



Atrial Fibrillation -

Can we use polygenic risk to inform clinical care?

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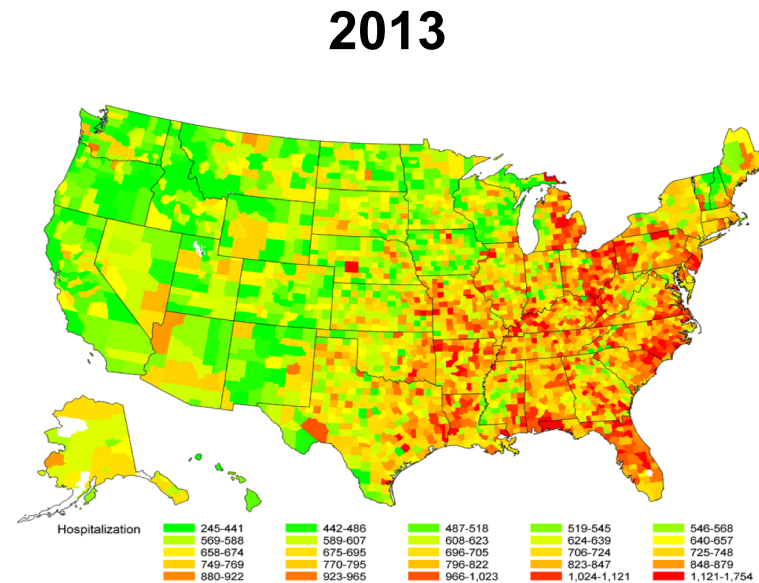
Sources of Funding

Research funding from National Institutes of Health grants R01HL092577, R01HL104156, K24HL105780; American Heart Association SFRN; Fondation Leducq and Bayer AG

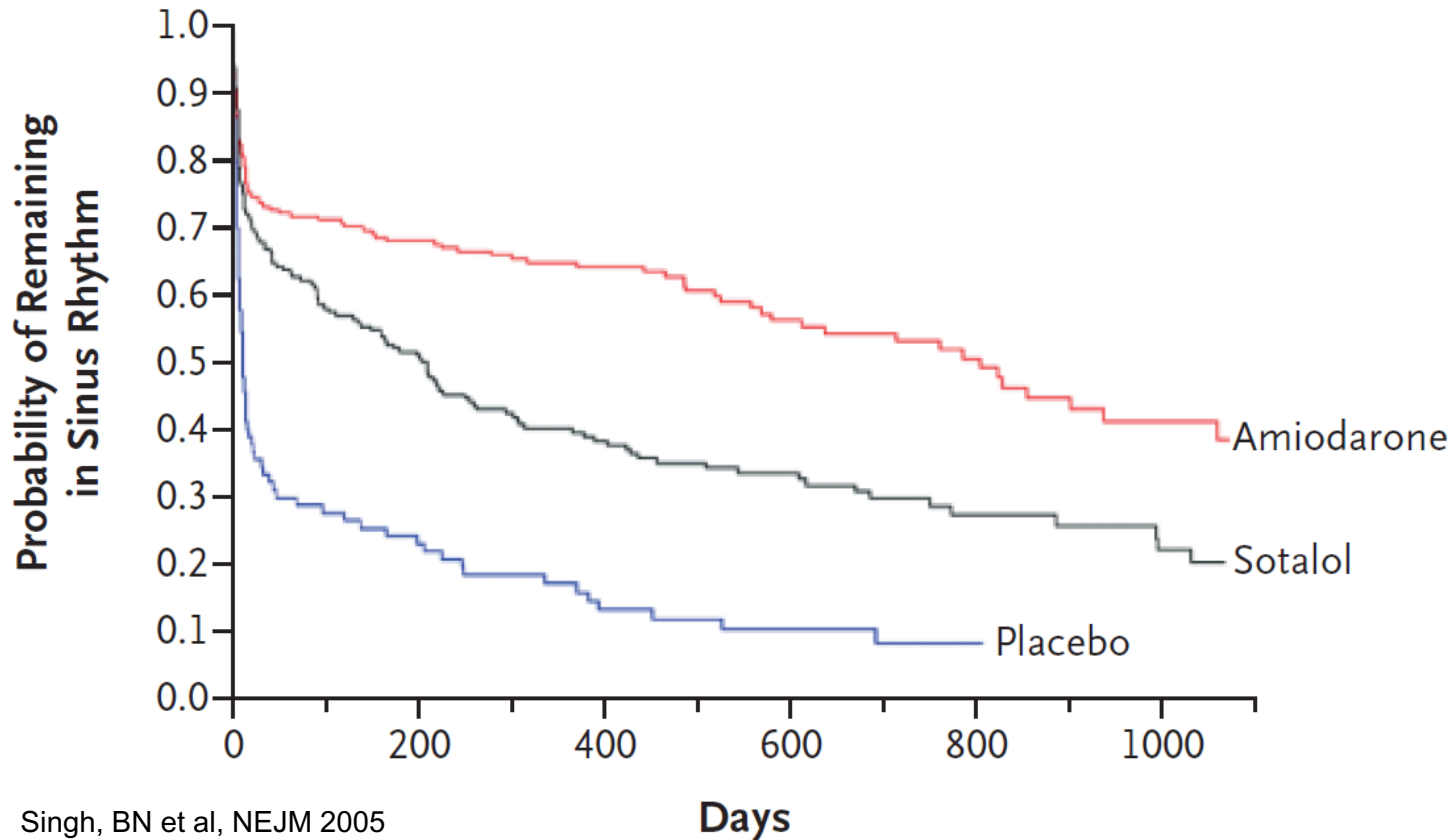
Consulting with Bayer AG, Novartis and Quest Diagnostics

Why do we care about atrial fibrillation?

