Integrating linguistics, social structure, and geography to model genetic diversity within India

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Supplementary Note

Normalized data sets

We assembled 48,225 genotypes for 891 samples from 90 well-defined ethnic groups (see **Supplementary Table 1**) which were collected from various sources [1–5]. After quality control for minor allele frequency (MAF) > 0.05, missingness rate less than 0.05 and Hardy-Weinberg test statistic less than 0.001 we removed 942 markers to end up with 47,283 autosomal SNPs. We did not use the Indian samples from the 1000 Genomes [6] project because of unavailability of their geographical coordinates as well as caste and language information. Additionally, three (GIH, STU, ITU) out of the five Indian populations in the 1000 Genomes project were collected from Indian Diaspora living in the USA (Houston) and the UK and might be biased and/or lead to gross underestimation of genetic diversity.

Social and language group encodings

India primarily has five language groups namely Andamanese (AND), Austro-Asiatic (AA), Dravidians (DR), Indo-Europeans (IE) and Tibeto-Burmese (TB). AND is split further into two groups: Ongan and the Great Andamanese languages. Apart from these it has some language isolates across the country but we have not included them in our study. PCA plot on Indian populations (Supplementary Figure S2 and Figure 1) reveal clusters corresponding to these language groups showing correlation of genetic mixture and langauge groups. Caste on the other hand further stratifies mixing of people due to the long imposed endogamy practiced in India. Caste has been a category of exclusion and social stratification in Indian society for the past 2000 years [7]. The society was mainly divided into privileged and under-privileged groups, constituted of upper or forward castes and lower or backward castes, respectively. Outside this caste structure were the Dalits or “untouchables” who were mostly subsistence farmers. They usually encompass broader range of communities apart from Scheduled Castes, as used by the Government of India. These communities usually constituted of tribal societies of the forest habitats and often practiced subsistence farming [7]. We encoded these forward and backward caste groups as Social Group A (SGA) and Social Group B (SGB), respectively. For the tribes outside of the caste system we used Social Group C (SGC).

As the consolidated data set was put together from so many varied sources, there was an imbalance of social group and language family representation (Table A) in the samples.

Language Groups					Social Groups		
AA	AND	DR	IE	TB	SGA	SGB	SGC
131	52	336	279	93	207	211	473

Table A: Number of samples per social and language groups in the entire consolidated data set as shown in Table S1A.

Language Groups				Social Groups		
AA	DR	IE	TB	SGA	SGB	SGC
92	93	94	89	107	43	218

Table B: Number of samples per social and language groups in the normalized data set. The normalization was done by language and geographical regions.

We had 16 SGA, 26 SGB, 48 SGC populations as well as 15 AA, 3 AND, 32 DR, 29 IE and 11 TB groups respectively for the entire data set. To create the normalized data set, we removed the population group Garo from the TB data set as the social group they belong to were unknown. Thus, the resulting data set had 90 individuals from TB and we sub-sampled a similar number of individuals from the other three language families. The sub-sampling was done with respect to the social group affiliation and geographical locations. As AA and TB speakers are more homogeneously located in the forests and hills of Central, East, and Northeast India, and, on the other hand, IE and DR speakers are more spread across the northern and southern India, we sampled individuals in order to guarantee a balanced representation of geographical variance. We also made sure that all language groups are equally represented in the normalized data set. This resulted in having 368 individuals sampled across 33 populations from all over India (Table B). We created multiple normalized subsets of the original consolidated data set using the same technique. For example, as shown in Table S1B, we included Kashmiri Pandits and Kshatriya for IE_SGA in the normalized subset used in this study. However, to check robustness, we included Brahmins and Srivastava for another subset and the same was done for each sociolinguistic category. Indeed, all our analyses returned similar results with very minor changes in the squared correlation values.

Correlation Optimization of Genetics and Geodemographics (COGG)

We now describe in more detail the proposed Correlation Optimization of Genetics and Geodemographics (COGG) method, which maximizes the correlation between one of the top two principal components and the geodemographic matrix, containing geographical coordinates, caste, tribe and language information. We restrict our encoding into three castes: SGA, SGB and SGCs, naming them as such instead of widely used conventional socially stigmatizing terms. We noticed that the Middle castes are genetically closer to the SGA, such as Kshatriya or Brahmins, hence, we labelled both Forward and Middle castes as SGA. Although the term Backward Class (as well as Scheduled castes and Scheduled Tribes) is used by the Government of India to classify social groups which are socially and educationally disadvantaged, we chose to call them SGB.

Let $\mathbf{u}$ be the m-dimensional vector containing (say) either of the top two PCs of the genetic covariance matrix, as computed by a software such as EIGENSTRAT [8], and let $\mathbf{G}$ denote the geodemographic matrix, as follows:

$$\mathbf{G} = \begin{array}{c}
\begin{array}{ccccccccc} G_1 & G_2 & G_3 & G_4 & G_5 & G_6 & G_7 & G_8 & G_9 \end{array} \\
\left[\begin{array}{c|c|c|c|c|c|c|c|c}
\vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \\
\vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \\
\mathit{Latitude} & \mathit{Longitude} & \mathit{SGA} & \mathit{SGB} & \mathit{SGC} & \mathit{AA} & \mathit{DR} & \mathit{IE} & \mathit{TB} \\
\vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \\
\vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots
\end{array}\right]
\end{array}$$

The social groups (SGA, SGB and SGC) and language (AA, DR, IE, TB) encoding was done as follows:

$$\textbf{Social groups (or Languages)} = \begin{cases} 1, & \text{if the sample belongs to that social group (or Language)} \\ 0, & \text{otherwise} \end{cases}$$

Let $\mathbf{a}$ be the k-dimensional vector whose elements are $a_1 \ldots a_k$ (in our case, $k = 9$). COGG solves the following optimization problem:

$$\max_{\mathbf{a}} \mathbf{Corr}\left(\mathbf{u}, \sum_{i=1}^{k} a_i \mathbf{G}_i\right). \tag{1}$$

Recalling the definition of the Pearson correlation coefficient, we can rewrite the above optimization problem as

$$\max_{\mathbf{a}} \mathbf{Corr}\left(\mathbf{u}, \sum_{i=1}^{k} a_i \mathbf{G}_i\right) = \max_{\mathbf{a}} \frac{\mathbf{u}^T(\sum_{i=1}^{k} a_i \mathbf{G}_i)}{\sqrt{\mathbf{Var}\left[\mathbf{u}\right] \mathbf{Var}\left[\sum_{i=1}^{k} a_i \mathbf{G}_i\right]}} = \max_{\mathbf{a}} \frac{\sum_{i=1}^{k} a_i(\mathbf{u}^T \mathbf{G}_i)}{\sqrt{\mathbf{Var}\left[\mathbf{u}\right] \sum_{i,j=1}^{k} a_i(\mathbf{G}_i^T \mathbf{G}_j) a_j}}. \tag{2}$$

Let $d_i = \mathbf{u}^T \mathbf{G}_i / \sqrt{\mathbf{Var}\left[\mathbf{u}\right]}$ for $i = 1 \ldots k$ and let $\mathbf{d}$ be the vector of the d_i's. Also, let $\mathbf{M}_{ij} = \mathbf{G}_i^T \mathbf{G}_j$ for all $i, j = 1 \ldots k$ and let $\mathbf{M}$ be the matrix of the $\mathbf{M}_{ij}$'s. By definition, $\mathbf{M}$ is a square, symmetric positive definite matrix and hence its square root $\mathbf{M}^{1/2}$ is well-defined. We can now rewrite the above equation as

$$\max_{\mathbf{a}} \left(\mathbf{u}, \sum_{i=1}^{k} a_i \mathbf{G}_i\right) = \max_{\mathbf{a}} \frac{\mathbf{d}^T \mathbf{a}}{\sqrt{\mathbf{a}^T \mathbf{M} \mathbf{a}}} = \max_{\mathbf{a}} \frac{\mathbf{d}^T \mathbf{a}}{\|\mathbf{M}^{1/2} \mathbf{a}\|_2}.$$

To understand the last equality let $\|\mathbf{x}\|_2$ denote the Euclidean norm of the vector $\mathbf{x}$ and recall that: *(i)* since $\mathbf{M}$ is symmetric positive definite matrix, $\mathbf{M} = (\mathbf{M}^{1/2})^T \mathbf{M}^{1/2}$ and *(ii)* $\sqrt{\mathbf{x}^T \mathbf{x}} = \|\mathbf{x}\|_2$ for any vector $\mathbf{x}$, including $\mathbf{x} = \mathbf{M}^{1/2} \mathbf{a}$. Now assume that $\mathbf{M}$ is invertible and make the change of variable $\mathbf{p} = \mathbf{M}^{1/2} \mathbf{a} / \|\mathbf{M}^{1/2} \mathbf{a}\|_2$. Notice that $\mathbf{p}$ is a unit norm vector (its Euclidean norm is equal to one) and that

$$\mathbf{a} = \|\mathbf{M}^{1/2} \mathbf{a}\|_2 \mathbf{M}^{-1/2} \mathbf{p}. \tag{3}$$

Thus, we get:

$$\max_{\mathbf{p}, \|\mathbf{p}\|_2 = 1} \left(\mathbf{u}, \sum_{i=1}^{k} a_i \mathbf{G}_i\right) = \max_{\mathbf{p}, \|\mathbf{p}\|_2 = 1} \mathbf{d}^T \mathbf{M}^{-1/2} \mathbf{p}. \tag{4}$$

Using sub-multiplicativity and the fact that $\mathbf{p}$ is a unit norm vector,

$$\mathbf{d}^T \mathbf{M}^{-1/2} \mathbf{p} \leq \|\mathbf{d}^T \mathbf{M}^{-1/2}\|_2 \|\mathbf{p}\|_2 = \|\mathbf{d}^T \mathbf{M}^{-1/2}\|_2 = \sqrt{\mathbf{d}^T \mathbf{M}^{-1} \mathbf{d}}. \tag{5}$$

The last equality follows from the fact that $\|\mathbf{x}\|_2 = \sqrt{\mathbf{x}^T\mathbf{x}}$ for any vector $\mathbf{x}$. The above upper bound is true for any unit norm vector $\mathbf{p}$ and can actually be achieved by the vector $\mathbf{p}_{\max}$:

$$\mathbf{p}_{\max} = \frac{\mathbf{M}^{-1/2}\mathbf{d}}{\|\mathbf{M}^{-1/2}\mathbf{d}\|_2}.$$

Indeed, it is easy to verify that $\mathbf{p}_{\max}$ is a unit norm vector that satisfies

$$\mathbf{d}^T\mathbf{M}^{-1/2}\mathbf{p}_{\max} = \mathbf{d}^T\mathbf{M}^{-\frac{1}{2}}\frac{\mathbf{M}^{-1/2}\mathbf{d}}{\|\mathbf{M}^{-1/2}\mathbf{d}\|_2} = \frac{\mathbf{d}^T\mathbf{M}^{-1}\mathbf{d}}{\sqrt{\mathbf{d}^T\mathbf{M}^{-1}\mathbf{d}}} = \sqrt{\mathbf{d}^T\mathbf{M}^{-1}\mathbf{d}}.$$

Thus, from eqn. (5), it follows that $\mathbf{p}_{\max}$ is a maximizer for the optimization problem of eqn. (4). If we let

$$\mathbf{a}_{\max} = \mathbf{M}^{-1}\mathbf{d},$$

it is easy to see that the above values for $\mathbf{a}_{\max}$ and $\mathbf{p}_{\max}$ satisfy

$$\mathbf{a}_{\max} = \|\mathbf{M}^{1/2}\mathbf{a}_{\max}\|_2\mathbf{M}^{-1/2}\mathbf{p}_{\max},$$

as stipulated by the change of variables from eqn. (3), and thus $\mathbf{a}_{\max}$ maximizes COGG. Plugging in the solution for $\mathbf{a}$, COGG revealed a squared Pearson correlation coefficient $r^2 = 0.93$ for PC1 vs $\mathbf{G}$ and $r^2 = 0.85$ for PC2 vs $\mathbf{G}$. These values represent a many fold increase from the original correlation values of $r^2 = 0.6$ for PC1 vs $\mathbf{G}'$ and $r^2 = 0.06$ for PC2 vs $\mathbf{G}'$, where $\mathbf{G}'$ is the matrix G without the sociolinguistic features, containing only the geographical coordinates. This highlights that geography is not enough as a feature to understand the genetic structure of the Indian populations.

To evaluate COGG without zero-one indicator variables we also applied a different encoding for $\mathbf{G}$ where we assigned 1, 2 and 3 for SGA, SGB and SGC, respectively in the social category and similarly 1, 2, 3 and 4 for AA, DR, IE and TB in language category. Running COGG with this encoding resulted in values of r^2 equal to 0.79 for PC1 and 0.82 for PC2, respectively. We observe that the value of r^2 for PC1 shows a decrease from 0.92 (when the previous encoding of zero-one indicator variable was used) to 0.79, whereas for PC2 it shows a smaller decrease.

We also investigated whether the values returned by COGG are statistically significant. We performed 1,000 iterations with randomly permuted values of the columns related to caste and language encoding in $\mathbf{G}$. We do not permute the columns corresponding to the geographical coordinates in order to maintain a baseline for the comparison. We randomly permuted the rows (individuals) corresponding to the seven columns (variables related to castes and language affiliations) in $\mathbf{G}$ and in each iteration we run COGG to find the optimal $\mathbf{a}_{\max}$ and the respective r^2 value. We find that the random permutations return a maximal value of r^2 equal to 0.6422 for PC1 and 0.1679 for PC2 (Supplementary Figure S6). This is a minor increase from 0.6 and 0.06 respectively for PC1 and PC2, clearly indicating the importance of the caste and language encoding in $\mathbf{G}$.

If there is "multicolinearity" or strongly correlated variables in $\mathbf{G}$, the inverse of that matrix might exhibit numerical instability as the smallest singular value of the covariance matrix might be close to zero. To avoid this, we regulate the smallest singular value by taking a regularized pseudoinverse of the covariance matrix.

Prior work attempted to disentangle the effects of non-genetic variables such as geography, linguistics, subsistence, social or ecological factors from the genetic variables captured by the top principal components. One such study [9] regressed the top 20 PCs computed from the genotypes of the Khoe-San populations with various combinations of geographic, linguistic and subsistence covariates, and used cross-validation scores to understand which non-genetic variable can predict the observed genetic patterns. They observed that languages improve the predictive capacity of a model that includes only geography in the sub-Saharan and the Southern African data set. This is similar to the intuition of COGG, which provides a conceptually straightforward model to do an in-depth study to account for the factors within the broad generic non-genetic factors, such as which language and social group explain most of the genetic variation captured by the top principal components. Also, in addition, we do a feature selection procedure to obtain the most significant variables in the geodemographic matrix, unlike previous studies. Another study [10] employed a Bayesian framework to isolate ecological factors from geographic distances. Broadly, COGG tries to achieve the same goal, but it provides the ease of use in this setting, where one can just encode the environmental and ecological factors as covariates and solve the underlying optimization problem to obtain the maximum correlation. Along with this, it is easier to comprehend, as it is closer to a linear regression setting.

