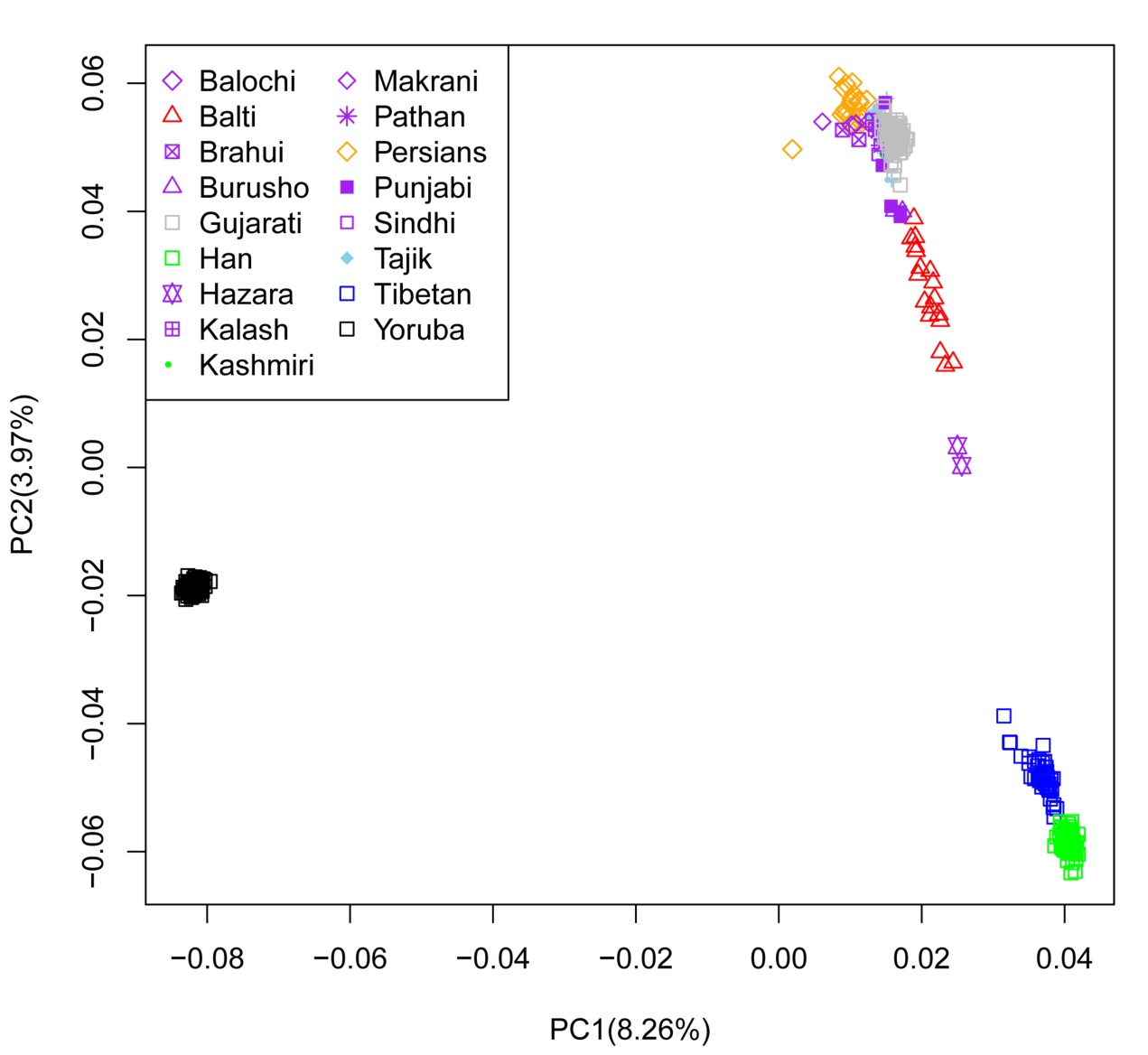
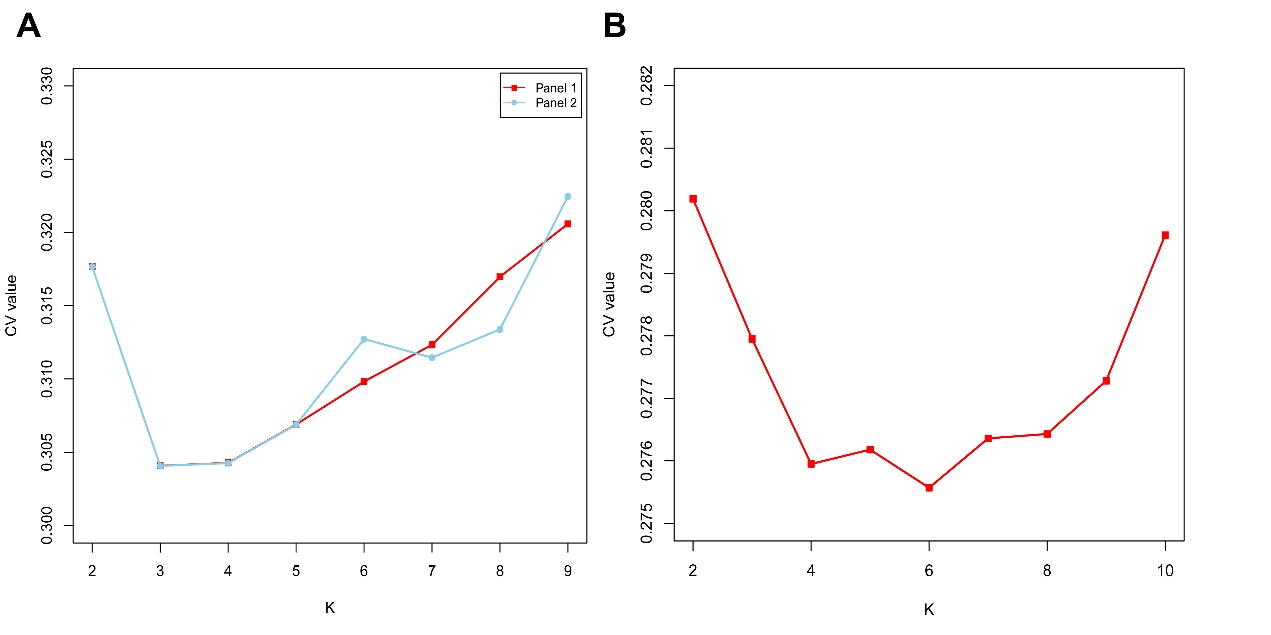
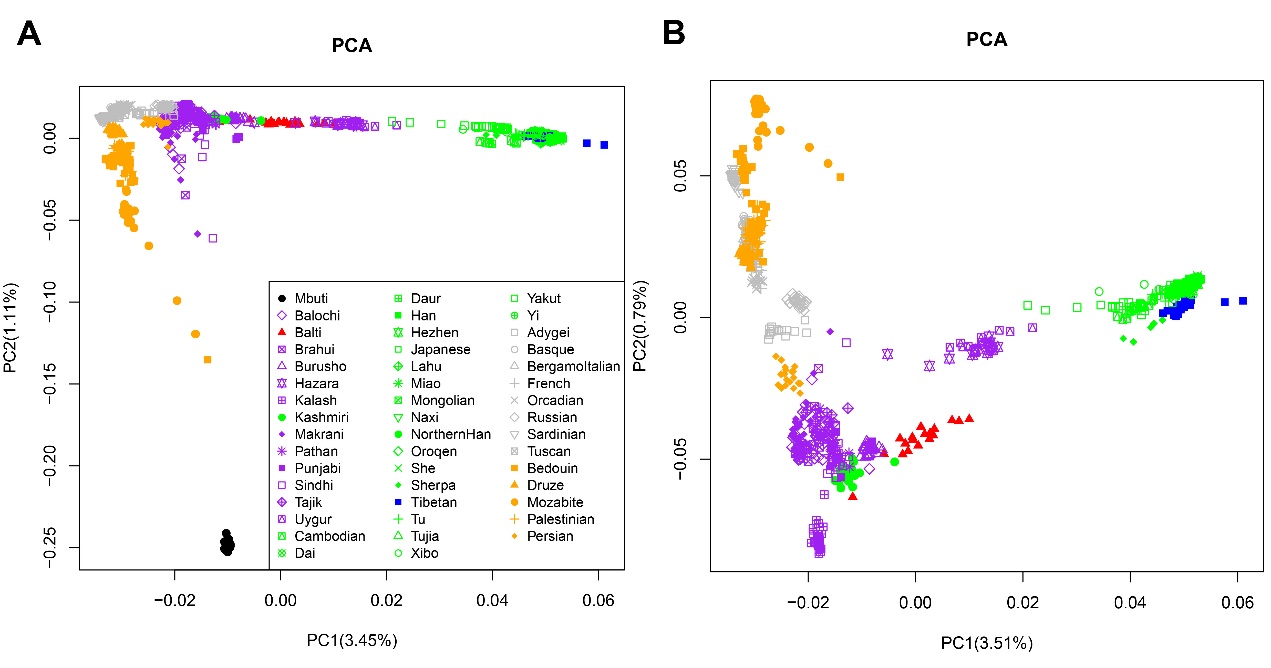
**Supplementary Figures**

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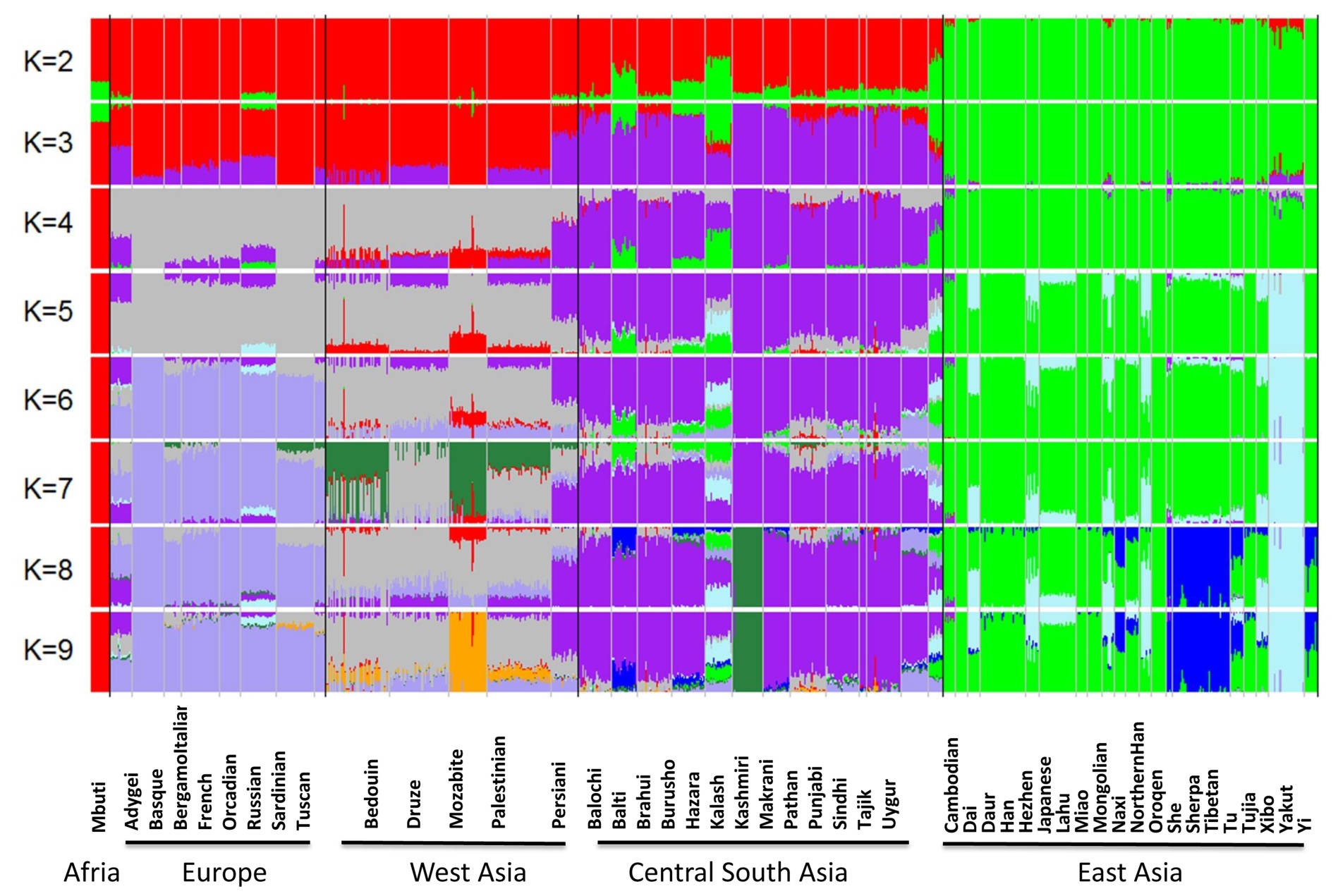
**Fig. S1. The principal component analysis of the individuals from 16 Asian populations with Yoruba.** A total of 472,755 SNPs in 455 individuals from 17 populations based on WGS data were used. See supplementary table S2 for sample information.

