Supplemental Figures for:

Fine-Scaled Human Genetic Structure Revealed by SNP Microarrays

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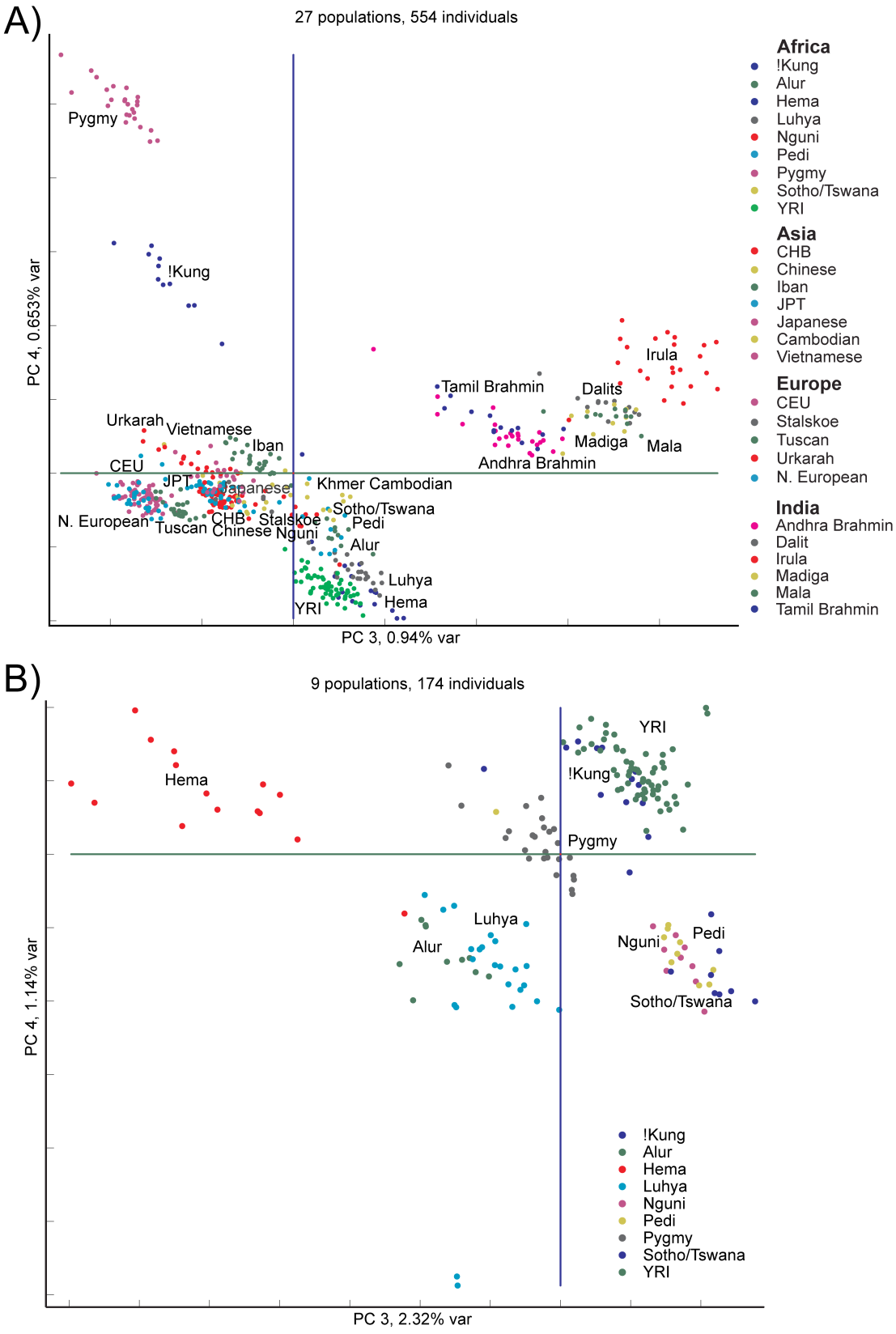
Supplemental Figure S1. Principal components analysis of population structure. A) All 554 individuals; B) African individuals. PC3 and PC4 are shown. Each individual is represented by one dot and the color label corresponding to their self-identified population origin. The percentage of the variance in genetic distance explained by each PC is shown on the axis.

Supplemental Figure S2. Principal components analysis of population structure in 554 individuals and HGDP samples. PC1 and PC2 are shown. Each individual is represented by one dot and the color label corresponding to their self-identified continental origin. The percentage of variant explained by each PC is shown on the axis.

