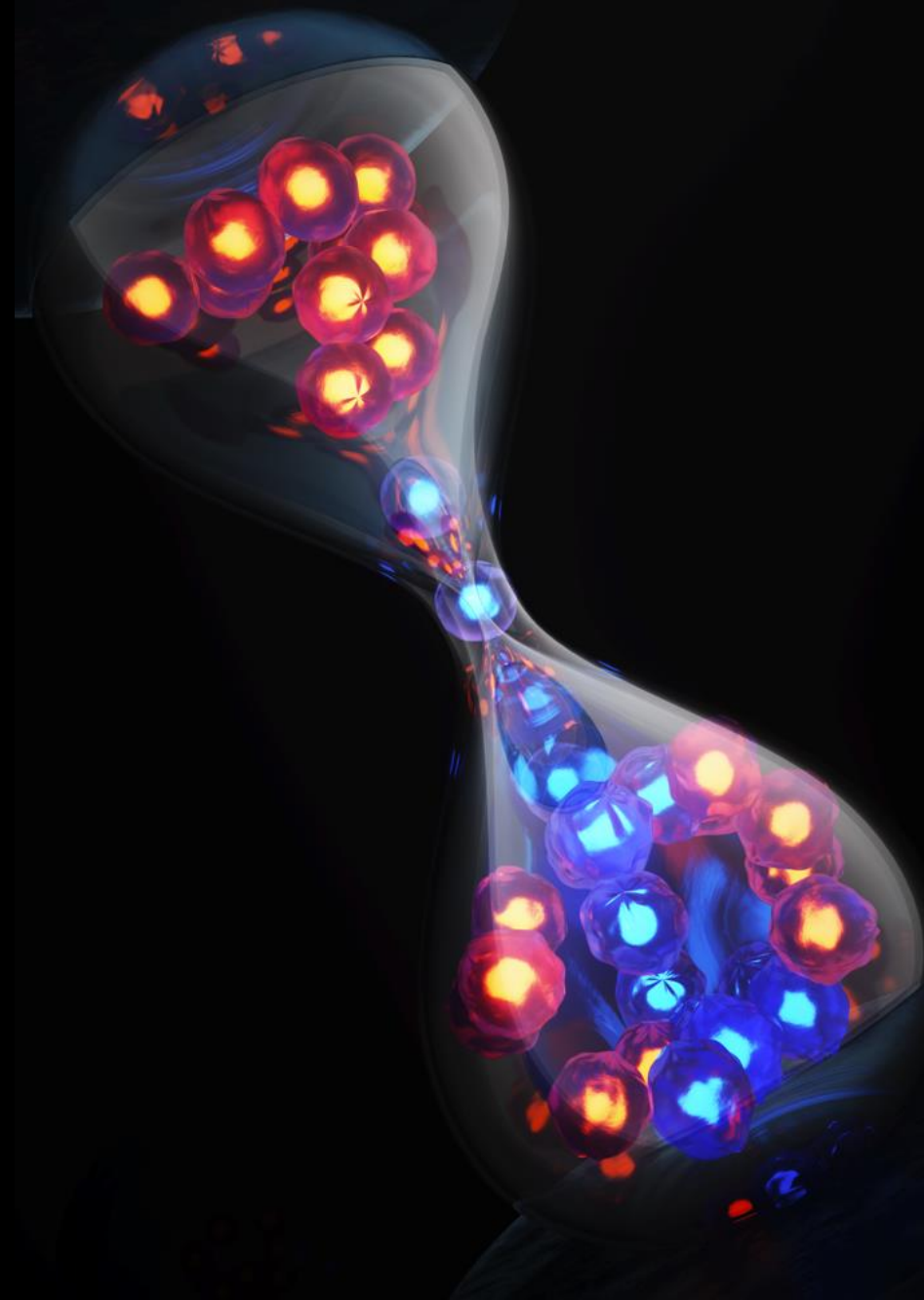




Clonal Hematopoiesis

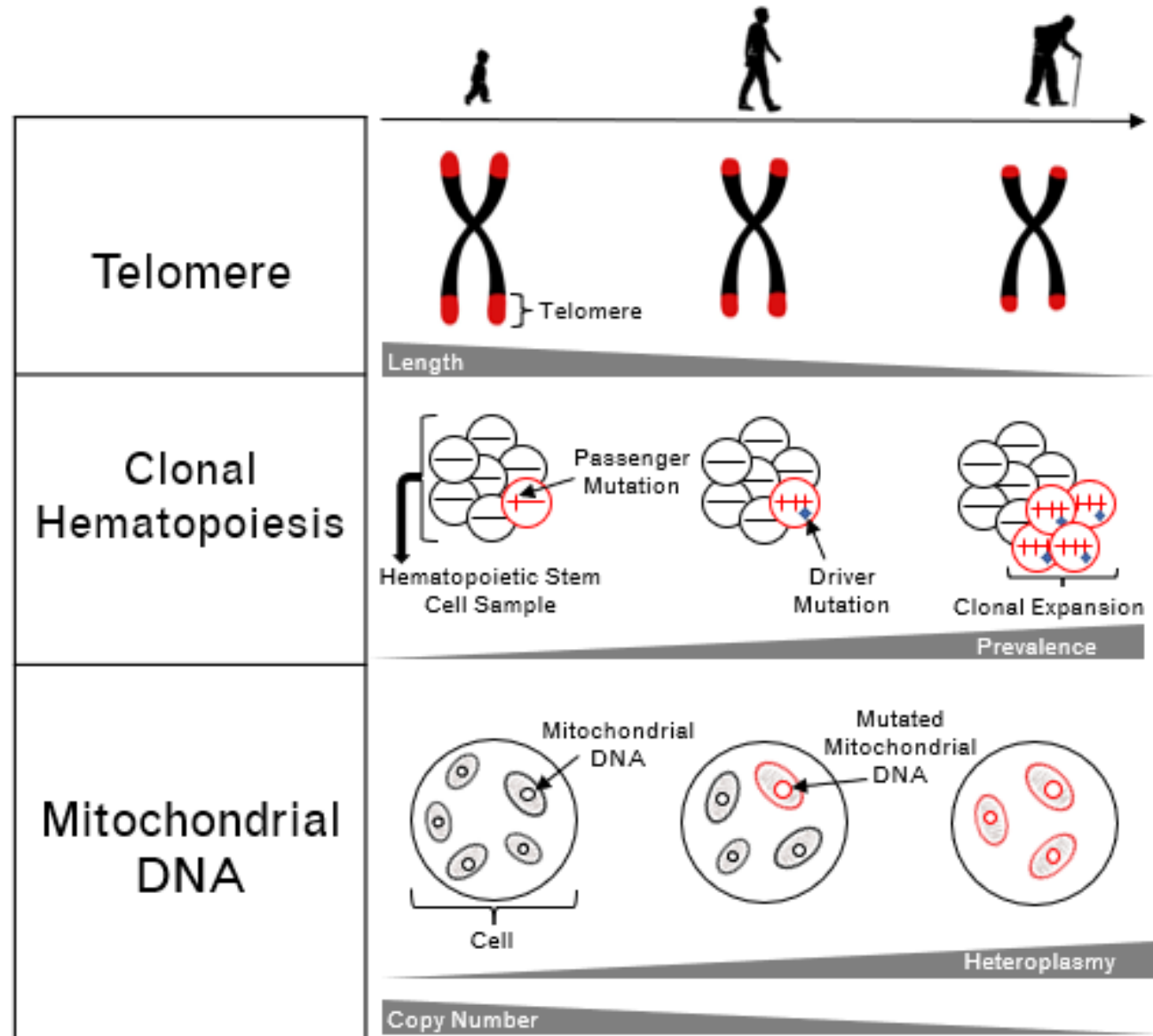
Alexander Bick, MD PhD
Assistant Professor, Div. Genetic Medicine
Vanderbilt School of Medicine



