

Chronic myelomonocytic leukemia (CMML)



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CMML: a hybrid disease

Clonal hematologic “overlap” disease (MDS/MPN) characterized by myeloid dysplasia, proliferation, and absence of the molecular lesions BCR/ABL, PDGFRA, PDGFRB, and FGFR1.

There are currently no FDA or EMA approved therapies for any MDS/MPN subtypes, except CMML-dysplastic .

Reactive and Clonal Mimickers of CMML

Reactive:

- Subacute bacterial endocarditis/endo-myocarditis
- Tuberculosis
- Malaria infection
- EB virus infections
- Syphilis
- Typhoid fever
- Trypanosomiasis
- Drug-induced toxic reactions
- Corticosteroid therapy
- Treatment with GM-CSF
- Paraneoplastic (T cell lymphoma, Hodgkin disease, solid tumors)
- Chronic and acute autoimmune diseases
- Sarcoidosis
- Chronic hepatitis plus cirrhosis
- Collagen disease
- Asplenic state
- Pregnancy

Clonal:

- CMUS
- Low risk MDS with monocytosis
- High risk MDS with monocytosis
- Monoblastic AML
- MPN with monocytosis
- GATA2 deficiency with monocytosis
- RASopathies: CBL syndromes and others*
- JMML
- Histiocytosis

WHO 2016 classification

Myelodysplastic/myeloproliferative neoplasms (MDS/MPN)

Chronic myelomonocytic leukemia

Atypical chronic myeloid leukemia, *BCR-ABL1*-negative

Juvenile myelomonocytic leukemia

Myelodysplastic/myeloproliferative neoplasm with ring sideroblasts and thrombocytosis (MDS/MPN-RS-T)

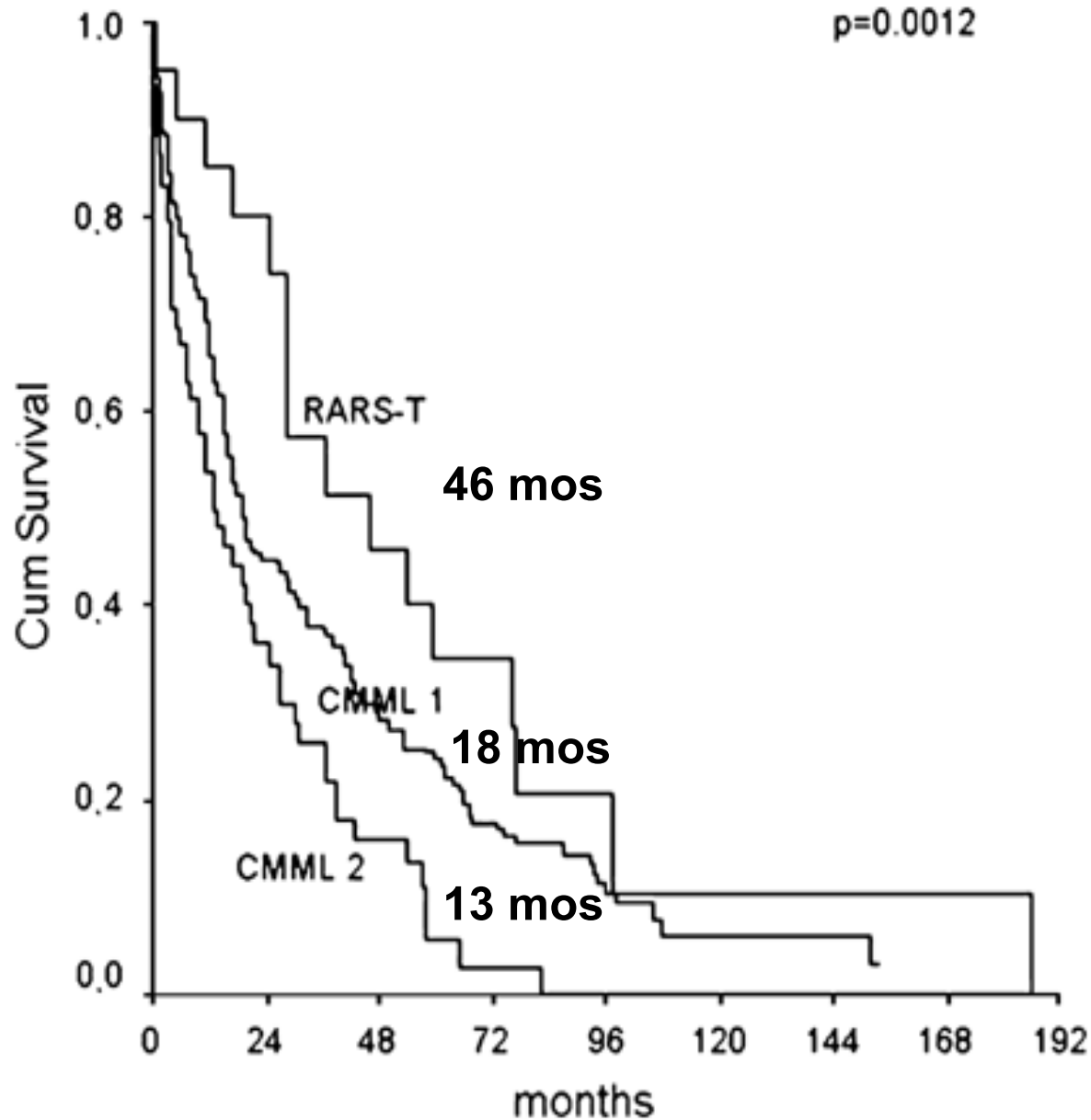
Myelodysplastic/myeloproliferative neoplasm, unclassifiable

CMML: WHO2016 diagnostic criteria

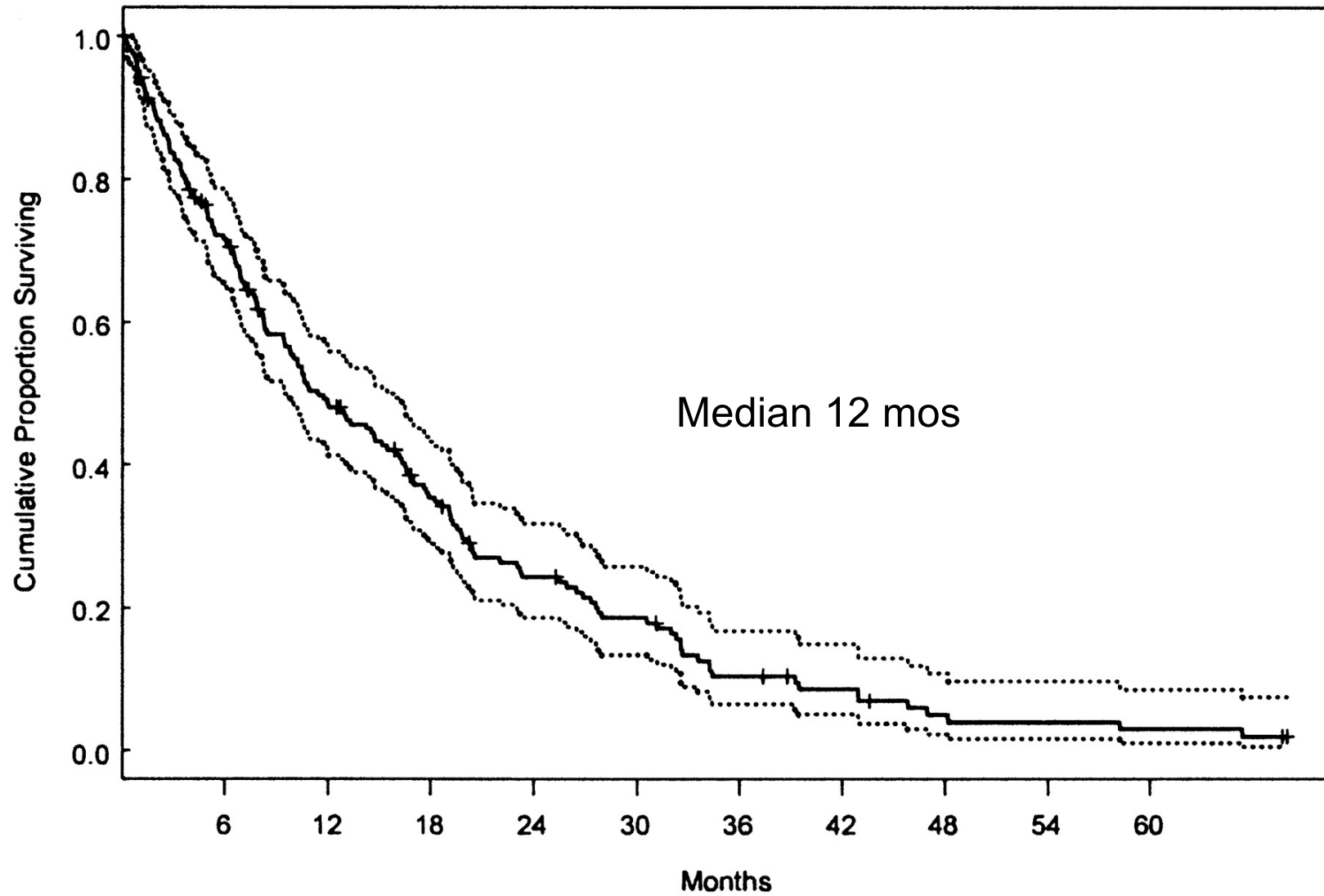
CMML diagnostic criteria

- Persistent PB monocytosis $\geq 1 \times 10^9/L$, with monocytes accounting for $\geq 10\%$ of the WBC count
 - Not meeting WHO criteria for *BCR-ABL1*⁺ CML, PMF, PV, or ET*
 - No evidence of *PDGFRA*, *PDGFRB*, or *FGFR1* rearrangement or *PCM1-JAK2* (should be specifically excluded in cases with eosinophilia)
 - $<20\%$ blasts in the blood and BM†
 - Dysplasia in 1 or more myeloid lineages. If myelodysplasia is absent or minimal, the diagnosis of CMML may still be made if the other requirements are met and
 - An acquired clonal cytogenetic or molecular genetic abnormality is present in hemopoietic cells‡
- or
- The monocytosis (as previously defined) has persisted for at least 3 mo and
 - All other causes of monocytosis have been excluded

Overall survival in MDS/MPN



Overall survival in CMML



Onida F et al. Blood 2002;99:840-849

CMML Classifications... the last one

Proposed Grading of Chronic Myelomonocytic Leukemia (CMML)*

Grading-based variants	Diagnostic features / criteria
CMML-0	<5% blasts in BM smears and <2% blasts in PB**
Dysplastic CMML-0	PB leukocytes $\leq 13 \times 10^9/L$
Proliferative CMML-0	PB leukocytes $> 13 \times 10^9/L$
CMML-1	6-9% blasts in BM smears and 2-4% blasts in PB**
Dysplastic CMML-1	PB leukocytes $\leq 13 \times 10^9/L$
Proliferative CMML-1	PB leukocytes $> 13 \times 10^9/L$
CMML-2***	10-19% blasts in BM smears and 5-19% in PB**
Dysplastic CMML-2	PB leukocytes $\leq 13 \times 10^9/L$
Proliferative CMML-2	PB leukocytes $> 13 \times 10^9/L$ ***

