



Initiatives based on genomes and e-health databases in Estonia

Lili Milani, PhD



estonian genome center
university of tartu

Estonian Biobank



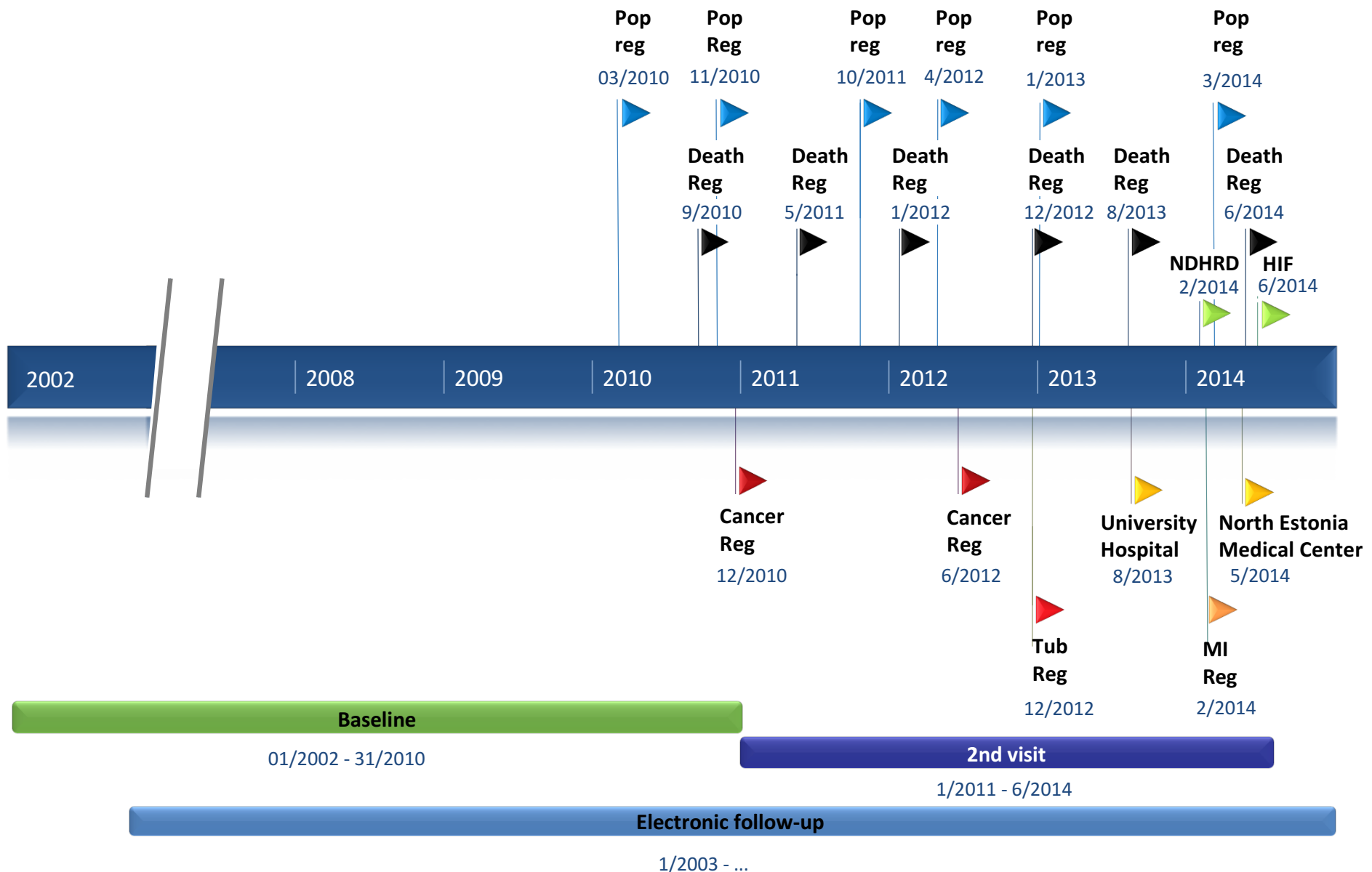
- Prospective, longitudinal, volunteer-based
- 52,000 participants - 5% of the adult population of Estonia
- Health records, diet, physical activity, etc.
- DNA, plasma and cell samples
- Estonian Human Genes Research Act
- Broad informed consent
- Open for research: Clear access rules