- Most common arrhythmia
- 33 million people worldwide
- Increased risk of stroke, heart failure, dementia, and death
- Treatments are limited



We clearly need new treatments for AF



Use genetics to identify underlying mechanisms of AF

Current AF resources

AF **Controls** **Status**

GWAS 120K >1M Available



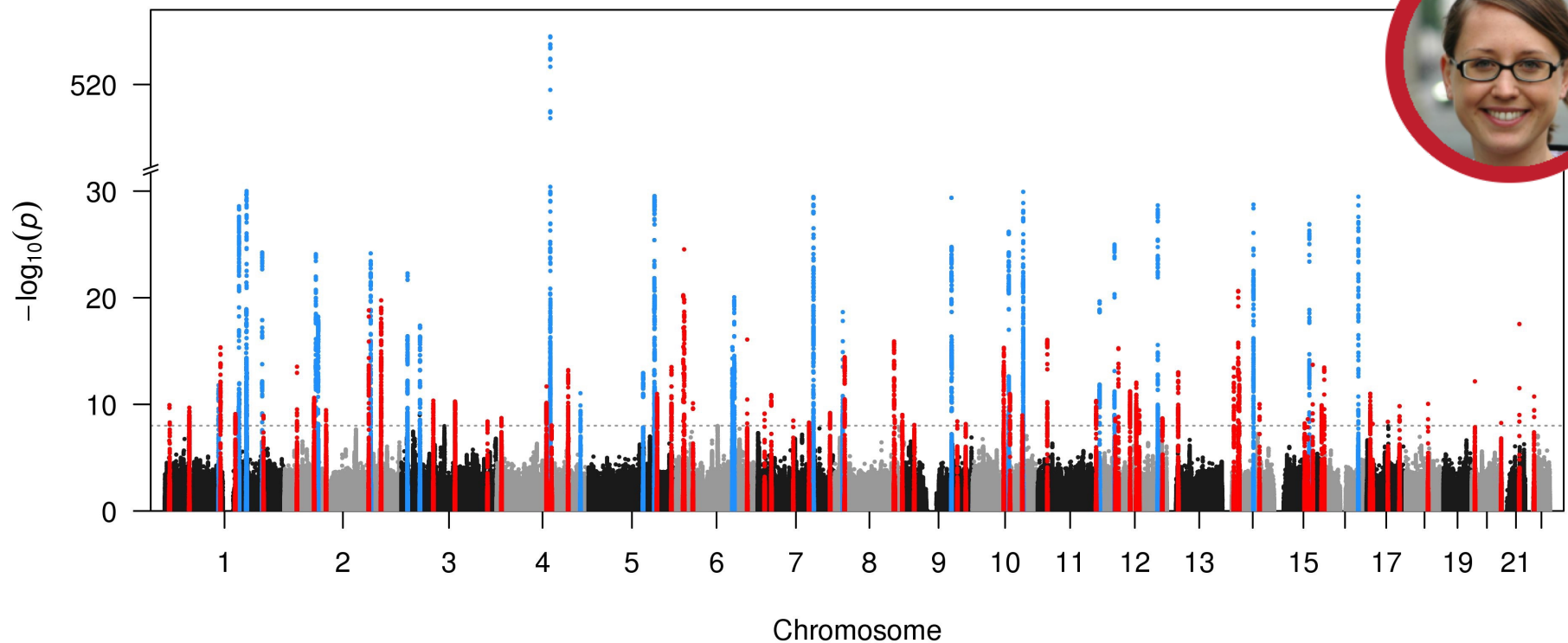
Broad AF Study



BIOBANK JAPAN



2018: 65K individuals, ~100 loci



known locus
novel locus

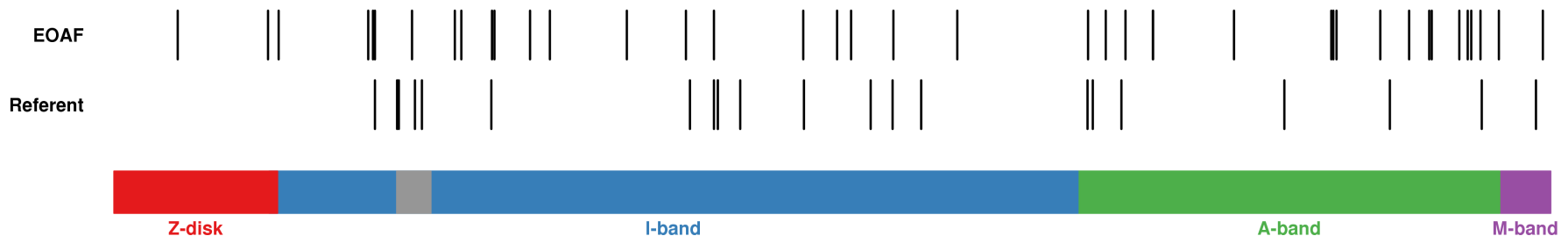
Roselli, Chaffin, et al *Nature Genetics*, 2018



