Ancestry inference and grouping from principal component analysis of genetic data

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Abstract

First, we show how Euclidean distance in the Principal Component Analysis (PCA) space is related to F_{ST} between populations. Then, we project the genetic data of individuals from the UK Biobank and the POPRES datasets onto the reference populations of the 1000 Genomes Project and show how to accurately infer global ancestry and group individuals in homogeneous clusters. Inferring ancestry for nearly 500,000 individuals is performed in 20 minutes only. The proposed method is particularly important for methods that needs to be applied in homogeneous samples. Finally, we conclude that our method and the community would benefit from having an easy access to a reference dataset with an even better coverage of the worldwide genetic diversity than the 1000 Genomes Project.

Introduction

Principal Component Analysis (PCA) has been widely used to correct for population structure in association studies and has been shown to mirror geography (Price *et al.* 2006; Novembre *et al.* 2008). Due to its popularity, many methods has been developed for efficiently computing PCs as well as appropriately projecting samples onto a reference PCA space (Abraham *et al.* 2017; Zhang *et al.* 2020; Privé *et al.* 2020), making these analyses available for ever increasing datasets in human genetics. Naturally, PCA has also been used for ancestry inference. However, among all studies where we have seen PCA used for ancestry inference, we have found there was no consensus on the most appropriate methods for inferring ancestry. For example, there may be divergences on which distance metric to use and the number of PCs to use to compute these distances.

Here, we first compare several distance metrics with the popular F_{ST} statistic between populations. We show that the simple Euclidean distance on PC scores is the most appropriate distance to use, then we show how to use it to infer global ancestry and to group individuals in homogeneous sub-populations. We do not provide a method to define admixture coefficients nor infer local ancestry, which are different problems for which there are several existing methods (Alexander *et al.* 2009; Frichot *et al.* 2014; Raj *et al.* 2014; Padhukasahasram 2014). However, inferring global ancestry in non-admixed individuals is still a very important problem since there are methods that specifically need to be applied in samples of ancestry homogeneous. This is the case e.g. for polygenic score methods that have been shown to underperform when applied to populations not homogeneous to the one used for training (Martin *et al.* 2017).

† Further defined in supplementary section "Defintions".

Measures of genetic dissimilarity between populations

We first compare four measures of genetic dissimilarity using populations of the 1000 Genomes Project (1000G†, 1000 Genomes Project Consortium *et al.* (2015)). The F_{ST}† is an ubiquitous measure of genetic dissimilarity between populations and the first measure we use in this comparison. We report F_{ST} between the 26 1000G populations in tables S1-S5. The other three measures compared are distances applied to the PC scores† of the genetic data: 1) the Bhattacharyya distance†; 2) the distance between the centers (geometric median†) of the two populations; 3) the shorter distance between pairs of PC scores from the two populations. The distance between population centers seems to be an appropriate PCA-based distance as this (squared) distance is approximately proportional to the F_{ST} (Figure S2) and provides an appropriate clustering of populations (Figure S5). In contrast, the two other Bhattacharyya and shortest distances do not provide as satisfactory results (Figures S4 and S6). For example, African Caribbeans in Barbados (ACB) and Americans of African Ancestry in SW USA (ASW) are close to Northern European populations (FIN, CEU and GBR) when using the Bhattacharyya distance. Using the shortest distance between pairs of individuals in two different populations is very sensitive to outliers being far from the other individuals in the population.

PCA-based ancestry inference

We project the dataset of interest onto the PCA space of the 1000G data using the fast tools developed in Privé *et al.* (2020). We recall that this uses a correction for shrinkage in projected PC scores, which has been shown to be particularly important when using PC scores for ancestry estimation (Zhang *et al.* 2020). Based on the results of the previous section, we propose to assign individual ancestry to one of the 26 1000G populations based on the distance to these reference population centers (geometric medians†). Since we showed previously that (squared) distances in the PCA space are proportional to F_{ST}, we can set a threshold on these distances that would correspond approximately to an F_{ST} of e.g. 0.002. This threshold is close to the dissimilarity between Spanish and Italian people (F_{ST}(IBS, TSI) of 0.0015). When an individual is not close enough to any of the 26 1000G populations, we leave its ancestry inference as unknown, otherwise we assign this individual to the closest population.

We first perform ancestry estimation for the individuals in the UK Biobank†. These individuals seem to originate from all over the world when we project onto the PCA space of the 1000G (Figure S7). Self-reported ancestry (Field 21000) is available for almost all individuals, with only 1.6% with unknown or mixed ancestry. Based on the threshold defined before, we could not infer ancestry for 4.6% of all 488,371 individuals. More precisely, among "British", "Irish" and "White" ancestries, this represented respectively 2.2%, 3.3% and 7.9% (Tables 1 and S7). This also represented 3.3% for "Chinese", 13.8% for "Indian" and 17.8% for "African" ancestries. Finally, mixed ancestries were particularly difficult to match to any of the 1000G populations, e.g. 97.3% unmatched within 'White and Black African' and 93.0% within 'White and Asian' ancestries. Only 47 individuals were wrongly classified in "super" population of the 1000G; e.g. six "British" were classified as South Asians, one "Chinese" as European and 25 "Caribbean" as South Asian by our method (Table 1). However, when comparing the location of these mismatched individuals to the rest of individuals on the PCA space computed on the UK Biobank (Bycroft *et al.* 2018), it seems more probable that our ancestry estimate is exact while the self-reported ancestry is wrong (Figure S8).

We also test the approach proposed in Zhang *et al.* (2020) which consists of finding the 20 nearest neighbors in 1000G and computing the frequency of (super) population membership, weighted by the inverse distance to these 20 closest 1000G individuals. When this probability is less than 0.875, they leave the ancestry as unknown, aiming at discarding admixed individuals. Less than 0.5% could not be matched by their method (Table S6). Of note, they could match much more admixed individuals, whereas they set a high probably aiming at discarding such admixed individuals. Morever, there are many more discrepancies between their method and the self-reported ancestry in the UK Biobank (Table S6) compared to the previous results with our method (Table 1). Finally, our method is able to accurately differentiate between sub-continental populations such as differentiating between Pakistani, Bangladeshi and Chinese people (Table S7). We also applied our ancestry detection technique to the European individuals of the POPRES data (Nelson *et al.* 2008). Only 16 out of the 1385 individuals (1.2%) could not be matched, of which 11 were from East or South-East Europe (Table S8). Note that all individuals that we could match were identified as of European ancestry. We could also identify accurately sub-regions of Europe; e.g. 261 out of 264 Spanish and Portugese individuals were identified as "Iberian Population in Spain" (EUR_IBS, Table S8).

Table 1: Self-reported ancestry (left) of UKBB individuals and their matching to 1000G continental populations (top) by our method. See the description of 1000G populations at `https://www.internationalgenome.org/category/population/`.

	AFR	AMR	EAS	EUR	SAS	Not matched
British	2		1	421457	6	9548
Irish				12328		425
White	1	1	1	499		43
Other White		40		11334	1	4440
Indian				5	4922	789
Pakistani					1421	327
Bangladeshi					217	4
Chinese			1453	1		50
Other Asian	1		279		939	528
Caribbean	3848				25	424
African	2633			1		570
Other Black	74				2	42
Asian or Asian British			2		20	20
Black or Black British	20			2		4
White and Black Caribbean	24	1		8	1	563
White and Black African	5			6		391
White and Asian		1	2	27	26	746
Unknown	835	173	576	2296	633	3307

PCA-based ancestry grouping

Finally, we show 3 possible ways how to use our ancestry inference method for grouping genetically homogeneous individuals. The first approach is to simply match individuals that are closed enough to one or more of the 1000G populations, as described in this paper. We can e.g. define a British ancestry cluster by identifying individuals close enough to the GBR 1000G population (Figure S9). Likewise, we can define "AFR", "AMR", "EAS" and "SAS" clusters of individuals who are close enough to any of the corresponding 1000G populations. We can then verify that these clusters define distinct sets of homogeneous individuals (Figure 1). Another solution, which does not require projecting individuals to the 1000G, but does require computing PC scores within the dataset instead, would consist in using reported ancestries and internal PC scores. Then, a British ancestry cluster could be defined by individuals close enough to the center of the people reported as "British" (Figure S10). We can also define an "AFR2" cluster if close enough to the center of either "Caribbean", "African" or "Other Black" individuals, "EAS2" if close to the "Chinese" cluster, and "SAS2" if close to either "Indian", "Pakistani" or "Bangladeschi" clusters. This enables e.g. to capture a larger set of individuals who are close enough to British people (e.g. Irish people), while discarding individuals whose genetic ancestry is not really "British" as self-reported. A third solution, useful when we know that the data is composed of a predominant ancestry is to keep individuals who are close enough to

the overall center of all individuals (Figure S11). We recall the we are using the geometric median as such center, which is robust to outliers. Overall, all these techniques approximately identify the same amount of people (Table S9).

