



KØBENHAVNS UNIVERSITET



**Herlev og Gentofte
Hospital**

PRSONAL

**(Population-based Randomized Study Of a Novel breast
cancer risk ALgorithm and stratified screening)**

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Funding of PRSONAL

nov
ordisk
fonden

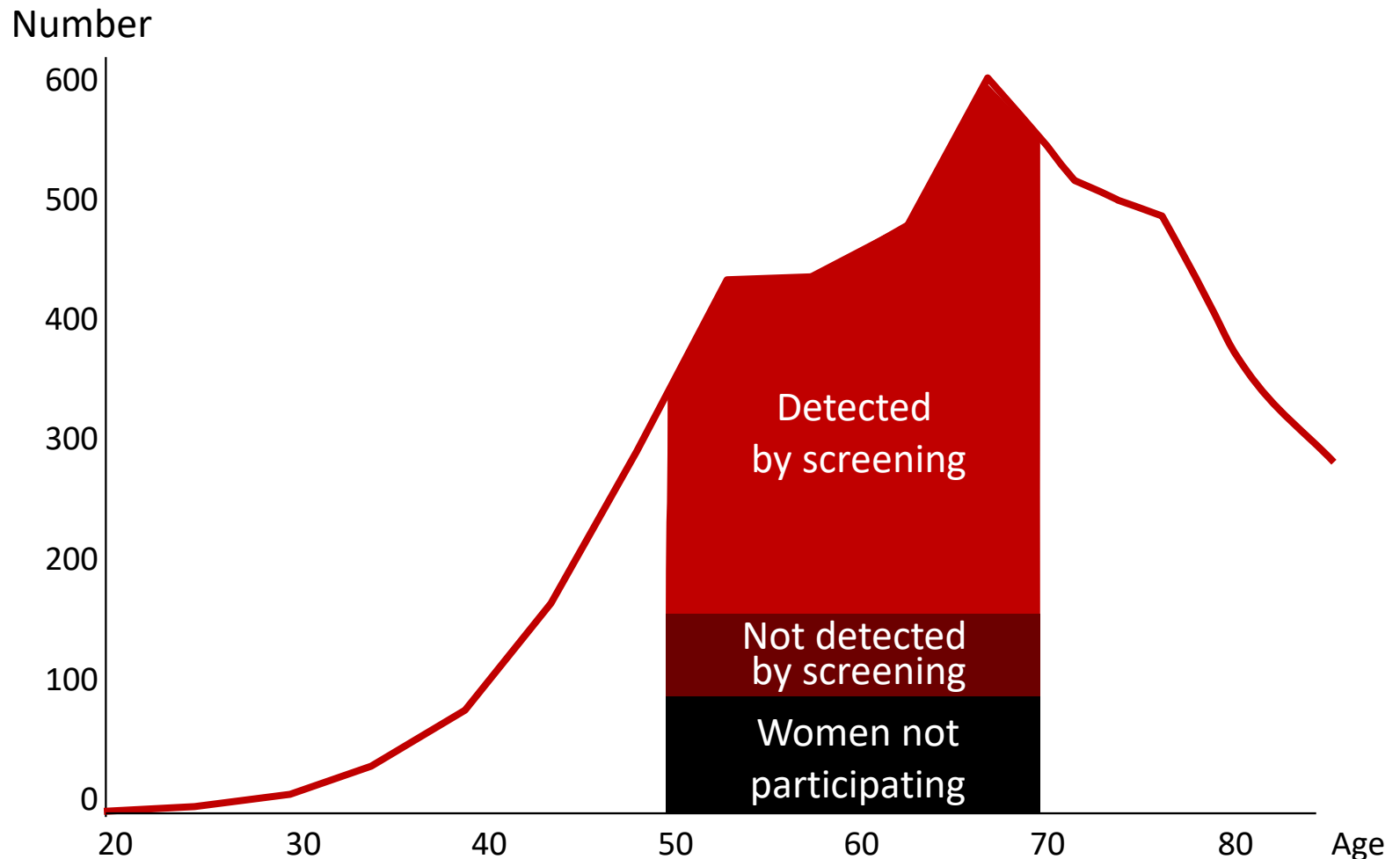
Investigator Initiated Clinical Trials

No other conflicts of interests (unfortunately...)

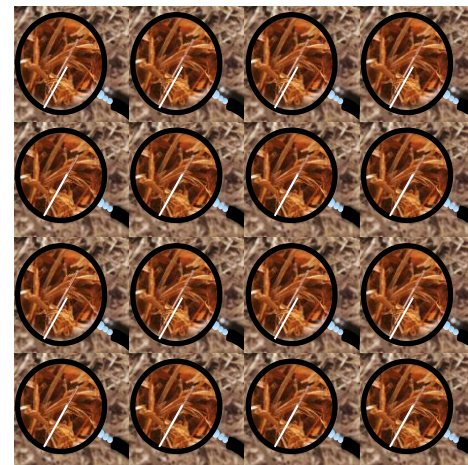
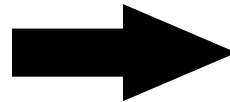
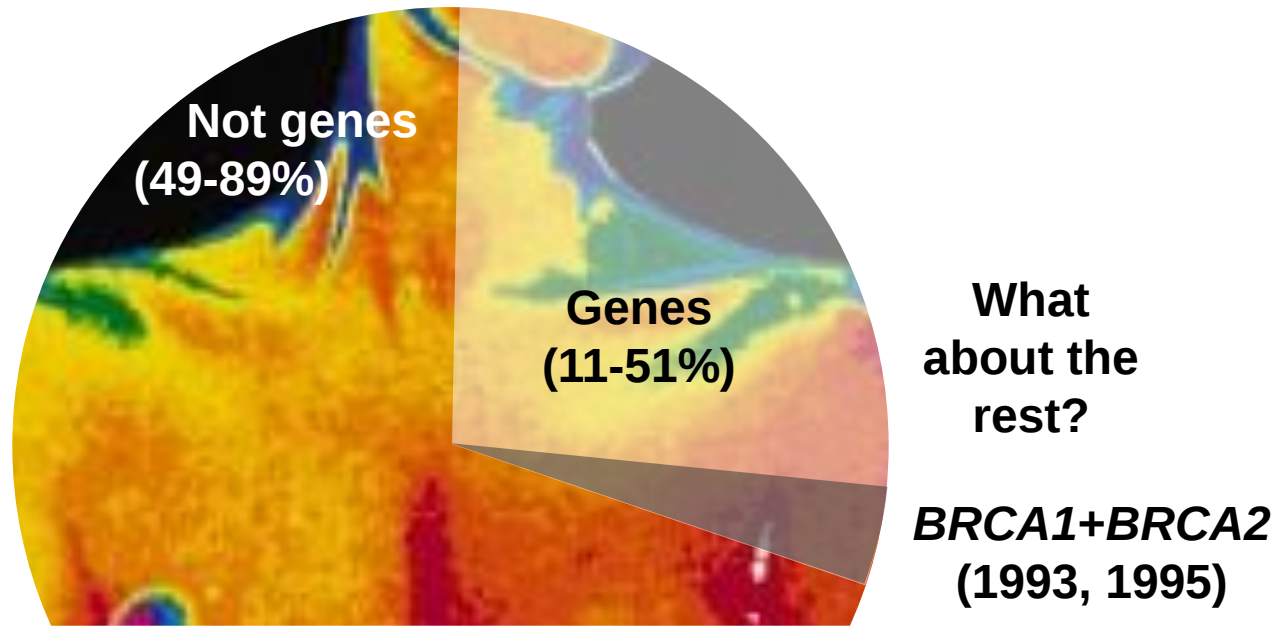
Breast cancer in Denmark, 2020.

