Blood DNA Sequence

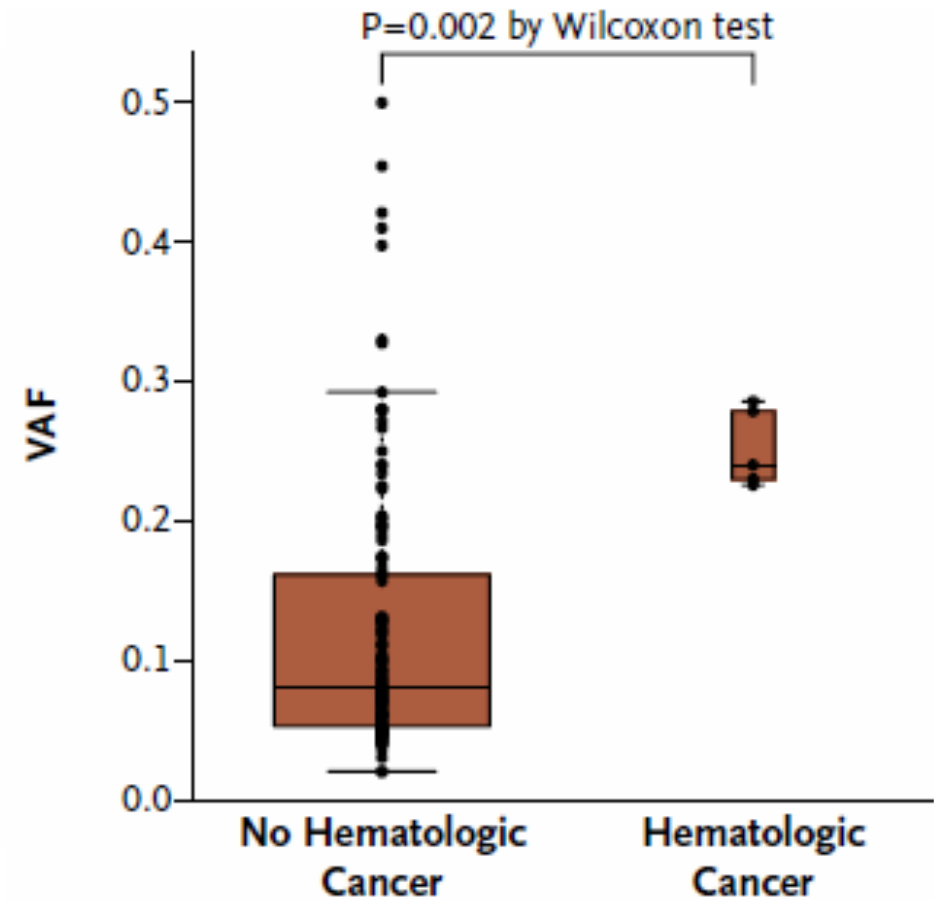
Giulio Genovese, Ph.D., Anna K. Kähler, Ph.D., Robert E. Handsaker, B.S.,



ORIGINAL ARTICLE

## Age-Related Clonal Hematopoiesis Associated with Adverse Outcomes

Siddhartha Jaiswal, M.D., Ph.D., Pierre Fontanillas, Ph.D., Jason Flannick, Ph.D.,



## **Clonal hemopoiesis of indeterminate potential (CHIP)**

**- Clonality defined by presence of MDS-associated genes:**

**DNMT3A, ASXL1, TET2, (JAK2) with loss of function**

**- Little propensity to develop MDS ( 0,5-1% /year)**

**- Present in 15% of persons aged > 70yrs**

**Triggered by (?) :**

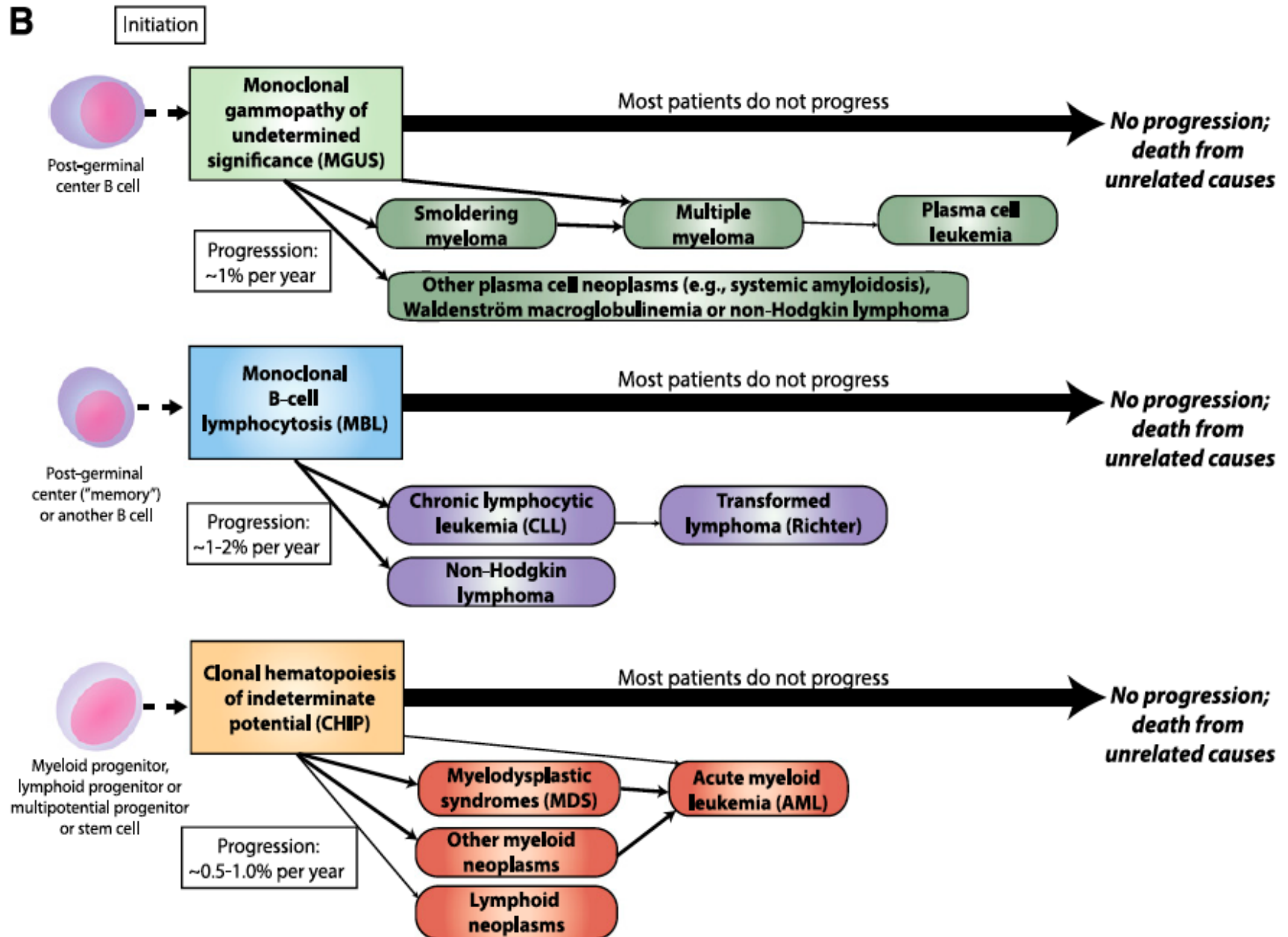
**Stochastic event**

**Environment (smoke, radiation, chemotherapy, inflammation)**

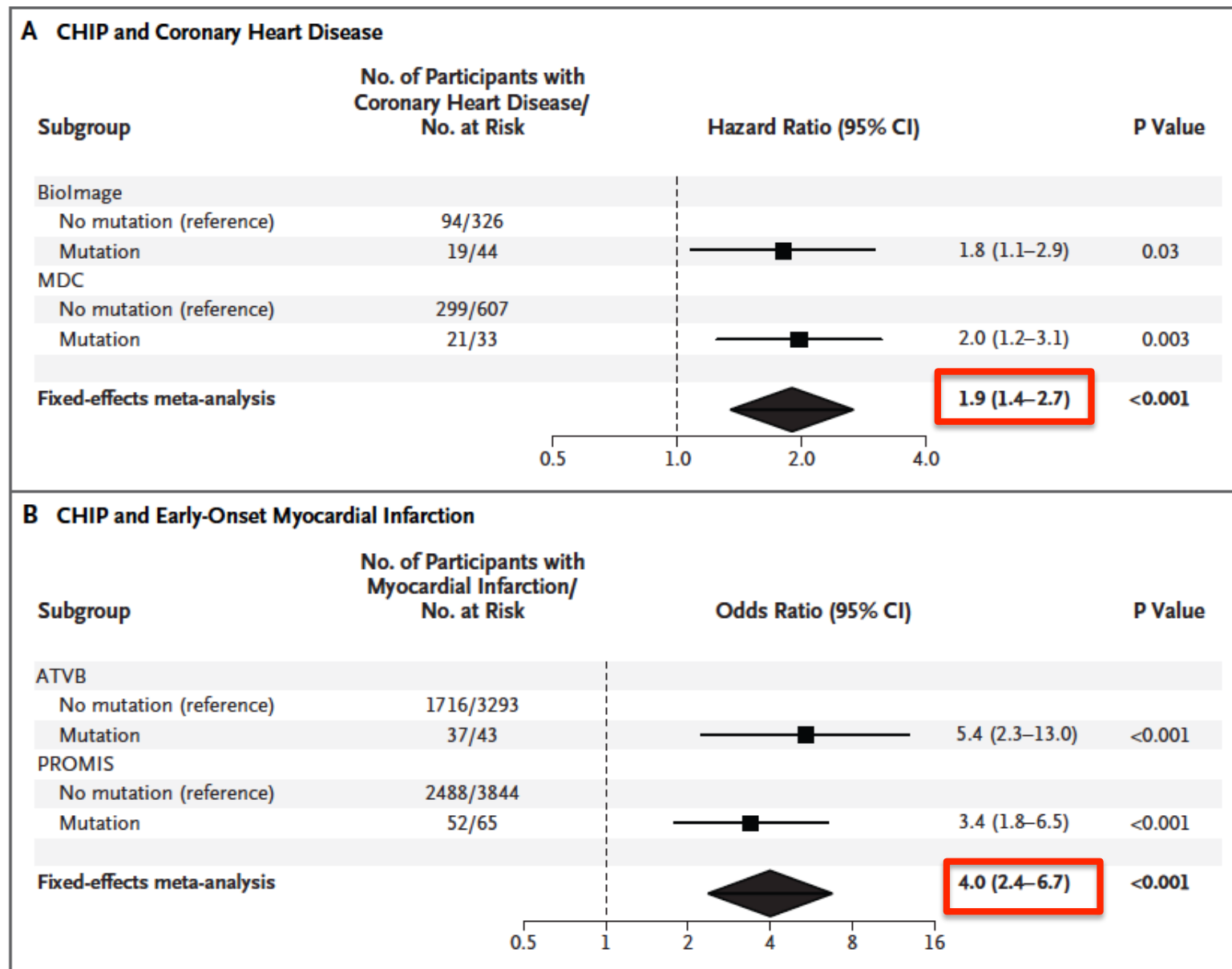
**Hereditary/predisposition conditions**

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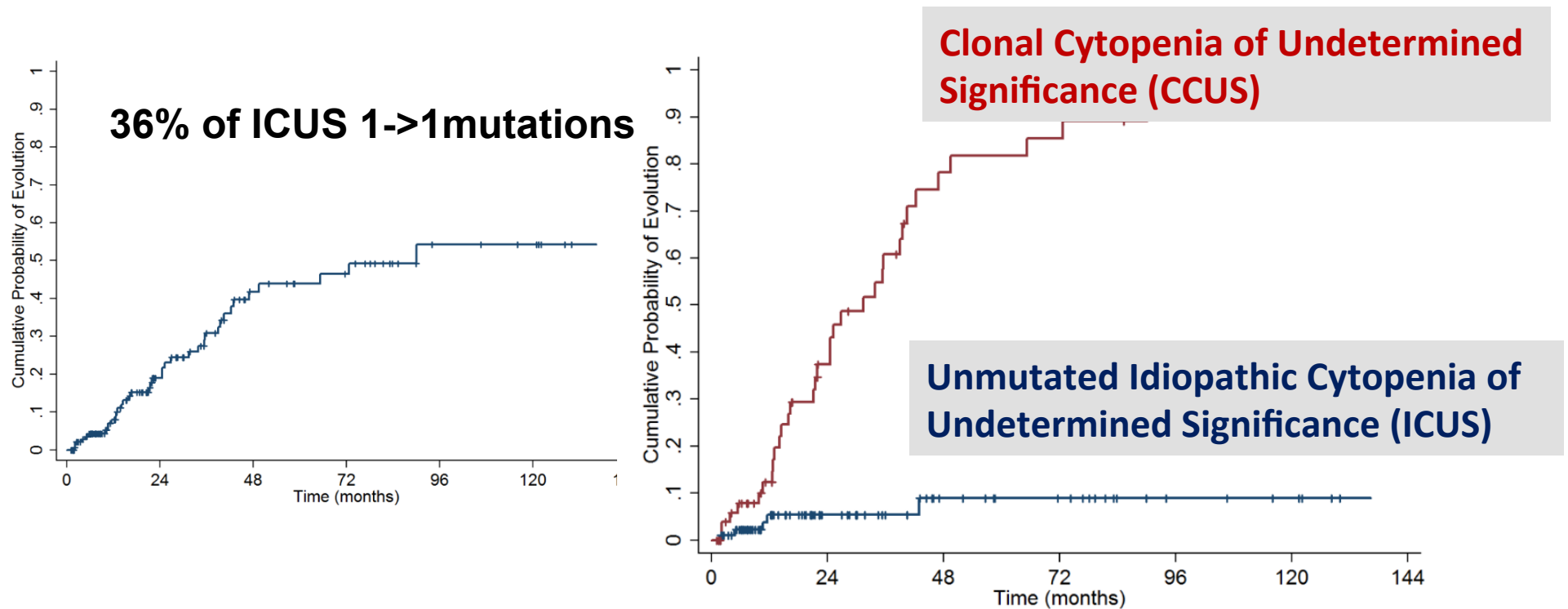
# Is CHIP so *innocent*??