Estonian biobank: omics profiling

Method	Sample size
Whole genome sequencing	2,400
Whole exome sequencing	2,500
Genome-wide genotyping arrays	50,000
Genome-wide methylation arrays	700
Genome-wide expression arrays	1,100
mRNA sequencing	600
Total RNA sequencing	50
Metabolomics (NMR)	11,000
Metabolomics (MS/MS)	1,100
Telomere length	5,200
Clinical biochemistry	2,700
IgG glycosylation	1,000

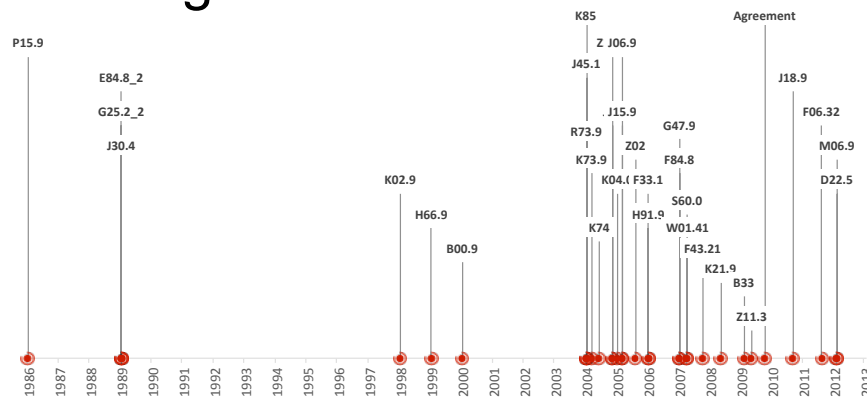


Timeline: linking to registries

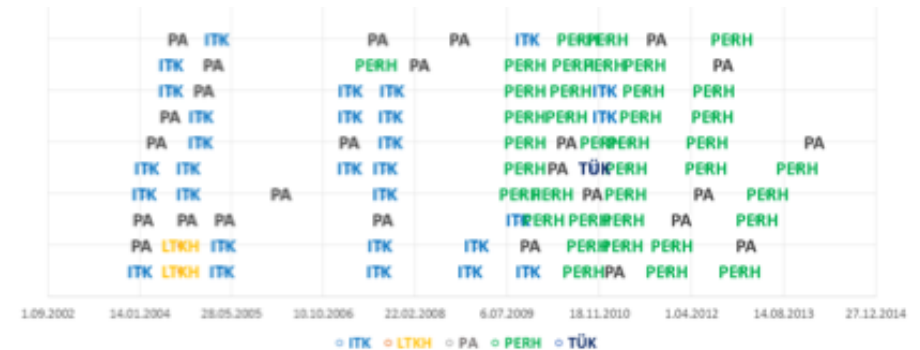


Disease trajectories