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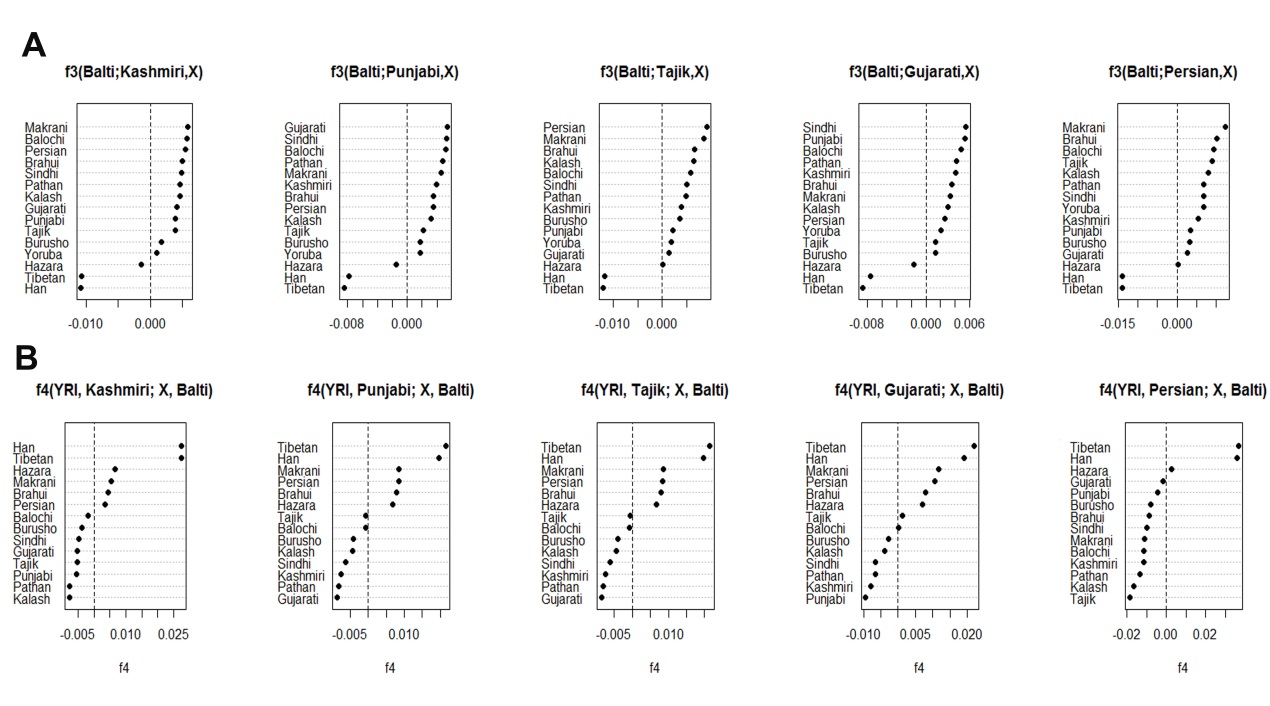
**Fig. S2. Error estimation for numbers of genetic clusters across populations.** The error rates were estimated using the cross-validation (CV) values, for each K values from the ADMIXTURE analyses shown in Fig. 2B (A) and Fig. S4(B). The CV values were calculated in two independent ADMIXTURE runs with two different seeds (noted with red and sky blue, respectively).