# CHIP correlates with coronary heart disease



# Mutations in patients with CCUS predict evolution compared to ICUS



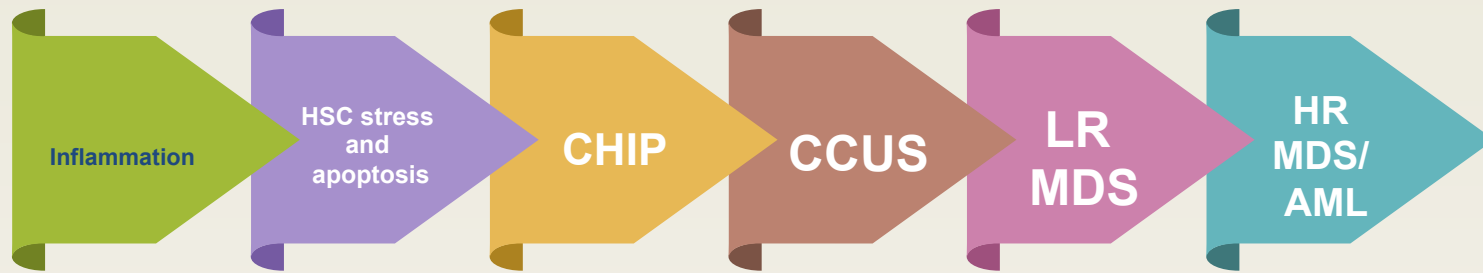
# Exposure to Radiation Therapy or Tobacco Use Increases Risk of Clonal Hemopoiesis More Than Chemotherapy Exposure

## Clonal Hematopoiesis

	Overall	No	Yes	<i>P</i> -value
Sample size (% of total cohort)	5649	4296	1353	
Prior Chemo *, N%	64%	64%	64%	0.89
Prior radiation*, N%	37%	35%	41%	<0,001
Current/former smoker, N%	46%	44%	53%	<0,001

**CHIP in 25% of solid tumor patients**, with 4.5% harboring presumptive leukemia driver mutations (CH-PD). Most frequent DNMT3A. PPM1D and TP53 mutations were associated with prior exposure to chemotherapy.

# inflammation could be a trigger for clonal hemopoiesis



Parainflammation  
Chronic  
smouldering  
Inflammation  
.....  
Multifactorial

Immunogenic  
Cell Death  
Antigen  
spreading

T cell  
recruitment  
and priming

Immune-  
subversion

Priming the  
adaptive response

Innate immune  
response

“Protective” T  
cell response

.....  
Th1, Th17 and  
Oligoclonal  
response

Active suppression of  
protective response

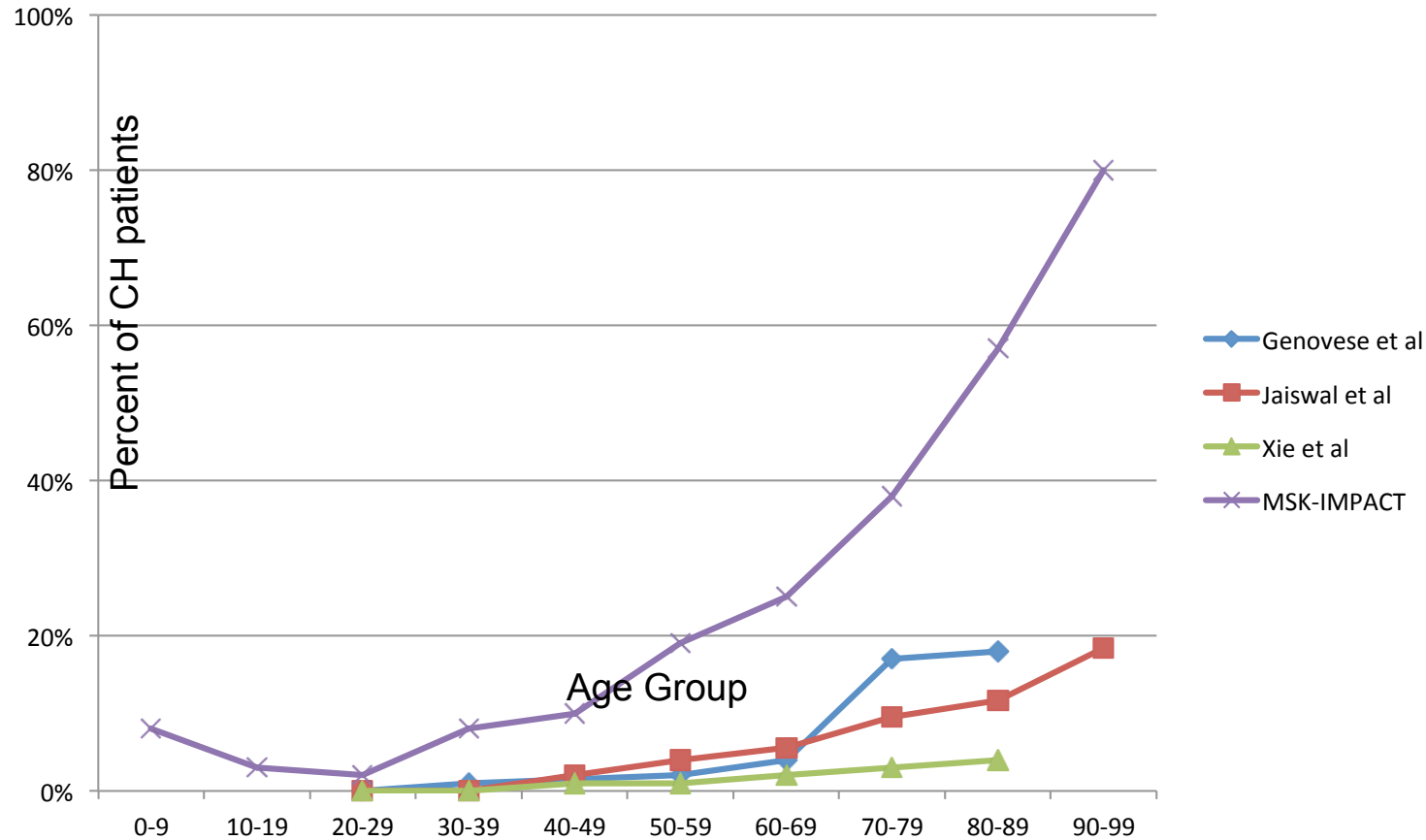
.....  
Increased Tregs,  
MDSCs and  
ineffective  
immune response

Courtesy Kordasti S, 2017



# Age-dependent clonal hemopoiesis is More Common Than Reported in Hotspot Focused Studies

*Senectus ipsa morbus est*



Coombs et al., 2017, Cell Stem Cell 21, 1–9  
Genovese G. et al NEJM. 2014;371(26):2477-87  
Jaiswal S et al NEJM. 2014 ;371(26):2488-98  
Xie et al; Nat Med. 2014 ;20(12):1472-8.



'YOU'RE DELIBERATLY PUTTING YOURSELF  
AT RISK OF ILL HEALTH BY BEING OVER 65...'

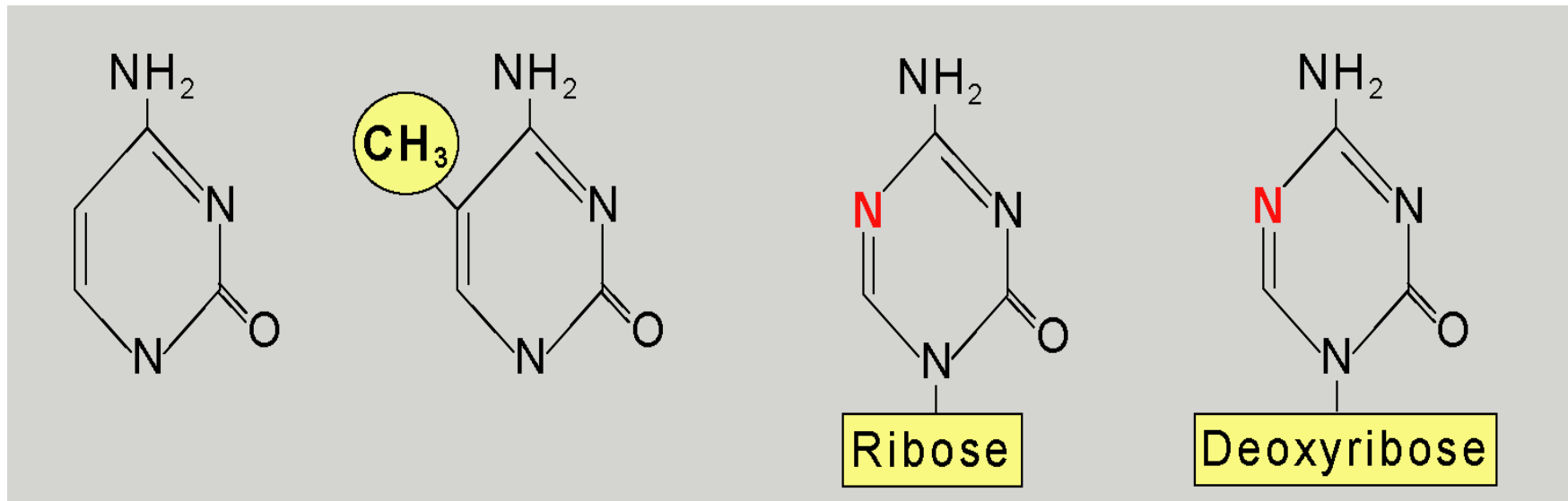
	ICUS	ARCH	CHIP	CCUS	Lower Risk MDS	Higher Risk MDS
<b>Clonality</b>	-	+	+	+	+	+
<b>Dysplasia</b>	-	-	-	-	+	+
<b>Cytopenia</b>	+	-	-	+	+	+
<b>BM Blast %</b>	<5%	<5%	<5%	<5%	<5%	<19%
<b>AML Overall Risk</b>	Very low	Very low	Very low but cardiopathy	Low / intermediate	Low	High
<b>Median Num of mutations</b>	0	1	1	>1<2	>2	>2
<b>Typical VAF</b>	-	1-10%	9-12% (>10)	30-40% (40)	>50%	>50%
<b>Types of mutations</b>		<i>DNMT3A, TET2,ASXL1, JAK2, TP53</i>	<i>DNMT3A, TET2,ASXL1, JAK2, TP53</i>	<i>TET2, DNMT3A,ASXL1, SRSF2, TP53 <b>Later</b> TET2, SRSF2, ASXL1, U2AF1, DNMT3A</i>	<b>SF3B1, TET2, ASXL1, SRSF2, DNMT3A</b> <i>and all the less frequent</i>	

