



# The Latest in Longevity Medicine: Predictive Genomics

Joel M Evans, MD

Chief of Medical Affairs

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# What is Longevity Medicine?

- The term is a real.
- 158,000,000 results on Google (10/8/23)
- National Academy of Medicine held a conference, *2023 Healthy Longevity Global Innovator Summit*, in Sept 2023.
- The therapeutic race is on between genetic changes, pharmaceuticals and natural compounds.
  - Genetic changes can increase lifespan 4x in the roundworm .
  - TAME trial (Targeting Aging by Metformin)
- Only single interventions studied so far.



# What is Longevity Medicine?

- Longevity medicine is advanced personalised preventive medicine powered by deep biomarkers of aging and longevity, and is a fast-emerging field. The field encompasses the likewise rapidly evolving areas of biogerontology, geroscience, and precision, preventive, and functional medicine.

- Longevity medicine: upskilling the physicians of tomorrow

The Lancet, Healthy Longevity, [VOLUME 2, ISSUE 4](#), E187-E188, APRIL 2021

[https://www.thelancet.com/journals/lanhl/article/PIIS2666-7568\(21\)00024-6/fulltext#%20](https://www.thelancet.com/journals/lanhl/article/PIIS2666-7568(21)00024-6/fulltext#%20)



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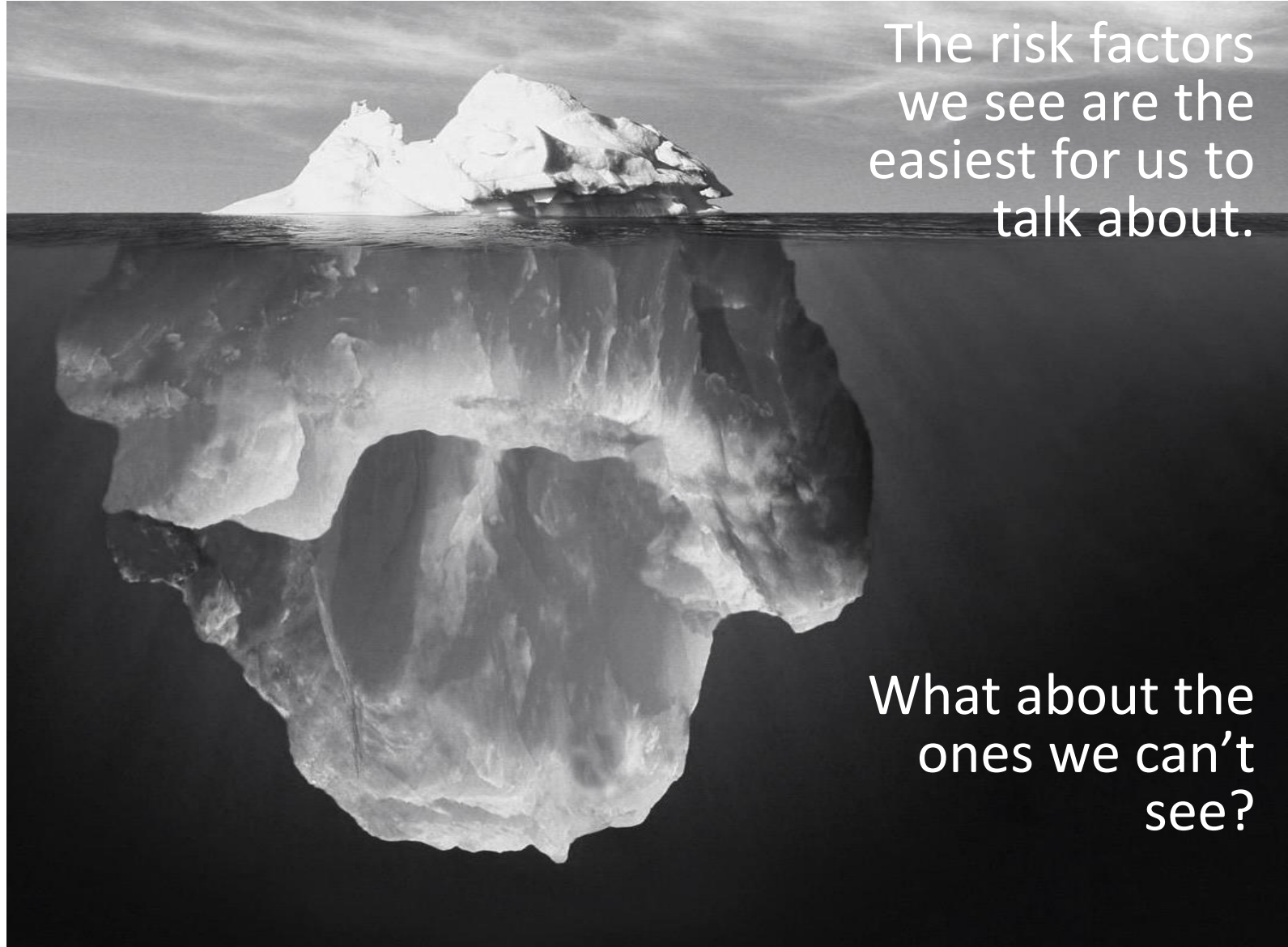


# What is Predictive Genomics?

- The new precision (personalized) medicine, where genome sequencing and data analysis are essential components. It allows tailored diagnosis and treatment according to the information from the patient's own genome and specific environmental factors. P4 (predictive, preventive, personalized and participatory) medicine is introducing new concepts, challenges and opportunities.
  - Carrasco-Ramiro F, Peiró-Pastor R, Aguado B. Human genomics projects and precision medicine. Gene Ther. 2017 Sep;24(9):551-561. doi: 10.1038/gt.2017.77.



Predictive genomics  
allows us to look beneath  
the surface



The risk factors  
we see are the  
easiest for us to  
talk about.

What about the  
ones we can't  
see?



For example, breast density for breast cancer.  
Or newer biomarkers, like DNA Methylation.  
But....



The risk factors we know about are the easiest for us to talk about.

What about the biomarkers we don't know about yet or can't test?

What about association, NOT causation?



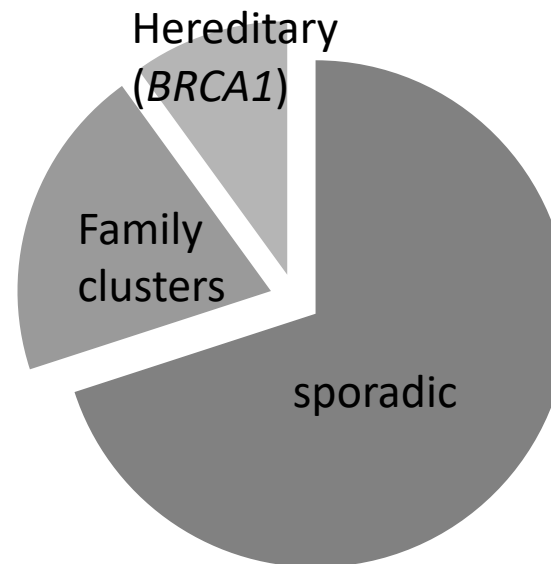
# The Human Genome:

- 23 pairs of chromosomes
- Three billion nucleotides (base pairs)
- 20-25,000 genes

