

Supplementary Information for

“Phenome-wide Heritability Analysis of the UK Biobank”

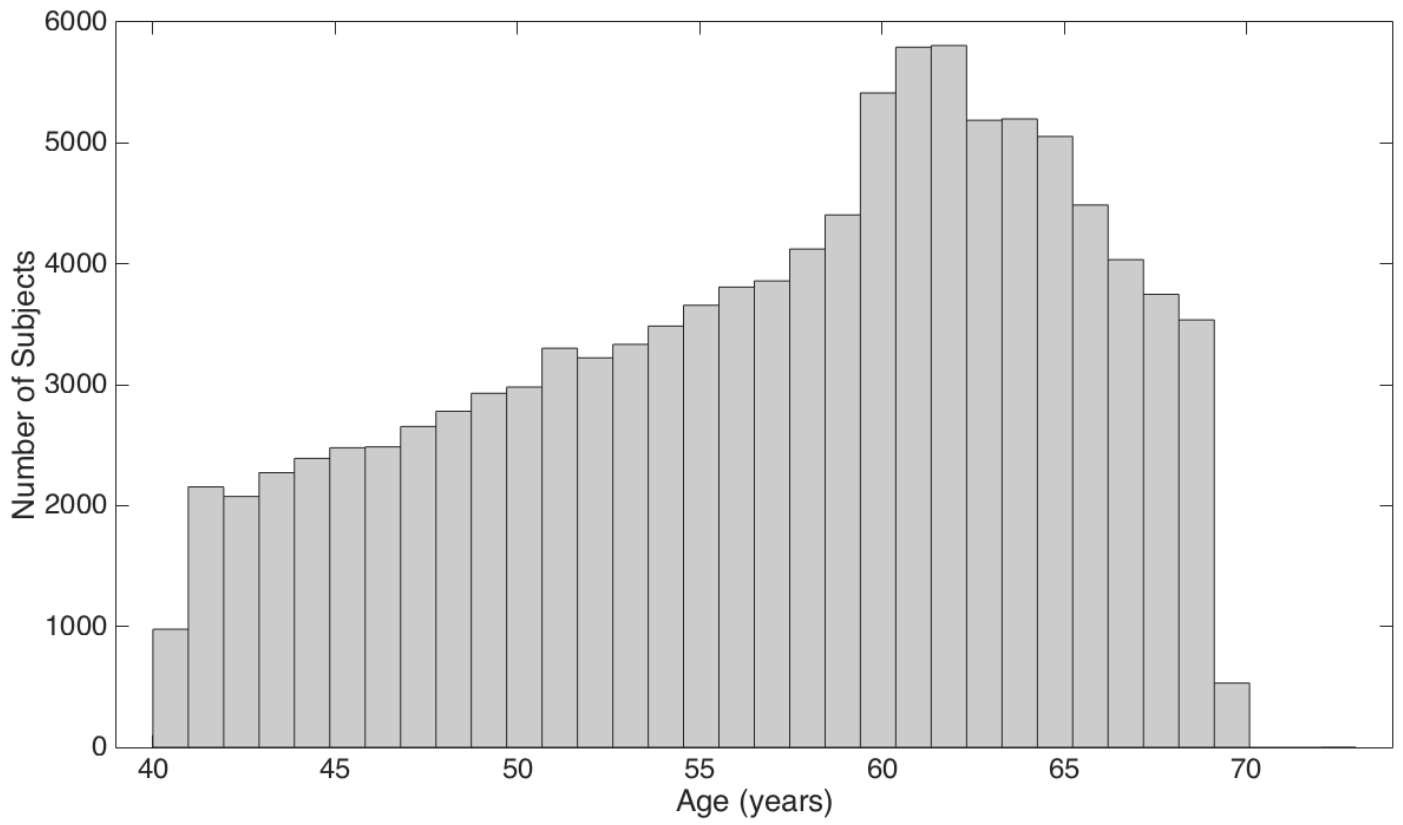
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Supplementary Tables 1: The heritability estimates, standard error estimates, sample sizes, covariates adjusted, prevalence in the sample (for binary traits) and other relevant information for all *non-disease traits* analyzed in the UK Biobank. Heritability estimates stratified by sex and socioeconomic status (SES) measured by the Townsend deprivation index are also presented.