Nationwide screening since 2008:

Biennial mammography of 50-69-year aged women

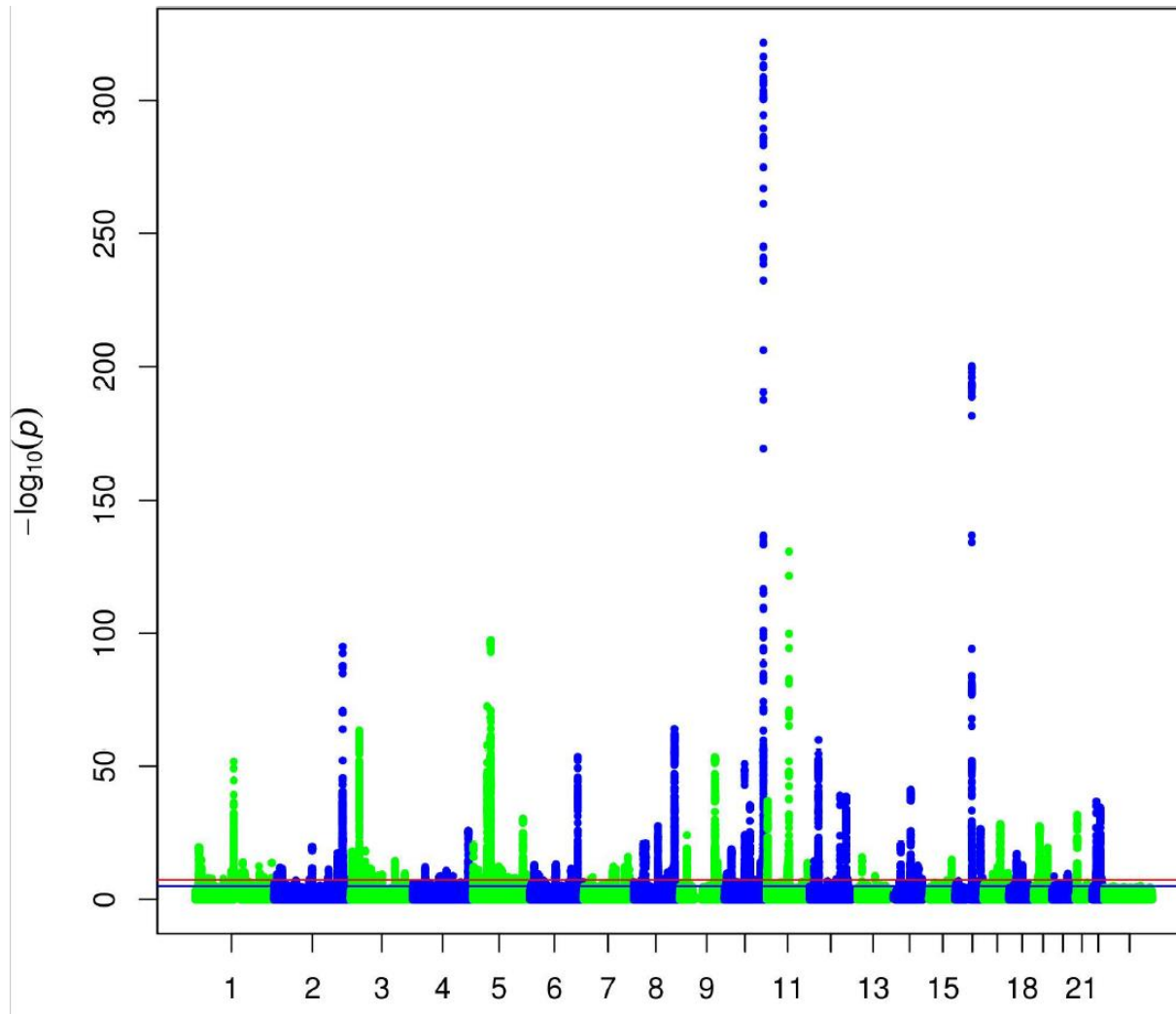


Genetic variation and breast cancer – a brief history



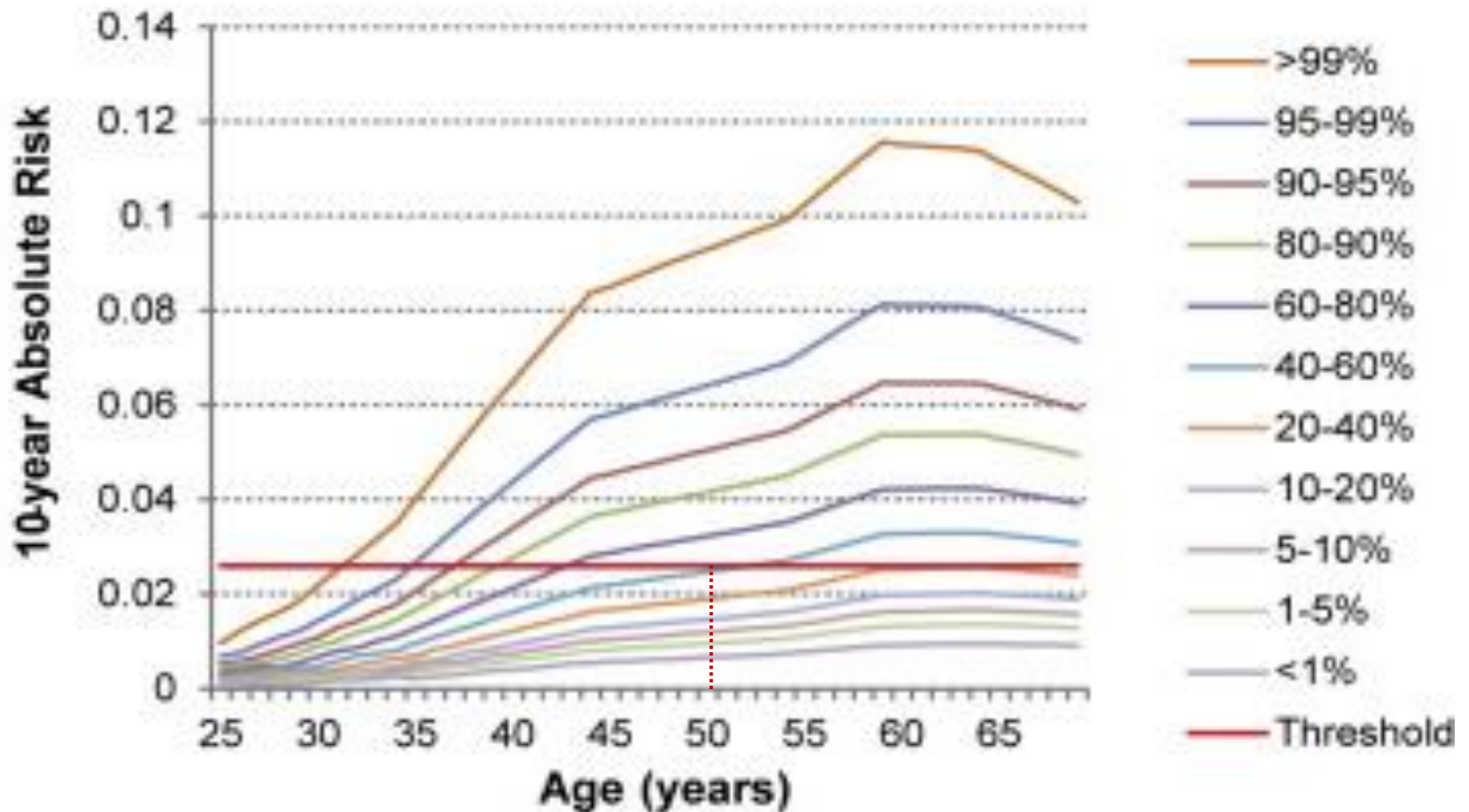
Statistical power!

Association analysis identifies 65 new breast cancer risk loci



Michailidou K. et al. Nature 551:92-94 (2017).

Polygenic risk score of breast cancer. 313 SNPs



“...A powerful and reliable predictor of breast cancer risk that may improve breast cancer prevention programs”

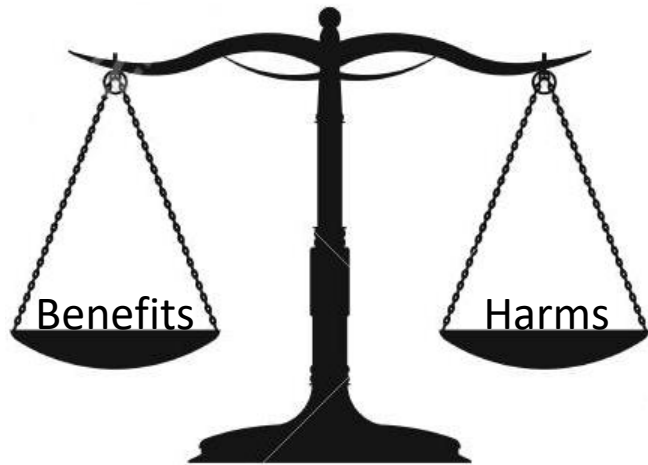
“Listen: You are all individuals. You are all different!”