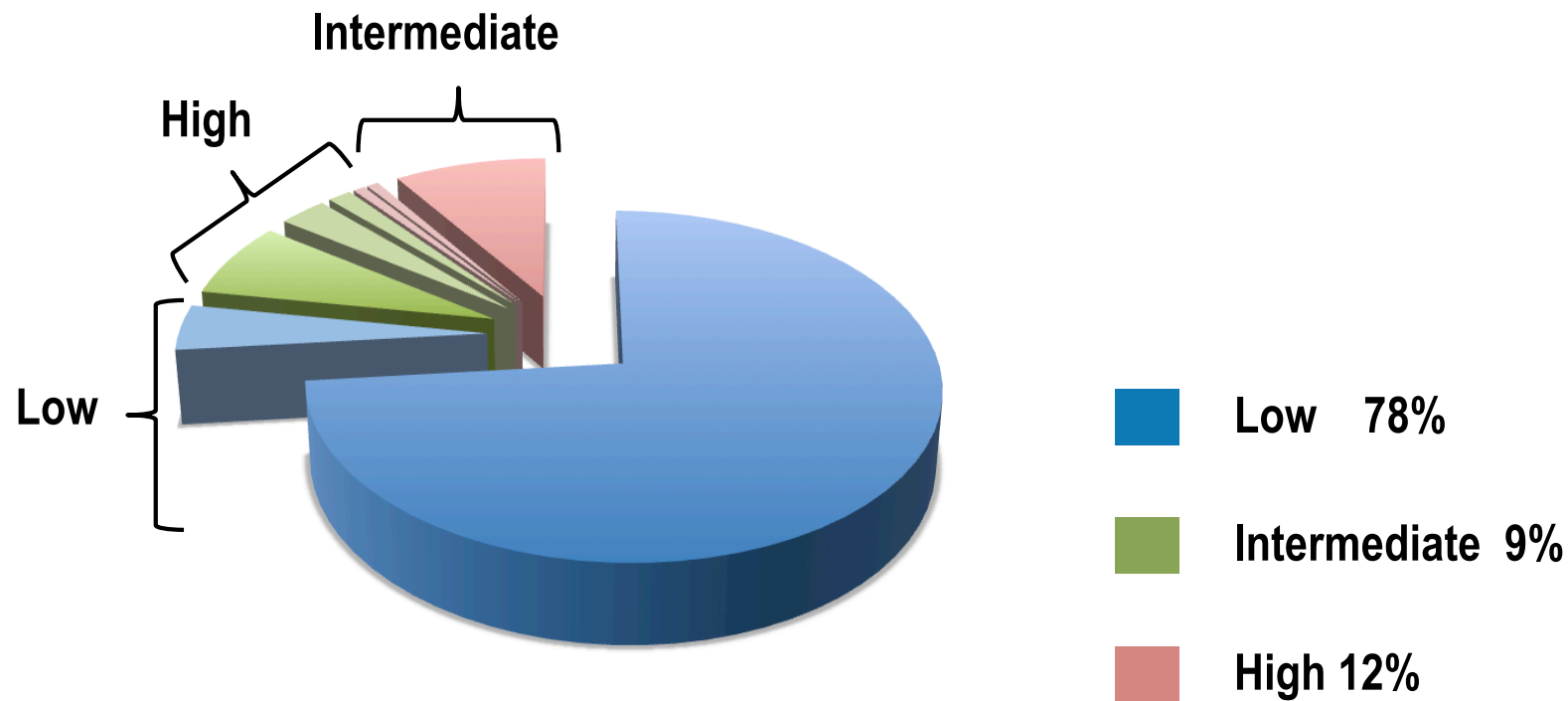
CMML Classifications... the last one

Phenotypic Classification of Monocytes and Distribution of Monocyte-Subsets in CMML and Controls*

Monocyte -Subset	Defining Phenotype	Typical Relative Frequency in*		
		CMML	MDS or MPN	Reactive BM
Classical (MO1)	CD14 ^{bright} /CD16 ⁻	≥94%	70-97%	<94%
Intermediate (MO2)	CD14 ^{bright} /CD16 ⁺	<20%	5-20%	5-15%
Non-classical (MO3)	CD14 ^{dim} /CD16 ⁺	<5%	5-10%	5-20%

Cytogenetic classification

- **Low risk:** normal, -Y (unique alteration).
- **High risk :** +8, -7/del(7q) complex karyotype
- – **Intermediate risk:** everything else



CMML-specific prognostic scoring system (CPSS)

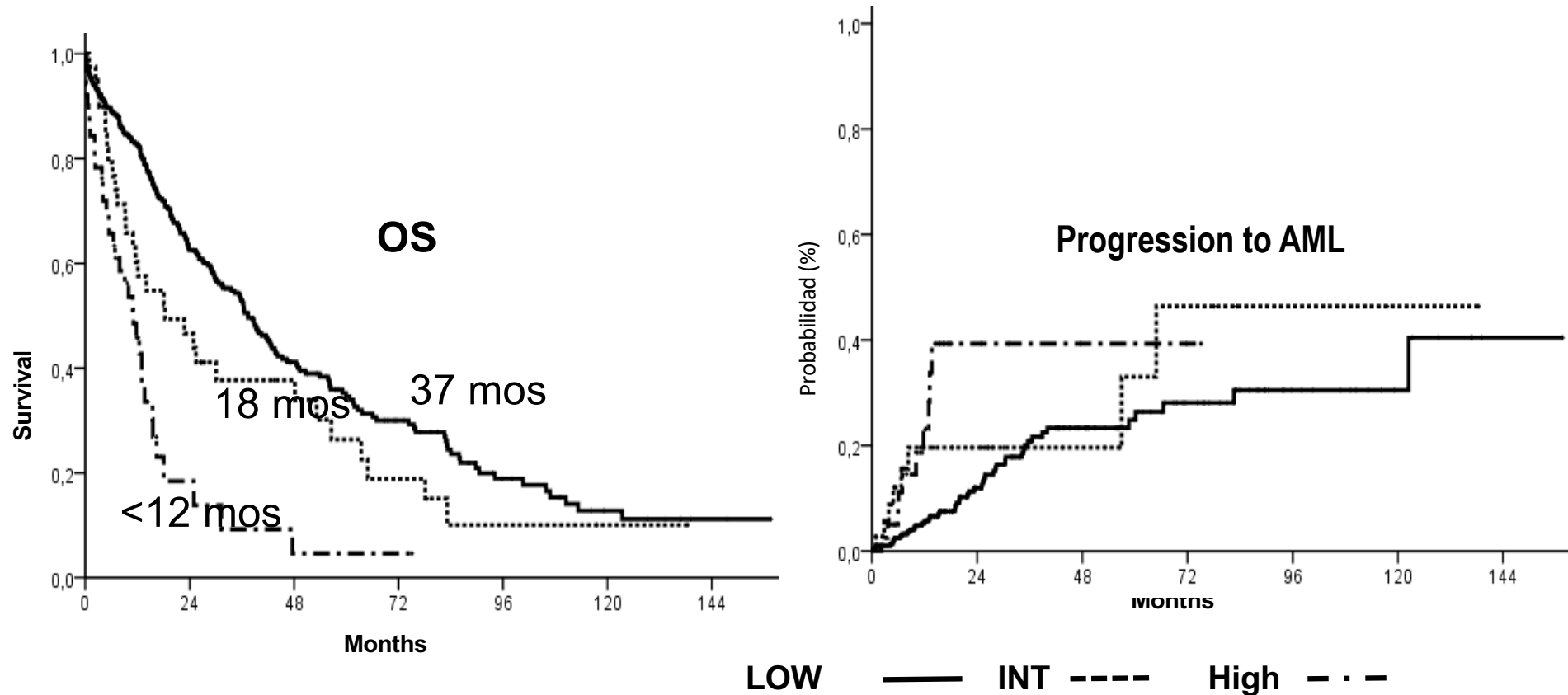
Training cohort: 558 pts (Spanish Group of Myelodysplastic Syndromes)

Validation cohort: 274 pts (Düsseldorf, Pavia)

Variable	Variable scores		
	0	1	2
WHO subtype	CMML-1 blasts (including promonocytes) <5% in the PB and <10% in the BM	CMML-2 blasts (including promonocytes) from 5% to 19% in the PB and from 10% to 19% in the BM, or when Auer rods are present irrespective of blast count	—
FAB subtype	CMML-MD (WBC count <13 × 10 ⁹ /L)	CMML-MP (WBC count ≥13 × 10 ⁹ /L)	—
CMML-specific cytogenetic risk classification*	Low	Intermediate	High
RBC transfusion dependency†	No	Yes	—

Risk group	Overall score
Low	0
Intermediate-1	1
Intermediate-2	2-3
High	4-5

Outcome of CMML pts according to cytogenetic risk



Low risk:

- normal or -Y (single)

High risk:

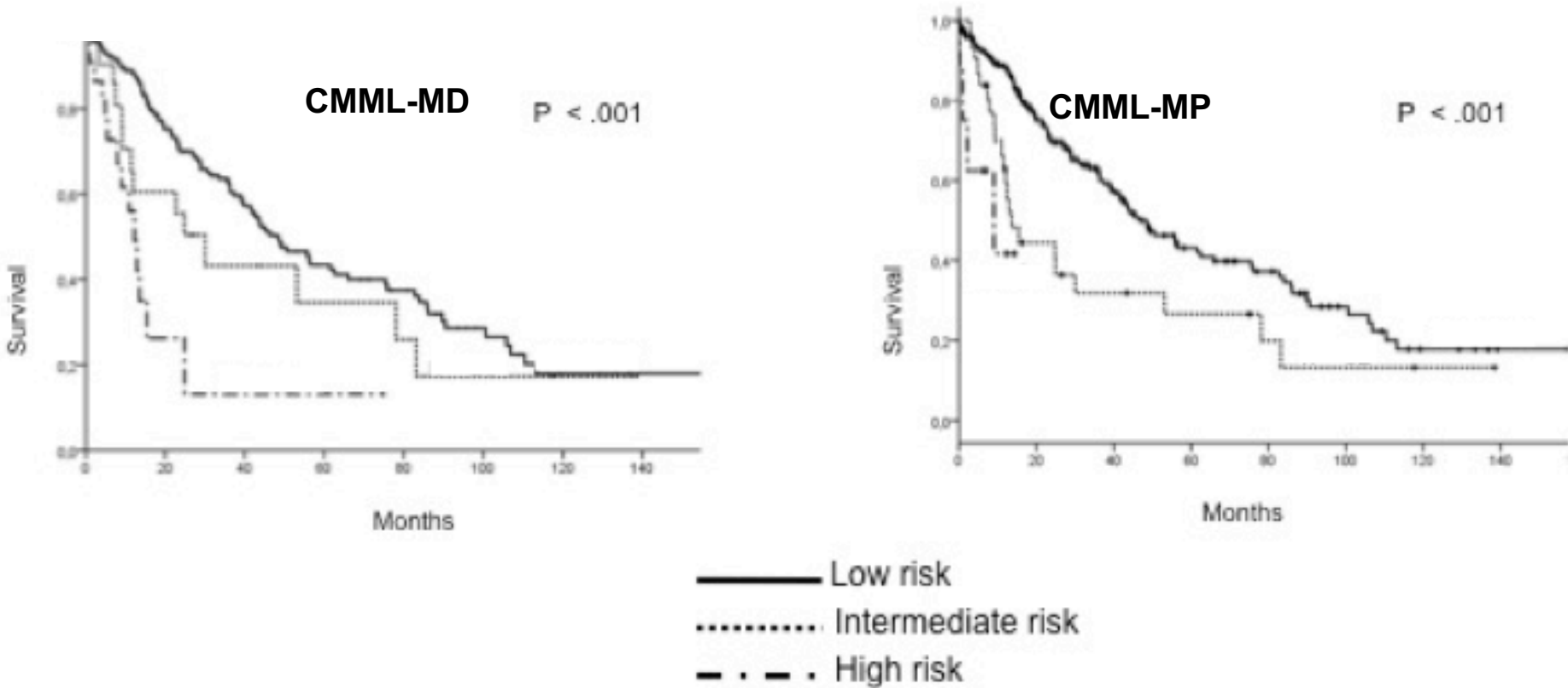
- abn chr 7, complex, +8

Intermediate risk:

