

Polygenic epilepsies

September 13, 2020

Epilepsy Genetics Update 2020



Every life deserves world class care.

Costin Leu, PhD

Genomic Medicine Institute, Lerner Research Institute *Cleveland Clinic, Cleveland, Ohio, USA*

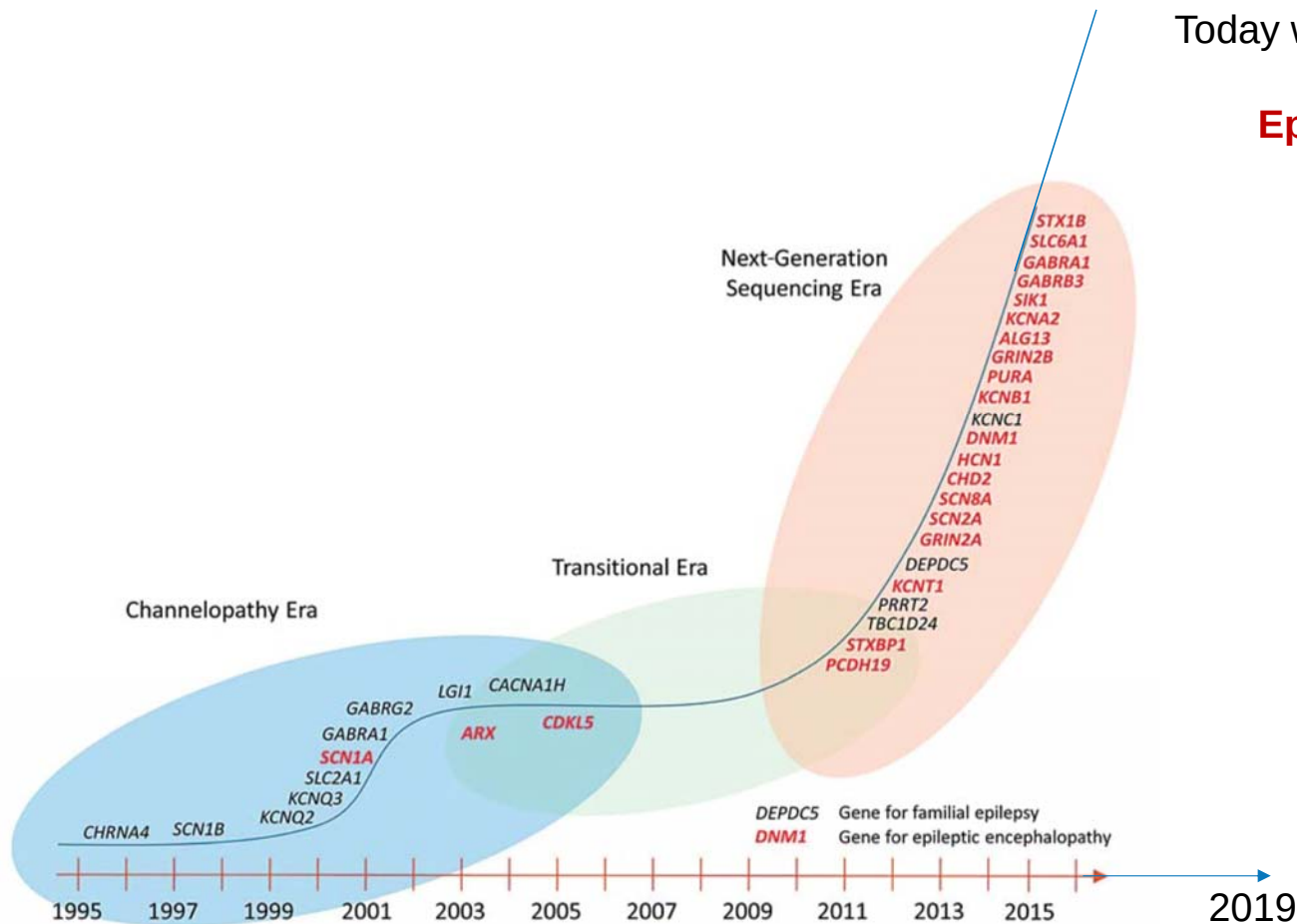
Institute for Neurology, *University College London, London, UK*

Stanley Center for Psychiatric Research, *Broad Institute of Harvard and M.I.T, Cambridge, USA*



leuc@ccf.org

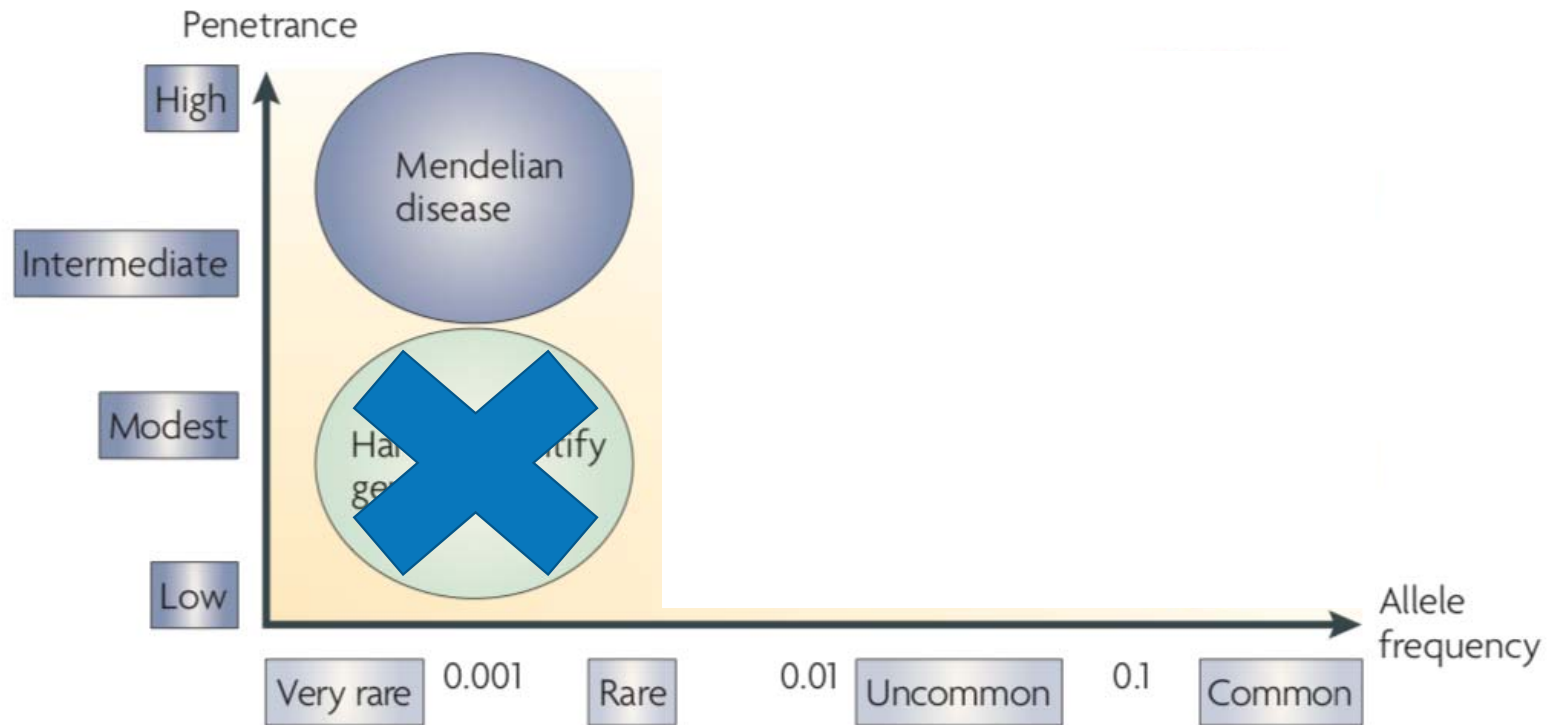
The number of known genes for rare (monogenic) epilepsies is growing



Today we know with high confidence about
30 – 100 genes associated with
Epilepsy – Neurodev. disorder with seizures

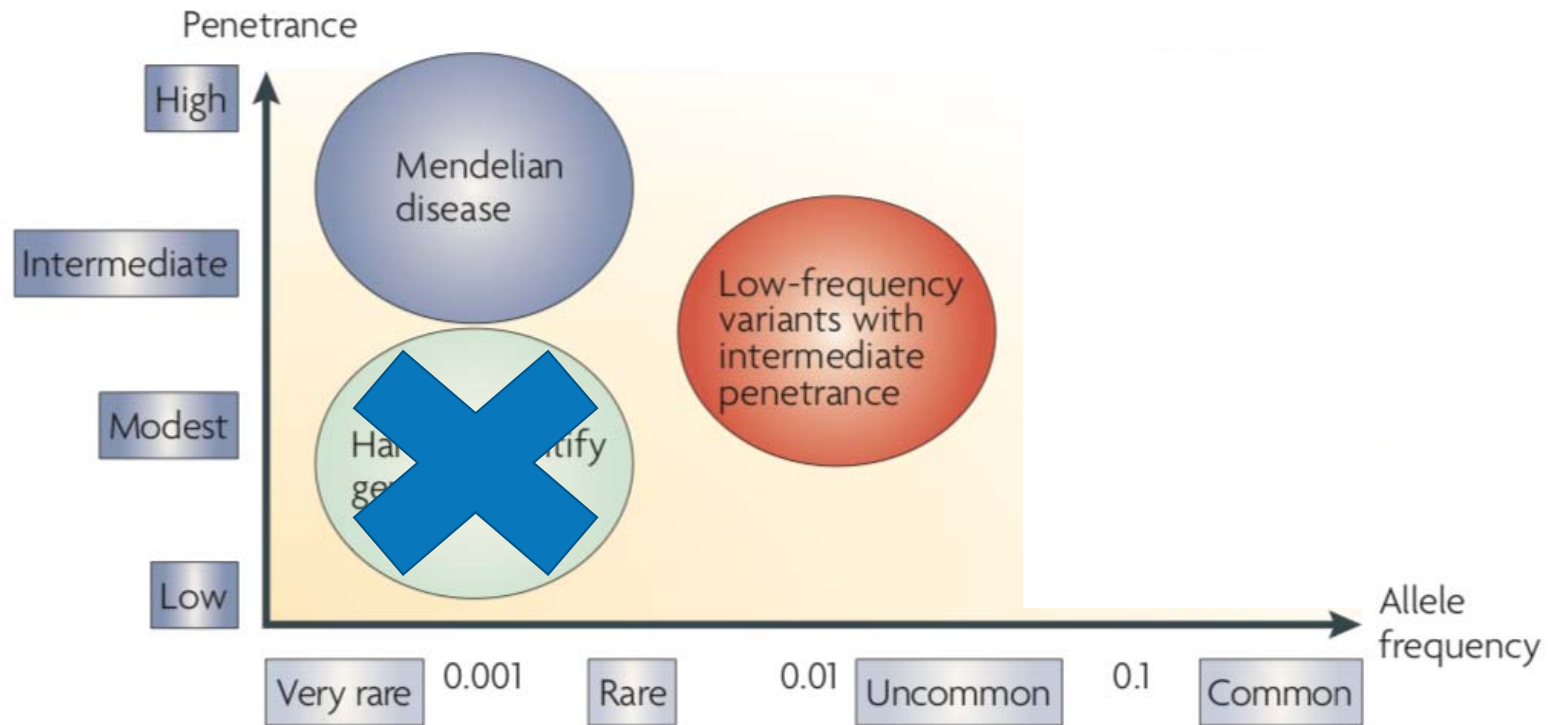
Modified from Helbig et al., 2016
PMID: 27781027