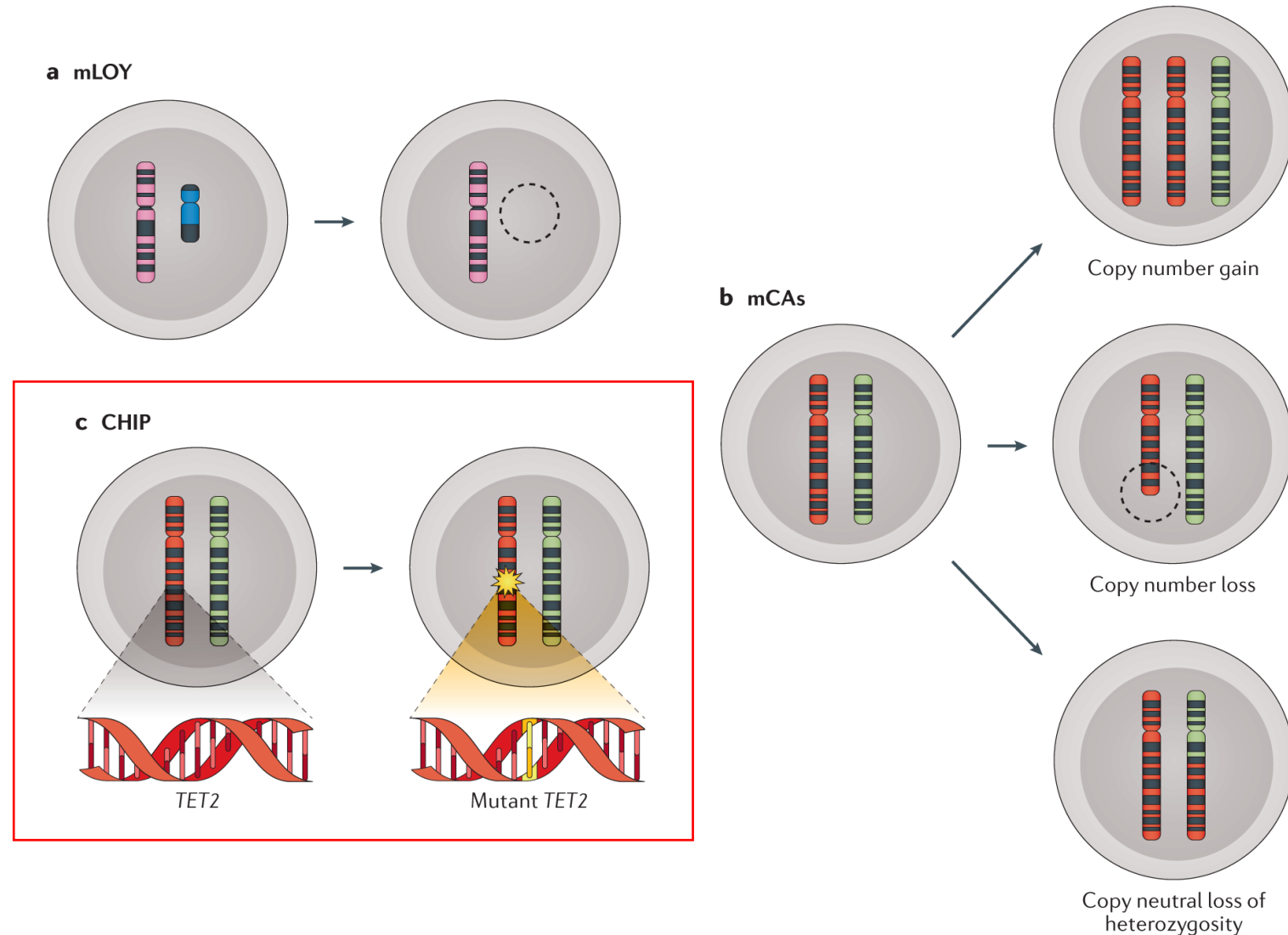
Disclosures

I am on the scientific Advisory Board of TenSixteen Bio.

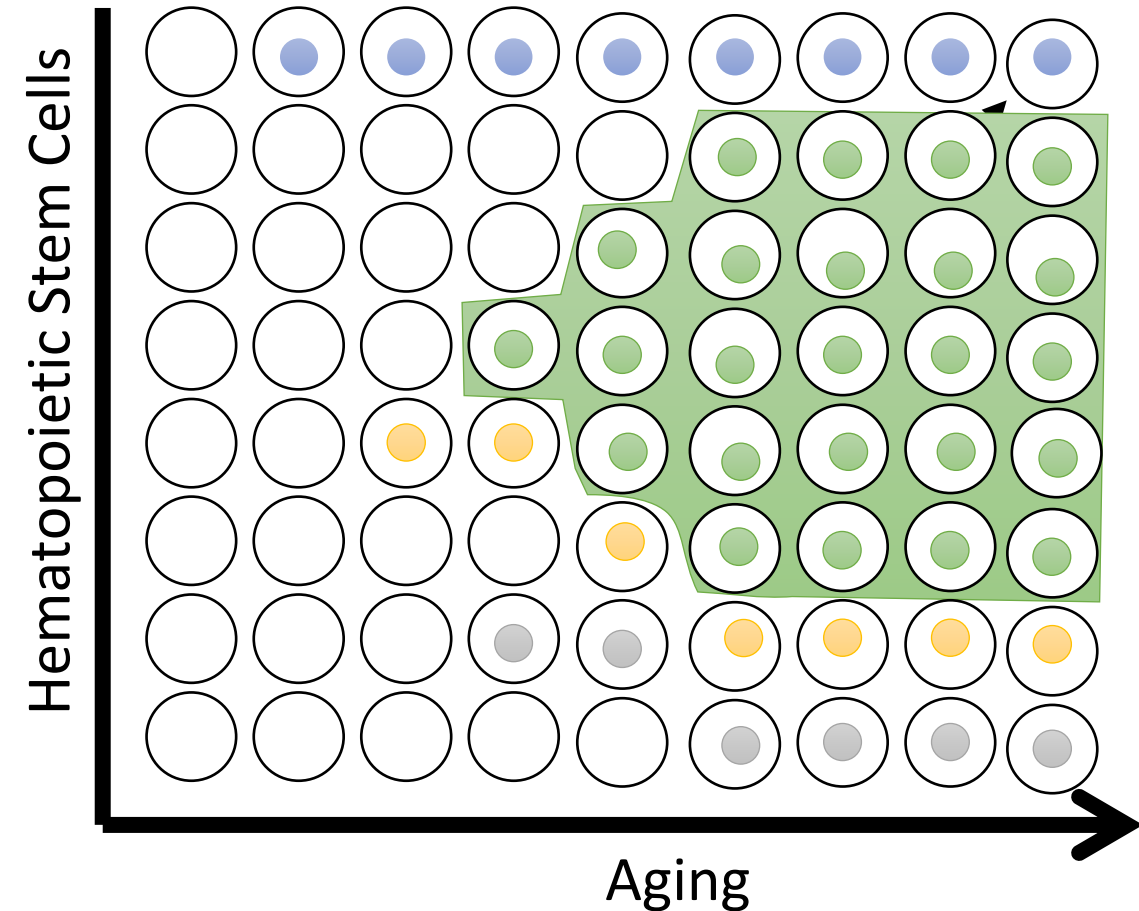
Although some things never change ... our genome does



Clonal Hematopoiesis



WHO Classification of Haemato-lymphoid Tumours 5th edition



Clonal Hematopoiesis of Indeterminate Potential (CHIP)

- Myeloid driver mutation
- Variant Allele Fraction >2%
- No other blood abnormalities