Canonical Correlation Analysis (CCA)

Finally, there is no mathematical reason to restrict COGG to the top two PCs of the genetic similarity covariance matrix. Prior work has exclusively focused on studying the correlation between longitude and latitude and the top two principal components; COGG goes beyond this by adding geodemographic features to study more general correlations. Our next method applies Canonical Correlation Analysis (CCA, introduced in [11]) to simultaneously study the correlation between the top q Principal Components (where q is a user-defined parameter) and the geodemographic matrix $\mathbf{G}$. CCA extracts linear components that capture correlations between two input datasets, in a manner analogous to PCA. From a statistical point of view, CCA extracts directions of maximal "correlation" between a pair of datasets represented by matrices. From a linear algebraic point of view, CCA measures the similarities between the subspaces spanned by the columns of each of the two datasets, represented by matrices [12]. In our case, we extend the optimization problem of eqn. (1) to identify the maximal correlation to include the matrix of top q principal components denoted as $\mathbf{U} \in \mathbb{R}^{m \times q}$ for m individuals and $\mathbf{G}$, the geodemographic matrix as described earlier. We obtain $\mathbf{U}$ by considering the top q left singular vectors of the genetic covariance matrix of the normalized subset. Formally, we define the following optimization problem, which we call COGG-CCA:

$$\max_{\mathbf{a},\mathbf{b}} \mathbf{Corr}\left(\sum_{j=1}^{q} b_j \mathbf{U}_j, \sum_{i=1}^{k} a_i \mathbf{G}_i\right), \tag{6}$$

where $\mathbf{b}$ is a p-dimensional vector whose entries are the b_j's and $\mathbf{a}$ is a k-dimensional vector whose entries are the a_i; $\mathbf{U}_j$ and $\mathbf{G}_i$ represent the j-th and i-th column of $\mathbf{U}$ and $\mathbf{G}$ as column vectors. Solving COGG-CCA analytically dates back to the work of [11] and allows us to obtain the following closed form solution for the vectors $\mathbf{a}$ and $\mathbf{b}$, the unknown coefficient vectors associated with the matrices $\mathbf{G}$ and $\mathbf{U}$, respectively.

Let $\mathbf{\Sigma}_{UU} = \mathbf{Cov}\left[U, U\right]$, $\Sigma_{GU} = \mathbf{Cov}\left[G, U\right]$, and $\Sigma_{GG} = \mathbf{Cov}\left[G, G\right]$ denote three covariance matrices and construct

$$\mathbf{\Sigma} = \mathbf{\Sigma}_{GG}^{-1/2}\mathbf{\Sigma}_{GU}\mathbf{\Sigma}_{UU}^{-1/2}.$$

Then, $\mathbf{a}$ is the top right singular vector of the matrix $\mathbf{\Sigma}$ and $\mathbf{b}$ is the top left singular vector of $\mathbf{\Sigma}$; it is well-known that the maximum correlation coefficient is equal to the largest singular value of the matrix $\mathbf{\Sigma}$. Applying COGG-CCA on our data, we obtain the maximum value $r^2 = 0.94$ for $q = 8$. To check for statistical significance of COGG-CCA, we first formed the baseline of r^2 by just including the geographical coordinates in the geodemographic matrix $\mathbf{G}$. This resulted in $r^2 = 0.74$. Next, we permuted the features in both the matrices, $\mathbf{G}$ and $\mathbf{U}$, respectively which resulted in a very small increase from the baseline with $r^2 = 0.76$, whereas COGG-CCA, even with smaller values of q resulted in very high r^2 (Supplementary Figure S7).

Feature selection using Orthogonal Matching Pursuit (OMP)

We used a greedy feature selection algorithm described in [13] to select features in the geodemographic matrix $\mathbf{G} \in \mathbb{R}^{m \times k}$ containing m individuals and k demographic features. The precise algorithm is described below.

Algorithm 1 OMP Algorithm for Feature Selection

```
**Input:** matrix $\mathbf{G}$, column vector $\mathbf{U} \in \mathbb{R}^m$, $\epsilon > 0$
**Output:** matrix $\mathbf{C} \in \mathbb{R}^{m \times p}$ which has columns of $\mathbf{G}$ with indices in $\tau$, $|\tau| = p$, $p < k$
$\tau \leftarrow \phi$; $r \leftarrow 0$; $\mathbf{U}^{(0)} \leftarrow \mathbf{U}$; $\mathbf{G}^{(0) \leftarrow \mathbf{G}}$;$\mathbf{C} \leftarrow \phi$
**while** $\|\mathbf{U}^{(r)}\|_2 > \epsilon$ **do**
    **for** $i \in \{1, 2, \cdots, k\} - \tau$ **do**
        choose $\mathbf{i}$ corresponding to maximum $\boldsymbol{corr}\Big(\mathbf{U}^{(r)}, \mathbf{G}_i^{(r)}\Big)$
    **end for**
    $\tau \leftarrow \tau \cup \{i\}$; $\mathbf{V} \leftarrow \mathbf{G}_i^{(r)}$
    remove column $i$ from $\mathbf{G}^{(r)}$ to form $\mathbf{G'}^{(r)}$
    project $\mathbf{G'}^{(r)}$ onto the subspace orthogonal to $\mathbf{V}$, i.e., $\mathbf{G}^{(r+1)} \leftarrow \mathbf{G'}^{(r)} - \left(\mathbf{V}\mathbf{V}^{\dagger}\right)\mathbf{G'}^{(r)}$
    project $\mathbf{U}^{(r)}$ onto the subspace orthogonal to $\mathbf{V}$, i.e., $\mathbf{U}^{(r+1)} \leftarrow \mathbf{U}^{(r)} - \left(\mathbf{V}\mathbf{V}^{\dagger}\right)\mathbf{U}^{(r)}$
    $r \leftarrow r + 1$
**end while**
$\mathbf{C} \leftarrow \mathbf{G}_\tau$
```

Ridge Leverage Scores

We start with the definition of the *statistical leverage scores* of a matrix.

Definition 1 Given an arbitrary $m \times n$ matrix $\mathbf{A}$ with $m > n$, let $\mathbf{U}$ denote the $n \times d$ matrix consisting of the d *left singular vectors* of $\mathbf{A}$ and let U_{i*} denote the i^{th} row of the matrix $\mathbf{U}$ as a *row vector*. Then, the statistical leverage scores of the rows of $\mathbf{A}$ are given by

$$\ell_i = \|\mathbf{U}_{i*}\|_2^2$$

Classical leverage scores quantify the importance of each column i for the range space of the data matrix $\mathbf{A}$. They are widely used in regression problems, outlier detection and randomized matrix algorithms. They are used to select important features from an under-determined system. To address instability issues in a regression, ridge regression is performed and an extension of this notion of *classical* leverage scores to a ridge regression setting is known as *ridge leverage scores*. It is defined as follows.

Definition 2 The ridge leverage score ${\tau_i}^{\lambda}(\mathbf{A})$ is defined as,

$${\tau_i}^{\lambda}(\mathbf{A}) = \Big(\mathbf{A}\mathbf{A}^\top \left(\mathbf{A}\mathbf{A}^\top + \lambda \mathbf{I}_n\right)^{-1}\Big)_{ii}$$

where $\lambda > 0$ is the regularization parameter. Further simplifying, the row ridge leverage scores boil down to the following,

$$\begin{aligned}
{\tau_i}^{\lambda}(\mathbf{A}) &= \Big(\mathbf{A}\mathbf{A}^\top \left(\mathbf{A}\mathbf{A}^\top + \lambda \mathbf{I}_n\right)^{-1}\Big)_{ii} \\
&= \left(\mathbf{U}\boldsymbol{\Sigma}\mathbf{V}^\top\mathbf{V}\boldsymbol{\Sigma}^\top\mathbf{U}^\top(\mathbf{U}\boldsymbol{\Sigma}\mathbf{V}^\top\mathbf{V}\boldsymbol{\Sigma}^\top\mathbf{U}^\top + \lambda\mathbf{I}_n)^{-1}\right)_{ii} \\
&= \left(\mathbf{U}\boldsymbol{\Sigma}^2\mathbf{U}^\top(\mathbf{U}\boldsymbol{\Sigma}^2\mathbf{U}^\top + \lambda\mathbf{U}\mathbf{U}^\top)^{-1}\right)_{ii} \\
&= \left(\mathbf{U}\boldsymbol{\Sigma}^2(\boldsymbol{\Sigma}^2 + \lambda)^{-1}\mathbf{U}^\top\right)_{ii} \\
&= \left(\mathbf{U}\boldsymbol{\Sigma}_\lambda\mathbf{U}^\top\right)_{ii}
\end{aligned}$$

For the above, we have assumed that $\mathbf{A}$ has full row rank as $d >> n$. Therefore the thin SVD (Singular Value Decomposition) of $\mathbf{A}$ is $\mathbf{U}\boldsymbol{\Sigma}\mathbf{V}^\top$, where $\mathbf{U} \in \mathbb{R}^{n \times n}$, $\mathbf{V} \in \mathbb{R}^{d \times n}$ and $\boldsymbol{\Sigma} \in \mathbb{R}^{n \times n}$ whose diagonal elements are the singular values of $\mathbf{A}$. For the above simplification we have used the fact that $\mathbf{U}$ and $\mathbf{V}$ are orthogonal matrices with orthonormal columns hence, $\mathbf{U}\mathbf{U}^\top = \mathbf{U}^\top\mathbf{U} = \mathbf{I}_n$ and $\mathbf{V}\mathbf{V}^\top = \mathbf{V}^\top\mathbf{V} = \mathbf{I}_d$ and their inverse is equal to transpose. Also, from above, $\boldsymbol{\Sigma}_\lambda \in \mathbb{R}^{n \times n}$ and the i^{th} diagonal entry of it is defined as,

$$\left(\boldsymbol{\Sigma}_\lambda\right)_{ii} = \sqrt{\frac{\sigma_i^2}{\sigma_i^2 + \lambda}}, \; i = \{1, 2, \cdots, n\} \tag{7}$$

Thus, we can write the row ridge leverage scores as,

$$\tau^{\lambda}(\mathbf{A}) = \|\mathbf{U}\mathbf{\Sigma}_{\lambda}\|_2^2$$

Armed with this definition we devise the algorithm to calculate the RLS statistic.

Algorithm 2 Row Ridge leverage score algorithm

```
1: Input: A matrix, $\mathbf{A} \in \mathbb{R}^{m \times n}$
2: Output: $\tau^{\lambda}(A) \in \mathbb{R}^{m \times 1}$
3: $\mathbf{B} = \mathbf{A}\mathbf{A}^{\top}$
4: Compute thin SVD of $\mathbf{B} = \mathbf{U}\mathbf{\Sigma}\mathbf{V}^{\top}$
5: Choose $\lambda = \text{mean}\{\sigma_1, \sigma_2, \cdots, \sigma_n\}$ where $\sigma_i$ is the $i^{th}$ diagonal element of $\mathbf{\Sigma}$
6: Compute $(\mathbf{\Sigma}_{\lambda})$ as defined in 7
7: Compute $\tau^{\lambda}(\mathbf{A}) = \|\mathbf{U}\mathbf{\Sigma}_{\lambda}\|_2^2$
8: Return the vector $\tau^{\lambda}(\mathbf{A})$
```

We obtain the row ridge leverage scores in this manner for the respective mean-centered (the columns of the matrix are centered around it's mean i,e. the mean of each column is subtracted from values corresponding to each row of the column) genotype matrix consisting of m individuals and n SNPs and the geodemographic matrix (described earlier). Thereafter, we compute the additive ridge leverage score per population as described in the Materials and Methods. This ensures important observations from both matrices are considered together.

Running COGG with the significant ethnic groups as shown in Table 1 on 90 pan-Indian populations further confirmed the importance of these populations in shaping Indian genetics. The r^2 value between geographical coordinates and the PCs came out to be 0.21 for PC1 and 0.08 for PC2, when COGG was run with populations from Table 1. COGG was run for the same populations and the values returned were $r^2 = 0.853$ for PC1 and the geodemographic matrix $\mathbf{G}$ and $r^2 = 0.794$ for PC2 and $\mathbf{G}$. Thus, COGG returns very high correlations using only the populations selected using the RLS statistics, capturing most of the variance reflected by the top PCs of the genetic matrix.

Estimating population admixture

We applied ADMIXTURE on the three data sets namely, the pan-Indian data set, the normalized Indian data set and the Eurasian data set just like we did for PCA. ADMIXTURE on the entire Indian data set (Supplementary Figure S3A), with all populations, revealed that the groups SGB and SGCs for AA and TB, along with some DR_SGB and SGCs (such as Paniyas, Kadar and Irulas) show divergence from DR_SGA and IE populations (Supplementary Figure S9). This is replicated in the ADMIXTURE output of the normalized Indian data set. When applied on the Eurasian data set, the IE and DR_SGAs, along with IE_SGB and SGCs cluster together with most Northwestern Frontier populations. The TB_SGC and SGA show signs of admixture from the Chinese populations. Some Middle Eastern populations and Caucasians share the same ancestral components as the IE and DR_SGA. The European populations seem to be sharing very small amount of ancestral components with the IE and DR speaking groups. To investigate further and quantify the shared ancestry between these populations we employed a quantitative meta-analysis of ADMIXTURE which was first developed in [14].

We now describe in more detail our quantitative analysis of ADMIXTURE's output. Given a target population X and reference populations Y, Z, etc., we were interested in quantifying the amount of ancestry of population X that is captured by populations Y, Z, etc. Towards that end we devised a new approach to quantitatively analyze the output of ADMIXTURE. Recall that ADMIXTURE, for a particular value of K, will represent each sample using K coordinates. Thus, for a particular value of K and for a particular population Y with n samples, we can represent the output of ADMIXTURE for this population as an n-by-K table. Then, for each reference population Y, we summarize this n-by-K matrix using its top right singular vector only; in all our analyses, the top singular value corresponding to the top right singular vector captured at least 80% of the reference population variance as represented by ADMIXTURE. Let v_Y be the top right singular vector (a K-dimensional vector) for population Y; similarly, let v_Z be the top right singular vector (a K-dimensional vector) for population Z, etc. Now that we have represented the ADMIXTURE output for each population as a K-dimensional signature vector, we can apply standard vector space calculus in order to answer our original question: how much of the ancestry of population X is captured by population Y, or population Z, etc. More specifically, in order to compute the percentage of the ancestry of population X that is captured by population Y, we compute the percentage of the norm of V_X that is captured (in projection sense) by v_Y. Formally, we compute

$$\frac{\|V_X - v_Y \cdot v_Y^{\dagger} \cdot V_x\|_F}{\|V_X\|_F}$$

which returns a value between zero and one. In the above, V_X denotes the m-by-K matrix representing the m samples of population X with respect to the K coordinates returned by ADMIXTURE. The notation $v_Y^{\dagger}$ indicates the pseudoinverse of the vector v_Y, which is equal to the transpose of the vector v_Y, suitably normalized. It is also worth noting that the norm used in the above equation is the standard matrix Frobenius norm. In order to quantify the amount of ancestry of population X that is captured by both populations Y and Z, we form the K-by-2 matrix $V = [v_Y v_Z]$ whose columns are the vectors v_Y and v_Z and we compute

$$\frac{\|V_X - V \cdot V^{\dagger} \cdot V_x\|_F}{\|V_X\|_F}$$

In the above equation, $V^{\dagger}$ denotes the pseudoinverse of the matrix V; the matrix $VV^{\dagger}$ is a projector on the subspace spanned by the column space of V. Thus, we basically extract from the matrix V_X the part of V_X that is captured by the (subspace spanned by the) vectors v_Y and v_Z.