All types of causal variants



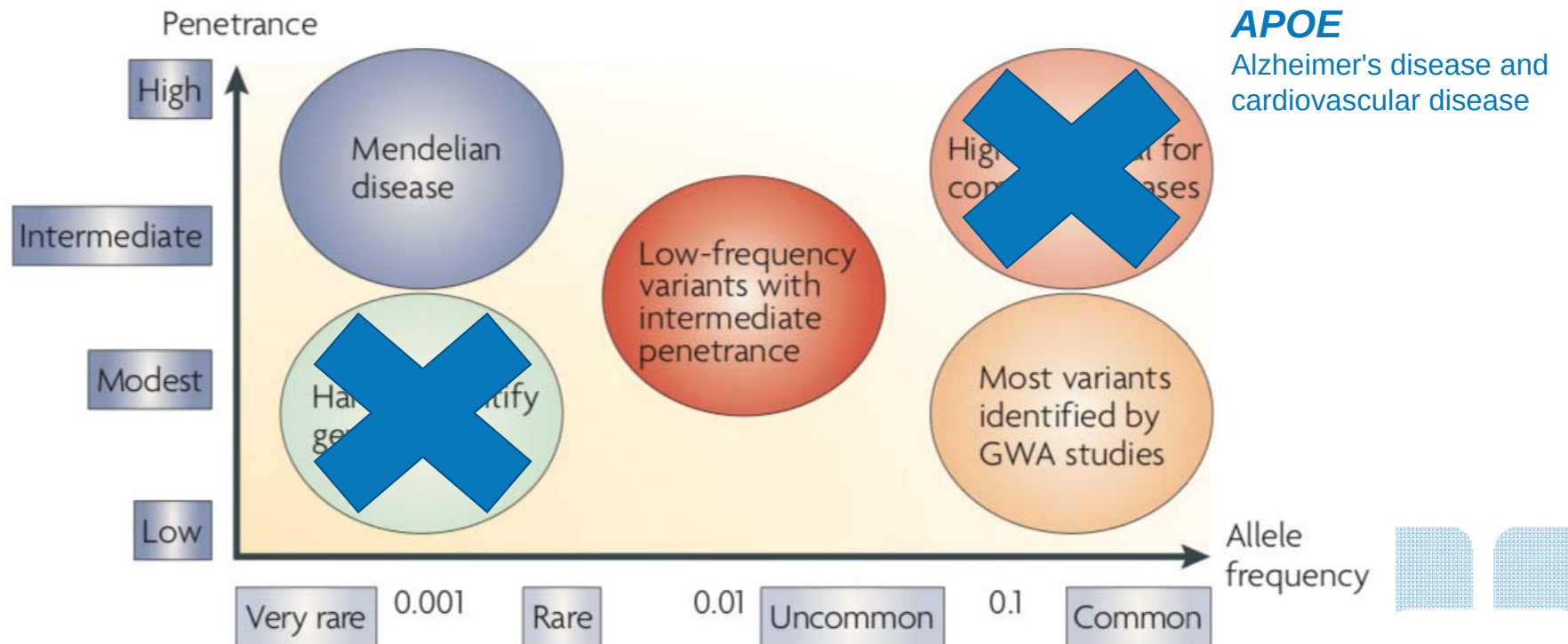
Modified from McCarthy et al., 2008
PMID: 18398418

All types of causal variants



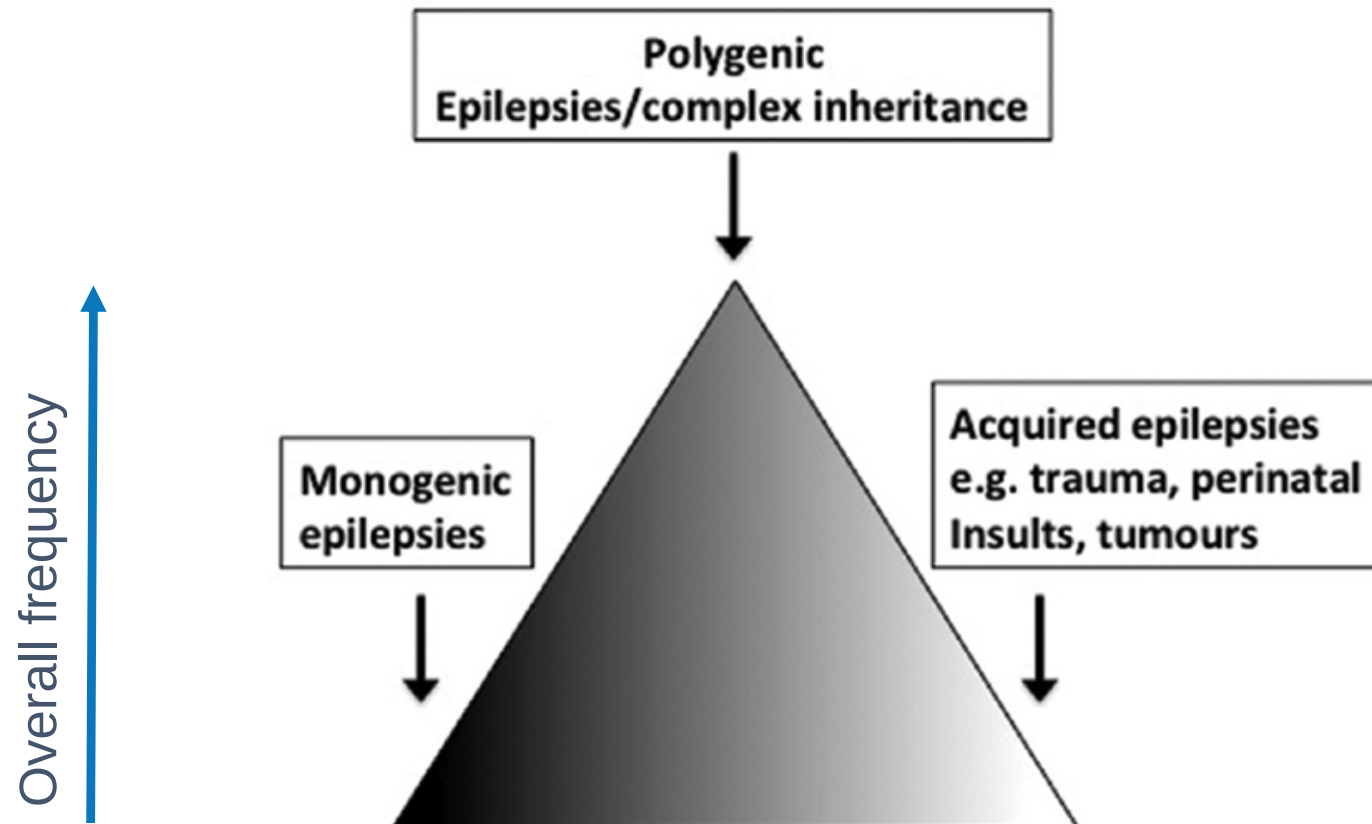
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All types of causal variants



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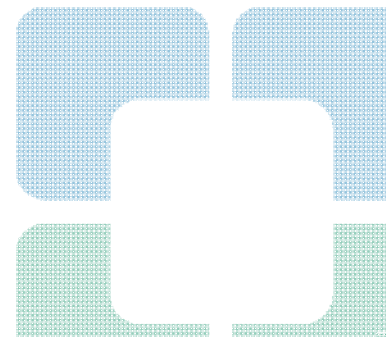
Monogenic vs. polygenic epilepsies



from Dhiman, 2017
PMID: 28615892

Genes known to cause Mendelian forms of epilepsy play only minor roles for common forms of epilepsy.

There is an unmet need for predictive genetic markers for the common epilepsies.



Polygenic risk scores

- The **utility of PRS as biomarkers** has been demonstrated virtually all complex traits and diseases, including neuropsychiatric disorders

Analysis | Published: 15 May 2017

Polygenic transmission disequilibrium confirms that common and rare variation act additively to create risk for autism spectrum disorders

Daniel J Weiner, Emilie M Wigdor, Stephan Ripke, Raymond K Walters, Jack A Kosmicki, Jakob Grove, Kaitlin F Samocha, Jacqueline I Goldstein, Aysu Okbay, Jonas Bybjerg-Grauholm, Thomas Werge, David M Anttila, ...

Neuron

Volume 98, Issue 4, 16 May 2018, Pages 743-753.e4

Letter | Published: 13 August 2018

Genome-wide polygenic scores for common diseases identify individuals with risk equivalent to monogenic mutations

Amit V. Khera, Mark Chaffin, Krishna G. Aragam, Mary E. Haas, Carolina Roselli, Seung Hoan Choi, Pradeep Natarajan, Eric S. Lander, Steven A. Lubitz, Patrick T. Ellinor & Sekar Kathiresan

THE PREPRINT SERVER FOR BIOLOGY

New Results

Genomic risk prediction of coronary artery disease in nearly 500,000 adults: implications for early screening and primary prevention

Michael Inouye, Gad Abraham, Christopher P. Nelson, Angela M. Wood, Michael J. Sweeting, Frank Dudbridge, Florence Y. Lai, Stephen Kaptoge, Marta Brozyna, Tingting Wang, Shu Ye, Thomas R Webb, Martin K. Rutter, Ioanna Tzoulaki, Riyaz S. Patel, Ruth J.F. Loos, Bernard Keavney, Harry Heringway, John Thompson, Hugh Watkins, Panos Deloukas, Emanuele Di Angelantonio, Adam S. Butterworth, John Danesh, Nilesh J. Samani, for The UK Biobank CardioMetabolic Consortium CHD Working Group

BRAIN

A JOURNAL OF NEUROLOGY

Polygenic burden in focal and generalized epilepsies

Costin Leu, Remi Stevelink, Alexander W Smith, Slavina B Goleva, Masahiro Kanai, Lisa Ferguson, Ciaran Campbell, Yoichiro Kamatani, Yukinori Okada, Sanjay M Sisodiya, Giampiero L Cavalleri, Bobby P C Koeleman, Holger Lerche, Lara Jehi, Lea K Davis, Imad M Najm, Aarno Palotie, Mark J Daly, Robyn M Busch, Epi25 Consortium, Dennis Lal

