Genetic Analysis of Disease in Diverse Individuals
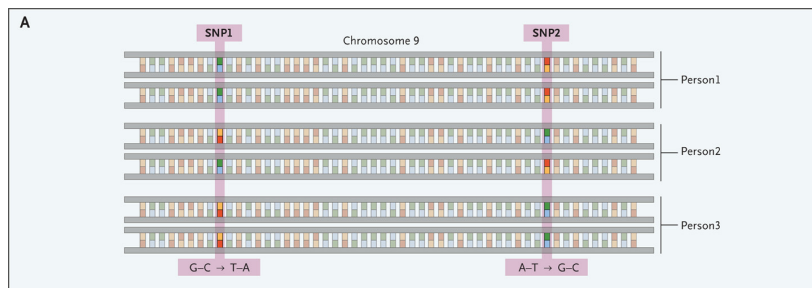
LA's Best

6/16/2025

Nicholas Mancuso, PhD

Center for Genetic Epidemiology

Keck School of Medicine, USC
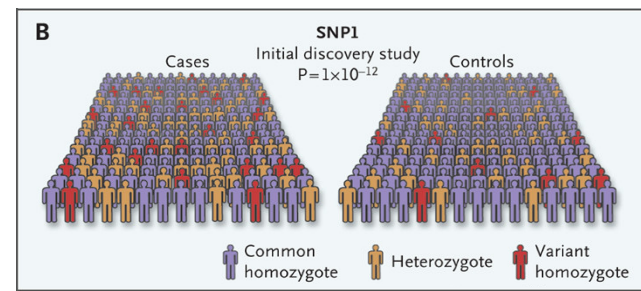
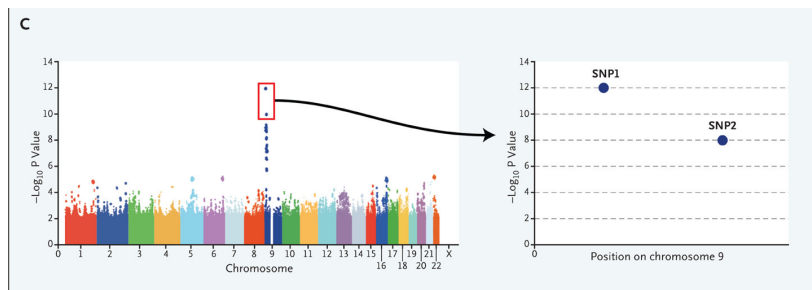Keck School of
Medicine of USC

Genome-wide association studies

Quantify common genetic variation (SNPs)

