

Supplementary Datasets

Supplementary Table 1: Details of all phenotypes studied in this dataset.

Supplementary Table 2: Most significant genotype-phenotype associations from variant-level exome-wide association study.

Supplementary Table 4: Significant missense variants from the binary trait ExWAS annotated with known GWAS associations within 50 kilobases.

Supplementary Table 5: Significant PTVs from the binary trait ExWAS annotated with known GWAS associations within 50 kilobases.

Supplementary Table 7: Lambda distributions from SAIGE, REGENIE, and Fisher's exact test comparisons

Supplementary Table 8: Collapsing analysis top hits

Supplementary Table 10: OMIM status of significant binary collapsing analysis associations

Supplementary Table 12: Oncology-related collapsing analysis associations

Supplementary Table 14: Non-intersecting PTV signals between ExWAS and collapsing analyses

Supplementary Table 15: Binary trait collapsing analyses in non-European populations

Supplementary Table 16: Pan-ancestry binary collapsing analysis

Supplementary Table 17: Pan-ancestry quantitative collapsing analysis

Supplementary Table 19: ExWAS dominant model n-of-1 permutation results

Supplementary Table 20: Collapsing analysis null distribution

Supplementary Table 22: Lambda distributions from collapsing analyses

Supplementary Table 24: Gene informativeness

Supplementary Table 26: Variant-level cautions

Supplementary Table 28: Cross-study comparison of 50K UKB exomes

Supplementary Table 29: Correlated Chapter XI phenotypes