ILAE2 Genetic Generalized Epilepsy (GGE) GWAS – 3708 cases vs. 24218 controls

PRS

=

Number (Alleles)
* $\log(\text{OR}_{\text{SNP1}})$

+

Number (Alleles)
* $\log(\text{OR}_{\text{SNP2}})$

+

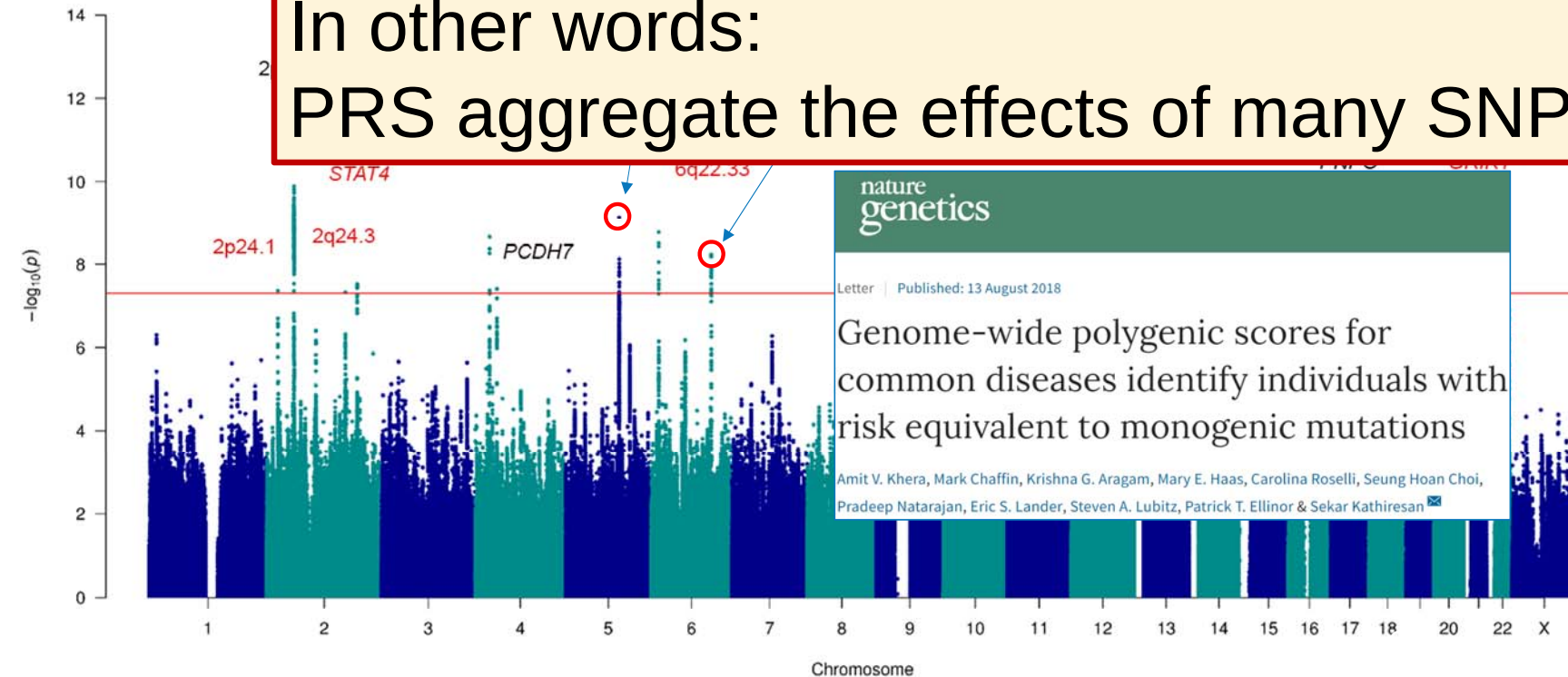
Number (Alleles)
* $\log(\text{OR}_{\text{SNP3}})$

=

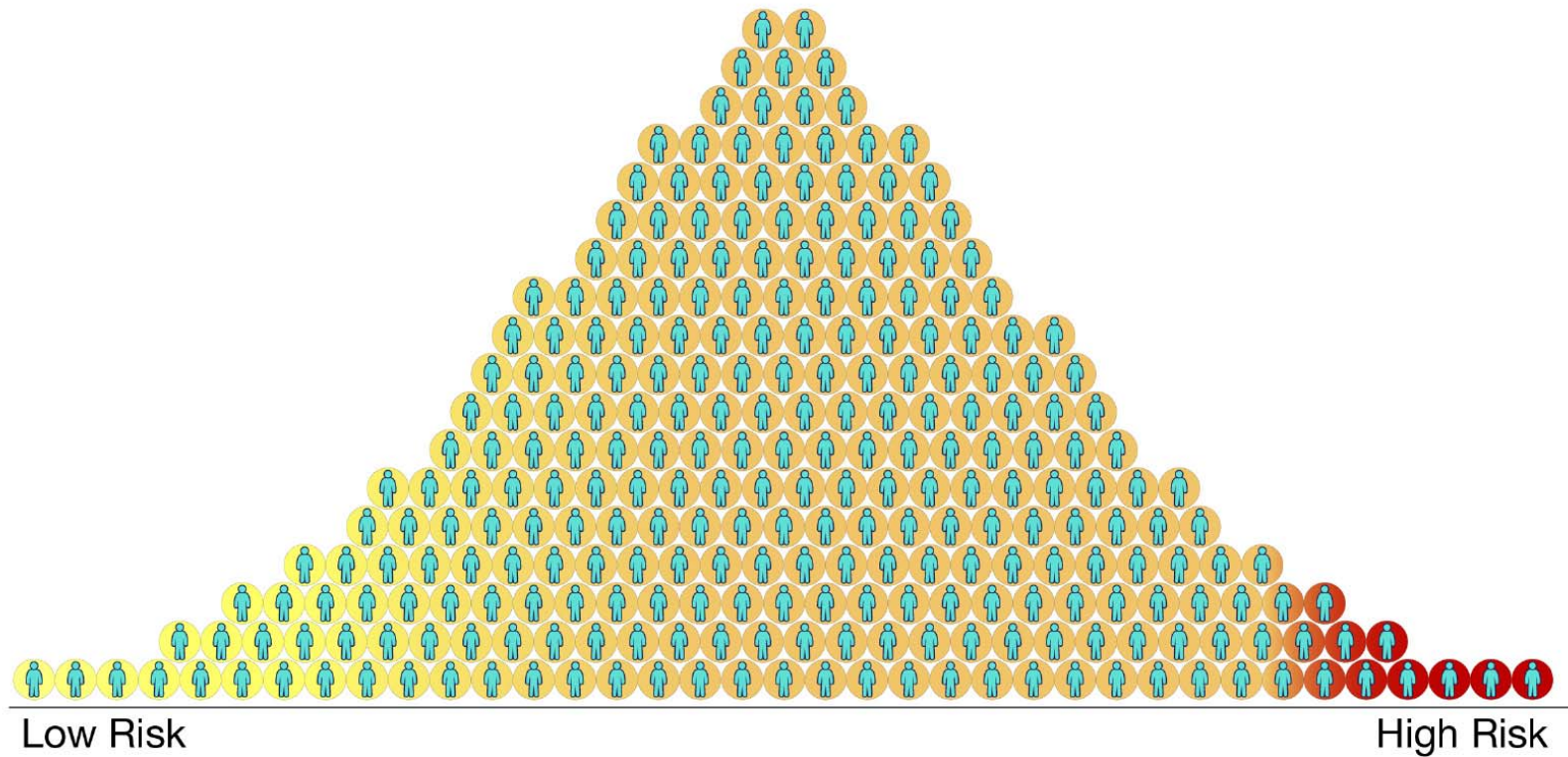
$\sum [\log(\text{OR}_i) * N_{\text{allele } i}] / \text{Number SNP}_i$

Per
person

In other words:
PRS aggregate the effects of many SNPs

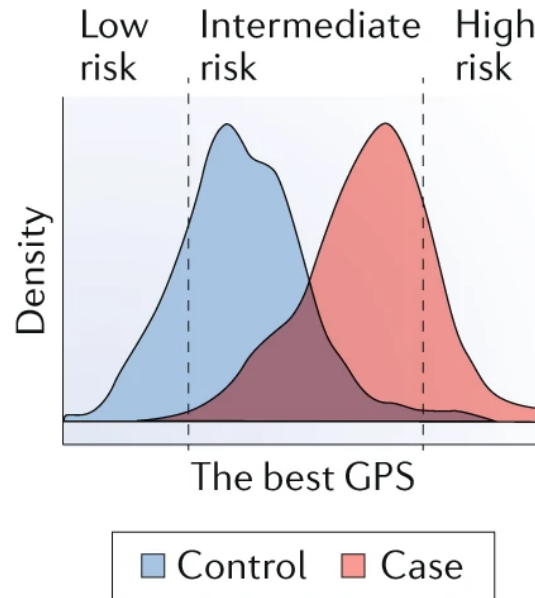


Polygenic risk scores are normally distributed



From <https://www.genome.gov>

Evaluation of the Polygenic Risk Scores



Polygenic score for
relative risk stratification

Modified from Liu and Kiryluk, 2018
PMID: 30279535

Can epilepsy PRS be used as
genetic biomarkers



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A JOURNAL OF NEUROLOGY

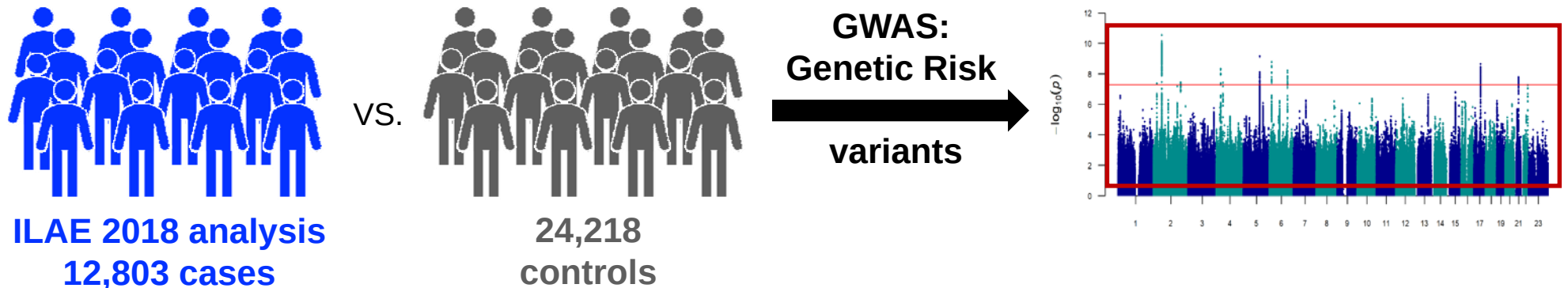
Polygenic burden in focal and generalized epilepsies



Costin Leu, Remi Stevelink, Alexander W Smith, Slavina B Goleva, Masahiro Kanai,
Lisa Ferguson, Ciaran Campbell, Yoichiro Kamatani, Yukinori Okada, Sanjay M Sisodiya,
Gianpiero L Cavalleri, Bobby P C Koeleman, Holger Lerche, Lara Jehi, Lea K Davis,
Imad M Najm, Aarno Palotie, Mark J Daly, Robyn M Busch, Epi25 Consortium ,
Dennis Lal ✉

PRS are derived from a GWAS and can only be generated in independent samples

1. Genome-wide association study (GWAS) for risk score generation



Epi25-EUR

♂ = 5,705

Cleveland-EUR

♂ = 620

EUR controls

♂ = 20,435

Epi25-FIN

♂ = 449

FINRISK

♂ = 1,559

UK biobank (UKB)

♂ = 459 ♀ = 383,197

Vanderbilt biobank (BioVU)