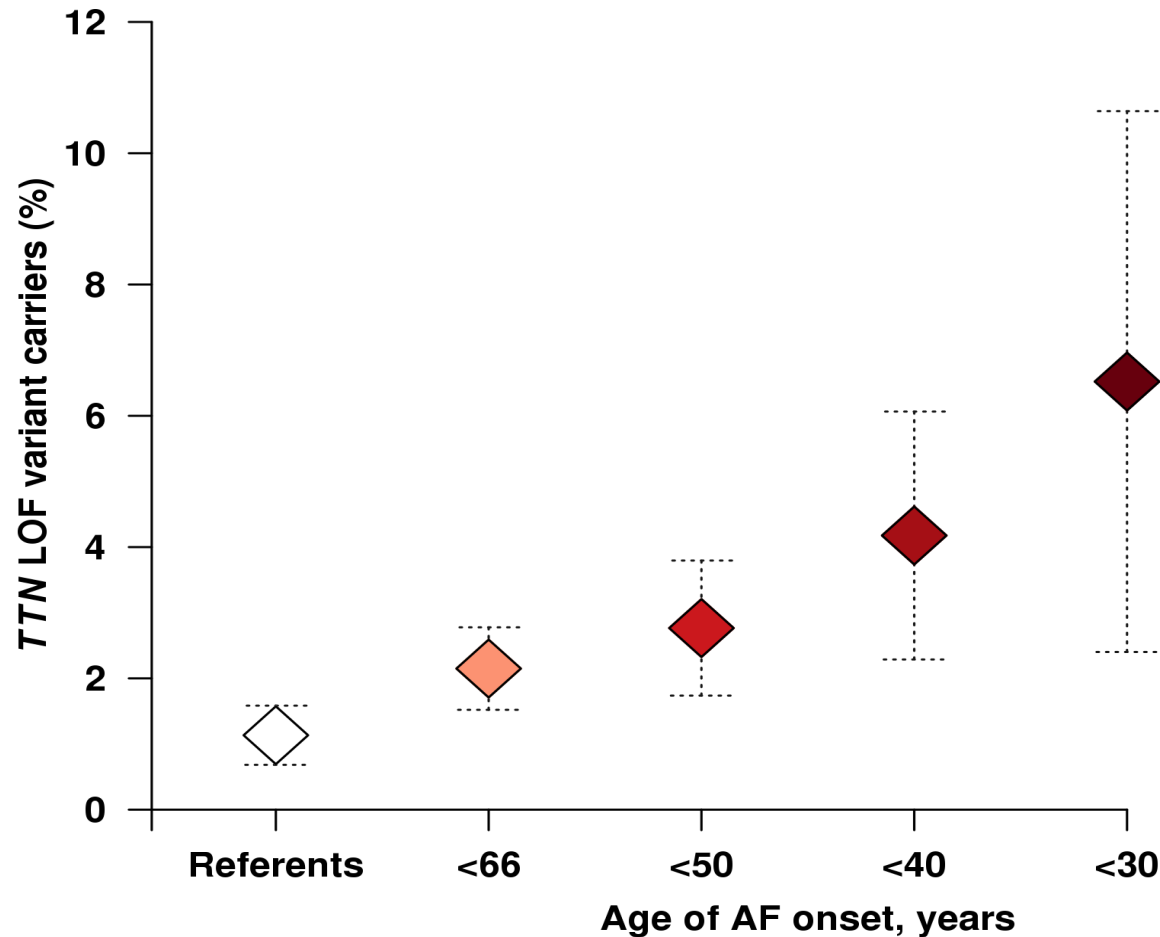
TTN loss of function mutations in early-onset AF



2800
AF cases + 5000
controls



Increasing frequency of *TTN* loss of function variants with decreasing age of AF onset