Large cohorts and simple models

Test for association between SNP and disease

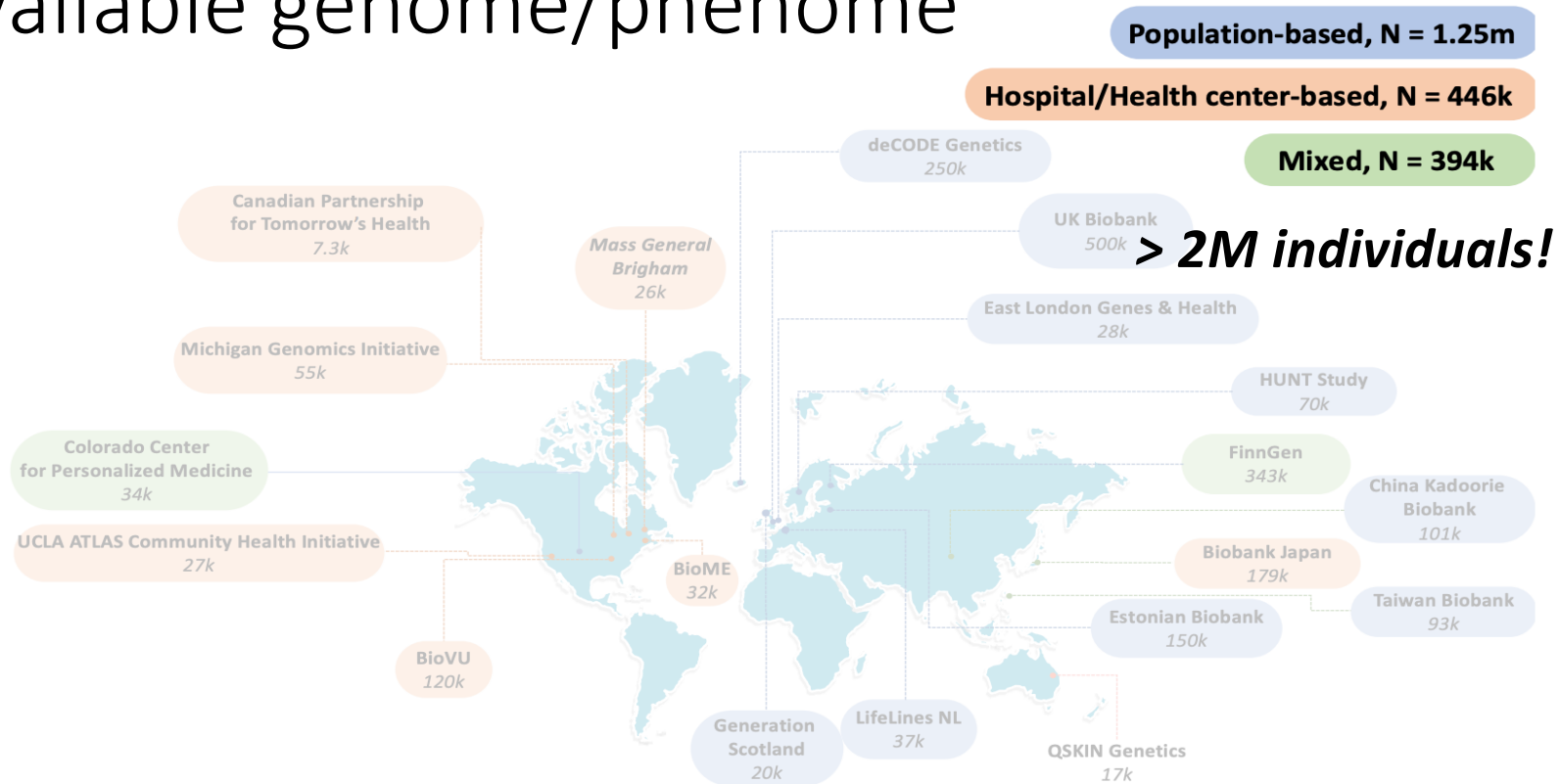Manolio TA. N Engl J Med 2010

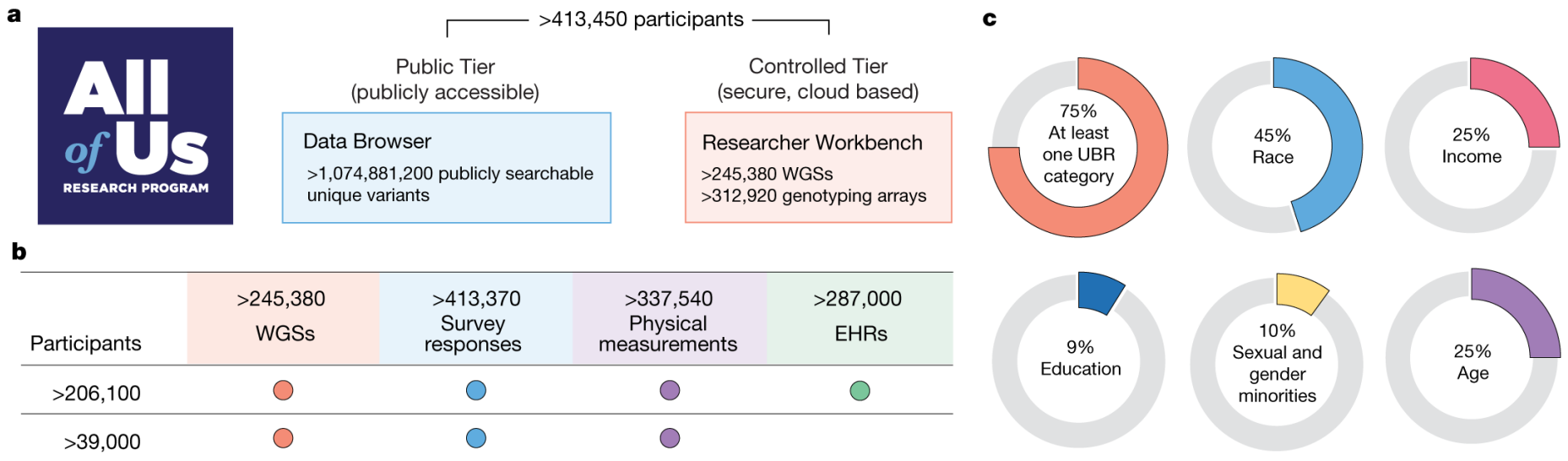# GWAS does not provide *causal mechanisms*