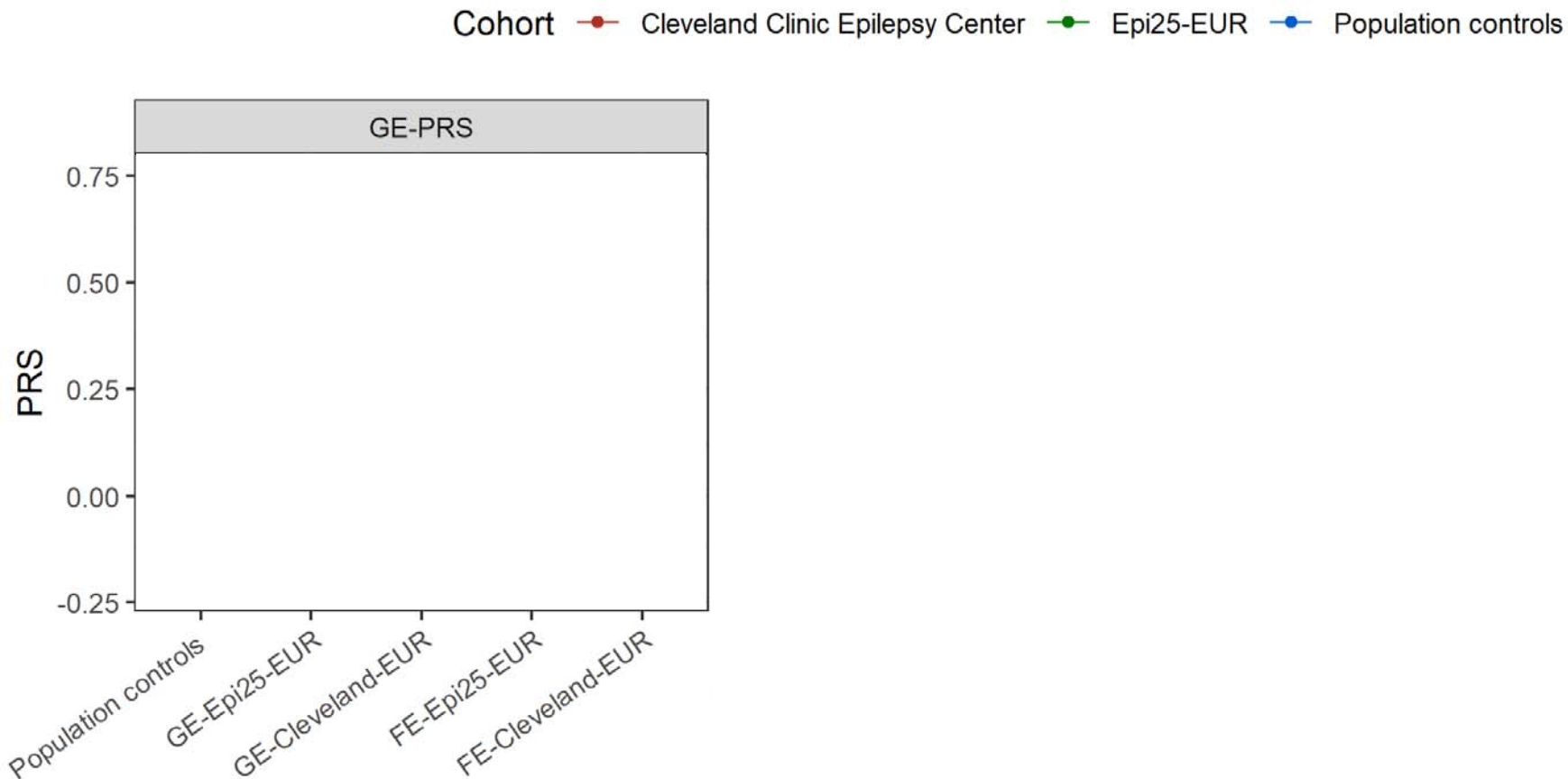
♂ = 829 ♀ = 48,670

BioBank Japan (BBJ)

♂ = 324 ♀ = 168,356

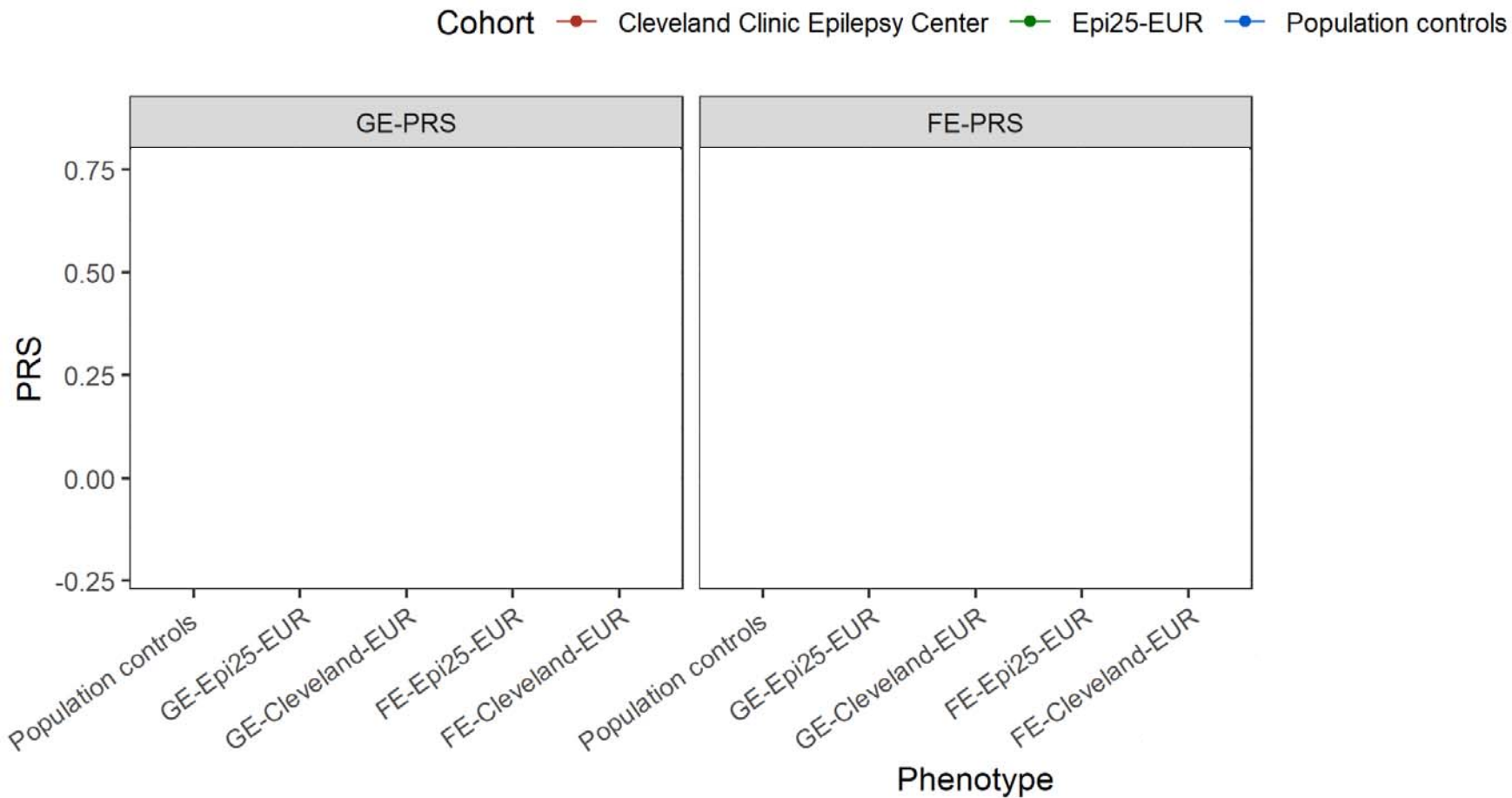
8,386 people with epilepsy and 622,217 population controls available across six cohorts

Polygenic risk scores for focal (FE) and generalized (GE) epilepsy



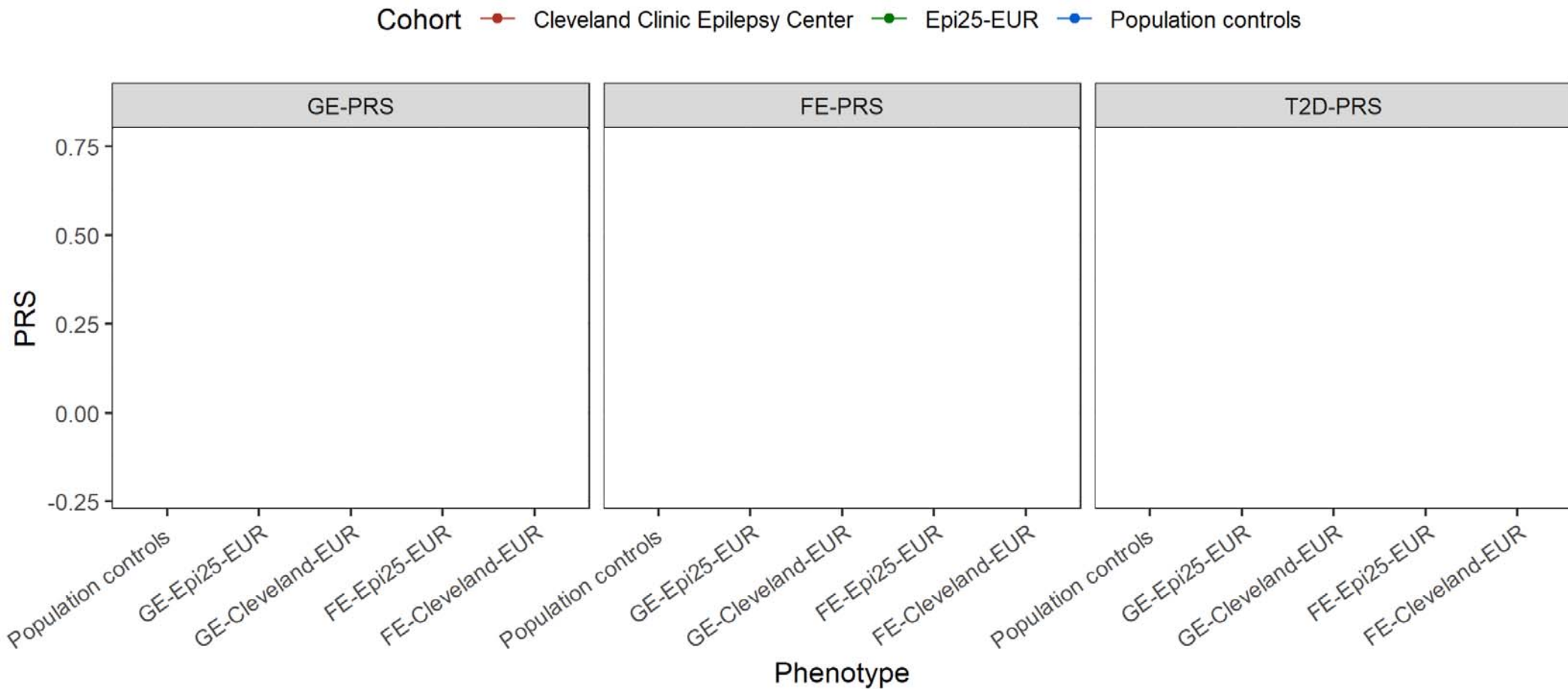
PRS = Polygenic risk score; GE = Generalized epilepsy; FE = Focal epilepsy; T2D = Type 2 diabetes; CC = Cleveland Clinic cohort, Epi25 = Consortium cohort

