

Supplementary information

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Supplementary Table 1

Number of high-quality biallelic variants in different datasets before and after LD pruning.

dataset	biallelic variants				
	unpruned	pruned			
		sliding window		difference between pruning windows	
		50k	10000k	count	percent (%)
GENOME	483100	232194	206253	25941	11.17%
EXOME	405496	184258	149453	34805	18.89%
BEADCHIP	567187	79492	72701	6791	8.54%
HUN-EXOME	408790	186984	151259	35725	19.11%

The unpruned datasets were LD pruned by Plink with two different sliding windows (50k and 10,000k respectively), and the difference of pruned markers between the two parameter settings is also summarized.

Supplementary Table 2

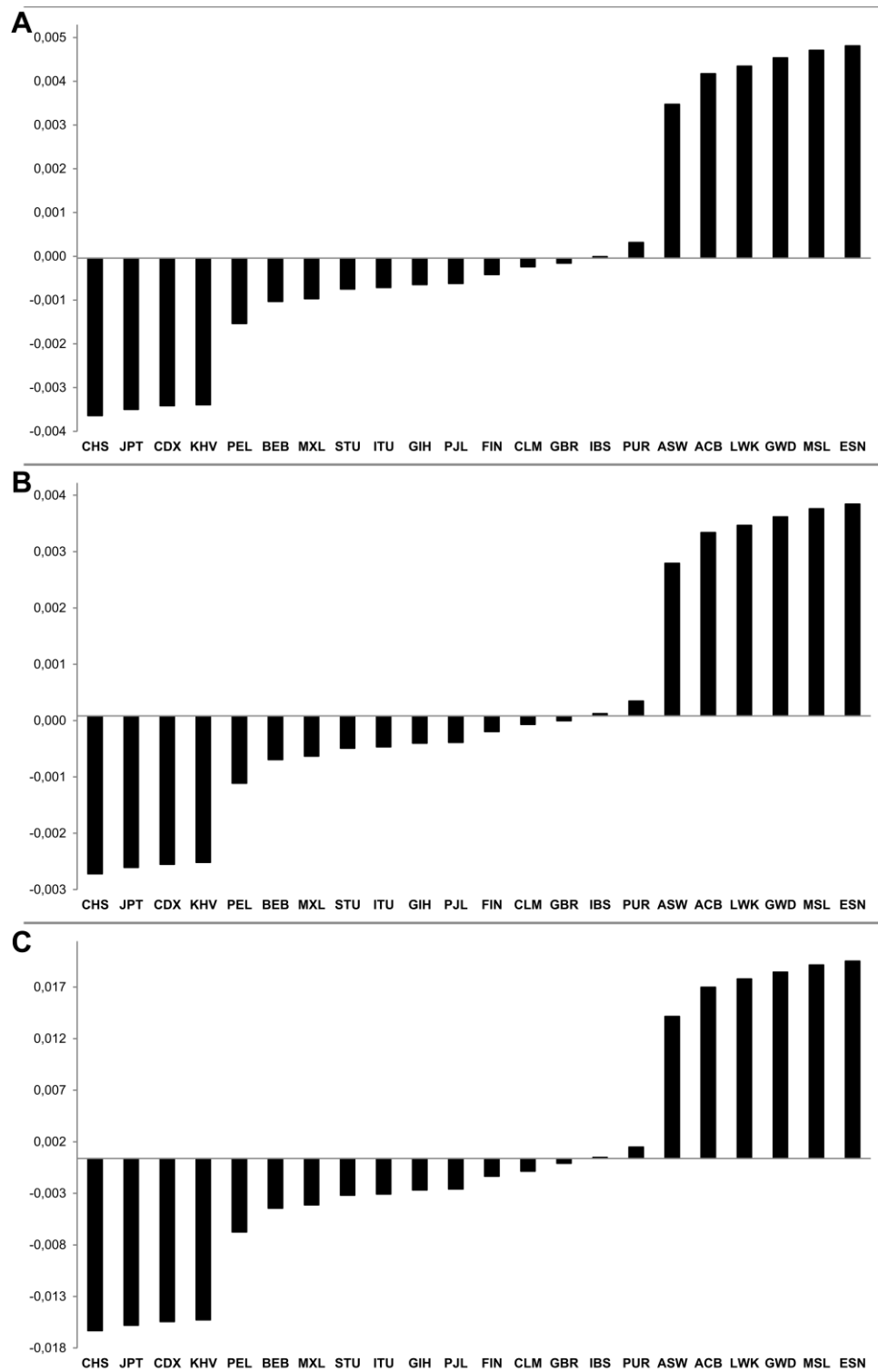
f_3 -statistics of Hungarian and selected South Asian populations.