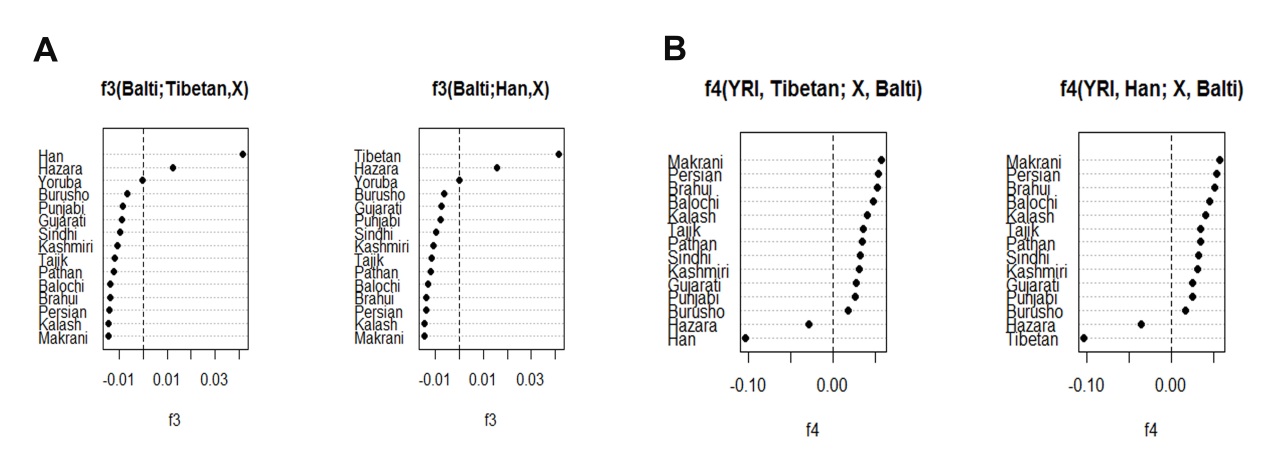
**Fig. S3. The principal component analysis for the extended dataset.** Genome-wide continental genetic affinity for the Balti population as compared to global reference populations with (A) or without Mbuti (B). A total of 2,714,036 SNPs in 879 individuals from 47 populations based on WGS data were used. See supplementary table S2 for sample information.



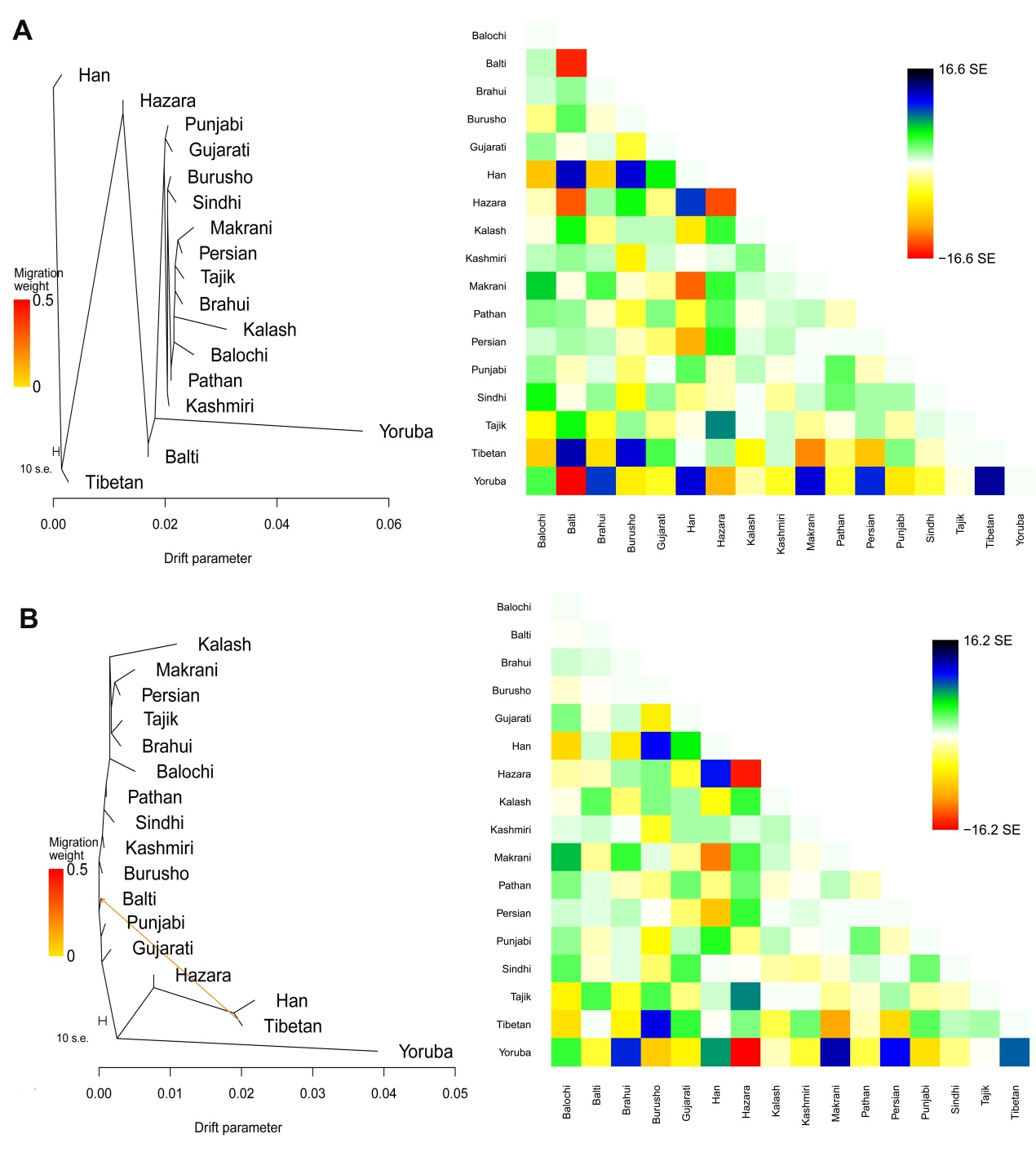
**Fig. S4. Unsupervised ADMIXTURE clustering for the WGS dataset of 879 individuals**. A total of 2,714,036 SNPs in 879 individuals from 47 populations based on WGS data were used. The lowest cross-validation error value was observed at K = 4 (Fig. S2B). See supplementary table S2 for sample information



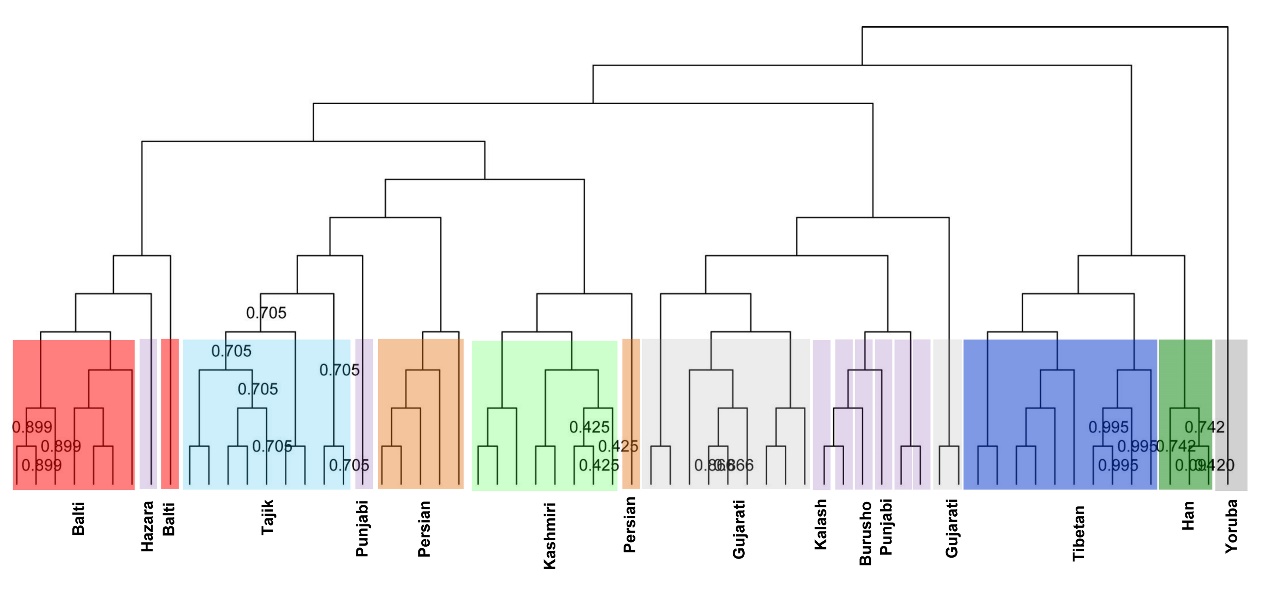
**Fig. S5. F statistics between the Balti and Central/South /West Asian populations.