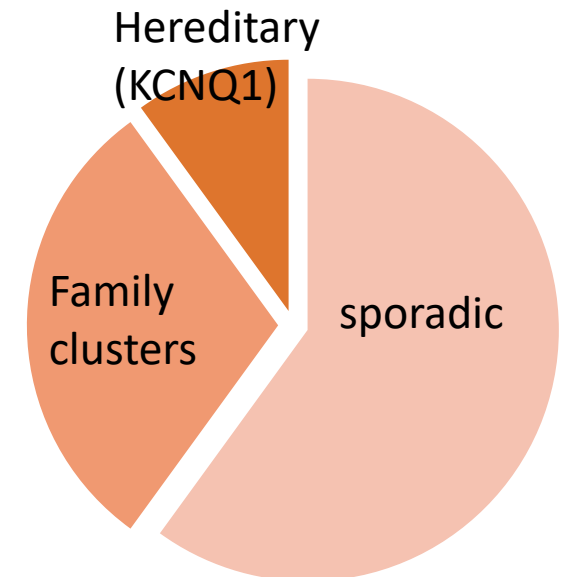
# Clinical Genetics 101

- Hereditary
- Familial
- Sporadic

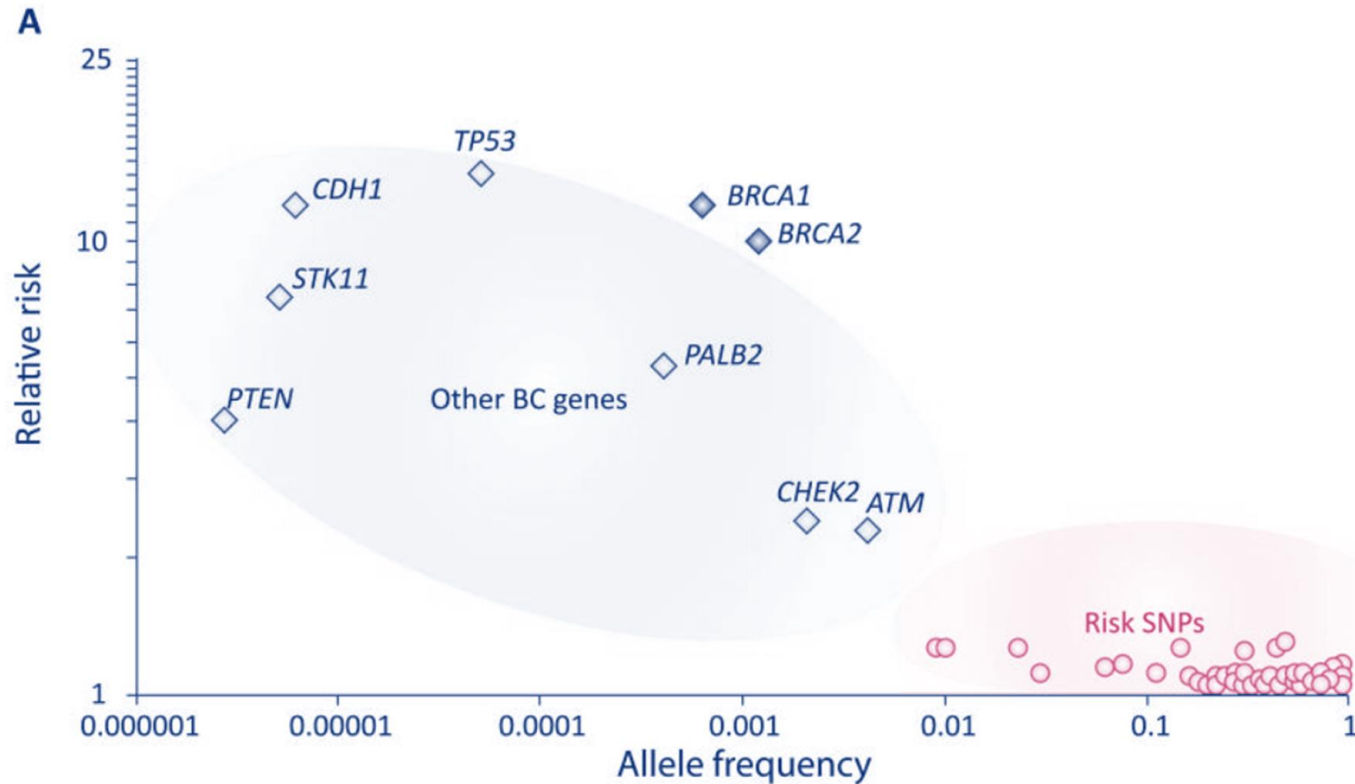
## Cancers



## Cardiovascular

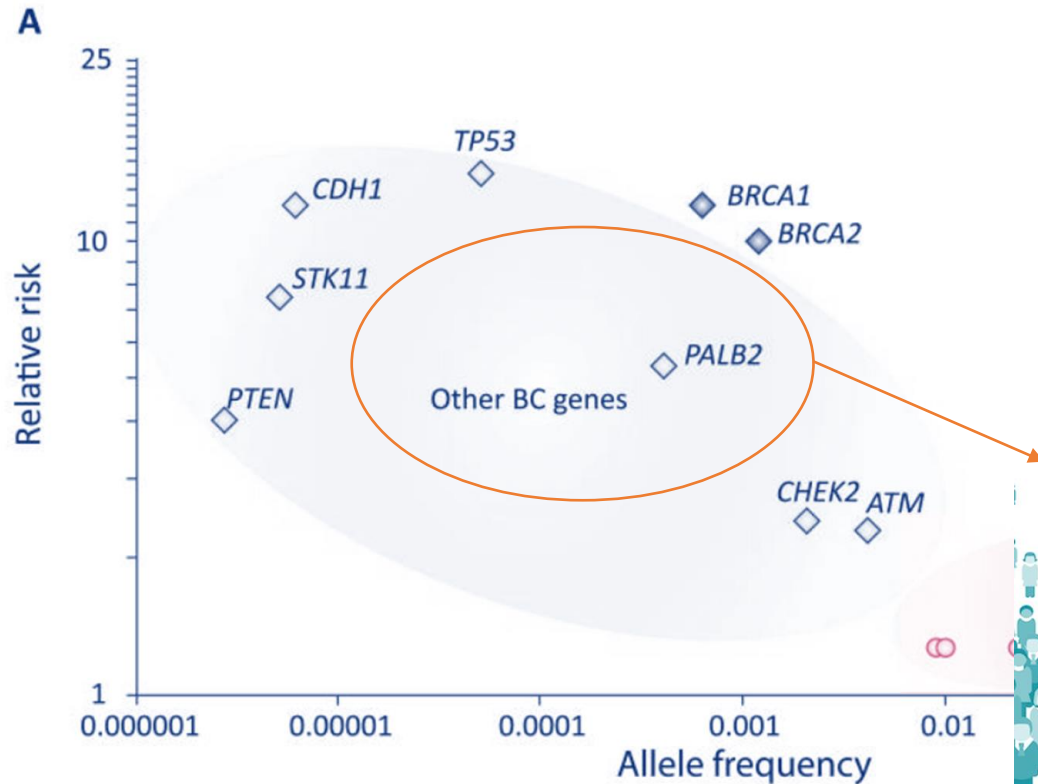


# Clinical Genetics 101



- High, moderate and low penetrance

# Clinical Genetics 101



- Low penetrance SNP originally derived from genome wide association studies

Thousands of adults **without** the disease

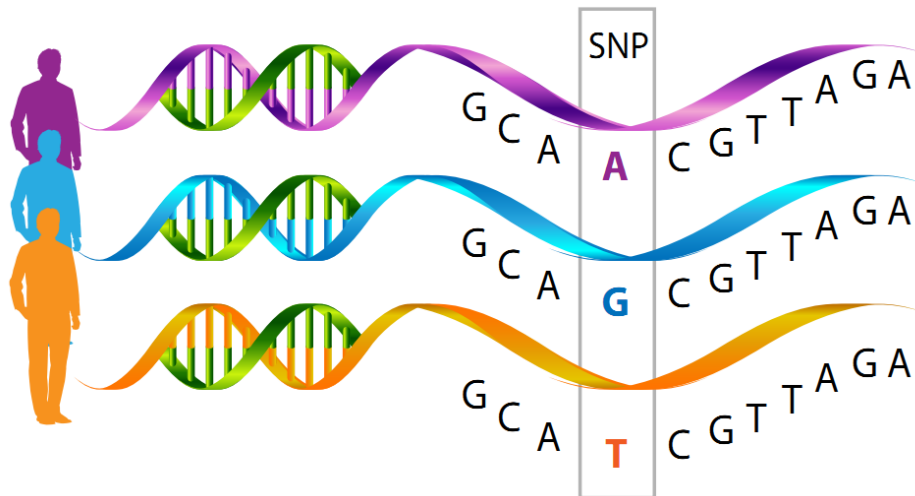


Thousands of adults **with** the disease





# Low penetrance risk alleles = SNP

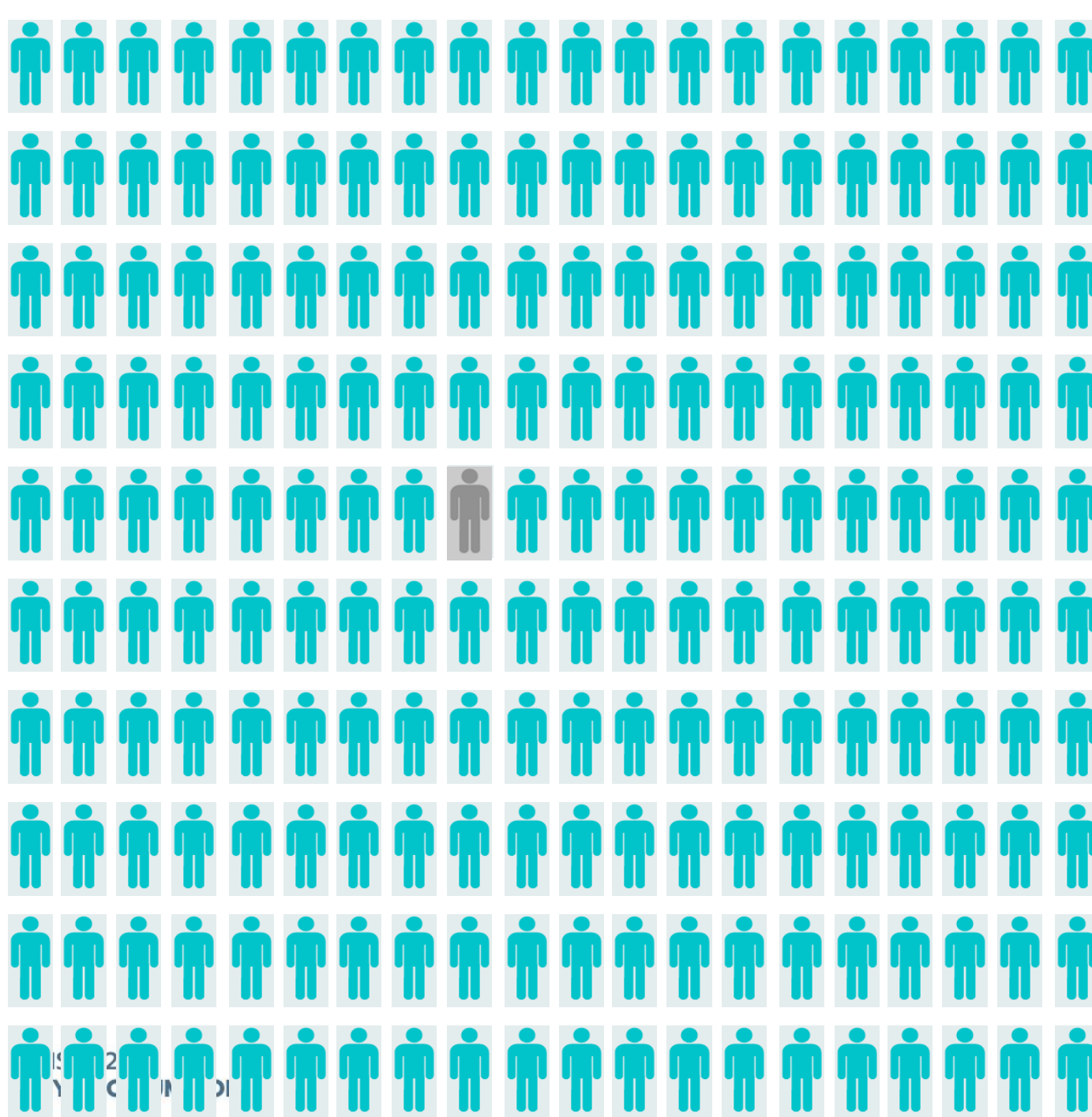


- SNP = Single Nucleotide Polymorphisms
- All of us have 99.9% DNA in common. Some of the 0.1% differences in our DNA are due to SNP
- Predictive genomics has exploited these SNP by using ones that appear more often in adults who develop disease (like breast cancer) compared to those who don't



# Putting SNP's together helps us calculate genetic risk

- What is polygenic Risk?
- What is a Polygenic Risk Score (PRS)?
- How does that differ from BRCA?



1 in 200+ adults  
will carry a  
pathogenic variant  
(*ex: BRCA1*)

High Penetrance  
Low Prevalence



# 1 in 8

- women develop breast cancer
- men develop prostate cancer

Every adult has a disease-specific polygenic risk score





# Polygenic Risk Scores

High Prevalence  
Low Penetrance

Each **SNP** alone only as a small  
association with the disease...



Risk of disease

...but in combination, the SNPs can have a  
measurable association with disease.



# PRS: Each of us has a different combination of SNP risk alleles



PRS: Each of us has a different combination of SNP risk alleles

Patient



“Baseline” risk



■ SNP

Single Nucleotide Polymorphisms

# Predictive genomics alone:



## Predictive genomics alone:

- Genome-wide association studies have shown unequivocally that common complex disorders have a polygenic architecture
- Researchers can identify genetic variants associated with diseases.
- These variants can be combined into a polygenic risk score to capture part of an individual's risk of diseases.
- Much of the research is on CVD, type 2 diabetes, breast, prostate cancers, Alzheimer's disease atrial fibrillation and inflammatory bowel disease
  - Lewis CM, Vassos E. Polygenic risk scores: from research tools to clinical instruments. *Genome Med.* 2020 May 18;12(1):44. doi: 10.1186/s13073-020-00742-5. PMID: 32423490; PMCID: PMC7236300.