Pop A	Pop B	Pop C	F3 value	Std Err	Z score	SNP count
STU	HUN	PJL	-0.003761	0.000140	-26.782	76834
ITU	HUN	PJL	-0.003641	0.000141	-25.752	76845
BEB	HUN	PJL	-0.002865	0.000138	-20.743	80622

Negative F_3 values with significant Z score indicate complex relations (admixture) between the Hungarian and South Asian populations.

Supplementary Figure 1

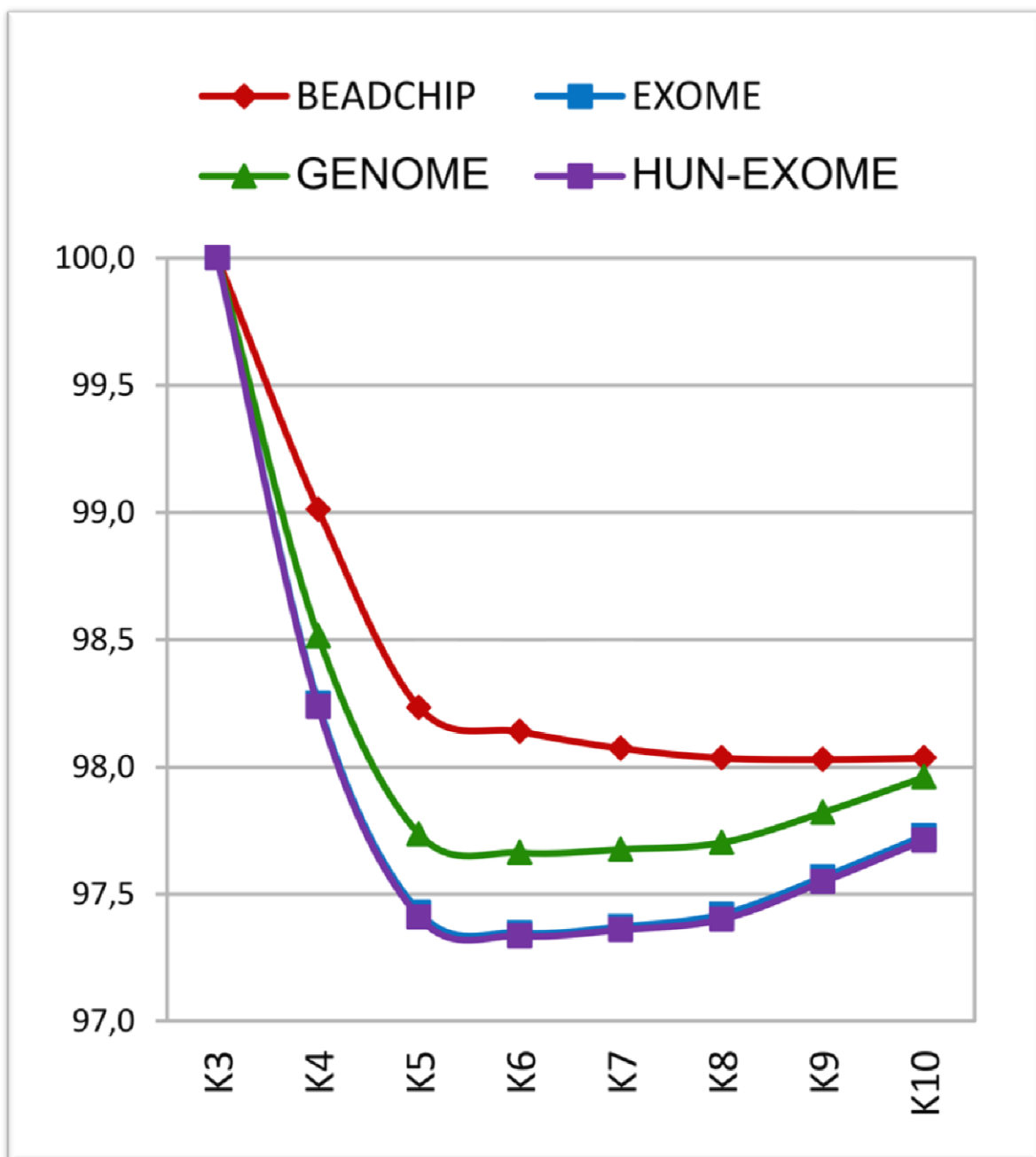
$F_4(\text{TSI}, X; \text{CHB}; \text{YRI})$ values of the analyzed datasets



A) GENOME, B) EXOME and C) BEADCHIP, where X denotes the test population indicated on the x-axis.