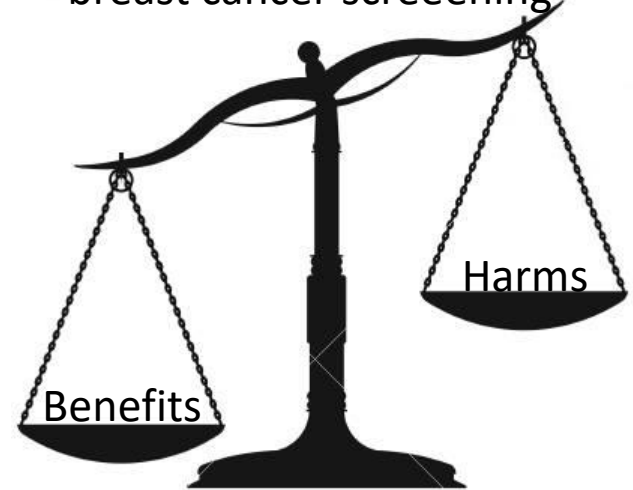
Life of Brian, Monty Python, 1980

Allocate Resources by Risk

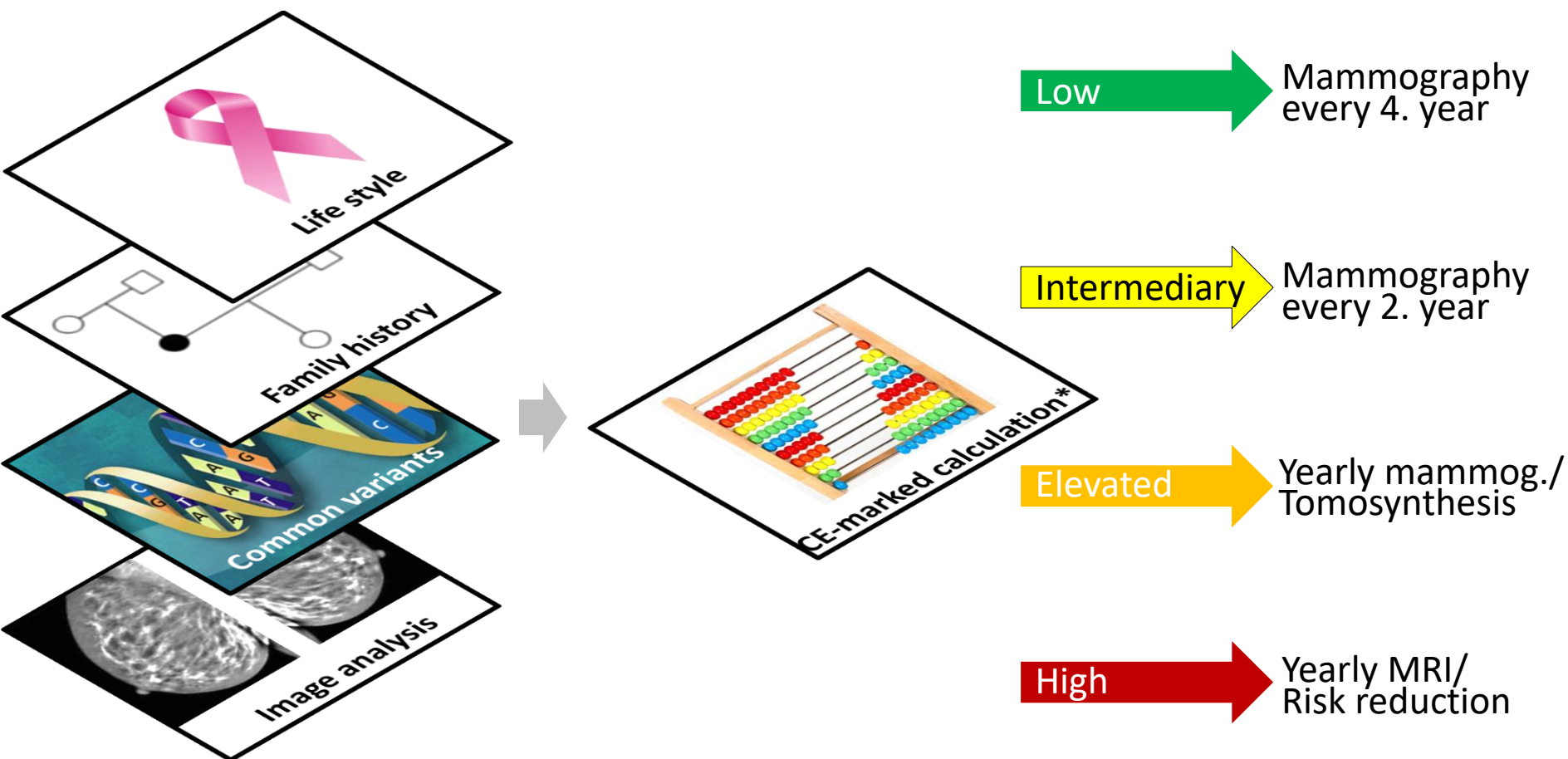
One-size-fits-all:
50-69-year olds have
mammography every 2nd year