WHO Classification of Haemato-lymphoid Tumours 5th edition

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5TH EDITION OF THE WORLD HEALTH CLASSIFICATION OF TUMORS OF THE HEMATOPOIETIC AND LYMPHOID TISSUES

[Sanam Loghavi](#) • [Rashmi Kanagal-Shamanna](#) • [Joseph D. Khoury](#) • ... [Reza Nejati](#) • [Mrinal M. Patnaik](#) •

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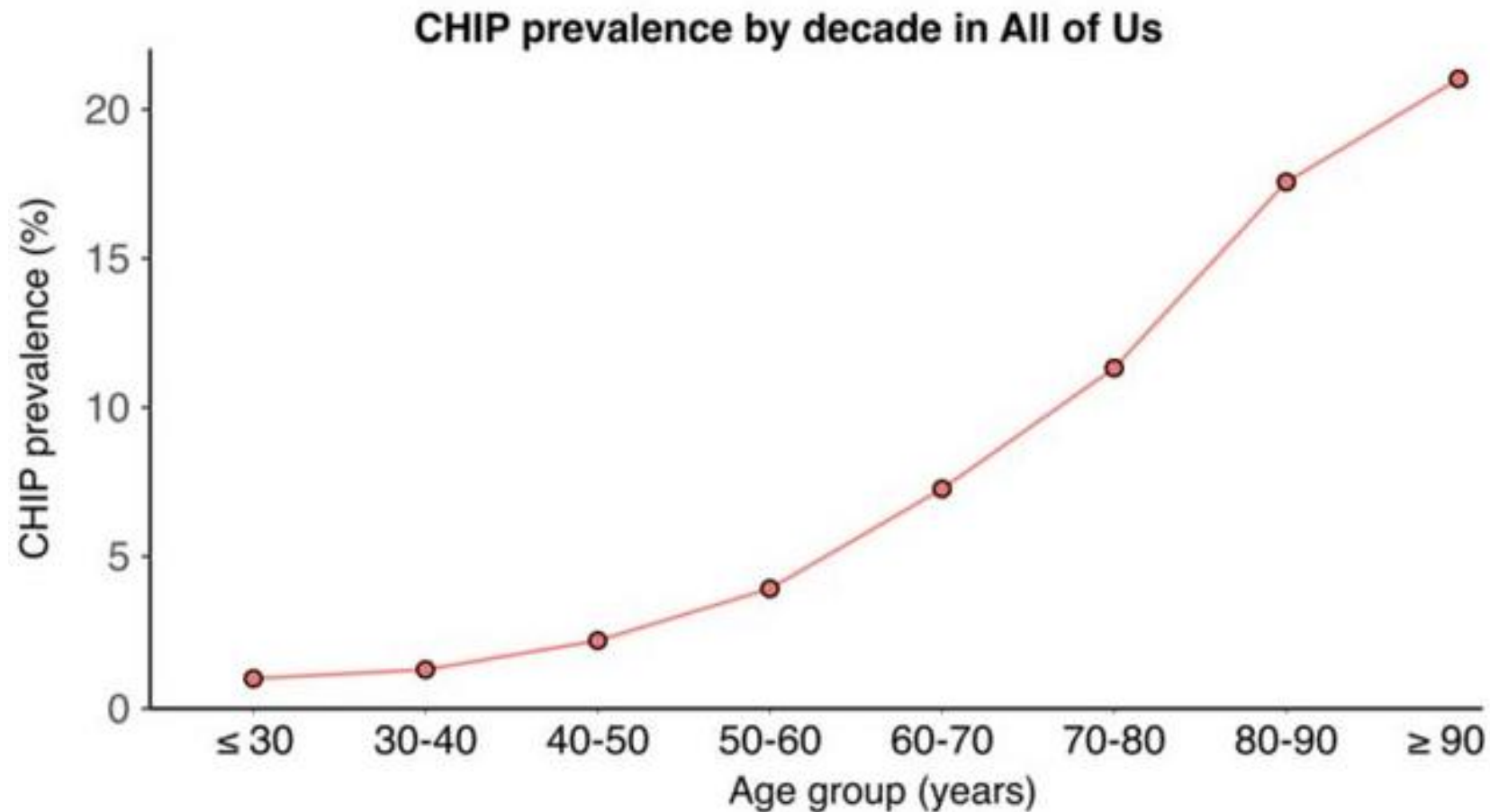
Published: December 01, 2023 • DOI: <https://doi.org/10.1016/j.modpat.2023.100397>