** (A) f3 tests detected gene flow between the Balti and Central/South/ West Asian populations. The f3 statistics were significantly negative (with Z score ≤ -3) when X was Tibetan or Han. (B) f4 tests with the Yoruba of Nigeria (YRI) set as the outgroup. Genetic affinity of Central/South/West Asian populations to the Balti population was revealed. Positive scores indicated that Central/South/West Asian populations shared more alleles with the Balti population than other populations.



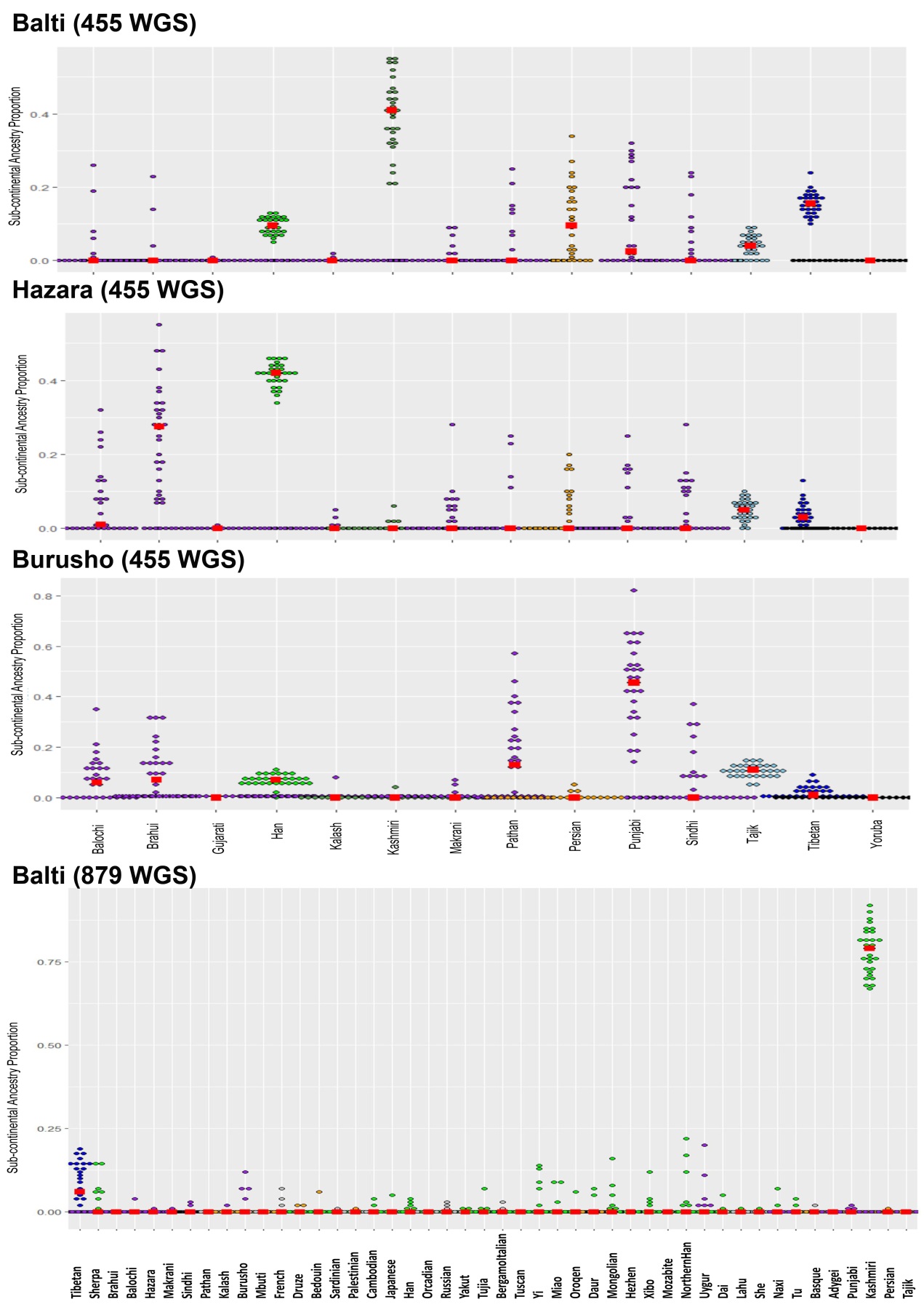
**Fig. S6. F statistics to estimate the relative amount of contribution from East Asian populations to the Balti population. (**A) f3 tests detected gene flow between the Balti and East Asian populations. The f3 statistics were significantly negative (with Z score ≤ -3), except where X was Han, Hazara, or Yoruba (not shown). (B) Genetic affinity of East Asian populations to the Balti population was revealed. Positive scores of f4 tests indicated that East Asians shared more alleles with the Balti population than other populations.