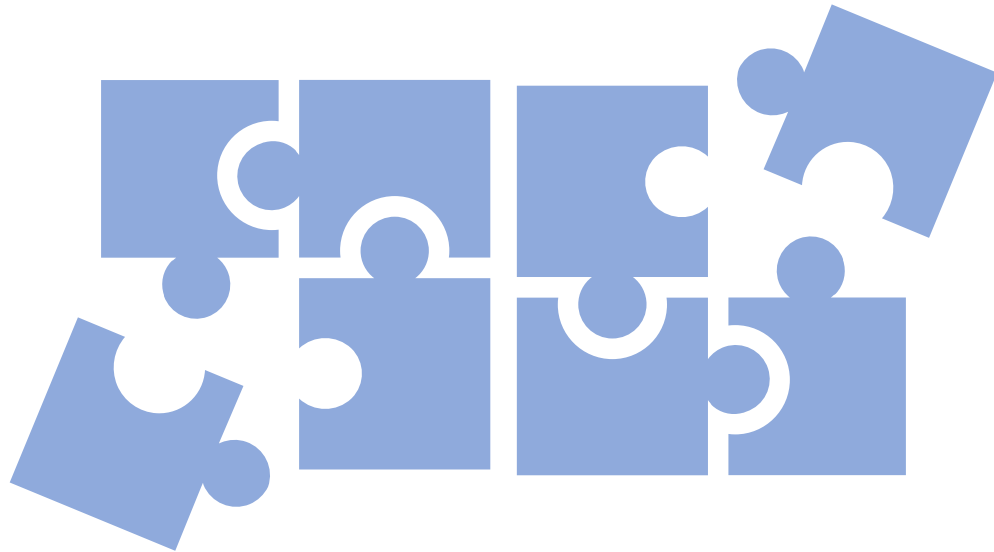


# Many companies are in the commercial space

- So much so that The Guardian published a piece, **“Will genome sequencing bring precision medicine for all?”**
  - The health secretary wants to introduce genetic screening to the NHS
  - The commercial space is clear: there are three main phases in the advancement of personalised medicine. First, improved diagnosis, then improved treatment as a result of better diagnosis. And the third stage, he says, will be much earlier detection and prevention.
- <https://www.theguardian.com/science/2019/sep/28/genome-sequencing-precision-medicine-bespoke-healthcare-nhs>



# What if we could integrate the power of predictive genomics with clinical (phenotypic) factors?



- Might they be more powerful **together?**

## CVD



# Integrated Polygenic Tool Substantially Enhances Coronary Artery Disease Prediction

- Can genetic data can be used to improve standard cardiovascular disease risk calculators?
- We developed our own polygenic risk score for CAD and developed an integrated risk tool (IRT) that combined our polygenic risk score with established risk tools.
- *Circ Genom Precis Med.* 2021;14:e003304. DOI: 10.1161/CIRCGEN.120.003304



# Integrated Polygenic Tool Substantially Enhances Coronary Artery Disease Prediction

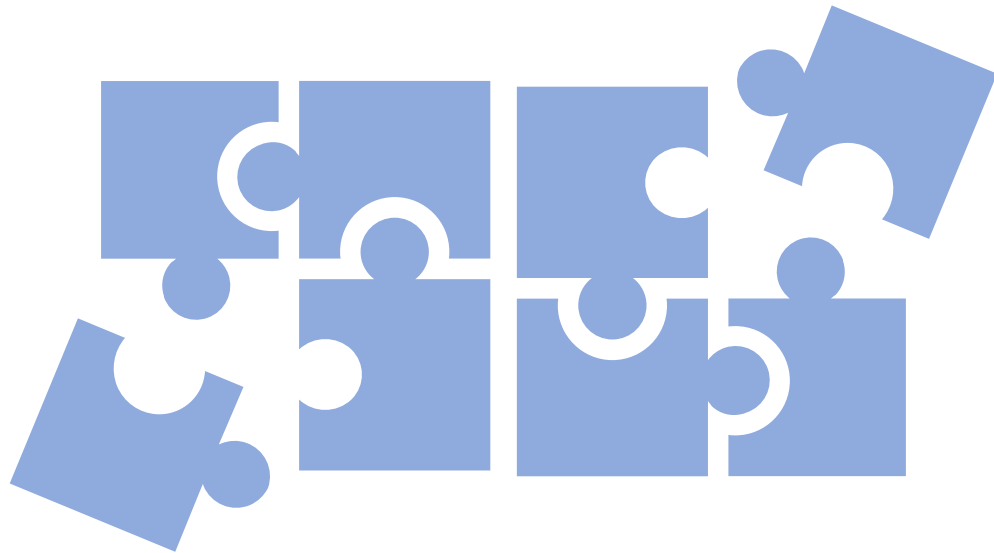
- The addition of our PRS to PCE (pooled cohort equations) would up-classify 7% of people to a level of cardiovascular risk that warrants statin prevention
- **CONCLUSIONS:** An IRT that **includes** polygenic risk outperforms current risk stratification tools and offers greater opportunity for early interventions.

• *Circ Genom Precis Med.* 2021;14:e003304. DOI: 10.1161/CIRCGEN.120.003304





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**Colon Cancer**



Colorectal cancer risk stratification is crucial to improve screening and risk-reducing recommendations, and consequently **do better than a one-size-fits-all screening regimen.**

We investigated adding a polygenic risk score (45 SNP's) to a family history model to quantify how it improves risk stratification

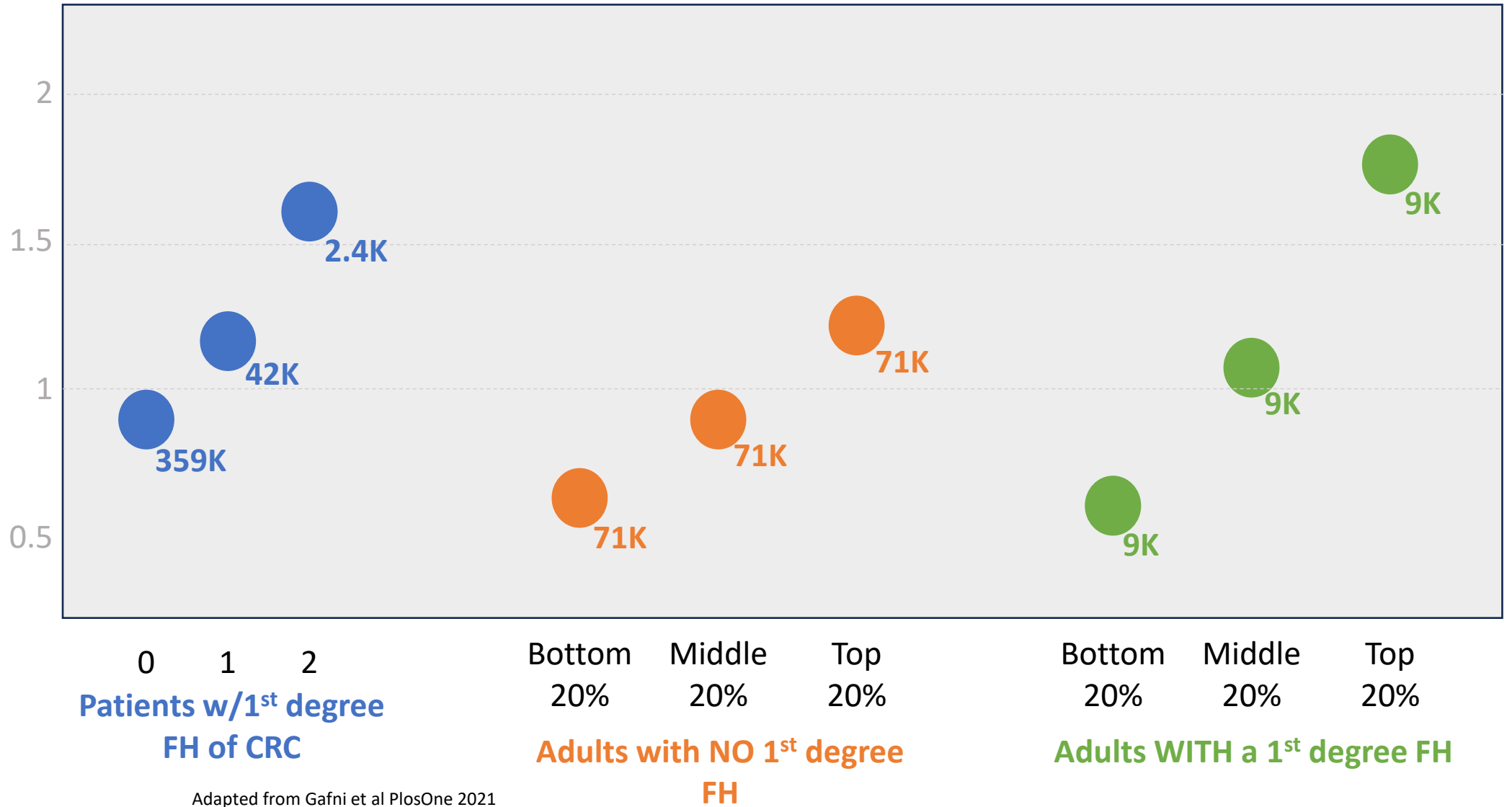


For both 10-year and full lifetime risk, the combined model had a wider risk distribution compared with family history alone, resulting in improved risk stratification of nearly 2-fold between the top and bottom risk quintiles of the full lifetime risk model. I

Importantly, the combined model can identify people who do not have family history of colorectal cancer but have a predicted risk that is equivalent to having at least one affected first-degree relative.



Standard incidence ratio







For both 10-year and full lifetime risk, the combined model had a wider risk distribution compared with family history alone, resulting in improved risk stratification of nearly 2-fold between the top and bottom risk quintiles of the full lifetime risk model. I

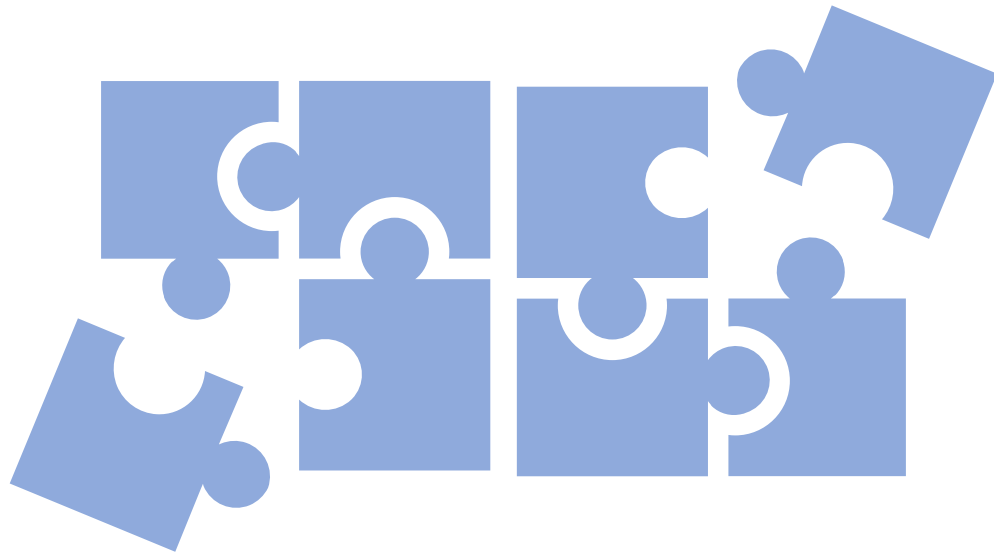
Importantly, the combined model can identify people who do not have family history of colorectal cancer but have a predicted risk that is equivalent to having at least one affected first-degree relative.



- The combined full lifetime risk model significantly improves discriminatory accuracy compared with a simple family history model
- Therefore, a combined polygenic risk score and first-degree family history model could be used to improve risk stratified population screening programs.



# What if we could integrate the power of predictive genomics with clinical (phenotypic) factors?



- Might they be more powerful **together?**

## Prostate Cancer



- Accurate prostate cancer risk assessment will enable identification of men who are at increased risk of the disease
- Current screening options include the DRE and the PSA test
- Risk factors for prostate cancer include age, family history, and ethnicity. Familial risk confers a two- to threefold increased risk based on a first-degree family history of prostate cancer and represents 10%–20% of cases.
- Twin studies have suggested that heritable factors explain 42% of prostate cancer risk.
- Interestingly, there remains a genetic susceptibility in the form of low-penetrance single-nucleotide polymorphisms (SNPs) that explain a large portion of risk.