- all others

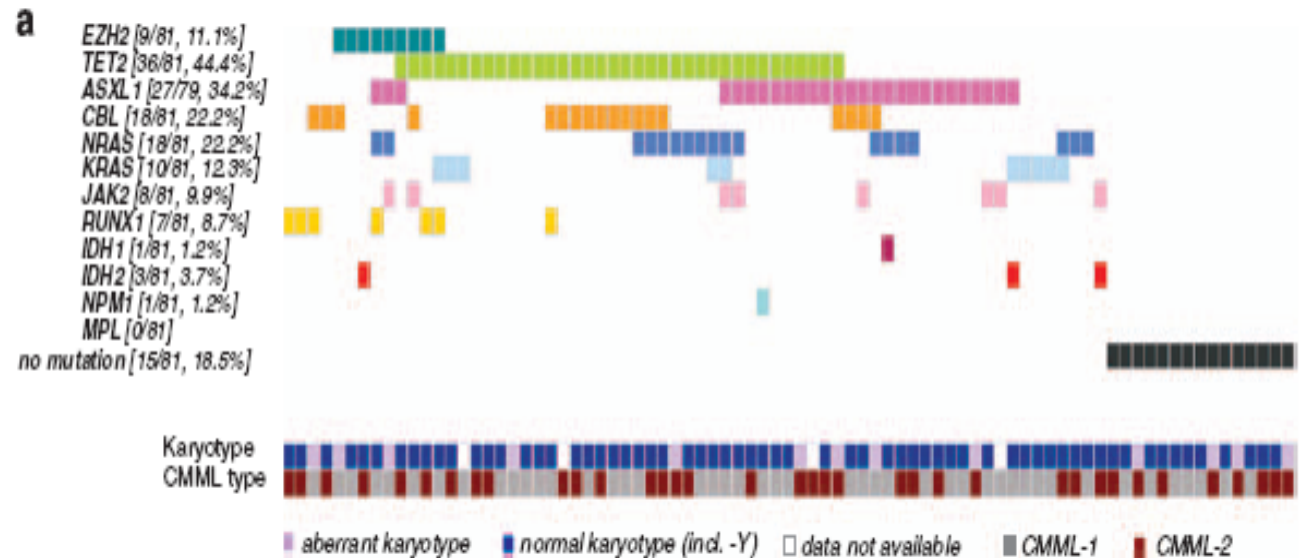
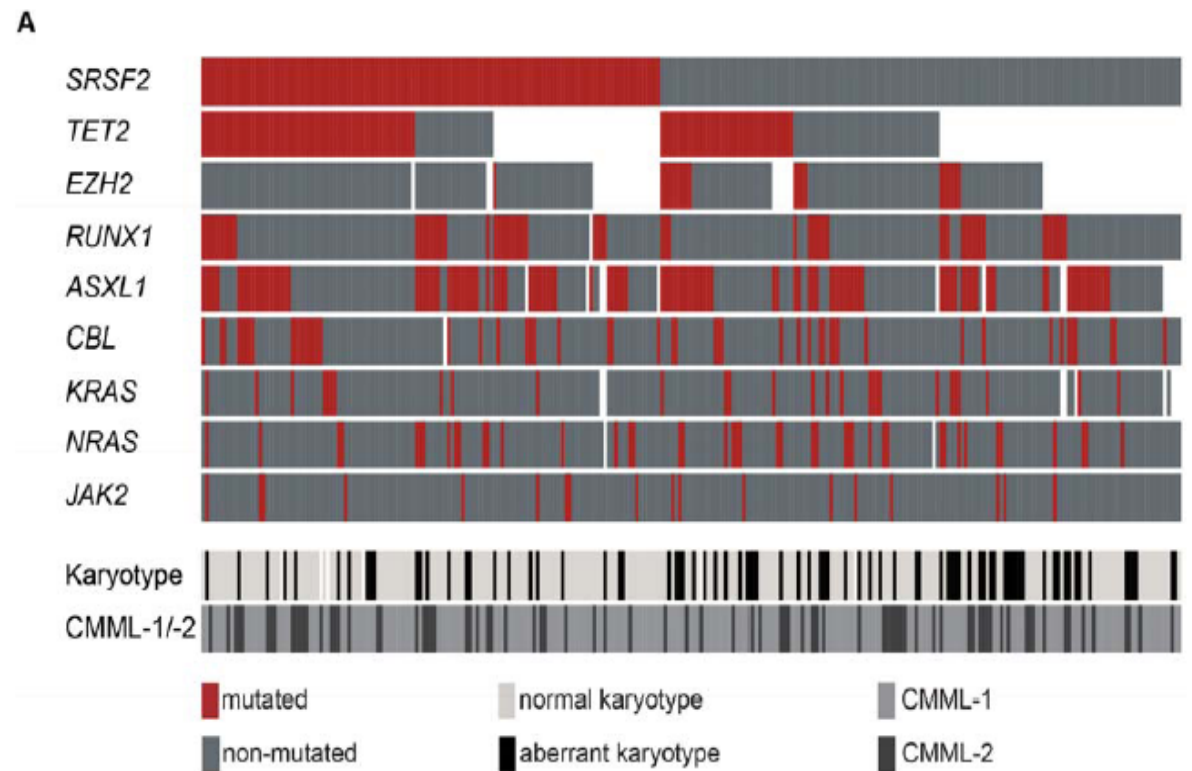
Cytogenetic risk groups are predicting outcome in CMML MD and CMML MP

A

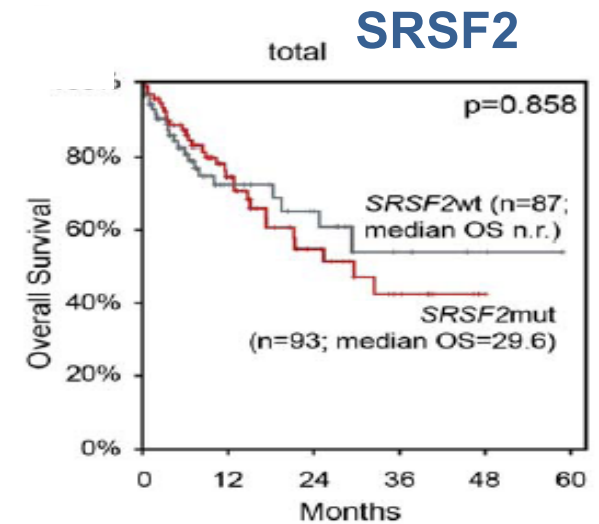
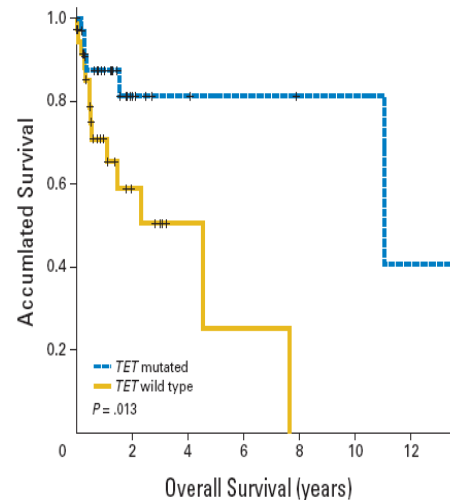
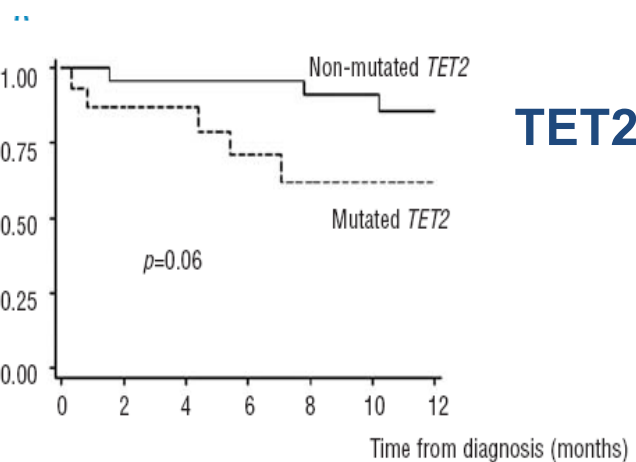
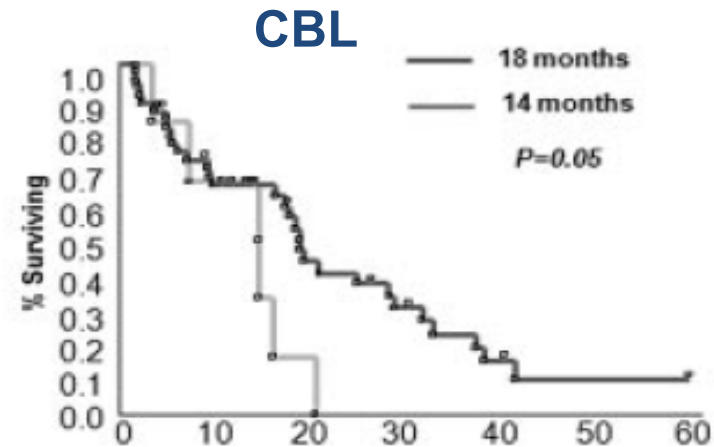
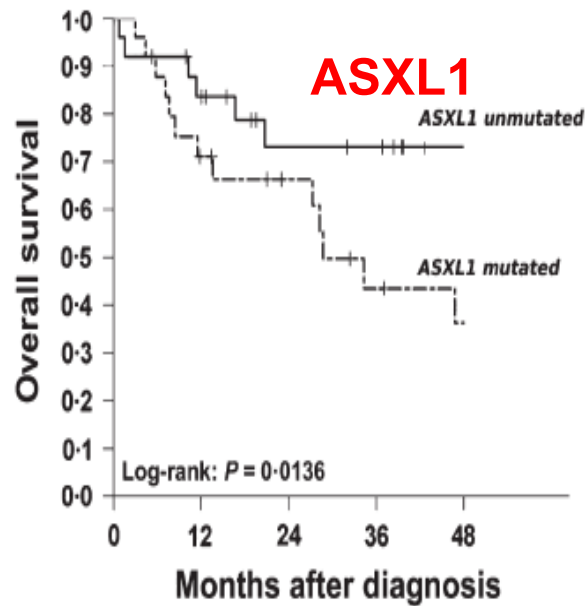


Molecular mutations in CMML

GENES	frequency
<i>TET2</i>	36 - 61%
<i>SRSF2</i>	28 - 47 %
<i>ASXL1</i>	27 - 52%
<i>RUNX1</i>	9 - 37%
<i>CBL</i>	5 - 19%
<i>RAS</i>	11 - 27%
<i>EZH2</i>	6 - 10%
<i>JAK2</i>	1 - 13%
<i>DNMT3A</i>	4 - 10%
<i>IDH1/2</i>	5 - 10%
<i>SF3B1</i>	5%
<i>U2AF1</i>	4 - 8%



Prognostic relevance of different somatic mutations



Meggendorfer *et al.* Blood 2012

Geisi-Boyer *et al.* BJH 2010

Jankowska *et al.*, Blood 2011

Kosmider *et al.*, Haematologica. 2009

Kohlmann *et al.*, JCO 2010

MYELOID NEOPLASIA

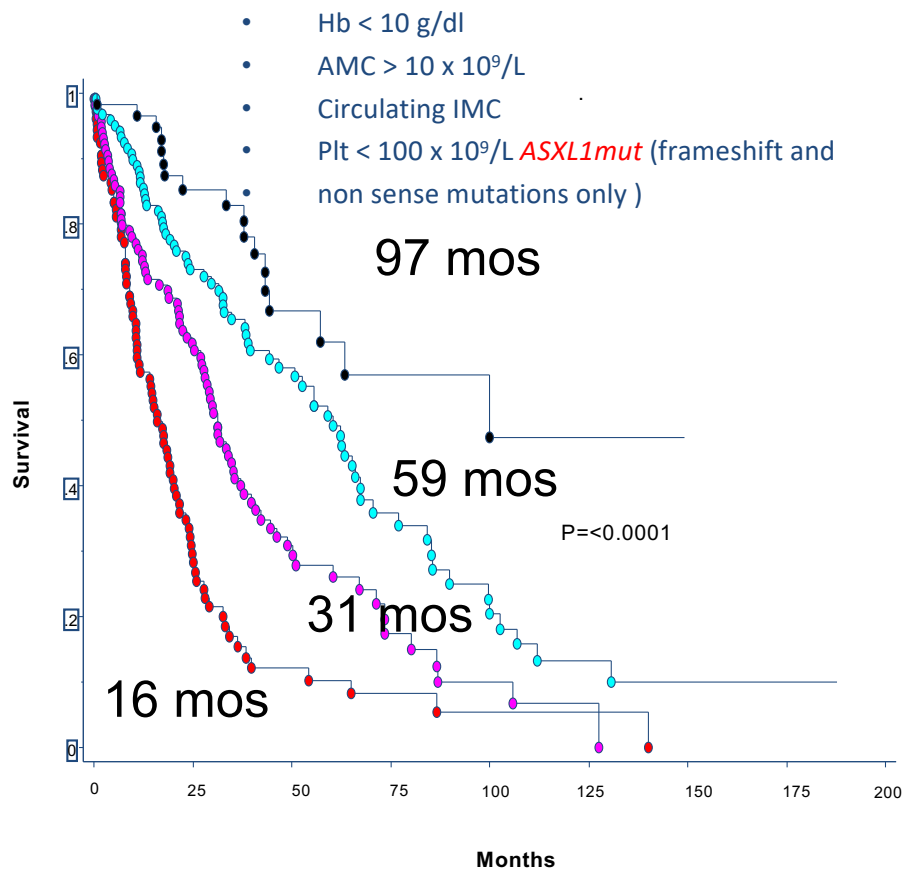
Integrating clinical features and genetic lesions in the risk assessment of patients with chronic myelomonocytic leukemia