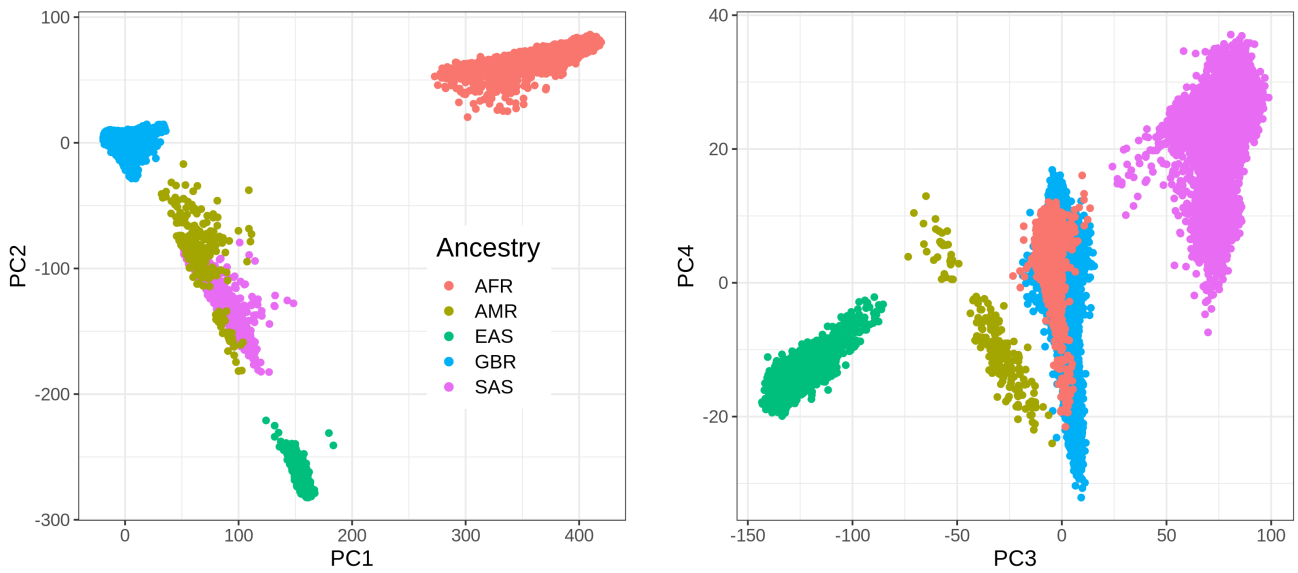

Figure 1: The UK Biobank PC scores (first four) colored by the homogeneous ancestry group we infer for these individuals.

Discussion

Here we propose a PCA-based method for ancestry inference and grouping into genetically homogeneous clusters. We show how the PCA-based distance is related to the F_{ST}, which allows to compute distances based on PC scores directly. Previously, we and others proposed to use (robust) Mahalanobis distances to infer ancestry or identify a homogeneous group of individuals (Peterson *et al.* 2017; Privé *et al.* 2020). When looking at distances between two populations, this corresponds to using the Bhattacharyya distance, which appear suboptimal here compared to using a simple Euclidean distance. We hypothesize that the main issue with this approach is that, when there is a very tight population cluster, all distances to this cluster are large because of the covariance component in the Mahalanobis distance. In contrast, here we propose to directly use the global scale of the PC scores, which is invariant from the cluster scattering. This global scale makes it also more robust to infer ancestry with our method as compared to using relative proportions from k=20 nearest neighbors (kNN, Zhang *et al.* (2020)). Indeed, consider an example of an admixed individual with say 25% European ancestry and 75% African ancestry. The kNN-based method is likely to identify this individual as of African ancestry, while our method will probably be unable to match it, which is a beneficial feature when we are interested in defining genetically homogeneous groups. We also believe our proposed method to be more robust than machine learning methods, because a machine learning method would try e.g. to differentiate between GBR and CEU 1000G populations, which are two very close populations of Northwest Europe (F_{ST} of 0.0002). In other words, our distance-based method should benefit from the

inclusion of any new reference population while it would make it increasingly complex to apply machine learning methods.

Yet, our proposed method also has limitations. First, since we match target individuals to 1000G populations, if individuals are far from all 26 1000G populations, then they would not be matched. When looking at the POPRES data, more individuals from East Europe could not be matched. This is not surprising because there are no East European population in the 1000G data. Moreover, if we look at the location of the 1000G populations on a map (Figure S1), we can see that it lacks representation of many parts of the world. This issue has also been reported e.g. for Asian populations (Lu and Xu 2013). Therefore more diverse populations should be aggregated to better cover the worldwide genome diversity. This probably would make our method better and, if a sufficient coverage is achieved, allow for approximating geographic coordinates by triangulation. Nevertheless, we also show how to define homogeneous ancestry groups without the use of the 1000G data. When a predominant genetic ancestry is present in the data, such as British in the UK Biobank (Bycroft *et al.* 2018) or Danish in the iPSYCH data (Pedersen *et al.* 2018), it is possible to directly restrict to a homogeneous subset of the data.

A second potential limitation of our method is that it has two hyper-parameters: the number of PCs used to compute the distances and the threshold on the minimum distance to any cluster above which the ancestry is not matched. Several studies have used only the first two PCs for ancestry inference. This is not enough to distinguish between Admixed Americans and South Asians (see AMR and SAS in figure 1), let alone for distinguishing between populations at the sub-continental level. As in Privé *et al.* (2020), we recommend to use all PCs that visually separate some populations. Moreover, we believe our proposed method to be robust to the number of PCs used because contribution to the Euclidean distance is smaller for later PCs than for first PCs. As for the distance limit, we have shown here how to define it to approximately correspond to an F_{ST} of 0.002. Alternatively, a threshold can be chosen based on the visual inspection of the histogram of distances (on a log scale). This threshold can also be adjusted depending on how stringent you want the selection to be.

In conclusion, we believe our proposed approach to be a simple and robust way to infer global ancestry and to define groups of homogeneous ancestry. It is also very fast, allowing to infer ancestry for 488,371 individuals in 20 minutes using 16 cores.

Software and code availability

The newest version of R package bigsnpr can be installed from GitHub (see `https://github.com/privefl/bigsnpr`). The code used in this paper is available at `https://github.com/privefl/paper-ancestry-matching/tree/master/code`.

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Declaration of Interests

The authors declare no competing interests.

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Supplementary Materials

Definitions † and methods

- The **1000 Genomes Project (1000G)** data is composed of approximately 100 individuals for each of 26 populations worldwide (described at `https://www.internationalgenome.org/category/population/`), including 7 African (AFR), 5 East Asian (EAS), 5 South Asian (SAS), 5 European (EUR) and 4 admixed American (AMR) populations. Here we used the transformed data in PLINK format provided in Privé *et al.* (2020).
- The $\boldsymbol{F_{ST}}$ measures the relative amount of genetic variance between populations compared to the total genetic variance within these populations (Wright 1965). We use the weighted average formula proposed in Weir and Cockerham (1984), which we now implement in our package bigsnpr (Privé *et al.* 2018).
- The **Principal Component (PC) scores** are defined as $U\Delta$, where $U\Delta V^T$ is the singular value decomposition of the (scaled) genotype matrix (Privé *et al.* 2020). They are usually truncated, e.g. corresponding to the first 20 principal dimensions only.
- The **Bhattacharyya distance** between two multivariate normal distributions $\mathcal{N}(\boldsymbol{\mu}_1,\ \boldsymbol{\Sigma}_1)$ and $\mathcal{N}(\boldsymbol{\mu}_2,\ \boldsymbol{\Sigma}_2)$ is defined as $D_B = \frac{1}{8}(\boldsymbol{\mu}_2 - \boldsymbol{\mu}_1)^T \boldsymbol{\Sigma}^{-1}(\boldsymbol{\mu}_2 - \boldsymbol{\mu}_1) + \frac{1}{2}\log\left(\frac{|\boldsymbol{\Sigma}|}{\sqrt{|\boldsymbol{\Sigma}_1|\,|\boldsymbol{\Sigma}_2|}}\right)$, where $\boldsymbol{\Sigma} = \frac{\boldsymbol{\Sigma}_1 + \boldsymbol{\Sigma}_2}{2}$ and $|M|$ is the absolute value of the determinant of matrix M (Bhattacharyya 1943; Fukunaga 1990). The mean and covariance parameters for each population are computed using the robust location and covariance parameters as proposed in Privé *et al.* (2020).
- The **geometric median** of points is the point that minimizes the sum of all Euclidean distances to these points. We now implement this as function `geometric_median` in our R package bigutilsr.
- The **UK Biobank** is a large cohort of half a million individuals from the UK, for which we have access to both genotypes and multiple phenotypes (`https://www.ukbiobank.ac.uk/`). We apply some quality control filters to the genotyped data; we remove individuals with more than 10% missing values, variants with more than 1% missing values, variants having a minor allele frequency < 0.01, variants with P-value of the Hardy-Weinberg exact test < 10^{-50}, and non-autosomal variants. This results in 488,371 individuals and 504,139 genetic variants.

