

Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: Hc.cutoff determination using FDR in simulated data.

File Name: Supplementary Data 2

Description: UKBB phenotypes used as query traits.

File Name: Supplementary Data 3

Description: Additional phenotypes used for the analysis of TYK2 variants.

File Name: Supplementary Data 4

Description: Query variants identified in the FinnGen dataset. Mapped table: where variants of the FinnGen primary traits are mapped to equivalent UKBB traits.

File Name: Supplementary Data 5

Description: Query variants identified in the FinnGen dataset. Unmapped table: where no equivalent traits in UKBB were mapped to FinnGen primary traits or where r_g information was not available.

File Name: Supplementary Data 6

Description: Query variants identified in the pQTL dataset from Ferkingstad et al., 2021

File Name: Supplementary Data 7

Description: Query variants from the UKBB dataset which are protein truncating variants with $MAF > 0.001$.

File Name: Supplementary Data 8

Description: UKBB traits with high Hc with the variants from the FinnGen dataset.

File Name: Supplementary Data 9

Description: UKBB traits with high Hc with the variants from the pQTL dataset.

File Name: Supplementary Data 10

Description: UKBB traits with high Hc with the variants from the protein truncating variants dataset.

File Name: Supplementary Data 11

Description: UKBB and GWAS catalog traits with high Hc with the TYK2 and SLC39A8 variants.

File Name: Supplementary Data 12

Description: Priors inferred from real data.