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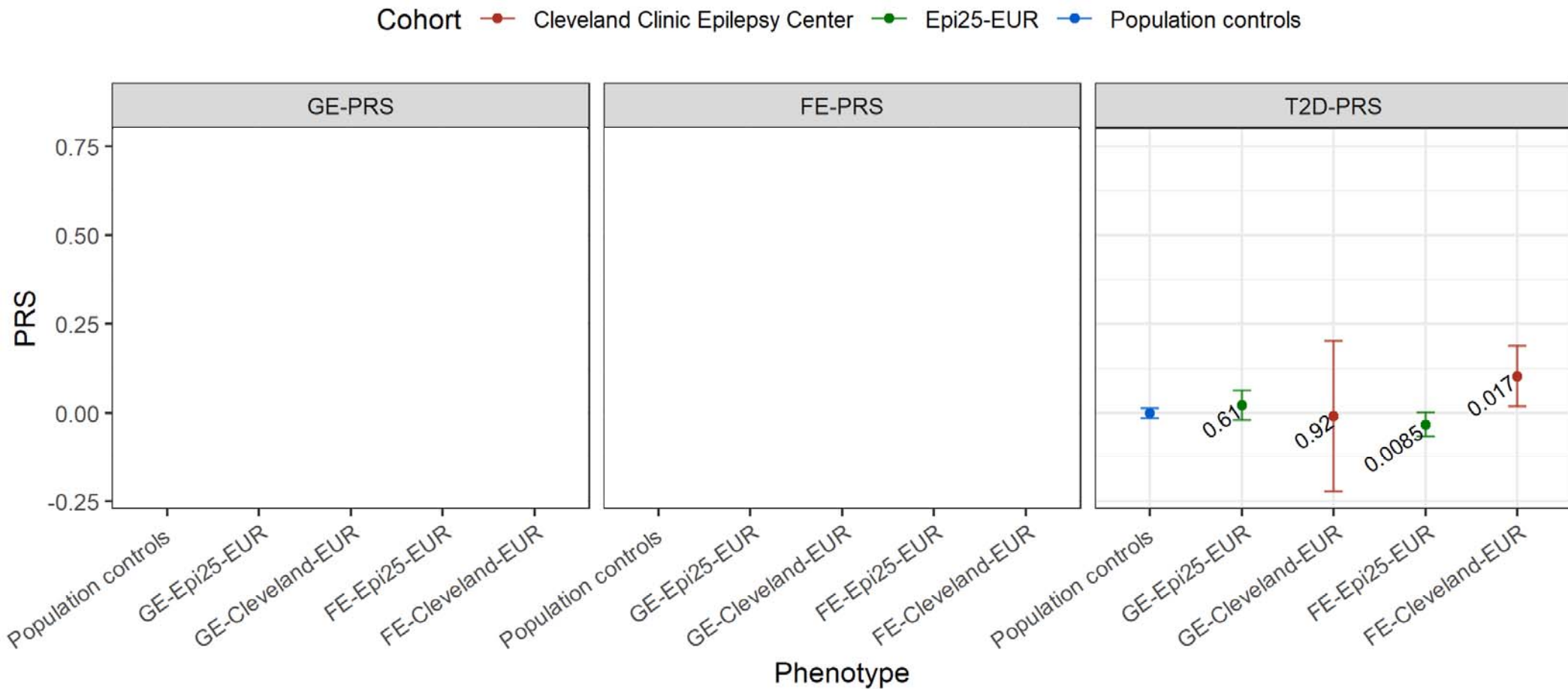
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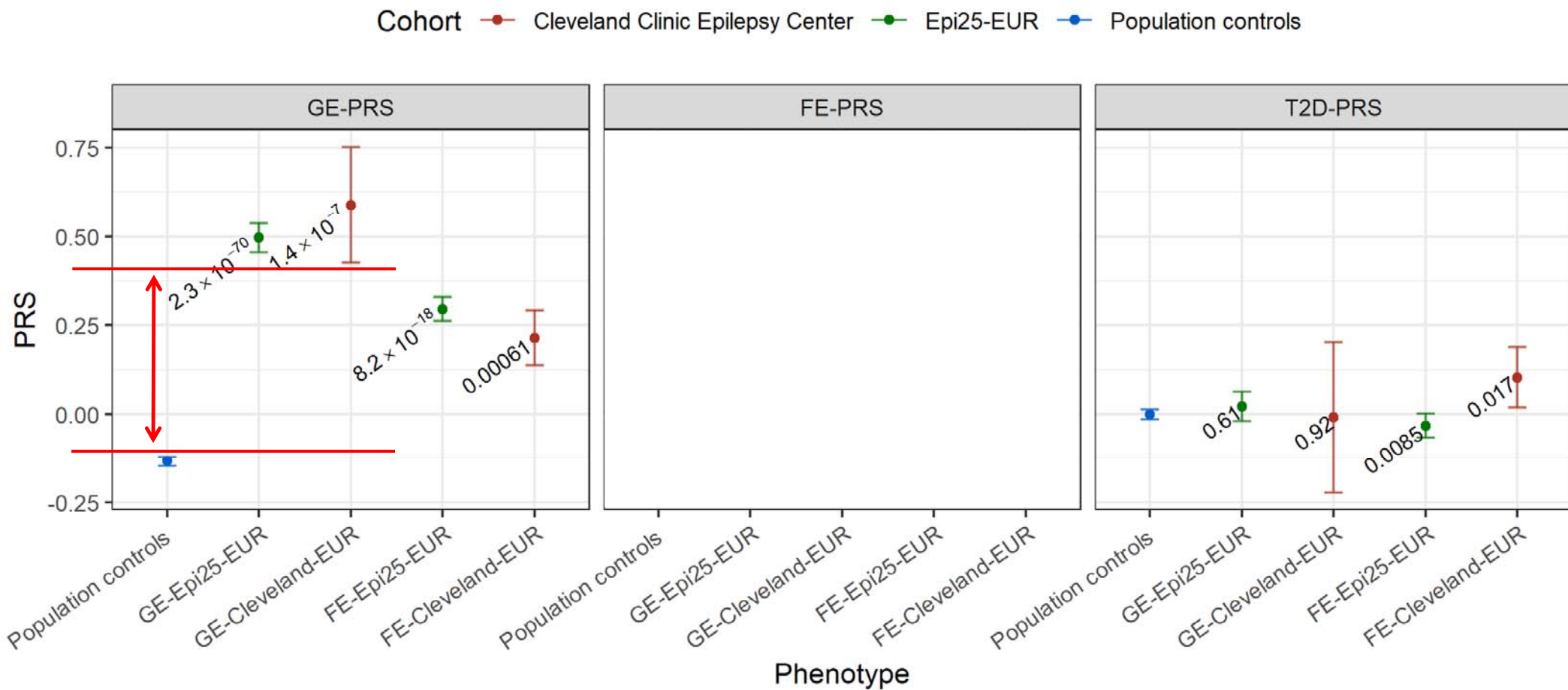
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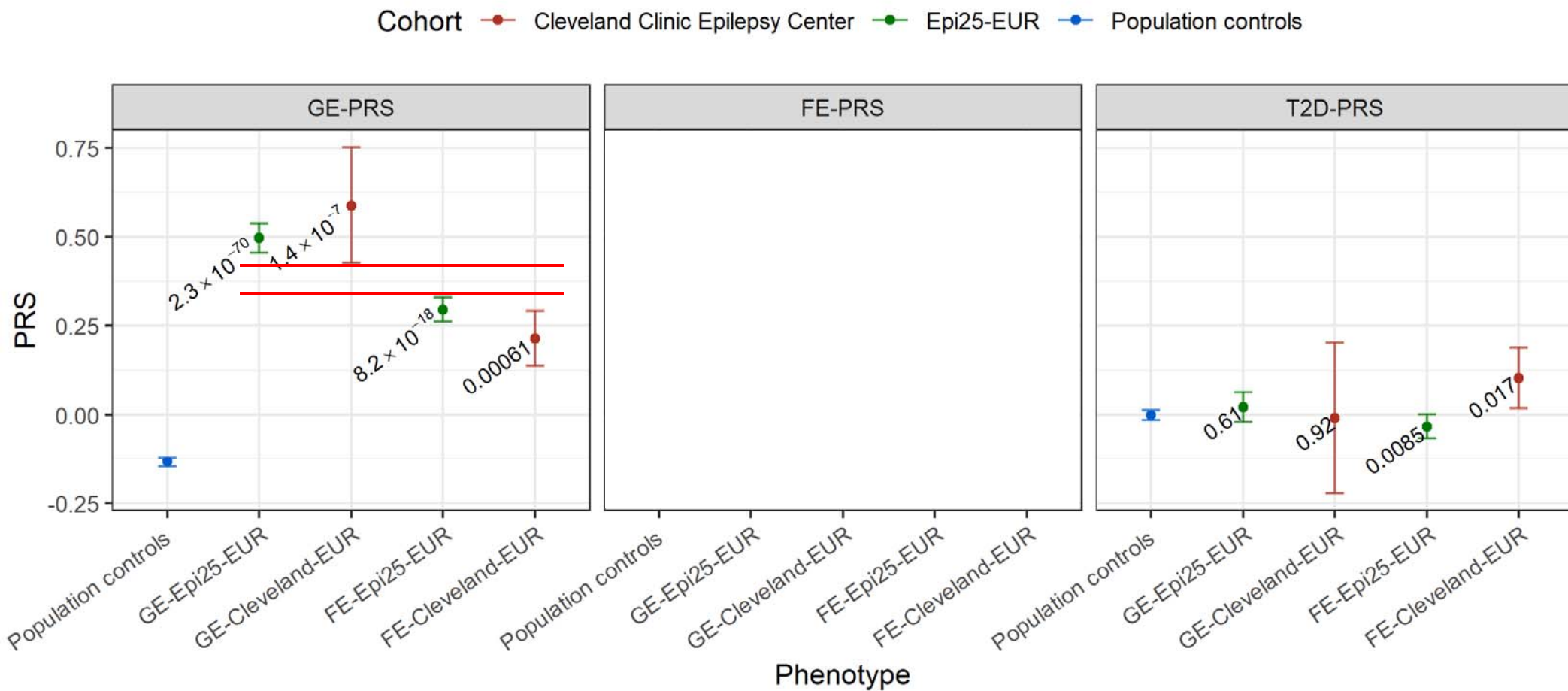
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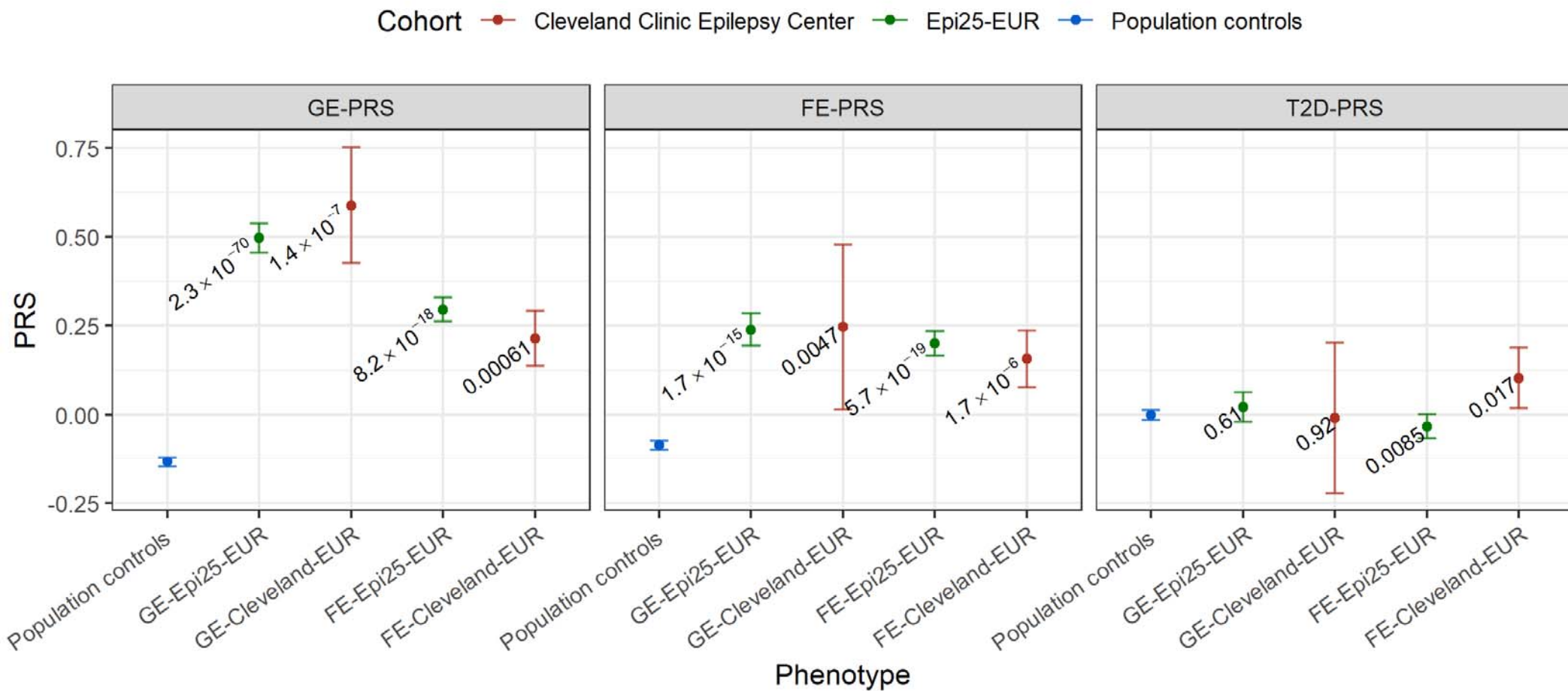
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How are the PRS distributed