Aging

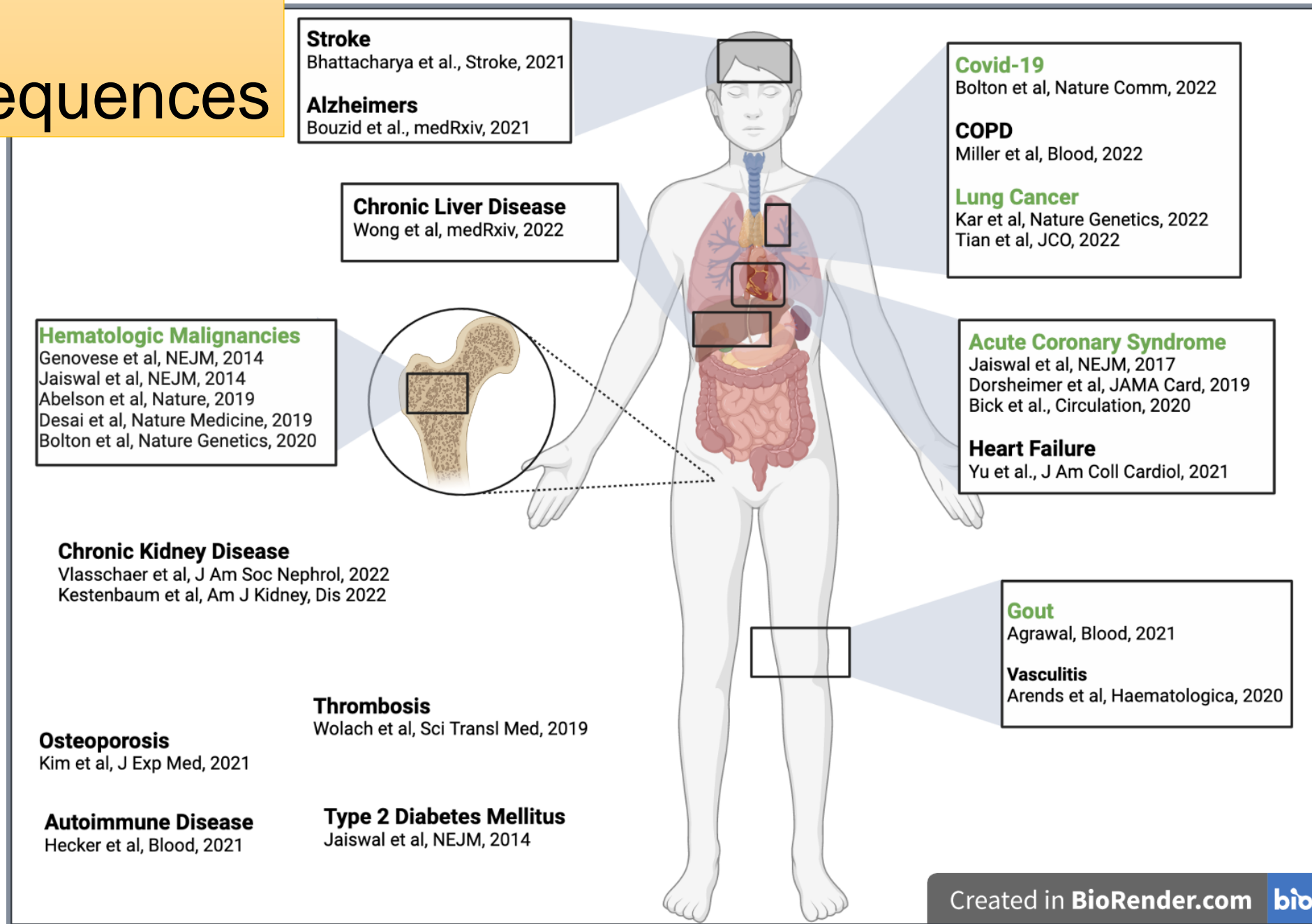


- CHIP + unexplained cytopenia

CHIP is common in the elderly



CHIP consequences




Genetics and epidemiology of mutational barcode-defined clonal hematopoiesis

Received: 9 May 2023

Accepted: 28 September 2023

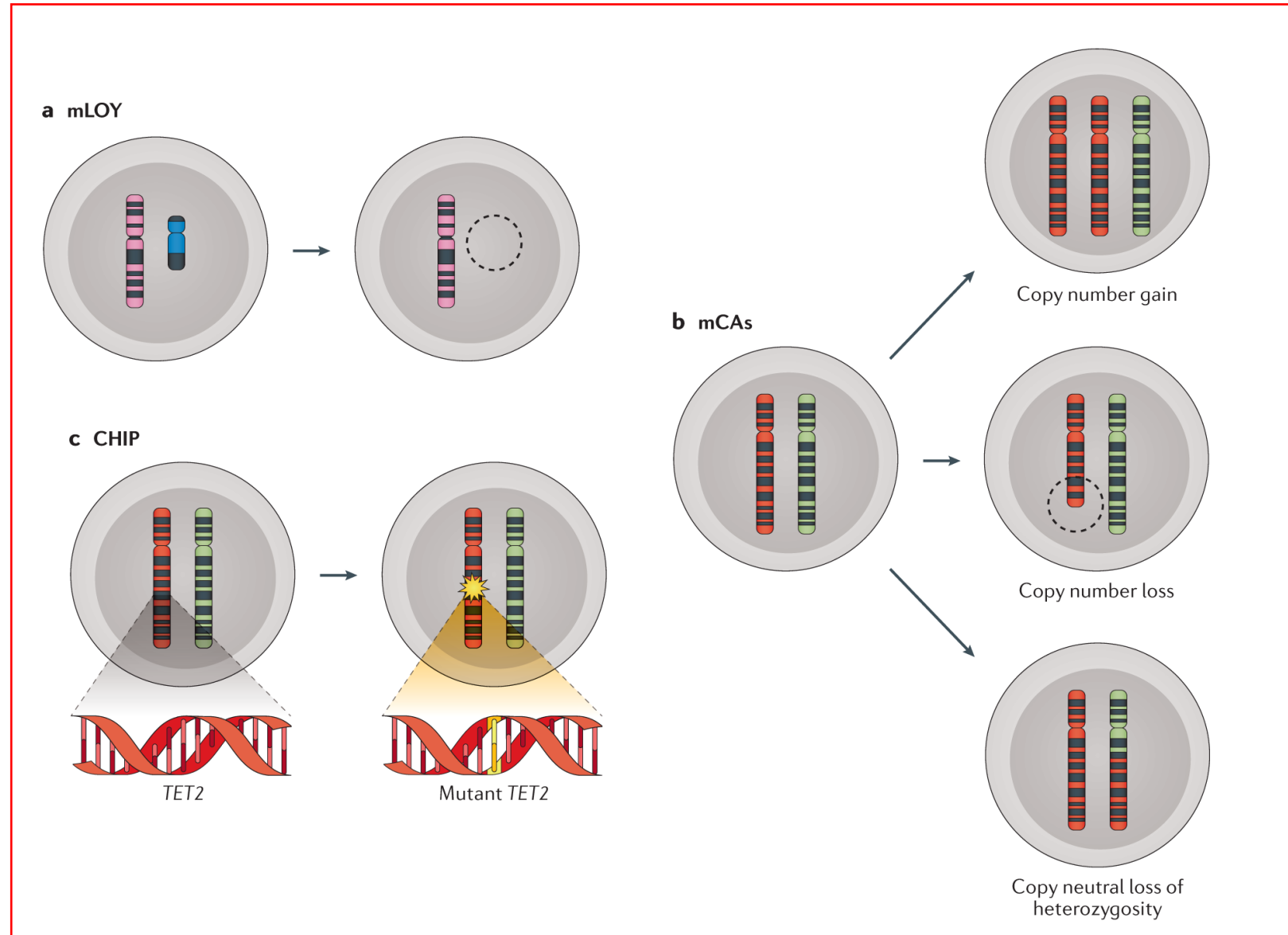
Published online: 06 November 2023

 Check for updates

Simon N. Stacey^{1,8}✉, Florian Zink^{1,8}, Gisli H. Halldorsson^{1,2}, Lilja Stefansdottir¹, Sigurjon A. Gudjonsson¹, Gudmundur Einarsson¹, Grimur Hjörleifsson¹, Thjodbjorg Eiriksdottir¹, Anna Helgadottir¹, Gyda Björnsdottir¹, Thorgeir E. Thorgeirsson¹, Thorunn A. Olafsdottir^{1,3}, Ingileif Jonsdottir^{1,3,4}, Solveig Gretarsdottir¹, Vinicius Tragante¹, Magnus K. Magnusson^{1,3}, Hakon Jonsson¹, Julius Gudmundsson¹, Sigurgeir Olafsson¹, Hilma Holm¹, Daniel F. Gudbjartsson^{1,2}, Patrick Sulem¹, Agnar Helgason^{1,5}, Unnur Thorsteinsdottir^{1,3}, Laufey Tryggvadottir⁶, Thorunn Rafnar¹, Pall Melsted^{1,2}, Magnus Ö. Ulfarsson^{1,2}, Brynjar Vidarsson^{3,7}, Gudmar Thorleifsson¹ & Kari Stefansson^{1,3}✉

Smoking demonstrates a dosage-dependent impact on risk of CH. CH associates with several smoking-related diseases. Contrary to published claims, we find no evidence that CH is associated with cardiovascular disease. We provide evidence that CH is driven by genes that are commonly mutated in myeloid neoplasia and implicate several new driver genes.