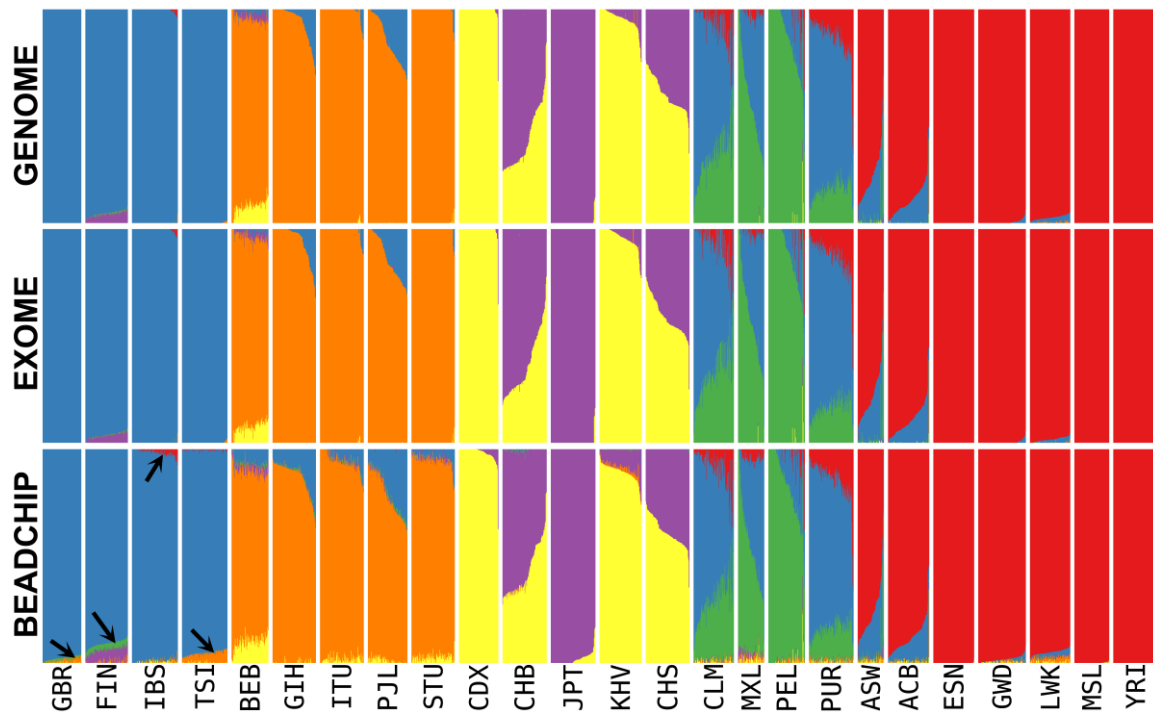
Supplementary Figure 2

Calculated Cross Validation error for different admixture models (K=3 to 10) for each dataset.