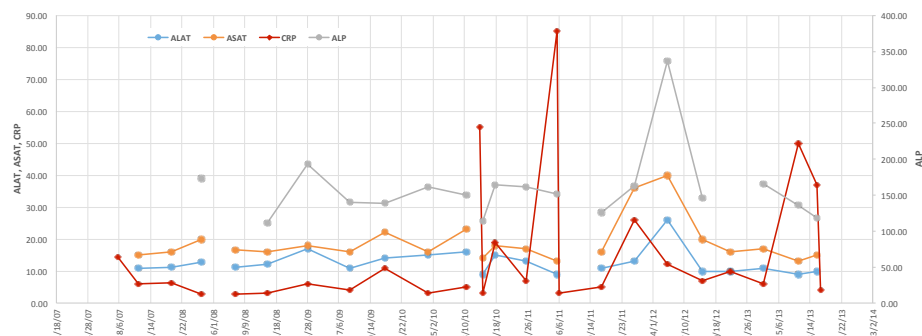
- Diagnosed diseases



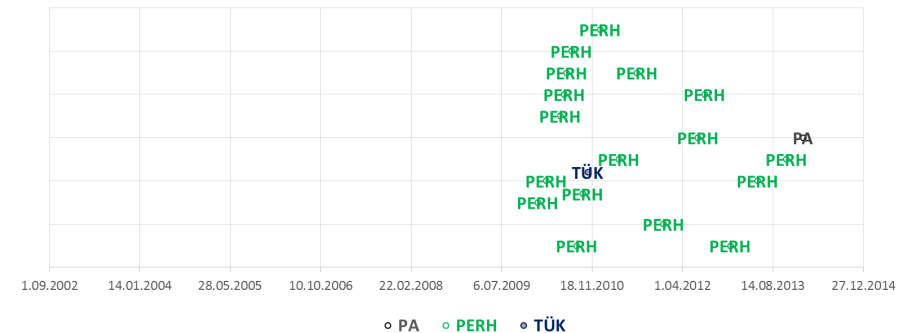
- Health insurance bills



- Clinical lab measurements



- Full free-text records



RESEARCH



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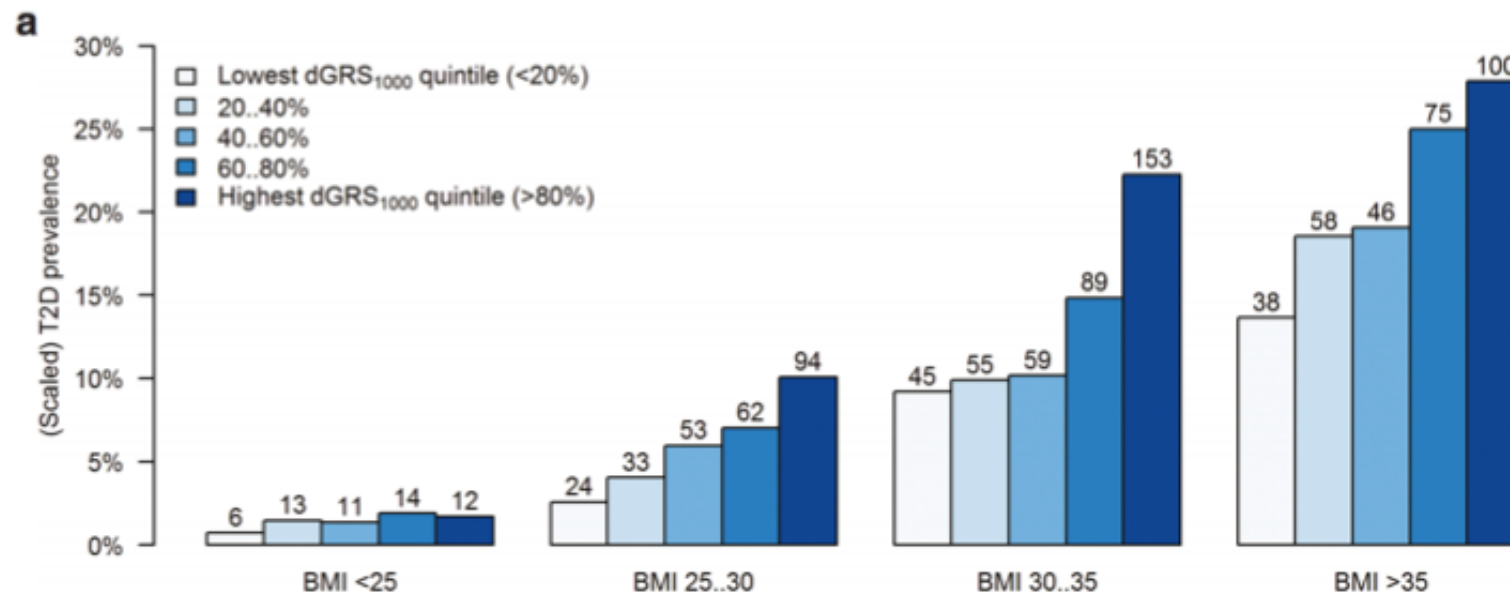


Open

Personalized risk prediction for type 2 diabetes: the potential of genetic risk scores

Kristi Läll, MSc^{1,2}, Reedik Mägi, PhD¹, Andrew Morris, PhD^{1,3,4}, Andres Metspalu, MD, PhD^{1,5}
and Krista Fischer, PhD¹