Location of 1000G populations

Figure S1: Locations of the 1000G populations, accessed from `https://www.internationalgenome.org/data-portal/population` and represented using R package leaflet. Note that Gujarati Indian from Houston, Texas were manually moved to Gujarat (22.309425, 72.136230), Sri Lankan Tamil from the UK to Sri Lanka (6.927079, 79.861244), and Indian Telugu from the UK to (16.5, 79.5) to better reflect the location of their ancestors. Also note that Utah Residents with Northern and Western European Ancestry, Americans of African Ancestry in SW USA, African Caribbeans in Barbados and Mexican Ancestry from Los Angeles USA are not located at their ancestral location.

Measures of genetic dissimilarity between populations

Table S1: F_{ST} values between African populations of the 1000G and all 26 1000G populations.

	LWK	ESN	YRI	ACB	ASW	GWD	MSL
LWK	0.0000	0.0077	0.0071	0.0064	0.0090	0.0108	0.0093
ESN	0.0077	0.0000	0.0008	0.0034	0.0088	0.0075	0.0051
YRI	0.0071	0.0008	0.0000	0.0025	0.0080	0.0062	0.0039
ACB	0.0064	0.0034	0.0025	0.0000	0.0020	0.0060	0.0044
ASW	0.0090	0.0088	0.0080	0.0020	0.0000	0.0098	0.0094
GWD	0.0108	0.0075	0.0062	0.0060	0.0098	0.0000	0.0036
MSL	0.0093	0.0051	0.0039	0.0044	0.0094	0.0036	0.0000
JPT	0.1475	0.1564	0.1545	0.1344	0.1194	0.1517	0.1574
CHB	0.1456	0.1546	0.1527	0.1324	0.1174	0.1499	0.1556
CHS	0.1466	0.1555	0.1536	0.1335	0.1186	0.1509	0.1565
CDX	0.1456	0.1544	0.1526	0.1324	0.1178	0.1498	0.1555
KHV	0.1435	0.1525	0.1507	0.1304	0.1154	0.1479	0.1535
GIH	0.1101	0.1200	0.1186	0.0954	0.0773	0.1156	0.1200
PJL	0.1069	0.1167	0.1154	0.0920	0.0735	0.1124	0.1167
BEB	0.1077	0.1174	0.1161	0.0934	0.0755	0.1131	0.1174
ITU	0.1096	0.1195	0.1181	0.0954	0.0778	0.1151	0.1195
STU	0.1091	0.1189	0.1175	0.0949	0.0774	0.1145	0.1189
PEL	0.1472	0.1559	0.1541	0.1325	0.1144	0.1515	0.1567
MXL	0.1125	0.1219	0.1205	0.0972	0.0772	0.1175	0.1218
CLM	0.0970	0.1063	0.1051	0.0816	0.0620	0.1021	0.1061
PUR	0.0849	0.0938	0.0927	0.0699	0.0515	0.0898	0.0935
FIN	0.1219	0.1319	0.1306	0.1044	0.0837	0.1272	0.1319
CEU	0.1189	0.1291	0.1278	0.1014	0.0805	0.1244	0.1290
GBR	0.1193	0.1295	0.1282	0.1017	0.0808	0.1248	0.1294
IBS	0.1145	0.1247	0.1234	0.0975	0.0772	0.1199	0.1247
TSI	0.1154	0.1258	0.1245	0.0986	0.0783	0.1210	0.1258

Table S2: F_{ST} values between admixed American populations of the 1000G and all 26 1000G populations.

	PEL	MXL	CLM	PUR
LWK	0.1472	0.1125	0.0970	0.0849
ESN	0.1559	0.1219	0.1063	0.0938
YRI	0.1541	0.1205	0.1051	0.0927
ACB	0.1325	0.0972	0.0816	0.0699
ASW	0.1144	0.0772	0.0620	0.0515
GWD	0.1515	0.1175	0.1021	0.0898
MSL	0.1567	0.1218	0.1061	0.0935
JPT	0.0795	0.0643	0.0707	0.0773
CHB	0.0786	0.0628	0.0689	0.0752
CHS	0.0811	0.0650	0.0708	0.0769
CDX	0.0849	0.0675	0.0719	0.0773
KHV	0.0817	0.0643	0.0689	0.0744
GIH	0.0725	0.0370	0.0278	0.0269
PJL	0.0688	0.0327	0.0230	0.0220
BEB	0.0669	0.0344	0.0278	0.0282
ITU	0.0732	0.0391	0.0308	0.0303
STU	0.0728	0.0390	0.0309	0.0305
PEL	0.0000	0.0170	0.0380	0.0548
MXL	0.0170	0.0000	0.0090	0.0180
CLM	0.0380	0.0090	0.0000	0.0056
PUR	0.0548	0.0180	0.0056	0.0000
FIN	0.0772	0.0338	0.0178	0.0149
CEU	0.0804	0.0334	0.0143	0.0100
GBR	0.0809	0.0338	0.0146	0.0102
IBS	0.0820	0.0339	0.0134	0.0081
TSI	0.0825	0.0345	0.0143	0.0090

Table S3: F_{ST} values between East Asian populations of the 1000G and all 26 1000G populations.

	JPT	CHB	CHS	CDX	KHV
LWK	0.1475	0.1456	0.1466	0.1456	0.1435
ESN	0.1564	0.1546	0.1555	0.1544	0.1525
YRI	0.1545	0.1527	0.1536	0.1526	0.1507
ACB	0.1344	0.1324	0.1335	0.1324	0.1304
ASW	0.1194	0.1174	0.1186	0.1178	0.1154
GWD	0.1517	0.1499	0.1509	0.1498	0.1479
MSL	0.1574	0.1556	0.1565	0.1555	0.1535
JPT	0.0000	0.0068	0.0086	0.0166	0.0140
CHB	0.0068	0.0000	0.0010	0.0084	0.0062
CHS	0.0086	0.0010	0.0000	0.0047	0.0031
CDX	0.0166	0.0084	0.0047	0.0000	0.0016
KHV	0.0140	0.0062	0.0031	0.0016	0.0000
GIH	0.0693	0.0673	0.0685	0.0685	0.0650
PJL	0.0669	0.0647	0.0660	0.0660	0.0626
BEB	0.0542	0.0518	0.0528	0.0527	0.0494
ITU	0.0656	0.0636	0.0647	0.0646	0.0611
STU	0.0642	0.0623	0.0634	0.0633	0.0598
PEL	0.0795	0.0786	0.0811	0.0849	0.0817
MXL	0.0643	0.0628	0.0650	0.0675	0.0643
CLM	0.0707	0.0689	0.0708	0.0719	0.0689
PUR	0.0773	0.0752	0.0769	0.0773	0.0744
FIN	0.0924	0.0901	0.0920	0.0925	0.0893
CEU	0.0985	0.0960	0.0977	0.0978	0.0946
GBR	0.0993	0.0968	0.0985	0.0985	0.0953
IBS	0.0981	0.0957	0.0973	0.0973	0.0942
TSI	0.0981	0.0956	0.0972	0.0972	0.0940

Table S4: F_{ST} values between European populations of the 1000G and all 26 1000G populations.