deCODE CH



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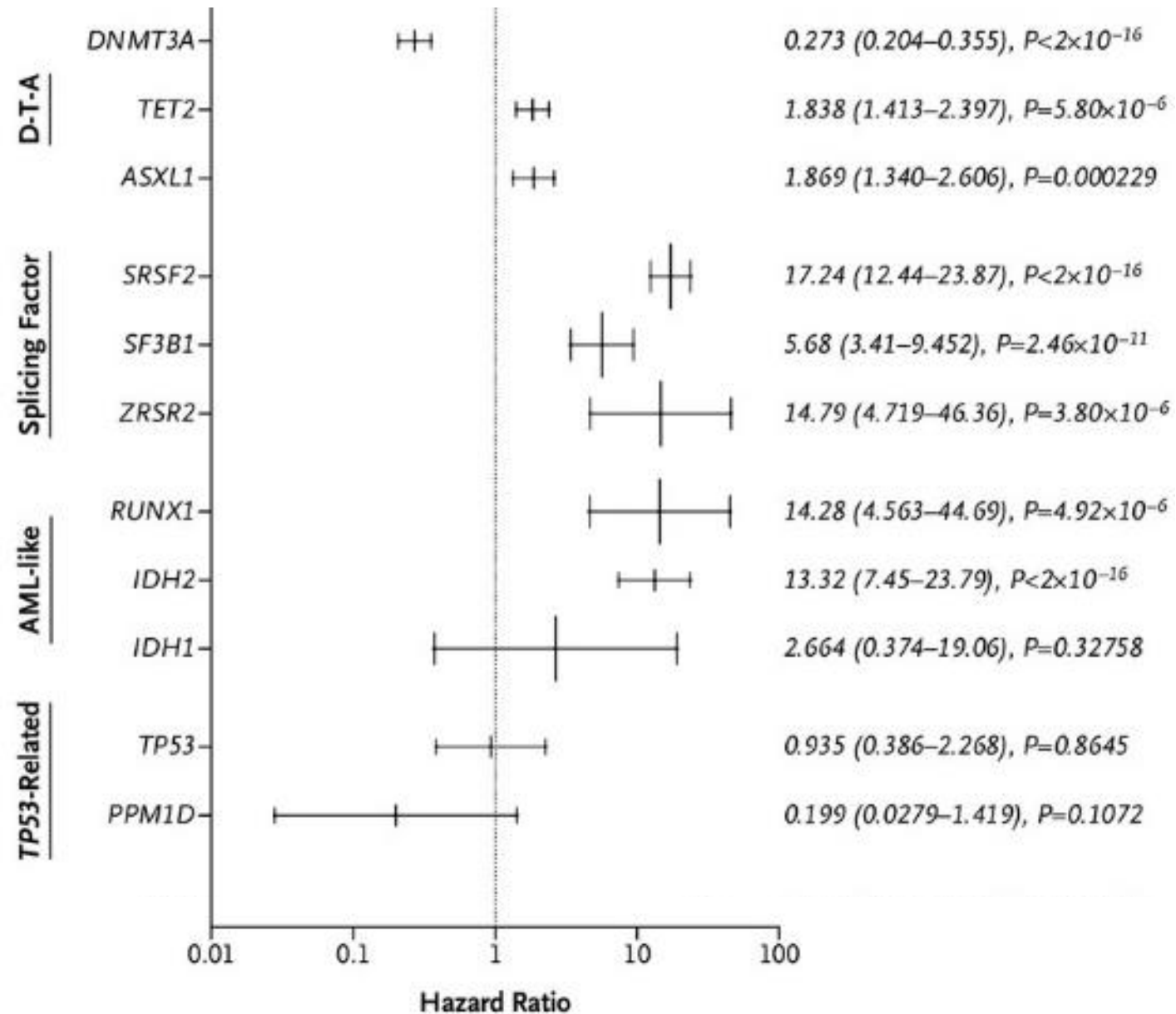
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CHIP is associated with cardiovascular disease in the UK Biobank

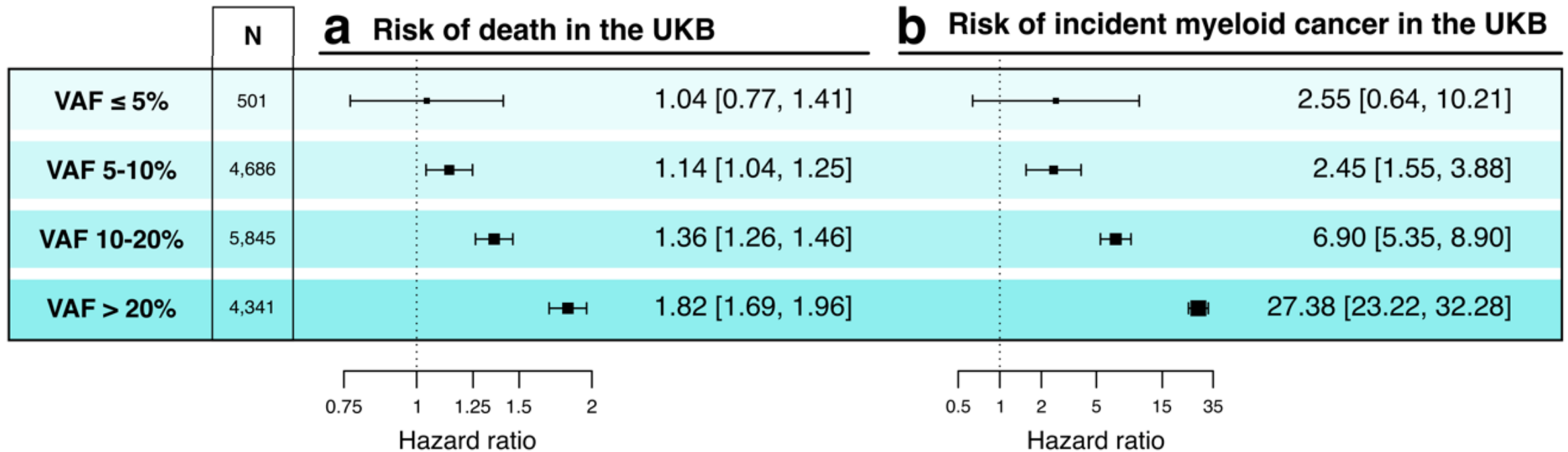
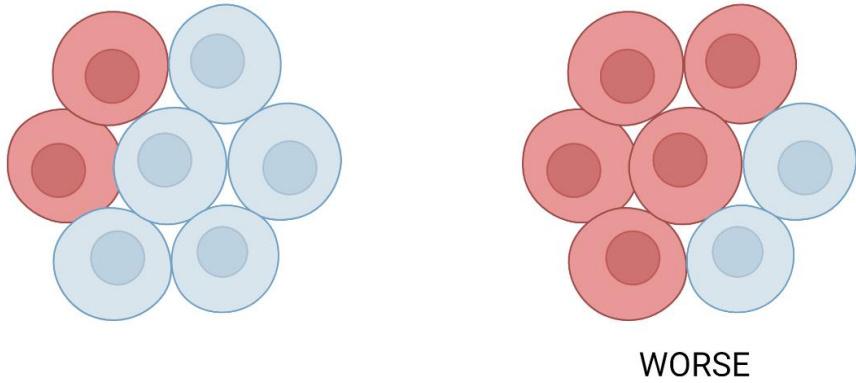
Caitlyn Vlasschaert, Giulio Genovese, Yash Pershad, Siddhartha Jaiswal, Pradeep Natarajan, Alexander G. Bick

doi: <https://doi.org/10.1101/2023.11.30.23299001>

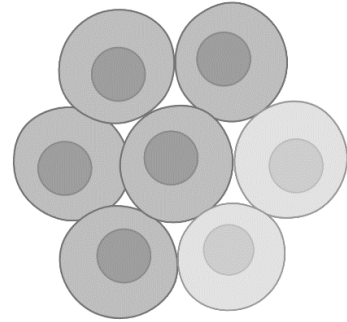
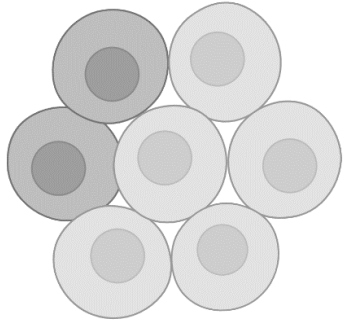
Myeloid Malignancy risk differs by CHIP gene



Larger CHIP clones have worse outcomes

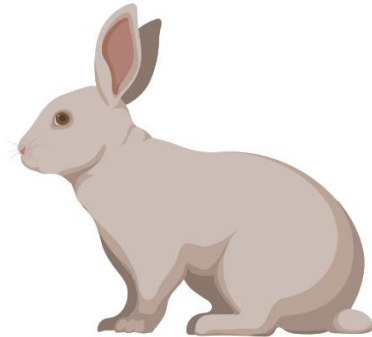


Larger CHIP clones have worse outcomes



WORSE

Bigger clones have worse outcomes.