Modified from Steensma et al, *Blood* 2015 and  
Bejar R *Leukemia*, 2017 online

# **Molecular variables: DNA methylation**



# Azanucleosides, Cytosine Analogues with hypomethylating properties



Cytosine

5-methyl-  
cytosine

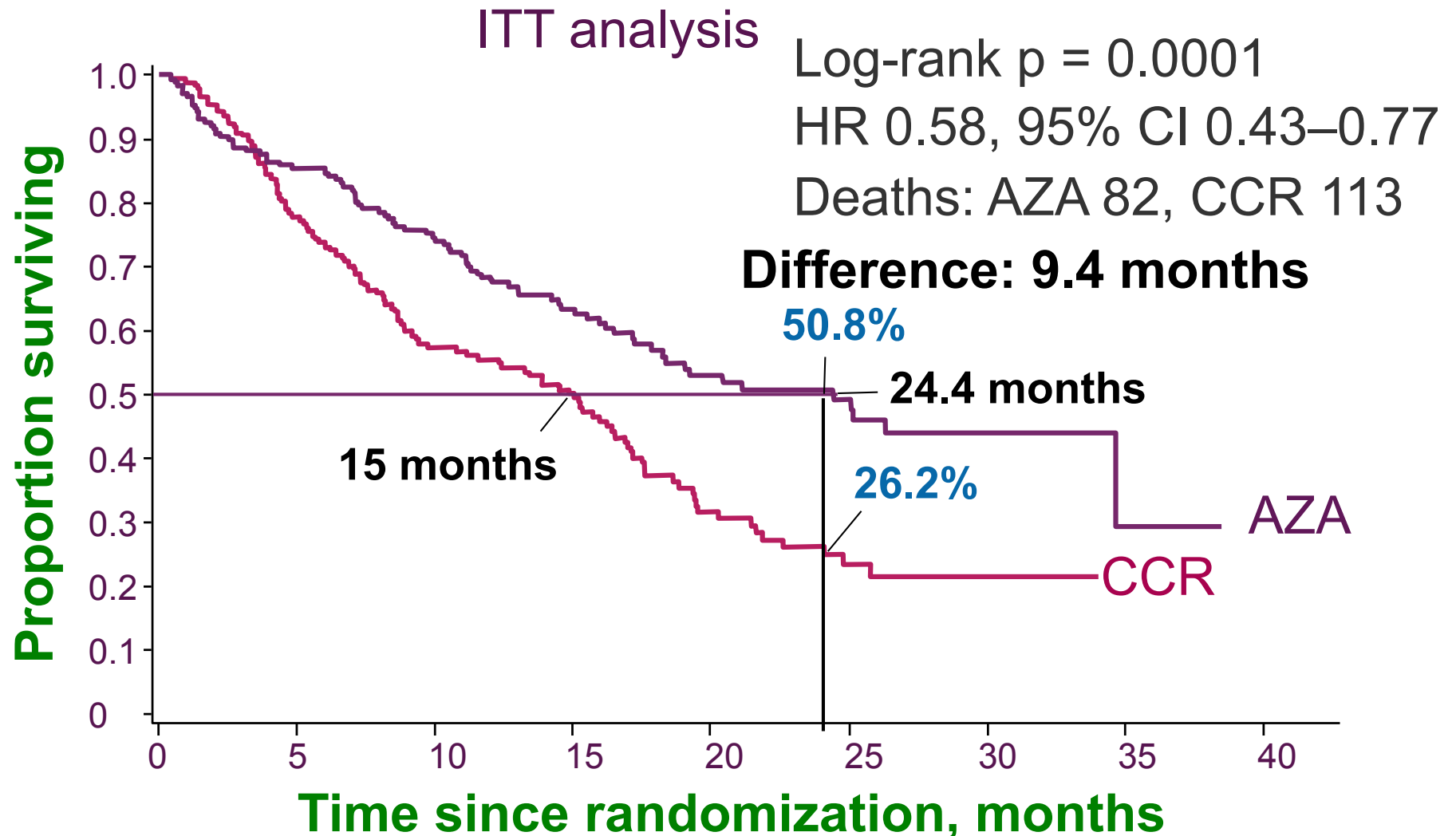
5-aza-  
cytosine

5-aza-2'-deoxy-  
cytosine

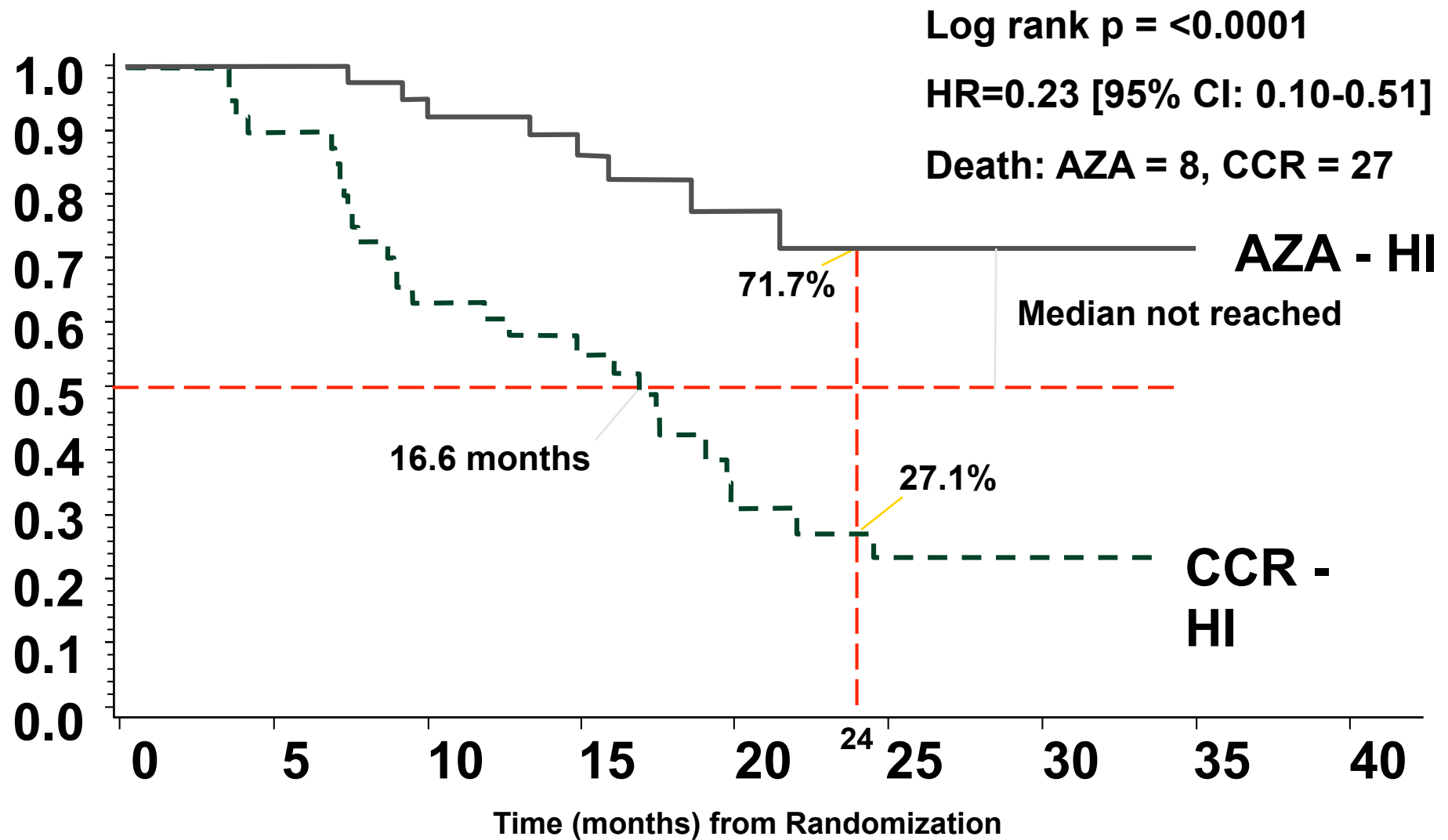
Azacitidine

Decitabine

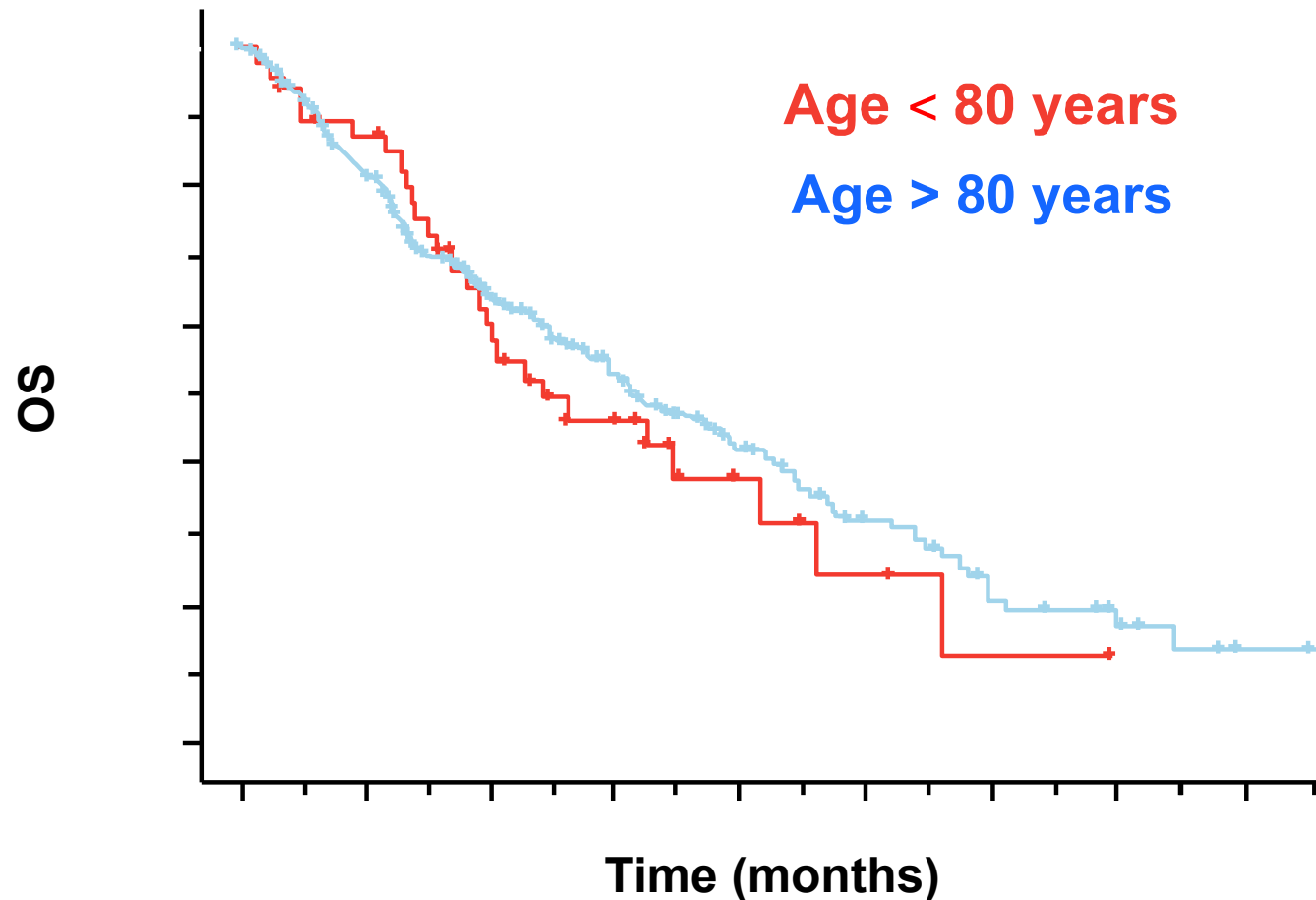
# Overall survival: AZA vs CCR



# AZA vs CCR: OS in Pts with Best Response of HI



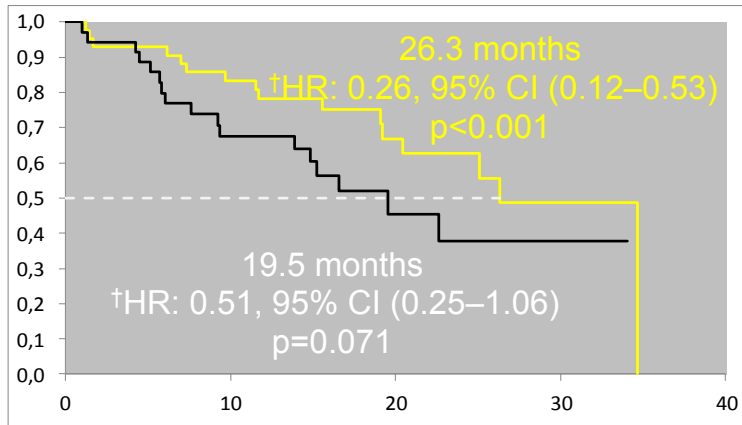
# Azacitidine (AZA) in Higher Risk MDS Patients (pts) Aged $\geq 80$ Years : OS