- Few patients with very high PRS burden
- Slight shift toward higher PRS burden in all patients



BRAIN

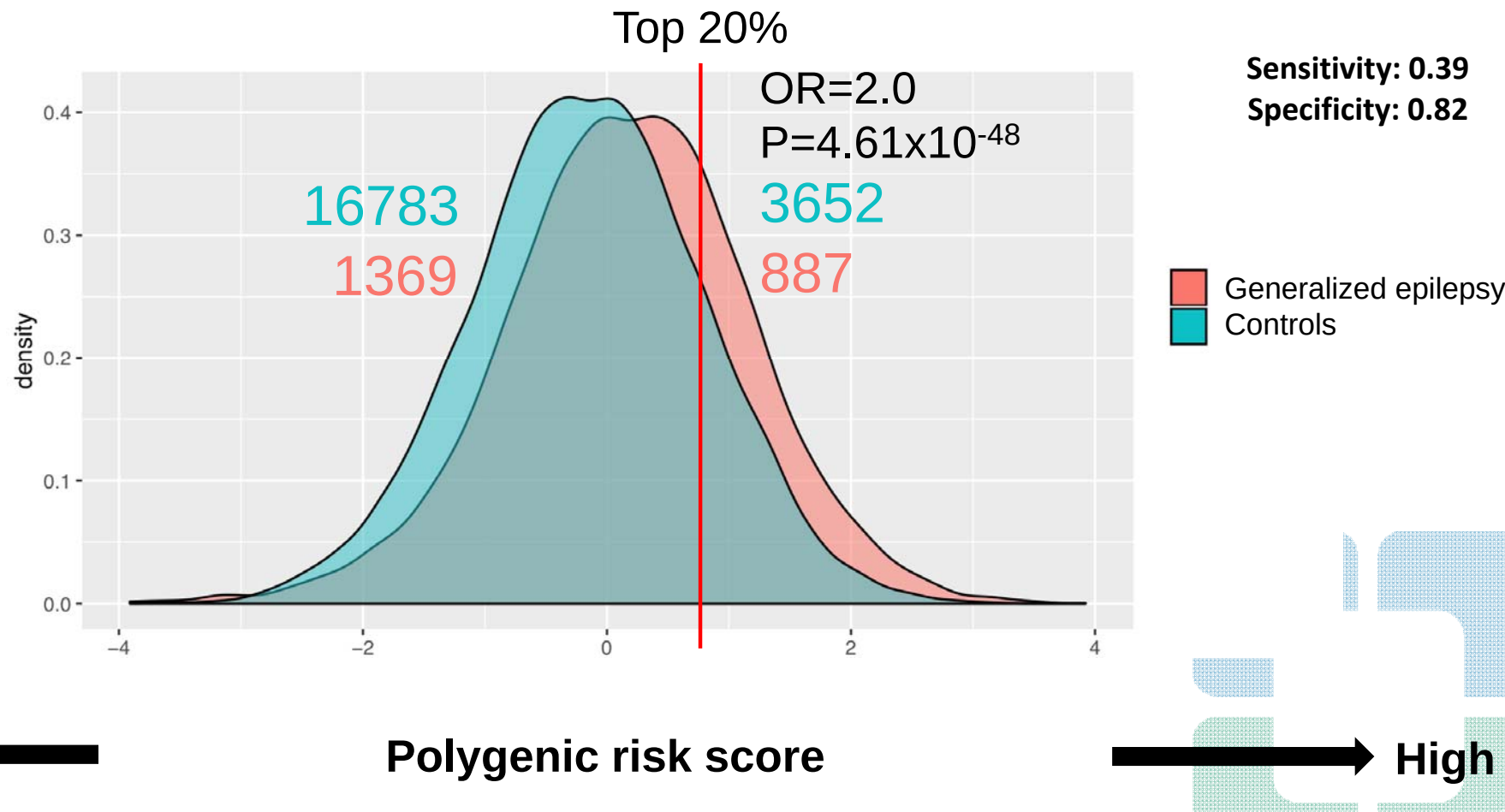
A JOURNAL OF NEUROLOGY

Polygenic burden in focal and generalized epilepsies

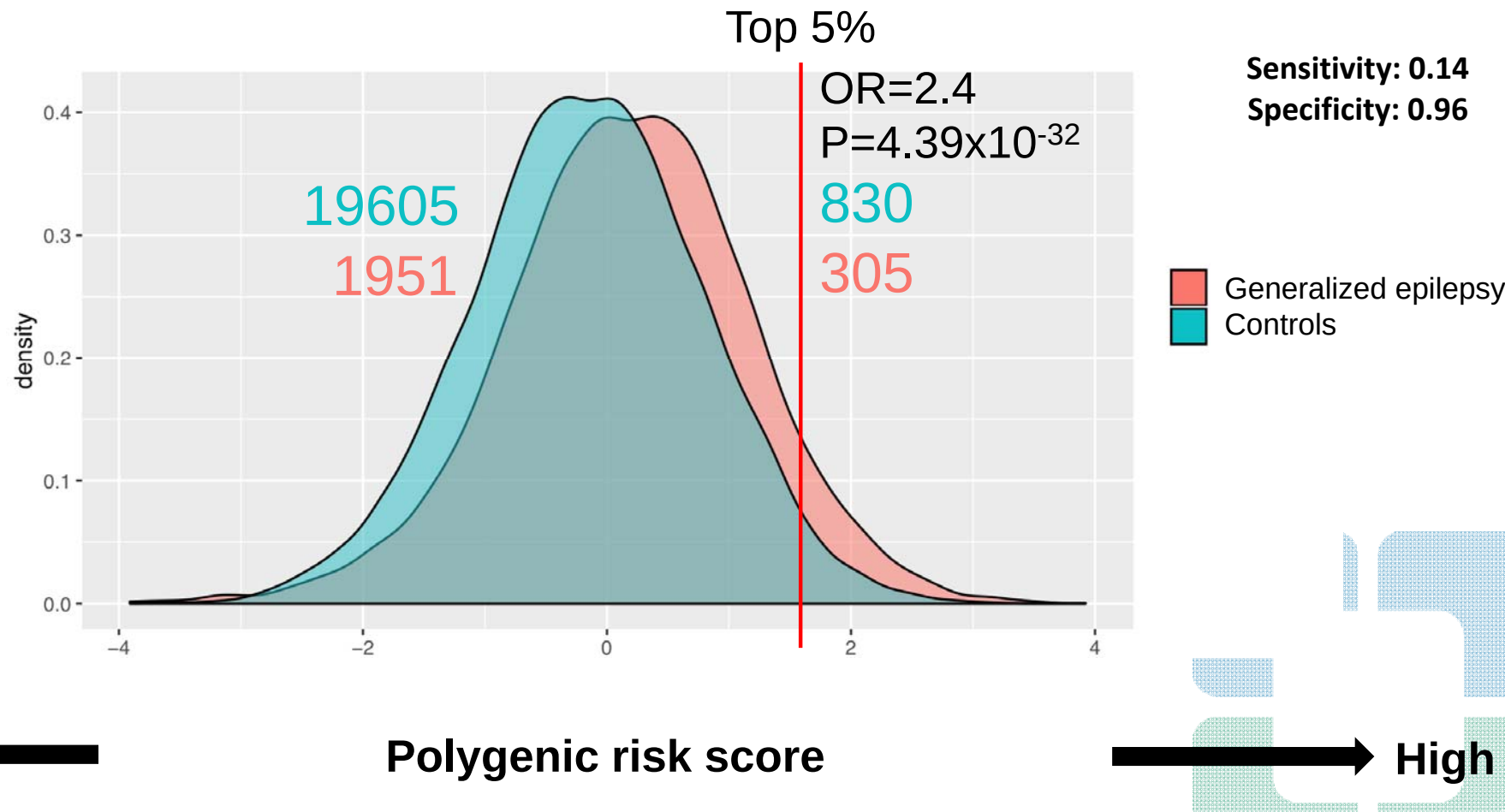


Costin Leu, Remi Stevelink, Alexander W Smith, Slavina B Goleva, Masahiro Kanai, Lisa Ferguson, Ciaran Campbell, Yoichiro Kamatani, Yukinori Okada, Sanjay M Sisodiya, Gianpiero L Cavalleri, Bobby P C Koeleman, Holger Lerche, Lara Jehi, Lea K Davis, Imad M Najm, Aarno Palotie, Mark J Daly, Robyn M Busch, Epi25 Consortium, Dennis Lal ✉