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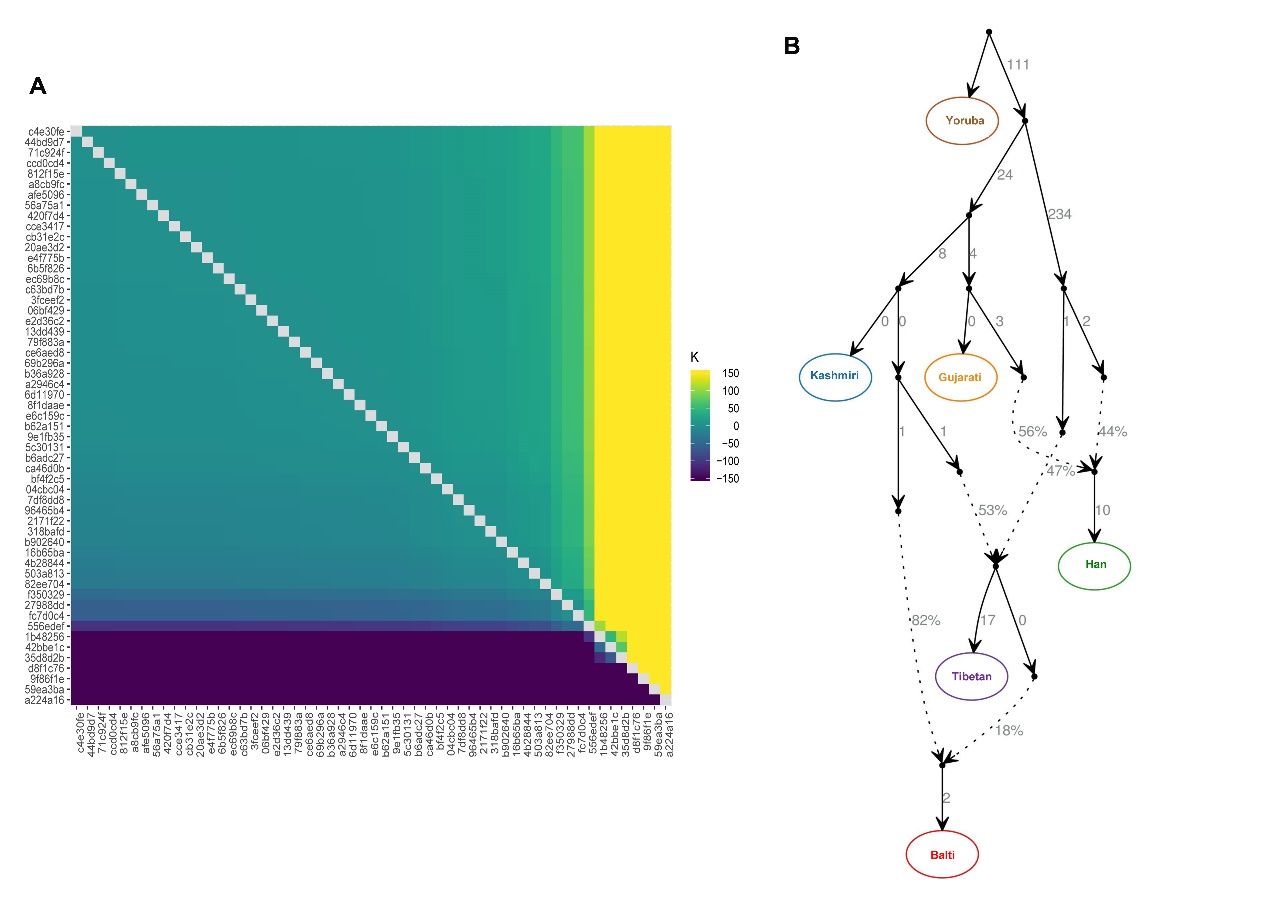
**Fig. S7. Population tree and gene flow inferred by TreeMix.** (A) A simple tree-like model without admixture (m=0). The data fit poorly, as indicated by the matrix of residuals between empirical and modeled allele frequency covariance on the right. (B) The single admixture event (m=1) from the branch of Tibetan to Balti. The data presented a better fit compared those of the model without migration (m=0) (A).