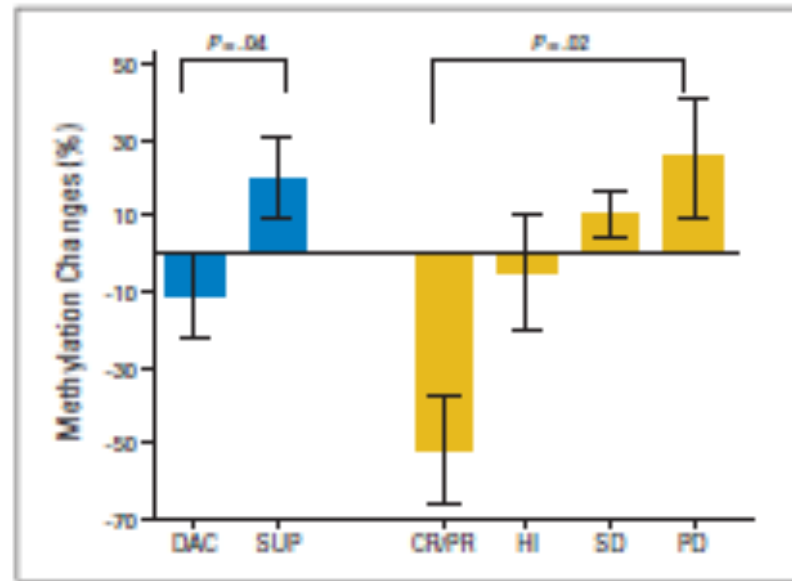
- OS similar in patients aged  $< 80$  and  $\geq 80$  years ( $P = .6$ )
- Median OS 12.1 months; 1- and 2-year OS: 50% and 23.2%



# Methylation pattern and response to therapy

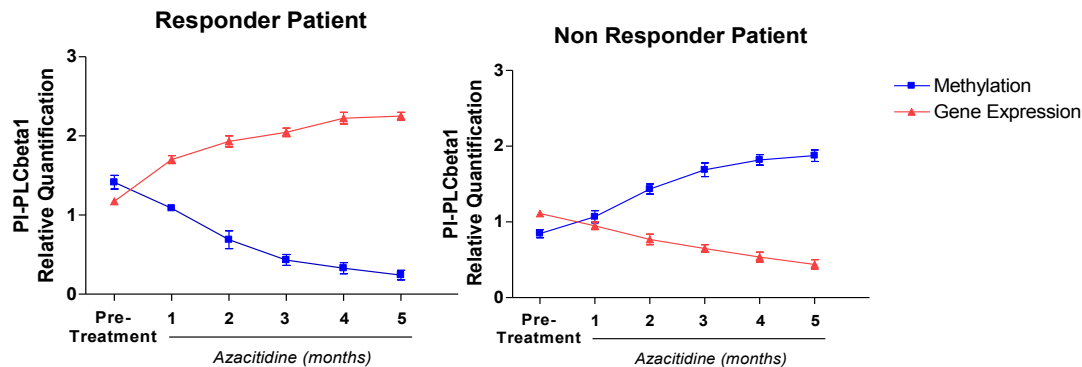


OS after AZA according to CDH1 methylation levels  
 Herman JG, et al. Presented at AACR 2009 [Abstract 4746]



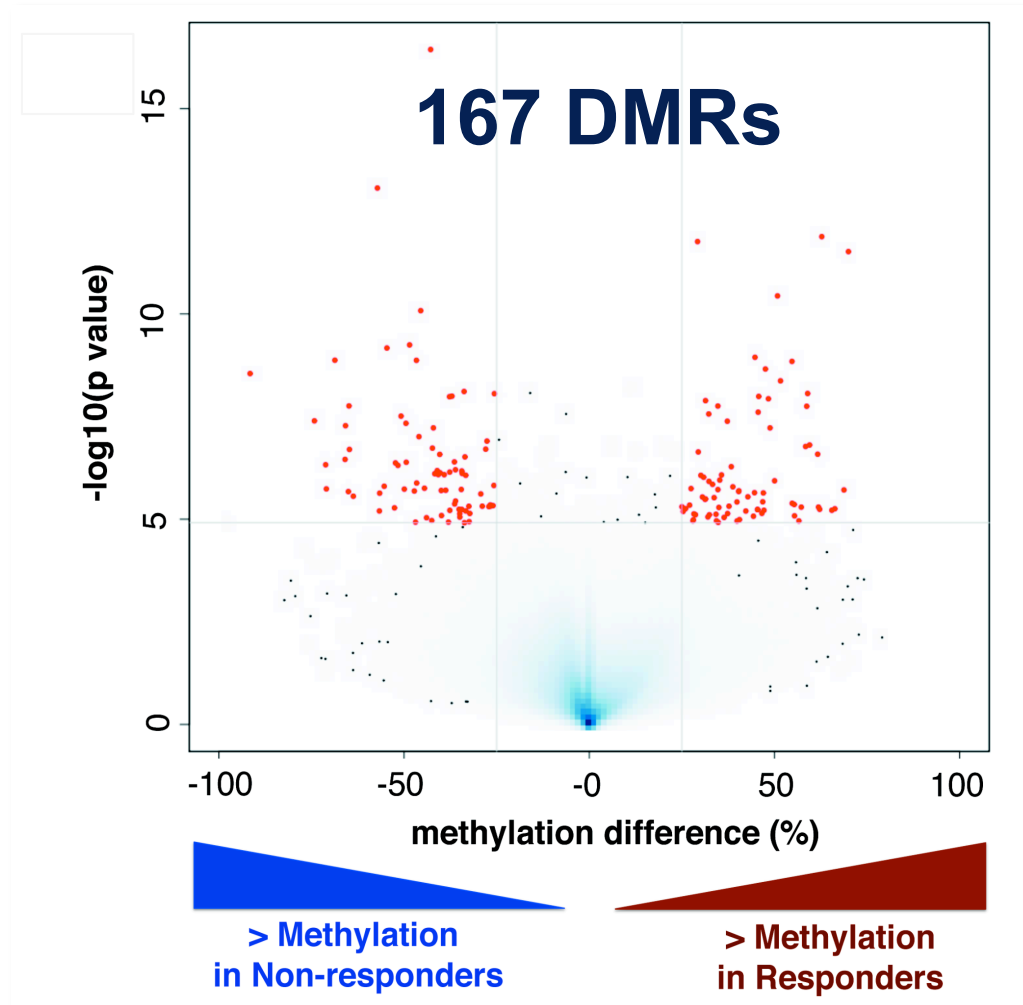
## Global methylation and response to Decitabine

Shen, J Clin Oncol. 2010 1;28(4):605-13

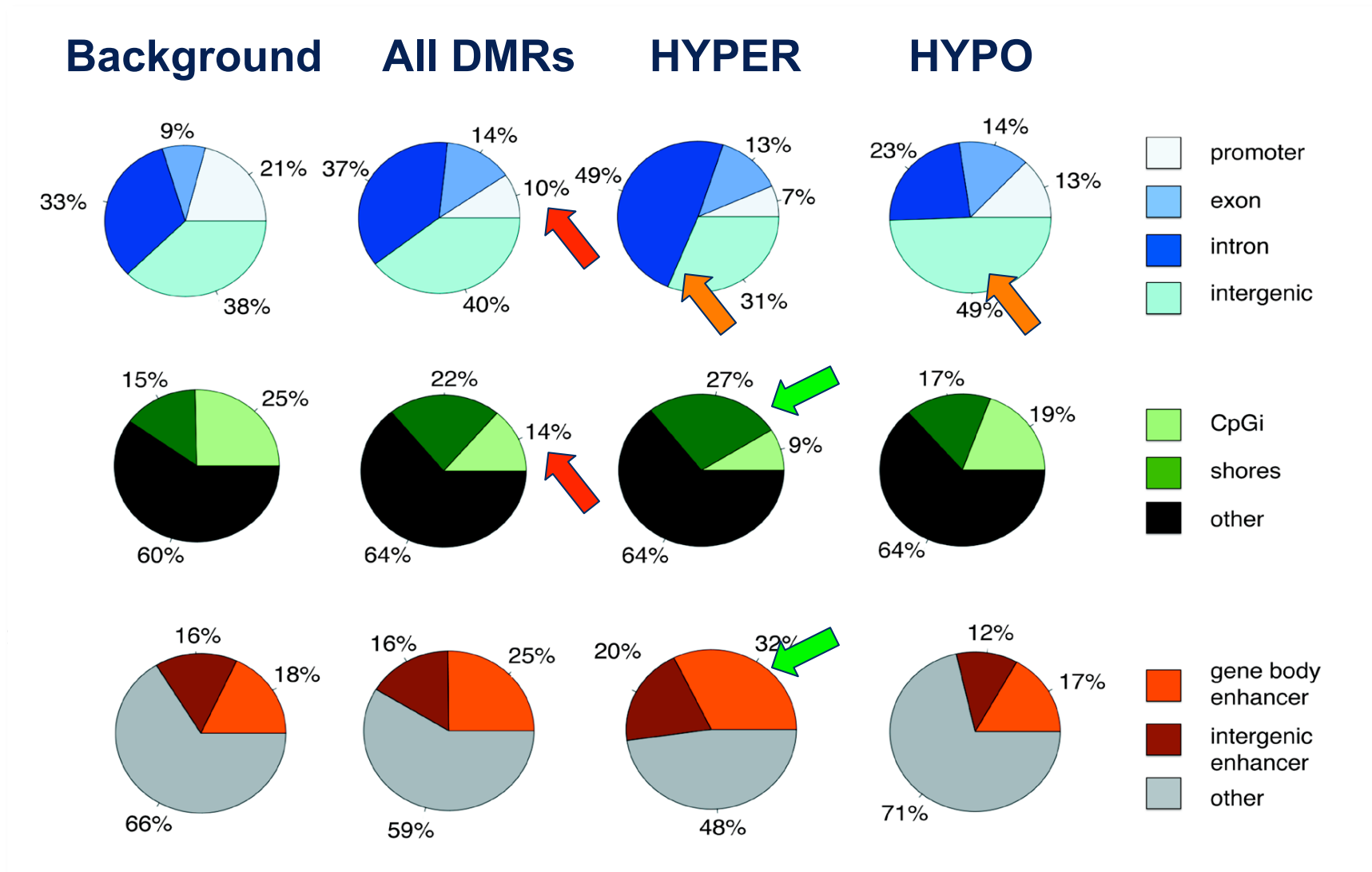


PI-PLCbeta1 promoter methylation and gene expression correlate with response to azacitidine  
 Follo et al PNAS 2009 29;106(39):16811-6

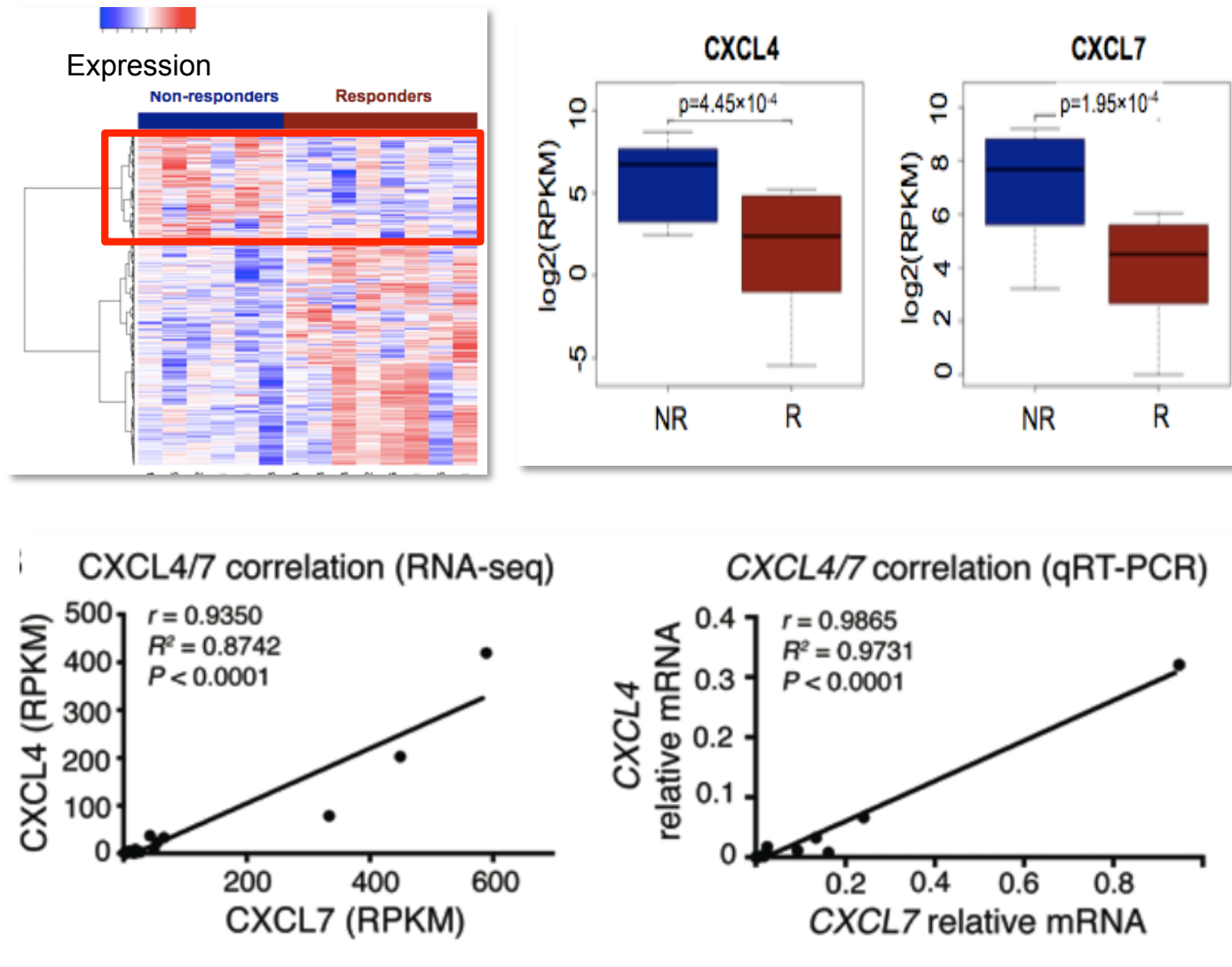
# Distinct DNA methylation profiles at diagnosis of CMML is associated with response to decitabine