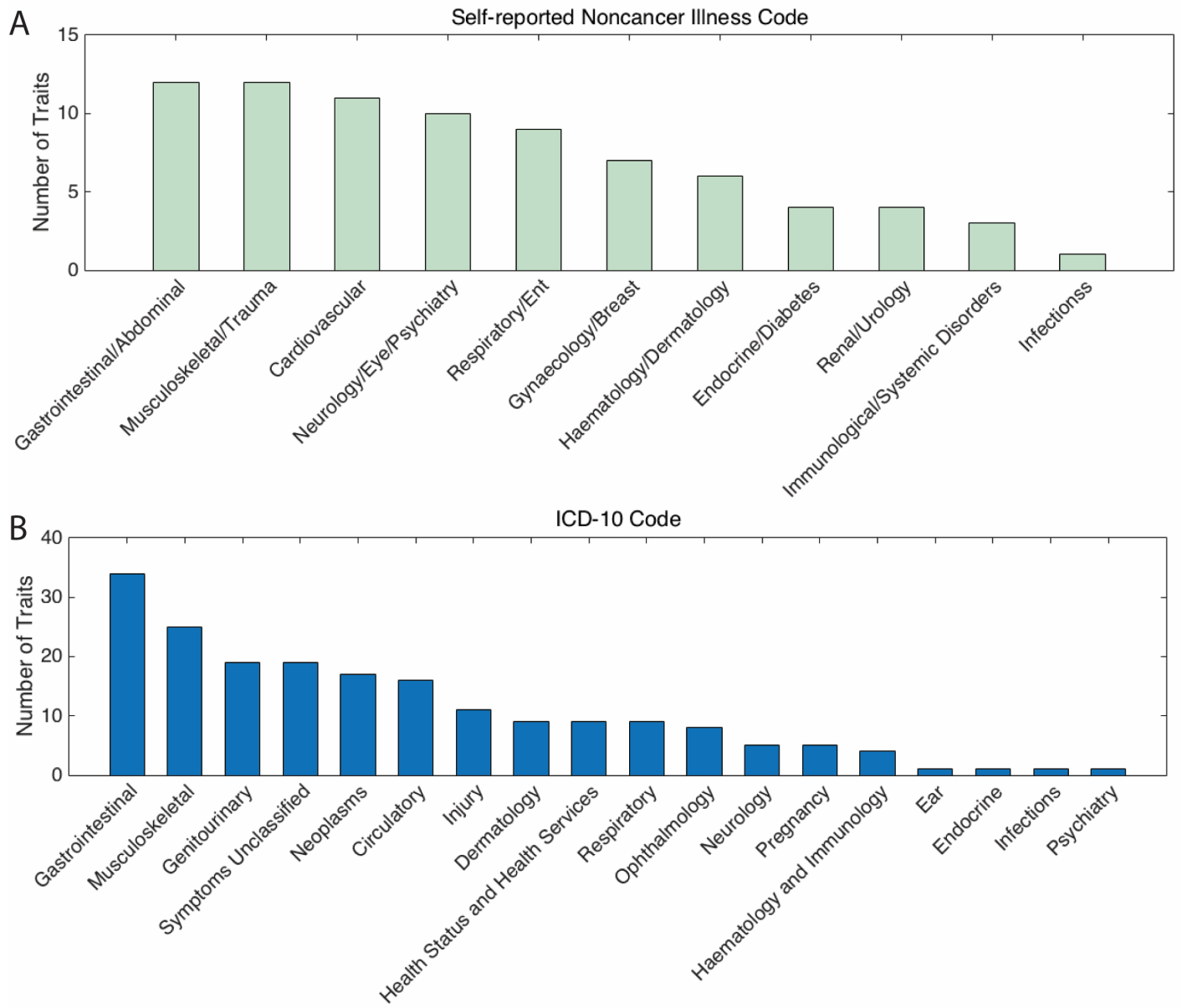
Supplementary Tables 2: The heritability estimates, standard error estimates, sample sizes, prevalence in the sample and other relevant information for all *self-reported illness codes and ICD-10 codes* analyzed in the UK Biobank. Heritability estimates stratified by sex and socioeconomic status (SES) measured by the Townsend deprivation index are also presented.

Supplementary Tables 3: Heritability estimates stratified by age.

Supplementary Tables 4: Traits whose heritability estimates decrease by 0.2 or more when the major histocompatibility complex (MHC) region (chr6:25-35Mb) is removed when computing the genetic similarity matrix.



Supplementary Figure 1: Age distribution of the sample analyzed in the UK Biobank.



Supplementary Figure 2: (A) A breakdown of the 79 self-reported non-cancer illness codes into different functional domains; (B) A breakdown of the 194 ICD-10 codes into different functional domains.