Prevalence in biobank



GRS for Type 2 Diabetes: incident cases

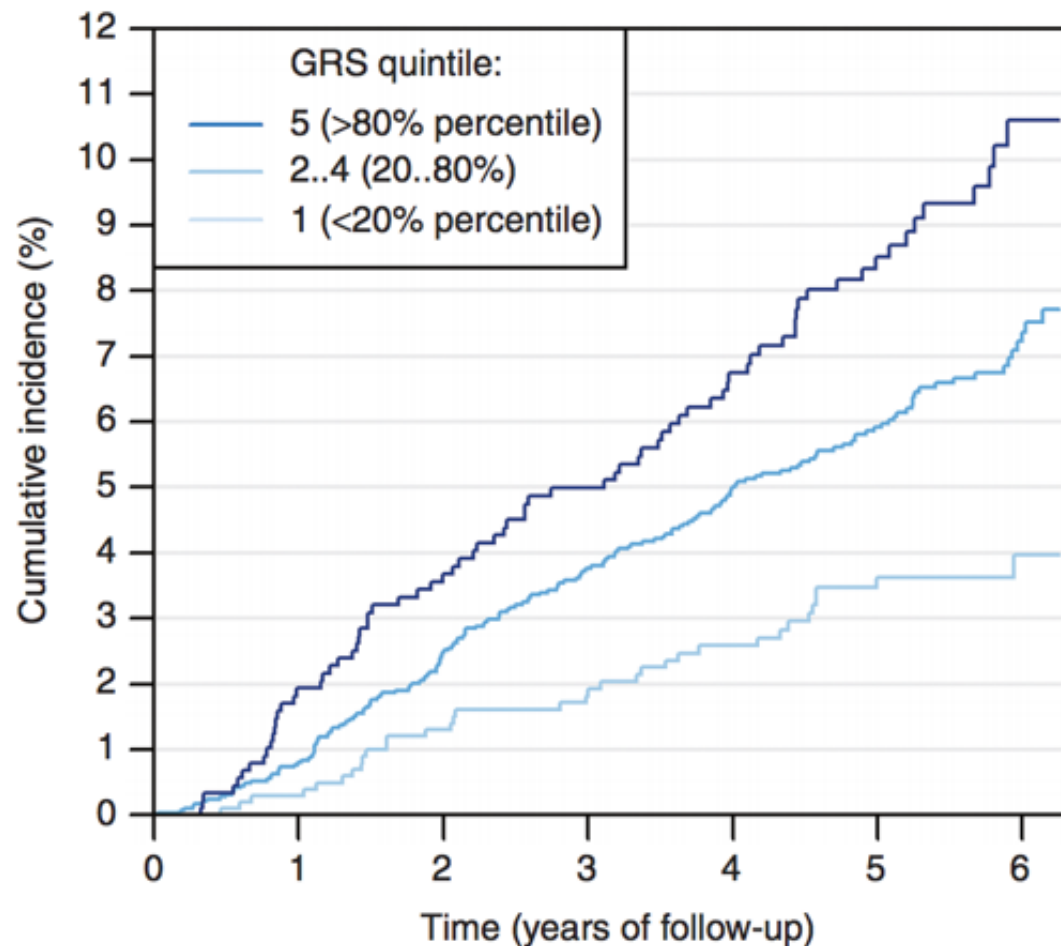
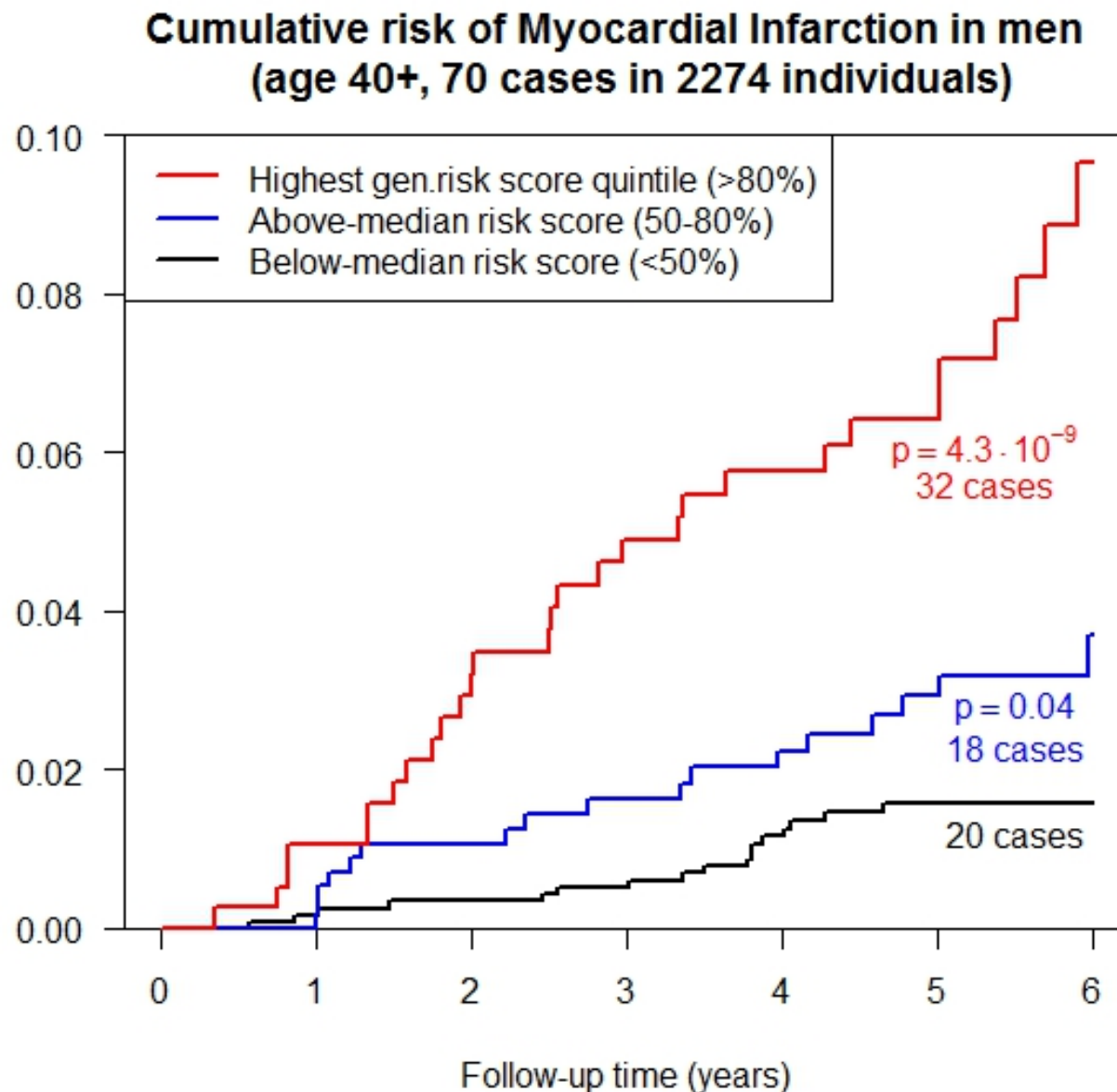