# Differentially methylated regions are enriched at distal intergenic regions and enhancers



# CXCL4 and CXCL7 are up-regulated in the bone marrow of non-responders



# CXCL4 and CXCL7 are up-regulated in the bone marrow of non-responders

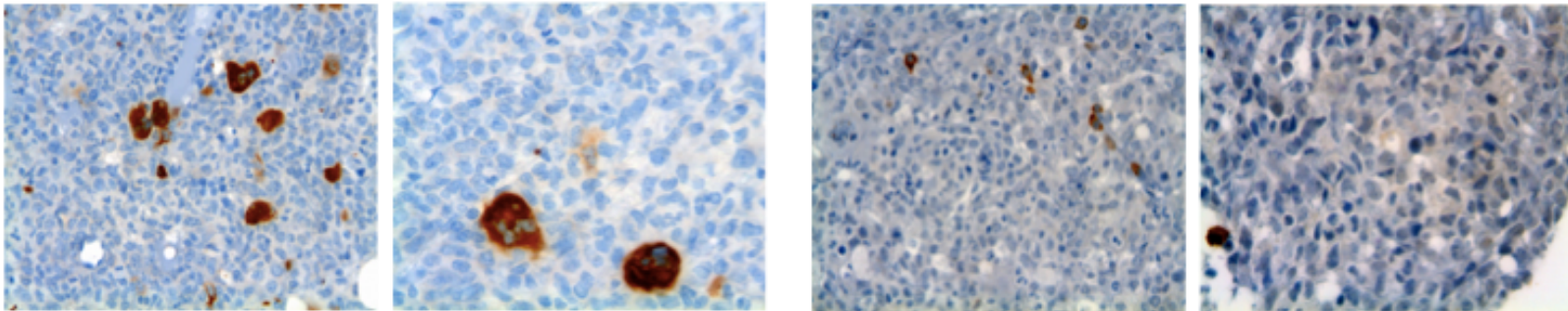


Francesca Buchi

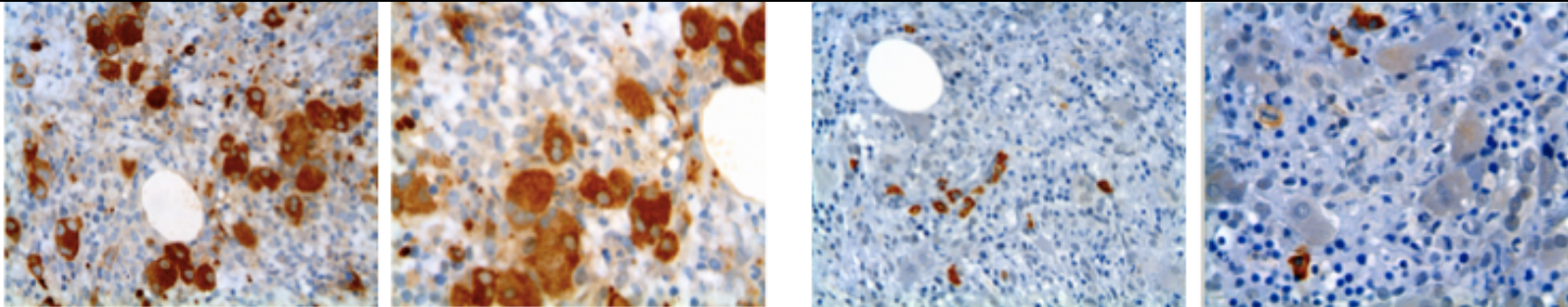
40X **CXCL4** 63X

40X **CXCL7** 63X

**R**



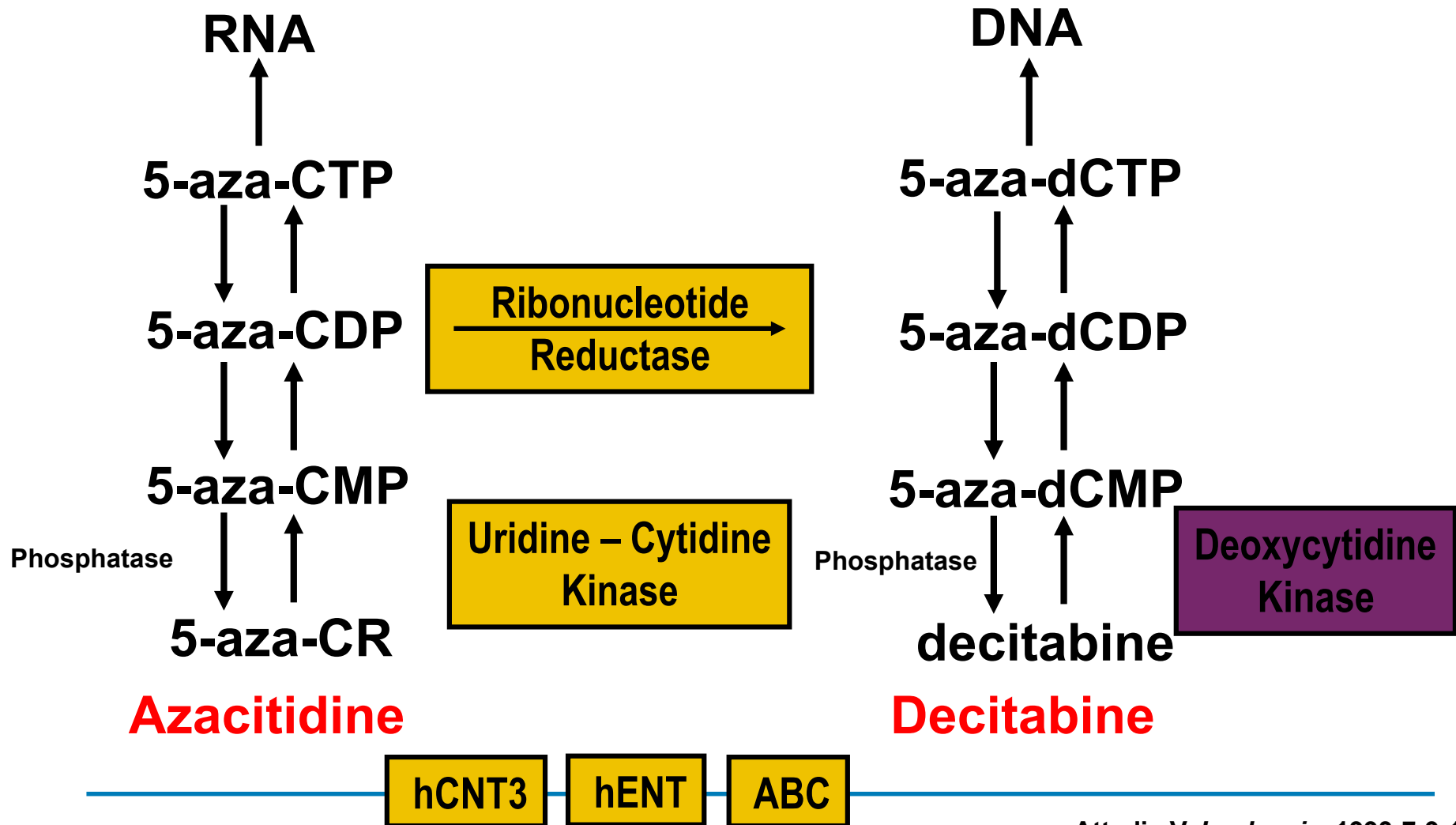
**NR**



**Uptake and metabolism of drugs  
may be impaired genetically and  
alter outcome**

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# RNA/DNA uptake of hypomethylating agents

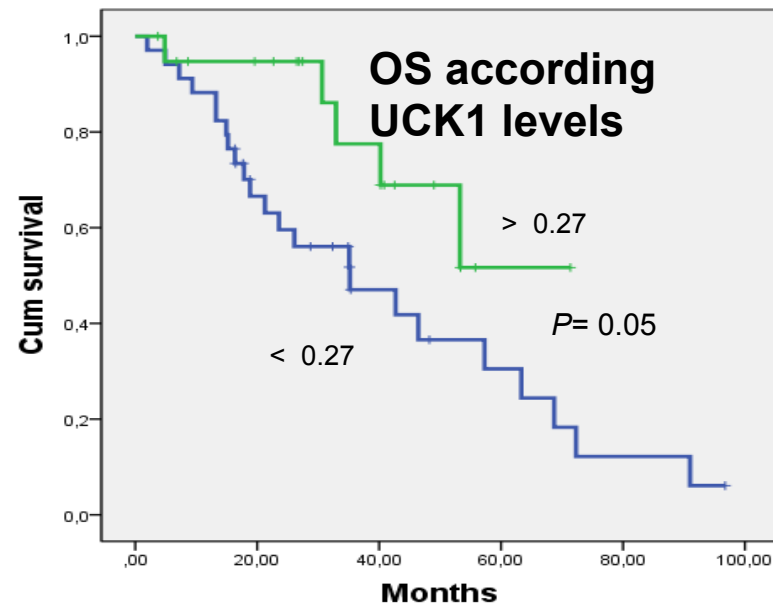
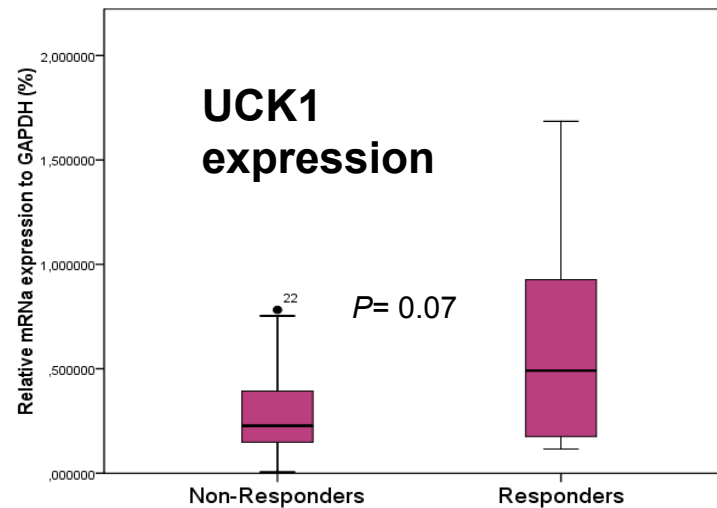


