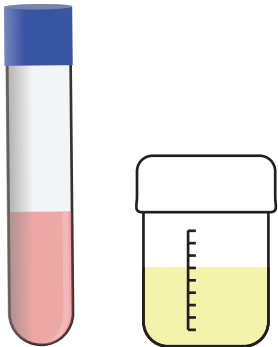


STUDY COHORT

UK Biobank

363,228 individuals
35 serum and urine labs
Genome array, imputation,
HLA, and Copy number variants



ASSESSING GENETIC ASSOCIATION

A GWAS

5792 independent loci
28 rare protein-truncating variants
192 rare protein-altering variants
31 HLA allelotypes
10 CNVs
28 aggregate rare CNV loci

B Heritability

Up to 57% heritability explained

C PheWAS

61 associations across 28 phenotypes for 34 LD independent coding variants

CAUSAL INFERENCE AND PREDICTION

A Mendelian randomization

51 causal relationships across 14 diseases & 3 quantitative traits

B PRS & PheWAS

70/10/20% training/validation/test
PRS with R^2 up to 0.51
median up to 0.24
139 associations $p < 10^{-4}$

C multi-PRS

Improves prediction of complex disease; renal failure, cirrhosis, gout, t2d, and heart failure