The meta-analysis when applied on the pan-Indian data set (891 individuals; 90 populations) showed that AA_SGC share a small amount of ancestry with other IE and DR tribal speakers (19%), whereas TB_SGC are completely isolated (Supplementary Figure S3B). DR_SGC show divergence from other populations, which is due to a few tribal populations such as Irula, Kadar, and Paniyas (as pointed out in Figure S2A). We investigate this further when we apply the meta-analysis on the pan-Indian data set and study the meta-analysis of each population group (Supplementary Table S2). The most significant observation is that IE and DR populations across their caste affiliations (except DR_SGC) cluster together, showing high shared ancestry among the SGA and SGB. The IE_SGC also share very high ancestry with the IE and DR SGA and SGC. This supports the autochthonous origin of the caste system in India. Applying the meta-analysis of ADMIXTURE to the Eurasian data along with the normalized Indian data set shows that the IE and DR speakers, along with the TB_SGA, share significant amount of ancestry with Northwestern Frontier provinces (maximum in IE_SGA, who share close to 80%), which is further validated by f_3 statistics. The TB_SGC and TB_SGA share approximately 94% and 68% ancestry with the Chinese populations, as well as with Mongolia. The Uygurs, along with the whole of Central Asia seems to share a small amount of ancestry with the IE populations across social groups, as well as with DR_SGA. We see similar trends in Turkey, Caucasia and European populations, sharing more ancestry with IE and DR SGAs. These populations also share close to 20% ancestry with IE_SGCs. This shows that with the spread of IE languages, some tribes have been in touch with the migrating populations who followed the path from Siberia and Mongolia through Central Asia and Northwestern Frontier provinces. We validate these findings with f_3 statistics and TreeMix analyses.

Linear Discriminant Analysis

The genotype score value was assigned as the sum of a value of 0 for the major allele and 1 for the minor allele for each strand. The counts for each genotype out of N samples are n_{00} for homozygous major allele, n_{01} for a heterozygous genotype, and n_{11} for the homozygous minor allele. The total score across N samples will be $1 \cdot n_{01} + 2 \cdot n_{11}$, with the average being $\bar{s} = (n_{01} + 2 \cdot n_{11})/(2N)$. The average squared score is $\bar{s^2} = (n_{01} + 4 \cdot n_{11})/(2N)$, so the variance is $\mathbf{Var}[s] = \bar{s^2} - (\bar{s})^2$. Scores assigned to each genotype are scaled to be $(s - \bar{s})/\sqrt{\mathbf{Var}[s]}$. In the case of Hardy-Weinberg equilibrium, this reduces to a form proportional to that employed in Eigenstrat [8]. This adjustment was applied to PCA computations performed for comparisons with LDA in this study, as well as in the normalization of the LDA input scores.

We maintain a matrix, $d \in \mathcal{R}^{N \times D}$, where N rows represent the individuals and D columns represent a genotype score. There are G groups of populations and each group has p individuals. The matrix d

is indexed as $d_{gpi,k}$, where $p \in g$ ($g \in G$) and $i \in p$, each with a vector of genotype scores indexed by $k \in D$. We define, $n_{gp} = |p|$ for $p \in g$, and $n_{g.} = \sum_{p \in g} n_{pg}$, then $N = \sum_{g \in G} n_{g.}$, the data are decomposed into components $d_{gpi,k} = x_{...,k} + x_{g..,k} + x_{gp.,k} + x_{gpi,k}$ such that $\sum_{i \in p} x_{gpi,k} = 0$, $\sum_{p \in g} n_{gp} x_{gp.,k} = 0$, and $\sum_{g \in G} n_{g.} x_{g..,k} = 0$.This produces a hierarchic decomposition of the variations among groups and populations similar to AMOVA [15], but each population and group is weighted by the number of samples they contain. Their values are determined from $x_{...,k} = N^{-1} \sum\limits_{g \in G, p \in g, i \in p} d_{gpi,k}$, $x_{g..,k} = n_{g.}^{-1} \sum\limits_{p \in g, i \in p} d_{gpi,k} - x_{...,k}$, $x_{gp.,k} = n_{gp}^{-1} \sum\limits_{i \in p} d_{gpi,k} - x_{...,k} - x_{g..,k}$, and $x_{gpi,k} = d_{gpi,k} - x_{...,k} - x_{g..,k} - x_{gp.,k}$.

The total covariance is

$$\begin{aligned} c_{k',k} &= N^{-1} \sum_{g \in G, p \in g, i \in p} \left(d_{gpi,k'} - x_{...,k'}\right)\left(d_{gpi,k} - x_{...,k}\right) \\ &= N^{-1} \sum_{g \in G} n_{g.} x_{g..,k'} x_{g..,k} + N^{-1} \sum_{g \in G, p \in g} n_{gp} x_{gp.,k'} x_{gp.,k} + N^{-1} \sum_{g \in G, p \in g, i \in p} x_{gpi,k'} x_{gpi,k}. \end{aligned}$$

Then $N^{-1} \sum\limits_{g \in G, p \in g, i \in p} x_{gpi,k'} x_{gpi,k}$ represents the variation within populations, $N^{-1} \sum\limits_{g \in G, p \in g} n_{gp} x_{gp.,k'} x_{gp.,k}$ represents the variation between populations within groups, and $(S_B)_{k'k} = N^{-1} \sum\limits_{g \in G} n_{g.} x_{g..,k'} x_{g..,k}$ represents the variation between groups. The total variation within groups is:

$$(S_W)_{k'k} = N^{-1} \sum_{g \in G, p \in g} n_{gp} x_{gp.,k'} x_{gp.,k} + N^{-1} \sum_{g \in G, p \in g, i \in p} x_{gpi,k'} x_{gpi,k}$$

.

While this could be evaluated for each individual SNP by choosing $k = k'$ and probing those, it is desirable to find combinations of SNPs that are most informative of the genetic differences among groups. Those combinations may be expressed in terms of vectors $\hat{u}$ with components $\hat{u}_k$. Then the projections on the x's would have the form $\sum\limits_{k \in [D]} x_{gpi,k} \hat{u}_k$. Along these projections, it is possible to write a ratio expressing the variation between groups vs within groups as $f(\hat{u}) = \frac{\hat{u}^T S_B \hat{u}}{\hat{u}^T S_W \hat{u}}$ [16,17]. Identifying $v = S_W^{1/2} \hat{u}$, this becomes $f(u(\hat{v})) = \hat{v}^T S_W^{-1/2} S_B S_W^{-1/2} \hat{v}$. This yields stationary values where $\hat{v}$ are eigenvectors of $S_W^{-1/2} S_B S_W^{-1/2}$, with eigenvalues directly corresponding to f.

The genetic associations identified by the $\hat{u}$ were tested by comparing the f's computed from the populations to those obtained for samples randomly permuted among the groups. Another caveat is that the largest eigenvalues of $S_W^{-1/2}$ correspond to the smallest eigenvalues of S_W. Yet, these are the most sensitive to sampling variation, genotyping errors, and cumulative computational errors. Further, the smallest, most error prone eigenvalues in S_W tend to dominate $S_W^{-1/2}$, as well as f's, even though they do not carry useful information. We apply a threshold for a ratio between eigenvalues of S_W between maximum and threshold, yielding a reciprocal square root ratio for included eigenvalues and eigenvectors in constructing $S_W^{-1/2}$. This restricts the computation to the subspace operationally spanned (or explored) by $S_W^{-1/2}$.

In general, d will be $N \times D$ dimensional with S_B and S_W being $D \times D$. Eigenvector computational space requirements for these tend to be prohibitive. Further, d will span an $N \ll D$ dimensional space. In the singular value decomposition $d = USV^T$ where V is orthonormal, then $dd^T = US^2U^T$, with S^2 diagonal. Since dd^T is symmetric, U is also orthonormal. Once U and S were determined by diagonalization of dd^T, $V = d^T US^{-1}$. V then represents a basis of N orthogonal D dimensional vectors. In that basis, $dV = US$ and $V^T S_B V$ and $V^T S_W V$ are $N \times N$ matrices. Computations of f were performed in this basis. LDA was run the normalized Indian data set of 33 populations, but now the groupings were by language affiliations of the individuals. The top two discriminants when plotted against each other, revealed a very strong evidence on the langauge-caste interplay, as pointed out in the selected features from COGG. In Figure S3A, separate clines appear from left to right, with the first cline of IE_SGC, followed by AA_SGC, DR_SGC and TB_SGC and TB_SGA. Further clines of DR_SGB, DR_SGA and IE_SGA and IE_SGB appear. This clearly shows the genetic stratification influenced by caste groups and then language groups within the caste groups. Thus, we see a two-layer stratification, when LDA was run with the language-caste groups.

Next, we applied LDA to the same dataset, to look further into the geography-social group-language interplay which was revealed by COGG. We first computed LDA with the supervised regional groups such as 'North', 'South', 'East', 'Northeast', 'Central-East' and 'Central'. The first two discriminants (Supplementary Figure S5B) reveals the stratification by the geographical locations of the individuals under study. There is a clear gradient from TB speakers in the left forming a cline with IE speakers on the right reflecting the east-west span of India with IE speakers in the northwestern regions surrounding Pakistan and TB speakers in northeastern states. However, LDA does not pick up the north-south variation between IE, AA and DR speakers. Instead we get a blob of IE_SGC, IE_SGA with DR speakers. This is probably attributed to the strict imposition of endogamy on IE and DR speakers across India.

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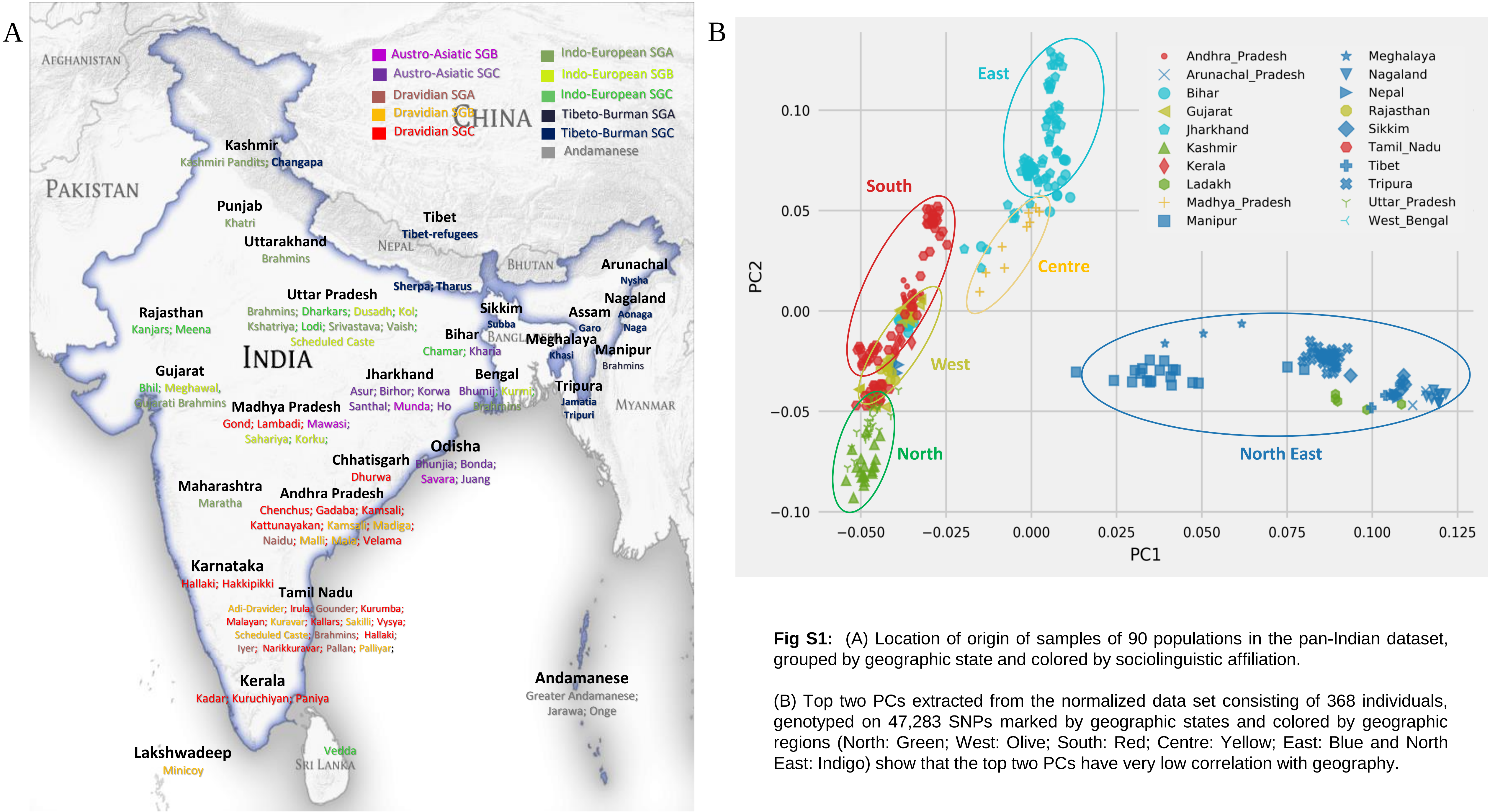


Fig S1: (A) Location of origin of samples of 90 populations in the pan-Indian dataset, grouped by geographic state and colored by sociolinguistic affiliation.

(B) Top two PCs extracted from the normalized data set consisting of 368 individuals, genotyped on 47,283 SNPs marked by geographic states and colored by geographic regions (North: Green; West: Olive; South: Red; Centre: Yellow; East: Blue and North East: Indigo) show that the top two PCs have very low correlation with geography.