Personalized
breast cancer screening

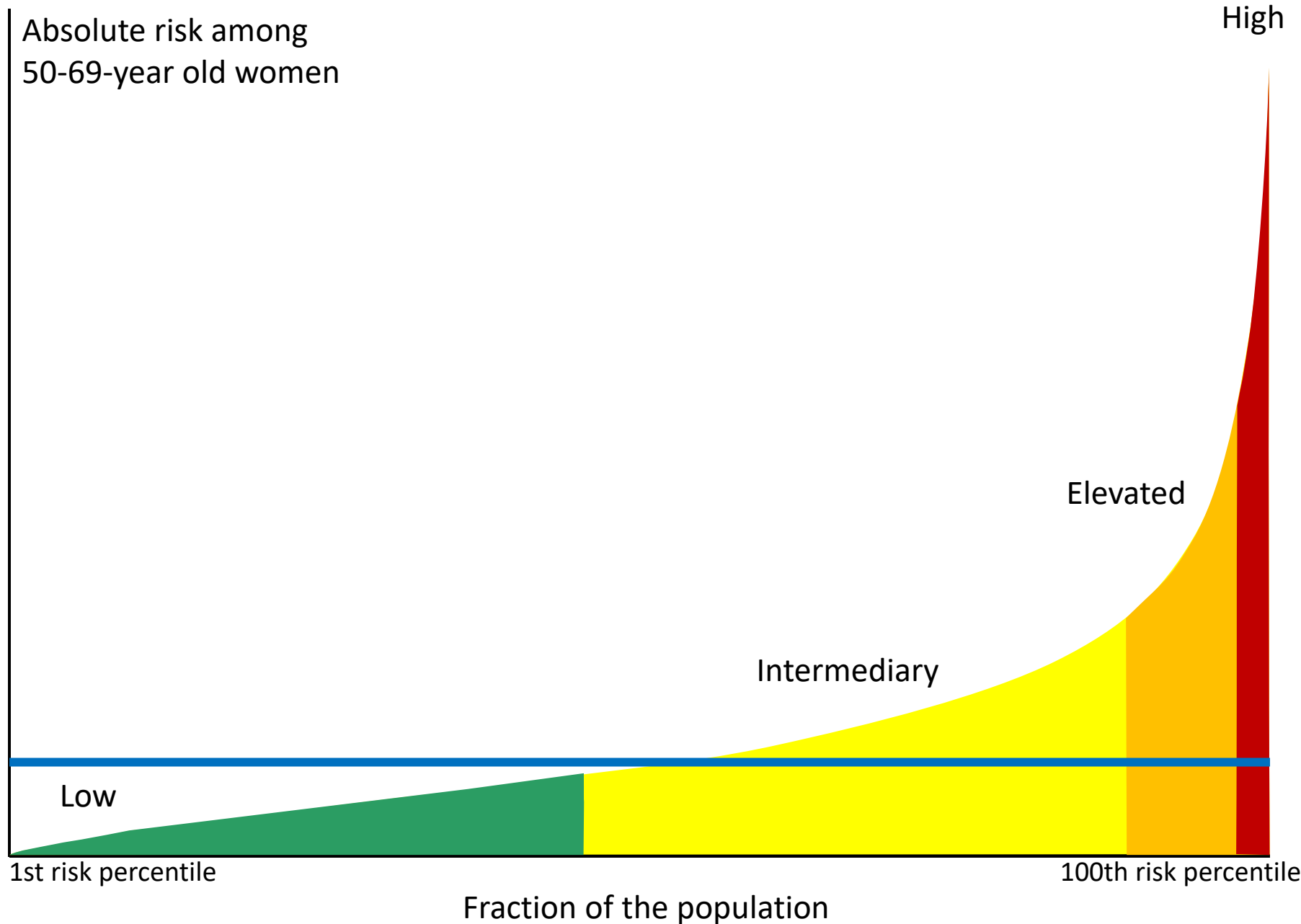


Vision for risk stratified breast cancer screening

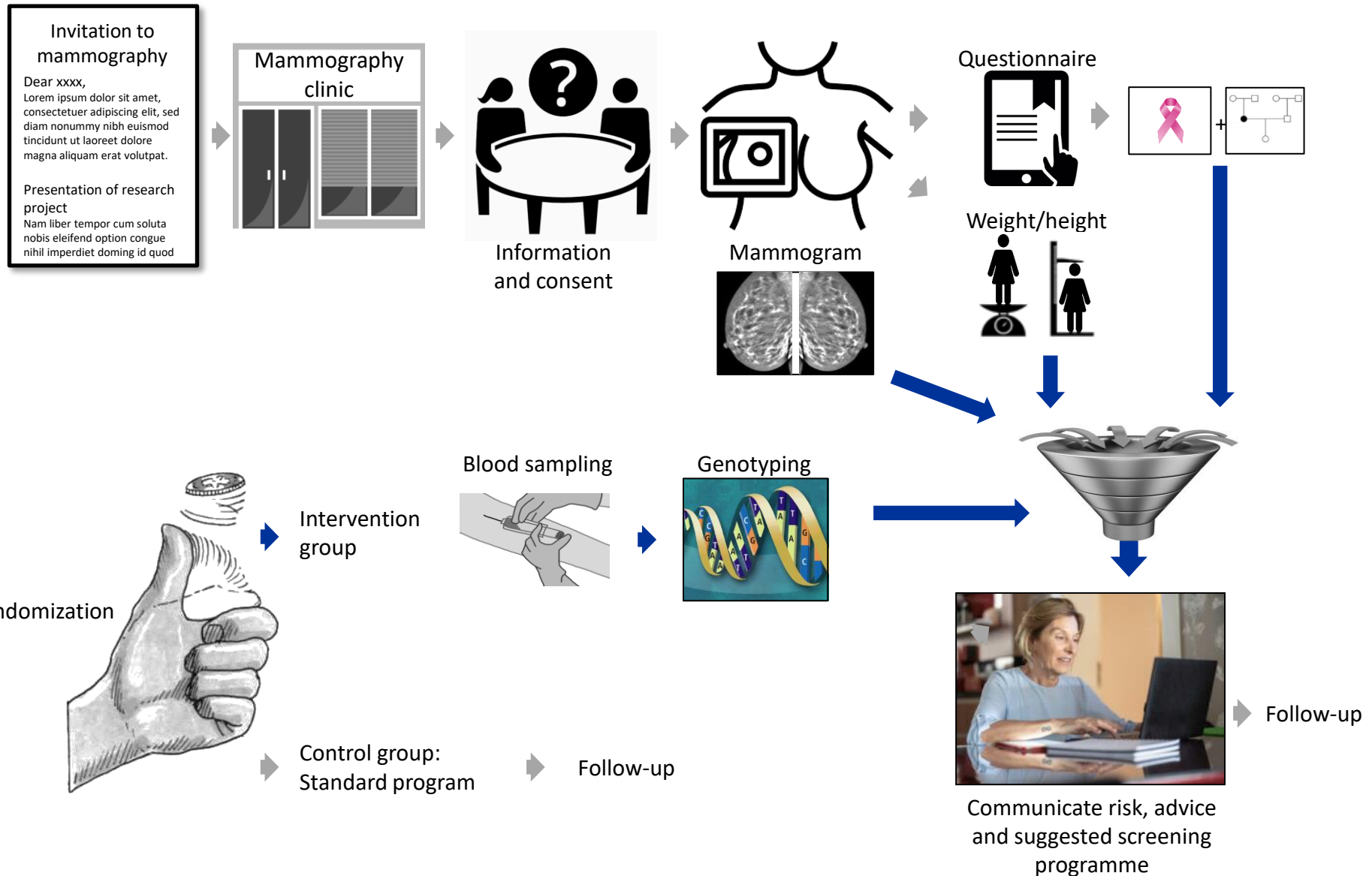


*BOADICEA in CanRisk

Risk Stratified Screening



PRSONAL – Randomized Clinical Trial



PRSONAL - Sample size and power

Primary outcome	Measure	Recording time point	Previously	Reference/ Country	Number of women needed
Acceptance	Mammography in low-risk women within 2 years <30%	Day 730	41% would be unhappy or very unhappy to have less intensified screening if they had lower risk.	Meisel SF, Pashayan N, Rahman B, et al: Adjusting the frequency of mammography screening on the basis of genetic risk: Attitudes among women in the UK. Breast 24:237-41, 2015/ UK	90% statistical power and significance level of 0.05: 1:1 Randomization of 962 women . Assumptions: 95% eligible, 50% agree to be randomized; randomization will last 2½ months.

A clear criterium of success:

If more than 30% of the women in the low-risk group opt out of the de-escalated screening and have their mammography within 2 years from baseline, PRSONAL will not have achieved its goals, in terms of acceptance and projected economic sustainability

Secondary outcomes	Measure	Recording time points	Expected in the control group	Reference/ Country	Detectable change in PRSONAL, 90% power
Anxiety	PROMIS anxiety scale	Day 1, 180, 365, 800	Mean=52.4, SD=8.2	Xie Z, Wenger N, Stanton AL, et al: Risk estimation, anxiety, and breast cancer worry in women at risk for breast cancer: A single-arm trial of personalized risk communication. Psychooncology 28:2226-2232, 2019/ US	+1.7 in all +7.7 in high-risk women
Breast cancer worry	Lerman breast cancer worry scale	Day 1, 180, 365, 800	Mean=7, SD=1	Xie Z, Wenger N, Stanton AL, et al: Risk estimation, anxiety, and breast cancer worry in women at risk for breast cancer: A single-arm trial of personalized risk communication. Psychooncology 28:2226-2232, 2019/ US	+0.4 in all +1.9 in high-risk women
Quality of life	EQ-5D-5L	Day 1, 180, 365, 800	Mean=0.86, SD=0.17	Sorensen J, Davidsen M, Gudex C, et al: Danish EQ-5D population norms. Scand J Public Health 37:467-74, 2009/ DK	-0.04 in all -0.16 in high-risk women

Potential Benefits

Breast cancer at screening visits: +10%

Breast cancer after screening visits: -24%

Number of screening visits: -15%

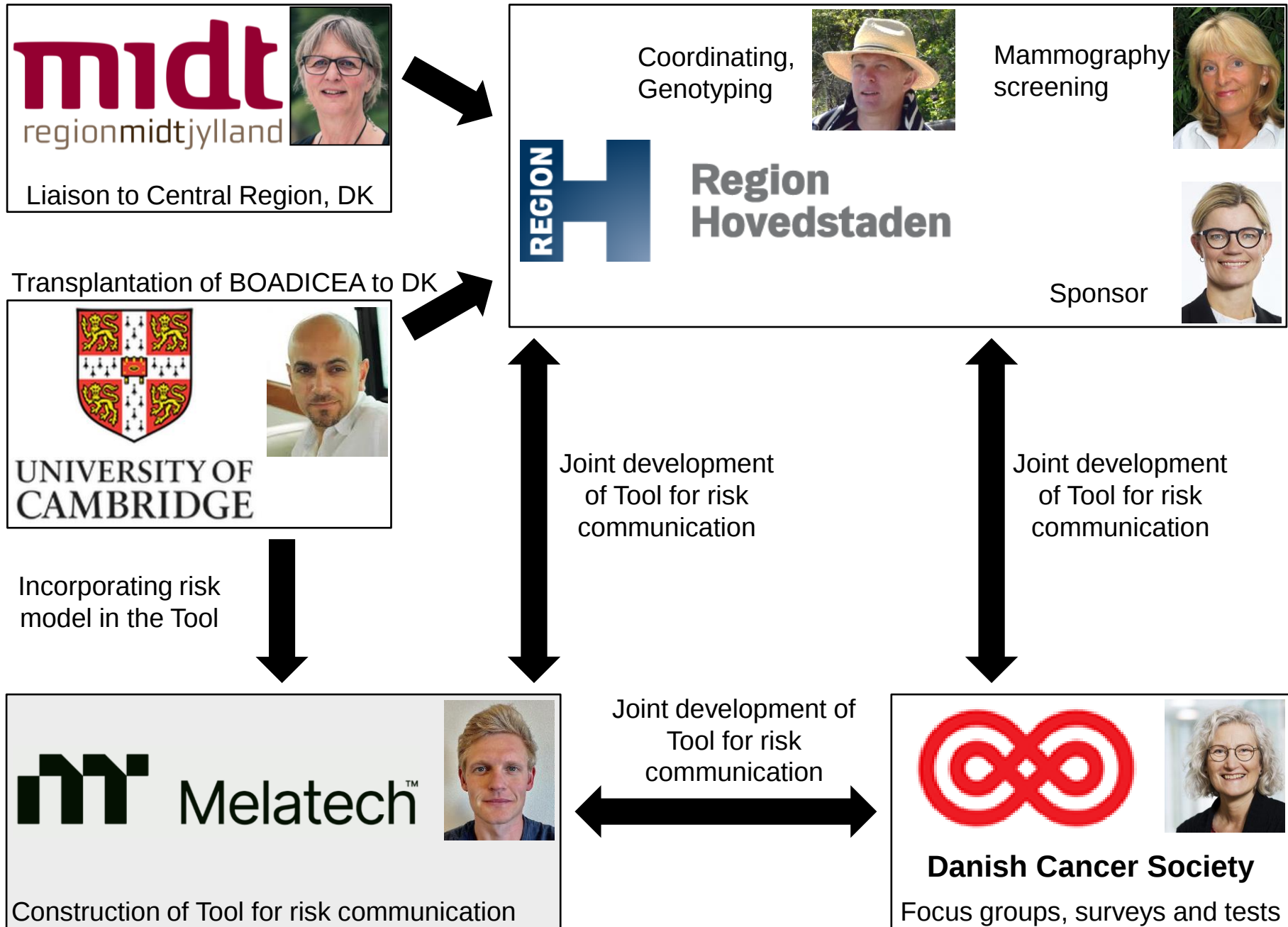
Fewer breast cancers detected at advanced stage

Reduced screening costs

Reduced treatment costs

Fewer breast cancer deaths?

