

Description of Additional Supplementary Files

Supplementary Data 1: Overview of all cardiovascular diseases included in this study among European populations

Supplementary Data 2: Univariate and bivariate LDSC results for the 6 cardiovascular diseases in European populations

Supplementary Data 3: Univariate and bivariate MiXeR results for the 6 cardiovascular diseases in European populations

Supplementary Data 4: Univariate LAVA results for each of the 6 cardiovascular diseases in European populations

Supplementary Data 5: Bivariate LAVA results for the 6 cardiovascular diseases in European populations

Supplementary Data 6: GWAS-PW results for the 6 cardiovascular diseases in European populations

Supplementary Data 7: LCV results for the 6 cardiovascular diseases in European populations

Supplementary Data 8: MRlap, MVMR, and LHCMR results for the 6 cardiovascular diseases in European populations

Supplementary Data 9: Genomic risk loci identified for MTAG results of 6 cardiovascular diseases in European populations by functional annotation of genomic risk loci using FUMA

Supplementary Data 10: Genomic risk loci identified for original GWAS results of 6 cardiovascular diseases in European populations by functional annotation of genomic risk loci using FUMA

Supplementary Data 11: Genomic risk loci identified for CPASSOC results of 6 cardiovascular diseases in European populations by functional annotation of genomic risk loci using FUMA

Supplementary Data 12: Prioritized genes identified for MTAG results of 6 cardiovascular diseases in European populations by functional annotation of genomic risk loci using FUMA

Supplementary Data 13: Prioritized genes identified for original GWAS results of 6 cardiovascular diseases in European populations by functional annotation of genomic risk loci using FUMA

Supplementary Data 14: Prioritized genes identified for CPASSOC results of 6 cardiovascular diseases in European populations by functional annotation of genomic risk loci using FUMA

Supplementary Data 15: Gene-based analysis for all genes that were nominally significant for any of the 6 cardiovascular diseases in European populations and/or for the MTAG analysis

Supplementary Data 16: Transcriptome-wide association study analysis for 10 related tissue-specific genes that were Bonferroni-corrected significant for any of the 6 cardiovascular diseases in European populations and/or for the MTAG analysis

Supplementary Data 17: Genomic risk loci overlapping among MTAG results of the 6 cardiovascular diseases in European populations and significantly colocalized loci identified by multi-trait colocalization using HyPrColoc

Supplementary Data 18: Lead SNPs overlapping among MTAG results of the 6 cardiovascular diseases in European populations and corresponding *P*-values

Supplementary Data 19: Gene sets significantly associated with each of MTAG results of the 6 cardiovascular diseases in European populations based on the susceptibility genes using MAGMA

Supplementary Data 20: Gene sets significantly associated with each of MTAG results of the 6 cardiovascular diseases in European populations based on the tissue-specific genes using Metascape

Supplementary Data 21: S-LDSC-based heritability enrichment estimates in 49 tissue types for MTAG results of the 6 cardiovascular diseases in European populations using LDSC-SEG

Supplementary Data 22: S-LDSC-based heritability enrichment estimates in 489 functional categories for MTAG results of the 6 cardiovascular diseases in European populations using LDSC-SEQ

Supplementary Data 23: Functional enrichment analysis for MTAG results of the 6 cardiovascular diseases in European populations using GARFIELD

Supplementary Data 24: MRlap results for the metabolic traits/diseases and 6 cardiovascular diseases in European populations

Supplementary Data 25: Proteome-wide MR analysis for causal effects of plasma protein levels with the 6 cardiovascular diseases in European populations (based on MTAG results) including colocalization and sensitivity analysis

Supplementary Data 26: Identification of druggable targets using OpenTargets

Supplementary Data 27: Overview of all Cardiovascular diseases and Metabolic traits included in this study among East Asian populations

Supplementary Data 28: Univariate and bivariate LDSC results for the 5 cardiovascular diseases in East Asian populations

Supplementary Data 29: Univariate and bivariate MiXeR results for the 5 cardiovascular diseases in East Asian populations

Supplementary Data 30: Univariate LAVA results for each of the 5 cardiovascular diseases in East Asian populations

Supplementary Data 31: Bivariate LAVA results for the 5 cardiovascular diseases in East Asian populations

Supplementary Data 32: GWAS-PW results for the 5 cardiovascular diseases in East Asian populations

Supplementary Data 33: LCV and MRlap results for the 5 cardiovascular diseases in East Asian populations

Supplementary Data 34: Genomic risk loci identified for original GWAS results of 5 cardiovascular diseases in East Asian populations by functional annotation of genomic risk loci using FUMA

Supplementary Data 35: Prioritized genes identified for 5 cardiovascular diseases in East Asian populations by mapping of genomic risk loci using FUMA

Supplementary Data 36: Gene-based analysis for all genes that were nominally significant for any of the 5 cardiovascular diseases in East Asian populations

Supplementary Data 37: Genomic risk loci overlapping among the 5 cardiovascular diseases in East Asian populations and significantly colocalized loci identified by multitrait colocalization using HyPrColoc

Supplementary Data 38: Lead SNPs overlapping among GWAS results of the 5 cardiovascular diseases in East Asian populations and corresponding p-values

Supplementary Data 39: Gene sets significantly associated with each of GWAS results of the 5 cardiovascular diseases in East Asian populations based on the susceptibility genes using MAGMA