

Description of Additional Supplementary Files

File name: Supplementary Data 1

Description: Epigenome-wide significant methylation sites ($p\text{-value} < 1.16e-7$) associated with self-reported race in the Veterans Aging Cohort Study (VACS) discovery group (N=527) and replications in the VACS replication group (N=467) and Women's Interagency HIV Study (WIHS) replication cohort (N=230)

File name: Supplementary Data 2

Description: Epigenome-wide significant methylation sites ($p\text{-value} < 1.16e-7$) associated with global ancestry in the Veterans Aging Cohort Study (VACS) discovery group (N=478) and replications in the VACS replication group (N=422) and Women's Interagency HIV Study (WIHS) replication cohort (N=131)

File name: Supplementary Data 3

Description: Epigenome-wide significant methylation sites ($p\text{-value} < 1.16e-7$) associated with local ancestry in the Veterans Aging Cohort Study (VACS) discovery group (N=478) and replications in the VACS replication group (N=422) and Women's Interagency HIV Study (WIHS) replication cohort (N=131)

File name: Supplementary Data 4

Description: The SNP-based heritability estimates of local ancestry-associated DNA methylation (mean $h^2=0.45$, median $h^2=0.43$) and the overall heritability (mean $h^2=0.06$, median $h^2=0.01$) estimated from all methylation sites

File name: Supplementary Data 5

Description: The trait enrichment of the differentially methylated CpG sites identified in the EWAS of local ancestry, global ancestry, and self-reported race

File name: Supplementary Data 6

Description: Methylation quantitative trait loci (meQTL) identified from the conventional model for local ancestry associated DNA methylation in the Veterans Aging Cohort Study (VACS) discovery group (N=478)

File name: Supplementary Data 7

Description: Methylation quantitative trait loci (meQTL) identified from the ancestry model for local ancestry associated DNA methylation in the Veterans Aging Cohort Study (VACS) discovery group (N=478), and replications in the VACS replication group (N=422) and Women's Interagency HIV Study (WIHS) replication cohort (N=131)

File name: Supplementary Data 8

Description: Methylation quantitative trait loci (meQTL) with genetic effects significantly differed by ancestry for local ancestry associated DNA methylation in the Veterans Aging Cohort Study (VACS) discovery group (N=478), and replications in the VACS replication group (N=422) and Women's Interagency HIV Study (WIHS) replication cohort (N=131)

File name: Supplementary Data 9

Description: meQTL rs9370878 of CpG site cg20133046: the genetic effects on the methylations are opposite for the African and European ancestry

File name: Supplementary Data 10

Description: meQTL rs1552489 of CpG site cg08033130: the genetic effects from the two ancestries contribute to the methylation in the same direction but with different effect sizes

File name: Supplementary Data 11

Description: meQTL rs2955229 of CpG site cg24599650: the African alleles are associated with differential methylations while the European alleles are not

File name: Supplementary Data 12

Description: meQTL rs4074196 of CpG site cg23611477: the European alleles are associated with differential methylations while the African alleles are not

File name: Supplementary Data 13

Description: meQTL rs6774733 of CpG site cg02527881: the genetic effects are comparable between ancestries