

Prevenzione delle neoplasie ematologiche: è oggi una realtà?

Bari, October 21th, 2019

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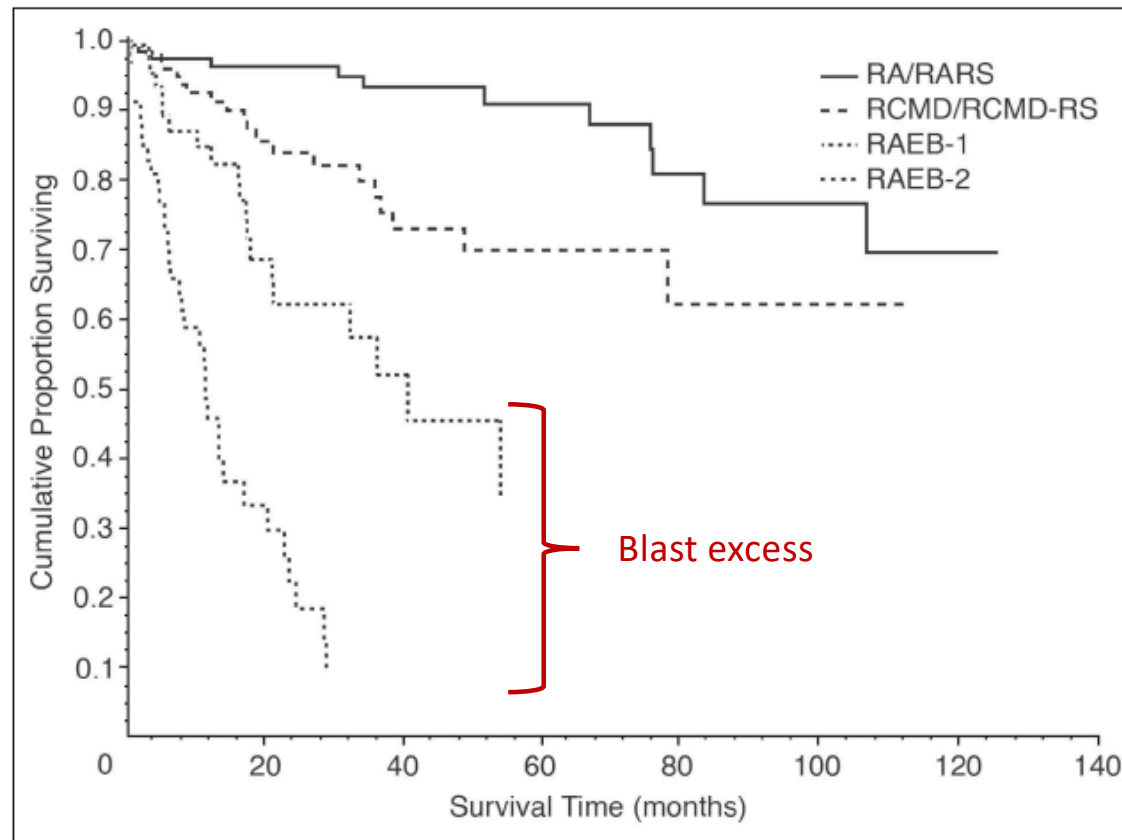
Fondazione IRCCS Policlinico San Matteo & University of Pavia

Outline of presentation

- Predicting progression to AML



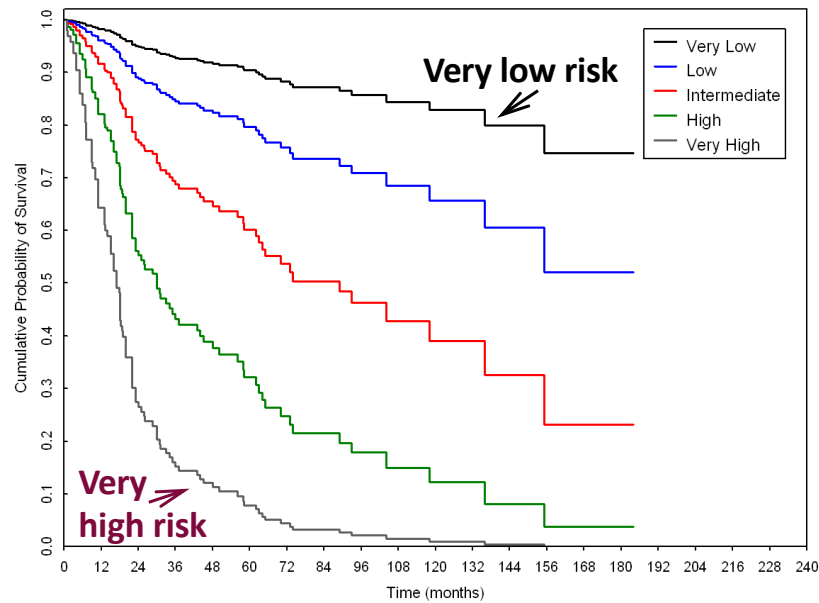
Risk of leukemic evolution according to the WHO subtype