Dite, G. S., Spaeth, E., Murphy, N. M., & Allman, R. (2023). Development and validation of a simple prostate cancer risk prediction model based on age, family history, and polygenic risk. *Prostate*, 83(10), 962-969. <https://doi.org/10.1002/pros.24537>



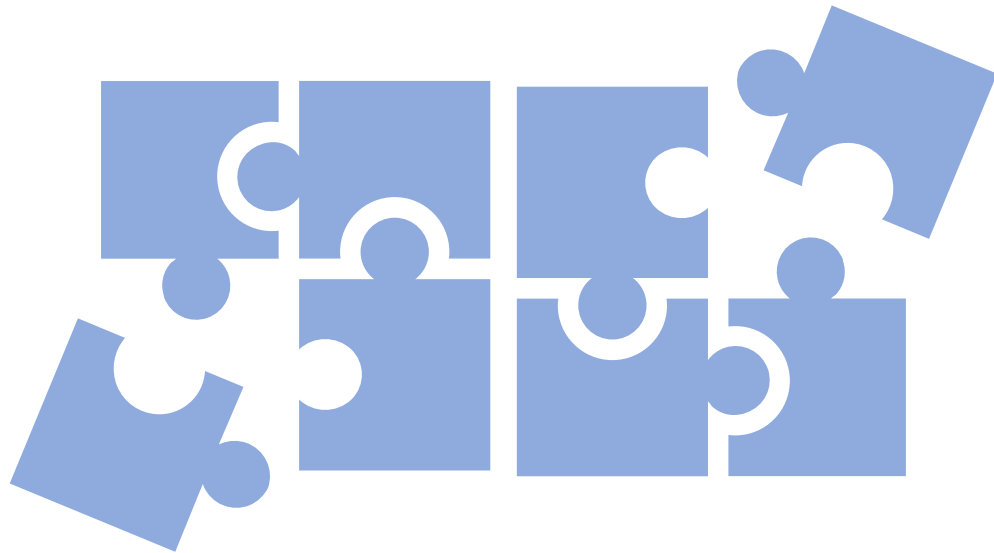


- The model can identify the top 10% of men who are at 2.8 times population risk and the next highest 10% of men at 1.5 times population risk
- At the other end, it can identify men who are at a very low risk
- Accurate knowledge of risk can **inform decision-making** when clinicians and patients discuss the risks and benefits of prostate cancer screening.
- Polygenic risk-tailored screening for prostate cancer is cost-effective and would result in a **30%–56% reduction in overdiagnosis**.

Dite, G. S., Spaeth, E., Murphy, N. M., & Allman, R. (2023). Development and validation of a simple prostate cancer risk prediction model based on age, family history, and polygenic risk. *Prostate*, 83(10), 962-969. <https://doi.org/10.1002/pros.24537>



What if we could integrate the power of predictive genomics with clinical (phenotypic) factors?



- Might they be more powerful **together?**

Ovarian Cancer



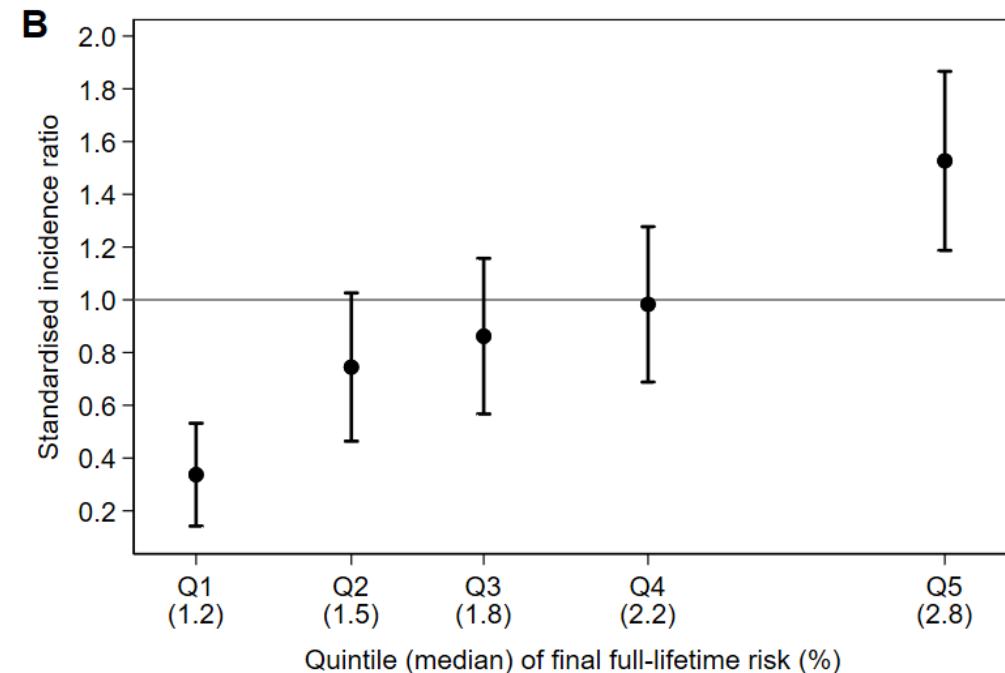
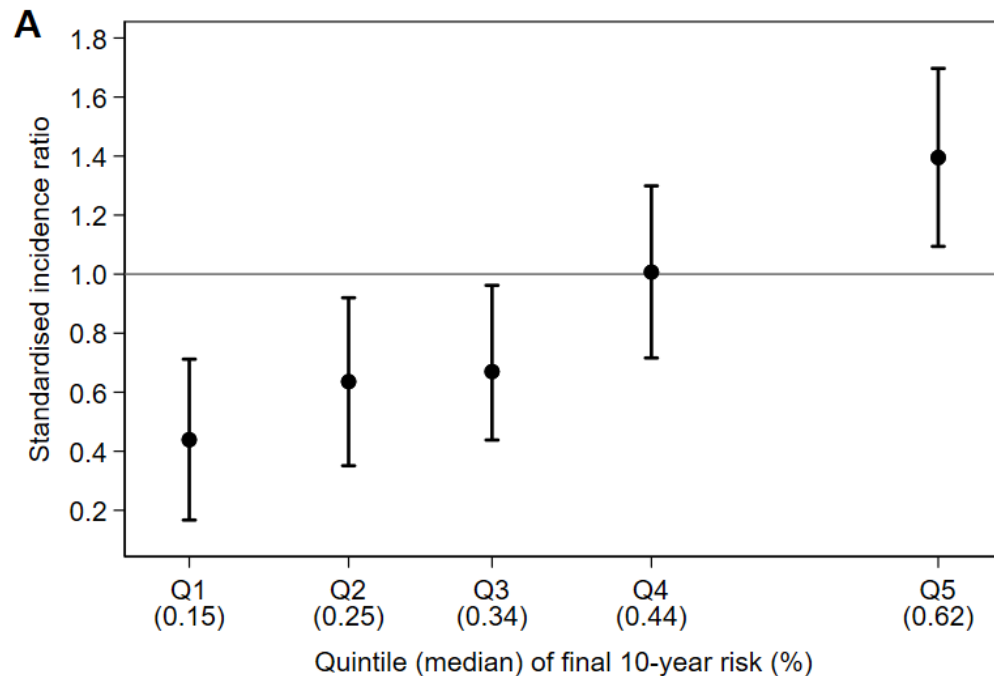
# A combined clinical and genetic model for predicting risk of ovarian cancer

- Women with a family history of ovarian cancer or gene variants are at high risk of the disease, but very few women have these risk factors.
- GWAS studies have identified common genetic variants associated with ovarian cancer to construct PRS.
- We assessed whether **a combined** polygenic and clinical risk score could predict risk of ovarian cancer in population-based women who would otherwise be considered as being at average risk.
- Clinical factors: being menopausal, ever taking hormone replacement therapy, ever taking hormonal birth control and ever having had a full-term pregnancy.



# A combined clinical and genetic model for predicting risk of ovarian cancer

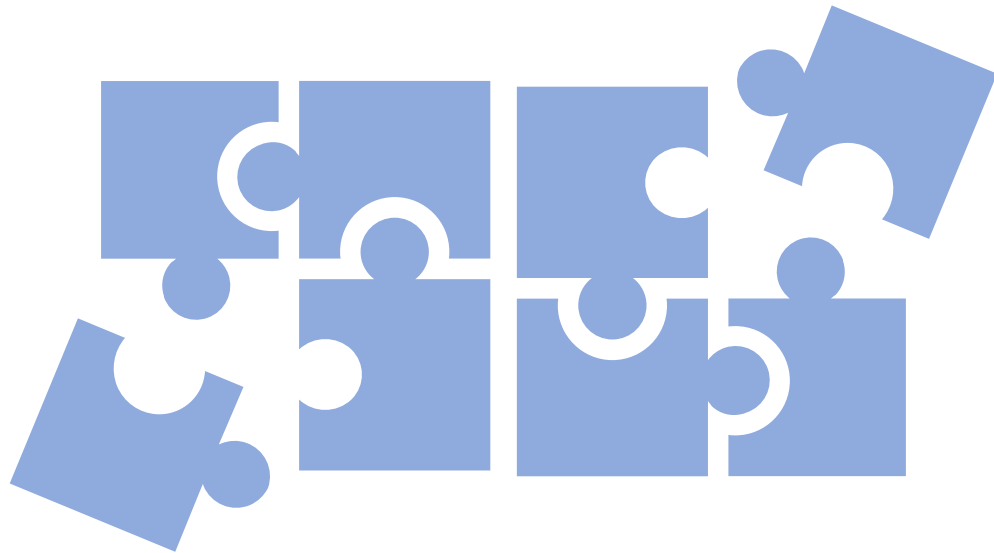
- A combined risk score incorporating a PRS and a clinical risk score has improved discrimination of ovarian cancer over 10 yrs.







# What if we could integrate the power of predictive genomics with clinical (phenotypic) factors?



- Might they be more powerful **together?**

## Pancreatic Cancer

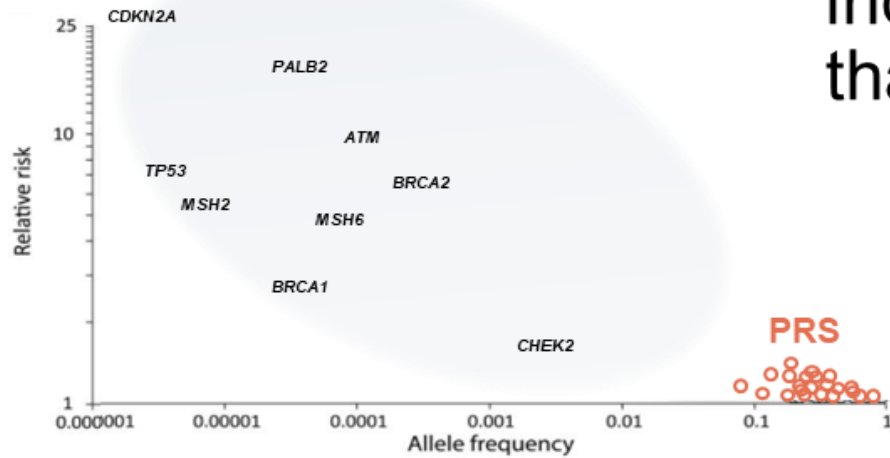


# Predicting 10-Year Risk of Pancreatic Cancer Using a Combined Genetic and Clinical Model

- Population screening is impractical because pancreatic cancer is rare with a lifetime risk of 1.7%.
- Accurate risk stratification in the general population could enable health care providers to focus early detection strategies to at-risk individuals. We already do this in BRCA+ patients (risk 5-10%).
- Clinical variables:
  - Smoking
  - T2 DM >3 yrs
  - FH (not in study)
  - ETOH (>3/d)
  - BMI
  - ABO Blood type (AO < AA < BO < BB < AB)

Dite, Gillian S., et al. "Predicting 10-year risk of pancreatic cancer using a combined genetic and clinical model." *Gastro Hep Advances* (2023).