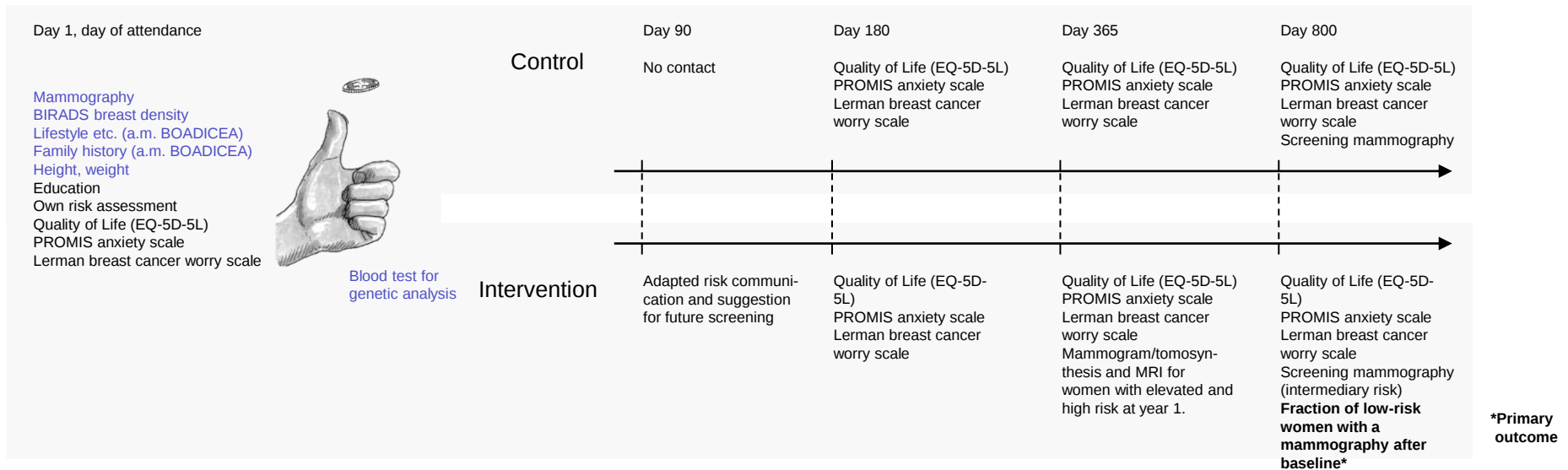
Partners of PRSONAL



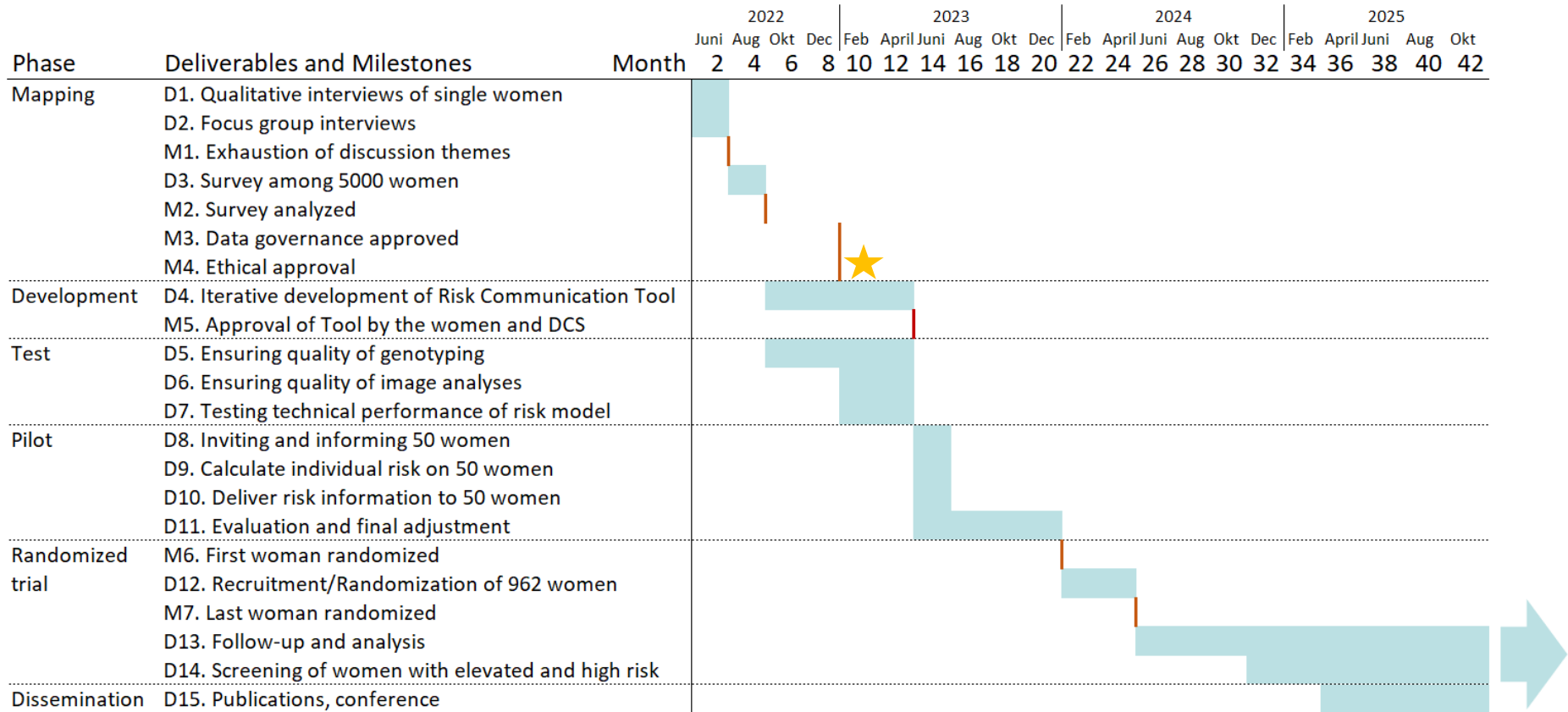
PRSONAL – Risk data flow



Collection of data used for risk calculation and data for safety monitoring



PRSONAL – Status



Challenges

Complex data vs. comprehension

Strong communication vs. no staff

Reduce invisible inequality in health (One-size-fits-all is inequality...)

Don't lose socioeconomic disadvantaged citizens

Probably more...

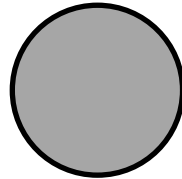


Relevant risk communication

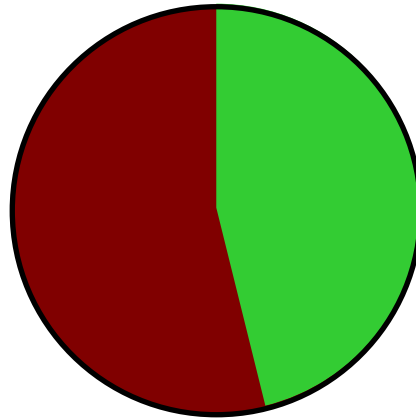


HOTLINE: XXXX XXXX

Average for all women at your age



Your risk to get breast cancer within the next 5 years is 8.2%.



Risk factors you can change:

Physical inactivity

Use of alcohol

Weight

Hormone treatment

What does this mean?