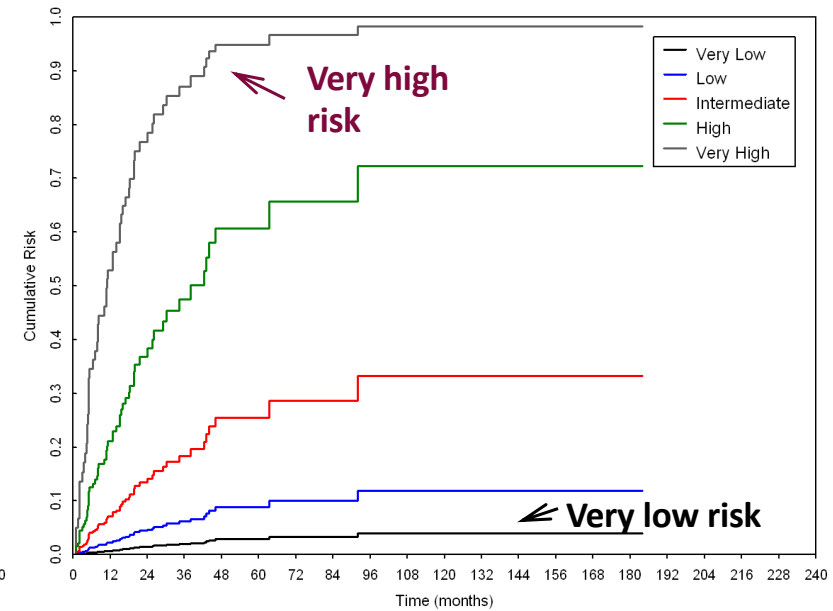
Malcovati et al. J Clin Oncol. 2005 Oct 20;23(30):7594-603

Time-dependent WPSS

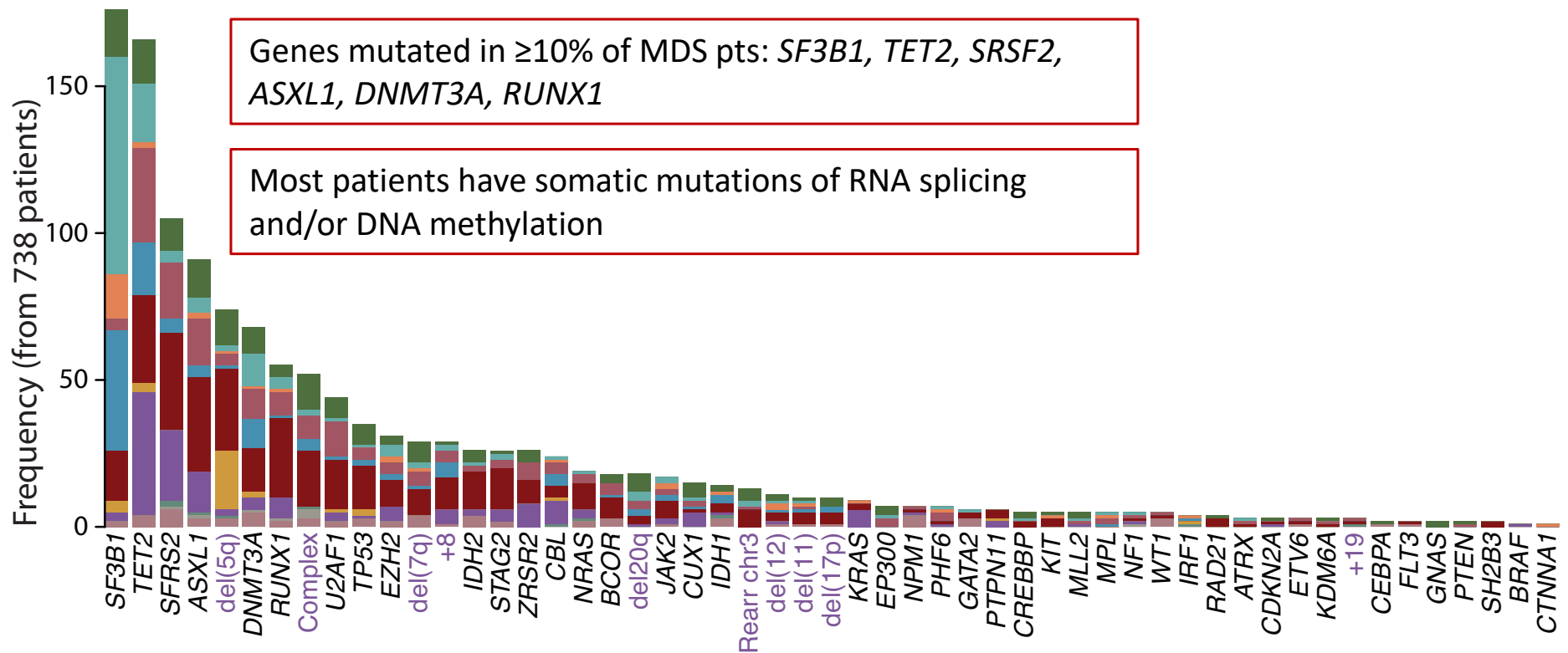
Overall survival
($P < .001$)