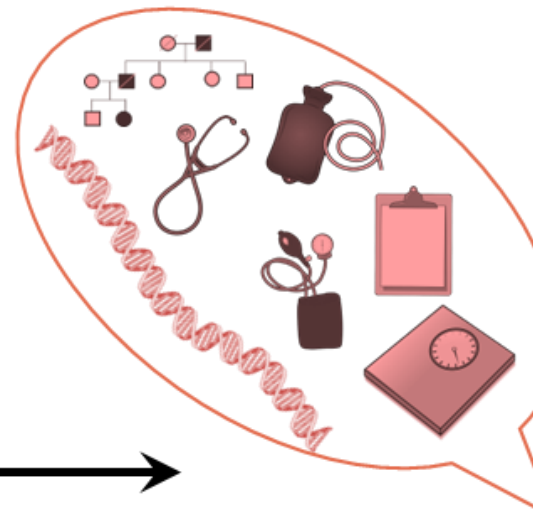
45% more *general population adults* identified at increased risk\* of pancreatic cancer using a model that combines polygenic risk with clinical risk factors.



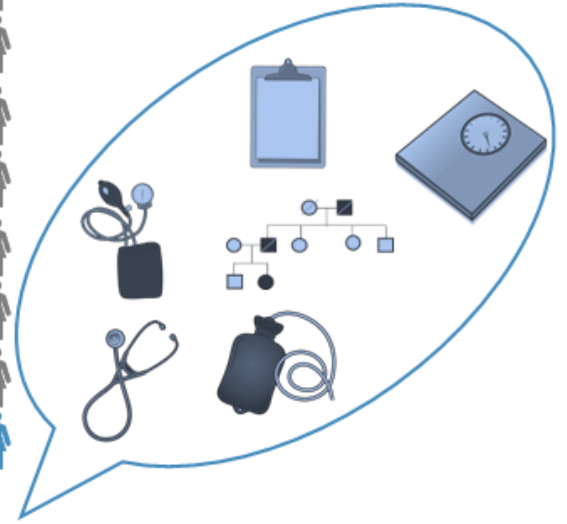
Adults that are ***not carriers*** of high/moderate cancer susceptibility variants can benefit from polygenic risk-integrated risk assessment.

\*defined as >4-fold population average

Combined model



Clinical alone model



3.8%



A risk-stratification tool, paired in a step-wise manner with existing or emerging pancreatic cancer screening techniques could lead to clinically significant downstaging of pancreatic cancer diagnoses.

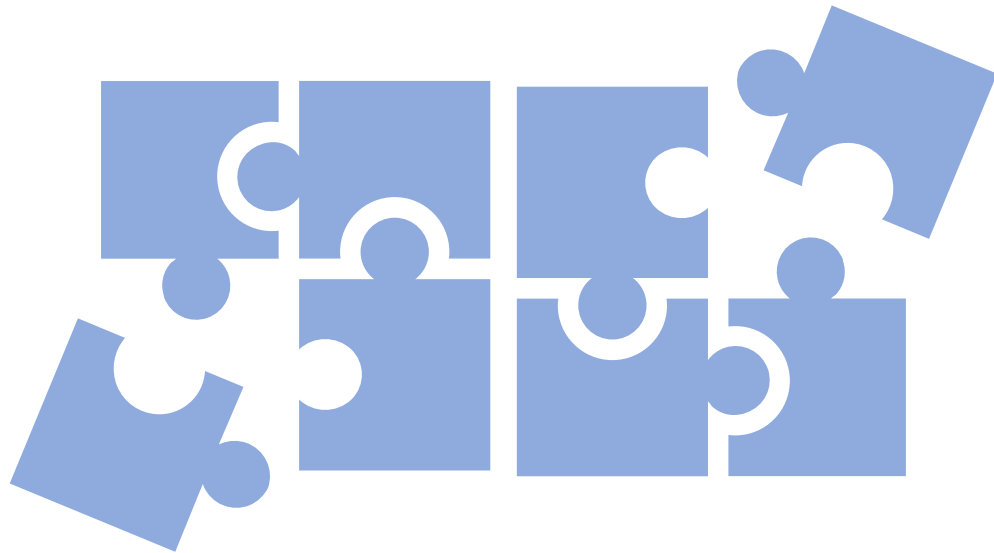




This is important because identifying at-risk adults at early stage diagnosis where surgical resection is still possible is associated with increased survival rates.



# What if we could integrate the power of predictive genomics with clinical (phenotypic) factors?



- Might they be more powerful **together?**

## Breast Cancer



# Breast cancer genetics and risk assessment: an overview for the clinician

- Breast cancer is the most common cancer in women in the world.
- Prevention of breast cancer is therefore a public health imperative everywhere.
- **Prevention** starts with **identification** of individuals at **high risk**.
- **Identification of high-risk women** starts with **identification of those who carry genetic mutations** associated with an elevated risk of breast cancer.
- Once high-risk women are identified then **early detection** and **risk reduction** efforts can be instituted.

L. Larkin (2023): Breast cancer genetics and risk assessment: an overview for the clinician, Climacteric, DOI: 10.1080/13697137.2023.2184254



# Breast Cancer Risk Assessment: The Basics of **Genetic** Risk Assessment

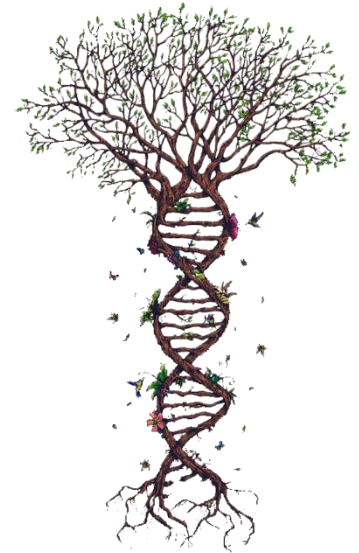


# Sporadic vs Hereditary Breast Cancer

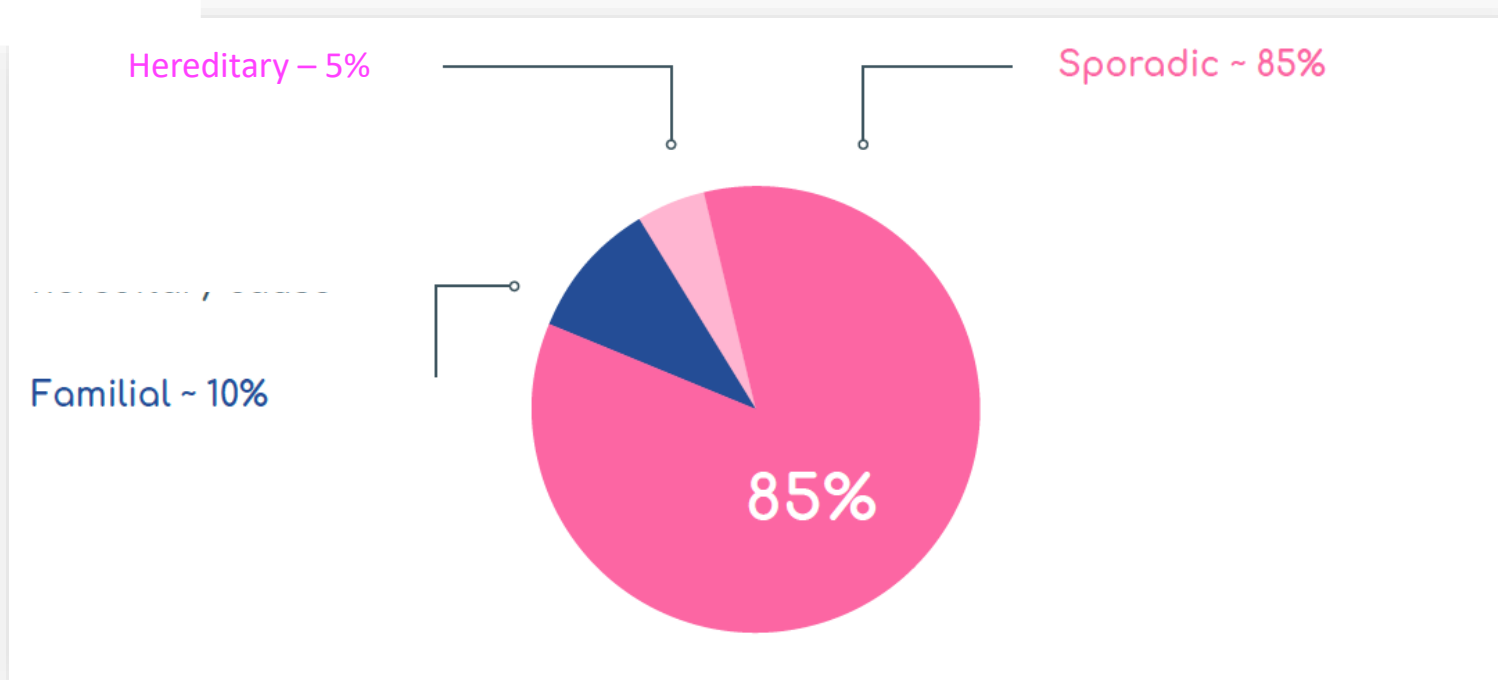


**Sporadic** = appearing or happening at irregular intervals in time; occasional

**Hereditary** = genetic event passed on from parents to their offspring

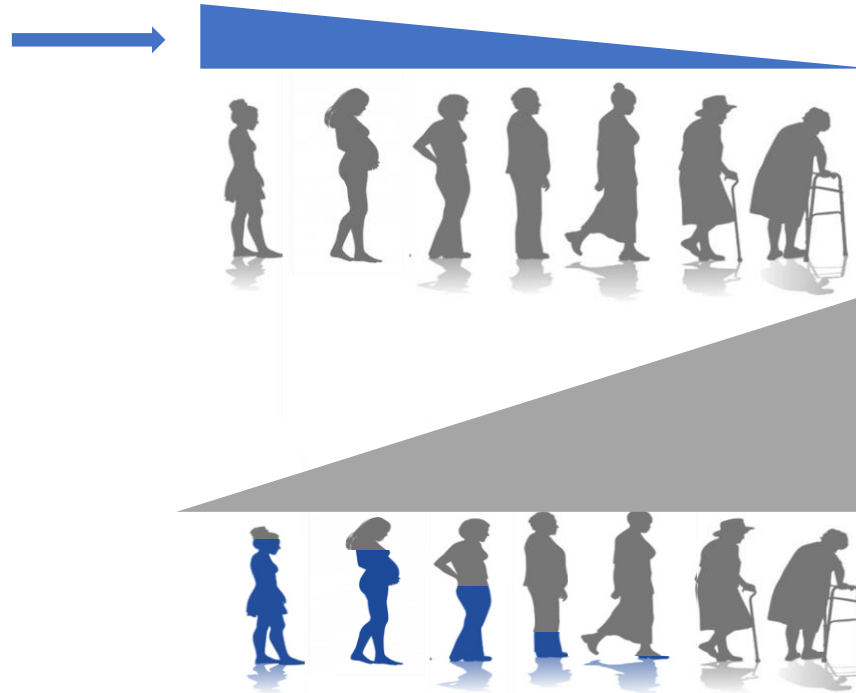


# Most women who develop breast cancer have little or no family history of the disease





Hereditary/familial  
risk of breast cancer is  
less common, but  
develops earlier



The majority of  
women develop  
sporadic breast  
cancer, and it  
develops later:  
**avg age at dx is 60**



1 in 400+ women  
will carry a *BRCA1*  
pathogenic variant





# Toward more personalized breast cancer risk assessment: The polygenic risk score

- Oct 2023
- Healthcare providers are uncertain about how best to assess and manage breast cancer risk.
- Patients who carry gene mutations have more complex risk management choices, but only some are aware of their status.
- This article helps clinicians stratify breast cancer risk and discusses a newer genomic test, the polygenic risk score, that may enable more personalized risk management and decision-making.