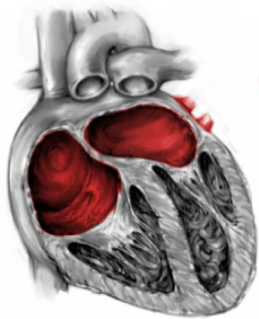
AF onset <30 yrs

OR 5.94

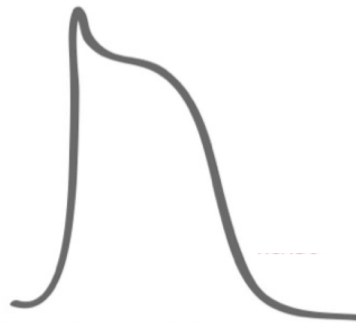
CI 2.64-13.36

$p=1.64 \times 10^{-5}$

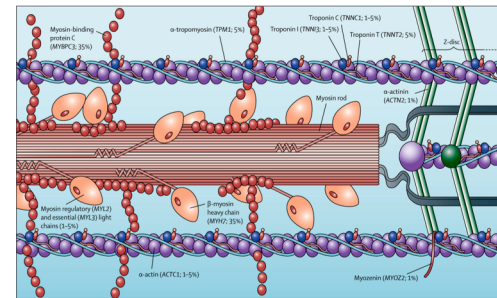
Some expected pathways have emerged



Atrial
development



Ion
channels



Contractile
proteins

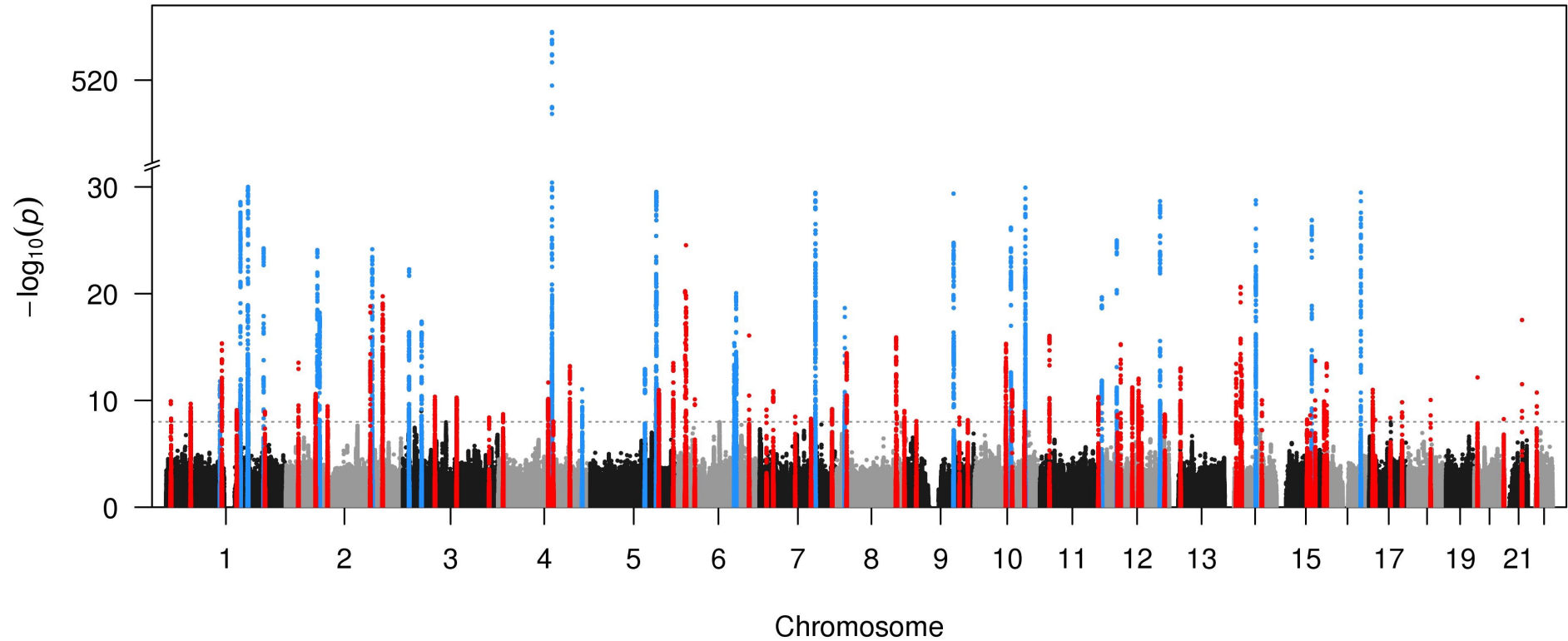
But many genes have unknown relation to AF
Challenge is linking gene to mechanism

How can we use polygenic risk of AF?



- AF risk prediction in general population
- Biomarker in high risk individuals – cryptogenic stroke
- Differential outcomes – HF, stroke, mortality
- Interaction between common and rare variation

A dominant locus for AF at *PITX2*/4q25



3 SNPs at top AF locus can identify high risk of AF

rs2200733 / rs17570669 / rs3853445

genotype combination,
(No. AF risk alleles)

Sample
frequency (%)

CC / TA / CC (1)

1.2

CT / TA / CC (2)

0.5

CC / AA / CC (2)

4.0

CC / TA / CT (2)

4.3

CT / TA / CT (3)

3.1

CC / AA / CT (3)

25.9

CC / TA / TT (3)

1.5

CT / AA / CC (3)

0.4

CC / AA / TT (4)

38.4

CT / TA / TT (4)

3.0

CT / AA / CT (4)

4.5

TT / TA / CT (4)

0.3

CT / AA / TT (5)

10.4

TT / TA / TT (5)

0.5

TT / AA / CT (5)