I wish another risk description

A women like you, but with average scores for these factors, will have a risk of 5.2%

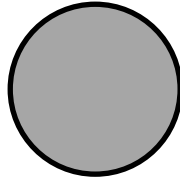
We suggest that next screening examination will be an MRI and will take place between 01-MM-ÅÅÅÅ and 01-MM-ÅÅÅÅ. You will be invited by electronic mail as usual.

Relevant risk communication

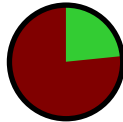


HOTLINE: XXXX XXXX

Average for all women at your age



Your risk to get breast cancer within the next 5 years is 0.8%.



Risk factors you can change:



Physical inactivity

Weight

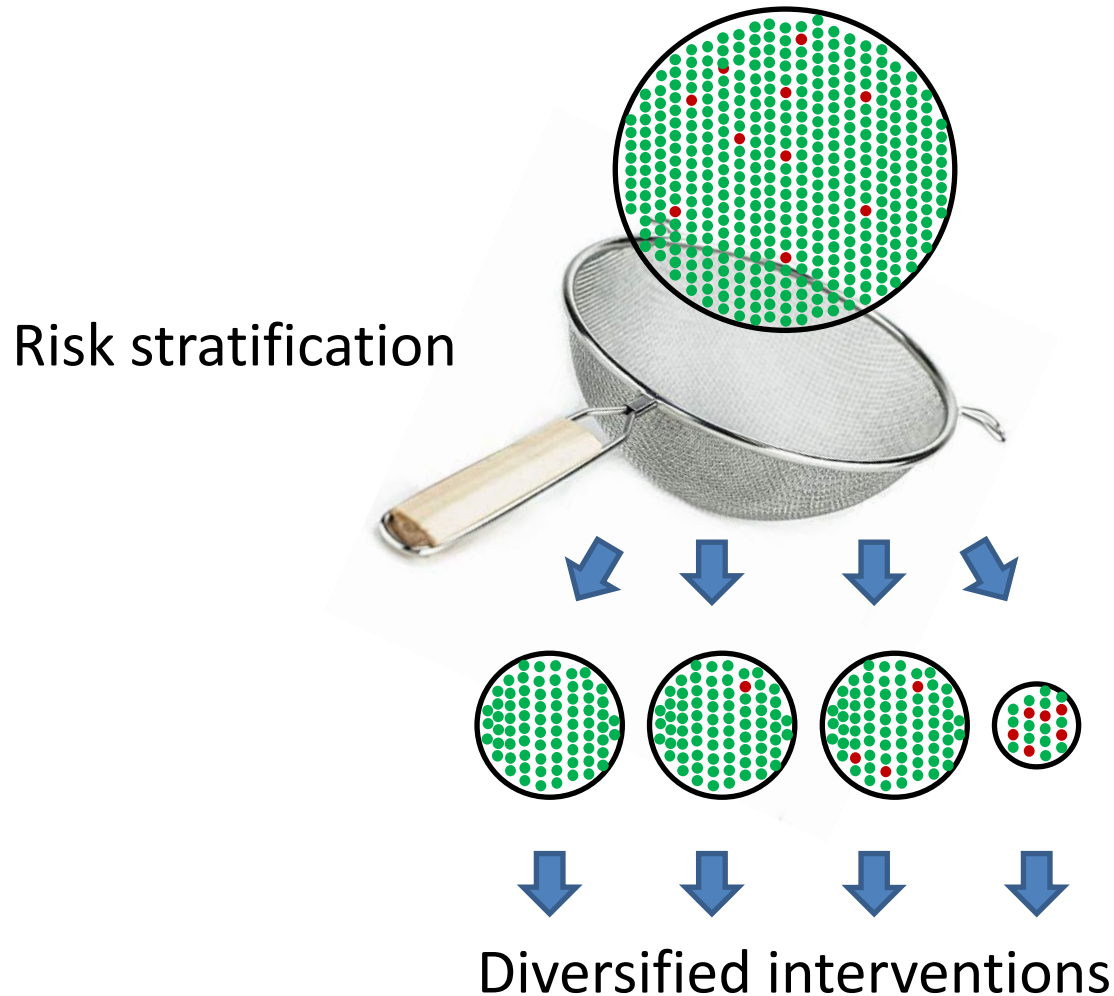
A women like you, but with average scores for these factors, will have a risk of 0.6%

What does this mean?

I wish another risk decription

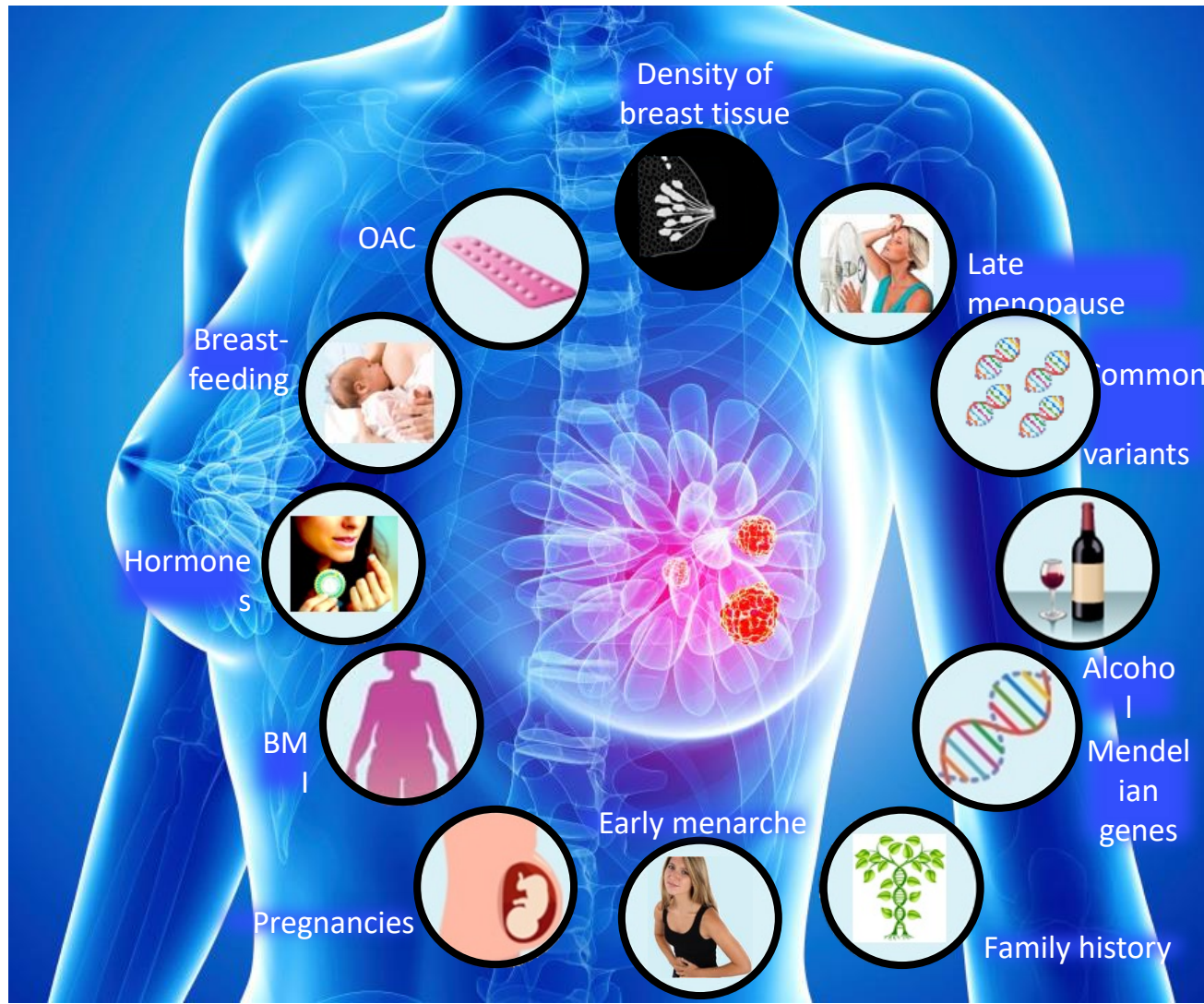
We suggest that the screening mammography will take place between 01-MM-ÅÅÅÅ and 01-MM-ÅÅÅÅ. You will be invited by electronic mail as usual. Please note that you have the right according to the law to have a screening mammography already in 2 years. For the group of women with your risk, however, we estimate that the harms will the exceed the benefits.