Chiara Elena,^{1,2} Anna Gallì,² Esperanza Such,³ Manja Meggendorfer,⁴ Ulrich Germing,⁵ Ettore Rizzo,⁶ Jose Cervera,³ Elisabetta Molteni,¹ Annette Fasan,⁴ Esther Schuler,⁵ Ilaria Ambaglio,² Maria Lopez-Pavia,³ Silvia Zibellini,² Andrea Kuendgen,⁵ Erica Travaglino,² Reyes Sancho-Tello,⁷ Silvia Catricalà,² Ana I. Vicente,⁸ Torsten Haferlach,⁴ Claudia Haferlach,⁴ Guillermo F. Sanz,³ Luca Malcovati,^{1,2,*} and Mario Cazzola^{1,2,*}

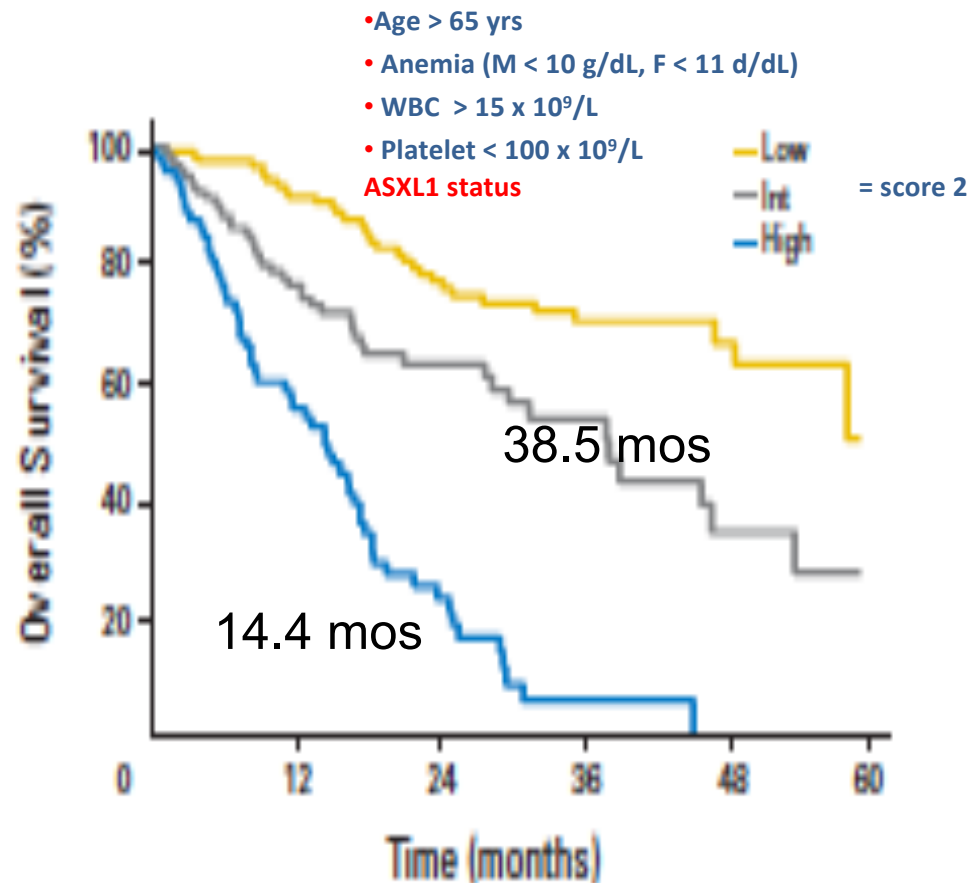
« mutations in RUNX1, NRAS, SETBP1, and ASXL1 were independently associated with overall survival (OS) »

OS according to Prognostic scores including ASXL1

Molecular Mayo



GFM



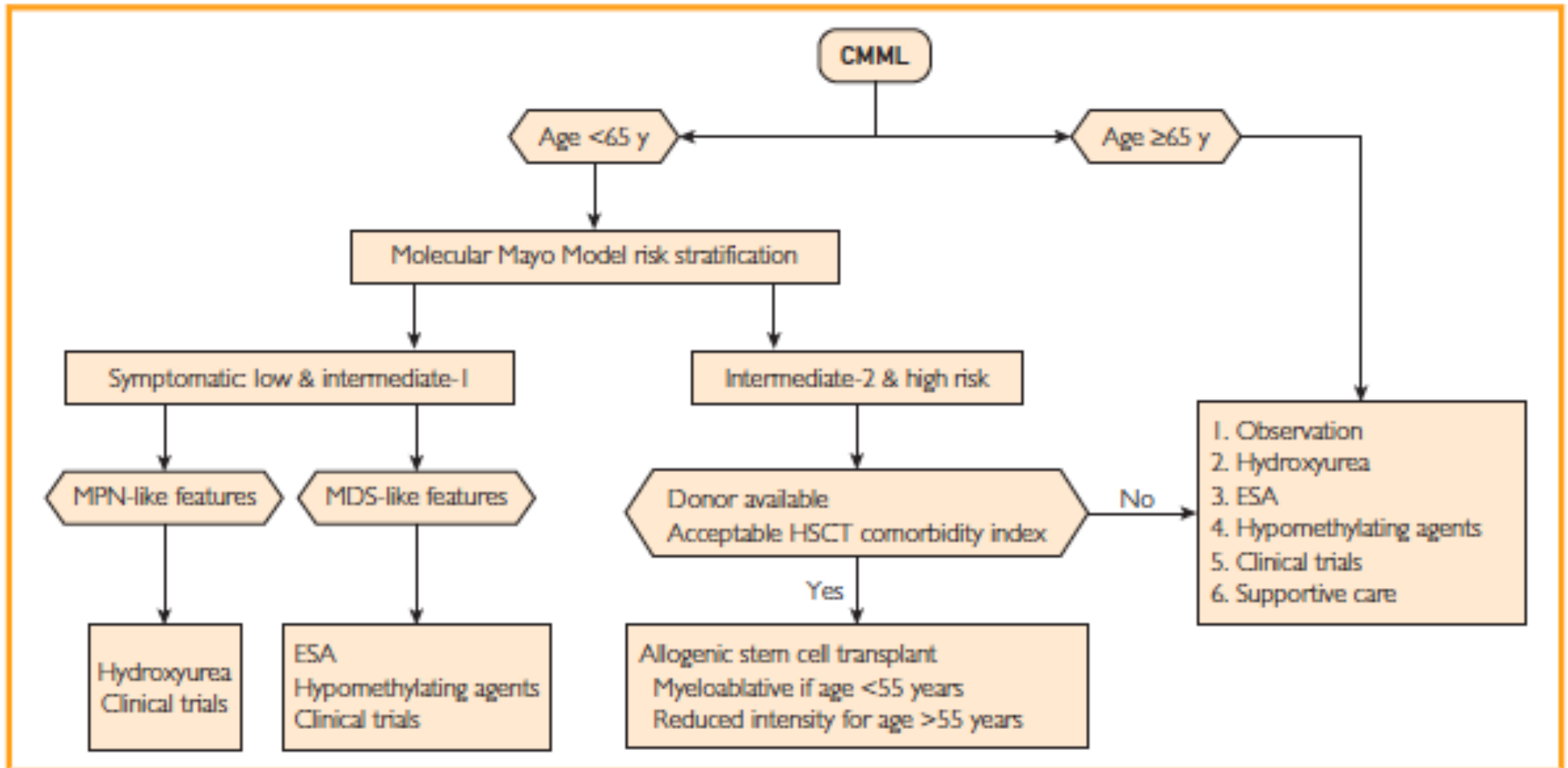
An international consortium proposal of uniform response criteria for myelodysplastic/myeloproliferative neoplasms (MDS/MPN) in adults

Michael R. Savona,¹ Luca Malcovati,² Rami Komrokji,³ Ramon V. Tiu,⁴ Tariq I. Mughal,⁵ Attilio Orazi,⁶ Jean-Jacques Kiladjian,⁷ Eric Padron,³ Eric Solary,⁸ Raoul Tibes,⁹ Raphael Itzykson,⁷ Mario Cazzola,² Ruben Mesa,⁹ Jaroslaw Maciejewski,⁴ Pierre Fenaux,⁷ Guillermo Garcia-Manero,¹⁰ Aaron Gerds,⁴ Guillermo Sanz,¹¹ Charlotte M. Niemeyer,¹² Francisco Cervantes,¹³ Ulrich Germing,¹⁴ Nicholas C. P. Cross,¹⁵ and Alan F. List,³ on behalf of the MDS/MPN International Working Group

Table 2. Proposed criteria for measurement of treatment response in adult MDS/MPN

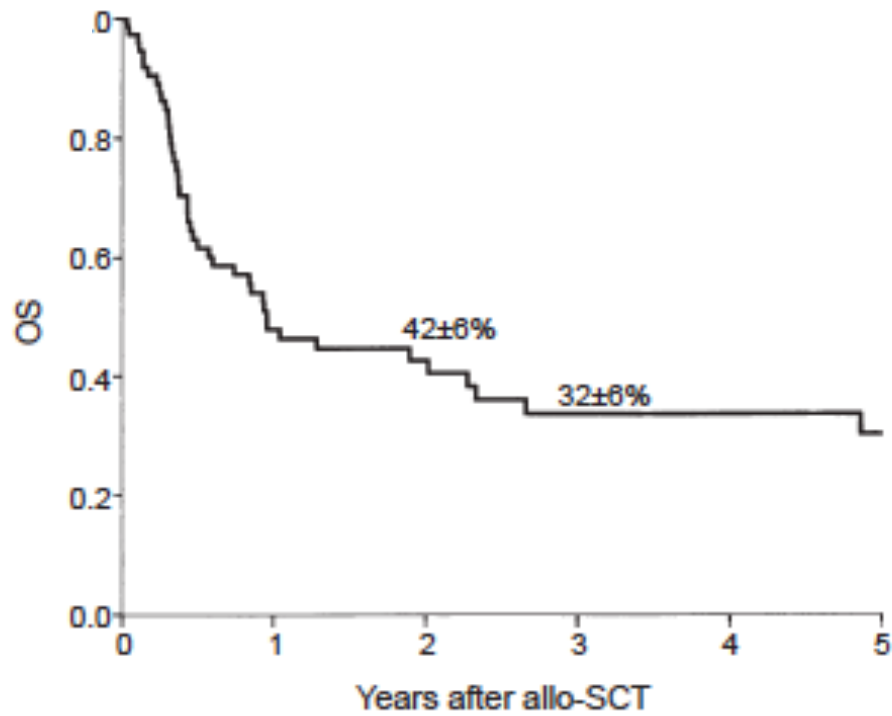
CR (presence of all of the following improvements)*
Bone marrow: $\leq 5\%$ myeloblasts (including monocytic blast equivalent in case of CMML) with normal maturation of all cell lines and return to normal cellularity*
Osteomyelofibrosis absent or equal to "mild reticulin fibrosis" (\leq grade 1 fibrosis)†
Peripheral blood‡
WBC $\leq 10 \times 10^9$ cells/L
Hgb ≥ 11 g/dL
Platelets $\geq 100 \times 10^9/L$; $\leq 450 \times 10^9/L$
Neutrophils $\geq 1.0 \times 10^9/L$
Blasts 0%
Neutrophil precursors reduced to $\leq 2\%$
Monocytes $\leq 1 \times 10^9/L$
Extramedullary disease: Complete resolution of extramedullary disease present before therapy (eg, cutaneous disease, disease-related serous effusions), including palpable hepatosplenomegaly
Provisional category of CR with resolution of symptoms:‡ CR as described above, and complete resolution of disease-related symptoms as noted by the MPN-SAF TSS
Persistent low-level dysplasia is permitted given subjectivity of assignment of dysplasia*