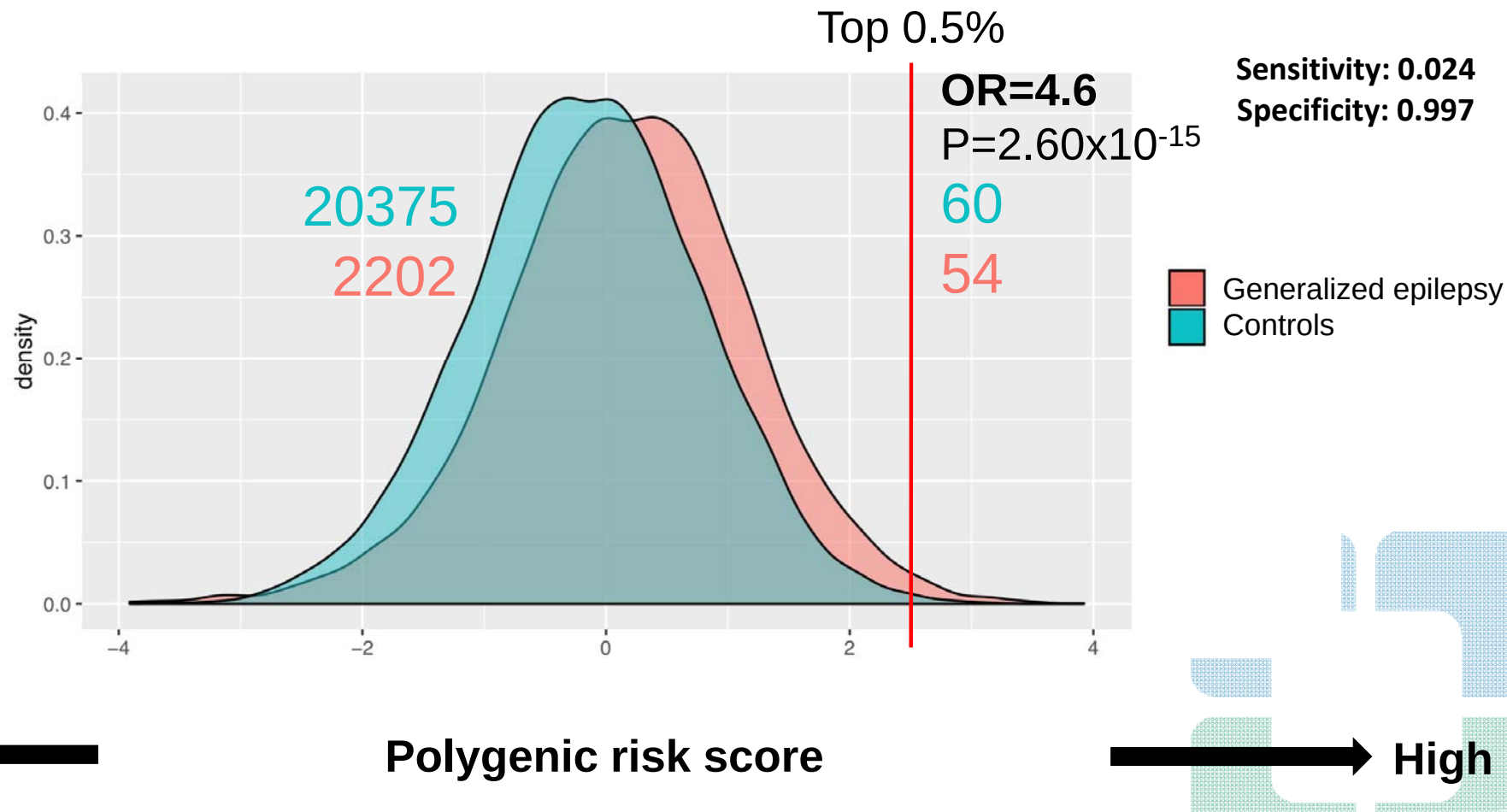
Individuals with GE are enriched in the extreme tail of the PRS distribution



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Polygenic risk score in large datasets
To learn more about genetics of complex disorders



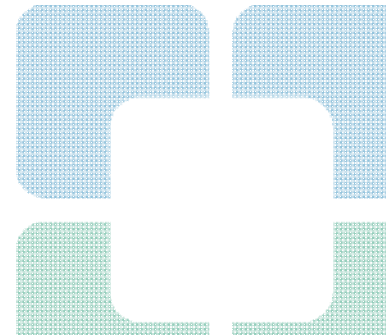
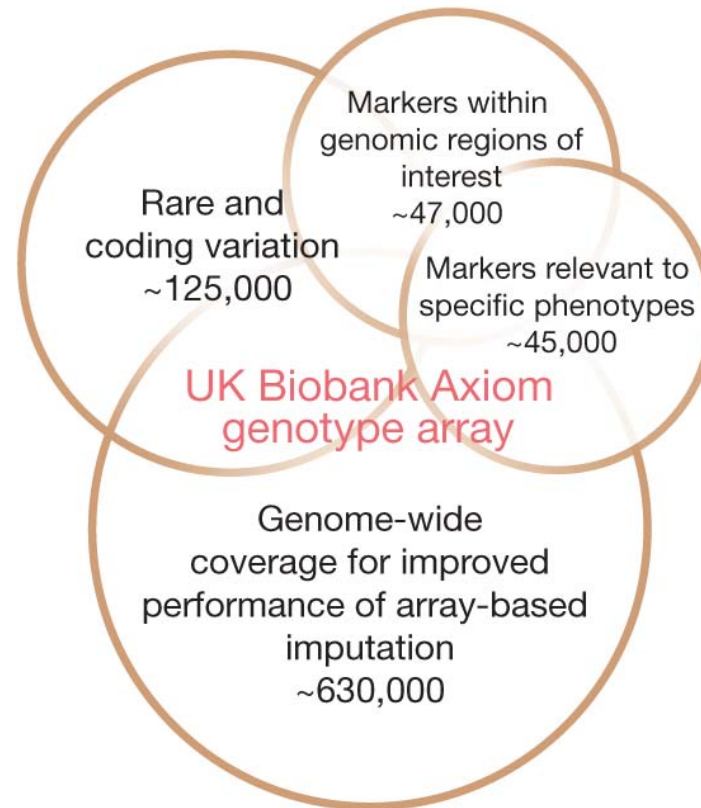
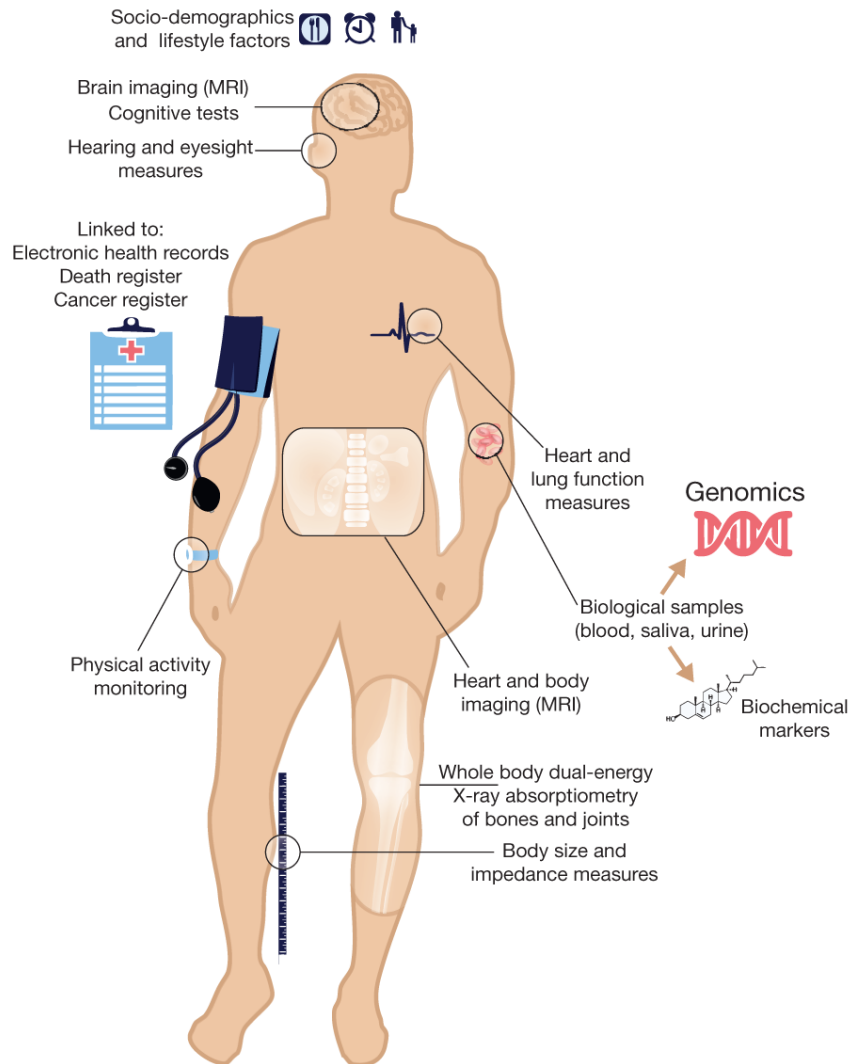
PLOS ONE

Pleiotropy of polygenic factors associated with focal and generalized epilepsy in the general population

Costin Leu , Tom G. Richardson, Tobias Kaufmann, Dennis van der Meer, Ole A. Andreassen, Lars T. Westlye, Robyn M. Busch, George Davey Smith, Dennis Lal 