Risk of leukemic evolution
($P < .001$)



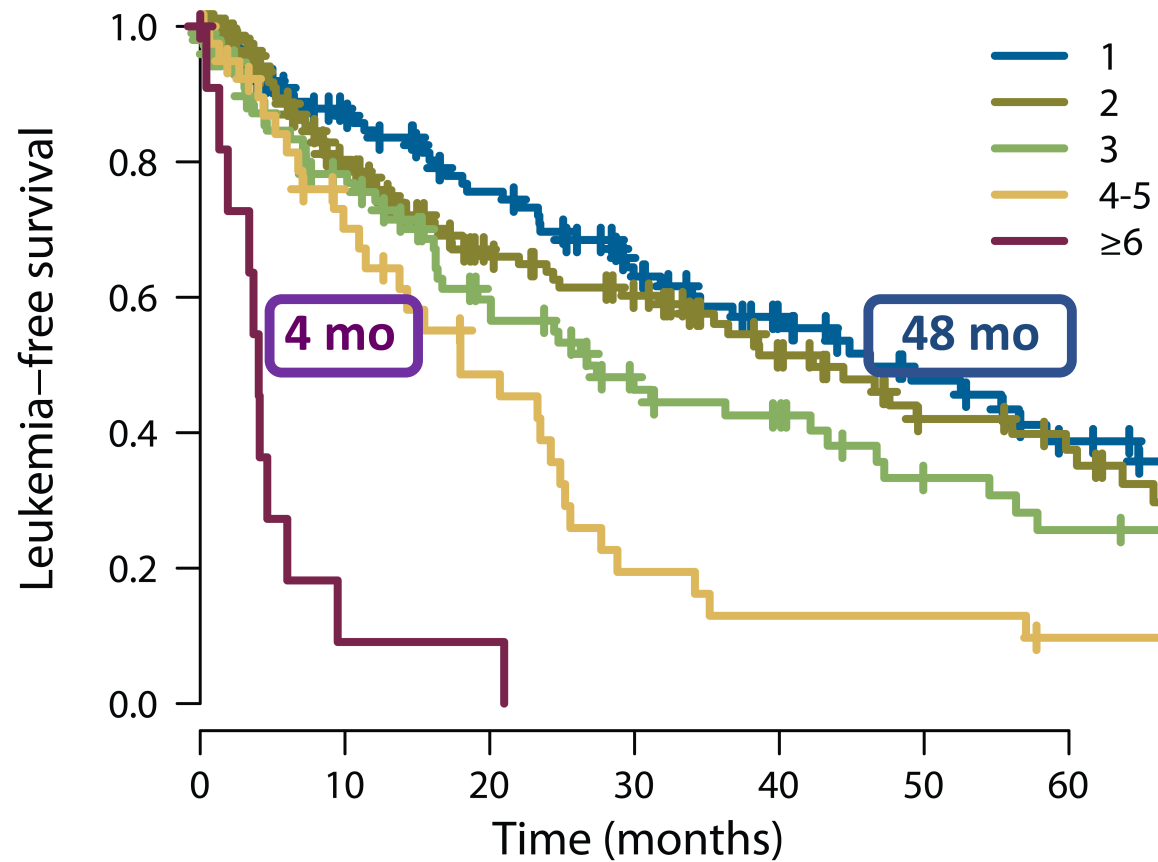
Genetic lesions in patients with MDS



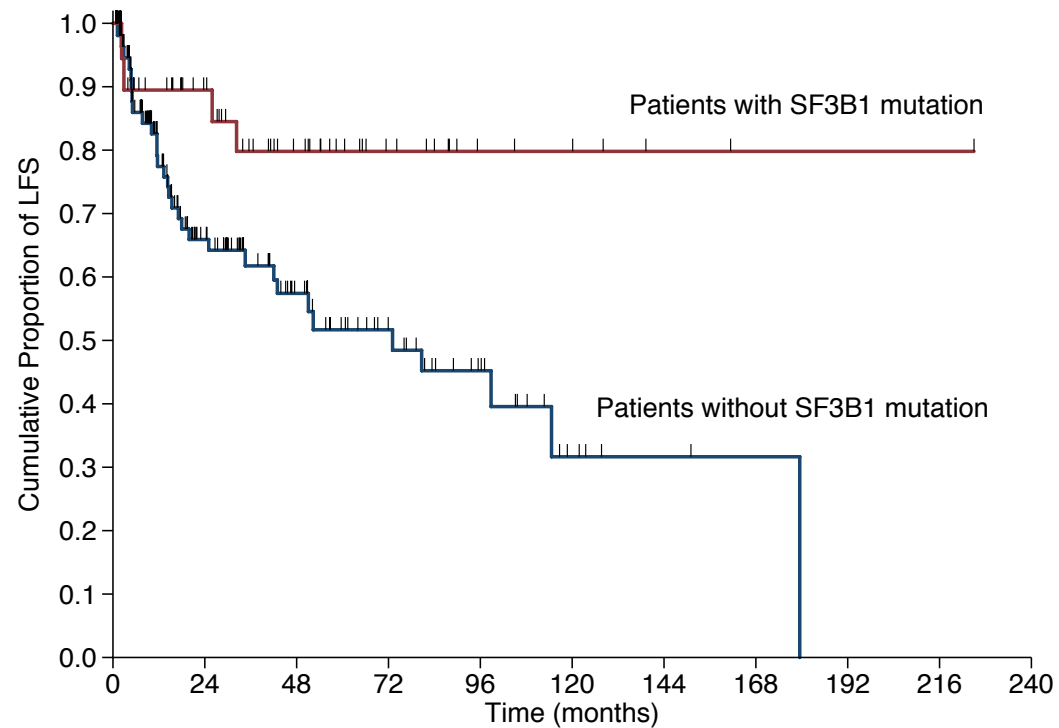
Papaemmanuil et al. Blood. 2013 Nov 21;122(22):3616-27