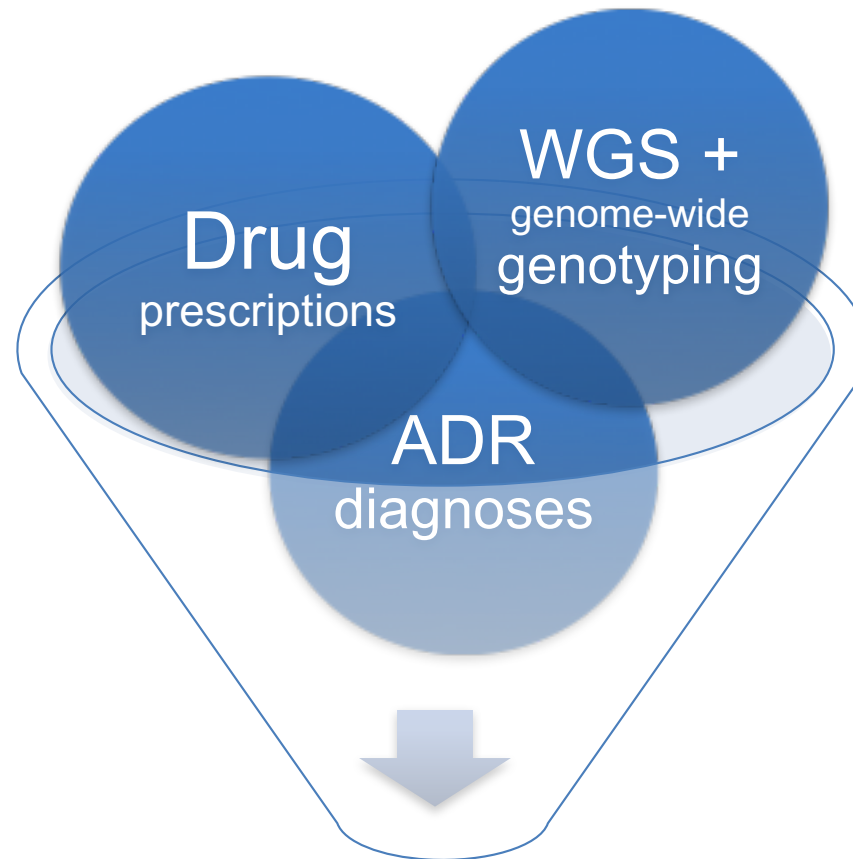
Figure 2 Cumulative incidence of type 2 diabetes in 4,881 genotyped individuals free of T2D aged 35–79 and with BMI >23 at baseline. In the figure, 6.25-year follow-up is presented because only 25% of individuals were followed for more than 6.25 years. Cumulative incidence is presented separately in three $dGRS_{1000}$ categories.

