

Description of Additional Supplementary Files

Supplementary Data 1: Demographics, lifestyle, physiological, molecular measurements and clinical conditions of participants at baseline, HELIOS 2018-2022

Supplementary Data 2: A comparison of the HELIOS Study with the Singapore National Statistics

Supplementary Data 3: A comparison of disease prevalence between HELIOS and the populations of China, Malaysia and India (Overall, Urban and Rural)

Supplementary Data 4: Summary of variant count by ethnicity and annotations

Supplementary Data 5: Rare variant annotations and ancestry-specific carrier counts for the three actionable pathogenic genes in FH

Supplementary Data 6: Summary Statistics used for PRS estimation and validation in the HELIOS Study

Supplementary Data 7: Methylation levels (Mean/SD) and P-values for 16,444 CpG sites differentially methylated between ethnic groups

Supplementary Data 8: Summary results of enrichment analysis of ethnically diverse CpGs at DNase I hotspots, H3 Marks and chromatin states across 39 cell types

Supplementary Data 9: Summary results of enrichment analysis of ethnically diverse CpGs at Transcription Factor Binding Sites

Supplementary Data 10: Summary results of enrichment analysis of ethnically diverse CpGs across 191 traits

Supplementary Data 11: Summary of results from regression analysis between top 5 epigenetic PCs and 191 traits and top 5 genetics PCs

Supplementary Data 12: Summary of results from association analysis of 153 metabolites

Supplementary Data 13: Summary of significant results from correlation analysis of 153 metabolites

Supplementary Data 14: Summary results of pairwise differential expression analysis for 12,434 genes across three ethnic groups

Supplementary Data 15: Gene Set enrichment analysis (GSEA) of the 2,972 differentially expressed genes across three pathway databases

Supplementary Data 16: Summary of Metabolite-Gene pairs with significant SMR associations and the respective Coloc posterior probability of shared casual variant using metabolite GWAS and eQTL data from eqtlgen

Supplementary Data 17: Summary of Metabolite-Gene pairs with significant SMR associations and the respective Coloc posterior probability of shared casual variant using metabolite GWAS and eQTL data from HELIOS Study

Supplementary Data 18: Correlations of measurements between baseline and repeat visit measurements (N=398)

Supplementary Data 19: Demographics of participants in the pilot studies

Supplementary Data 20: Demographics of recalled participants in the reproducibility study

Supplementary Data 21: Spectrum of baseline measurements and biological samples in the HELIOS

Supplementary Data 22: Summary Statistics used for PRS estimation in the HELIOS Study