	FIN	CEU	GBR	IBS	TSI
LWK	0.1219	0.1189	0.1193	0.1145	0.1154
ESN	0.1319	0.1291	0.1295	0.1247	0.1258
YRI	0.1306	0.1278	0.1282	0.1234	0.1245
ACB	0.1044	0.1014	0.1017	0.0975	0.0986
ASW	0.0837	0.0805	0.0808	0.0772	0.0783
GWD	0.1272	0.1244	0.1248	0.1199	0.1210
MSL	0.1319	0.1290	0.1294	0.1247	0.1258
JPT	0.0924	0.0985	0.0993	0.0981	0.0981
CHB	0.0901	0.0960	0.0968	0.0957	0.0956
CHS	0.0920	0.0977	0.0985	0.0973	0.0972
CDX	0.0925	0.0978	0.0985	0.0973	0.0972
KHV	0.0893	0.0946	0.0953	0.0942	0.0940
GIH	0.0343	0.0325	0.0328	0.0334	0.0317
PJL	0.0289	0.0269	0.0272	0.0278	0.0262
BEB	0.0372	0.0368	0.0372	0.0375	0.0362
ITU	0.0393	0.0380	0.0384	0.0384	0.0367
STU	0.0398	0.0385	0.0389	0.0389	0.0373
PEL	0.0772	0.0804	0.0809	0.0820	0.0825
MXL	0.0338	0.0334	0.0338	0.0339	0.0345
CLM	0.0178	0.0143	0.0146	0.0134	0.0143
PUR	0.0149	0.0100	0.0102	0.0081	0.0090
FIN	0.0000	0.0062	0.0066	0.0101	0.0116
CEU	0.0062	0.0000	0.0002	0.0022	0.0034
GBR	0.0066	0.0002	0.0000	0.0024	0.0037
IBS	0.0101	0.0022	0.0024	0.0000	0.0015
TSI	0.0116	0.0034	0.0037	0.0015	0.0000

Table S5: F_{ST} values between South Asian populations of the 1000G and all 26 1000G populations.

	GIH	PJL	BEB	ITU	STU
LWK	0.1101	0.1069	0.1077	0.1096	0.1091
ESN	0.1200	0.1167	0.1174	0.1195	0.1189
YRI	0.1186	0.1154	0.1161	0.1181	0.1175
ACB	0.0954	0.0920	0.0934	0.0954	0.0949
ASW	0.0773	0.0735	0.0755	0.0778	0.0774
GWD	0.1156	0.1124	0.1131	0.1151	0.1145
MSL	0.1200	0.1167	0.1174	0.1195	0.1189
JPT	0.0693	0.0669	0.0542	0.0656	0.0642
CHB	0.0673	0.0647	0.0518	0.0636	0.0623
CHS	0.0685	0.0660	0.0528	0.0647	0.0634
CDX	0.0685	0.0660	0.0527	0.0646	0.0633
KHV	0.0650	0.0626	0.0494	0.0611	0.0598
GIH	0.0000	0.0035	0.0042	0.0039	0.0043
PJL	0.0035	0.0000	0.0035	0.0033	0.0036
BEB	0.0042	0.0035	0.0000	0.0022	0.0021
ITU	0.0039	0.0033	0.0022	0.0000	0.0013
STU	0.0043	0.0036	0.0021	0.0013	0.0000
PEL	0.0725	0.0688	0.0669	0.0732	0.0728
MXL	0.0370	0.0327	0.0344	0.0391	0.0390
CLM	0.0278	0.0230	0.0278	0.0308	0.0309
PUR	0.0269	0.0220	0.0282	0.0303	0.0305
FIN	0.0343	0.0289	0.0372	0.0393	0.0398
CEU	0.0325	0.0269	0.0368	0.0380	0.0385
GBR	0.0328	0.0272	0.0372	0.0384	0.0389
IBS	0.0334	0.0278	0.0375	0.0384	0.0389
TSI	0.0317	0.0262	0.0362	0.0367	0.0373

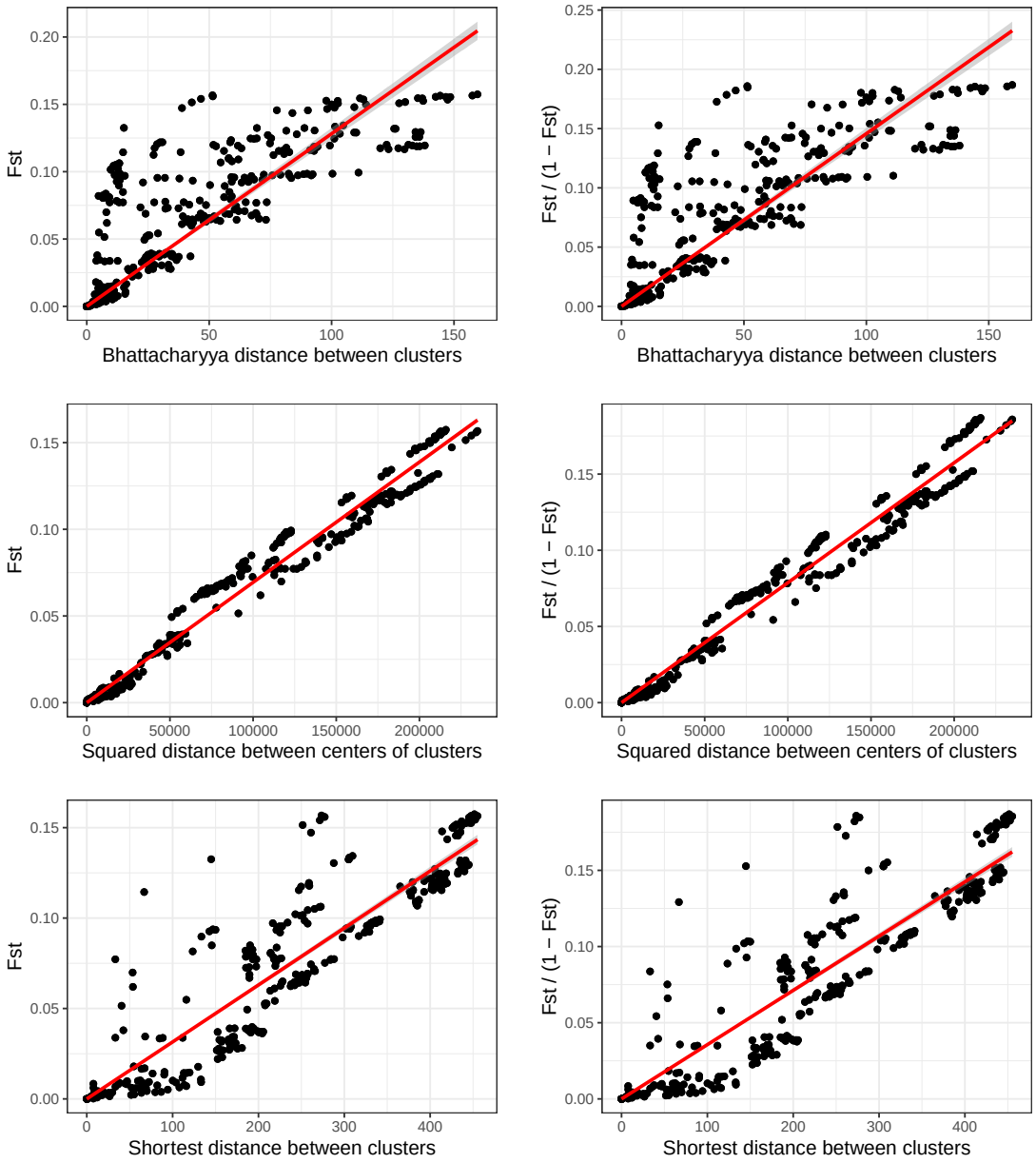

Figure S2: Comparing F_{ST} to different PCA-based distances between pairs of the 26 1000G populations.