Future screening programmes are multidimensional and multistep

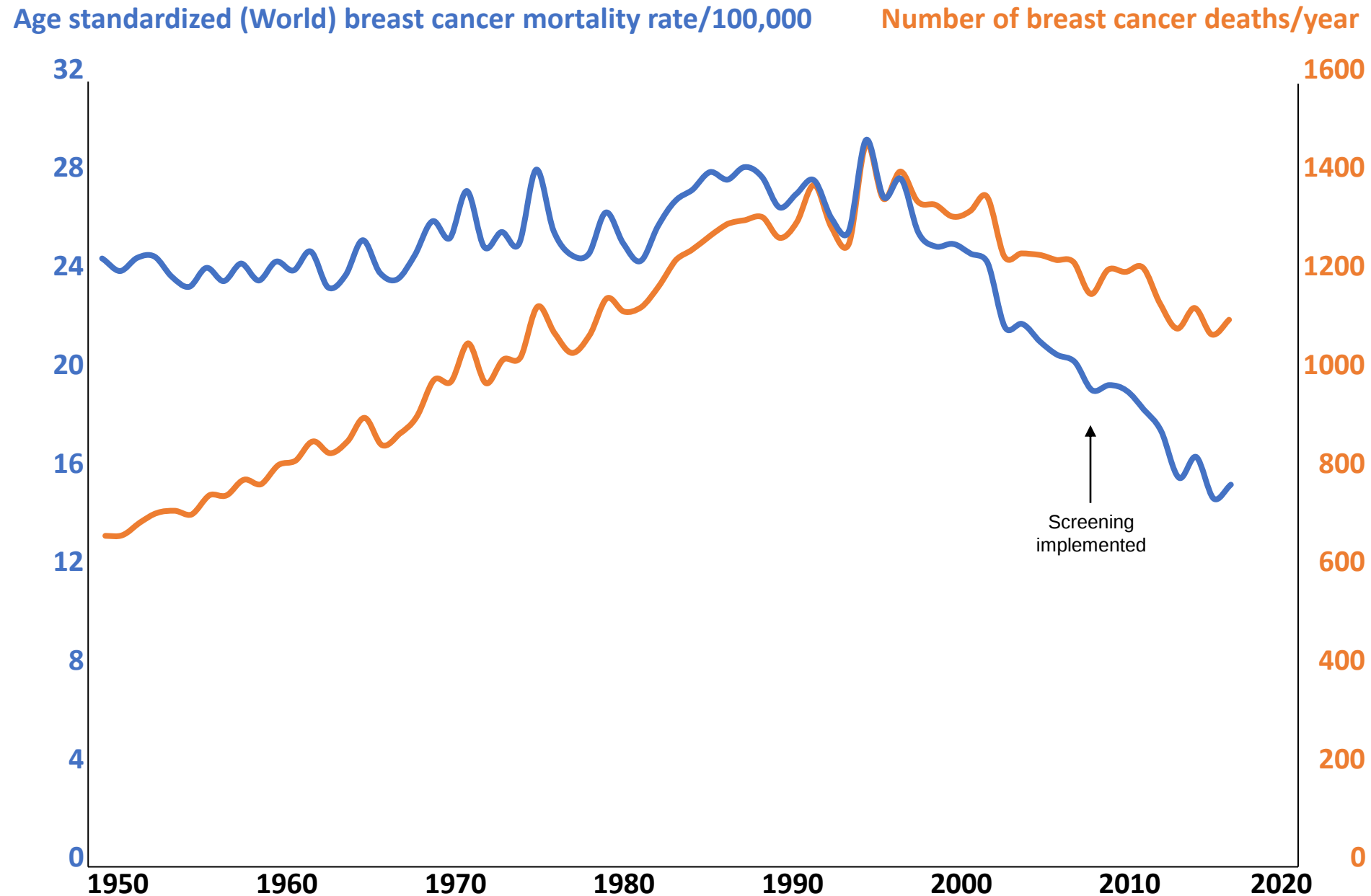


We know
the risk
factors

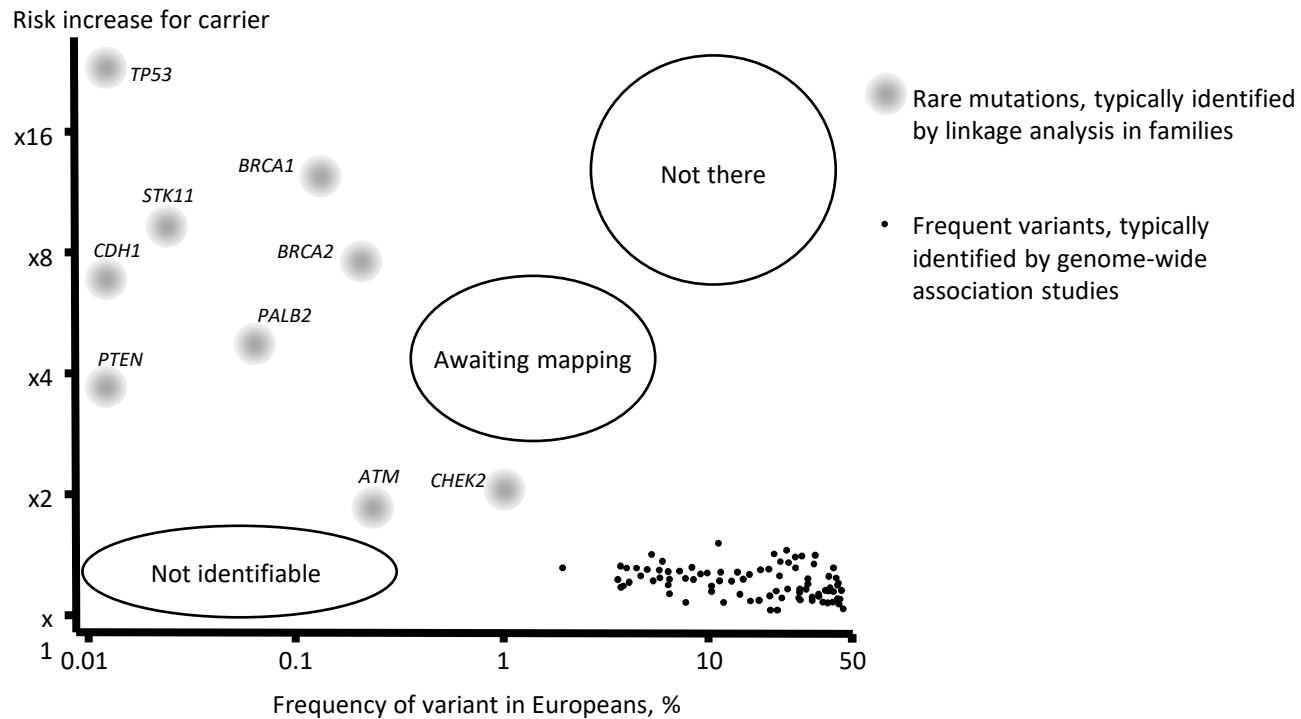
...and now
we know
have to
combine
them.