- GWAS provides **regions** associated with disease risk

- What are the **mechanisms** driving disease risk?

- Most associations are **non-coding**
  - SNPs with **regulatory** function are strong candidates

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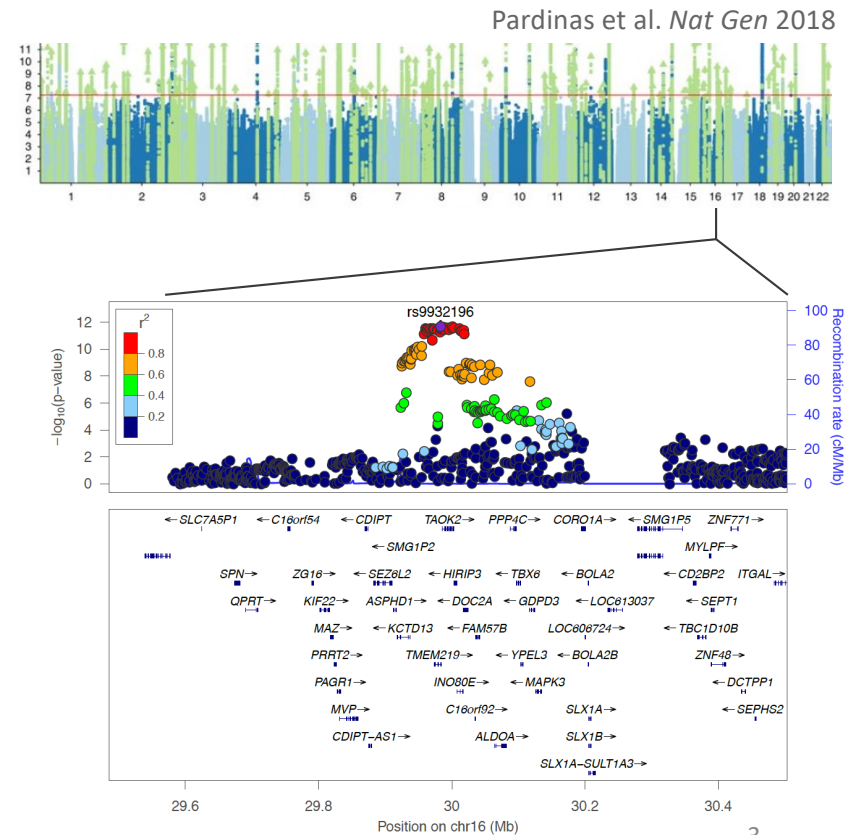
Global biobanks reflect *massive* scale of available genome/phenome

Population-based, N = 1.25m

Hospital/Health center-based, N = 446k

Mixed, N = 394k

> 2M individuals!

deCODE Genetics
250k

Canadian Partnership
for Tomorrow's Health
7.3k

Mass General
Brigham
26k

UK Biobank
500k

East London Genes & Health
28k

Michigan Genomics Initiative
55k

HUNT Study
70k

Colorado Center
for Personalized Medicine
34k

FinnGen
343k

China Kadoorie
Biobank
101k

UCLA ATLAS Community Health Initiative
27k

Biobank Japan
179k

BioME
32k

Taiwan Biobank
93k

Estonian Biobank
150k

BioVU
120k

Generation
Scotland
20k

LifeLines NL
37k

QSKIN Genetics
17k

All of US Biobank

LA's Best Project: All of Us Analysis

- Project Aims:
  - Learn to navigate genetic + phenotypic data on AOU portal
  - Select phenotype and construct analysis group (non EHR related!)
  - Visualize diverse ancestry components using PCA
  - Perform GWAS

- Deliverables
  - Small presentation/writeup on any potential genetic findings