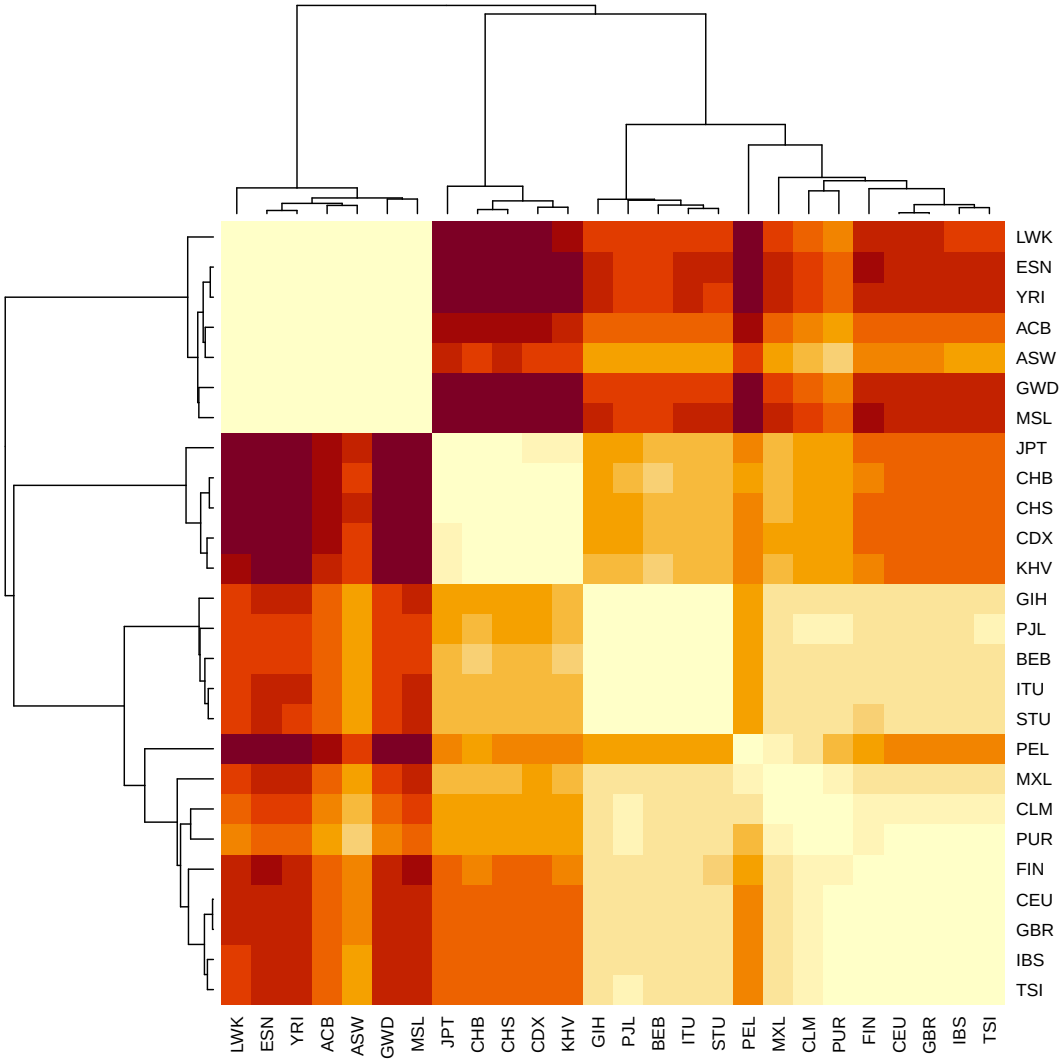

Figure S3: Heatmap with clustering based on the F_{ST} between pairs of the 26 1000G populations. Corresponding values are reported in tables S1-S5.

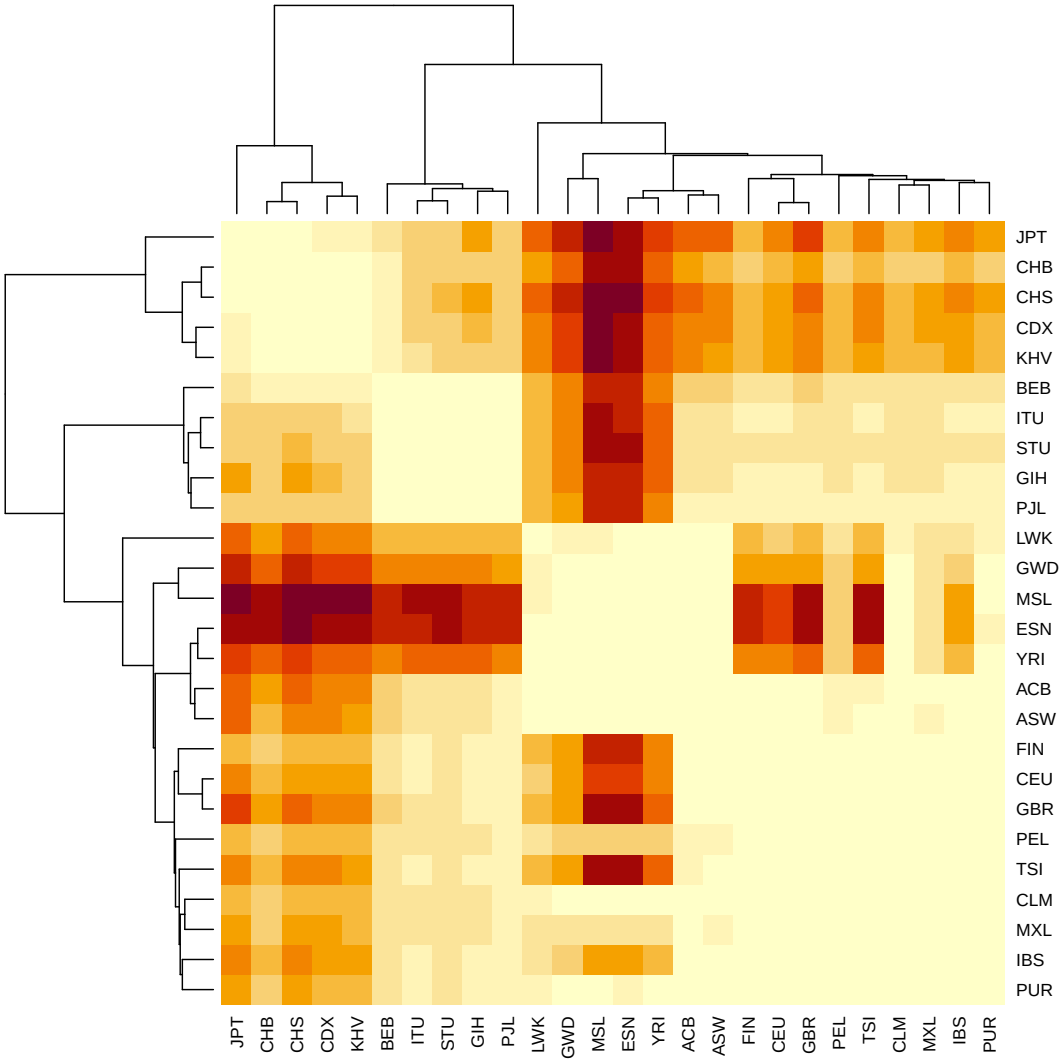

Figure S4: Heatmap with clustering based on the Bhattacharyya distances between pairs of the 26 1000G populations.

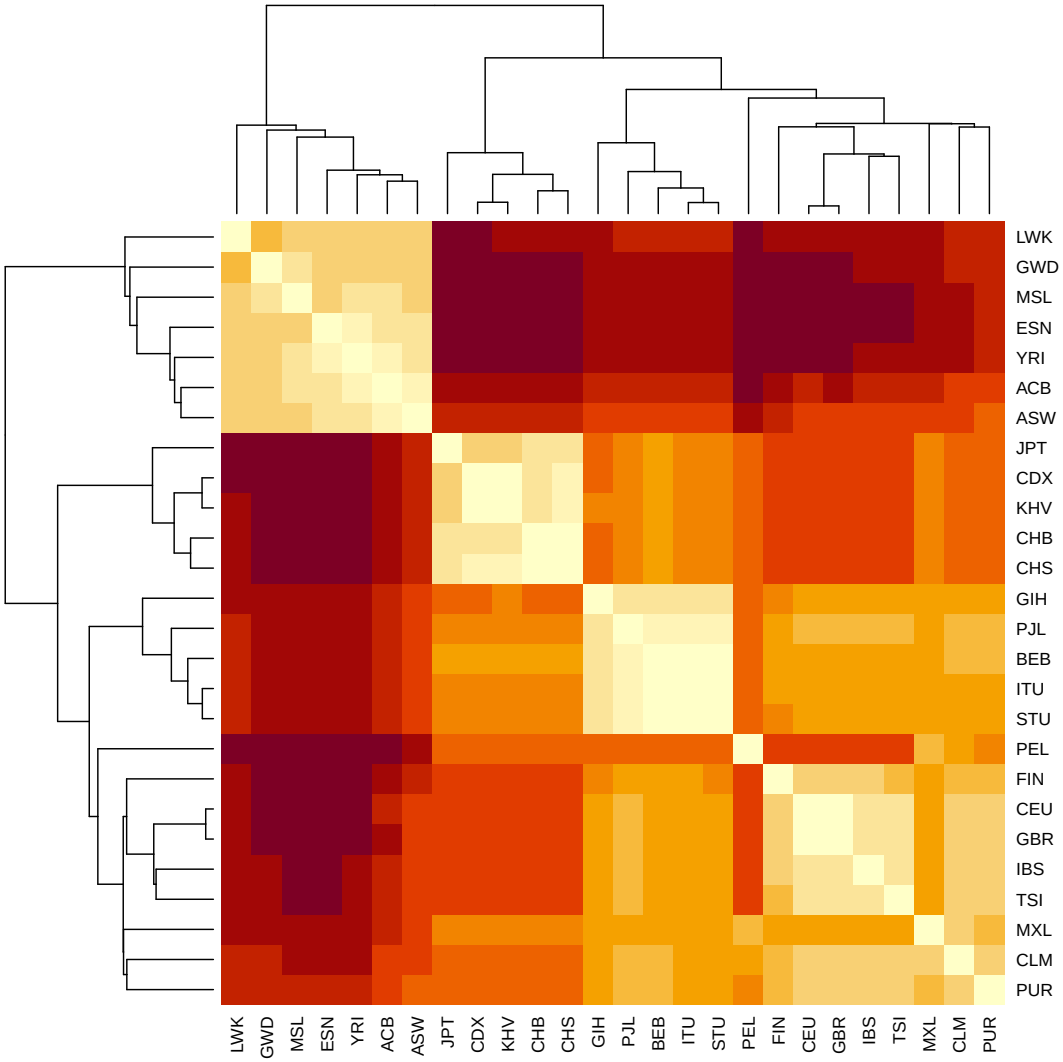

Figure S5: Heatmap with clustering based on the distances between centers of pairs of the 26 1000G populations.

