I generate PCA for all samples in the reference databases after LD filtration and calculated projection matrix by
$M'V'\Sigma^{-2}$, then plot target sample on this PCA.

I assume that any sample is either from a single population or a linear mixture of different populations and can be represented by the following linearly additive model (P represents each population, x represents the proportions and R_i represents the discrepancy of the observed value to the expected value):

$$S_i = \Sigma P_j x_{ij} + R_i$$
$$= \left(P_1 .... P_j\right)\begin{pmatrix} x_{i1} \\ ... \\ x_{ij} \end{pmatrix} + R_i \qquad ①$$
$$S_i = PX_i + R_i$$

and the variances should also follow linearly additive model.

$$V_i = \left(\sigma_1 .... \sigma_j\right) X_i = \sigma X_i \qquad ②$$

Thus, combining the ① and ②, the discrepancy relative to variance can be represented by

$$S_i = PX_i + R_i$$
$$= PX_i + diag(V_i)\, R_i' \qquad ③$$
$$diag^{-1}(V_i) S_i = diag^{-1}(V_i) PX_i + R_i'$$

While treating $\boxed{diag^{-1}(V_i)}$ as a constant matrix, and assuming that regardless with or with not relative to the variance, S_i's nearest point in space M should be close enough to each other.

Assuming the discrepancies correspond to the shortest distances to vector spaces formed by linear additive of super-populations, the discrepancy of each sample to any combination of populations can be determined as the following:

Any sample $diag^{-1}(V_i) S_i$'s shortest distance to space $diag^{-1}(V_i) P$ is the
$\mathrm{Re}\, jction_{S_i \to P} = diag^{-1}(V_i) S_i - \mathrm{Pr}\, ojection_{S_i \to P} = diag^{-1}(\sigma X_i)(I - P(P^T P)^{-1} P^T) S_i$
And any sample's ethnicity composition is estimated as $X_i = (P^T P)^{-1} P^T S$.

All samples' ethnicity compositions were estimated and minor components (proportion < 0.01). were discarded.