# UCK1 hyperexpression modulates response to Azacitidine in HR-MDS

Ana Valencia et al, Leukemia 2013

57 MDS pts  
↓  
Azacitidine  
75mg/m<sup>2</sup>/7 days  
every 28 gg

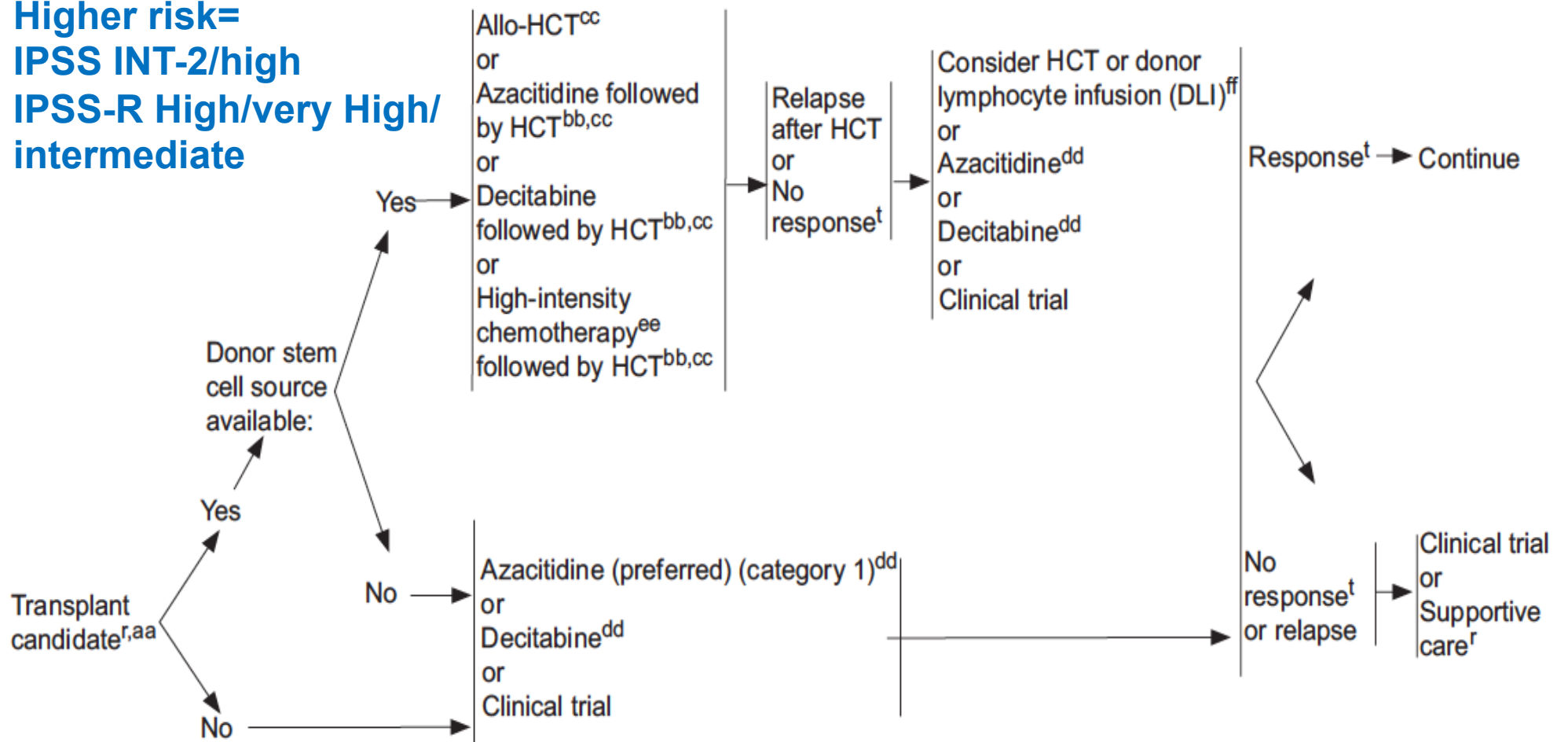
UCK1/2  
Gene expression  
Promoter methylation  
Gene sequence



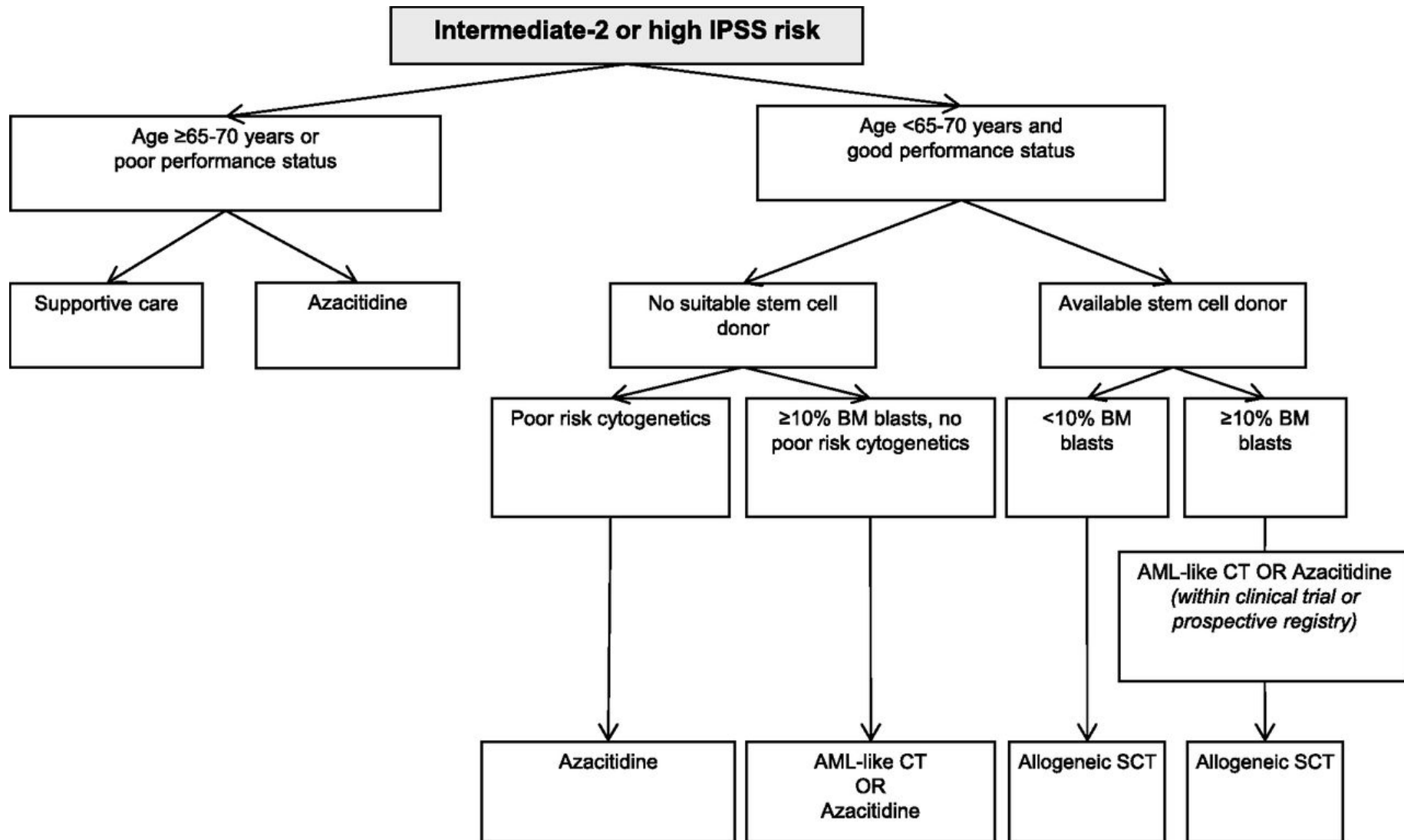


# Myelodysplastic Syndromes, Version 2.2017, NCCN Clinical Practice Guidelines in Oncology.

**Higher risk=**  
**IPSS INT-2/high**  
**IPSS-R High/very High/**  
**intermediate**



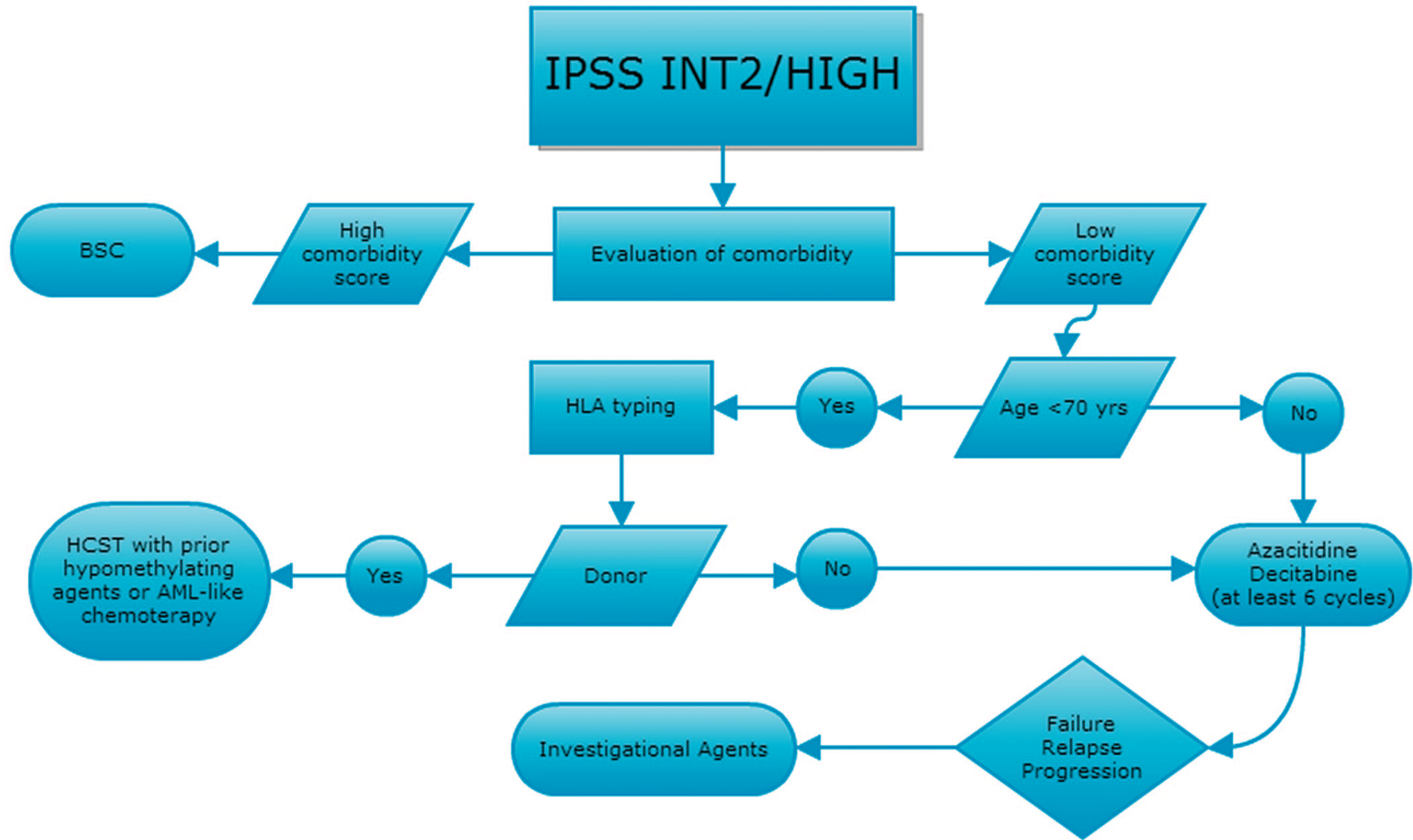
# Therapeutic algorithm for adult patients with primary MDS and intermediate-2 or high IPSS score.



Luca Malcovati et al. Blood 2013;122:2943-2964



# Therapeutical options for higher risk MDS



**Santini V.**

**Hematology** Am Soc Hematol Educ Program. 2012;2012:65-73.

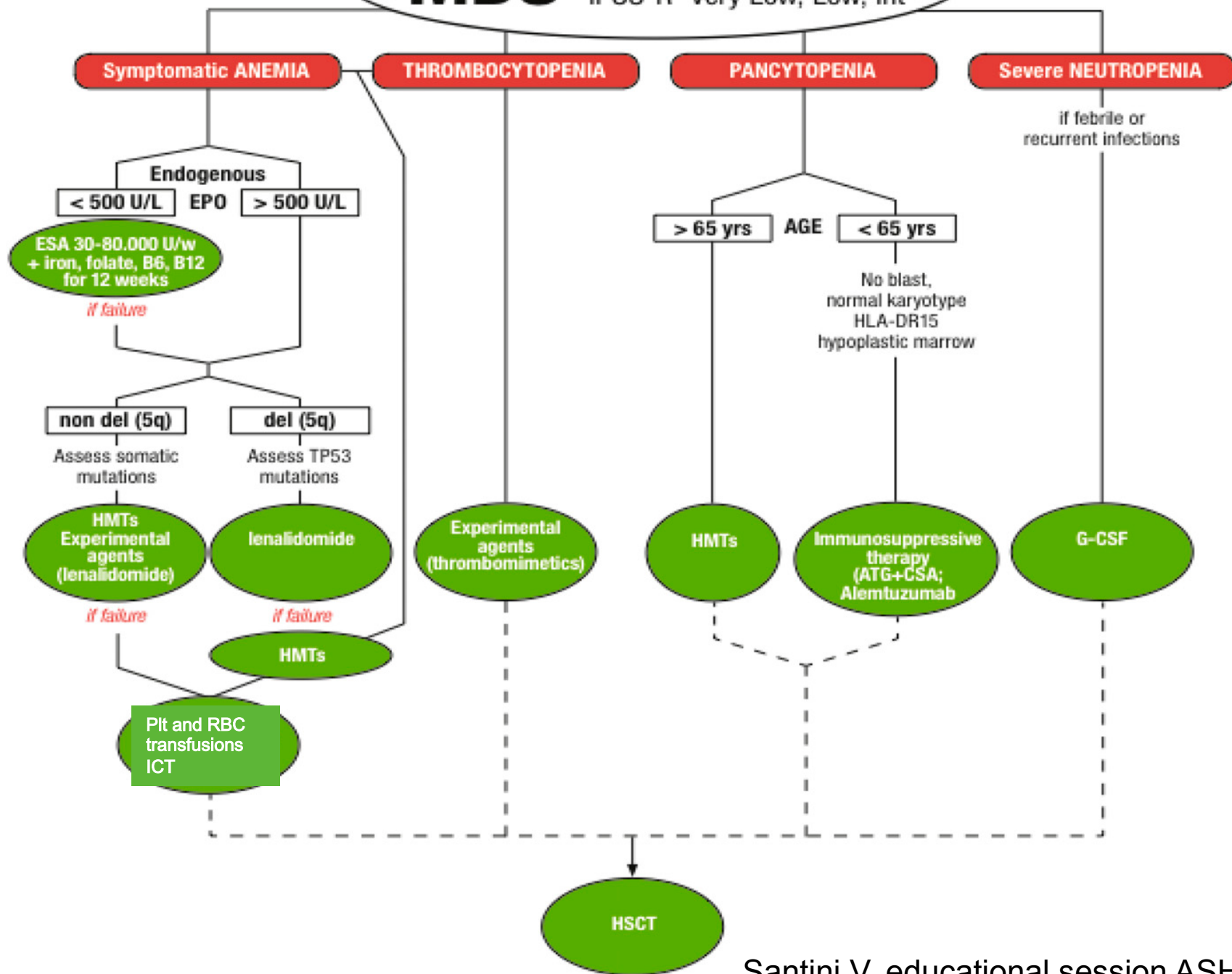
## **SIE-Italian Guideline Recommendations**