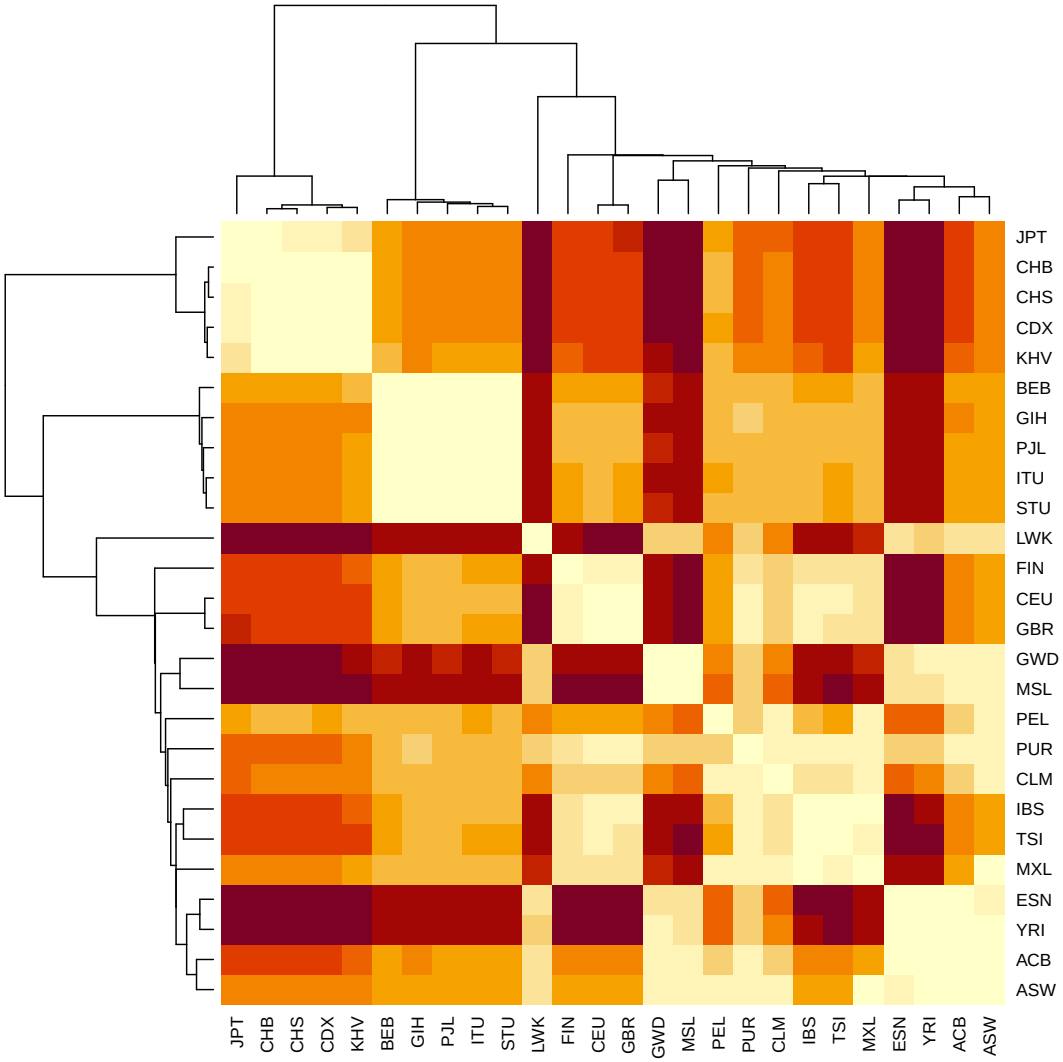

Figure S6: Heatmap with clustering based on the shortest distances between individuals in pairs of the 26 1000G populations.

PCA-based ancestry inference

Table S6: Self-reported ancestry (left) of the UK biobank individuals and their matching to 1000G continental populations (top) using 20-wNN (Zhang *et al.* 2020). See the description of 1000G populations at `https://www.internationalgenome.org/category/population/`.

	AFR	AMR	EAS	EUR	SAS	Not matched
British	4	50	6	430696	95	163
Irish				12748	3	2
White	1	2	1	540	1	
Other White		170	1	15533	18	93
Indian				21	5680	15
Pakistani				3	1742	3
Bangladeshi					220	1
Chinese		7	1483	3	3	8
Other Asian	1	1	359	216	1138	32
Caribbean	4117	1			36	143
African	3000		1	2	2	199
Other Black	90	1		1	5	21
Asian or Asian British			2	4	34	2
Black or Black British	23			2		1
White and Black Caribbean	93	16		74	11	403
White and Black African	102	13		52	4	231
White and Asian		42	10	242	349	159
Unknown	1024	541	712	3774	1020	749

Table S7: Self-reported ancestry (top) of the UK biobank individuals and their matching to 1000G populations (left) by our method. See the description of 1000G populations at `https://www.internationalgenome.org/category/population/`.

	British	Irish	White	Other White	Indian	Pakistani	Bangladeshi	Chinese	Other Asian	Caribbean	African	Other Black	Unknown
AFR_ACB										2024	66	34	198
AFR_ASW	2									1072	31	11	134
AFR_ESN										1	270	1	47
AFR_GWD											42		9
AFR_LWK			1								284	1	69
AFR_MSL										3	144	3	23
AFR_YRI									1	748	1796	24	404
AMR_CLM				18									27
AMR_MXL				21									117
AMR_PEL			1	1									30
AMR_PUR													1
EAS_CDX								4	15				10
EAS_CHB								218	23				33
EAS_CHS	1		1					907	17				42
EAS_JPT								10	53				221
EAS_KHV								314	171				274
EUR_CEU	183646	854	181	5802	2			1					883
EUR_FIN	1			126									1
EUR_GBR	235579	11461	294	2446	3						1		1066
EUR_IBS	68		7	775									24
EUR_TSI	2163	13	17	2185									365
SAS_BEB				1	229	17	215		92	20		1	209
SAS_GIH					416								4
SAS_ITU	1				813	12			220	4			135
SAS_PJL	5				3332	1392	2		203	1		1	238
SAS_STU					132				424				94
Not matched	9548	425	43	4440	789	327	4	50	528	424	570	42	5031

Table S8: Ancestry (left) of POPRES individuals and their matching to 1000G populations (top) by our method. See the description of 1000G populations at `https://www.internationalgenome.org/category/population/`.