GRS for Coronary Artery Disease and prediction of incident Myocardial Infarction



A weaker, but
still significant
effect seen
among females
($p=0.005$)

**98% of Europeans carry ≥ 1 mutation
relevant for drug treatment outcome**



Pharmacogenomic study



TRANSLATION



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Feedback to participants

1. Risk for common diseases
 - Genetic risk
 - Lifestyle risk factors
2. Incidental findings (BRCA1/2, FH, etc)
 - Cascade screening
3. Pharmacogenetics
4. Carrier status



Reporting disease risk: type 2 diabetes



BRCA1/2 mutations detected by WGS

Gene	cDNA	Prot.	Pathogenic/benign	AC
BRCA1	c.4258C>T	p.Gln1420*	Known pathogenic (BIC)	1
BRCA1	c.1840A>T	p.Lys614*	Known pathogenic (BIC)	1
BRCA1	c.5329dupC (5382insC)	p.Ser1756fs*	Known pathogenic (BIC)	4
BRCA1	c.4035delA (4154delA)	p.Glu1345fs*	Known pathogenic (BIC)	6
BRCA2	c.8572C>T	p.Gln2858*	Known pathogenic (BIC)	2
BRCA2	c.467_468insT	p.Lys157fs*	Expected pathogenic	1
BRCA2	c.9097_9098insT	p.Thr3033Ilefs*10	Expected pathogenic	1