•Sarkis-Tannous, Daad MPAS, PA-C; Sukol, Roxanne B. MD, MS; Sullivan, Erika MPAS, PA-C. Toward more personalized breast cancer risk assessment: The polygenic risk score. JAAPA 36(10):p 37-40, October 2023. | DOI: 10.1097/01.JAA.0000977692.63075.f3



# Polygenic risk scores and breast cancer risk prediction

- Polygenic Risk Scores (PRS) are a major component of accurate breast cancer risk prediction.
- They have the potential to improve screening and prevention strategies.
- The personalized risk assessment of PRS identify women at higher risk of breast cancer development and enables the implementation of stratified screening and prevention approaches.

•Roberts E, Howell S, Evans DG. Polygenic risk scores and breast cancer risk prediction. *Breast*. 2023 Feb;67:71-77. doi: 10.1016/j.breast.2023.01.003. Epub 2023 Jan 10. PMID: 36646003; PMCID: PMC9982311.



# Polygenic risk scores and breast cancer risk prediction

- PRS represent a significant advance in breast cancer risk prediction and their further development will undoubtedly enhance personalization.

• Roberts E, Howell S, Evans DG. Polygenic risk scores and breast cancer risk prediction. *Breast*. 2023 Feb;67:71-77. doi: 10.1016/j.breast.2023.01.003. Epub 2023 Jan 10. PMID: 36646003; PMCID: PMC9982311.



# Identifying women with increased risk of breast cancer and implementing risk-reducing strategies and supplemental imaging

Some women have a higher lifetime risk of BC because of genetic and lifestyle factors

Because BC risk is variable, screening and prevention strategies should be individualized.

Health care professionals need to be able to assess risk profiles, identify high-risk women, and individualize screening and prevention strategies



# Polygenic Risk Scores (PRS) Matter



# What about lifestyle risks for breast cancer?

## Do they matter?



# Breast Cancer Risk Assessment: The Basics of **Lifestyle** Risk Assessment



# The literature Supports:

- Dense Breasts
- Obesity
- Elevated Blood sugar, Insulin, Diabetes
- Inflammation
- Elevated Estrogen at Menopause
- Poor Estrogen Detoxification
- Lack of Exercise
- Diet (red meat, animal fat, dairy, non- organic, alcohol)
- EDC's



# What about combining lifestyle risk with polygenic risk in Breast Cancer?



1 in 5 women  
will have combination of  
common genetic markers  
and clinical factors that  
puts her at elevated risk  
of breast cancer



# Breast Cancer Risk Assessment: The Basics of combining **Polygenic and Lifestyle** Risk Assessment



# Scientific Support for PRS Combined with Lifestyle





# Identifying women with increased risk of breast cancer and implementing risk-reducing strategies and supplemental imaging

- Some women have a higher lifetime risk of BC because of **genetic** and **lifestyle factors**
- Screening and prevention strategies should be **individualized** after considering patient-specific risk factors
- We propose a stepwise approach to managing BC risk:
  1. Recognizing risk factors;
  2. Using a validated screening tool to assess the lifetime risk of BC



# Validation of a breast cancer risk prediction model based on the key risk factors: family history, mammographic density and polygenic risk

- Mammographic density, polygenic risk and clinical factors as a breast cancer risk prediction model (BRISK) was compared to clinical models (Gail and IBIS) and PRS with more clinical factors.
- **BRISK performs better** than two commonly used clinical risk models and **no worse** compared to a similar model with more risk factors.



# At what age is risk assessment beneficial?

Initially and at any point in time when a woman has had a change in clinical risk factors

At what age is risk assessment beneficial?

Pre-screening age (30 – 50 years)

A woman who has not yet had a mammogram

Menopause

Nearly 80% of breast cancers are diagnosed post-menopause<sup>1</sup>

AGE

35

45

55

65

75

**When high breast density is determined<sup>2</sup>**

- A woman who has dense breast tissue, as identified by mammogram, is at higher risk of breast cancer
- **Nearly half of all women have heterogeneously or extremely dense breast tissue (BI-RADS C or D, respectively)**

1. National Breast Cancer Foundation Australia. Breast Cancer Stats. Available at: <https://nbcf.org.au/about-breast-cancer/breast-cancer-stats/>. Accessed March 2022.

2. Cancer Australia, 2018. Risk factors for breast cancer: A review of the evidence, Cancer Australia, Surry Hills, NSW.



Breast density (c/d)

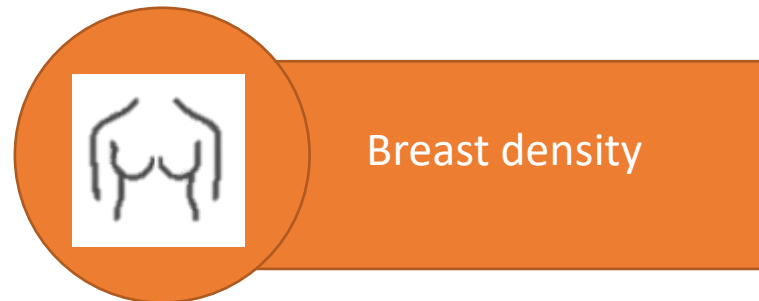
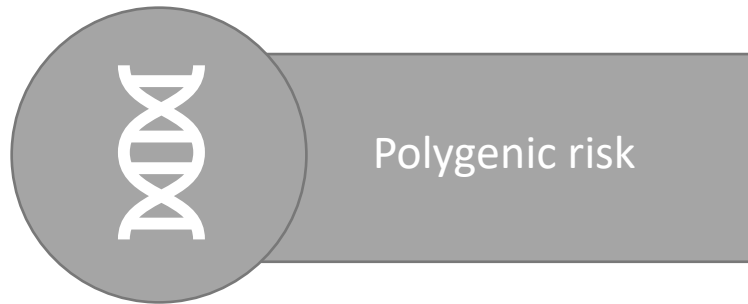
Absolute  
risk  
score

Out of 600,000+ women:  
47% of women had dense breasts but 60%  
of women with advanced breast cancers  
had dense breasts.

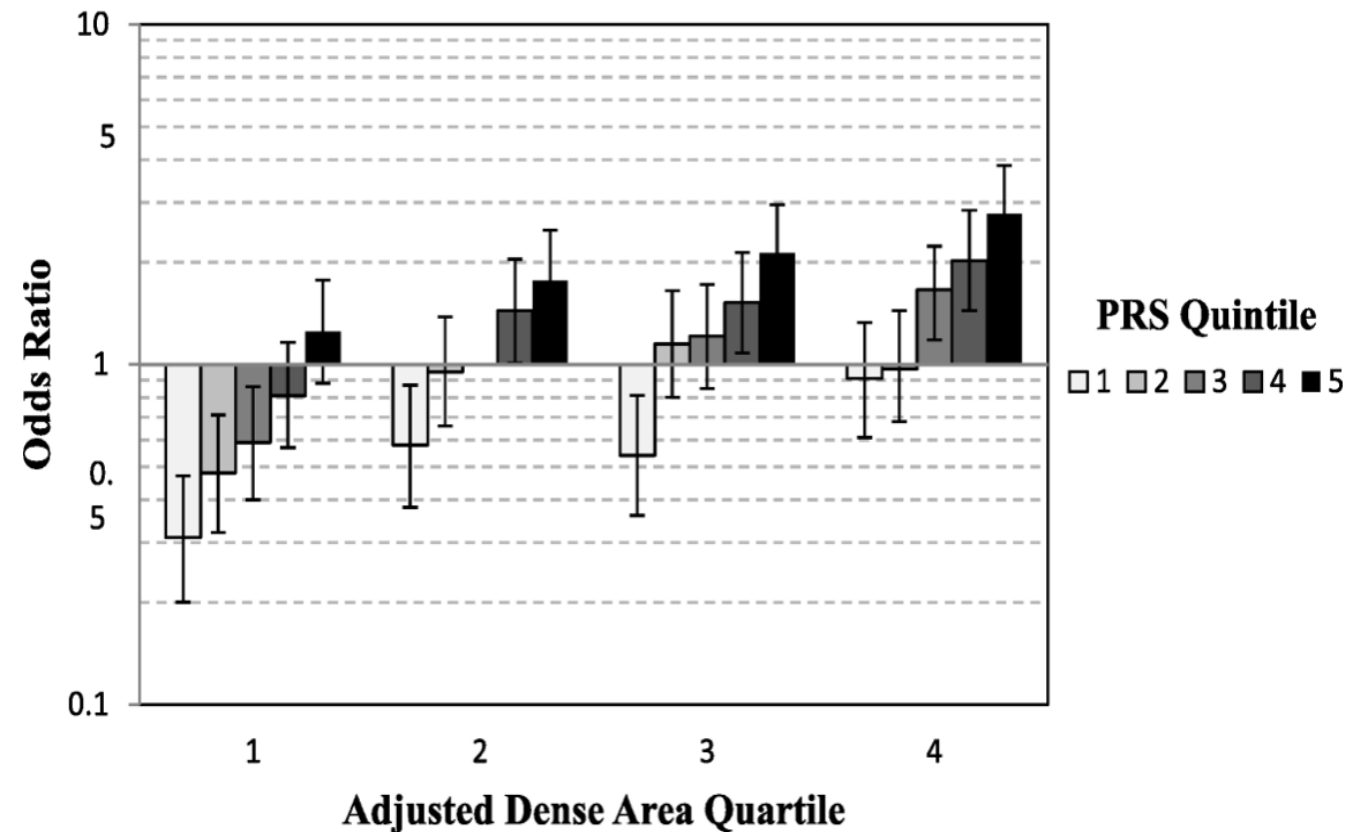
**“breast density notification should be  
combined with breast cancer risk so  
women at highest risk for advanced  
cancer are targeted for supplemental  
imaging discussions”  
(Kerlikowski *et al* 2019)**



# Independent risk factors can be added together



**Multiplicative capacity of breast density and polygenic risk score (PRS)<sup>2</sup>**





# Examples of clinical models combined with polygenic risk scores to improve risk prediction for Breast Cancer

- IBIS (Tyrer-Cuzick)
- Gail
- Boadicea (Breast and Ovarian Analysis of Disease Incidence and Carrier Estimation Algorithm )
- BCSC (Breast Cancer Surveillance Consortium)
- Other

# Clinical models are available that have an integrated PRS capability

CanRisk

BOADICEA v6

Breast and Ovarian Analysis of Disease Incidence and Carrier Estimation Algorithm

Welcome

CanRisk Tool

Load Save Reset Preferences

Polygenic Risk Score(s)

Has a SNP array / Polygenic Risk Score (PRS), ever been run?