Haferlach et al. Leukemia. 2014 Feb;28(2):241-7

Genetic complexity and risk of leukemic evolution

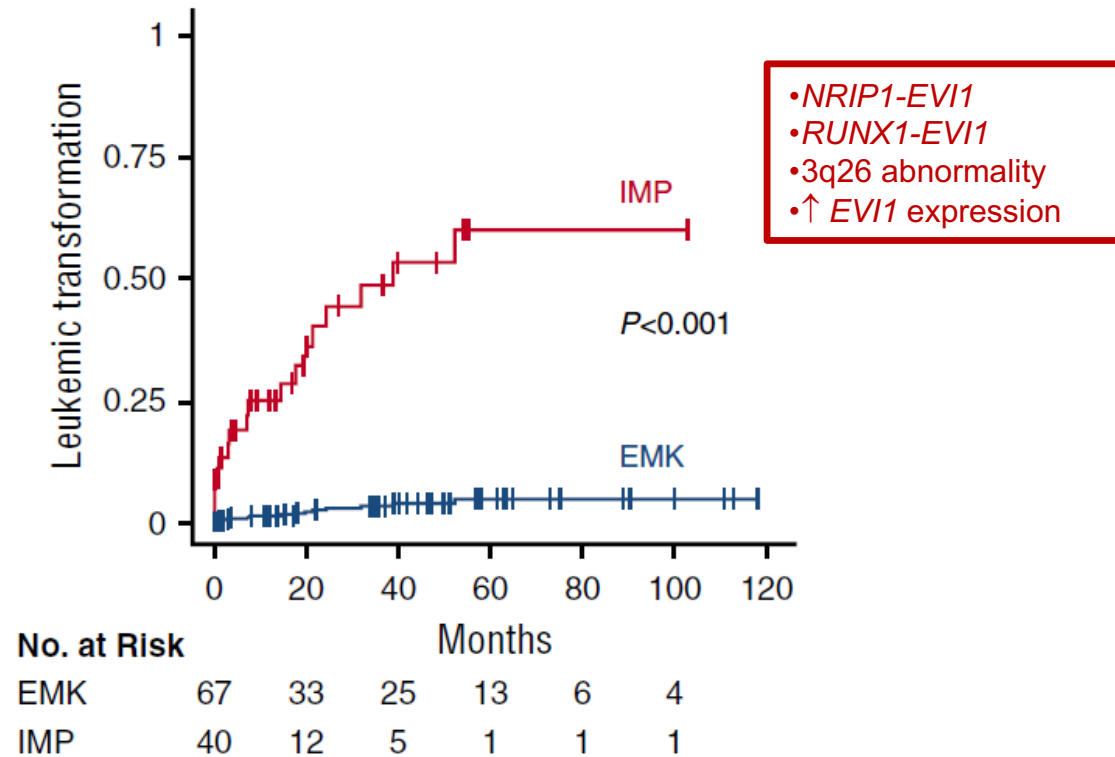


Risk of leukemic evolution according to *SF3B1* mutational status



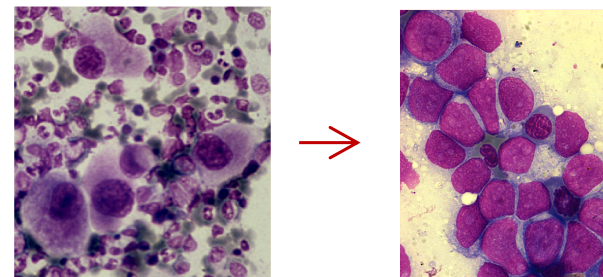
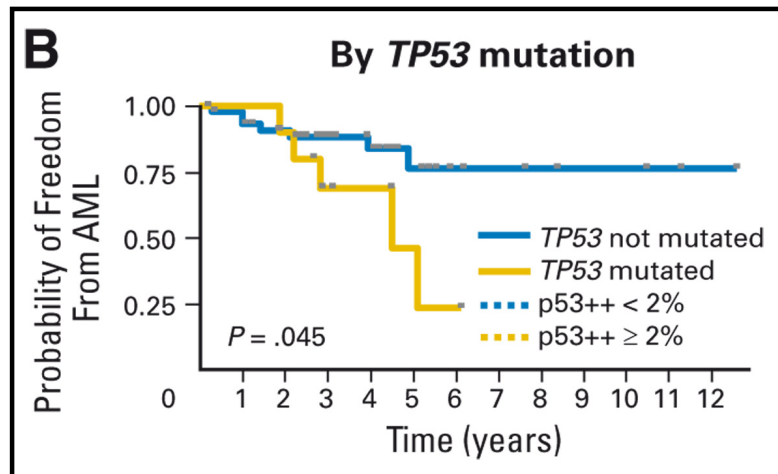