Fig S2: Population Structure of Indian populations

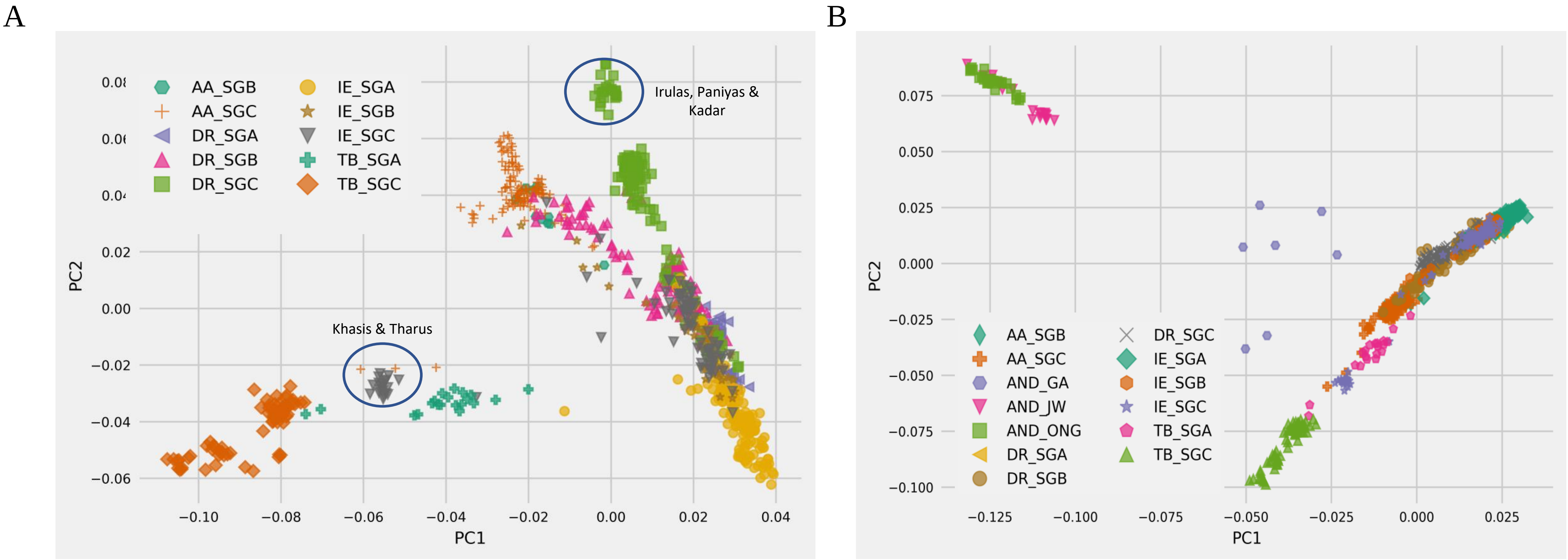


Fig S2: (A) PCA plot of all mainland Indian samples (839 individuals). We note that the formation of the clusters is primarily dominated by language groups, with TB_SGC and TB_SGA forming a cluster with Khasis (AA_SGC) and Tharus (IE_SGC) showing signs of admixture. The IE and DR speakers form a cline with a gradient of social groups within, IE_SGA and DR_SGC occupying the ends of the cline. We also observe that the Irulas, Paniyas, Kurumba and Kadars show divergence from other Dravidian tribal populations.

(B) ALL 891 Indian samples (including outliers from Andaman islands) projected as the top two PCs. In presence of outliers, we observe a cline for mainland Indian populations and an outlier cluster of Ongan language speaking Jarawa (AND_JW) and Onge (AND_ONG). However, the Great Andamanese (AND_GA) lies near the mainland Indian populations. Proportions of variance explained for the top 3 PCs are 33%, 22% and 12.7%,

Fig S3A: Admixture ancestry of Indian populations

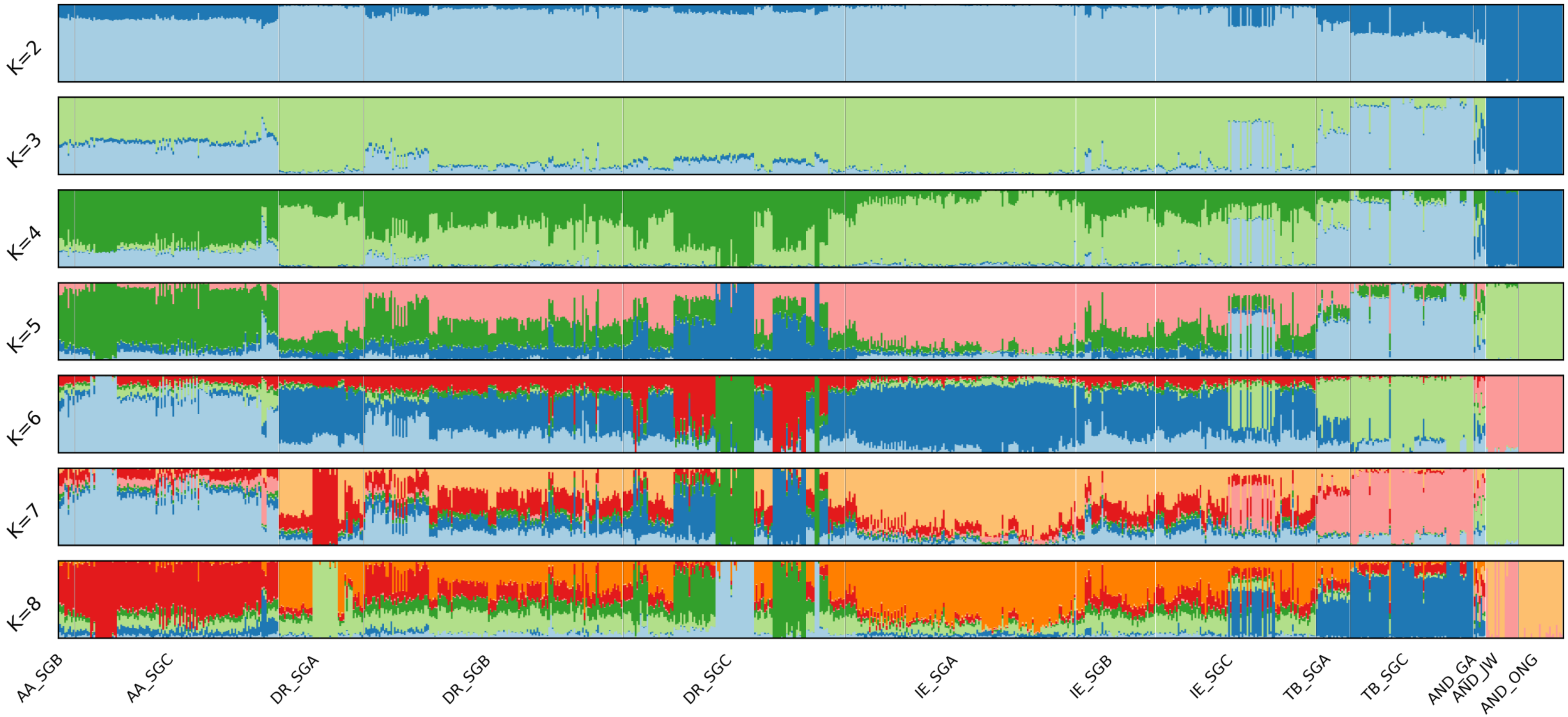
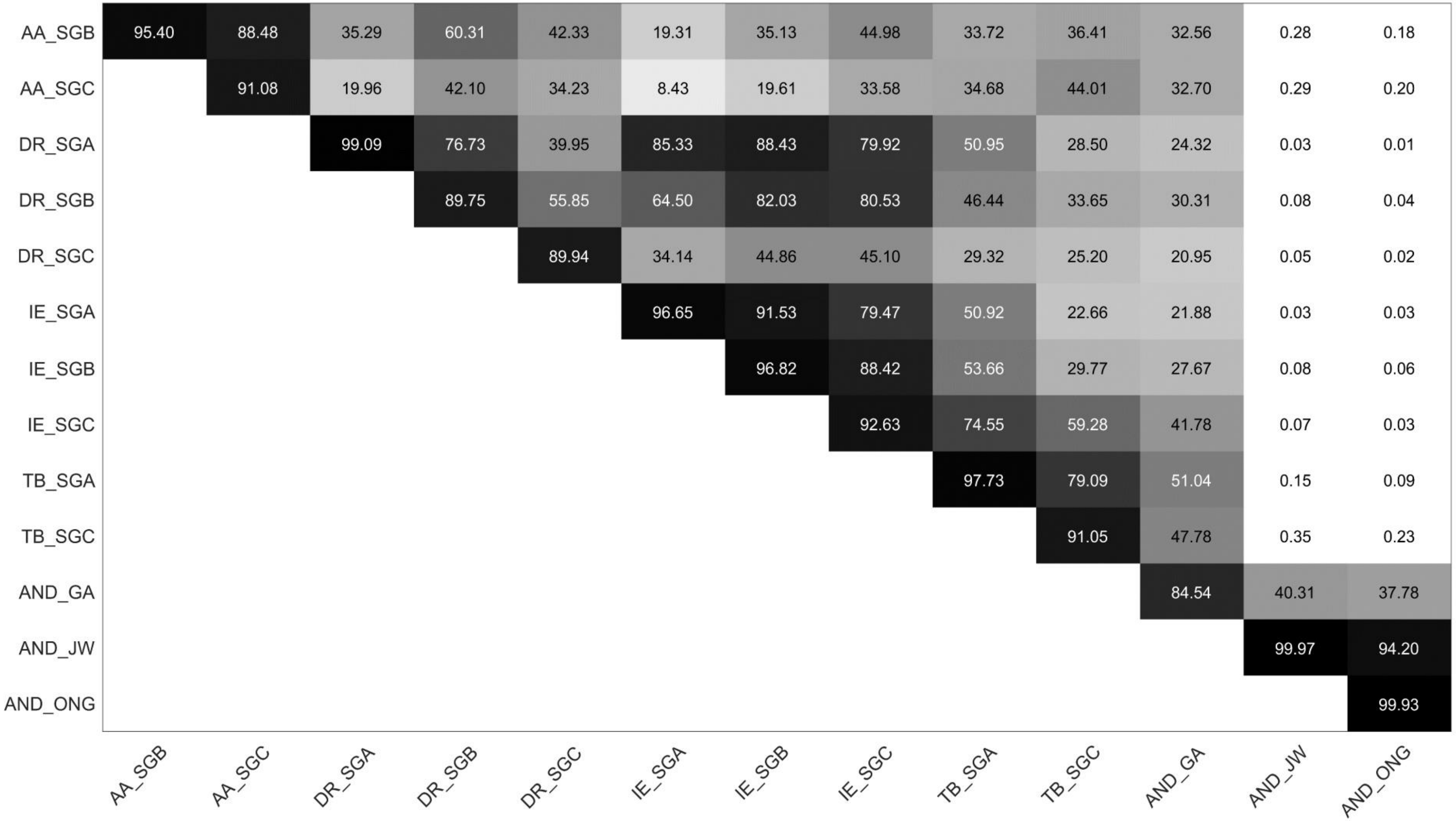


Fig S3A: An ADMIXTURE plot (for values of K between two and eight) of the pan-Indian data set (891 individuals; 47,283 SNPs) clearly shows the five main components related to language groups (Dravidian, Indo-European, Tibeto-Burman, Andamanese and Austro-Asiatic); see, for example, the plot for K equal to five or six. The plot also shows the divergence of the Dravidian SGC (DR_SGC) and the Andaman samples from rest of DR speakers and mainland India, respectively.

Fig S3B: Admixture ancestry of Indian populations



	AA_SGB	AA_SGC	DR_SGA	DR_SGB	DR_SGC	IE_SGA	IE_SGB	IE_SGC	TB_SGA	TB_SGC	AND_GA	AND_JW	AND_ONG
AA_SGB	95.40	88.48	35.29	60.31	42.33	19.31	35.13	44.98	33.72	36.41	32.56	0.28	0.18
AA_SGC		91.08	19.96	42.10	34.23	8.43	19.61	33.58	34.68	44.01	32.70	0.29	0.20
DR_SGA			99.09	76.73	39.95	85.33	88.43	79.92	50.95	28.50	24.32	0.03	0.01
DR_SGB				89.75	55.85	64.50	82.03	80.53	46.44	33.65	30.31	0.08	0.04
DR_SGC					89.94	34.14	44.86	45.10	29.32	25.20	20.95	0.05	0.02
IE_SGA						96.65	91.53	79.47	50.92	22.66	21.88	0.03	0.03
IE_SGB							96.82	88.42	53.66	29.77	27.67	0.08	0.06
IE_SGC								92.63	74.55	59.28	41.78	0.07	0.03
TB_SGA									97.73	79.09	51.04	0.15	0.09
TB_SGC										91.05	47.78	0.35	0.23
AND_GA											84.54	40.31	37.78
AND_JW												99.97	94.20
AND_ONG													99.93

Fig S3B: Meta-analysis of the results of the ADMIXTURE plot (see Methods for details) to visually and numerically quantify the amount of shared ancestry (as revealed by ADMIXTURE) between any pair of populations. Darker colors indicate larger amounts of shared ancestry; we observe a higher amount of shared ancestry between the Indo-European and Dravidian populations, across all social groups, indicating the existence of significant admixture between the two linguistic groups. The isolation of the Dravidian SGC samples is primarily due to the isolation of hill SGCs (such as Irula, Kadar, Paniyas, etc.). Greater Andamanese (AND_GA) shares more ancestry with mainland Indian populations than other Andamanese groups Jarawa (AND_JW) and Onge (AND_ONG).

Fig S4: Stratification in Indian populations

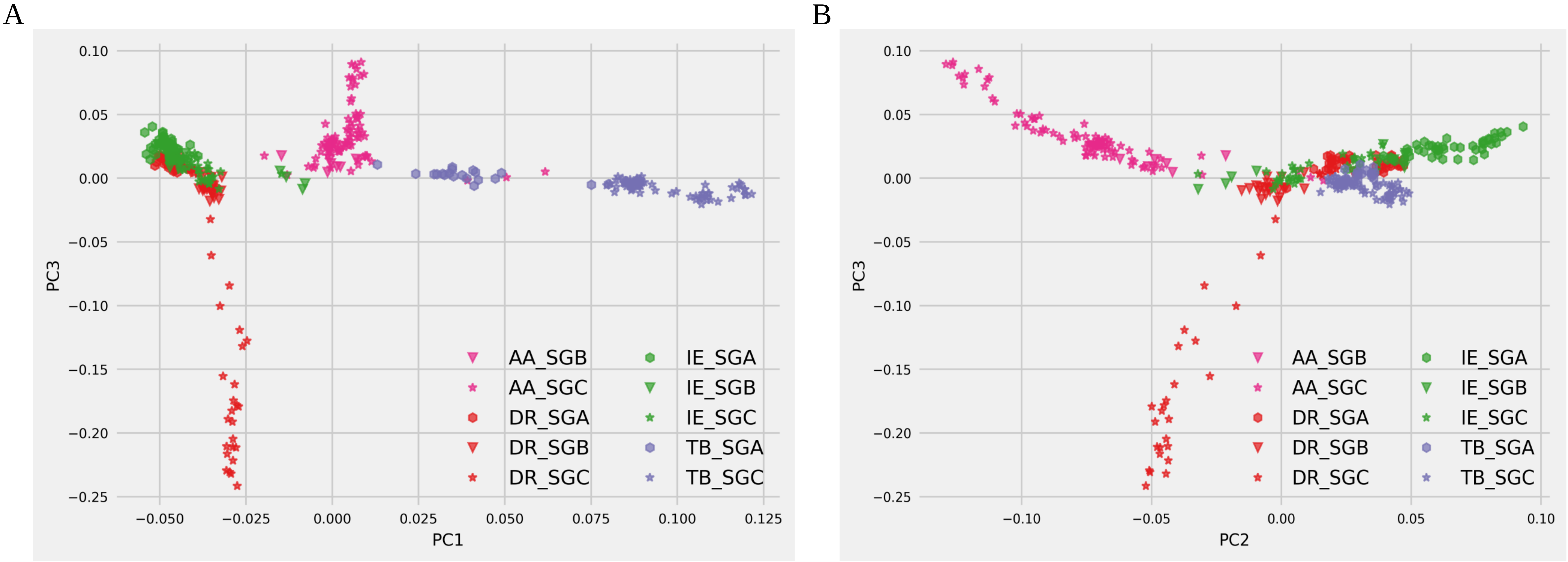


Fig S4: (A) First and third PCs reveal clusters stratified by sociolinguistic groups in the normalized data set of 368 individuals (33 populations). SGCs from different language groups diverge (IE_SGC is closer to other IE speakers) TB_SGC forms a cluster with TB_SGA being closer to IE and AA speakers. AA speakers form a cluster of their own.