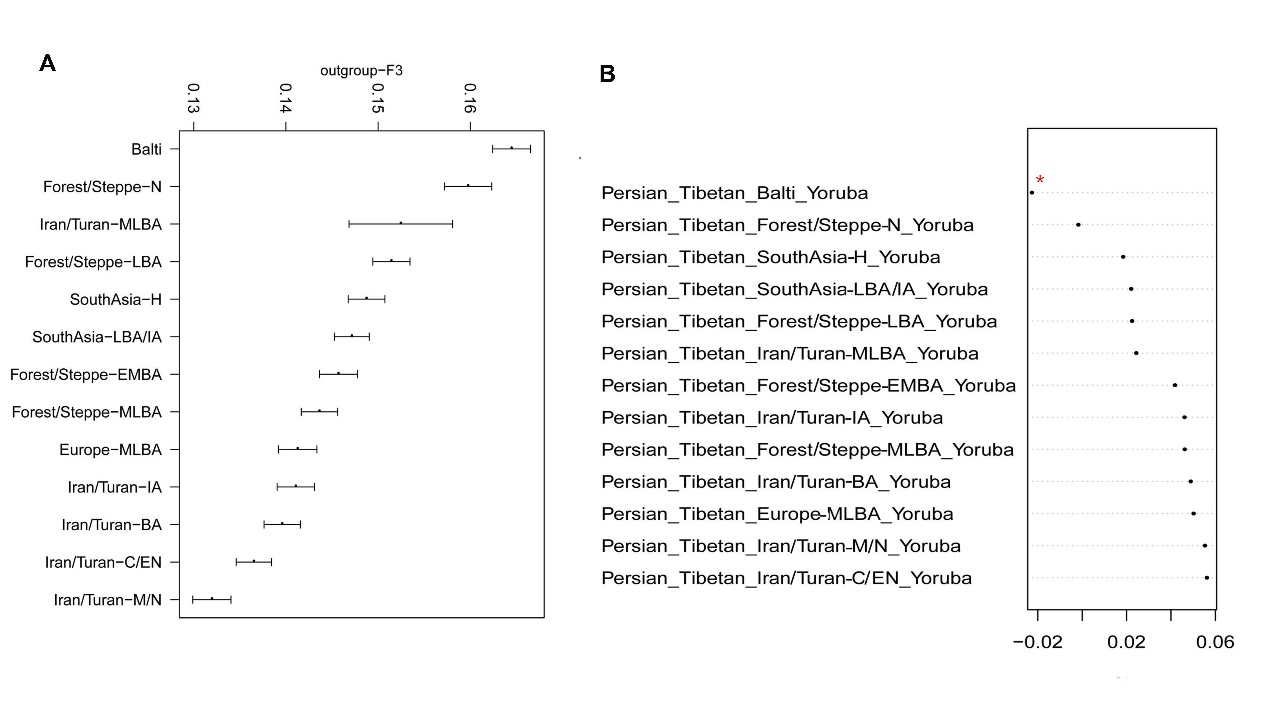
**Fig. S8. Hierarchical tree for population assignment of 455 individuals.** Each tip corresponded to a population grouped by FINESTRUCTURE. Population lables were noted with colors**.**

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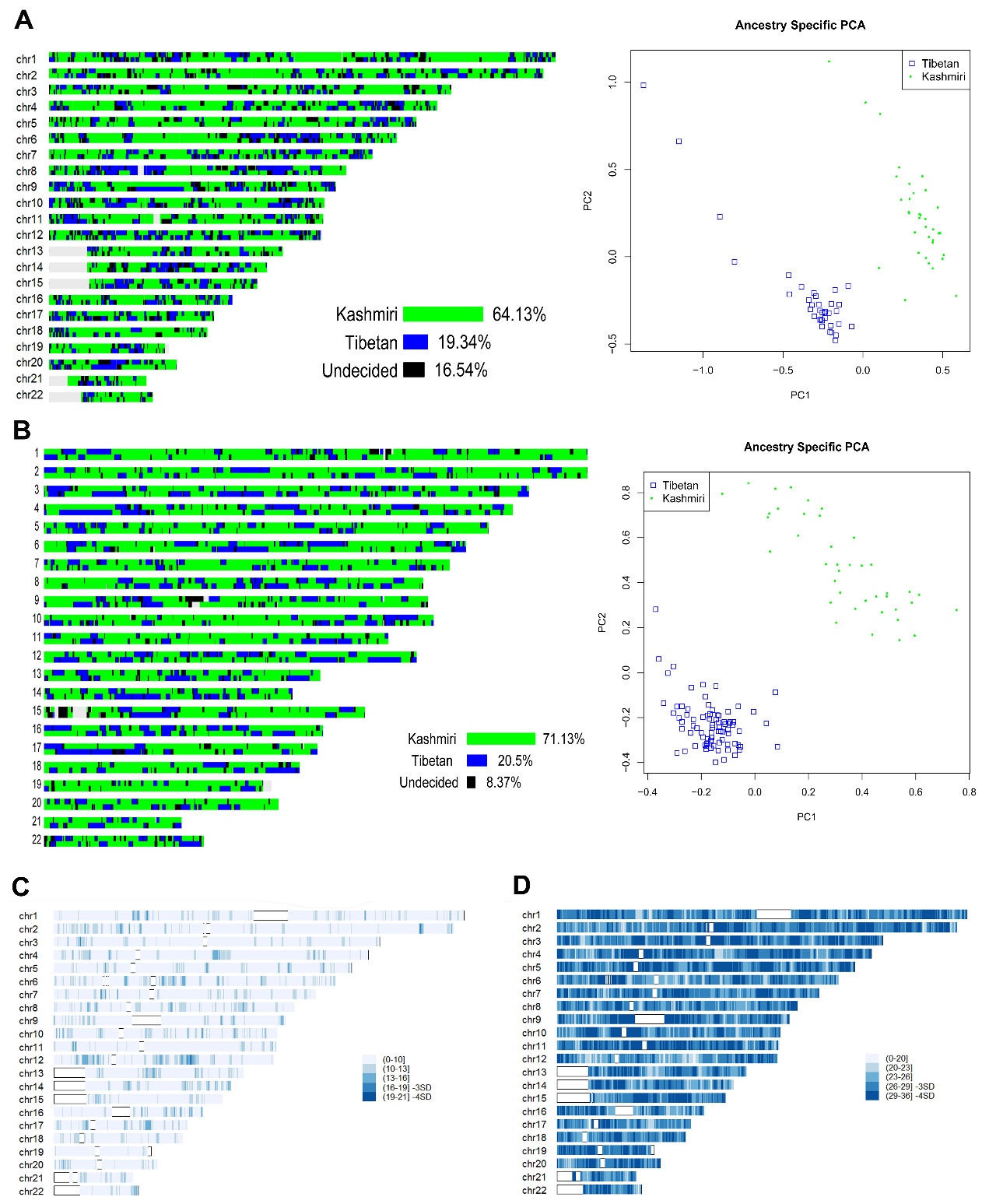
**Fig. S9. Sub-continental ancestry components inferred by SOURCEFIND.** The SOURCEFIND was performed with 30 independent runs using 200,000 iterations each run. Dot represents the result of each run. Red square indicates median value.