Yes

Upload a VCF (Variant Call Format) file Enter PRS values

Select the reference file to use to construct the PRS:

Breast Cancer

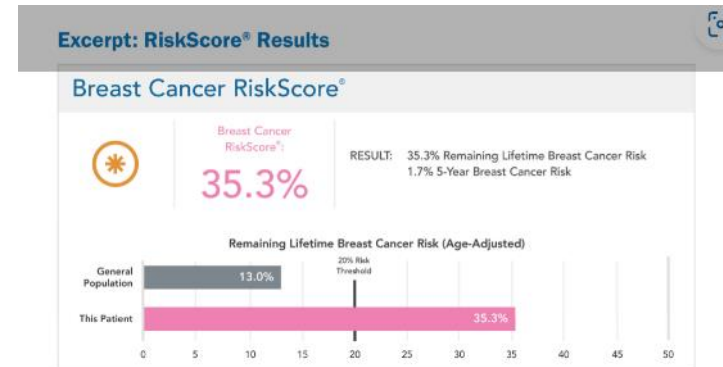
Select a reference

Ovarian Cancer

Select a reference

Upload VCF file

Give the sample name within the VCF file:



## Excerpt: MyRisk™ Management Tool

GENETIC RESULT: NEGATIVE - NO CLINICALLY SIGNIFICANT MUTATION IDENTIFIED

Note: "CLINICALLY SIGNIFICANT," as defined in this report, is a genetic change that is associated with the potential to alter medical intervention.

BREAST CANCER RISKSCORE®: REMAINING LIFETIME RISK 35.3%

This level of risk is at or above 20% threshold for consideration of modified medical management. See RiskScore Interpretation Section for more information.

CLINICAL HISTORY ANALYSIS: NO ADDITIONAL MANAGEMENT GUIDELINES IDENTIFIED BASED ON THE CLINICAL HISTORY PROVIDED

Other clinical factors may influence individualized management. This analysis may be incomplete if details about cancer diagnoses, ages, family relationships or other factors were omitted or ambiguous. If this patient also has a clinically significant mutation, the recommendations based on the clinical history analysis should be considered in light of the possibility that this mutation explains all or some of the cancer history in the family.

BREAST CANCER RISKSCORE™

At or above 20%

THIS BREAST CANCER RISKSCORE™ IS ASSOCIATED WITH THE FOLLOWING CANCER RISKS:

ELEVATED RISK: Female Breast

No clinically significant mutations were identified in this patient. However, based on personal/family history, the patient's cancer risks may still be increased over the general population. See information below.

Please see the Genetic Test Result for more details on any variant(s) detected in this patient, including variant classification information.

ADDITIONAL FINDINGS: NO VARIANT(S) OF UNCERTAIN SIGNIFICANCE (VUS) IDENTIFIED

TYRER-CUZICK BREAST CANCER RISK CALCULATION

REMAINING LIFETIME BREAST CANCER RISK: 16.6%

5-YEAR BREAST CANCER RISK: 0.7%

## Breast Cancer Risk Assessment Final Test Report

### GeneType for Breast Cancer



Laboratory Accession Number: NA0781  
Date of Specimen Collection: Feb-10-2022  
Date of Laboratory Receipt: Feb-17-2022  
Date of Report: Jul-12-2023

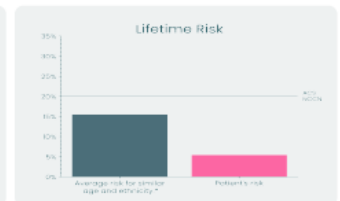
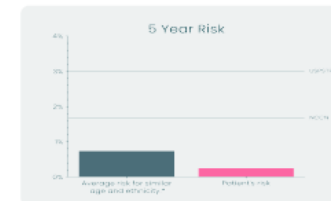
Patient Name: Jessica Patel  
Date of Birth: Jun-10-1986  
Patient Address: 1985 Thecondomina Via  
Union Hall, WI 54742

Ordering Medical Provider:  
Dr Rebecca Adams  
12345 Showwood Beach Rd  
West Covina, CA 94000

This patient is at an  
**AVERAGE**  
risk of breast cancer

0.25%  
Patient's  
5 year risk

5.48%  
Patient's  
Lifetime risk



\*The average risk is based on the same age, biological gender and race/ethnicity as the patient from the general population.

## Interpretation

This patient has a 5.48% chance of developing breast cancer within her remaining lifetime up to age 90 years. This is considered an average risk because it is below the 20% threshold defined by the American Cancer Society and other medical associations.

This patient has a 0.25% chance of developing breast cancer over the next 5 years which is considered within average risk. This is lower than the actionable threshold of 15% as defined by NCCN and lower than 3% as defined by USPSTF.

The patient should continue following general population breast screening protocols at a minimum, regardless of their estimated risk score. Also note that the risk scores are patient-specific and cannot be used to estimate risk in relatives. Furthermore, these results should be interpreted by a healthcare professional in the context of the patient's full clinical history, particularly for patients close to a threshold risk value.

Report continued on next page

v4 May 2023

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# Changing Risk:

Breast Cancer Research and Treatment (2023) 198:335–347  
<https://doi.org/10.1007/s10549-022-06834-7>

EPIDEMIOLOGY



## Validation of a breast cancer risk prediction model based on the key risk factors: family history, mammographic density and polygenic risk

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Received: 16 June 2022 / Accepted: 2 December 2022 / Published online: 7 February 2023  
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### Abstract

**Purpose** We compared a simple breast cancer risk prediction model, BRISK (which includes mammographic density, polygenic risk and clinical factors), against a similar model with more risk factors (simplified Rosner) and against two commonly used clinical models (Gail and IBIS).

**Methods** Using nested case–control data from the Nurses’ Health Study, we compared the models’ association, discrimination and calibration. Classification performance was compared between Gail and BRISK for 5-year risks and between IBIS and BRISK for remaining lifetime risk.

**Results** The odds ratio per standard deviation was 1.43 (95% CI 1.32, 1.55) for BRISK 5-year risk, 1.07 (95% CI 0.99, 1.14) for Gail 5-year risk, 1.72 (95% CI 1.59, 1.87) for simplified Rosner 10-year risk, 1.51 (95% CI 1.41, 1.62) for BRISK remaining lifetime risk and 1.26 (95% CI 1.16, 1.36) for IBIS remaining lifetime risk. The area under the receiver operating characteristic curve (AUC) was improved for BRISK over Gail for 5-year risk ( $AUC=0.636$  versus  $0.511$ ,  $P<0.0001$ ) and for BRISK over IBIS for remaining lifetime risk ( $AUC=0.647$  versus  $0.571$ ,  $P<0.0001$ ). BRISK was well calibrated for the estimation of both 5-year risk (expected/observed [ $E/O$ ]=1.03; 95% CI 0.73, 1.46) and remaining lifetime risk ( $E/O=1.01$ ; 95% CI 0.86, 1.17). The Gail 5-year risk ( $E/O=0.85$ ; 95% CI 0.58, 1.24) and IBIS remaining lifetime risk ( $E/O=0.73$ ; 95% CI 0.60, 0.87) were not well calibrated, with both under-estimating risk. BRISK improves classification of risk compared to Gail 5-year risk ( $NRI=0.31$ ; standard error [ $SE$ ]=0.031) and IBIS remaining lifetime risk ( $NRI=0.287$ ;  $SE=0.035$ ).

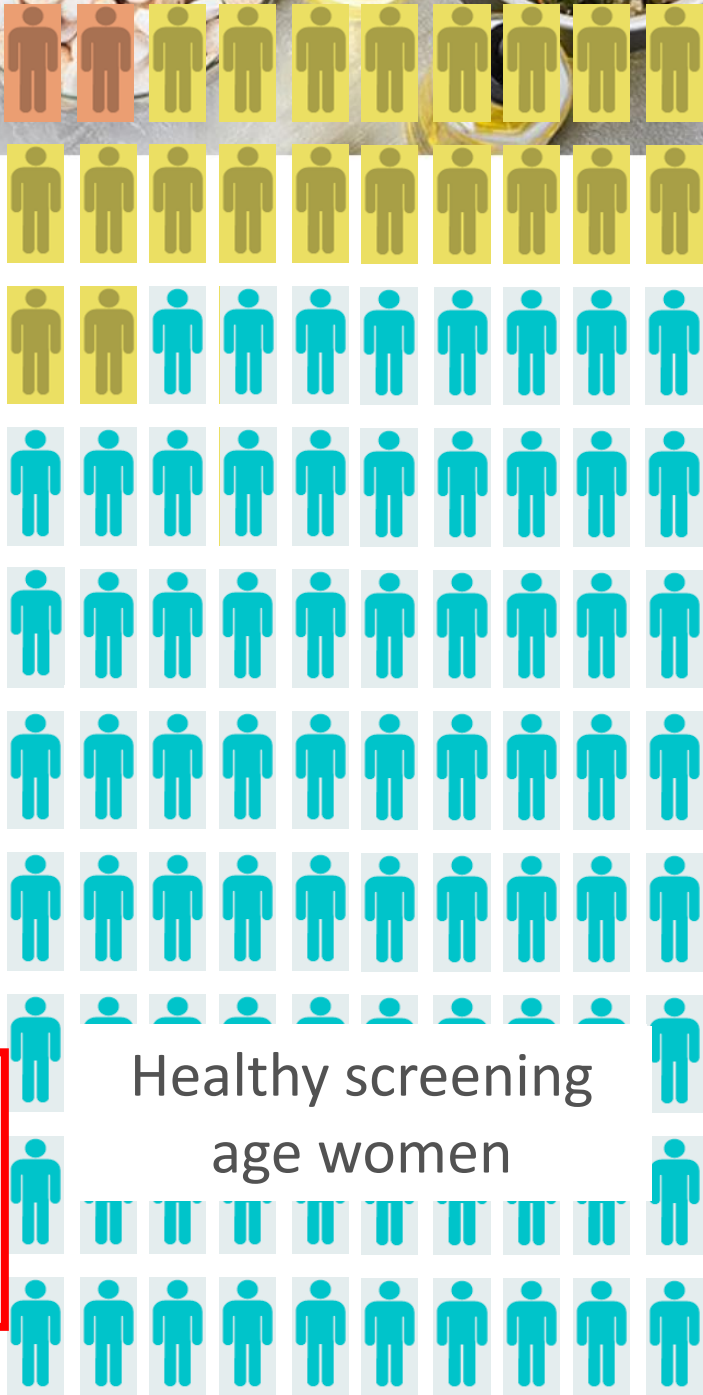
**Conclusion** BRISK performs better than two commonly used clinical risk models and no worse compared to a similar model with more risk factors.

9x

Integrated model

IBISv7

|                 | IBISv7 | Integrated model |
|-----------------|--------|------------------|
| % cases >20%    | 4.1%   | 41.3%            |
| % controls >20% | 2.5%   | 22.4%            |





# Which patients are eligible for risk assessment and who may benefit most?

## The ideal Criteria:

- Age 30 years and older
- No previous breast cancer (or ductal carcinoma in situ [DCIS]) diagnosis
- No *BRCA1/BRCA2* mutations
- Pre-mammogram
  - Is she eligible to start sooner?
- Dense breasts
  - ~50% of women have dense breast tissue<sup>1</sup>
- Menopausal
  - Should she re/consider hormone replacement therapy?