(B) Second and third PCs extracted from the normalized data set reveal clear clusters by the sociolinguistic groups. DR_SGC shows divergence from fellow DR speakers (SGA and SGB) who tightly cluster with IE_SGB and IE_SGC. IE_SGA forms one end of a cline with maximal variance along with AA_SGC forming the other end with AA_SGB and IE_SGB possibly mixing in Central India.

Fig S5: LDA plots

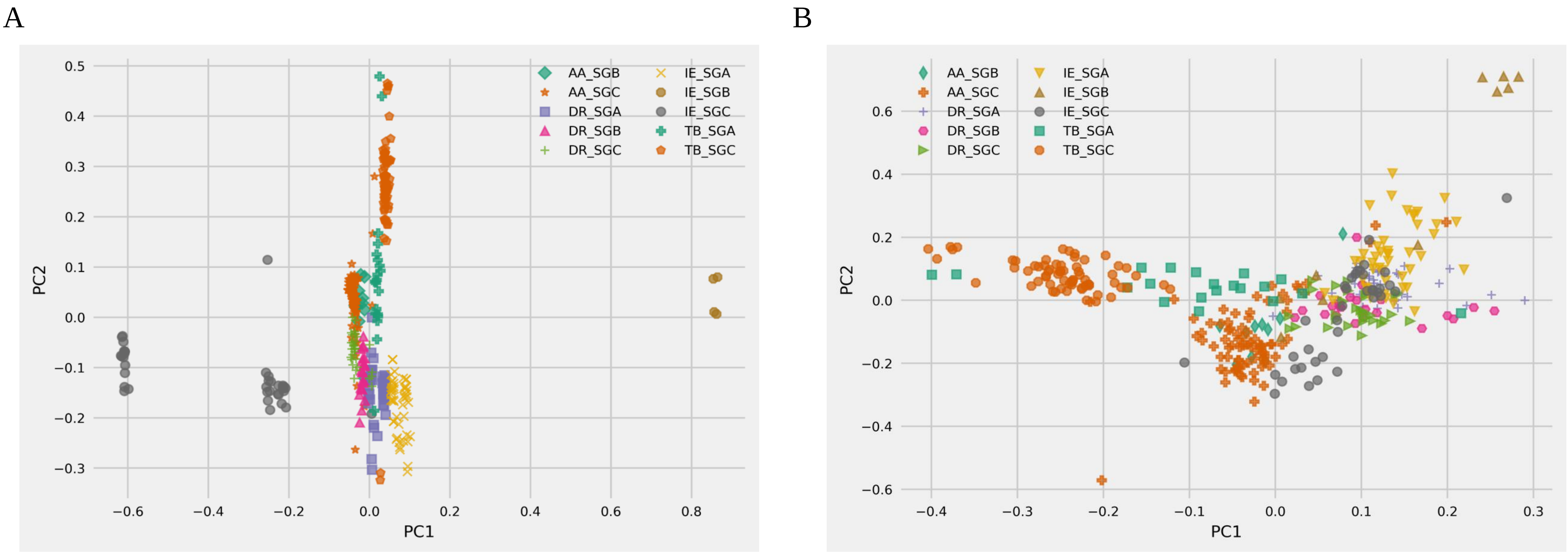
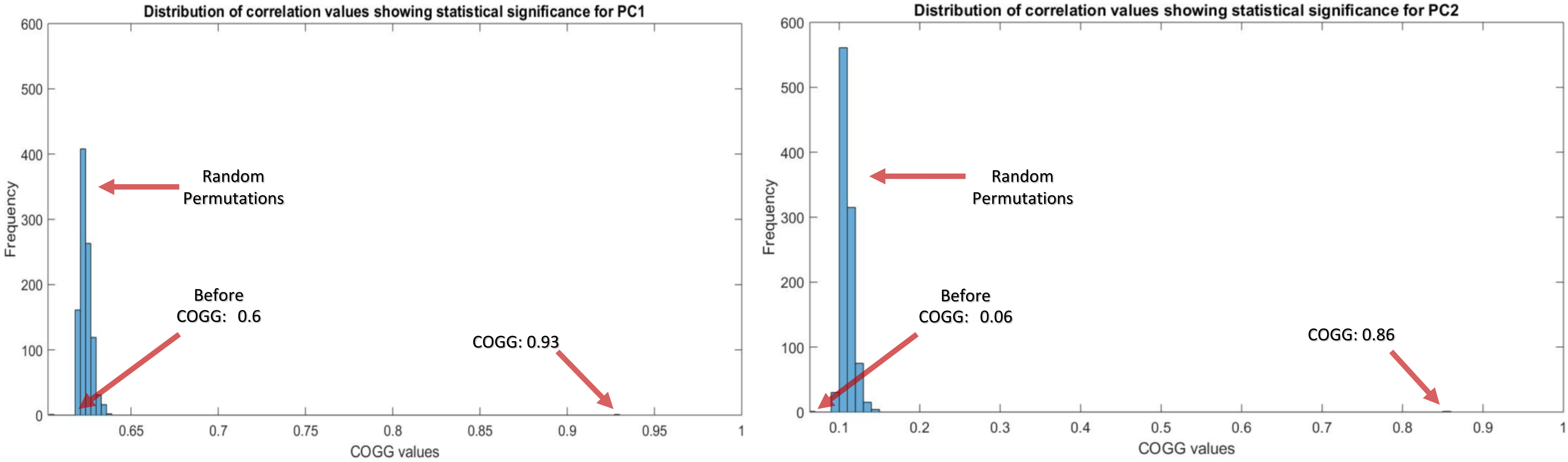


Fig S5: (A) Plotting the top two discriminants by language groups. Layers of stratification appear, from left to right. Although the LDA was performed by language groups, we see a two-layer stratification, first by castes and then by languages. The IE_SGA form a separate cline, followed by DR_SGA; then, the IE_SGC and DR_SGB follow. Then some DR and AA tribal populations cluster together, followed by a separate cluster of IE tribal populations.

(B) Plotting the top two discriminants by geographic regions. Layers of stratification appear from left to right. TB speakers occupy the left as IE speakers occupy the right side of the plot mirroring the east-west expanse of the map of India. However, the north-south variation does not appear as clearly as the east-west. This is perhaps confounded by the endogamy practiced by IE and DR populations.

Fig S6: Statistical Significance of COGG



Distribution of correlation values showing statistical significance for PC1

Random Permutations

Before COGG: 0.6

COGG: 0.93

Distribution of correlation values showing statistical significance for PC2

Random Permutations

Before COGG: 0.06

COGG: 0.86

Fig S6: Statistical significance of the COGG output (using random permutations of the features) Clearly, COGG is statistically significant for both the first and the second principal components.

Fig S7: COGG-CCA

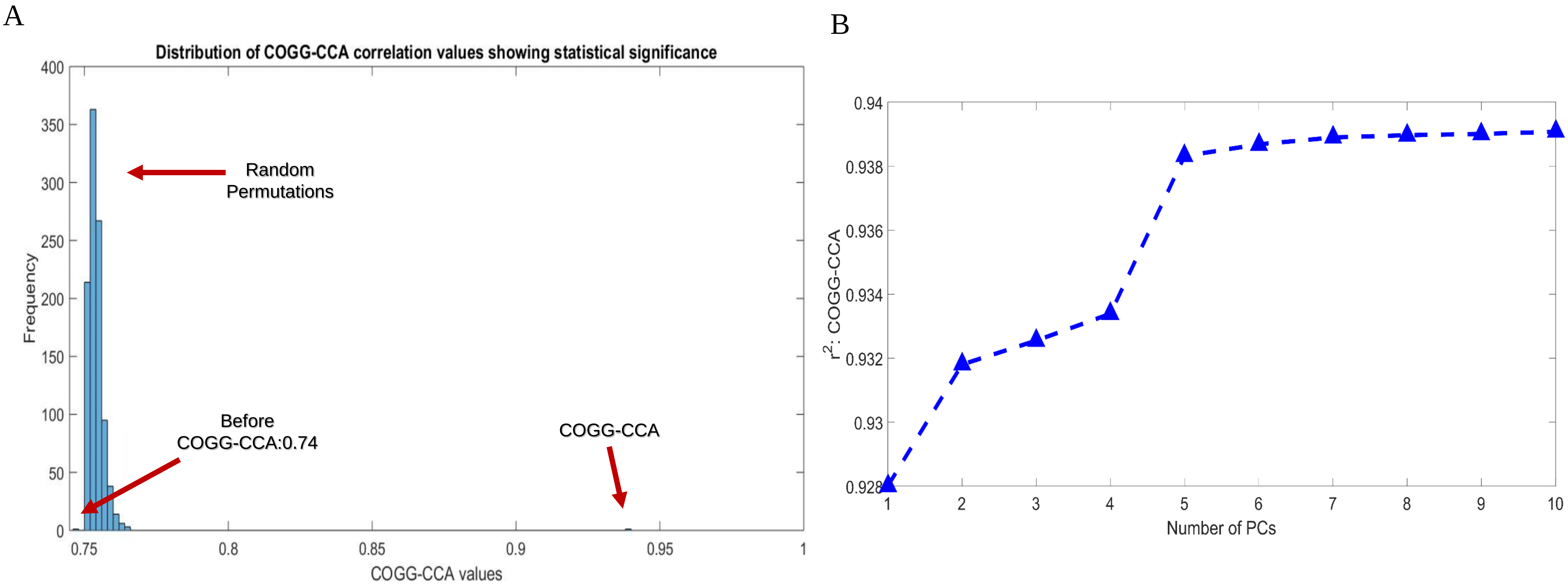


Fig S7a: COGG-CCA, when run with top 8 PCs, shows statistical significance with r^2 = 0.94 when compared against random permutations of the variables with average r^2 = 0.75.

Fig S7b: Varying number of PCs to perform COGG-CCA results in the maximum r^2 when top 6 to 8 PCs are used.

Fig S8: Shared ancestry of Indian populations

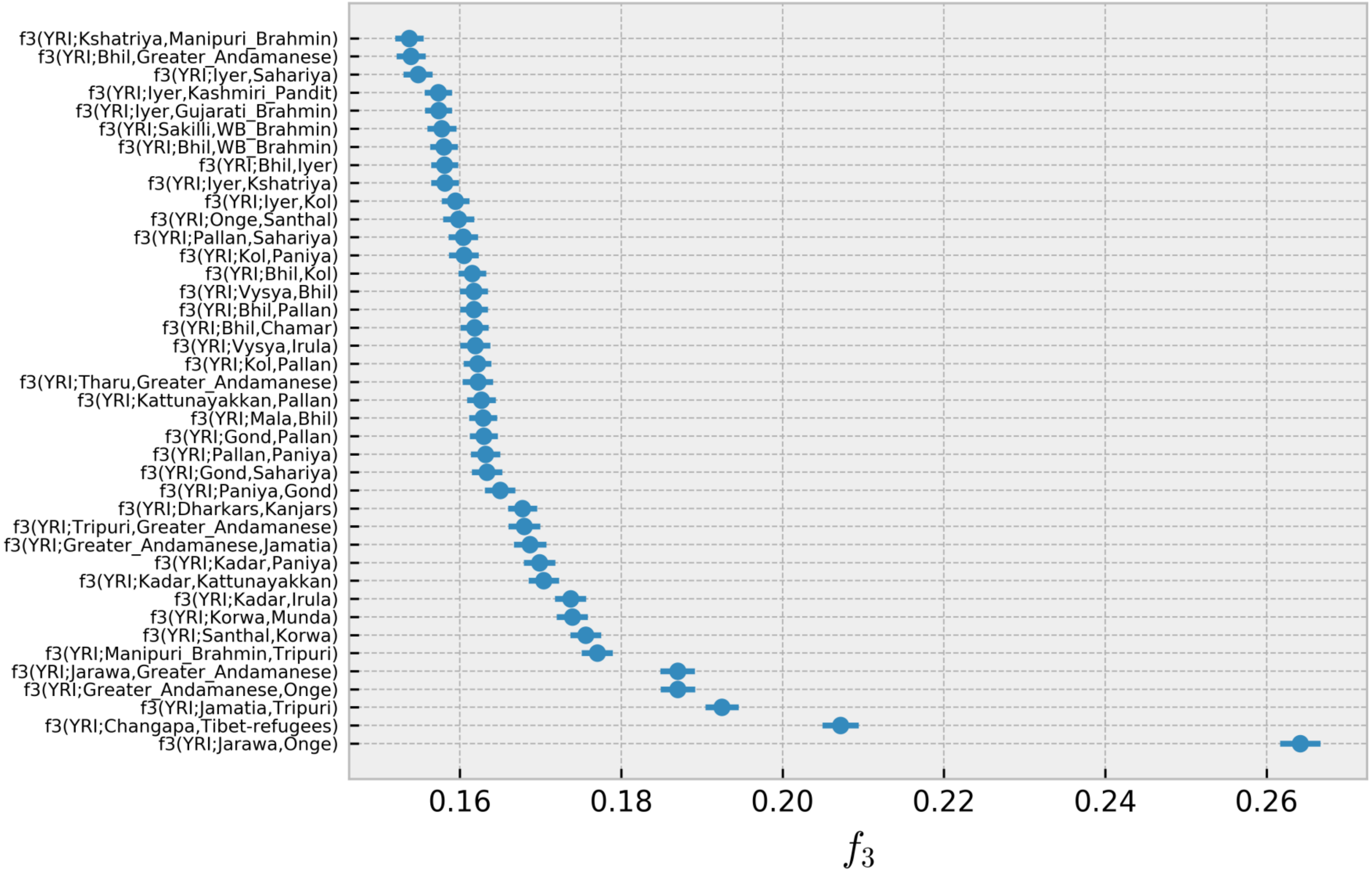
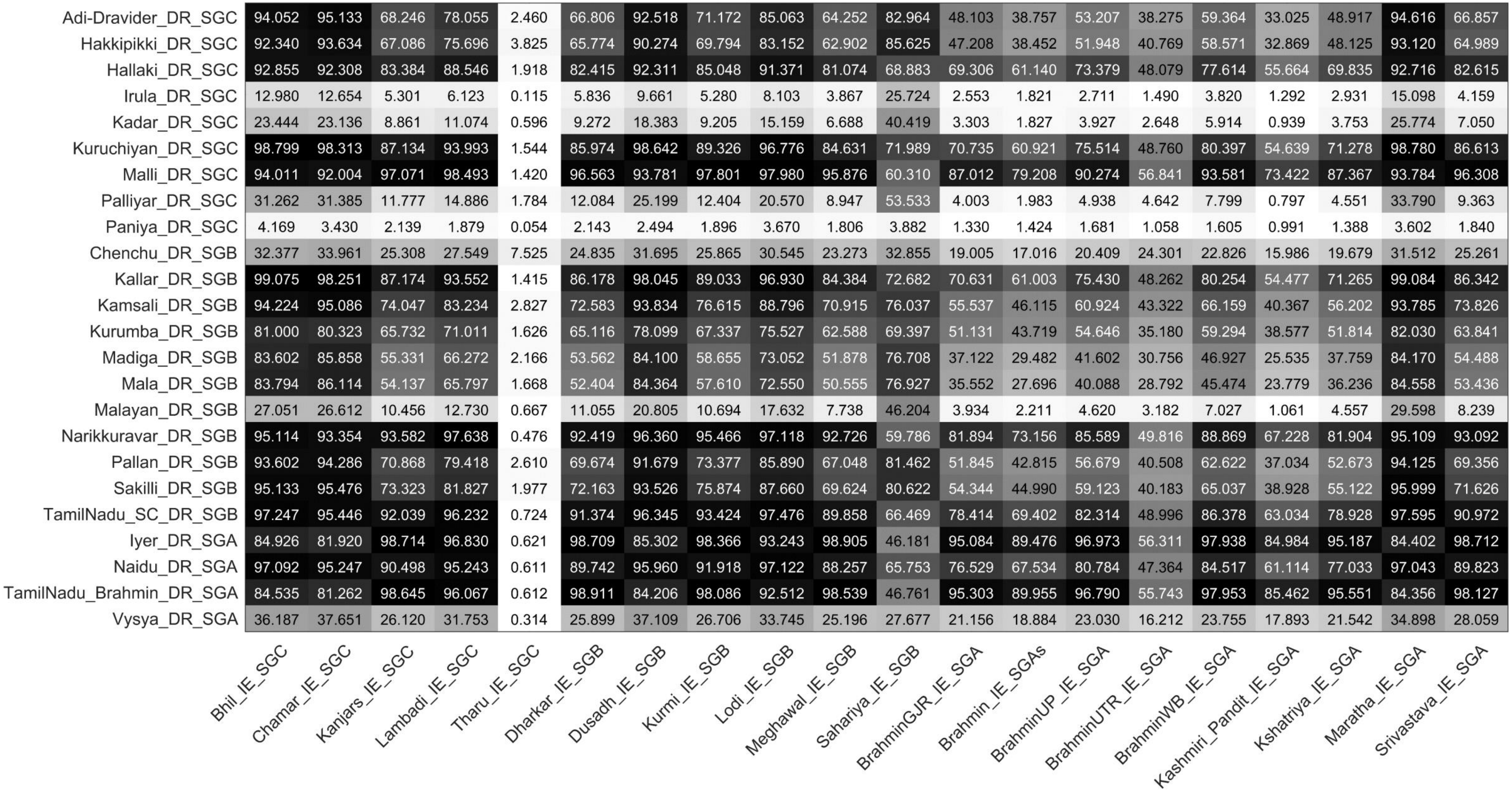