Supplementary Figure 3

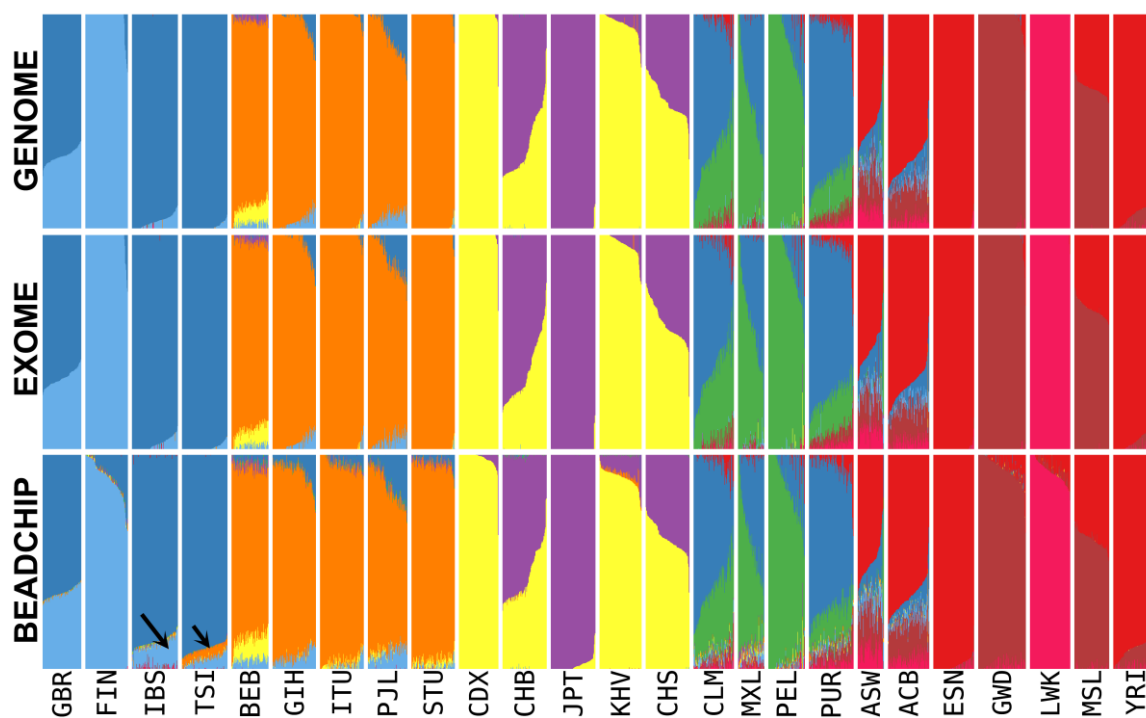
Admixture analysis of 25 populations using the GENOME, EXOME and BEADCHIP datasets with the K=6 admixture model.



The arrows denote examples of minor genetic admixture components within the European super-population.

Supplementary Figure 4

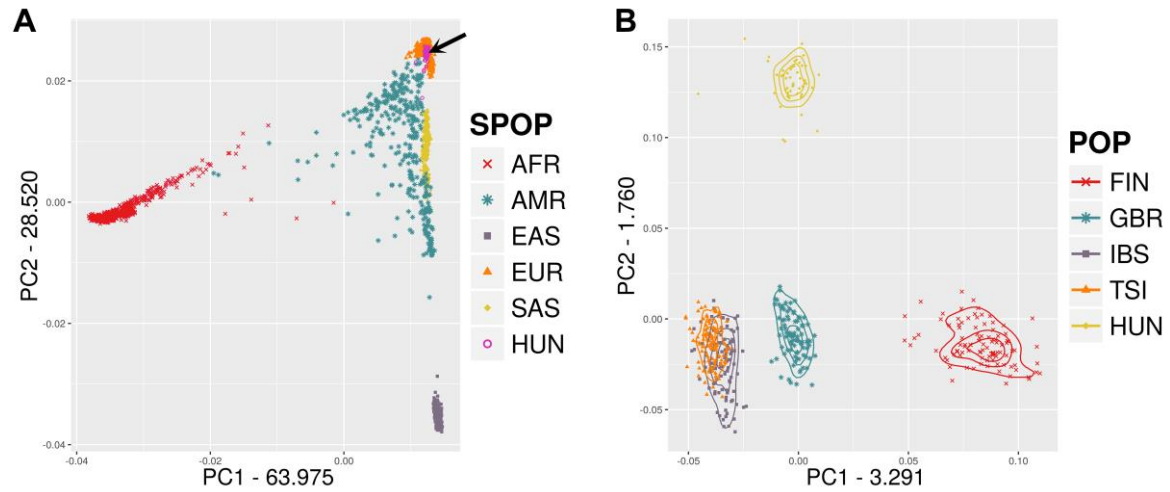
Admixture analysis of 25 populations using the GENOME, EXOME and BEADCHIP datasets with the K=9 admixture model.



The arrows denote examples of minor genetic admix components within the European super-population.