Gene expression and risk of leukemic transformation in MDS

- Erythroid/megakaryocytic (EMK) signature - Immature progenitor (IMP) signature



Shiozawa et al. Blood. 2017 Dec 14;130(24):2642-2653

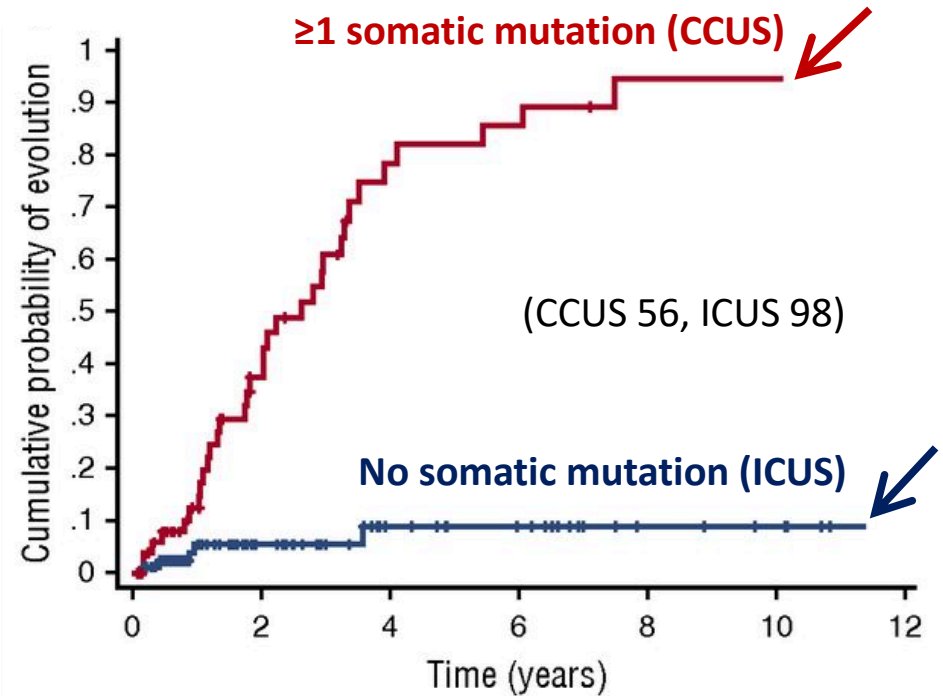
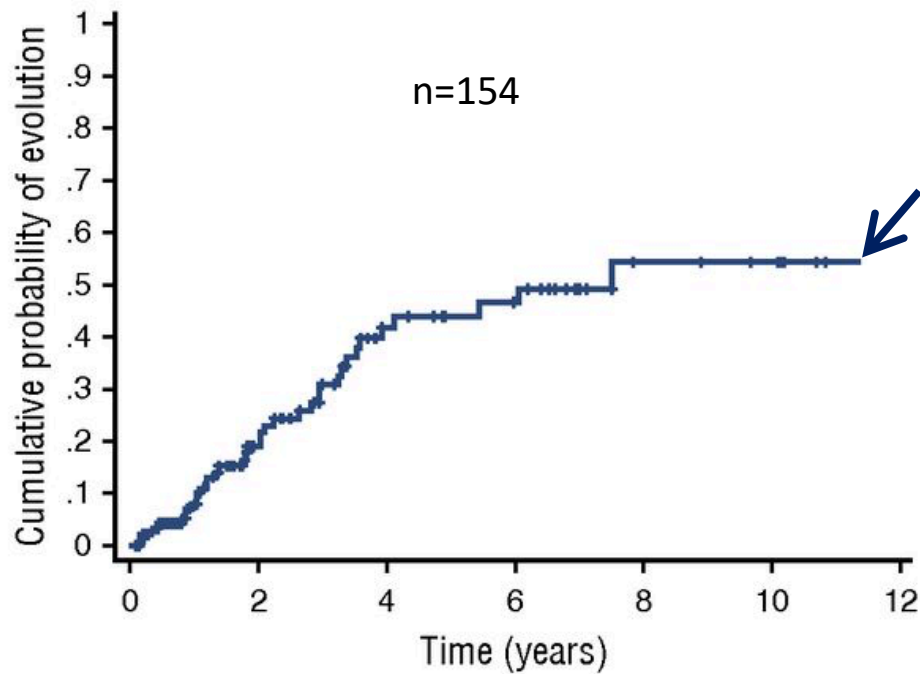
TP53 mutation and risk of progression to AML in MDS with del(5q)