0.2

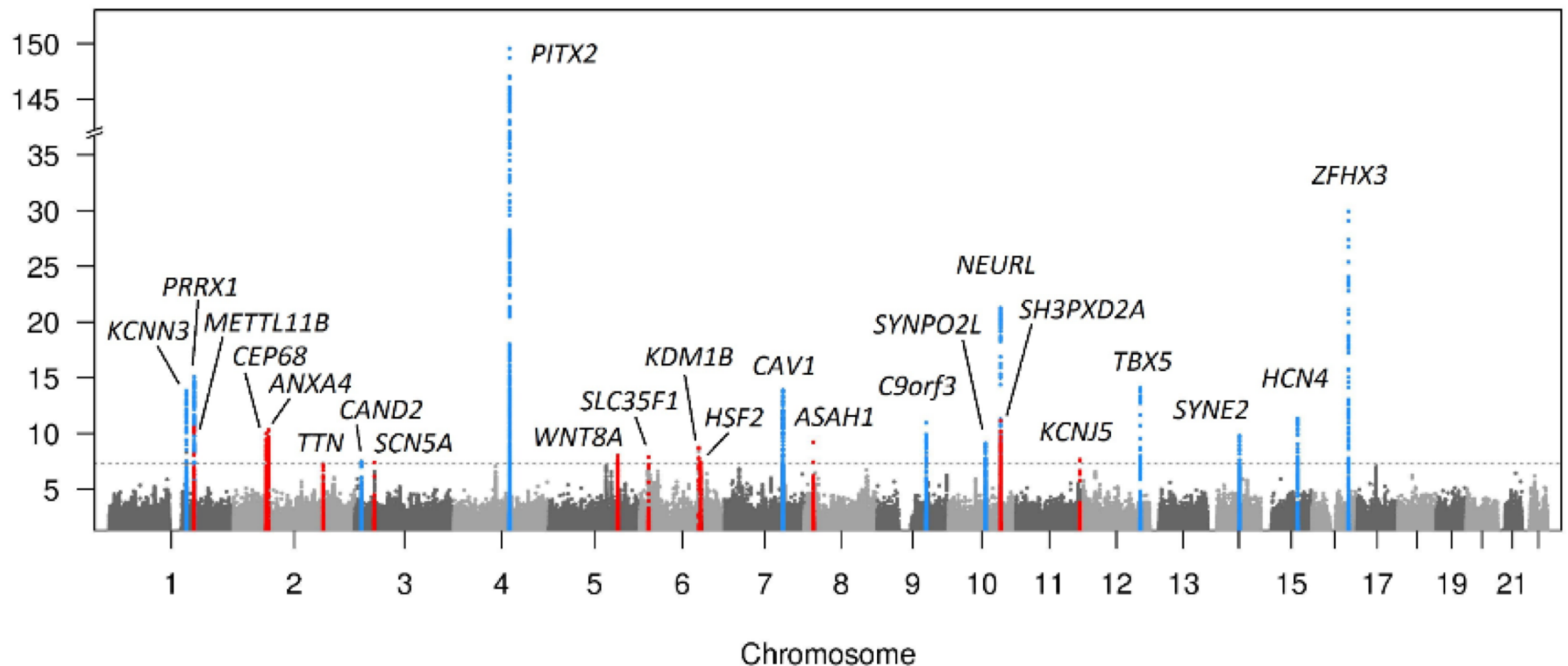
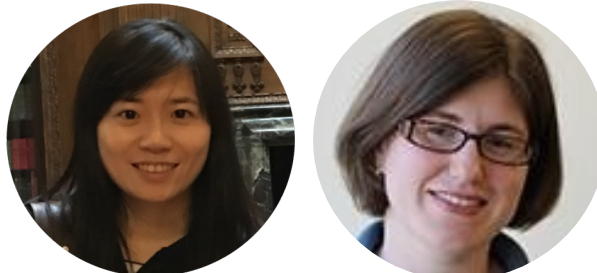
TT / AA / TT (6)

1.2

5,856 with AF
31,838 without AF

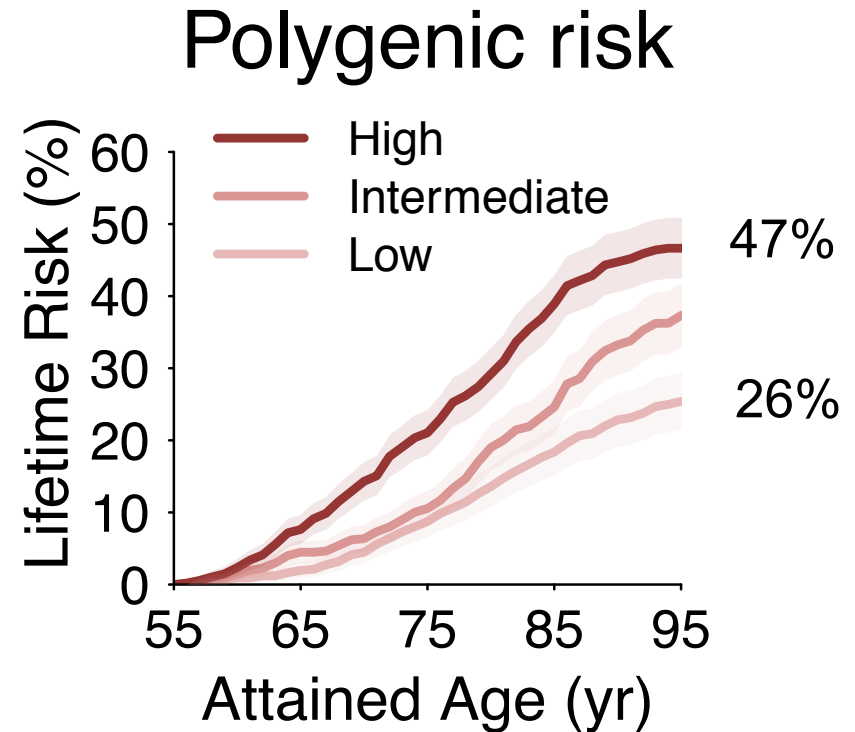
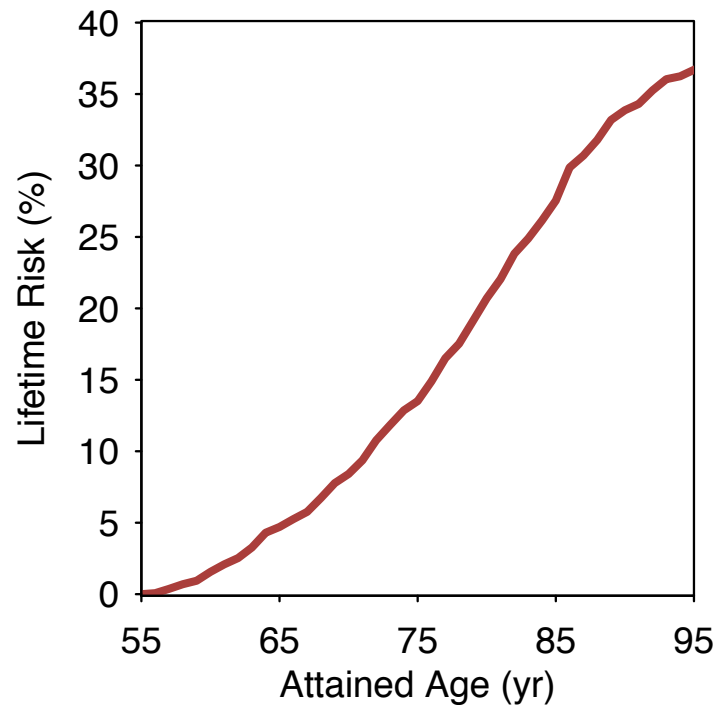
0.1 0.5 1 5 10 20
Relative risk