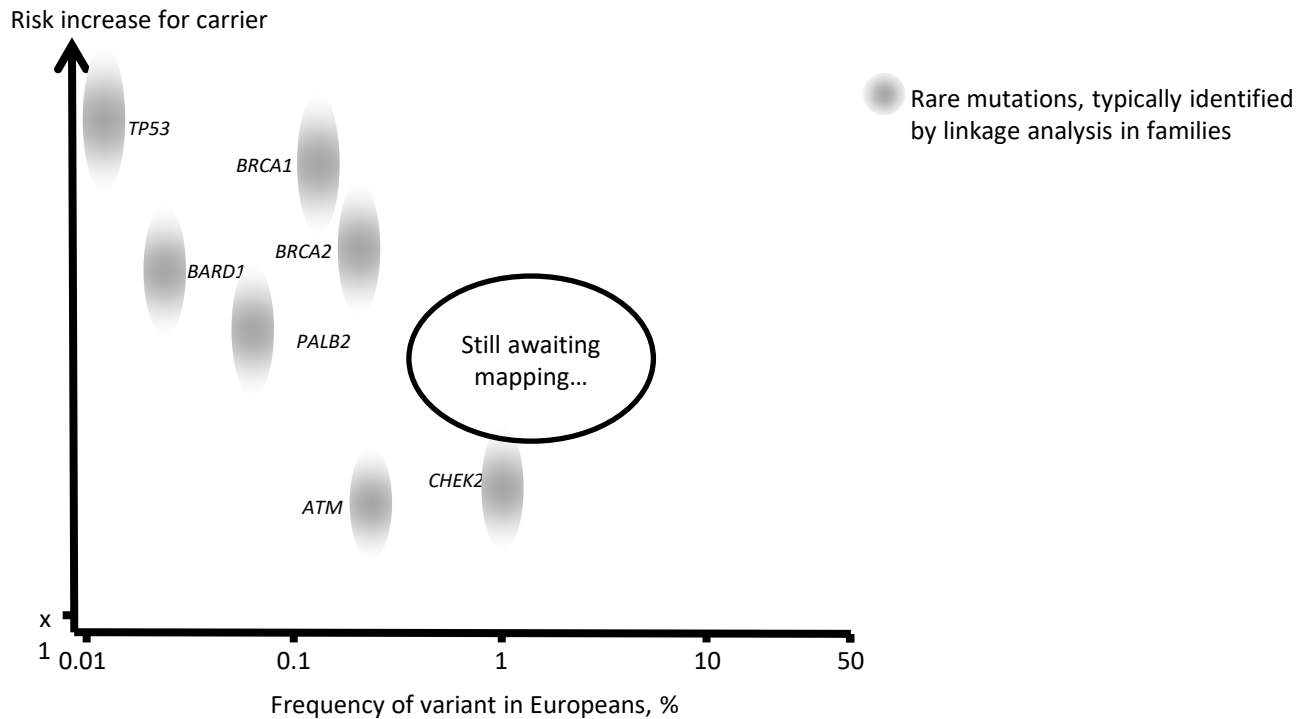
Breast cancer mortality in Denmark



Breast cancer and genetics



Better description of risk by each mendelian variant



ORIGINAL ARTICLE

Breast Cancer Risk Genes — Association Analysis in More than 113,000 Women

Breast Cancer Association Consortium*

ABSTRACT

BACKGROUND

Genetic testing for breast cancer susceptibility is widely used, but for many genes, evidence of an association with breast cancer is weak, underlying risk estimates are imprecise, and reliable subtype-specific risk estimates are lacking.

METHODS

We used a panel of 34 putative susceptibility genes to perform sequencing on samples from 60,466 women with breast cancer and 53,461 controls. In separate analyses for protein-truncating variants and rare missense variants in these genes, we estimated odds ratios for breast cancer overall and tumor subtypes. We evaluated missense-variant associations according to domain and classification of pathogenicity.

RESULTS

Protein-truncating variants in 5 genes (*ATM*, *BRCA1*, *BRCA2*, *CHEK2*, and *PALB2*) were associated with a risk of breast cancer overall with a P value of less than 0.0001. Protein-truncating variants in 4 other genes (*BARD1*, *RAD51C*, *RAD51D*, and *TP53*) were associated with a risk of breast cancer overall with a P value of less than 0.05 and a Bayesian false-discovery probability of less than 0.05. For protein-truncating variants in 19 of the remaining 25 genes, the upper limit of the 95% confidence interval of the odds ratio for breast cancer overall was less than 2.0. For protein-truncating variants in *ATM* and *CHEK2*, odds ratios were higher for estrogen receptor (ER)-positive disease than for ER-negative disease; for protein-truncating variants in *BARD1*, *BRCA1*, *BRCA2*, *PALB2*, *RAD51C*, and *RAD51D*, odds ratios were higher for ER-negative disease than for ER-positive disease. Rare missense variants (in aggregate) in *ATM*, *CHEK2*, and *TP53* were associated with a risk of breast cancer overall with a P value of less than 0.001. For *BRCA1*, *BRCA2*, and *TP53*, missense variants (in aggregate) that would be classified as pathogenic according to standard criteria were associated with a risk of breast cancer overall, with the risk being similar to that of protein-truncating variants.

CONCLUSIONS

The results of this study define the genes that are most clinically useful for inclusion on panels for the prediction of breast cancer risk, as well as provide estimates of the risks associated with protein-truncating variants, to guide genetic counseling. (Funded by European Union Horizon 2020 programs and others.)

The authors' full names, academic degrees, and affiliations are listed in the Appendix. Address reprint requests to Dr. Easton at the University of Cambridge, Strangeways Research Laboratory, Worts Causeway, Cambridge CB1 8RN, United Kingdom, or at dle20@medschl.cam.ac.uk.

*A complete list of collaborators and investigators is provided in the Supplementary Appendix, available at NEJM.org.

Dr. Döring, Dr. Carvalho, and Mr. Allen and Drs. Teo, Devilee, and Easton contributed equally to this article.

This article was published on January 20, 2021, at NEJM.org.

N Engl J Med 2021;384:428-39.
DOI: 10.1056/NEJMoa1913948

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2021

Cancer diseases are heterogenous

Strategies to detect them while small, must be diverse

Cancer is caused by infections

Cancer is inherited



Cancer is caused by mutations

Cancer is caused by environment

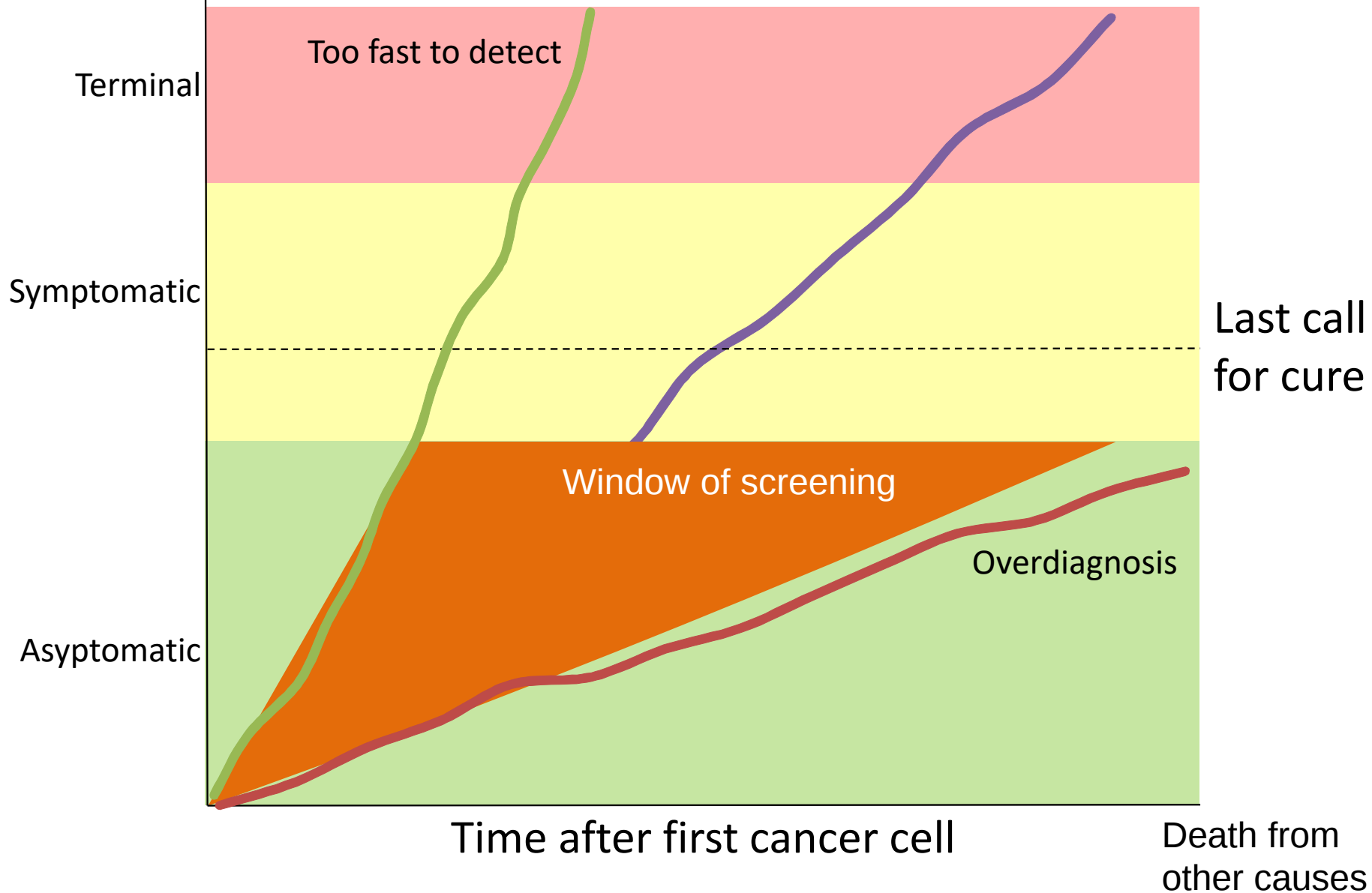
Cancer is frequent
(50% of the population)

Cancer is rare
(for a cell)

Cancer is an
old-age disease
Cancer is a
stochastic event

Screening is complex

Tumor size/
disease state



Three solutions

- 1) Stop smoking
(Reduces likelihood of first cancer cell)
- 2) Improve treatment
(Increases threshold for last call for cure)
- 3) Early detection/screening
(But not too early)

Cancer screening

Pro

With screening
we find tumors while they
are small and treatable



Con

We cannot use scarce resources on healthy
individuals