	EUR_CEU	EUR_FIN	EUR_GBR	EUR_IBS	EUR_TSI	Not matched
Anglo-Irish Isles	136		127		2	1
Belgium	43					
Central Europe	47				8	
Eastern Europe	27				1	2
France	49		3	35	2	
Germany	67		3		1	
Italy	1			11	204	3
Netherlands	13		4			
Scandinavia	13	1	1			
SE Europe	12			3	70	9
SW Europe	1			261	1	1
Switzerland	179			32	11	

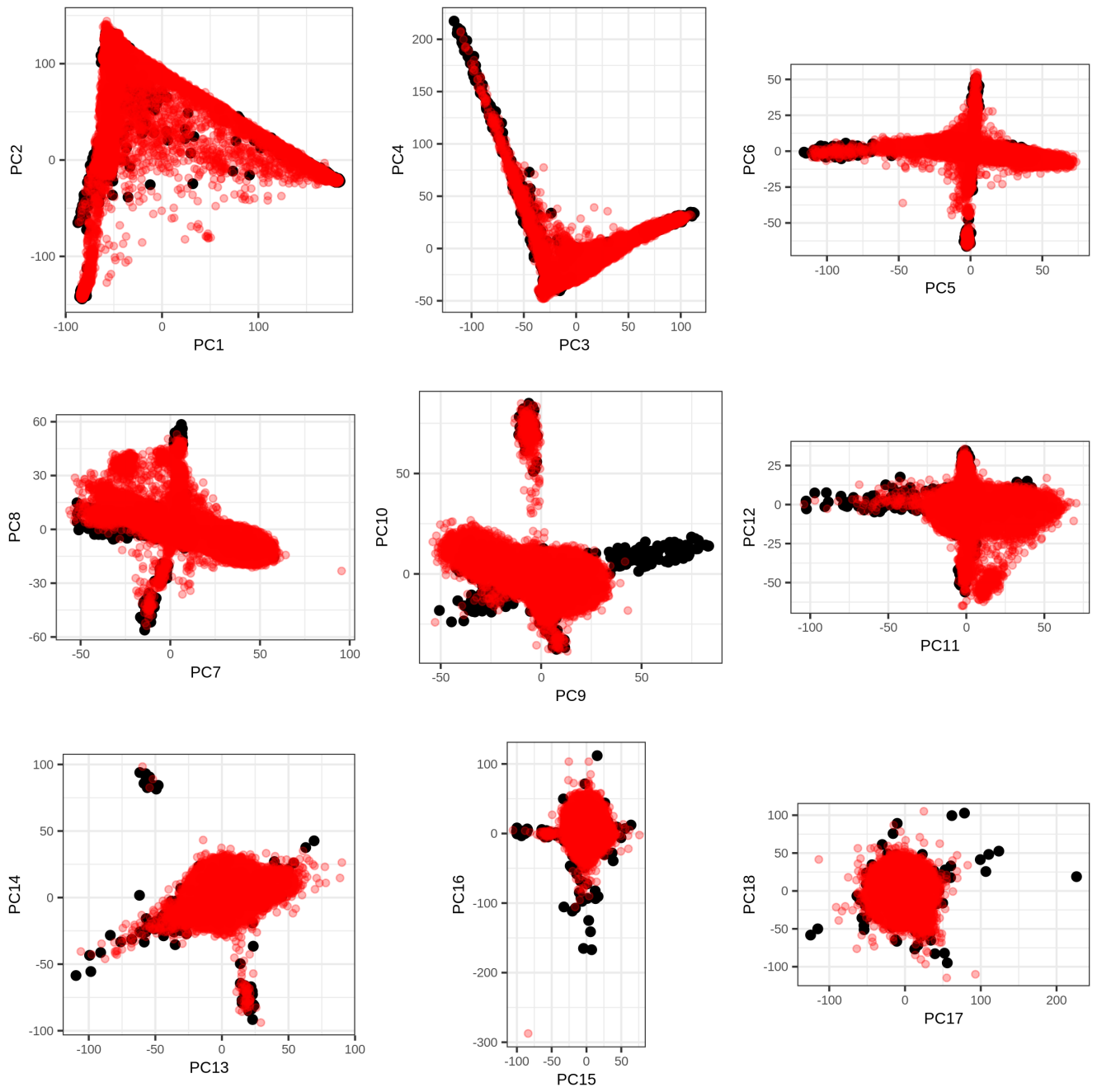

Figure S7: First 18 PC scores of the 1000G data (in black), onto which the UK Biobank data has been projected (in red).

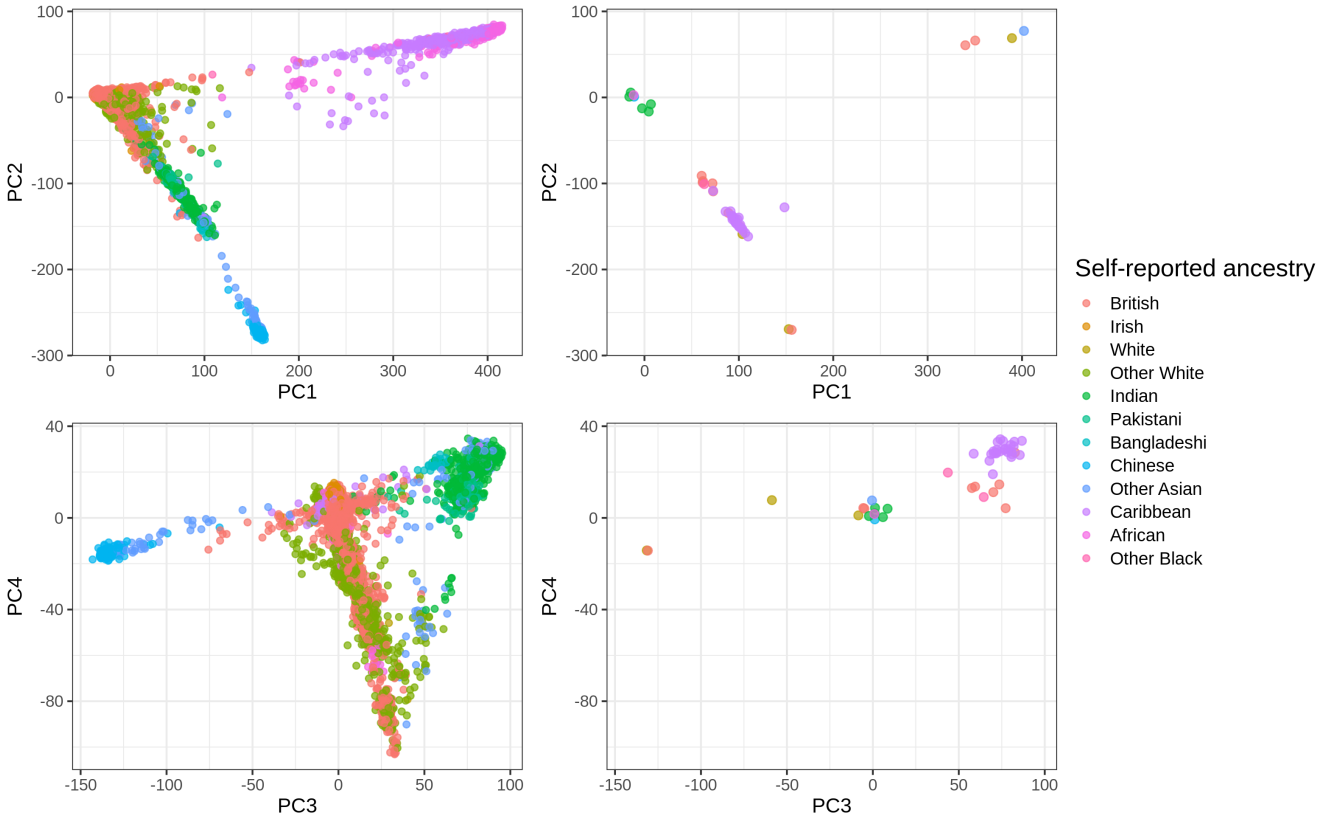

Figure S8: PC scores (computed in the UK Biobank) colored by self-reported ancestry. On the left, these are 50,000 random individuals. On the right, these are the 47 individuals with some discrepancy between their self-reported-ancestry and our ancestry estimation.

PCA-based ancestry grouping

Table S9: Number of individuals per self-reported ancestry in the UK Biobank (left) for each homogeneous ancestry group defined by our proposed methods.

	GBR	British	homogeneous	AFR	AFR2	EAS	EAS2	SAS	SAS2	AMR
British	416374	426210	421871	2	2	1	1	6	11	
Irish	12298	12712	12039							
White	471	492	467	1		1	1			1
Other White	7187	10932	8351					1	3	40
Indian	5	6	5					4922	5573	
Pakistani		1						1421	1724	
Bangladeshi								217	218	
Chinese	1	1	1			1453	1437		1	
Other Asian		4	1	1	1	279	62	939	1027	
Caribbean				3848	3578			25	25	
African	1	1	1	2633	2347				1	
Other Black				74	70			2	3	
Asian or Asian British						2	1	20	26	
Black or Black British	2	2	2	20	20					
White and Black Caribbean	7	7	4	24	14			1	1	1
White and Black African	5	6	4	5	3					
White and Asian	21	59	23			2		26	57	1
Unknown	1852	2008	1814	835	732	576	114	633	739	173
Total	438224	452441	444583	7443	6767	2314	1616	8213	9409	216