**Patients belonging to the IPSS  
int 2-high groups and not eligible  
to allogeneic HSCT, or eligible to  
allogeneic HSCT but lacking an  
immediately available donor, are  
recommended to receive  
hypomethylating therapy .**

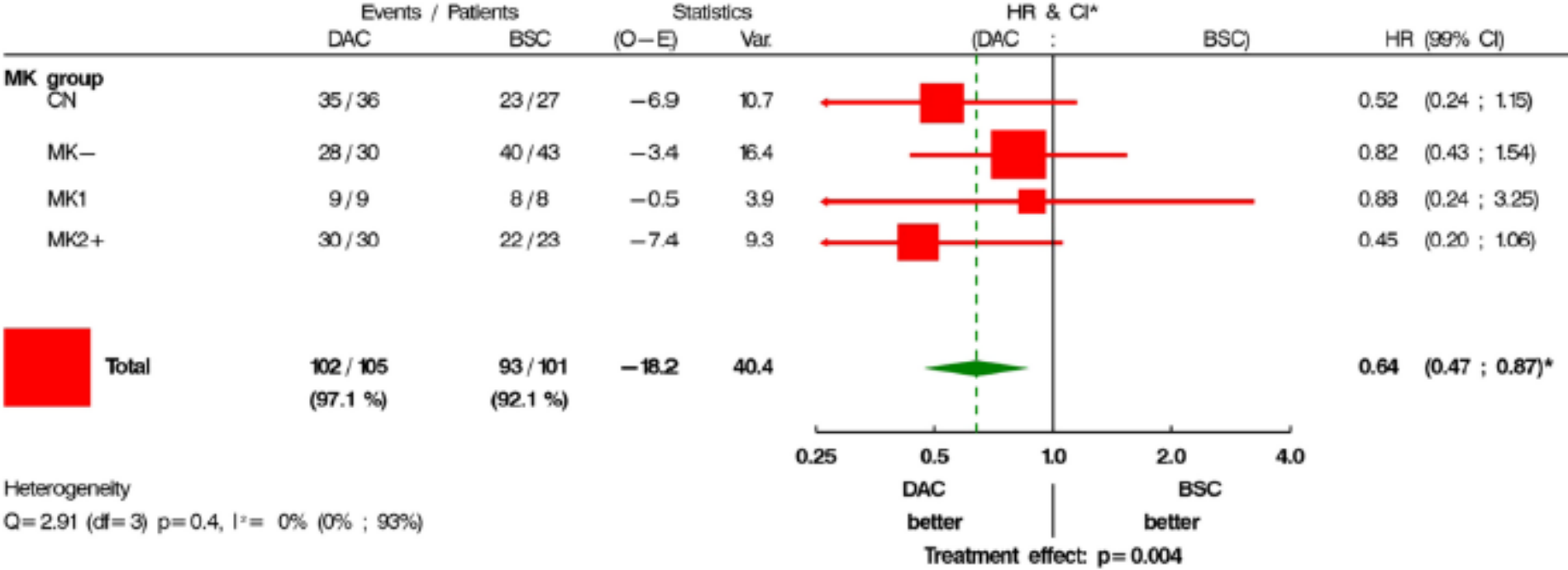
**(grade A)**

Santini et al, Leuk Res 2010

**MDS** IPSS Low, Int-1  
IPSS-R Very Low, Low, Int



# Progression-free survival after decitabine is strikingly prolonged in the presence of 2 or more monosomies



\*95% CI for totals and subtotals, 99% CI elsewhere

# *The* NEW ENGLAND JOURNAL *of* MEDICINE

ESTABLISHED IN 1812

NOVEMBER 24, 2016

VOL. 375 NO. 21

## TP53 and Decitabine in Acute Myeloid Leukemia and Myelodysplastic Syndromes

J.S. Welch, A.A. Petti, C.A. Miller, C.C. Fronick, M. O'Laughlin, R.S. Fulton, R.K. Wilson, J.D. Baty, E.J. Duncavage, B. Tandon, Y.-S. Lee, L.D. Wartman, G.L. Uy, A. Ghobadi, M.H. Tomasson, I. Pusic, R. Romee, T.A. Fehniger, K.E. Stockerl-Goldstein, R. Vij, S.T. Oh, C.N. Abboud, A.F. Cashen, M.A. Schroeder, M.A. Jacoby, S.E. Heath, K. Lubner, M.R. Janke, A. Hantel, N. Khan, M.J. Sukhanova, R.W. Knoebel, W. Stock, T.A. Graubert, M.J. Walter, P. Westervelt, D.C. Link, J.F. DiPersio, and T.J. Ley

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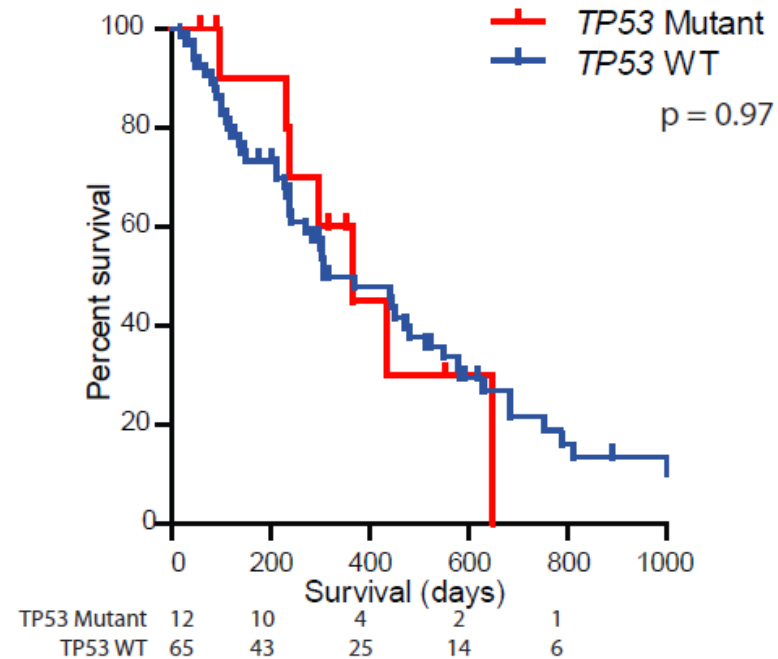
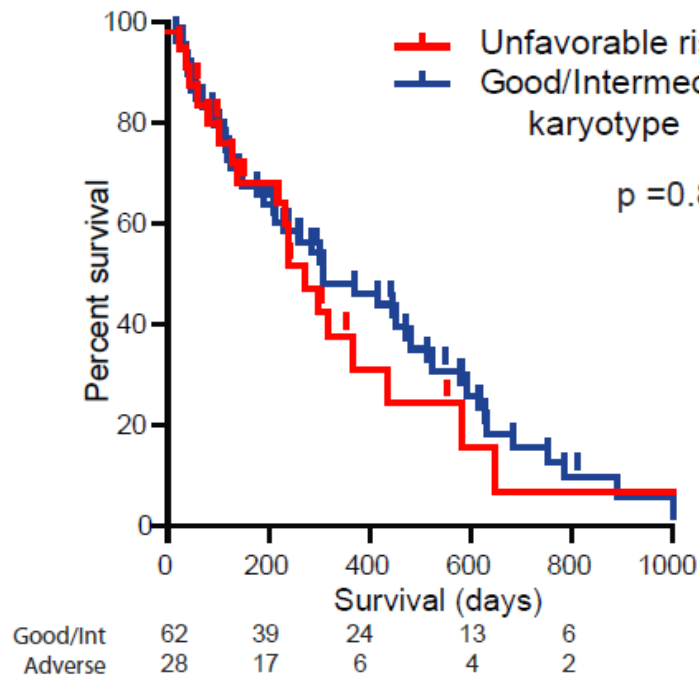
Welch JS et al. N Engl J Med 2016;

# 100% patients *TP53* mutations respond to Decitabine

Characteristic	All Patients (N=116)	<i>TP53</i> Mutations (N=21)	Wild-Type <i>TP53</i> (N=78)	<i>TP53</i> Not Evaluated (N=17)	P Value†
Response — no. (%)					
Bone marrow blast clearance <5% blasts	53 (46)	21 (100)	32 (41)	0	<0.001
Complete remission					
With recovery of peripheral-blood counts	15 (13)	4 (19)	11 (14)	0	0.73
With incomplete count recovery	24 (21)	9 (43)	15 (19)	0	0.04
Morphologic complete remission					
With hematologic improvement	6 (5)	5 (24)	1 (1)	0	0.002
Without hematologic improvement	8 (7)	3 (14)	5 (6)	0	0.36
No bone marrow blast clearance	63 (54)	0	46 (59)	5 (29)	<0.001
Partial response	9 (8)	0	9 (12)	0	0.05
Stable disease	23 (20)	0	18 (23)	5 (29)	0.006
Progressive disease	19 (16)	0	19 (24)	0	0.003
Samples not available for evaluation	12 (10)	0	0	12 (71)	



## OS according to risk karyotype and TP53 profile with decitabine

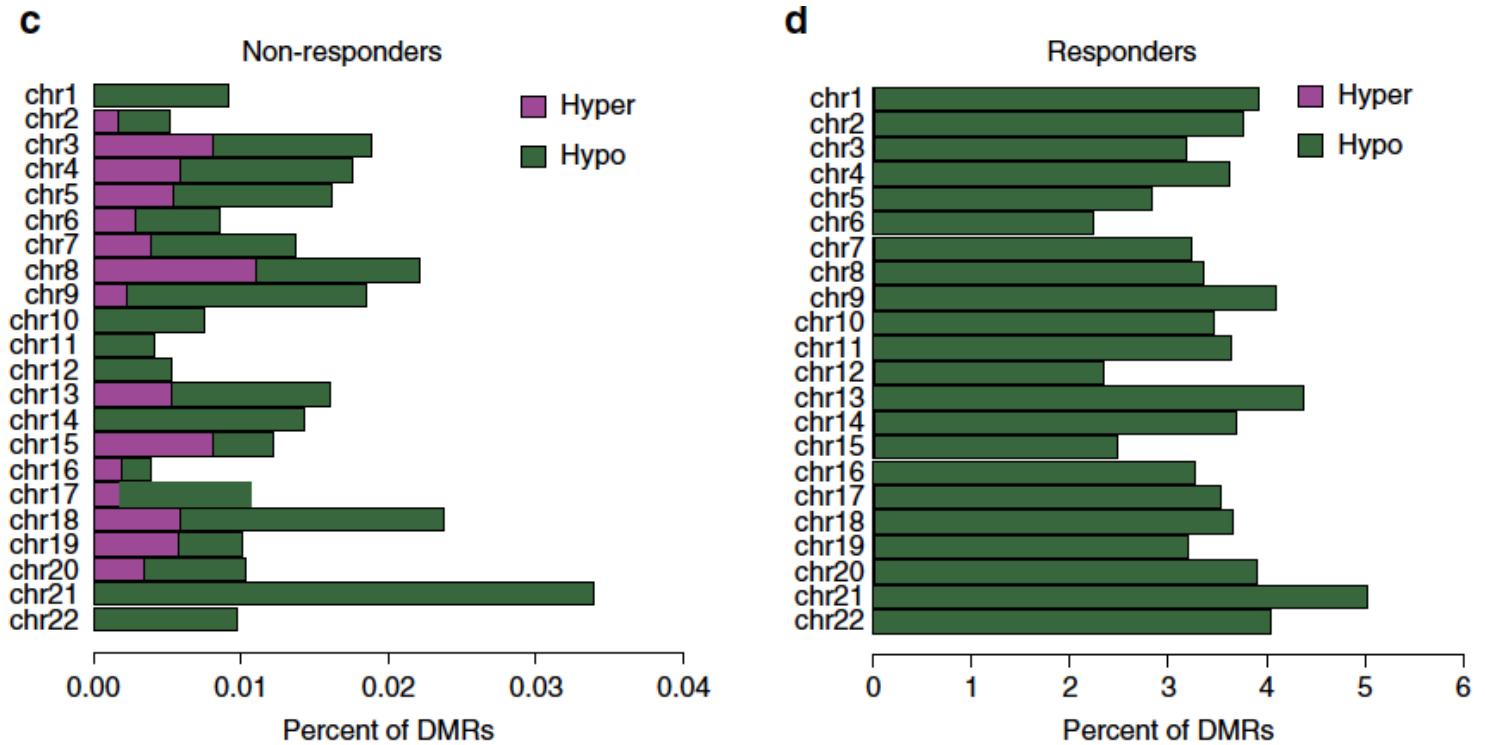


No differences between unfavourable and favourable risk karyotype  
No differences between per status TP53 mutant and wild type