Therapeutic recommendations for CMML

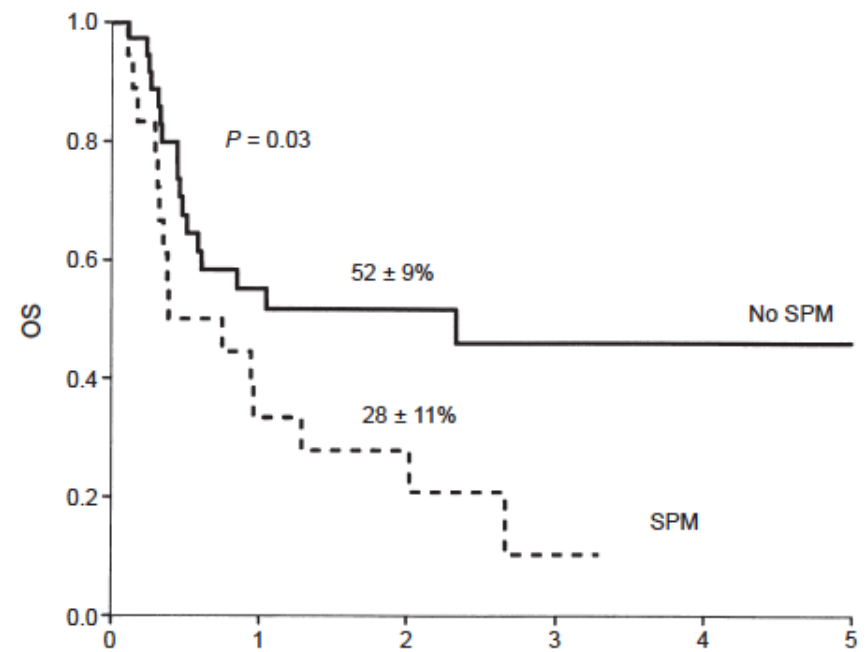


OS in CMML after allogeneic HSCT

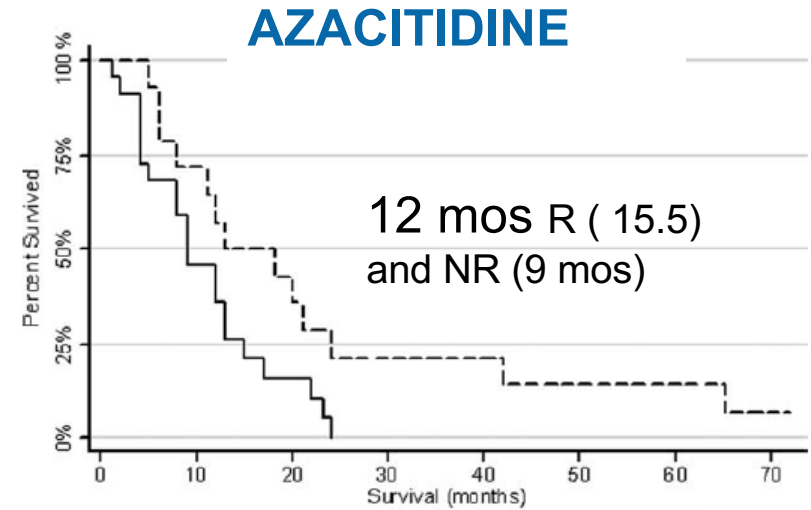
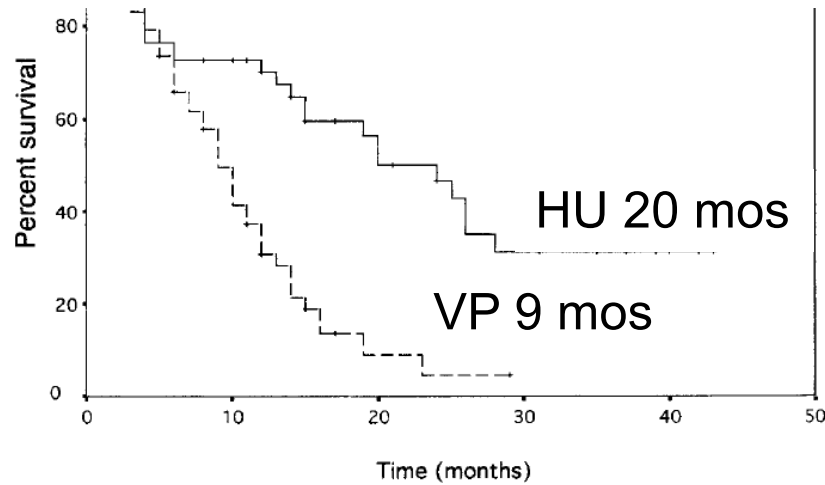
overall



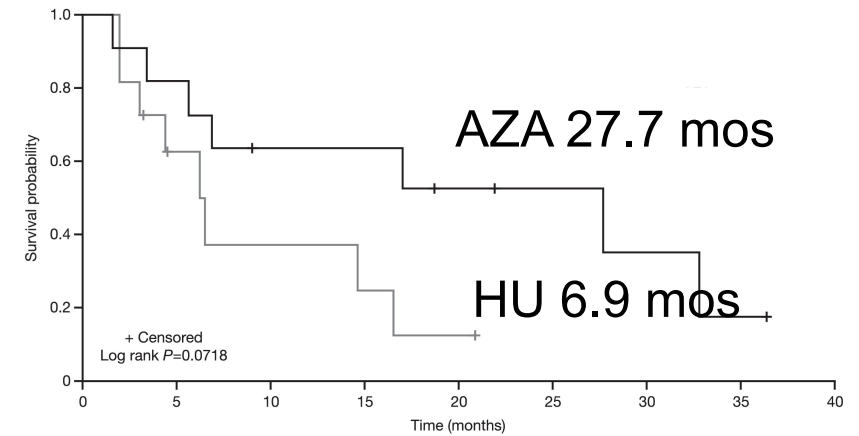
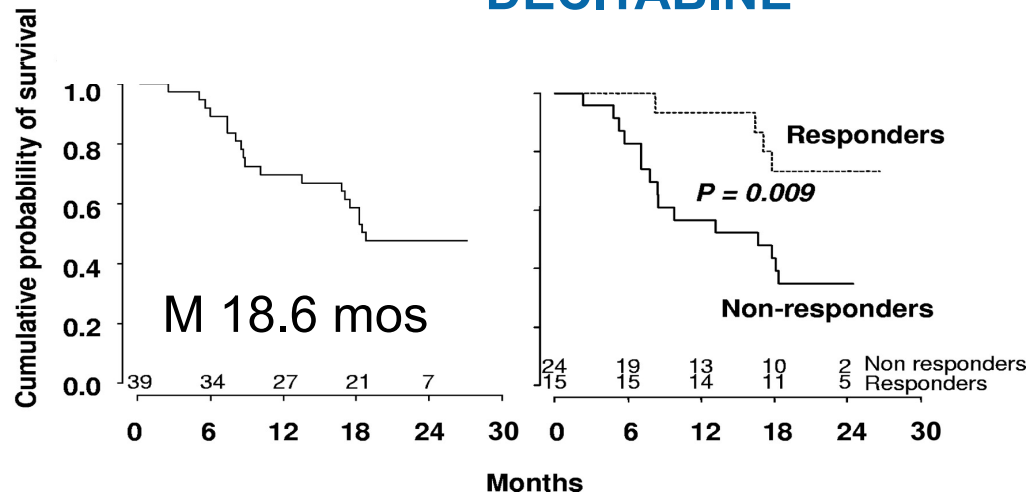
according spleen size



OS in CMML after therapy



DECITABINE



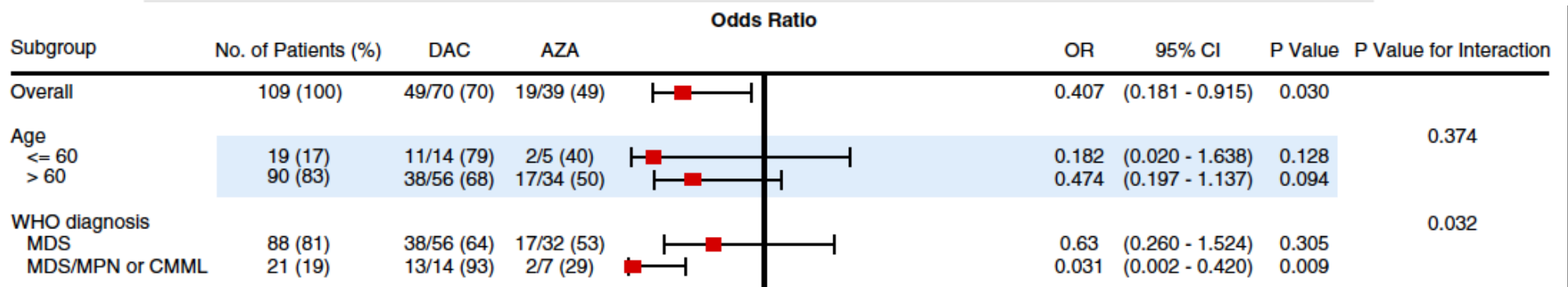
Wattel et al, Blood 1996
 Braun et al., Blood 2011

Costa et al, Cancer 2011;
 Pleyer et al., Leuk Res 2014

Low-Dose Decitabine or Azacitidine in MDS/MPN

- Bayesian adaptive randomization: DAC vs. AZA
- Regimens:
 - DAC 20 mg/m² IV D1-3 every 4 weeks
 - AZA 75 mg/m² IV/SC D1-3 every 4 weeks
- Response assessment by modified IWG 2006

	Overall	DAC	AZA
MDS/MPN-U	6 (5)	2 (3)	4 (10)
CMML	16 (14)	10 (14)	6 (15)





A phase II, multicentre trial of decitabine in higher-risk chronic myelomonocytic leukemia

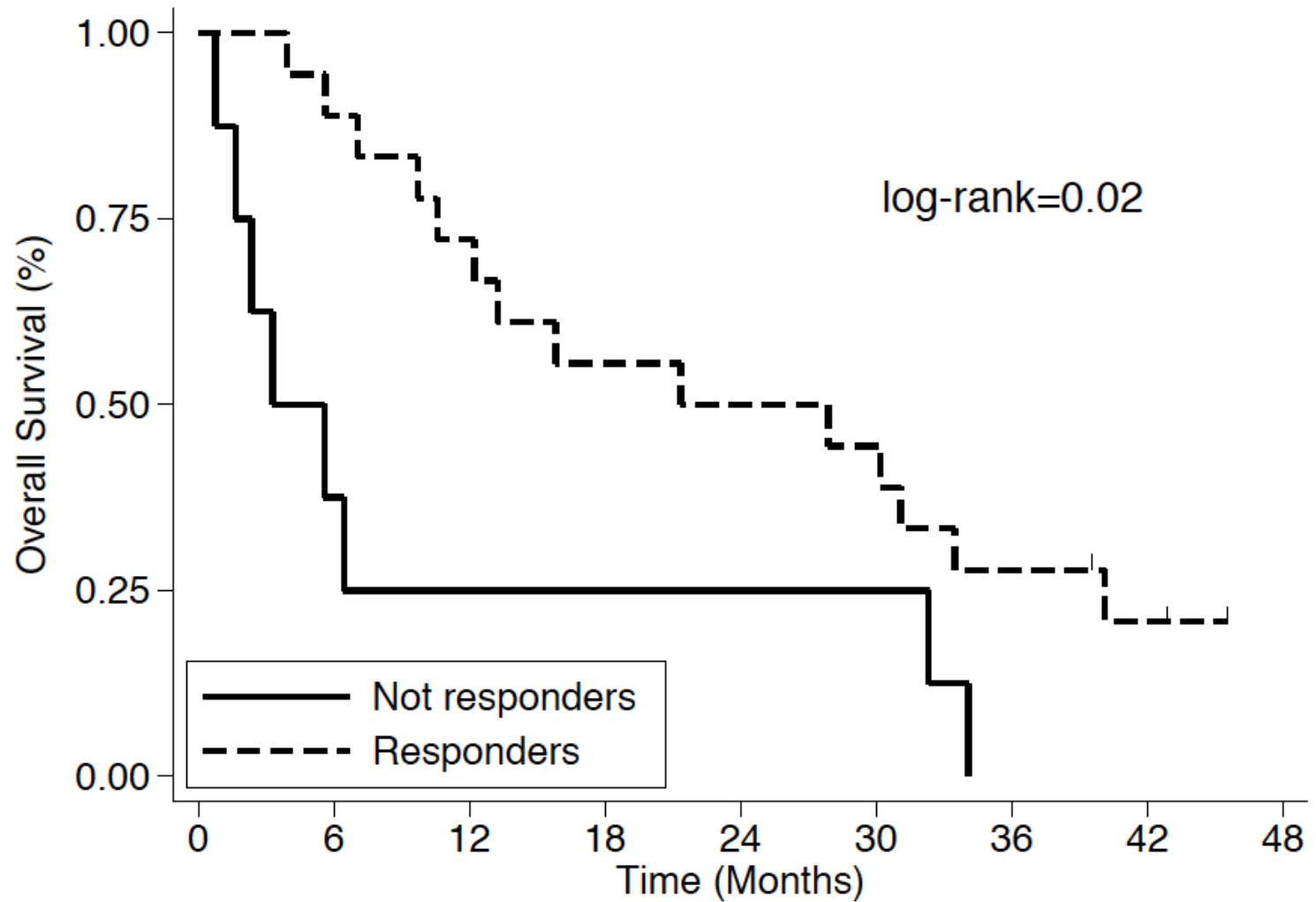
V Santini, B Allione, G Zini, D Gioia, M Lunghi, A Poloni, D Cilloni, A Sanna, E Masiera, M Ceccarelli, O Abdel-Wahab, A Terenzi, E Angelucci, C Finelli, F Onida, A M Pelizzari, D Ferrero, G Saglio, M Figueroa, A Levis

Santini et al; Leukemia. 2018 Feb;32(2):413-418.