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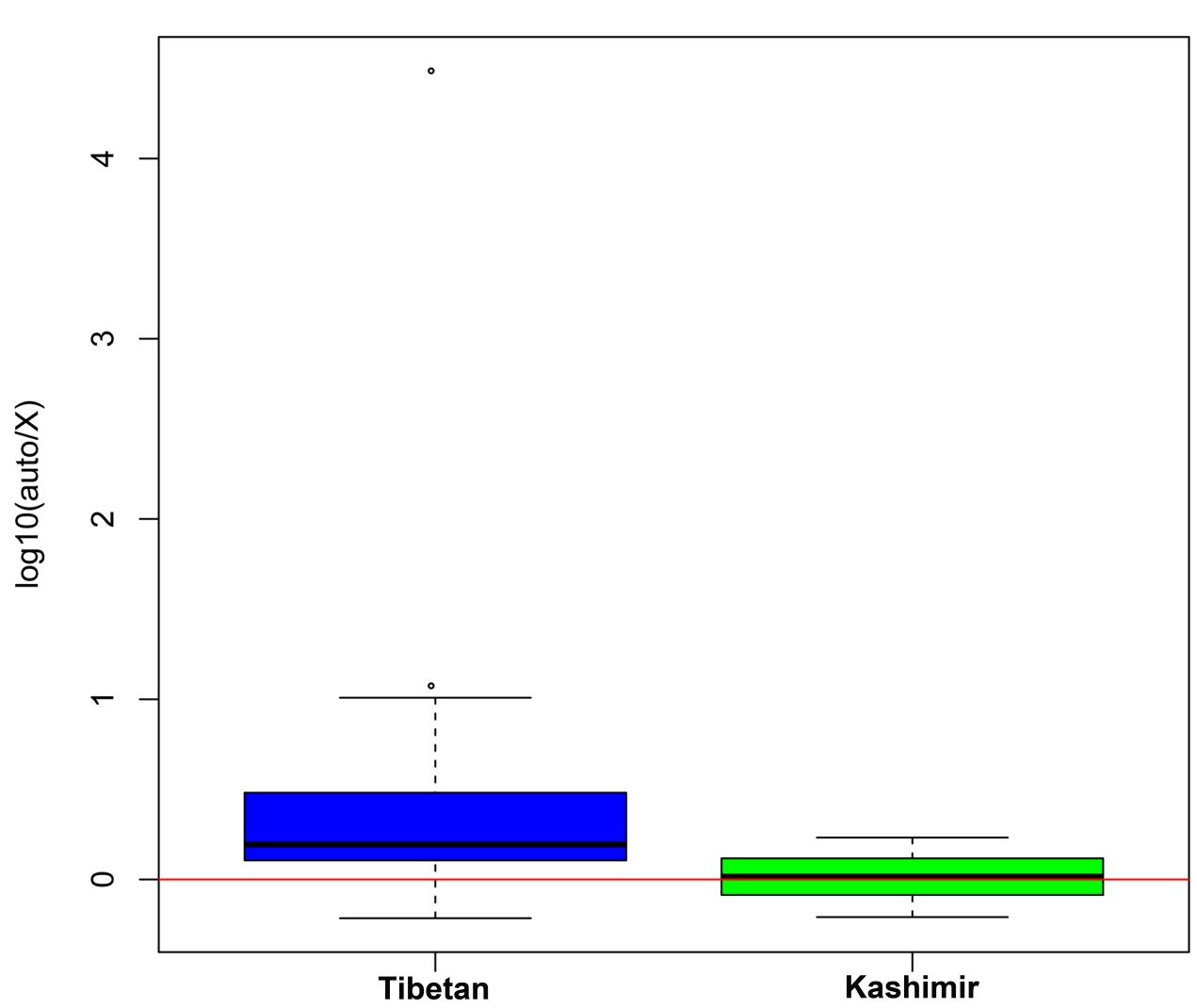
**Fig. S10. Admixture graph model.** (A) Heatmap of Bayes factors for graph pairs with |K|>3. The 55 graphs without f4 outliers (|Z| < 3) were included. (B) A good fitting graph of ID4b28844 with K < 83. Estimated genetic drift was indicated along the solid lines in units of f2 distance (parts per thousand). Admixture events were shown as dotted lines labeled by proportions.

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**Fig. S11. F statistics between Tibetan and ancient Central/South Asian populations.** (A) Outgroup f3 tests to detect gene flow between the Tibetan and Central/South Asian populations as compared with the Balti. (B) f4 tests with the Yoruba of Nigeria (YRI) set as the outgroup. Genetic affinity of ancient Central/South Asian populations to the Tibetan population was revealed. Negative score indicated that the Tibetan population share more alleles with the test population. \* represents statistic significantly (with |Z score|>3). The information of ancient samples was referred to the published reference (Narasimhan, et al. 2019).



**Fig. S12. Local ancestry inference in the Balti genomes.** (A) Local ancestry inference by PCAdmix and ancestry specific PCA.(B) Local ancestry inference by RFmix and ancestry specific PCA. (C) Local Tibetan ancestry inferred by RFMix. (D) Local Kashmiri ancestry inferred by RFMix.



**Fig. S13. Autosomal versus X chromosomal ancestry proportions.** The ratios of autosomal to X chromosomal ancestry proportions for Tibetan and Kashmiri-specific components as inferred by ADMIXTURE analysis (K = 5) in the Balti population were scaled in log10. The ratio more than 0 meant a higher contribution from source males than females into the gene pool of admixed population.