Fig S8:Most significant (Z-score higher than 85) outgroup $f_3$statistics of the form f3(YRI;A,B) where YRI is the outgroup, A are the groups from Table S1 and B are all the pan-Indian populations in our data spanning across social groups and language families.

Fig S9: Shared Ancestry between IE and DR



	Bhil_IE_SGC	Chamar_IE_SGC	Kanjars_IE_SGC	Lambadi_IE_SGC	Tharu_IE_SGC	Dharkar_IE_SGB	Dusadh_IE_SGB	Kurmi_IE_SGB	Lodi_IE_SGB	Meghawal_IE_SGB	Sahariya_IE_SGB	BrahminGJR_IE_SGA	Brahmin_IE_SGAs	BrahminUP_IE_SGA	BrahminUTR_IE_SGA	BrahminWB_IE_SGA	Kashmiri_Pandit_IE_SGA	Kshatriya_IE_SGA	Maratha_IE_SGA	Srivastava_IE_SGA
Adi-Dravider_DR_SGC	94.052	95.133	68.246	78.055	2.460	66.806	92.518	71.172	85.063	64.252	82.964	48.103	38.757	53.207	38.275	59.364	33.025	48.917	94.616	66.857
Hakkipikki_DR_SGC	92.340	93.634	67.086	75.696	3.825	65.774	90.274	69.794	83.152	62.902	85.625	47.208	38.452	51.948	40.769	58.571	32.869	48.125	93.120	64.989
Hallaki_DR_SGC	92.855	92.308	83.384	88.546	1.918	82.415	92.311	85.048	91.371	81.074	68.883	69.306	61.140	73.379	48.079	77.614	55.664	69.835	92.716	82.615
Irula_DR_SGC	12.980	12.654	5.301	6.123	0.115	5.836	9.661	5.280	8.103	3.867	25.724	2.553	1.821	2.711	1.490	3.820	1.292	2.931	15.098	4.159
Kadar_DR_SGC	23.444	23.136	8.861	11.074	0.596	9.272	18.383	9.205	15.159	6.688	40.419	3.303	1.827	3.927	2.648	5.914	0.939	3.753	25.774	7.050
Kuruchiyan_DR_SGC	98.799	98.313	87.134	93.993	1.544	85.974	98.642	89.326	96.776	84.631	71.989	70.735	60.921	75.514	48.760	80.397	54.639	71.278	98.780	86.613
Malli_DR_SGC	94.011	92.004	97.071	98.493	1.420	96.563	93.781	97.801	97.980	95.876	60.310	87.012	79.208	90.274	56.841	93.581	73.422	87.367	93.784	96.308
Palliyar_DR_SGC	31.262	31.385	11.777	14.886	1.784	12.084	25.199	12.404	20.570	8.947	53.533	4.003	1.983	4.938	4.642	7.799	0.797	4.551	33.790	9.363
Paniya_DR_SGC	4.169	3.430	2.139	1.879	0.054	2.143	2.494	1.896	3.670	1.806	3.882	1.330	1.424	1.681	1.058	1.605	0.991	1.388	3.602	1.840
Chenchu_DR_SGB	32.377	33.961	25.308	27.549	7.525	24.835	31.695	25.865	30.545	23.273	32.855	19.005	17.016	20.409	24.301	22.826	15.986	19.679	31.512	25.261
Kallar_DR_SGB	99.075	98.251	87.174	93.552	1.415	86.178	98.045	89.033	96.930	84.384	72.682	70.631	61.003	75.430	48.262	80.254	54.477	71.265	99.084	86.342
Kamsali_DR_SGB	94.224	95.086	74.047	83.234	2.827	72.583	93.834	76.615	88.796	70.915	76.037	55.537	46.115	60.924	43.322	66.159	40.367	56.202	93.785	73.826
Kurumba_DR_SGB	81.000	80.323	65.732	71.011	1.626	65.116	78.099	67.337	75.527	62.588	69.397	51.131	43.719	54.646	35.180	59.294	38.577	51.814	82.030	63.841
Madiga_DR_SGB	83.602	85.858	55.331	66.272	2.166	53.562	84.100	58.655	73.052	51.878	76.708	37.122	29.482	41.602	30.756	46.927	25.535	37.759	84.170	54.488
Mala_DR_SGB	83.794	86.114	54.137	65.797	1.668	52.404	84.364	57.610	72.550	50.555	76.927	35.552	27.696	40.088	28.792	45.474	23.779	36.236	84.558	53.436
Malayan_DR_SGB	27.051	26.612	10.456	12.730	0.667	11.055	20.805	10.694	17.632	7.738	46.204	3.934	2.211	4.620	3.182	7.027	1.061	4.557	29.598	8.239
Narikkuravar_DR_SGB	95.114	93.354	93.582	97.638	0.476	92.419	96.360	95.466	97.118	92.726	59.786	81.894	73.156	85.589	49.816	88.869	67.228	81.904	95.109	93.092
Pallan_DR_SGB	93.602	94.286	70.868	79.418	2.610	69.674	91.679	73.377	85.890	67.048	81.462	51.845	42.815	56.679	40.508	62.622	37.034	52.673	94.125	69.356
Sakilli_DR_SGB	95.133	95.476	73.323	81.827	1.977	72.163	93.526	75.874	87.660	69.624	80.622	54.344	44.990	59.123	40.183	65.037	38.928	55.122	95.999	71.626
TamilNadu_SC_DR_SGB	97.247	95.446	92.039	96.232	0.724	91.374	96.345	93.424	97.476	89.858	66.469	78.414	69.402	82.314	48.996	86.378	63.034	78.928	97.595	90.972
Iyer_DR_SGA	84.926	81.920	98.714	96.830	0.621	98.709	85.302	98.366	93.243	98.905	46.181	95.084	89.476	96.973	56.311	97.938	84.984	95.187	84.402	98.712
Naidu_DR_SGA	97.092	95.247	90.498	95.243	0.611	89.742	95.960	91.918	97.122	88.257	65.753	76.529	67.534	80.784	47.364	84.517	61.114	77.033	97.043	89.823
TamilNadu_Brahmin_DR_SGA	84.535	81.262	98.645	96.067	0.612	98.911	84.206	98.086	92.512	98.539	46.761	95.303	89.955	96.790	55.743	97.953	85.462	95.551	84.356	98.127
Vysya_DR_SGA	36.187	37.651	26.120	31.753	0.314	25.899	37.109	26.706	33.745	25.196	27.677	21.156	18.884	23.030	16.212	23.755	17.893	21.542	34.898	28.059

Fig S9: The shared ancestry matrix of relatedness between IE and DR speakers show that high relatedness with some divergent groups, following from the PC plot in Fig S5a. The DR_SGA share very high ancestry with IE SGA and SGC, showing that there was high admixture and contact between these groups prior to endogamy.

Fig S10A: Network analysis of Eurasia in light of Indian populations

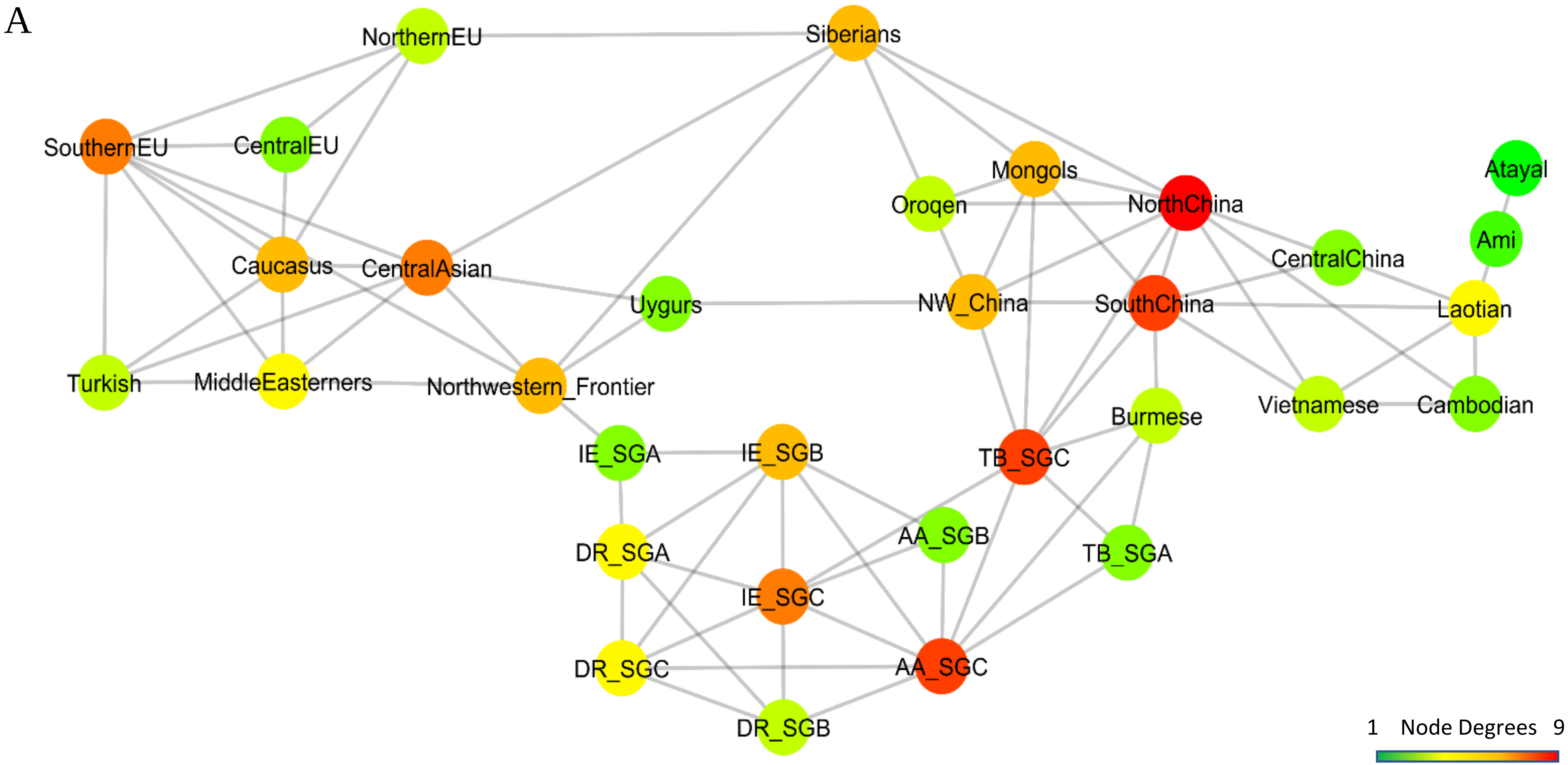
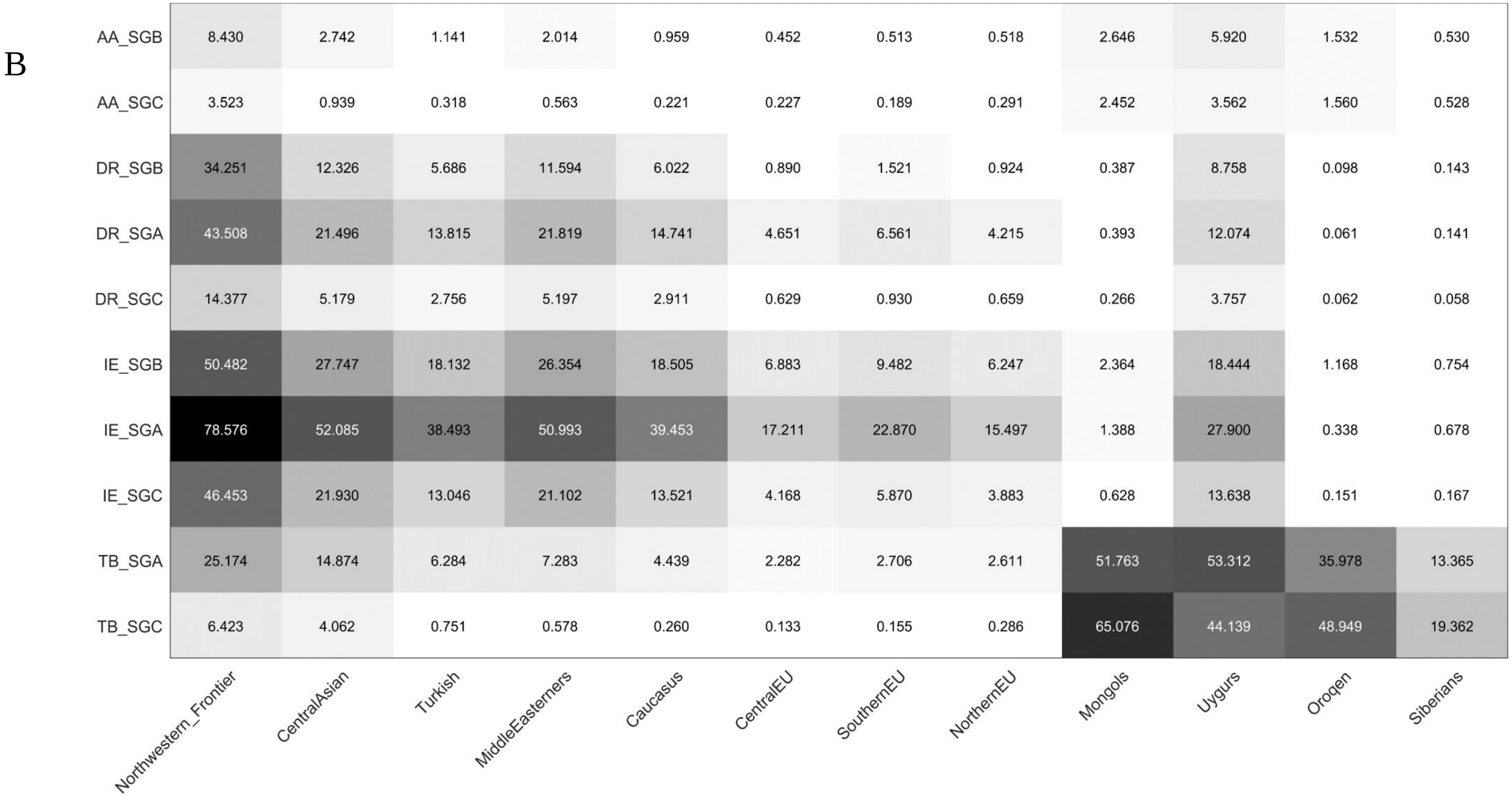