Response to decitabine in CMML patients (7% ORR in TP53 mut)

	Number (%) of patients				
	ITT (n = 42)	CMML-1 ^a (n = 26)	CMML-2 ^a (n = 16)	dCMML (n = 14)	pCMML (n = 28)
ORR	20 (47.6)	15 (57.6)	5 (31.25)	9 (64.3)	11 (39.3)
CR	7 (16.6)	5 (19.2)	2 (12.5)	3 (21.4)	4 (14.3)
mCR	8 (19.0)	6 (23.1)	2 (12.5)	4 (28.6)	4 (14.3)
PR	1 (2.4)	0 (0.0)	1 (6.2)	0 (0.0)	1 (3.5)
HI	4 (9.5)	4 (15.3)	0 (0.0)	2 (14.2)	2 (7.2)
SD	9 (21.4)	4 (15.3)	5 (31.3)	0 (0.0)	9 (32.1)
PD	13 (31.0)	7 (26.9)	6 (37.5)	5 (35.7)	8 (28.6)

Overall survival according to Response to DAC



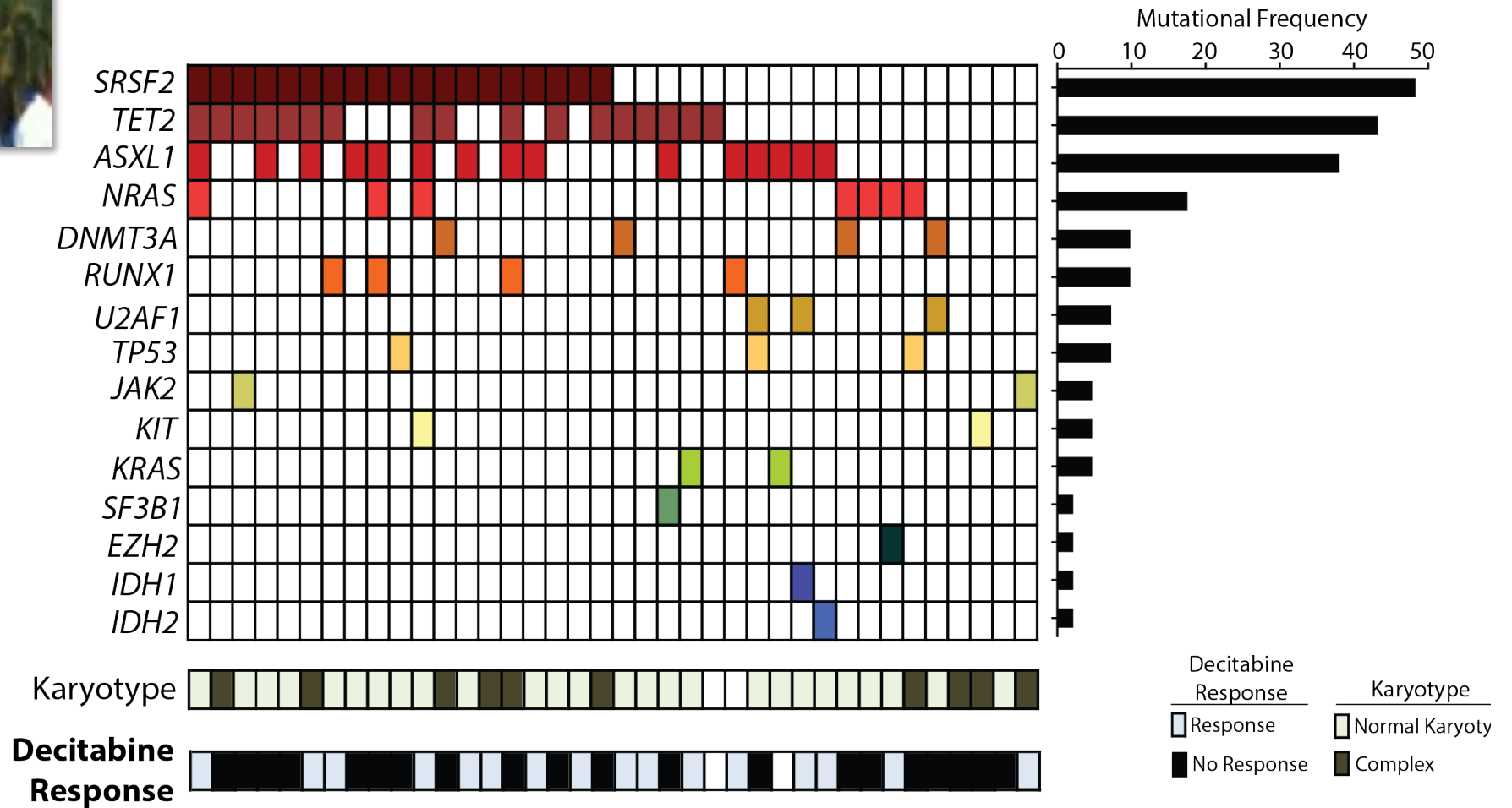
At risk:

Not responders	8	3	2	2	2	2	0	0	0
Responders	18	16	13	10	9	8	5	3	1

Mutational profiles do not correlate with response to DAC

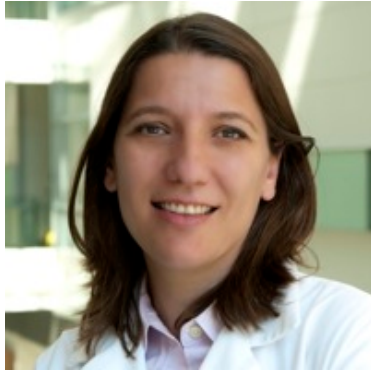


Omar Waab

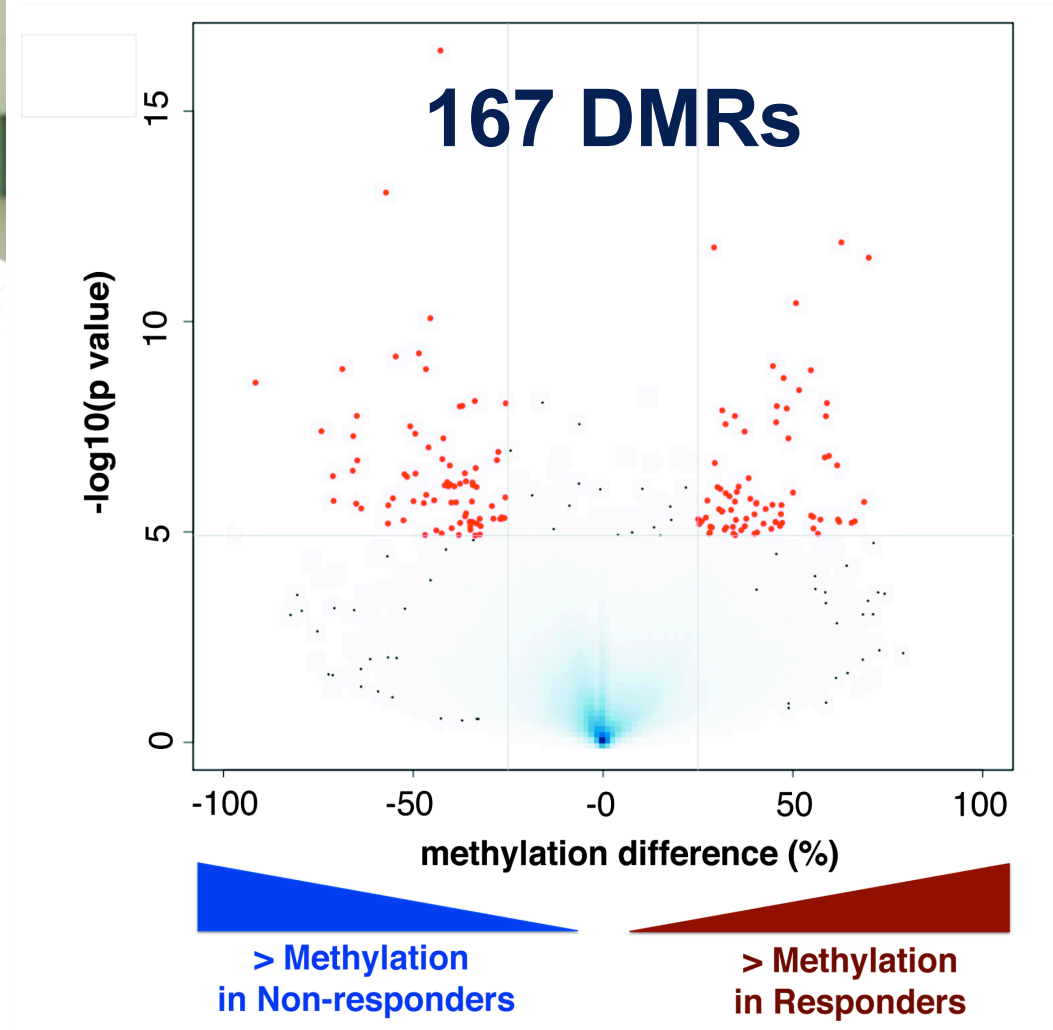


Santini et al, Leukemia 2017
Meldi et al; J Clin Invest. 2015

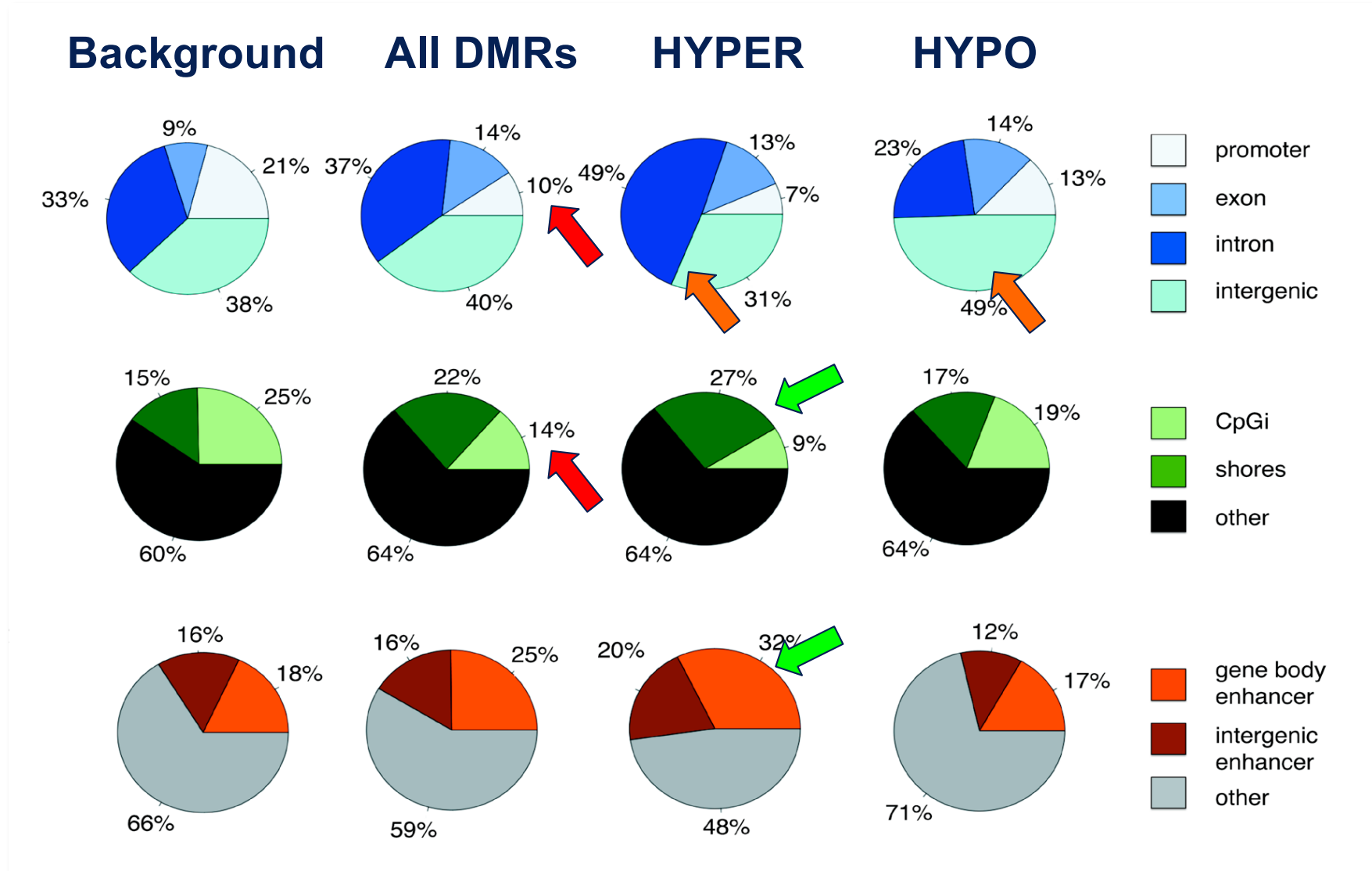
Distinct DNA methylation profiles at diagnosis is associated with response to DAC



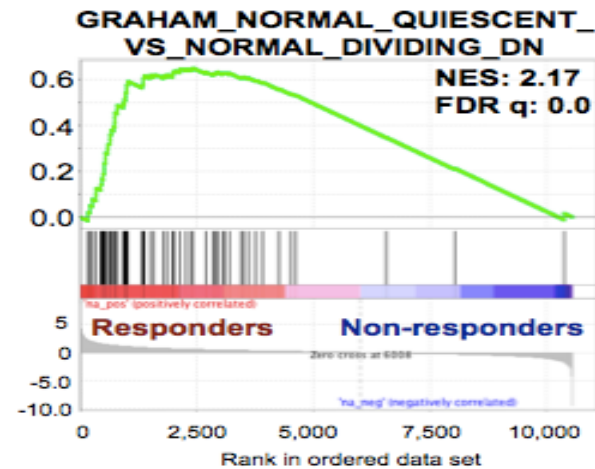
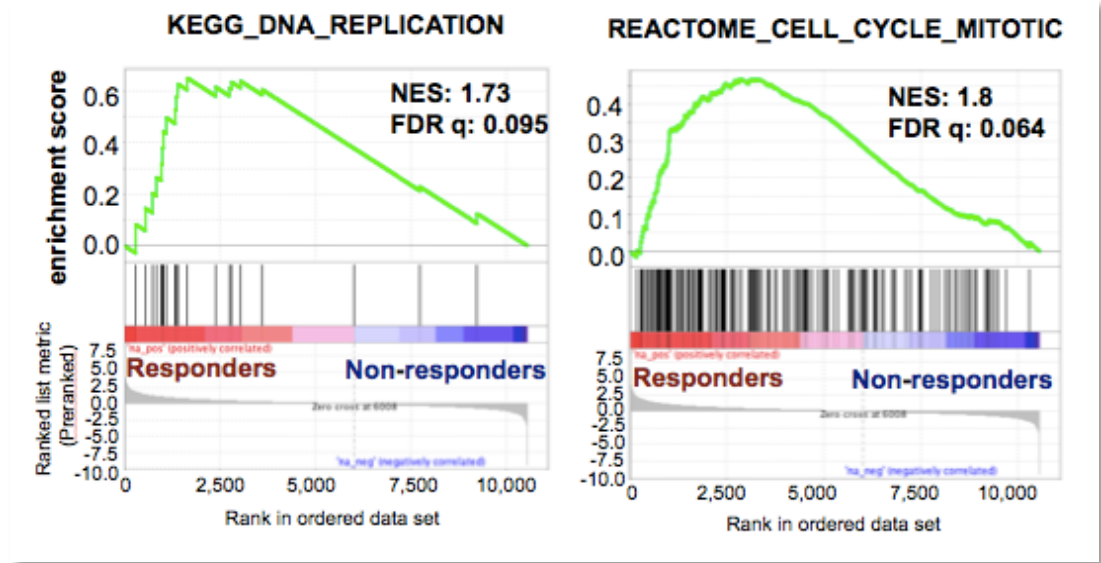
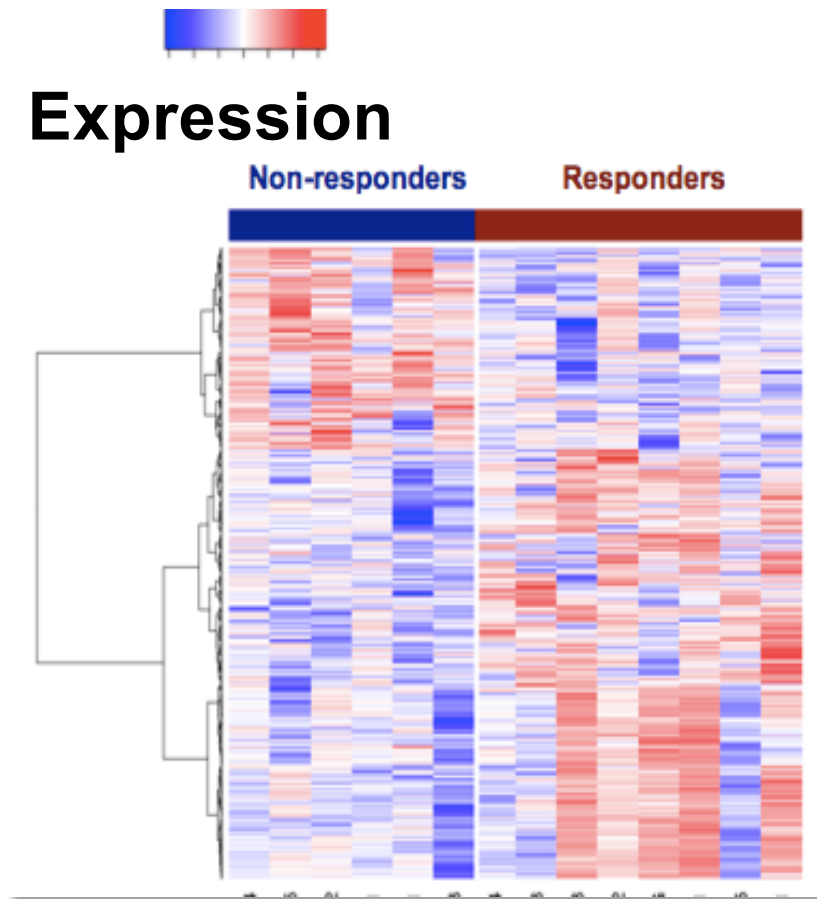
ME Figueroa
Michigan University
(now Miami U)



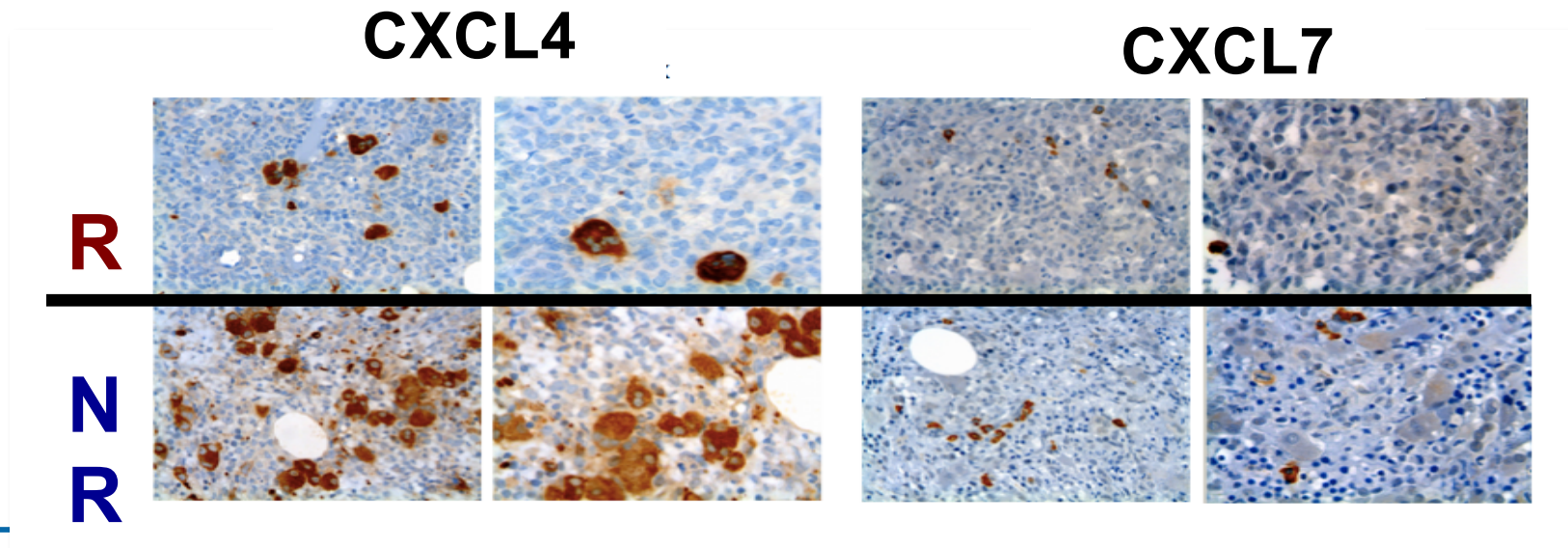
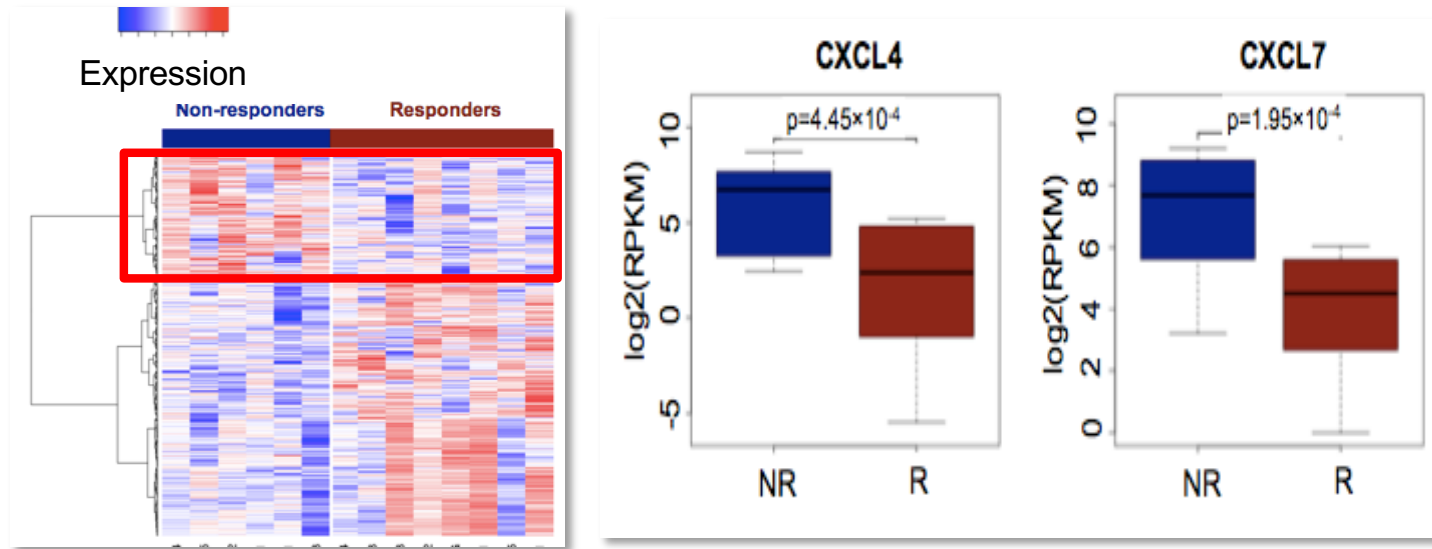
Differentially methylated regions are enriched at distal intergenic regions and enhancers