+ WES: 15 + Long-range haplotyping: 18
= Total 49 cases + cascade screening

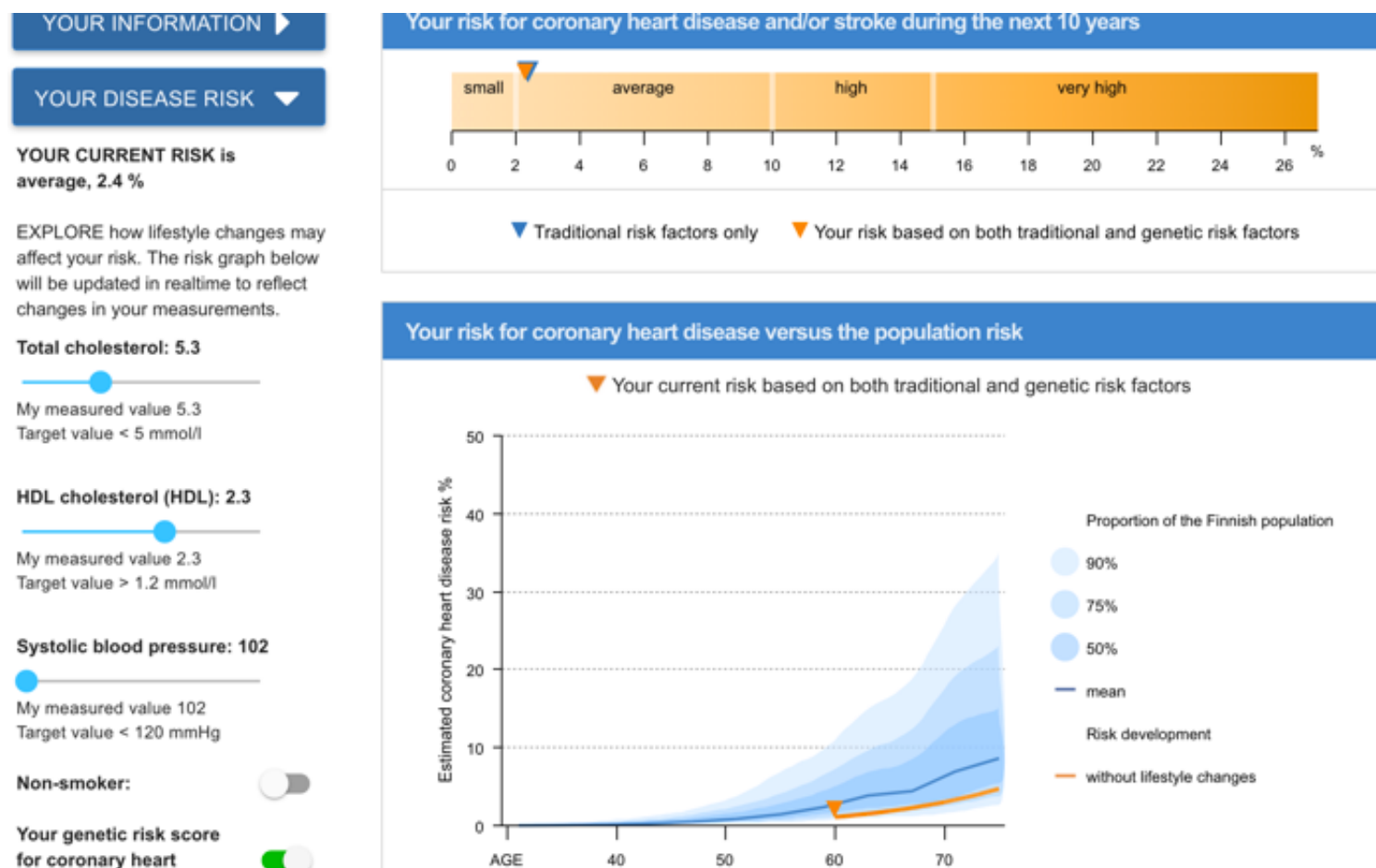
TRAINING



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ePerMed workshop for clinicians



Prof. Andres Metspalu, Tõnu Esko, Krista Fischer, Reedik Mägi, Maris Alver, Kristi Läll, Kristi Krebs, Tõnis Tasa, Mart Kals, Tom Haller, Neeme Tõnisson, Anu Reigo, Liis Leitsalu, Helene Alavere, Kristjan Metsalu, Kairit Mikkel, Mari-Liis Tammesoo



STACC

Software Technology and
Applications Competence Center

Prof. Jaak Vilo, Hedi Peterson, etc.

QureTEC

Regionaalhaigla



BioMed@STACC: the health data mining team

▼ 18 people



- ☐ Alexander Tkachenko ▼
- ☒ Anne-Liis Tanav ▼
- ☒ Dage Särg ▼
- ☒ Gea Pajula ▼
- ☐ Harry-Anton ▼
- ☐ Karl-Oskar Masing ▼
- ☒ Marek Oja ▼
- ☒ Margus Jäger ▼
- ☐ marje johanson ▼
- ☒ Markus Lippus ▼
- ☐ Mihkel Manguse ▼
- ☒ monika soosaar ▼
- ☒ Raul Sirel ▼
- ☐ Robert Roosalu ▼
- ☒ Sulev Reisberg ▼
- ☐ Sven Laur ▼
- ☒ Tormi Reinson ▼
- ☐ Uku R ▼

REPUBLIC OF ESTONIA
MINISTRY OF SOCIAL AFFAIRSE-HEALTH
ESTONIAN E-HEALTH FOUNDATION

Prof. Eric Lander, Dr Sekar
Kathiresan, Daniel McArthur

Dr Ain Aaviksoo, Dr Krista Kruuv-
Käo, Indrek Jakobson, Marju Raju