Clonal cytopenia of undetermined significance (CCUS)

- Persistent unexplained cytopenia (≥ 4 months)
- Insufficient criteria for diagnosis of MDS (dysplasia $< 10\%$, blast count $< 5\%$)
- Presence of a somatic mutation with a VAF $\geq 2\%$ in a hematologic malignancy-associated gene (eg, *TET2*, *ASXL1*, or *DNMT3A*) in the peripheral blood or bone marrow

Diagnostic value of mutation status in patients with cytopenia of undetermined significance



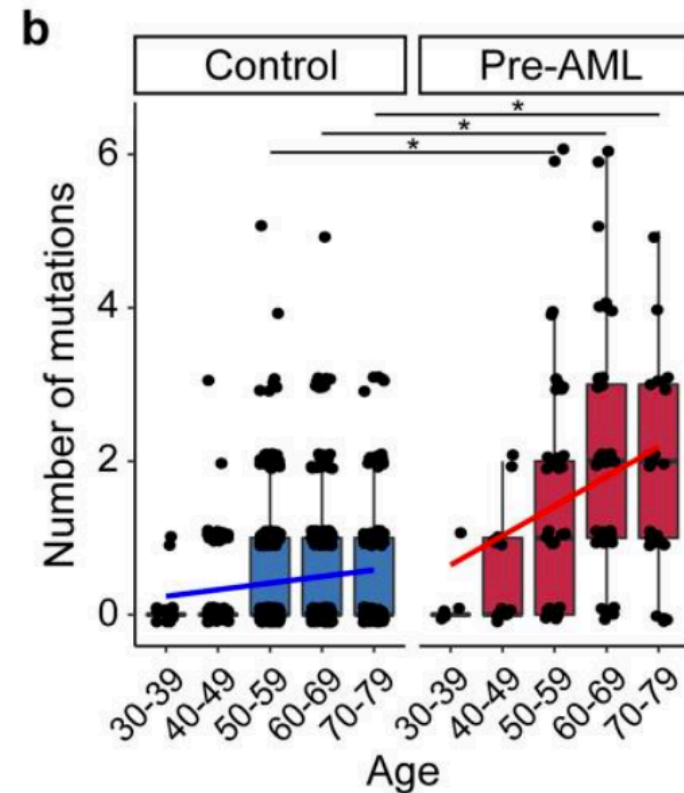
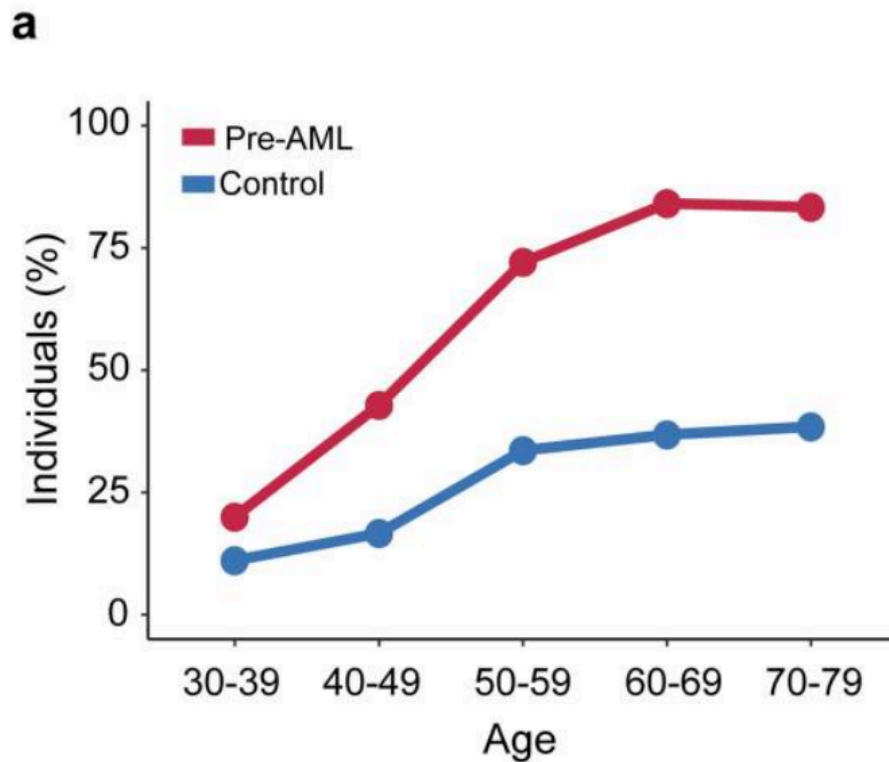
Somatic mutations precede acute myeloid leukemia years before diagnosis