# Response to DAC is associated with reversal of hypermethylation

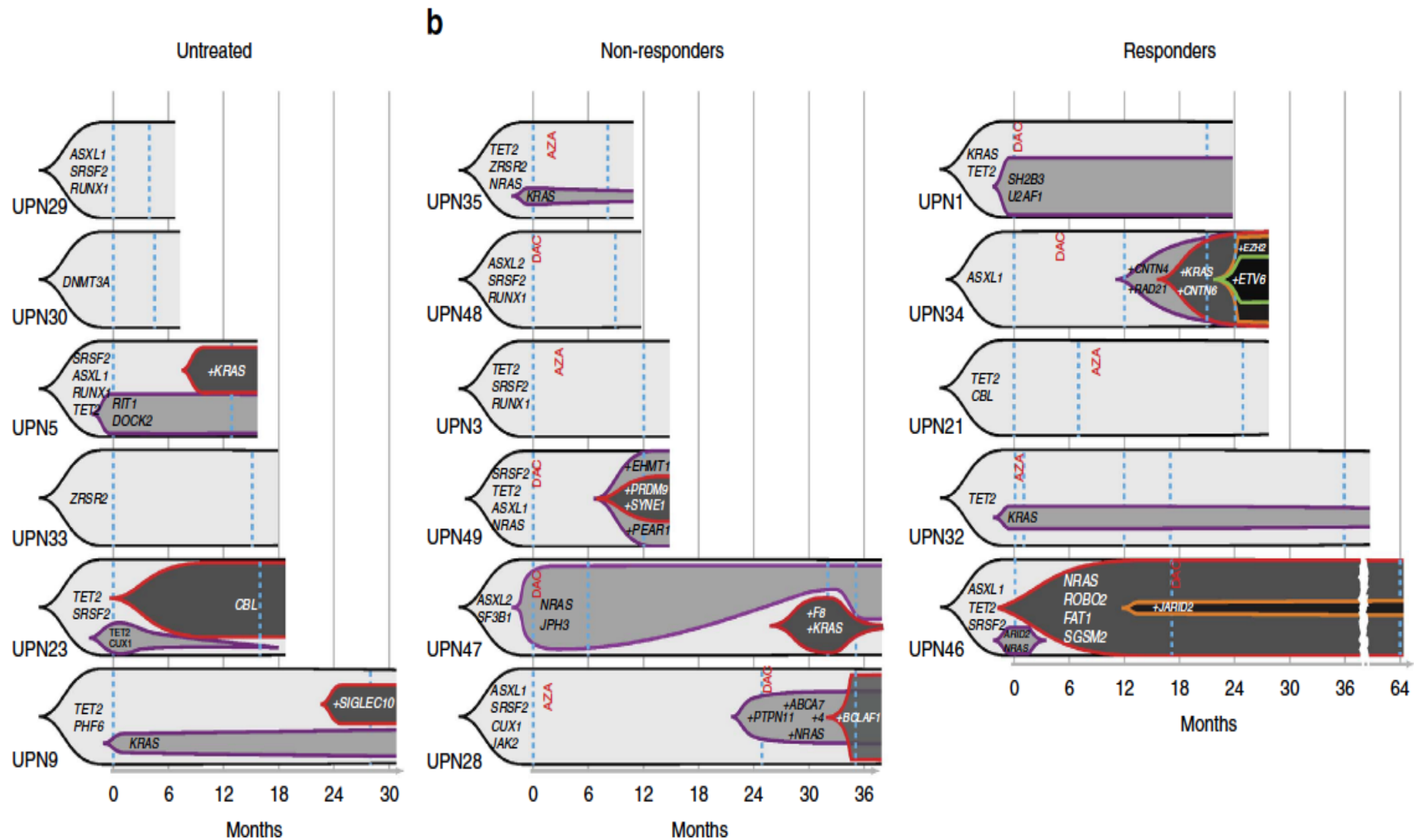
## Before DAC – After DAC

CHROMOSOMES

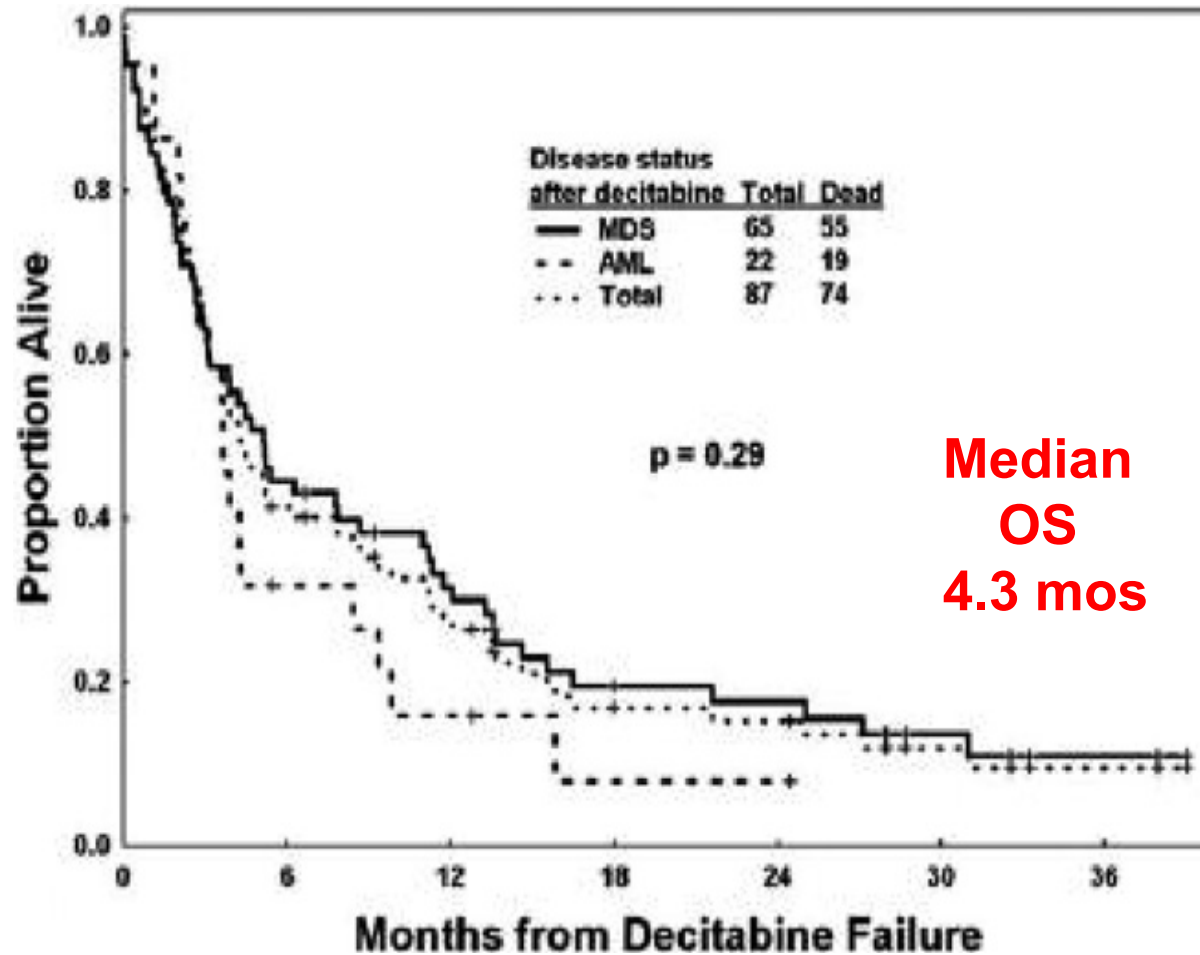


- Loss of mC  $\geq 25\%$  after DAC
- Gain of mC  $\geq 25\%$  after DAC

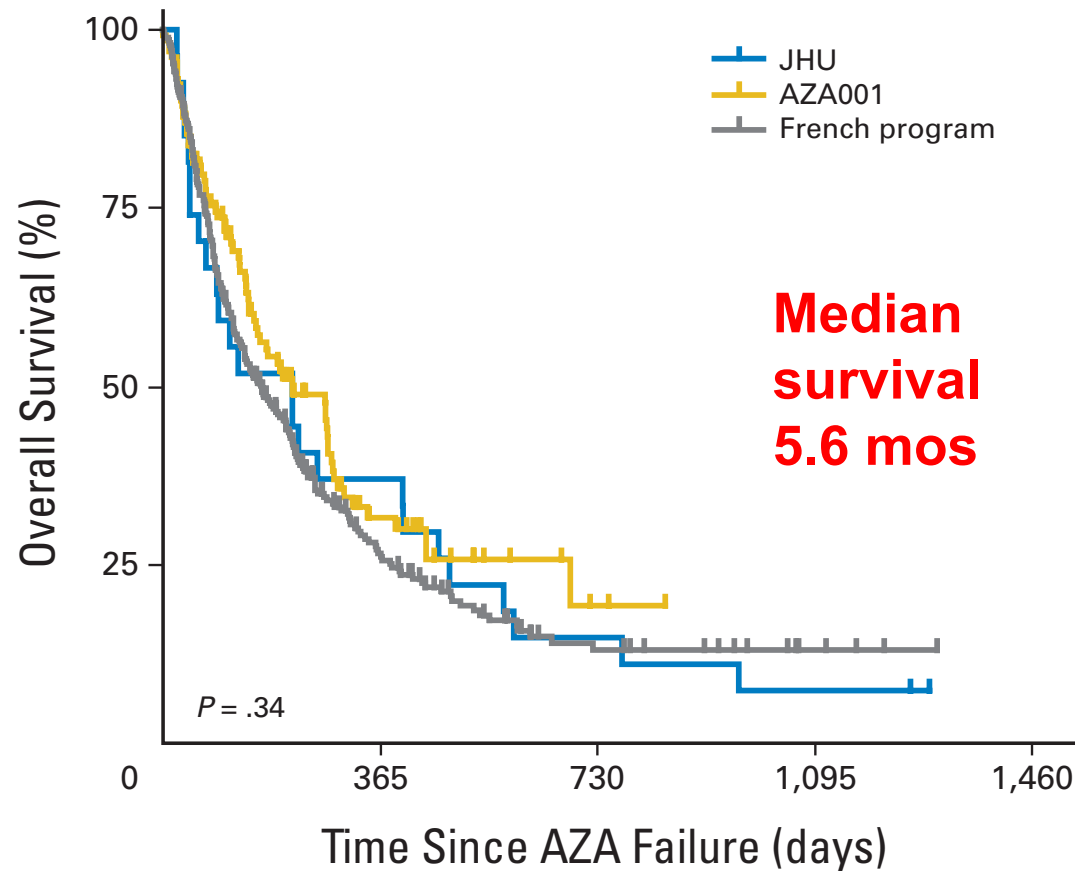
# Mutation allele burden remains unchanged after DAC



# Survival after decitabine failure in MDS/AML patients



# Survival after azacitidine failure in MDS/AML patients





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DEGLI STUDI  
FIRENZE

DIPARTIMENTO DI  
MEDICINA SPERIMENTALE  
E CLINICA



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Antonella Poloni

Emanuele Angelucci

Carlo Finelli

Alessandro Levis

Omar Abdel-Wahab



Ana Valencia

Erico Masala

Alice Brogi

Alessandro Sanna

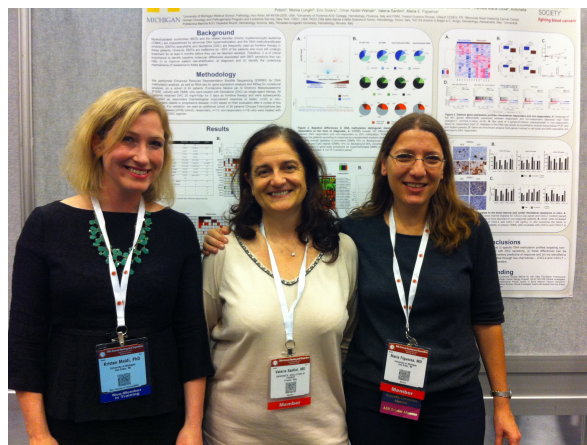
Valeria Santini



Maria E.Figueroa

Tingting Qin

Kristen Meldi



**Institute Gustave Roussy,  
Paris**

Eric Solary



Groupe  
Francophone des  
Myélodysplasies

Nathalie Droin

Dorothee Selimoglu-Buet