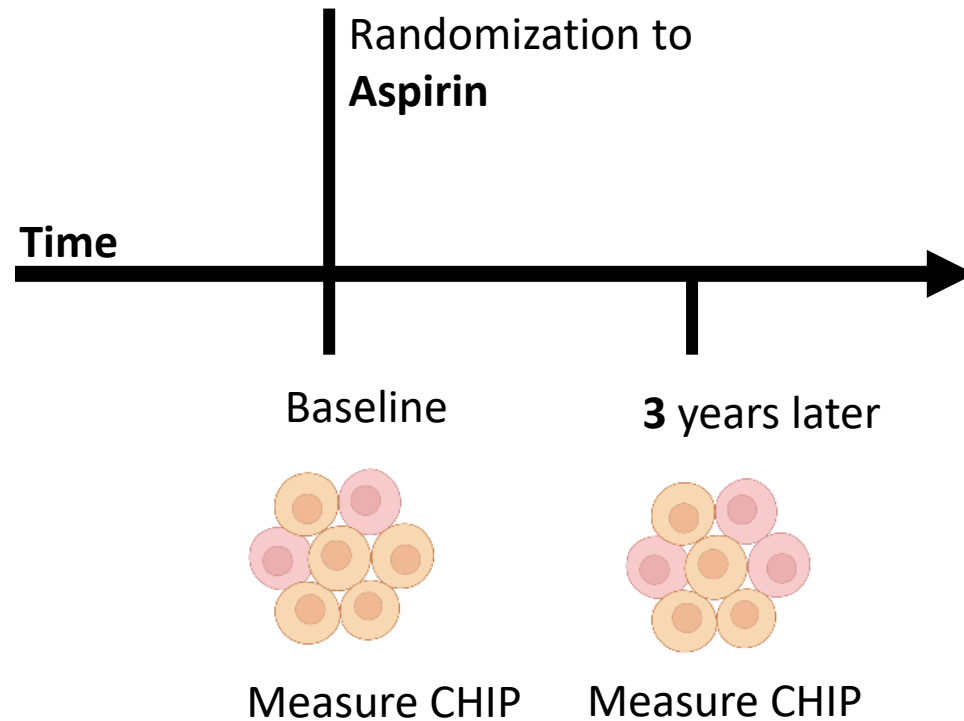


WORSE

Hypothesis:

Faster growth is worse than slower growth.

ASPREE-CHIP study



Participants: Community-dwelling age ≥ 70 or ≥ 65 US minorities

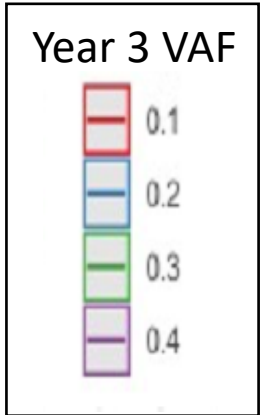
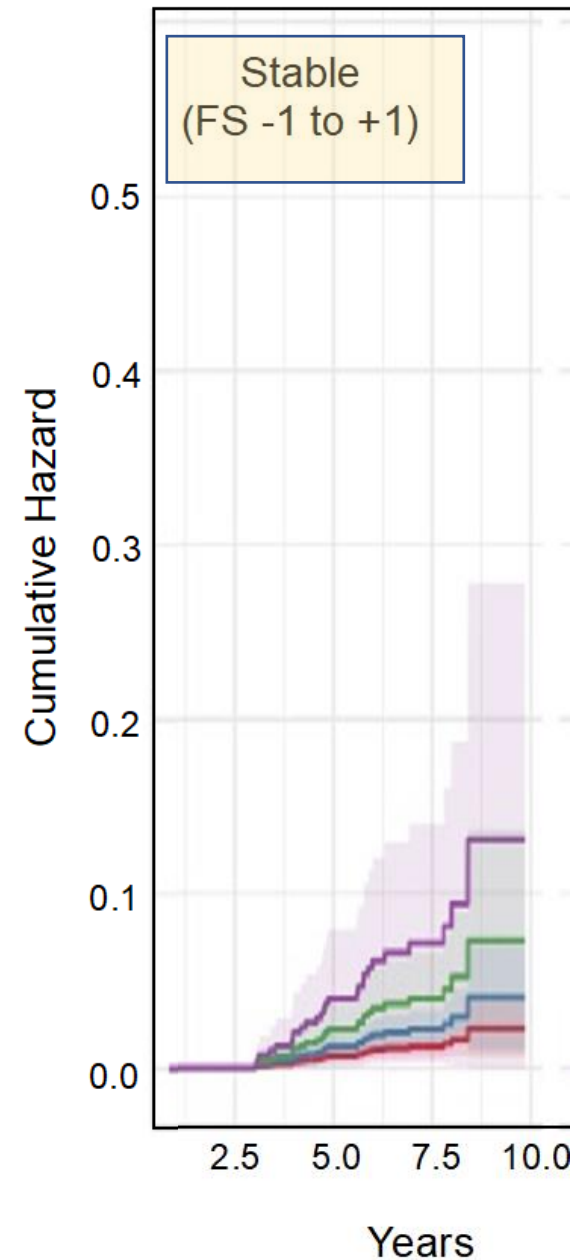
Intervention: randomization to 100mg aspirin daily or placebo