Fig S10A: Networks formed using the top five PCs (see Materials and Methods for the network formation algorithm) and five nearest neighbors showing three major paths leading to the two entry points of India.

Fig S10B: Shared ancestry of Eurasian populations



	Northwestern_Frontier	CentralAsian	Turkish	MiddleEasterners	Caucasus	CentralEU	SouthernEU	NorthernEU	Mongols	Uygurs	Oroqen	Siberians
AA_SGB	8.430	2.742	1.141	2.014	0.959	0.452	0.513	0.518	2.646	5.920	1.532	0.530
AA_SGC	3.523	0.939	0.318	0.563	0.221	0.227	0.189	0.291	2.452	3.562	1.560	0.528
DR_SGB	34.251	12.326	5.686	11.594	6.022	0.890	1.521	0.924	0.387	8.758	0.098	0.143
DR_SGA	43.508	21.496	13.815	21.819	14.741	4.651	6.561	4.215	0.393	12.074	0.061	0.141
DR_SGC	14.377	5.179	2.756	5.197	2.911	0.629	0.930	0.659	0.266	3.757	0.062	0.058
IE_SGB	50.482	27.747	18.132	26.354	18.505	6.883	9.482	6.247	2.364	18.444	1.168	0.754
IE_SGA	78.576	52.085	38.493	50.993	39.453	17.211	22.870	15.497	1.388	27.900	0.338	0.678
IE_SGC	46.453	21.930	13.046	21.102	13.521	4.168	5.870	3.883	0.628	13.638	0.151	0.167
TB_SGA	25.174	14.874	6.284	7.283	4.439	2.282	2.706	2.611	51.763	53.312	35.978	13.365
TB_SGC	6.423	4.062	0.751	0.578	0.260	0.133	0.155	0.286	65.076	44.139	48.949	19.362

Fig S10B: Meta-analysis of the ADMIXTURE output reveals that, overall, Indian populations share a great proportion of ancestry with the so-called Indian Northwestern Frontier populations, namely the SGC populations spanning Afghanistan and Pakistan. In concordance with previous studies we find higher degrees of shared ancestry in Central Asian populations with IE and DR SGA. In particular, IE SGA share large amounts of ancestry with other IE speaking populations (i.e., Europeans). However, IE, TB, and DR speakers also share considerable amounts of ancestry with the Uygurs. On the other hand, AA speakers, who have been suggested as the earliest settlers of India, appear more isolated.

Population Name	# of Samples	State/Province	Broad Region	Language	Caste	Latitude	Longitude	Dataset
Adi-Dravider	5	Tamil Nadu	South	Dravidian	Social Group B (SGB)	12.11	79.053	Moorjani et al. (2013)
Aonaga	4	Nagaland	NorthEast	Tibeto_Burmese	Unknown	25.6667	94.133	Reich et al. (2009) +Metspalu et al. (2011)
Asur	2	Jharkhand	Eastern States	Austro_Asiatic	Social Group C (SGC)	23.76	86.42	Chaubey et al. (2011) +Metspalu et al. (2011)
Bhil	17	Gujarat	NorthWest	Indo-European	SGC	23.0333	72.667	Moorjani et al. (2013) +Reich et al. (2009)
Bhumij	5	West Bengal	Eastern States	Austro_Asiatic	SGC	21.806	87.114	Moorjani et al. (2013)
Bhunjia	1	Odisha	Eastern States	Indo-European	SGC	21.27	81.56	Metspalu et al. (2011)
Birhor	20	Jharkhand	Eastern States	Austro_Asiatic	SGC	23.991	84.816	Basu et al. (2016) +Moorjani et al. (2013)
Bonda	4	Odisha	Eastern States	Austro_Asiatic	SGC	18.4	81.88	Metspalu et al. (2011)
Brahmin	15	Uttar Pradesh	North	Indo-European	Social Group A (SGA)	25.75	82.683	Moorjani et al. (2013)
Chamar	10	Bihar	Eastern States	Indo-European	SGC	25.37	83.04	Metspalu et al. (2011)
Changapa	5	Ladakh	North	Tibeto_Burmese	SGC	34.02	79.004	Moorjani et al. (2013)
Chenchus	10	Andhra Pradesh	South	Dravidian	SGC	18	79.59	Metspalu et al. (2011) + Reich et al. (2009)
Dhurwa	1	Bihar	Eastern States	Dravidian	SGC	18.78	82.68	Metspalu et al. (2011)
Dharkars	12	Uttar Pradesh	North	Indo-European	SGC	25.44	83.1	Metspalu et al. (2011)
Dusadh	10	Uttar Pradesh	North	Indo-European	SGB	25.44	84.56	Metspalu et al. (2011)
Gadaba	1	Andhra Pradesh	South	Austro_Asiatic	SGC	18.79	82.7	Chaubey et al. (2011)
Garo	4	Assam	NorthEast	Tibeto_Burmese	Unknown	26.17	90.62	Metspalu et al. (2011)
Gond	38	Madhya Pradesh	Central	Dravidian	SGC	22.1	82.16	Reich et al. (2009) +Metspalu et al. (2011) +Basu et al. (2016)
Gounder	5	Tamil Nadu	South	Dravidian	SGA	12.1	79.1	Moorjani et al. (2013)
Gujarati_Brahmin	20	Gujarat	NorthWest	Indo-European	SGA	22.29	70.94	Basu et al. (2016)
Hallaki	7	Kannada	South	Dravidian	SGC	13.9167	74.15	Reich et al. (2009)
Hakkipikki	4	Kannada	South	Dravidian	SGC	14.78	74.51	Metspalu et al. (2011)
Ho	28	Jharkhand	Eastern States	Austro_Asiatic	SGC	25.4	86.13	Reich et al. (2009) +Metspalu et al. (2011) +Basu et al. (2016)
Irula	25	Tamil Nadu	South	Dravidian	SGC	11.58	76.609	Basu et al. (2016) +Moorjani et al. (2013)
Iyer	20	Tamil Nadu	South	Dravidian	SGA	13.1	80.2	Basu et al. (2016)
Jamatia	18	Tripura	NorthEast	Tibeto_Burmese	SGC	23.84	92.17	Basu et al. (2016)
Juang	2	Odisha	Eastern States	Austro_Asiatic	SGC	21.49	83.98	Metspalu et al. (2011)
Kadar	20	Kerala	South	Dravidian	SGC	9.96	77.16	Basu et al. (2016)
Kallar	5	Tamil Nadu	South	Dravidian	SGC	10.99	78.22	Metspalu et al. (2011) +Moorjani et al. (2013)
Kamsali	4	Andhra Pradesh	South	Dravidian	SGB	15.49	78.29	Reich et al. (2009)
Kanjars	8	Rajasthan	North	Indo-European	SGC	26.45	80.32	Metspalu et al. (2011)
Kashmiri_Pandit	20	Kashmir	North	Indo-European	SGA	34.22	75.5	Reich et al. (2009) +Moorjani et al. (2013)
Kattunayakkan	5	Andhra Pradesh	South	Dravidian	SGC	9.55	76.8	Moorjani et al. (2013)
Kharia	8	Bihar	Eastern States	Austro_Asiatic	SGC	21.89	83.36	Metspalu et al. (2011) +Reich et al. (2009)
Khasi	3	Meghalaya	NorthEast	Austro_Asiatic	SGC	24.87	90.72	Metspalu et al. (2011)
Khatri	19	Punjab	North	Indo-European	SGA	30.52	76.76	Basu et al. (2016)
Kol	17	Uttar Pradesh	North	Indo-European	SGB	25.15	82.58	Metspalu et al. (2011)
Korku	4	Madhya Pradesh	Central	Austro_Asiatic	SGB	22.711	75.88	Moorjani et al. (2013)

Korwa	18	Jharkhand	Eastern States	Austro_Asiatic	SGC	22.39	82.79	Basu et al. (2016)
Kshatriya	27	Uttar Pradesh	North	Indo-European	SGA	25.45	82.41	Moorjani et al. (2013) +Metspalu et al. (2011)
Kurmi	1	West Bengal	East	Indo-European	SGB	22.85	88.3	Metspalu et al. (2011)
Kuruchiyan	5	Kerala	South	Dravidian	SGC	11.73	76.41	Moorjani et al. (2013)
Kurumba	13	Tamil Nadu	South	Dravidian	SGC	10.54	76.27	Reich et al. (2009) +Metspalu et al. (2011)
Lambadi	1	Madhya Pradesh	Central	Dravidian	SGC	17.45	78.5	Metspalu et al. (2011)
Lodi	5	Uttar Pradesh	North	Indo-European	SGB	26.45	83.24	Reich et al. (2009)
Madiga	19	Andhra Pradesh	South	Dravidian	SGB	17.58	79.35	Moorjani et al. (2013) +Reich et al. (2009)
Mala	18	Andhra Pradesh	South	Dravidian	SGB	17.22	78.29	Moorjani et al. (2013) +Reich et al. (2009)
Malayan	2	Tamil Nadu	South	Dravidian	SGC	9.58	76.51	Metspalu et al. (2011)
Malai_Kuravar	5	Tamil Nadu	South	Dravidian	SGB	13.84	80.22	Moorjani et al. (2013)
Malli	5	Andhra Pradesh	South	Dravidian	SGB	10.55	72.63	Moorjani et al. (2013)
Manipuri_Brahmin	20	Manipur	NorthEast	Tibeto_Burmese	SGA	24.812	93.94	Basu et al. (2016)
Mawasi	1	Madhya Pradesh	Central	Austro_Asiatic	SGB	23.15	77.42	Basu et al. (2016)
Maratha	7	Maharashtra	West	Indo-European	SGA	18.5	73.7	Basu et al. (2016)
Meghawal	6	Gujarat	NorthWest	Indo-European	SGB	26.18	73.04	Reich et al. (2009) +Metspalu et al. (2011)
Meena	1	Rajasthan	NorthWest	Indo-European	SGC	28.29	74.98	Metspalu et al. (2011)
Minicoy	5	Lakshwadeep	SouthWest	Indo-European	SGB	8.28	73.06	Moorjani et al. (2013)
Munda	5	Jharkhand	Eastern States	Austro_Asiatic	SGB	21.6	83.76	Moorjani et al. (2013)
Naga	4	Nagaland	NorthEast	Tibeto_Burmese	SGC	25.67	94.11	Metspalu et al. (2011)
Naidu	4	Andhra Pradesh	South	Dravidian	SGA	13.13	79.06	Reich et al. (2009)
Narikkuravar	5	Tamil Nadu	South	Dravidian	SGC	13.17	79.4	Moorjani et al. (2013)
Nysha	4	Arunachal Pradesh	NorthEast	Tibeto_Burmese	SGC	26.55	92.4	Reich et al. (2009)
Pallan	20	Tamil Nadu	South	Dravidian	SGA	9.92	78.12	Basu et al. (2016)
Palliyar	5	Tamil Nadu	South	Dravidian	SGC	10.89	76.84	Moorjani et al. (2013)
Pulliyar	5	Tamil Nadu	South	Dravidian	SGB	11.02	76.98	Metspalu et al. (2011)
Piramalai_Kallars	8	Tamil Nadu	South	Dravidian	SGC	10.99	78.22	Metspalu et al. (2011)
Paniyas	27	Kerala	South	Dravidian	SGC	9.5	76.8	Moorjani et al. (2013) + Metspalu et al. (2011) + Basu et al. (2016)
Sahariya	4	Madhya Pradesh	Central	Indo-European	SGB	25.28	81.54	Reich et al. (2009)
Sakilli	4	Tamil Nadu	South	Dravidian	SGB	9.86	76.97	Metspalu et al. (2011)
Santhal	28	Jharkhand	Central+East	Austro_Asiatic	SGC	24.3	87.3	Metspalu et al. (2011) +Reich et al. (2009) +Basu et al. (2016)
Satnami	4	Madhya Pradesh	Central	Indo-European	SGB	20.29	85.58	Reich et al. (2009)
Savara	2	Odisha	Central+East	Austro_Asiatic	SGB	18.8	82.7	Metspalu et al. (2011)
Sherpa	5	Nepal	NorthEast	Tibeto_Burmese	SGC	29.2	83.4	Moorjani et al. (2013)
Srivastava	2	Uttar Pradesh	North	Indo-European	SGA	25.1	82.37	Reich et al. (2009)
Subba	5	Sikkim	NorthEast	Tibeto_Burmese	SGC	27.34	88.6	Moorjani et al. (2013)
Tharu	31	Nepal	North	Indo-European	SGC	29.23	79.3	Reich et al. (2009) +Basu et al. (2016) + Metspalu et al. (2011)
Tibet-refugees	5	Tibet	North	Tibeto_Burmese	SGC	29.625	91.17	Moorjani et al. (2013)
Tripuri	19	Tripura	NorthEast	Tibeto_Burmese	SGC	23.81	91.2	Basu et al. (2016)
Vaish	4	Uttar Pradesh	North	Indo-European	SGA	25.46	82.44	Reich et al. (2009)
Vedda	4	Sri Lanka	SriLanka	Indo-European	SGC	6.44	80.5	Moorjani et al. (2013)
Velamas	14	Andhra Pradesh	South	Dravidian	SGA	17.05	79.27	Reich et al. (2009) + Metspalu et al. (2011)
Vysya	20	Tamil Nadu	South	Dravidian	SGA	14.41	77.39	Reich et al. (2009) +Moorjani et al. (2013)
WB_Brahmin	18	West Bengal	East	Indo-European	SGA	22.55	88.37	Basu et al. (2016)

UttarPradesh_SC	5	Uttar Pradesh	North	Indo-European	SGB	25.42	83.1	Metspalu et al. (2011)
TamilNadu_SC	2	Tamil Nadu	South	Dravidian	SGB	13.05	80.18	Metspalu et al. (2011)
UttarPradesh_Brahmins	8	Uttar Pradesh	North	Indo-European	SGA	26.06	83.18	Metspalu et al. (2011)
Uttaranchal_Brahmins	1	Uttar Pradesh	North	Indo-European	SGA	29.6	79.65	Metspalu et al. (2011)
Jarawa	19	Andaman	Andaman	Ongan	SGC	11.7	92.6	Basu et al. (2016)
Onge	26	Andaman	Andaman	Ongan	SGC	11.7	92.6	Basu et al. (2016)
Great Andmanese	7	Andaman	Andaman	Great Andamanese	SGC	12.2	93	Reich et al. (2009)
TamilNadu_Brahmin	2	Tamil Nadu	South	Dravidian	SGA	12.49	78.42	Metspalu et al. (2011)

Table S1A: A detailed description of the Indian samples, including their place of origin, language, caste affiliations, and respective longitude/latitude. The last column references the publication describing the respective dataset (we use the first author's last name and year of publication as a shortcut to the relevant reference from our bibliography).