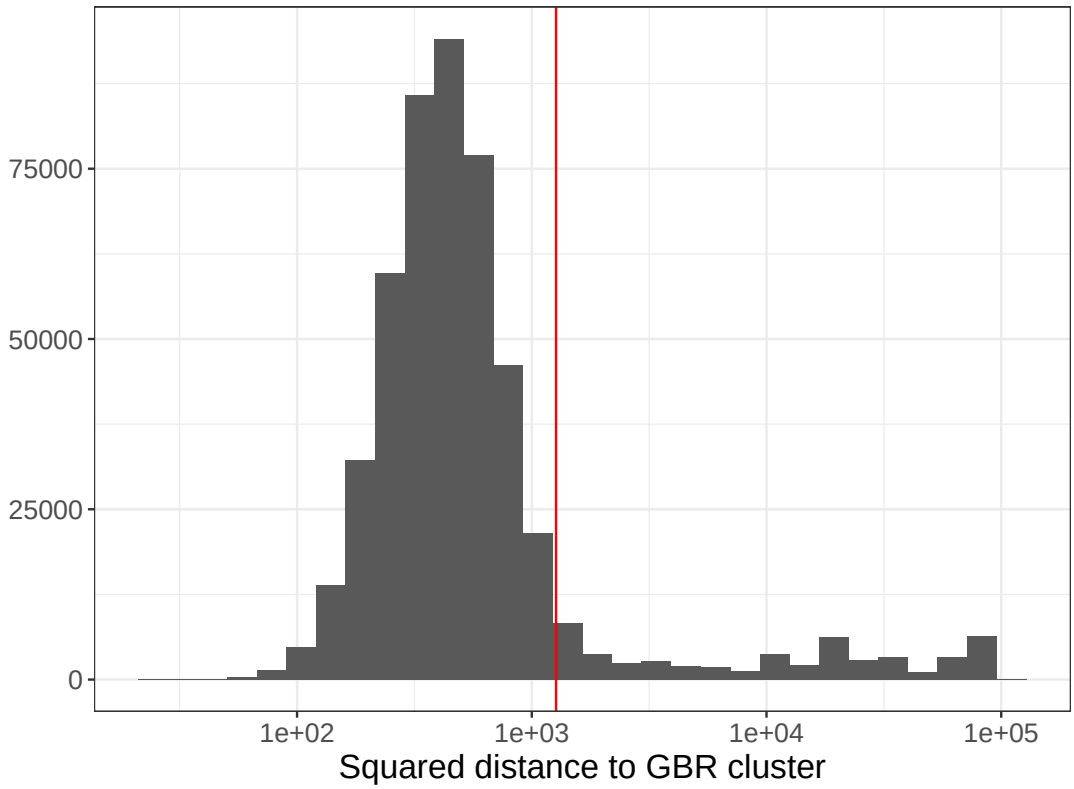

Figure S9: Histogram of squared distances (on a log scale) from the projected UK Biobank individuals to the geometric median of the GBR individuals from the 1000G data. The threshold in red assumes an F_{ST} of 0.002.

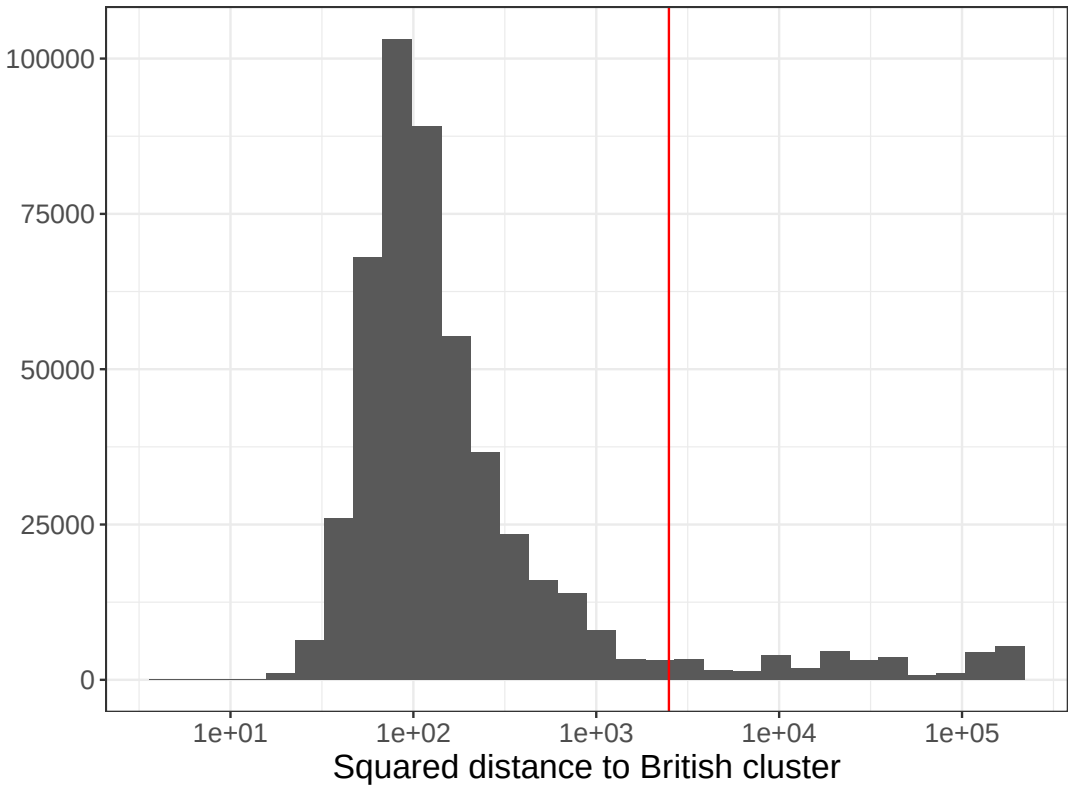

Figure S10: Histogram of squared distances (on a log scale) from the UK Biobank PC scores to the geometric median of the UKBB British individuals. The threshold in red assumes an F_{ST} of 0.002.

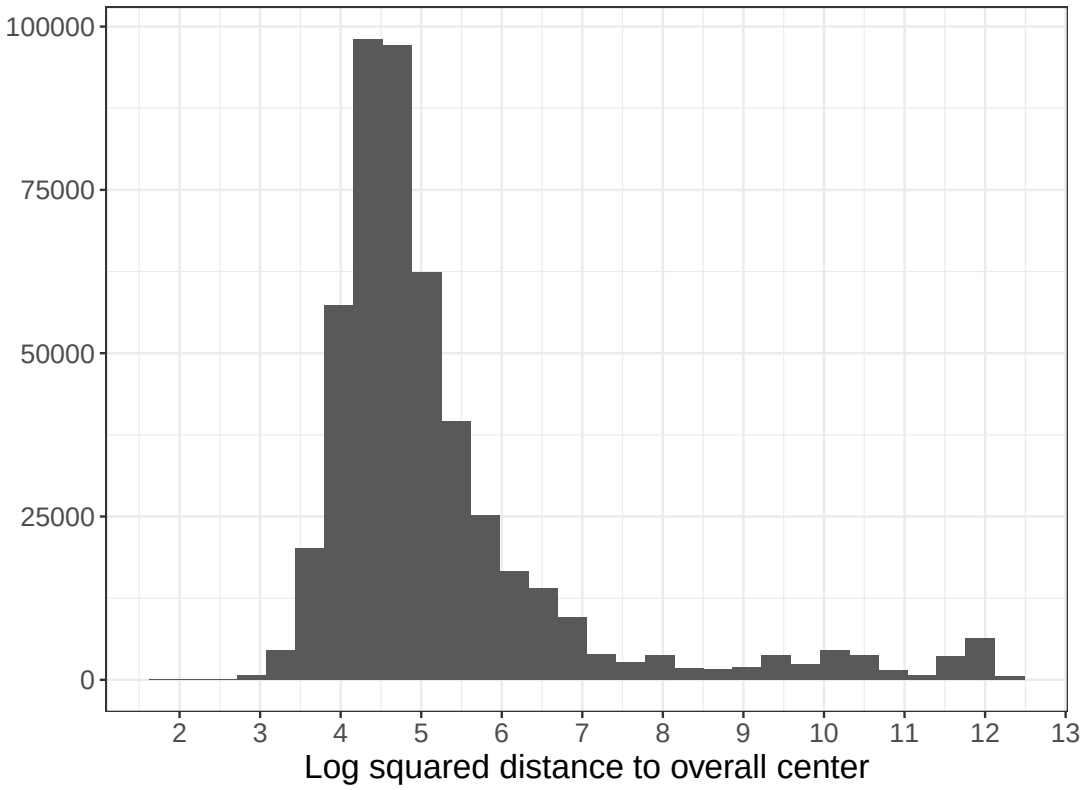

Figure S11: Histogram of (log) squared distances from the UK Biobank PC scores to the geometric median of the all UKBB individuals. Here we use a threshold at 7, based on visual inspection.