- 212 women from the Women's Health Initiative who were healthy at study baseline, but eventually developed AML during follow-up (median time: 9.6 years)
- Deep sequencing was performed on peripheral blood DNA of these cases and compared to age-matched controls that did not develop AML
- Mutations in *IDH1*, *IDH2*, *TP53*, *DNMT3A*, *TET2* and spliceosome genes significantly increased the odds of developing AML
- All subjects with *TP53* mutations (n = 21 out of 21 patients) and *IDH1* and *IDH2* (n = 15 out of 15 patients) mutations eventually developed AML

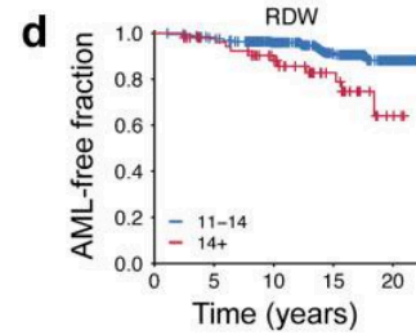
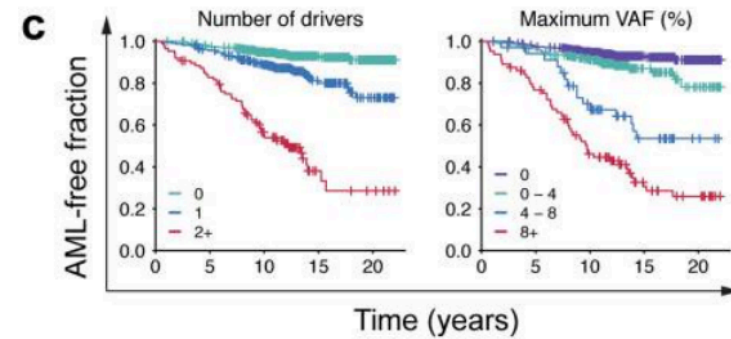
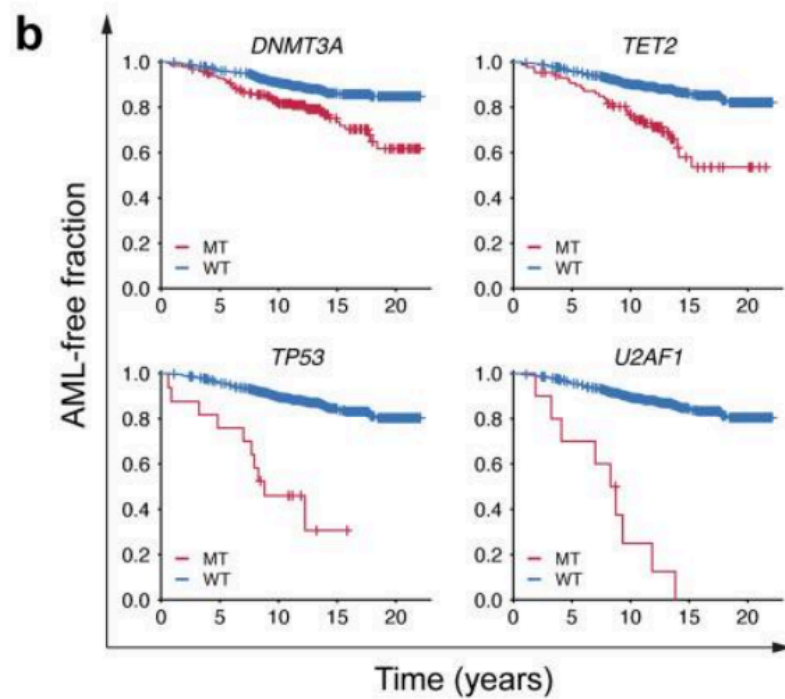
Prediction of AML risk in healthy individuals