# •Cases



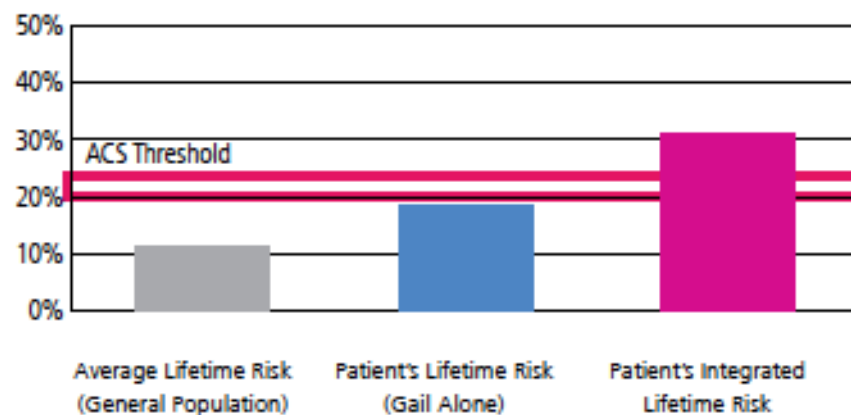
# 51 yo female, LMP 6 mo ago, wants Bio-Identical HRT for Hot Flashes: No FH, PMH Neg, PE WNL

| SELF                               |                                    | NON-HEREDITARY BREAST CANCER                                                                                                |
|------------------------------------|------------------------------------|-----------------------------------------------------------------------------------------------------------------------------|
| Y                                  | <input checked="" type="radio"/> N | Have you ever been diagnosed with any breast cancer or ductal carcinoma in situ (DCIS) or lobular carcinoma in situ (LCIS)? |
| Y                                  | <input checked="" type="radio"/> N | Did you start your menstrual period before age 12?                                                                          |
| Y                                  | <input checked="" type="radio"/> N | Did you have your first child AFTER 30 years of age?                                                                        |
| <input checked="" type="radio"/> Y | <input checked="" type="radio"/> N | Have you ever been told you have DENSE BREASTS?                                                                             |
| Y                                  | <input checked="" type="radio"/> N | Have you been tested for BRCA?                                                                                              |
| Y                                  | <input checked="" type="radio"/> N | Have you ever taken estrogen for hormone replacement therapy (HRT)?                                                         |
| <input checked="" type="radio"/> Y | <input checked="" type="radio"/> N | Have you ever had a (positive or negative) breast biopsy?                                                                   |

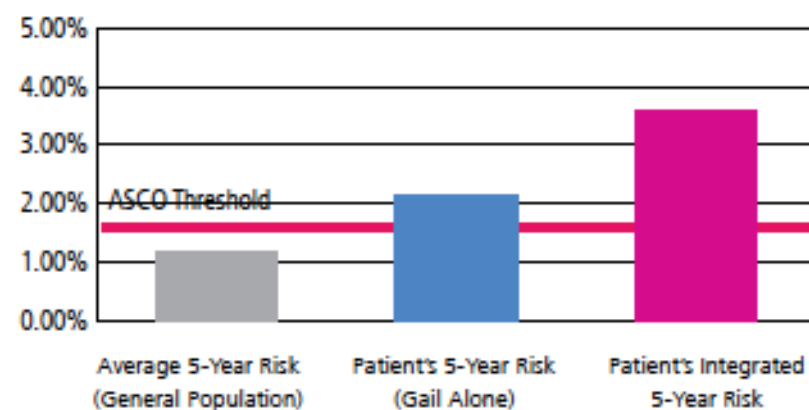


# NO HRT!!

**Patient's Integrated Lifetime Risk**



**Patient's Integrated 5-Year Risk**



60 yo for routine  
annual. No concerns.  
Ashkenazi Jewish.

BRCA Testing  
Indicated

BRCA Neg...  
When reviewing  
results.....

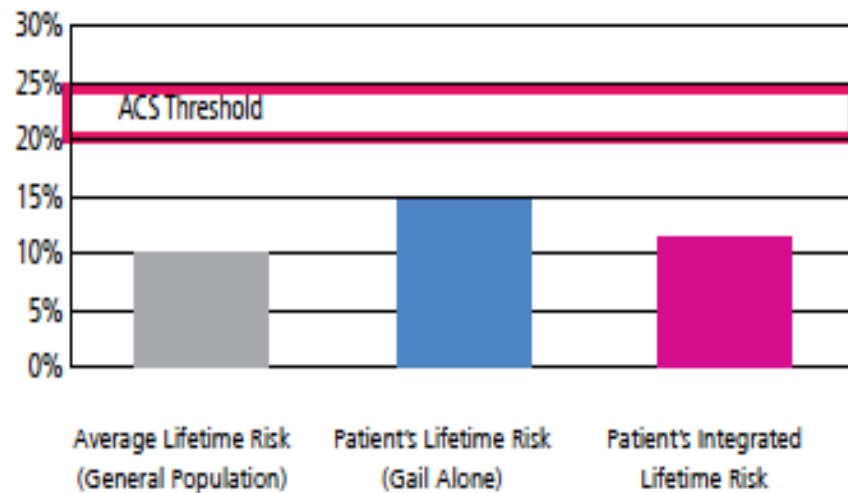
Instruction: Circle "Y" to below statements that apply to YOU and/or YOUR FAMILY on both your **mother's** and **father's** sides; list the diagnosed person's relationship to you (eg; self, paternal aunt, maternal uncle, paternal grandmother) and the age at diagnosis. Each statement should be answered individually, so you may list the same cancer more than once.

**BREAST AND OVARIAN CANCER**

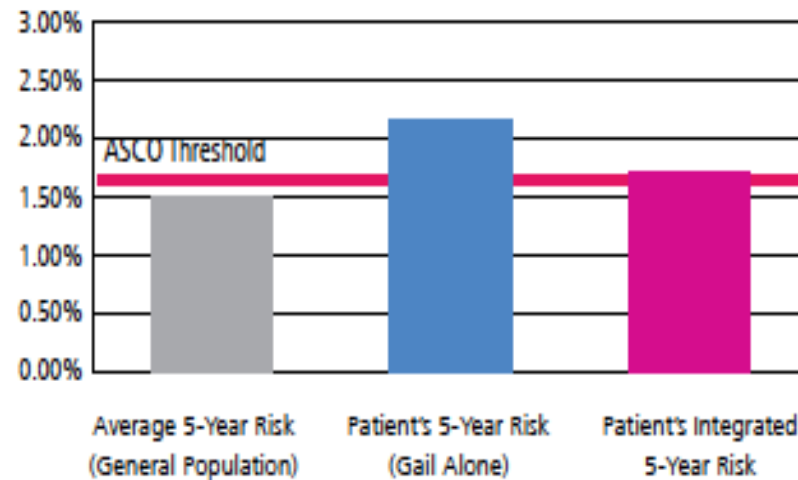
|                                    |                                    | RELATIONSHIP                                                                                      | AGE AT DIAGNOSIS        |
|------------------------------------|------------------------------------|---------------------------------------------------------------------------------------------------|-------------------------|
| <input checked="" type="radio"/> Y | N                                  | -Breast cancer before age 50                                                                      | <u>sister</u> <u>46</u> |
| <input type="radio"/> Y            | <input checked="" type="radio"/> N | -Ovarian cancer                                                                                   |                         |
| <input type="radio"/> Y            | <input checked="" type="radio"/> N | - Primary, unrelated breast cancer in same person or same side of family                          |                         |
| <input type="radio"/> Y            | <input checked="" type="radio"/> N | -Both breast & ovarian cancer (in an individual or family)                                        |                         |
| <input type="radio"/> Y            | <input checked="" type="radio"/> N | -Pancreatic cancer w/ breast or ovarian cancer in same person or same side of family              |                         |
| <input type="radio"/> Y            | <input checked="" type="radio"/> N | -Ashkenazi Jewish ancestry w/ breast, ovarian or pancreatic in same person or same side of family |                         |


# PATIENT REASSURED!!

**Patient's Integrated Lifetime Risk**



**Patient's Integrated 5-Year Risk**





**Should we really estimate  
breast cancer risk for all our  
patients?**





# The Endocrine Society says YES

Endocrine  
Society  
HRT Decision  
Tree

Evaluate breast cancer risk – for those with high to moderate risk, consider other options.



**And the public is aware  
of this  
recommendation..**



# Breast Cancer Drugs Urged for Healthy High-Risk Women in NYT

The United States Preventive Services Task Force recommended that, for healthy women ages 40 to 70, doctors help assess the odds of breast cancer



# Using integrated genomic models enables new screening paradigms





**Population level Risk stratification**



**Liquid biopsy assays**

↑ positive predictive value



**Multi-Cancer early detection**



# Reducing Breast Cancer Incidence and Mortality: Rethinking an Approach to Risk Assessment and Prevention

- Breast cancer prevention strategies continue to evolve with advances in research resulting in newer polygenic profiles to improve breast cancer prediction.
- Ongoing studies are exploring the impact of single-nucleotide polymorphisms to estimate the polygenic breast cancer risk and revolutionize personalized risk assessment.
- We have previously shown that after being informed about their personalized risk on the basis of polygenic risk score, women at increased risk for breast cancer were more likely to use endocrine preventive medication.
- Future trials may demonstrate that polygenic risk scores may not only improve adherence to pharmacologic risk-reduction strategies but potentially improve compliance with a risk-free, low-cost intervention that saves lives, a low-fat diet.



# What is Longevity Medicine?

- Equipping health-care providers with tools of obtaining and utilising an individualised precision dataset of each patient not only reduces the risks of the patient developing diseases, but mitigates and even eliminate diseases, and customizes **optimal preventive and therapeutic approaches**.

- Longevity medicine: upskilling the physicians of tomorrow

The Lancet, Healthy Longevity, [VOLUME 2, ISSUE 4](#), E187-E188, APRIL 2021

[https://www.thelancet.com/journals/lanhl/article/PIIS2666-7568\(21\)00024-6/fulltext#%20](https://www.thelancet.com/journals/lanhl/article/PIIS2666-7568(21)00024-6/fulltext#%20)



# What is Longevity Medicine?

- The notion of longevity and healthy aging as a major priority for healthcare will undoubtedly substantially impact primary, secondary, and tertiary prevention.

- Longevity medicine: upskilling the physicians of tomorrow

The Lancet, Healthy Longevity, [VOLUME 2, ISSUE 4](#), E187-E188, APRIL 2021

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## In Conclusion...

- Predictive genetic testing for complex diseases: a public health perspective (2014)
  - C. Marzuillo et al., Predictive genetic testing for complex diseases: a public health perspective, *QJM: An International Journal of Medicine*, Volume 107, Issue 2, February 2014, Pages 93–97
- The time is now ripe for the introduction of a range of genetic tests into healthcare practice



# Breast cancer genetics and risk assessment: an overview for the clinician (2023)

“It is only through identification of high-risk women that we can prevent breast cancer, not just screen for it.”



“It is only through identification of high-risk patients that we can prevent most complex chronic disease, not just screen for it.”

JME, Personal  
Communication, 2024



# Thank You





**Saturday 12:30pm – 1:30pm**

**The Latest in Longevity Medicine:  
Predictive Genomics**

Please scan this QR code on you mobile  
or tablet device to access the session feedback survey



The Latest in Longevity Medicine: Pr  
edictive Genomics