Main Outcomes and Measures: Disability-free survival, mortality, cancer and MACE

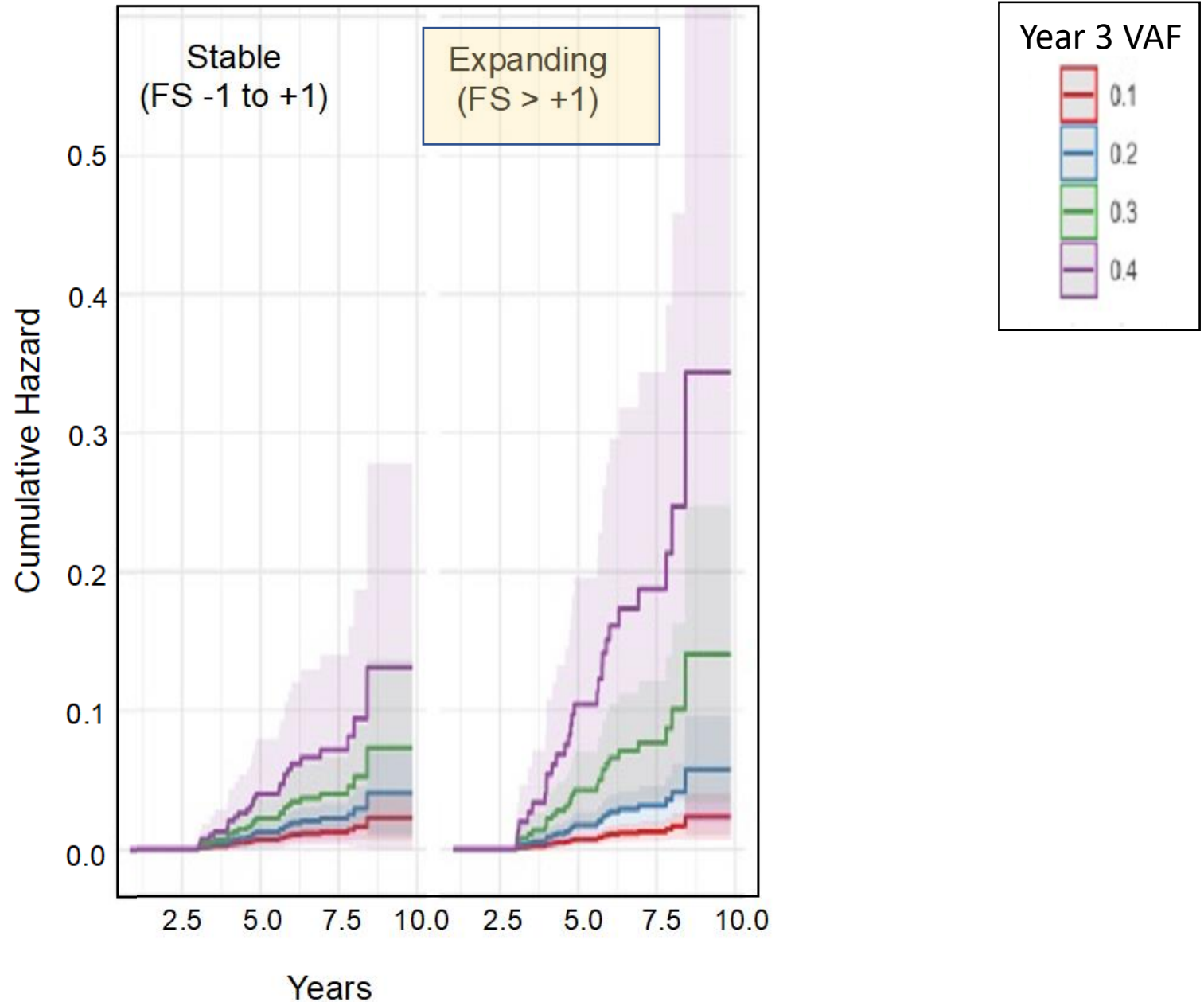
Median follow-up: 4.6 years

Observational f/u: 6.9 years

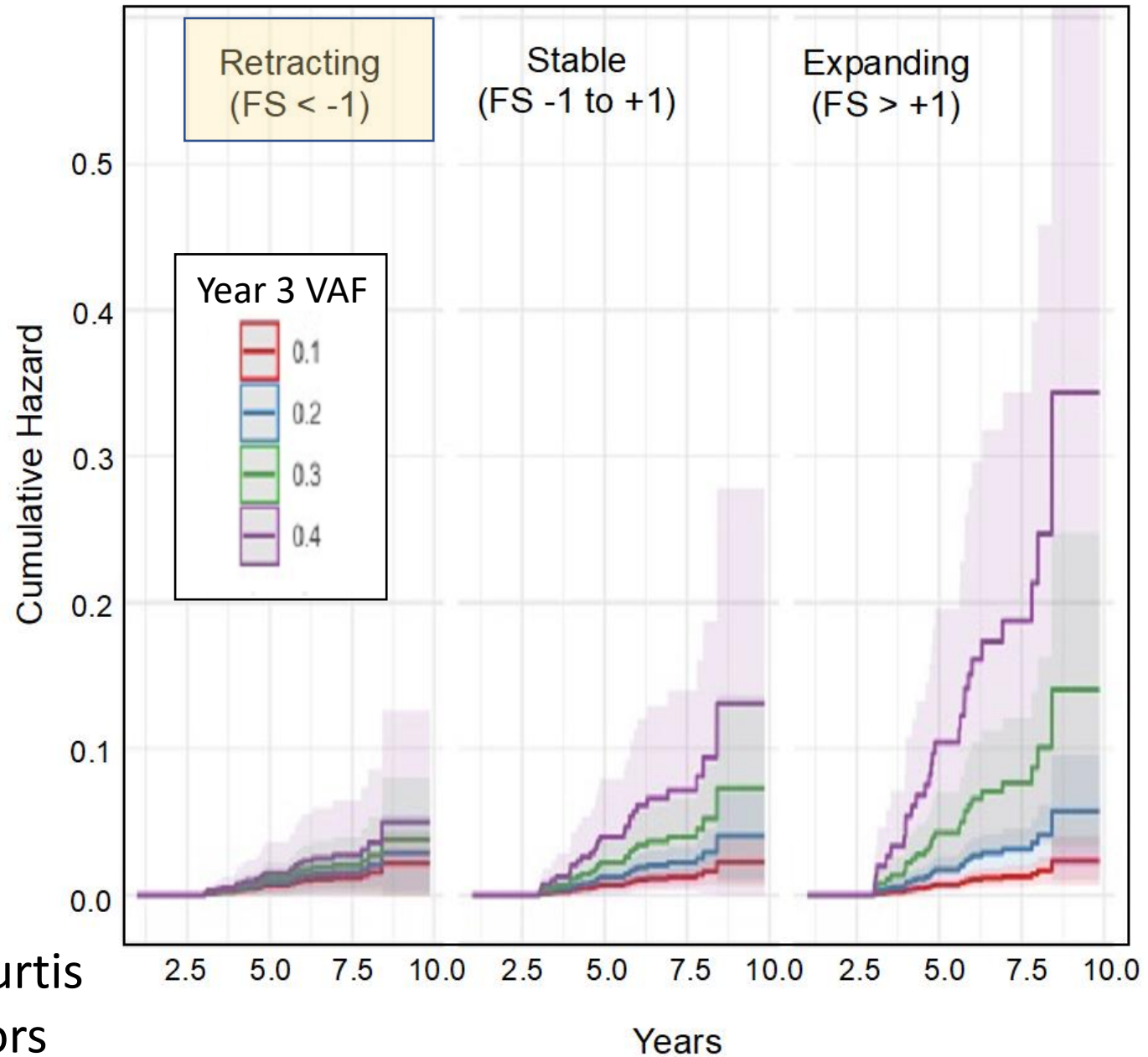
ASPREE: Faster growth is worse than slower growth



ASPREE: Faster growth is worse than slower growth



ASPRE: Faster growth is worse than slower growth



What causes CHIP?

HSC Intrinsic

- DNA damage
 - Aging
 - Smoking
 - Radiation exposure
 - Telomere attrition
 - DNA mismatch repair
- **Germline genetics**

Selective pressures

- Chemotherapy
- Immune-mediated marrow depletion
- Inflammation, infection, stress [...]

How are CHIP patients identified clinically?

Incidental finding from solid tumor genetic testing

GENOMIC VARIANTS

Biologically Relevant

Variant Allele Fraction

 **JAK2** p.V617F Missense variant - GOF

3.3% 

Median Variant Allele Fraction

3.3%

IMMUNOTHERAPY MARKERS

Microsatellite Instability Status

MSI-High not detected

TREATMENT IMPLICATIONS

No reportable treatment options found.

Reported variant(s) detected in this patient's sample may be associated with clonal hematopoiesis or an underlying hematologic process. Clinical correlation is recommended.


How are CHIP patients identified clinically?

Incidental finding from solid tumor genetic testing

GENOMIC VARIANTS

Biologically Relevant

Variant Allele Fraction

 JAK2 p.V617F Missense variant - GOF

3.3% 

Median Variant Allele Fraction

Myeloid NGS panel during cytopenia workup

TECHNICAL SUMMARY

Gene	Alteration	AMP Tier	Chr	Pos	Ref	Alt	Coverage	Allele Freq. or Fold Change
TET2	p.Gly1187Alafs*39	II	4	106164048	AG	A	14298	9%

Clonal Hematopoiesis Risk Score (CHRS)

Prognostic Variable	0.5	1	1.5	2	2.5
Single <i>DNMT3A</i>	present	absent	–	–	–
High Risk Mutation	–	absent	–	–	present
Mutation Number	–	1	–	≥ 2	–
Variant Allele Fraction	–	< 0.2	–	> 0.2	–
Red Cell Distribution Width	–	< 15	–	–	≥ 15
Mean Corpuscular Volume	–	< 100	–	–	> 100
Cytopenia	–	CHIP	CCUS	–	–
Age	–	< 65y	≥ 65y	–	–

Clonal Hematopoiesis Risk Score (CHRS) Calculator

Patient Characteristics

CHIP or CCUS

Number of mutations

Maximum VAF

Mean corpuscular volume (MCV)

Red cell distribution width (RDW)

Age

About this calculator

[CHRS Score and Clinical Outcomes](#)