Supplementary Figure 5

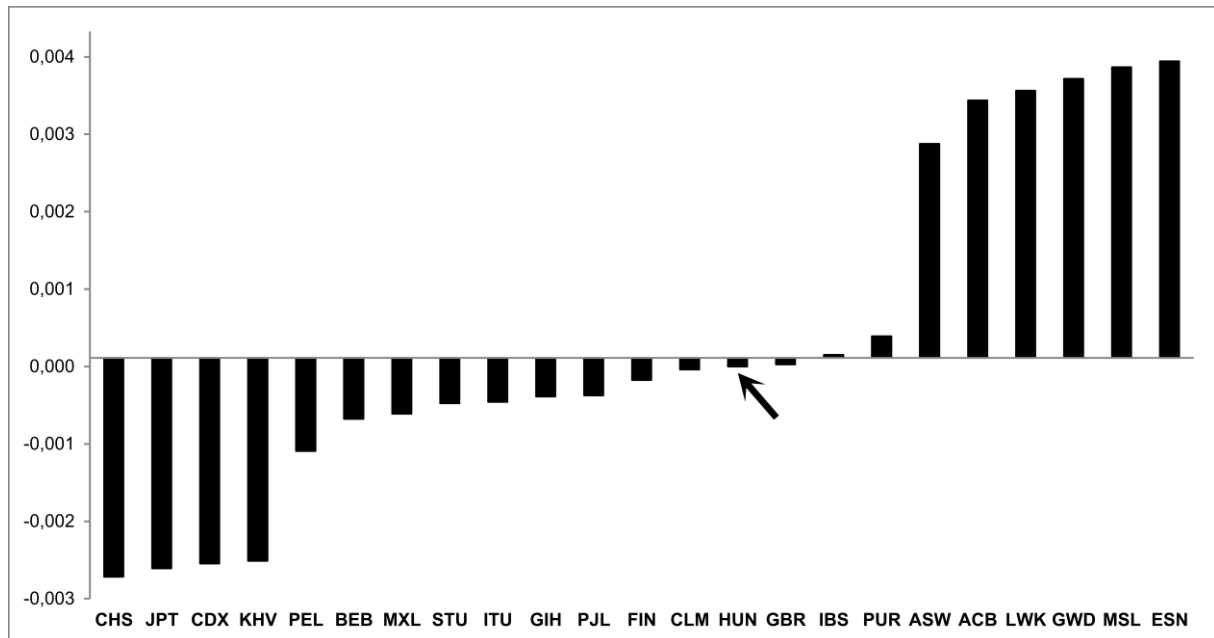
PCA of the HUN-EXOME dataset



A) Hungarians (highlighted by the arrow) in relation to the super-population, **B)** Hungarians in relation to European populations.

Supplementary Figure 6

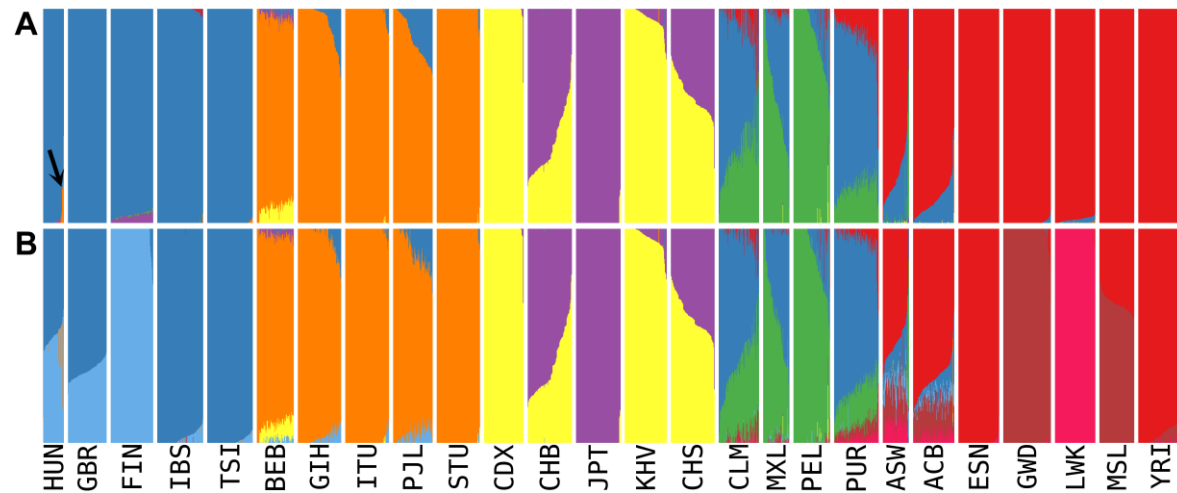
$F_4(\text{TSI}, X; \text{CHB}, \text{YRI})$ values of the HUN-EXOME dataset, where X denotes the test population indicated on the x-axis.



The arrow shows the relative position of Hungarians, indicating that they have higher East Asian admixture component than British but lower than Finnish population.

Supplementary Figure 7

Admixture analysis of 25 populations using the HUN-EXOME dataset for the **A)** K=6 and **B)** K=9 admixture models.



The arrow denotes Hungarian individuals with substantial South Asian admixture components.

Supplementary Data

We have deposited the Supplementary Data to figshare:

<https://figshare.com/s/e91794c7141a7eb16255>