How does genetics influence the risk of AF?



Lifetime risk of AF is high

Genetic risk can stratify lifetime risk of AF

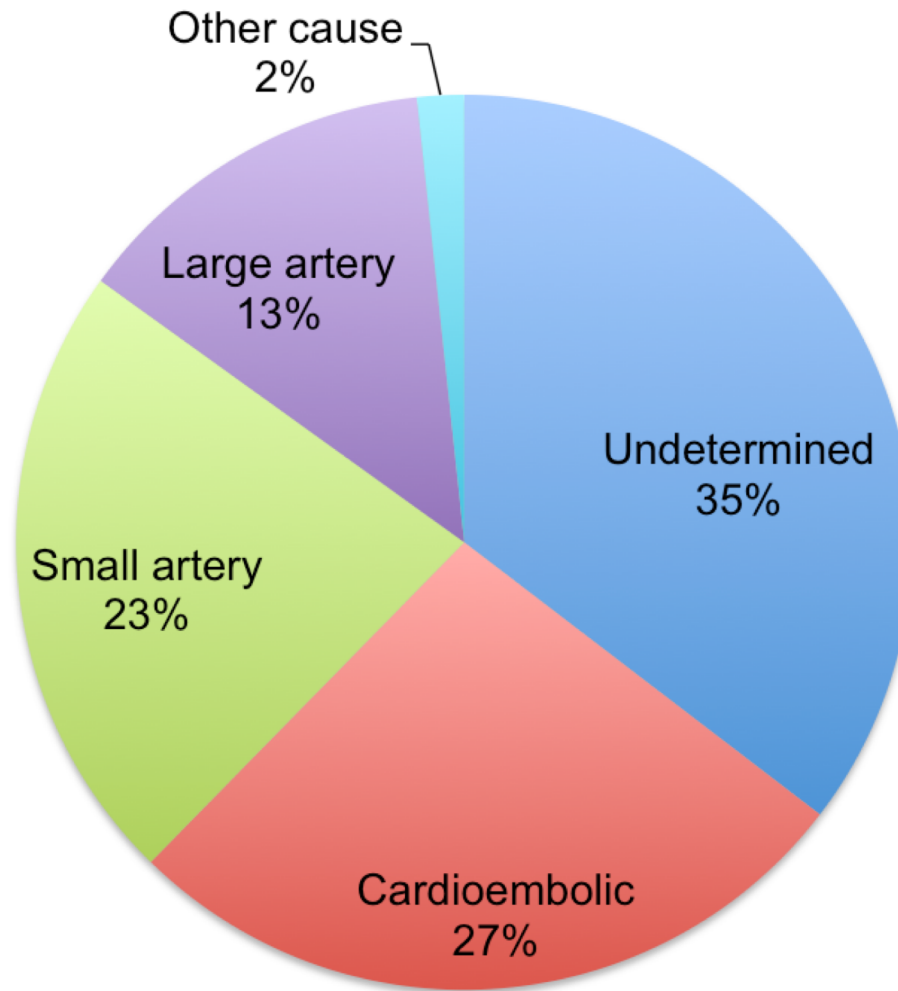


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One third of strokes are cryptogenic



Anticoagulation in cryptogenic stroke trials has failed



Trial	Anticoagulant	Comparator	Reduced recurrent stroke with anticoagulant
WARS 2001	Warfarin	ASA 325 mg	No
NAVIGATE-ESUS 2018	Rivaroxaban 15 mg	ASA 100 mg	No
RESPECT-ESUS 2018	Dabigatran 110 mg or 150 mg BID	ASA 100 mg	No
ATTICUS	Apixaban 5 mg BID	ASA 100 mg	Pending

Would genetically determined AF/cardioembolic stroke subgroups benefit from anticoagulation?