[Population Data](#)

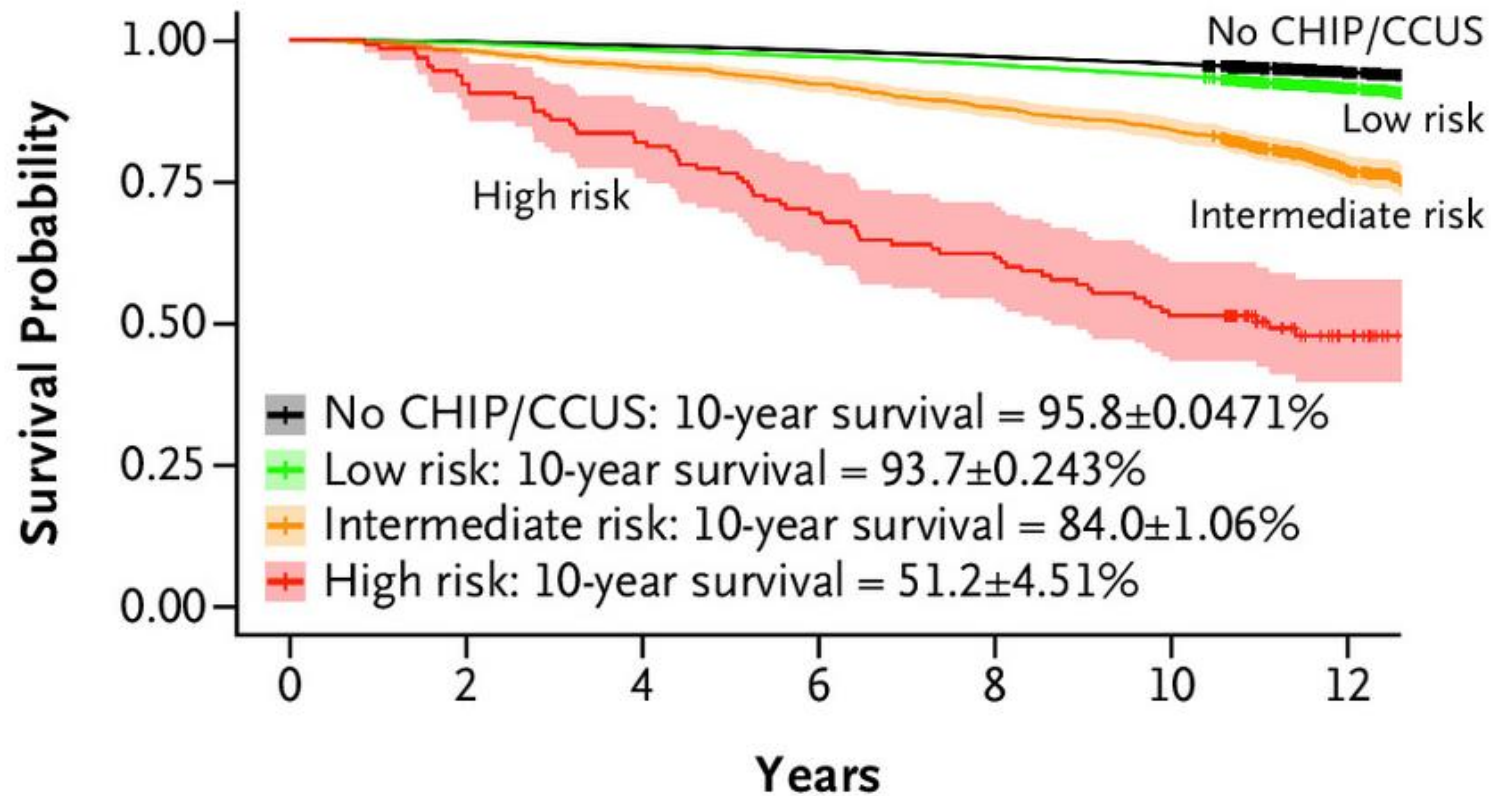
The clonal hematopoiesis risk score (CHRS) is a prognostic model for clonal hematopoiesis of indeterminate significance (CCUS) which can be used to estimate 5- and 10- year cumulative risk of myeloid malignancy data published in Weeks LD et al. 2023. *New England Journal of Medicine Evidence*. The CHRS was developed by the CHRS Biobank and validated using patient cohorts from Dana-Farber Cancer Institute, Boston, MA, USA and University of Michigan.

Cytopenia definitions in CCUS:

- anemia: hemoglobin < 12g/dL for females, <13 g/dL for males
- thrombocytopenia: platelet count < 150 K/uL
- neutropenia: absolute neutrophil count < 1.8 K/uL

Using the CHRS calculator:

- Outcome predictions are made using data/variables obtained at the time of next generation sequencing.
- Select a diagnosis of CHIP or CCUS.
- Select the number of pathogenic somatic variants (mutations) detected by peripheral blood or bone marrow.
- For patients with only 1 mutation, indicate whether the mutated gene is *DNMT3A* (single *DNMT3A*). This field will default to 'Absent' for patients with multiple mutations.
- Indicate whether there are mutations in high risk genes (*SF3B1*, *SRSF2*, *ZRSR2*, *JAK2*, *TP53*, *RUNX1*). This field defaults to 'Absent' when single *DNMT3A* mutations is selected.
- Indicate if the maximum variant allele fraction (VAF) - for any mutation - is ≥ 0.2 (20%)
- Indicate whether mean corpuscular volume (MCV) is ≥ 100 femtoliters, red cell distribution width is ≥ 13 %.
- After entering patient information, click 'Calculate CHRS'.



Number at Risk

Time (yr)	0	2	4	6	8	10	12
High risk	123	113	101	86	76	63	25
Int. risk	1,196	1,176	1,141	1,101	1,051	1,005	354
Low risk	10,018	9,963	9,830	9,717	9,567	9,386	3,793
No CHIP/CCUS	182,406	181,706	180,486	178,864	76,967	174,688	72,376

Ongoing Clonal Hematopoiesis Clinical Trials

There are no FDA approved therapies for CHIP

Targeting Specific Driver Mutations

- Ivosidenib for Patients With Clonal Cytopenia of Undetermined Significance and Mutations in IDH1 [NCT05030441]
- A Study of Enasidenib in People With Clonal Cytopenia of Undetermined Significance [NCT05102370]

Targeting bone marrow environment

- Canakinumab for the Prevention of Progression to Cancer in Patients With Clonal Cytopenias of Unknown Significance, IMPACT Study [NCT05641831]



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The under-appreciation of CHIP

It's time to drop the "indeterminate" and get serious about this biomarker

ERIC TOPOL

MAY 21, 2023

Share ...

Each day the 50,000 to 200,000 blood stem cells in our bone marrow, known as hematopoietic (HSC), produce billions of specialized blood cells—red blood cells, platelets, B and T lymphocytes, and various myeloid cells (white blood cells, such as neutrophils and monocytes). As we age, the repeated cell divisions of the HSCs lead to acquired (“somatic”) mutations. When such a mutation of an HSC leads to a clone that expands—which denotes some fitness advantage— it is known as clonal hematopoiesis. CHIP, which stands for clonal hematopoiesis of indeterminate potential, refers to presence of myeloid blood cells with a driver gene mutation (with a frequency of $\geq 2\%$) without any clinical criteria of a blood cancer. It turns out CHIP is a major biomarker, not just for blood cancer (an 11-fold risk of a blood malignancy, or absolute 0.5% risk per year), but also for heart disease, blood clot events such as stroke and pulmonary embolism, and many other chronic illnesses (simplified [Figure below](#)).



Clonal Hematopoiesis

Alexander Bick, MD PhD
Assistant Professor, Div. Genetic Medicine
Vanderbilt School of Medicine

