**Appendix 1. Genotyping and quality control**

HANDLS participants were genotyped using the Illumina 1M genotyping array. A total of 1,024 individuals were successfully genotyped. Sample quality control inclusion criteria were: **(1)** concordance between self-reported sex and X-chromosome based sex; **(2)** >95% call rate per participant (across all equivalent arrays), **(3)** concordance between self-reported African ancestry and genotyped SNPs confirmed ancestry, and **(4)** proportional sharing of genotypes < 15% between samples, excluding close relatives from the final sample. Moreover, SNPs in HANDLS were selected when the following criteria were met: **(1)** Hardy-Weinberg equilibrium (HWE) p-value>10-7; **(2)** Missing by haplotype p-values > 10-7; **(3)** Minor allele frequency>0.01, and **(4)** Call rate > 95%. Basic quality control and data management for each genotype was conducted using PLINKv1.06.([1](#_ENREF_1)) Cryptic relatedness was estimated via pairwise identity by descent analyses in PLINK and confirmed using RELPAIR.([2](#_ENREF_2)) STRUCTUREv2.3([3-5](#_ENREF_3)) and the multidimensional scaling (MDS) function in PLINKv1.06 were used to determine ancestry among HANDLS participants. HANDLS participants with component vector estimates consistent with the HapMap African ancestry samples for the first 4 component vectors were included. Moreover, in our main analyses, we adjusted for all 10 principal components to control for any residual effects of population structure.([6](#_ENREF_6)). SNPs that passed the above quality control criteria were used for genotype imputation using MACH and minimac softwares (<http://www.sph.umich.edu/csg/abecasis/mach/>). The 1000 Genomes Project phase 1 alpha freeze multiethnic panel were used as a reference population to impute SNPs. Imputed SNP with imputation quality measure of R2<0.3 or minor allele frequency of <1% were excluded from the analysis. Serum uric acid (SUA) associated SNPs identified by genome-wide association and candidate gene studies were selected from those SNPs that passed the imputation quality control criteria.

**References:**

1. Purcell S, Neale B, Todd-Brown K, Thomas L, Ferreira MA, Bender D, Maller J, Sklar P, de Bakker PI, Daly MJ, et al. PLINK: a tool set for whole-genome association and population-based linkage analyses. Am J Hum Genet 2007;81(3):559-75. doi: S0002-9297(07)61352-4 [pii]

10.1086/519795.

2. Epstein MP, Duren WL, Boehnke M. Improved inference of relationship for pairs of individuals. Am J Hum Genet 2000;67(5):1219-31. doi: S0002-9297(07)62952-8 [pii]

10.1016/S0002-9297(07)62952-8.

3. Pritchard JK, Stephens M, Donnelly P. Inference of population structure using multilocus genotype data. Genetics 2000;155(2):945-59.

4. Falush D, Stephens M, Pritchard JK. Inference of population structure using multilocus genotype data: linked loci and correlated allele frequencies. Genetics 2003;164(4):1567-87.

5. Falush D, Stephens M, Pritchard JK. Inference of population structure using multilocus genotype data: dominant markers and null alleles. Mol Ecol Notes 2007;7(4):574-8. doi: 10.1111/j.1471-8286.2007.01758.x.

6. Price AL, Patterson NJ, Plenge RM, Weinblatt ME, Shadick NA, Reich D. Principal components analysis corrects for stratification in genome-wide association studies. Nature genetics 2006;38(8):904-9. doi: ng1847 [pii]

10.1038/ng1847.