SiGN Consortium: AF genetic risk is specific for cardioembolism



Chris Anderson



Sara Pulit



Steve Lubitz



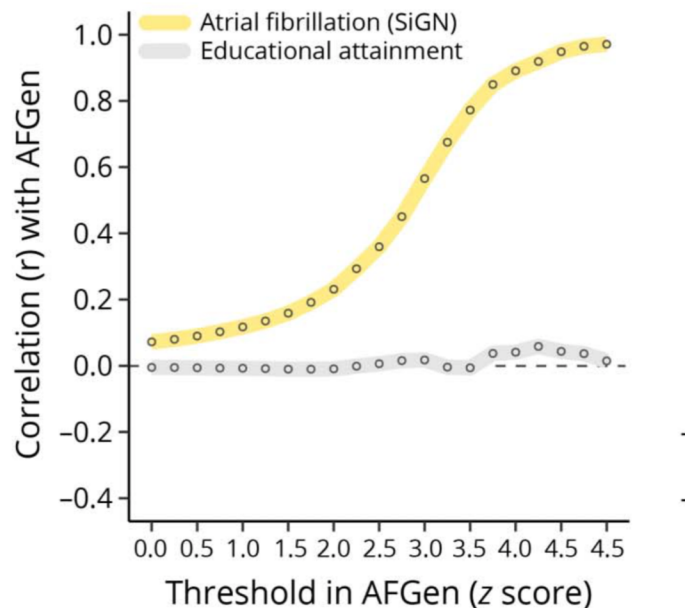
13K ischemic stroke cases &
28K referents

- ~25% cardioembolic
- ~20% large artery
- ~20% small vessel
- ~25% cryptogenic

SiGN Consortium: AF genetic risk is specific for cardioembolism



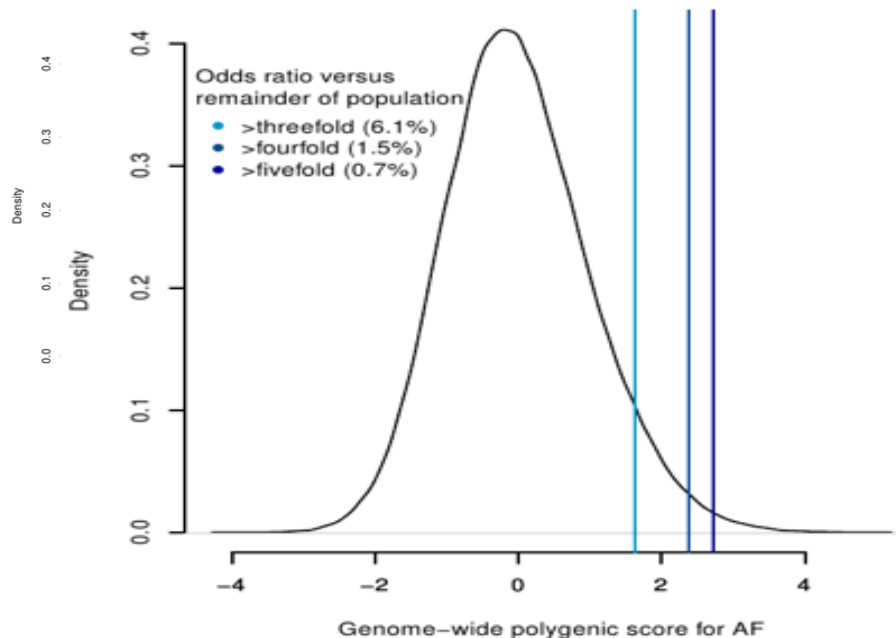
AF



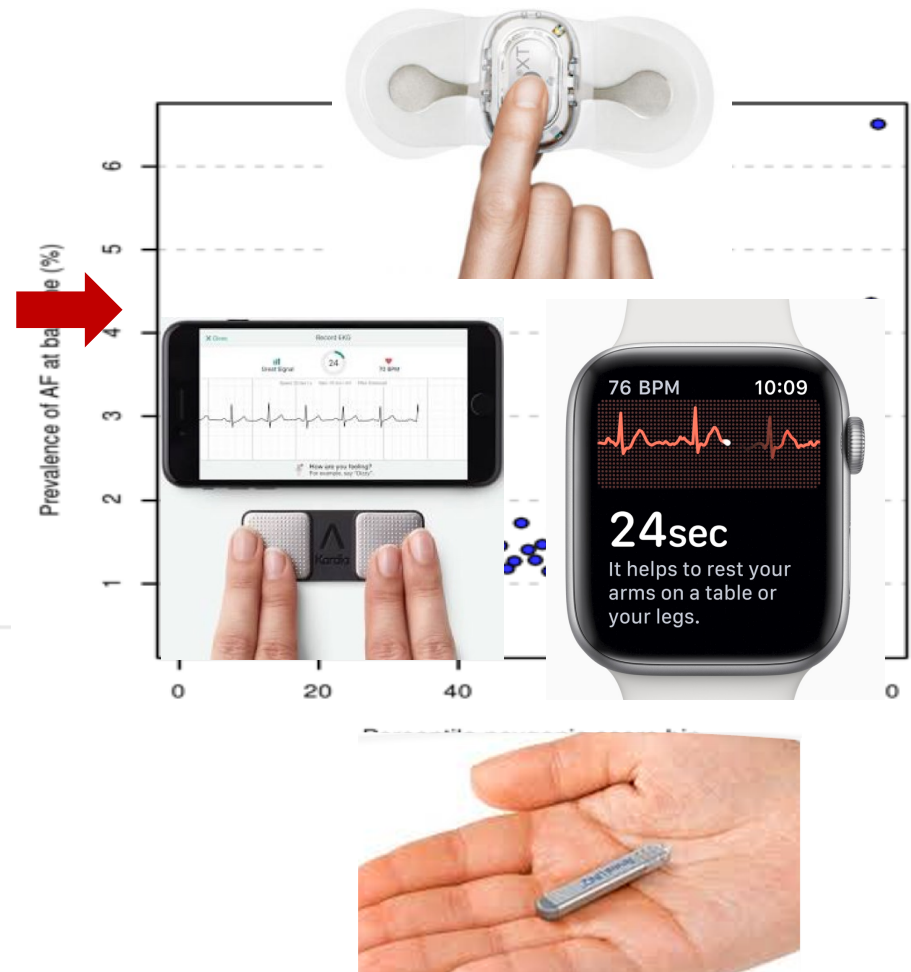
Using AF GRS to identify at risk patients