Published: April 28, 2020 • <https://doi.org/10.1371/journal.pone.0232292>

UK Biobank



PRS brain-focused PheWAS in the UKB

PRS for generalized
and focal epilepsy

in

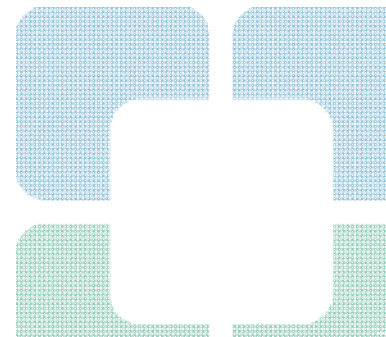


UK biobank (UKB)
= 334,398 without epilepsy

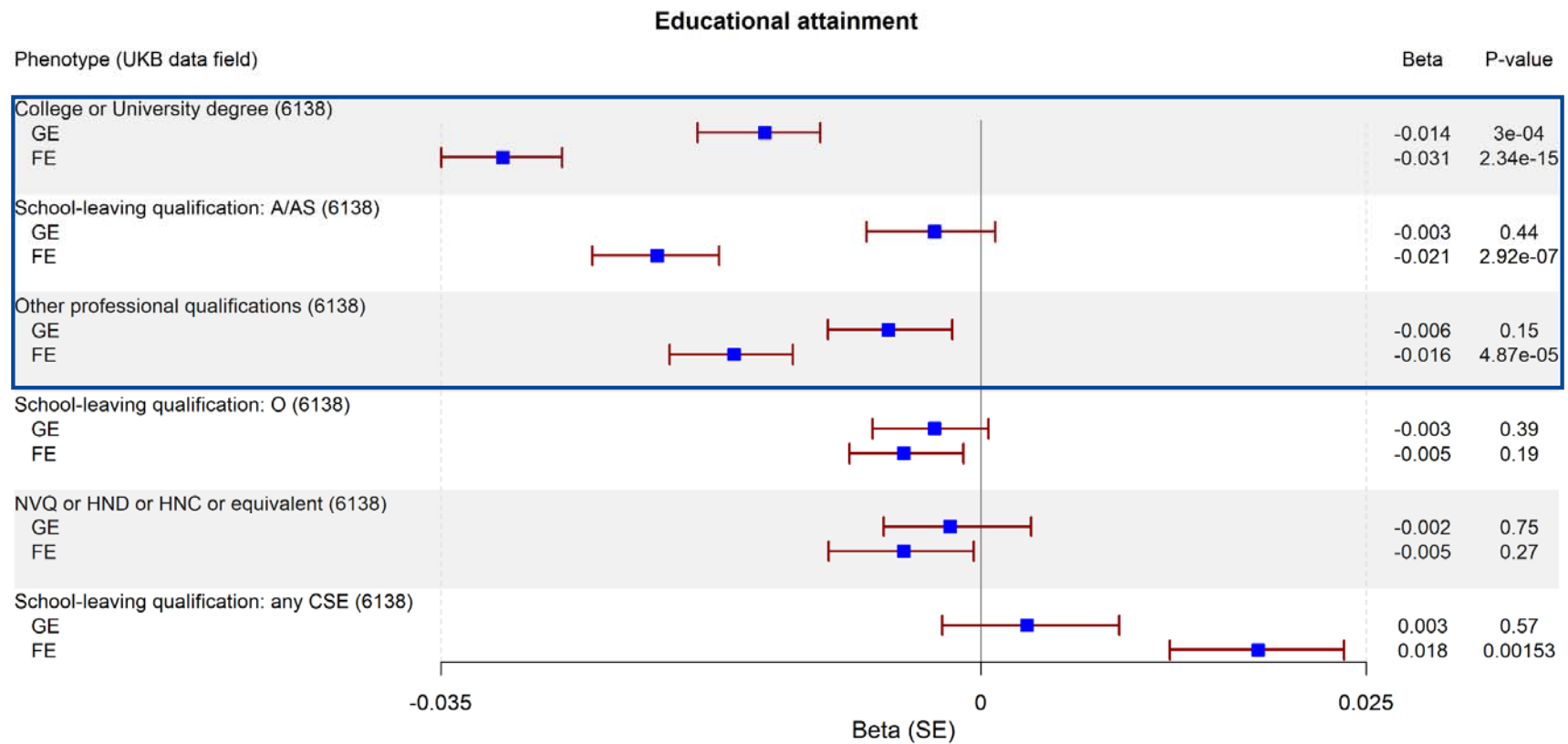
with

42 conditions, categorized six groups:

1. Educational attainment
2. Neuroticism
3. Mood [affective] disorders
4. Substance use/abuse/dependence
5. Diseases of the nervous system
6. Nonpsychotic mental disorders

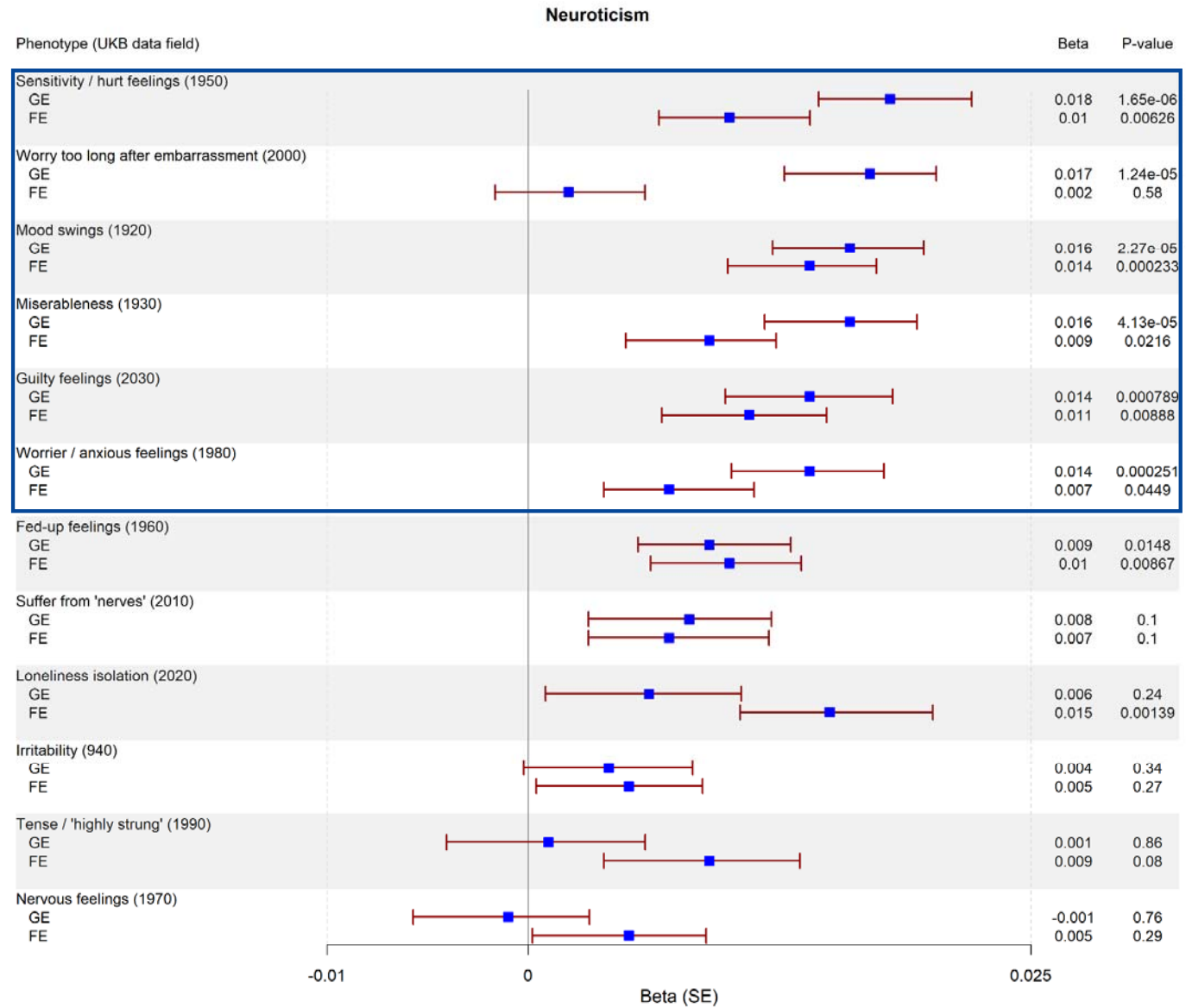


Educational attainment



Significant association if $P < 5.95 \times 10^{-4}$

Neuroticism

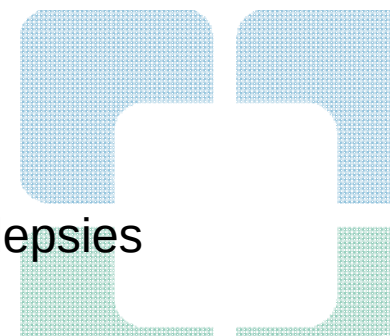


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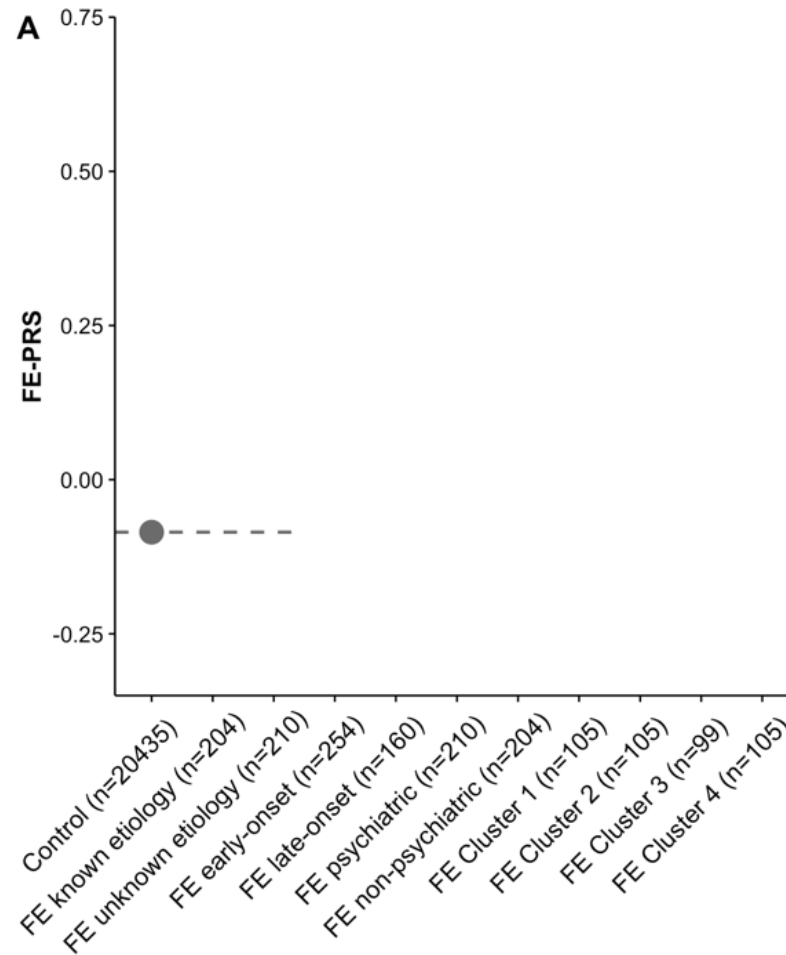
Polygenic risk score to evaluate
clustering algorithms for improved patient classification



Polygenic risk heterogeneity among focal epilepsies
Gramm*, Leu* et al., 2020 (accepted)



Cluster analysis can improve classifications



A Study cohort



Cleveland Clinic

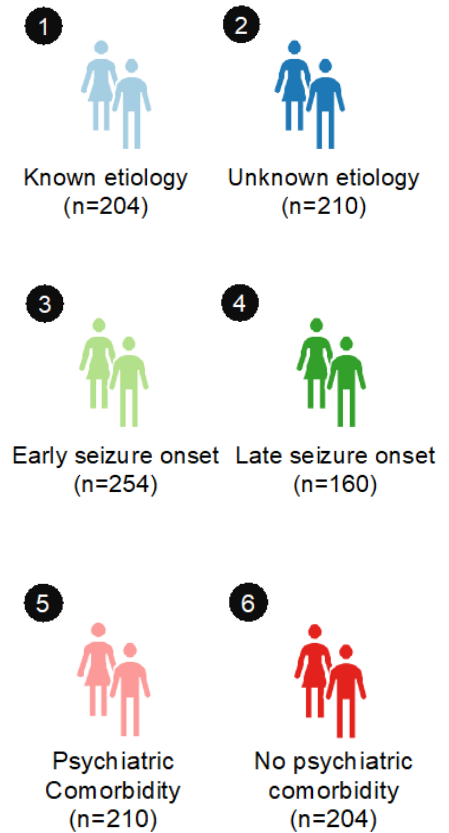
414 individuals with focal epilepsy (FE)

- Phenotype data
- Genotype data
- European ancestry



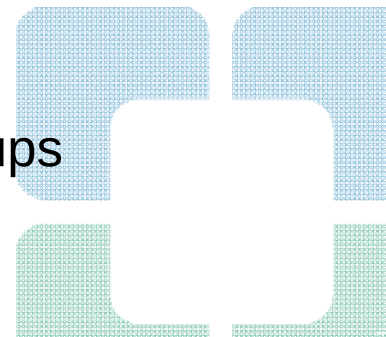
20,435 population controls

- Genotype data
- European ancestry



Summary

- Most epilepsy cases are not monogenic
- Polygenic factors are shown for other diseases to confer risk equivalent to monogenic risk variants
- Polygenic risk factors also play a role in epilepsy and can be measured
- Polygenic risk factors for epilepsy are associated with neurological and psychiatric traits in healthy individuals
- Polygenic risk factors can be used to test and potentially improve the genetic homogeneity within phenotype subgroups



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