Population Name	# of Samples	State/Province	BroadRegion	Language	Caste	Latitude	Longitude	Dataset
Bhil	17	Gujarat	NorthWest	Indo-European	SGC	23.0333	72.6667	Moorjani et al. (2013) [6]+Reich et al. (2009)
Kanjars	8	Rajasthan	North	Indo-European	SGC	26.45	80.32	Metspalu et al. (2011)
Kashmiri_Pandit	20	Kashmir	North	Indo-European	SGA	34.22	75.5	Reich et al. (2009) +Moorjani et al. (2013) [6]
Chamar	10	Bihar	Eastern States	Indo-European	SGC	25.37	83.04	Metspalu et al. (2011)
Kshatriya	27	Uttar Pradesh	North	Indo-European	SGA	25.45	82.41	Moorjani et al. (2013) [6]+Metspalu et al. (2011)
Meghawal	6	Gujarat	NorthWest	Indo-European	SGB	26.18	73.04	Reich et al. (2009) +Metspalu et al. (2011)
Tharus	2	Nepal	Central	Indo-European	SGC	27.12	83.45	Metspalu et al. (2011)
Sahariya	4	Madhya Pradesh	Central	Indo-European	SGB	25.28	81.54	Reich et al. (2009)
Sherpa	5	Nepal	NorthEast	Tibeto_Burmese	SGC	29.2	83.4	Moorjani et al. (2013) [6]
Changapa	5	Ladakh	North	Tibeto_Burmese	SGC	34.02	79.004	Moorjani et al. (2013) [6]
Nysha	4	Arunachal Pradesh	NorthEast	Tibeto_Burmese	SGC	26.55	92.4	Reich et al. (2009)
Jamatia	18	Tripura	NorthEast	Tibeto_Burmese	SGC	23.84	92.17	Basu et al. (2016)
Aonaga	4	Nagaland	NorthEast	Tibeto_Burmese	SGC	25.6667	94.1333	Reich et al. (2009) +Metspalu et al. (2011)
Naga	4	Nagaland	NorthEast	Tibeto_Burmese	SGC	25.67	94.11	Metspalu et al. (2011)
Tripuri	19	Tripura	NorthEast	Tibeto_Burmese	SGC	23.81	91.2	Basu et al. (2016)
Manipuri_Brahmin	20	Manipur	NorthEast	Tibeto_Burmese	SGA	24.812	93.94	Basu et al. (2016)
Tibet-refugees	5	Tibet	North	Tibeto_Burmese	SGC	29.625	91.17	Moorjani et al. (2013) [6]
Subba	5	Sikkim	NorthEast	Tibeto_Burmese	SGC	27.34	88.6	Moorjani et al. (2013) [6]
Khasi	3	Meghalaya	NorthEast	Austro_Asiatic	SGC	24.87	90.72	Metspalu et al. (2011)
Bhumij	5	West Bengal	Eastern States	Austro_Asiatic	SGC	21.806	87.114	Moorjani et al. (2013) [6]
Birhor	20	Jharkhand	Eastern States	Austro_Asiatic	SGC	23.991	84.816	Basu et al. (2016) +Moorjani et al. (2013) [6]
Munda	5	Jharkhand	Eastern States	Austro_Asiatic	SGB	21.6	83.76	Moorjani et al. (2013) [6]
Mawasi	1	Madhya Pradesh	Central	Austro_Asiatic	SGB	23.15	77.42	Basu et al. (2016)
Santhal	28	Jharkhand	Central+East	Austro_Asiatic	SGC	24.3	87.3	Metspalu et al. (2011) +Reich et al. (2009) +Basu et al. (2016)
Kharia	8	Bihar	Eastern States	Austro_Asiatic	SGC	21.89	83.36	Metspalu et al. (2011) +Reich et al. (2009)
Korku	4	Madhya Pradesh	Central	Austro_Asiatic	SGB	22.711	75.88	Moorjani et al. (2013) [6]
Korwa	18	Jharkhand	Eastern States	Austro_Asiatic	SGC	22.39	82.79	Basu et al. (2016)
Sakilli	4	Tamil Nadu	South	Dravidian	SGB	9.86	76.97	Metspalu et al. (2011)
Irula	25	Tamil Nadu	South	Dravidian	SGC	11.58	76.609	Basu et al. (2016)+Moorjani et al. (2013) [6]
Kuruchiyan	5	Kerala	South	Dravidian	SGC	11.73	76.41	Moorjani et al. (2013) [6]
Madiga	19	Andhra Pradesh	South	Dravidian	SGB	17.58	79.35	Moorjani et al. (2013) [6]+Reich et al. (2009)
Vysya	20	Tamil Nadu	South	Dravidian	SGA	14.41	77.39	Reich et al. (2009) +Moorjani et al. (2013) [6]
Iyer	20	Tamil Nadu	South	Dravidian	SGA	13.1	80.2	Basu et al. (2016)

Table S1B: Normalized subset of samples in India created after carefully selecting populations from Table S1A to equally represent, region, caste and languages. For each population, we include their place of origin, language, caste affiliations, and respective longitude/latitude. The last column references the publication describing the respective dataset (we use the first author's last name and year of publication as a shortcut to the relevant reference).

Population Name	# of samples	Region	Data Source
Adygei	38	Caucasus	Cann et al. (2002) +Rajeevan et al. (2003)
Afghan	24	NW_Frontier	Cann et al. (2002) + Di Cristofaro et al. (2013)
Albania	30	SouthernEU	Rajeevan et al. (2003)
Ami	38	SouthEast Asia	Rajeevan et al. (2003)
Atayal	34	SouthEast Asia	Rajeevan et al. (2003)
Azeris	23	CentralAsian	Yunusbayev et al. (2015)
Bedouin	48	MiddleEast	Cann et al. (2002)
Brahui	25	NW_Frontier	Cann et al. (2002) Di Cristofaro et al. (2013)
Burmese	15	Burmese	Chaubey et al. (2011)
Burusho	25	NW_Frontier	Cann et al. (2002) Di Cristofaro et al. (2013)
Buryats	22	Siberian	Yunusbayev et al. (2015)
Cambodian	26	SouthEast Asia	Cann et al. (2002)
Chechens	20	Caucasus	Yunusbayev et al. (2012)
Druze	50	MiddleEast	Cann et al. (2002)
French	29	CentralEU	Cann et al. (2002)
Georgians	30	Caucasus	Yunusbayev et al. (2012)
Germans	13	CentralEU	Yunusbayev et al. (2015)
Greek	20	SouthernEU	Behar et al. (2012) +d11
Hakka	37	SouthChina	Rajeevan et al. (2003)
Han	44	NorthChina	Cann et al. (2002)
Hazara	24	NW_Frontier	Cann et al. (2002) + Di Cristofaro et al. (2013)
Hezhen	9	NorthChina	Cann et al. (2002)
Iranians	20	MiddleEast	Behar et al. (2012)
Ishkashim	10	NW_Frontier	Cann et al. (2002) + Di Cristofaro et al. (2013)
Italian	37	SouthernEU	Cann et al. (2002) + Behar et al. (2012)
KHV	99	SouthEast Asia	Behar et al. (2012)
Kabardin	3	Caucasus	Auton et al. (2015) [41]
Kurds	6	MiddleEast	Yunusbayev et al. (2012)
Laotians	59	SouthEast Asia	Rajeevan et al. (2003)
Lebanese	8	MiddleEast	Behar et al. (2012)
Libya	17	MiddleEast	Rajeevan et al. (2003)
Mongolians	21	Mongolia	Cann et al. (2002)
Naxi	9	SouthChina	Cann et al. (2002)
Oroqen	10	NorthChina	Cann et al. (2002)
Romanians	32	SouthernEU	Behar et al. (2012)
Russians	83	NorthernEU	Cann et al. (2002) +Rajeevan et al. (2003) +Yunusbayev et al. (2015)
Selkups	20	Siberian	Raghavan et al. (2014)
She	10	SouthChina	Cann et al. (2002)
Swedish	18	NorthernEU	Behar et al. (2012)
Syrians	16	MiddleEast	Behar et al. (2012)
Tajiks	24	CentraAsian	Yunusbayev et al. (2015) +Yunusbayev et al. (2012)
Tu	10	NW_China	Cann et al. (2002)
Tujia	10	CentralChina	Cann et al. (2002)
Turkmens	23	CentralAsian	Behar et al. (2012) +Yunusbayev et al. (2012)
Turks	19	MiddleEast	Yunusbayev et al. (2015) +Cann et al. (2002)
Uyghur	11	Uyghurs	Behar et al. (2012)
Uzbeks	19	CentralAsian	Cann et al. (2002)
Xibo	9	NW_China	Rajeevan et al. (2003)
Yakuts	49	Siberian	Behar et al. (2012)
Yemenites	47	MiddleEast	Rajeevan et al. (2003)

Table S1C: Samples gathered from Europe and Asia, to be merged with the samples from Table S1B, to test hypotheses regarding Indo-European and Tibeto-Burman language dispersals into the Indian sub-continent.

Table S2: Shared Ancestry table between the 90 populations found in Table S1A. The matrix is ordered according to language and social group affiliations. We see that Austro-Asiatic and Tibeto-Burman populations usually show divergence from the rest of India and only cluster within themselves. Few DR_SGCs such as Paniyas, Irulas and Kadars, show little shared ancestry with other Dravidian SGC and SGBs, which is explained by their remote locations in the hills and their livelihood as nomadic hunter gatherers. The Gonds share a very high amount of ancestry with other Austro-Asiatic and Dravidian populations, which follows from linguistics, as Gondis are bilingual. The Dravidian SGB and SGAs share high ancestry with Indo-European SGA/SGB/SGCs.

A	B	C	F3	Err	Z
DR_SGB	IE_SGA	Gounder	-0.02328	0.000644	-36.114
IE_SGA	TB_SGC	Manipuri_Brahmin	-0.01583	0.000452	-35.019
DR_SGB	IE_SGC	Gounder	-0.02188	0.000657	-33.315
IE_SGA	TB_SGC	Tharu	-0.01364	0.000447	-30.518
DR_SGA	TB_SGC	Tharu	-0.01292	0.000429	-30.084
IE_SGC	TB_SGC	Tharu	-0.00843	0.000389	-21.647
DR_SGC	TB_SGC	Tharu	-0.00913	0.000436	-20.922
DR_SGC	TB_SGC	Manipuri_Brahmin	-0.0094	0.000484	-19.415
IE_SGA	AA_SGC	Iyer	-0.00343	0.000241	-14.211
IE_SGA	AA_SGC	Gond	-0.00449	0.000321	-13.989
DR_SGC	AA_SGC	Gond	-0.00419	0.000305	-13.722
IE_SGC	AA_SGC	Gond	-0.00226	0.000171	-13.245
IE_SGA	AA_SGC	Kol	-0.00347	0.000266	-13.002
IE_SGA	AA_SGC	Pallan	-0.00411	0.000325	-12.638
IE_SGA	AA_SGC	Bhil	-0.00326	0.000277	-11.758
IE_SGA	DR_SGC	Bhil	-0.0036	0.000343	-10.489
IE_SGC	TB_SGC	Khasi	-0.01008	0.001166	-8.648
IE_SGB	TB_SGC	Khasi	-0.00981	0.001155	-8.49
IE_SGA	AA_SGC	Chamar	-0.00292	0.000358	-8.152
IE_SGA	AA_SGC	Satnami	-0.00503	0.000853	-5.898

Table S3: Top 10% of the significant f_3 statistics (f_3(C; A,B)) highlighting the most admixed populations in India. Gounders, Manipuri Brahmins, Tharus and Gonds are the most admixed among all tribes in India. Detailed f_3 statistics (for all mainland Indian populations from Table S1A available in supplementary .xlsx file SuppTable3). The Indo-European tribes such as Bhil, Kol and Chamar show signs of admixture from Austro-Asiatic tribes and Indo-European forward and SGBs. Changapa, who are a tribe in Ladakh, Jammu and Kashmir in the extreme north surprisingly show signs of admixture from Dravidian tribes, Indo-European SGAs, SGBs and tribes, showing that they have been in contact with the rest of the tribes in India. The Gonds show signs of admixture from Austro-Asiatic, Dravidian and Indo-European tribes, which is much expected as Gondis are spanned across central India. Some Gondi samples also show admixture from Indo-European and Dravidian SGAs. Expectedly, the Khasis are an admixed population from Tibeto-Burman tribes and Austro-Asiatic tribes. The Khasis are Austro-Asiatic speakers located in the northeast, along with Tibeto-Burman tribes. Notably, Manipuri Brahmins uphold the view that they are an admixed population between Indo-European and Tibeto-Burman speakers. The Tharus also are an admixed population, as had been noted earlier, with admixture from Indo-European, Dravidian, Austro-Asiatic, and Tibeto-Burman tribes, but not just Indo-Europeans.

Table S4: Outgroup f3 statistic results for the tests: f3(YRI; X, Y) as visualized in Figure 3 in the pie charts showing shared genetic affinity of X and Y populations, where X is an Indian population and Y is an Eurasian/southeast Asian population. The maximum f3 values are returned for every population in X w.r.t Y and then represented here in descending order. The greater the maximum shared genetic affinity, the darker is the color used in the pie chart in Fig 3. This table shows that the Europeans share more genetic drift with the IE_SGA and East Asians with the TB_SGC, reflecting on the gateways of gene flow to the Indian subcontinent.