Individuals without AF, but high clinical or GRS



Screening



Single lead electrocardiogram

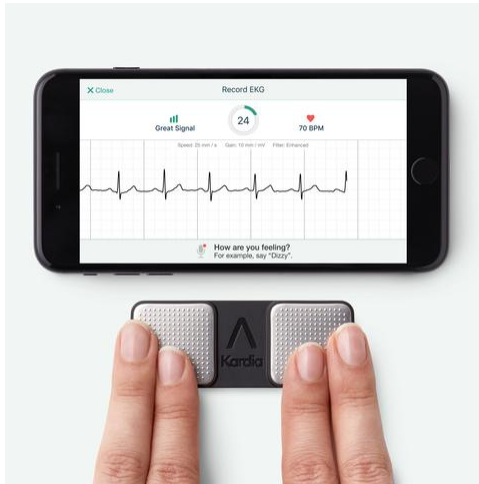


We will find AF, but at a cost...



yikes!

Plenty of other technologies



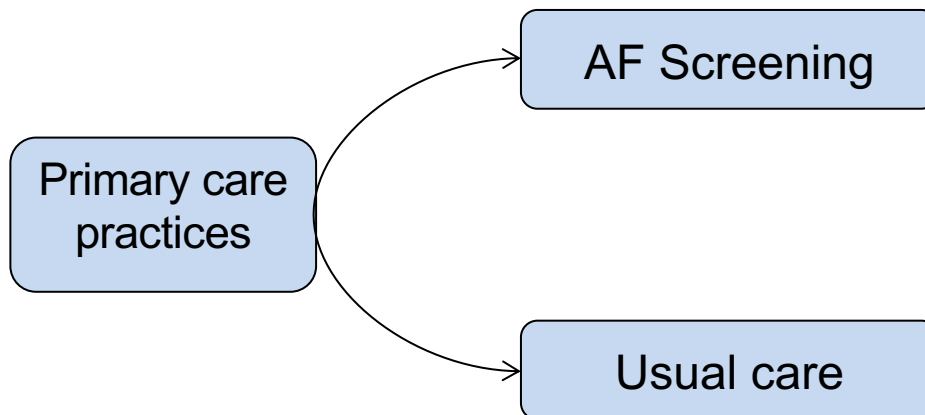
Google Fit



Large scale screening is already underway

VITAL-AF

- Cluster RCT
- N=35,000
- Age ≥ 65 years



How can we use polygenic risk of AF?

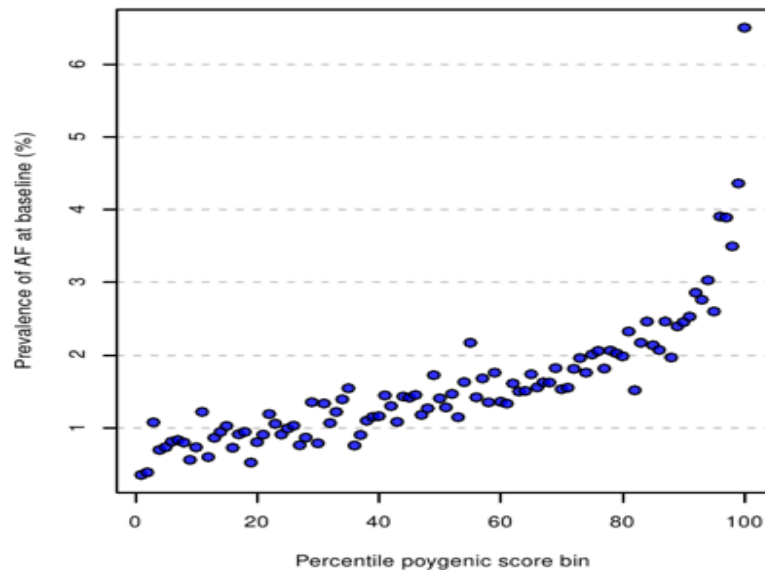


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Ongoing work to examine interaction between common and rare variation

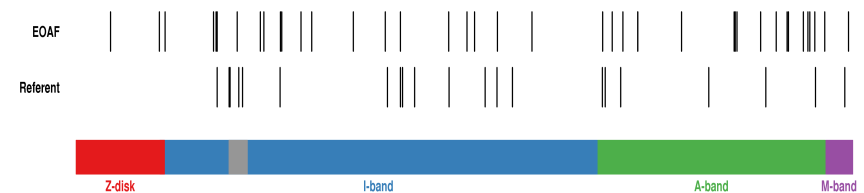


Polygenic risk



+

Rare variation



Conclusions



- Identified >130 genetic loci for AF
- Titin LOF variants in early-onset AF
- AF PRS
 - Can identify high risk individuals
 - May refine cryptogenic stroke risk
 - Should be considered with clinical RFs
- Screening of AF is increasingly widespread

Our team

MGH

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Lubitz, Milan and Kathiresan labs

Broad Institute

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AFGen Consortium

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