- To distinguish individuals at high risk of developing AML from those with benign ARCH, we undertook deep sequencing of genes recurrently mutated in AML in the peripheral blood cells of 95 individuals sampled on average 6.3 years before AML diagnosis (pre-AML group), together with 414 unselected age- and gender-matched individuals (control group)

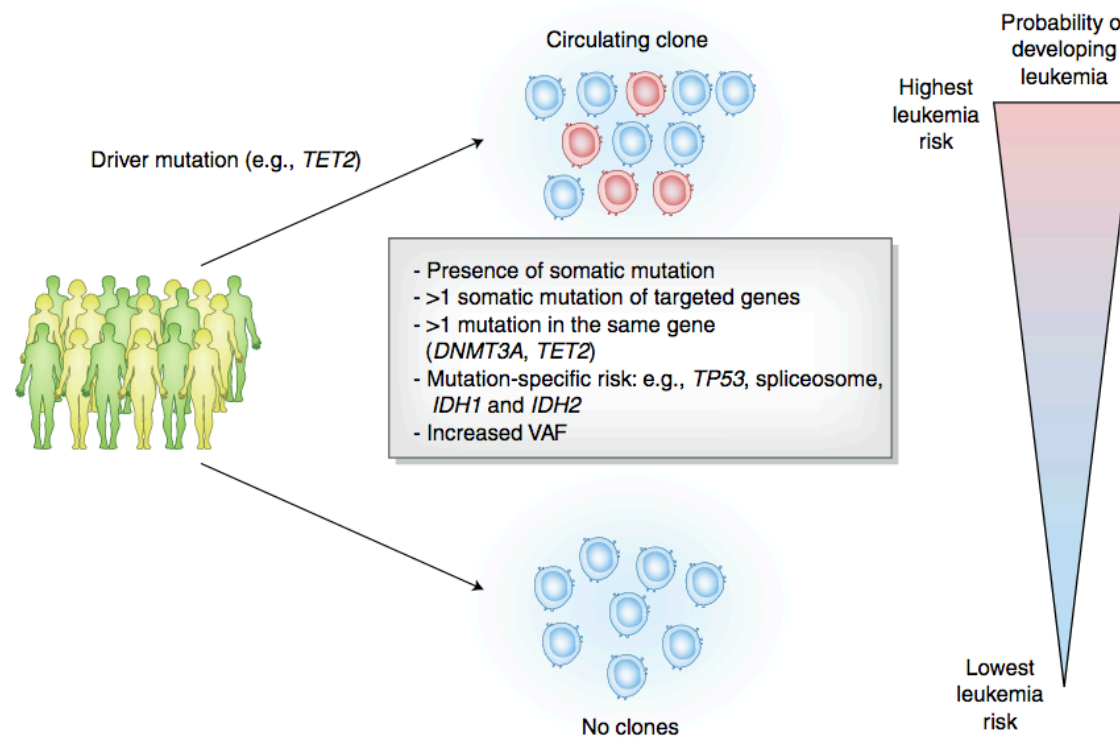
Prediction of AML risk in healthy individuals



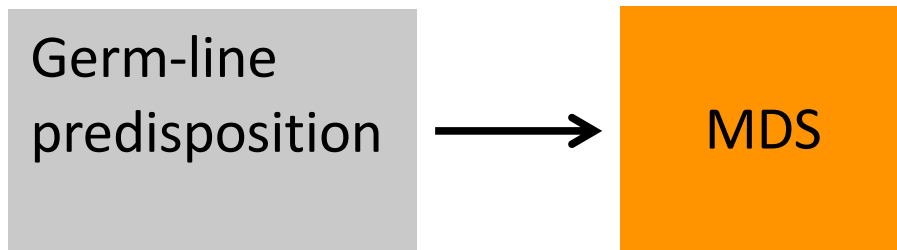
Prediction of AML risk in healthy individuals



Predicting progression to AML



Germline genetic predisposition to myeloid neoplasms with myelodysplasia



Patients under the age of 60 and/or with evidence of familial disease

Myeloid neoplasm classification

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*

Arber et al. Blood. 2016 May 19;127(20):2391-405

Acknowledgments