Differential gene expression at diagnosis associated with response to DAC



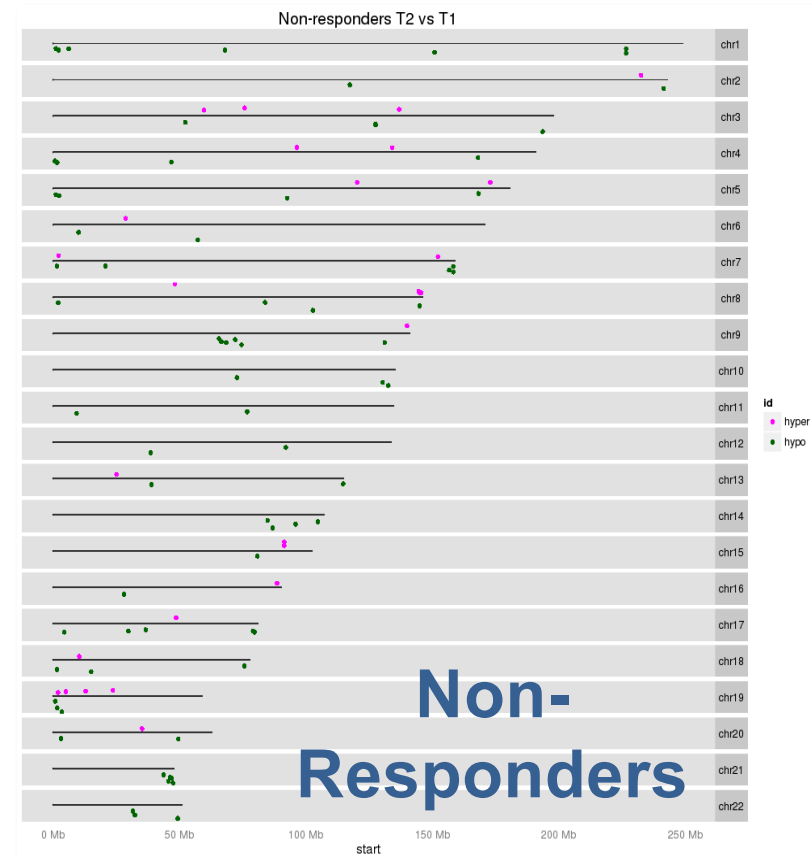
CXCL4 and CXCL7 are up-regulated in the bone marrow of non-responders



Response to DAC is associated with reversal of hypermethylation

Before DAC – After DAC

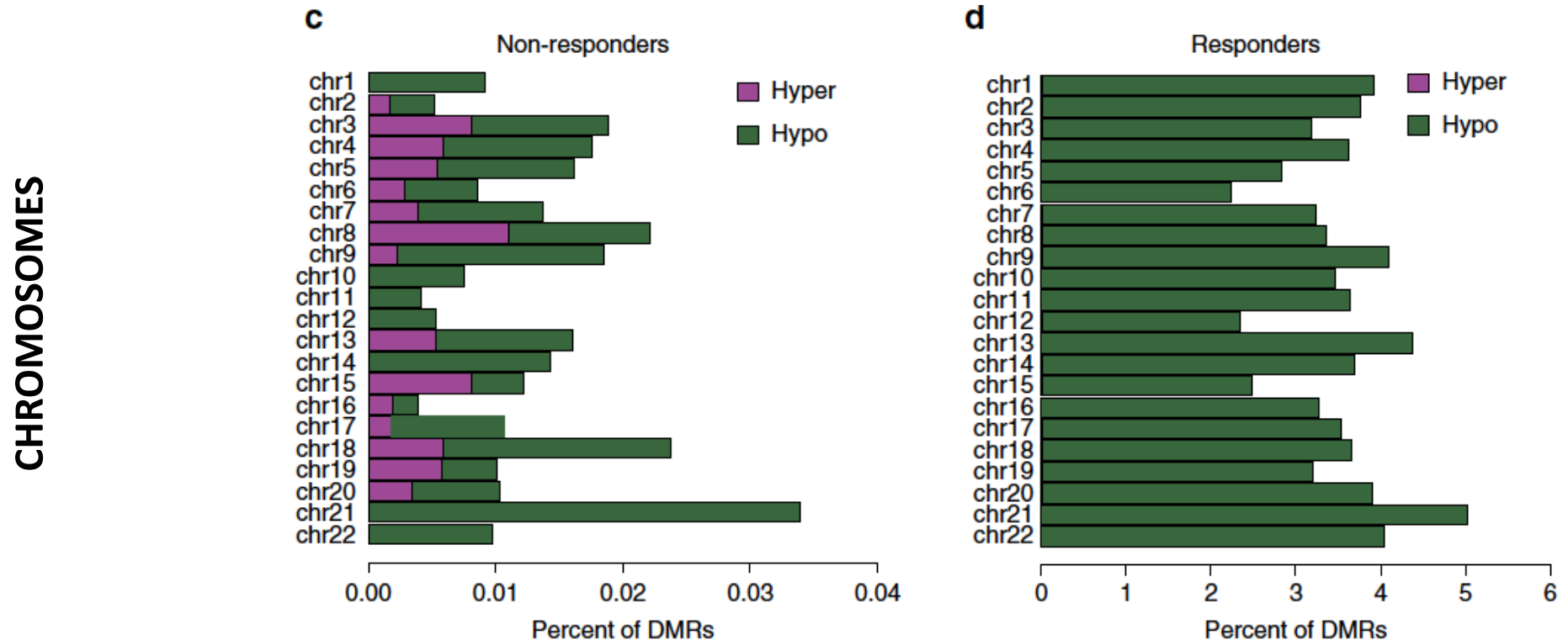
CHROMOSOMES



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

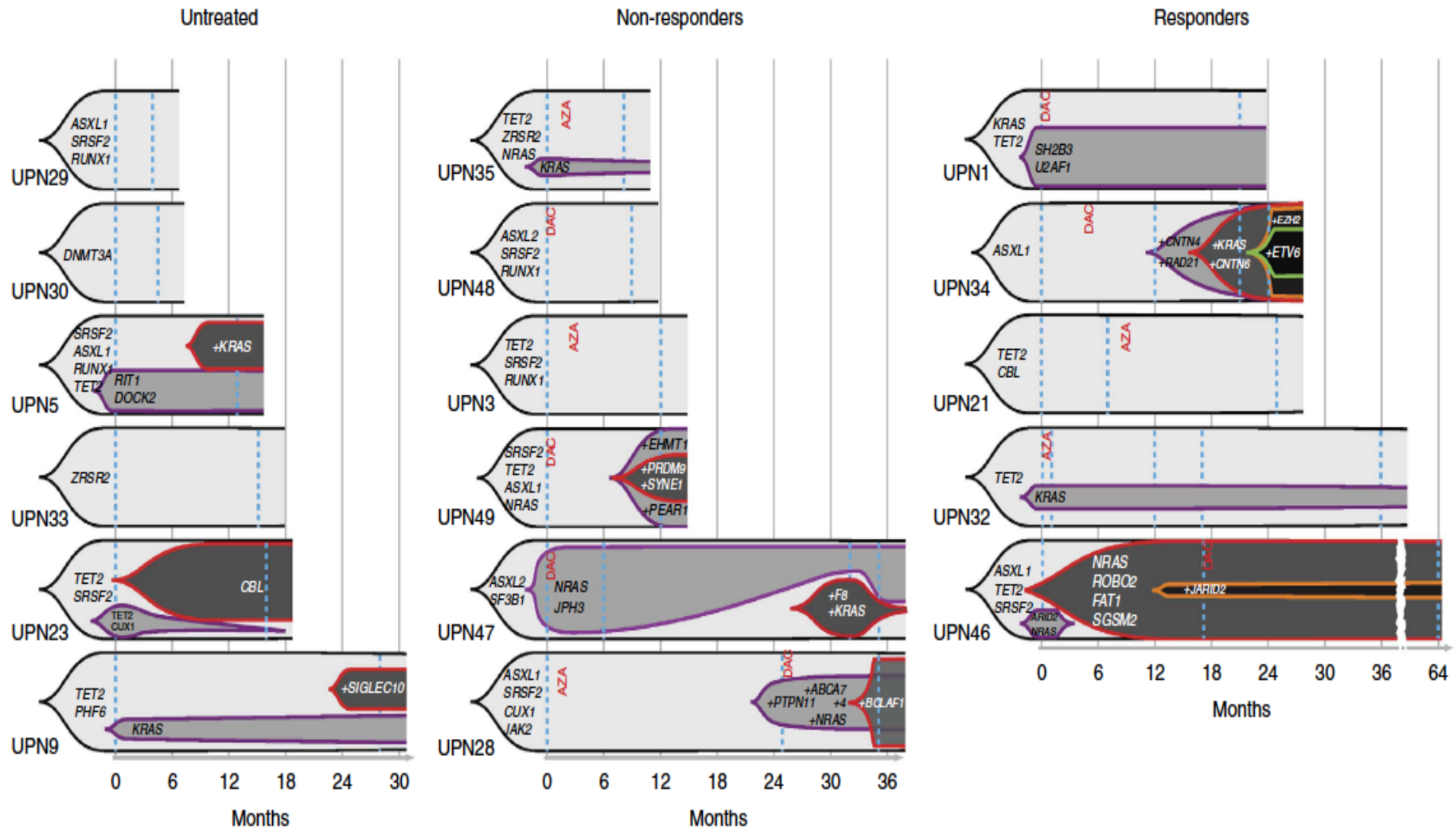
Response to DAC is associated with reversal of hypermethylation

Before DAC – After DAC



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

Mutation allele burden remains unchanged after DAC



DACOTA trial

Primary Objective
Event free survival

DAC 20 mg/m² x 5 days
every 28 days

Patient Randomized into Study
N = 168 1:1

Minimum 6 month treatment & follow-up

HU

Patient Population:
Advanced proliferative CMML
Centrally confirmed diagnosis



EHA CMMML panel

Participants:

- E Solary
- E Padron
- G F Sanz
- R Itzykson
- V Santini
- T de Witte
- U Platzbecker
- J Cortes
- A van de Loosdrecht
- F Onida
- U Germing
- D Bowen
- N Cross
- L Malcovati,
- P Fenaux, Steering Committee Chair

EHA Executive Office:

- C Smand
- G Rojková



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Bernardino Allione
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Alessandro Levis

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**Institute Gustave Roussy,
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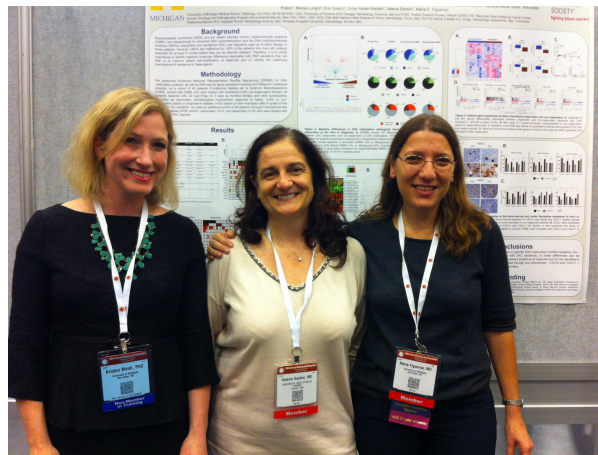


Groupe
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Myélodysplasies

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Maria E.Figueroa
Tingting Qin
Kristen Meldi



FISM

**FONDAZIONE
ITALIANA
SINDROMI
MIELODISPLASTICHE**



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