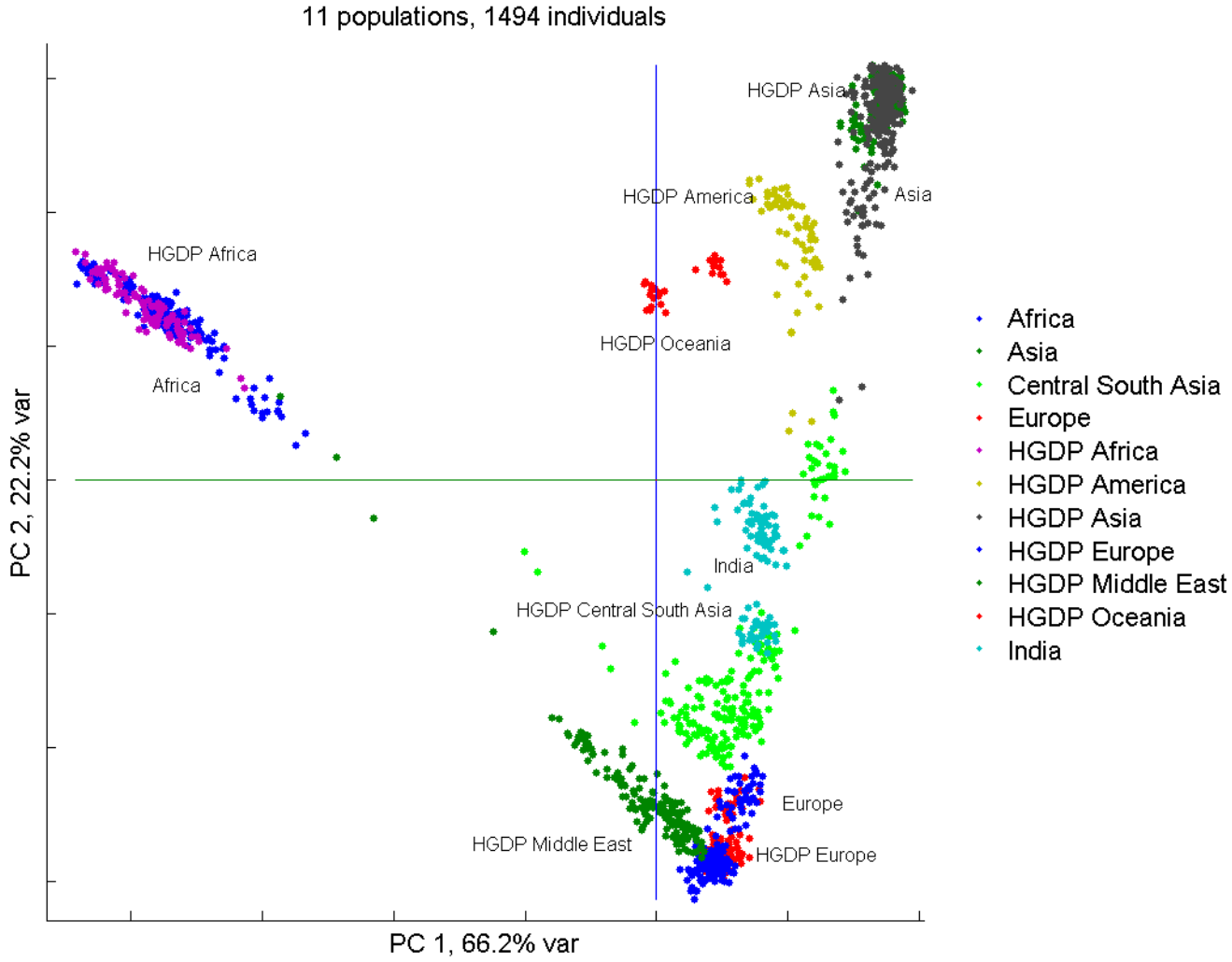
Supplemental Figure S3. Principal components analysis of population structure in each continental group for 554 individuals and HGDP samples. A) Africa; B) East/Southeast Asia; C) Europe; and D) South Asia. First two PCs are shown. For East/Southeast Asia, Chinese ethnic groups in the HGDP panel were grouped into Northern China (Oroqen, Daur, Hezhen, Mongola, Xibo, and Tu), Southern China (Dai, Lahu, Miao, Naxi, She, Tujia, Yi) and Han Chinese (Han and Han-NChina) to improve the resolution.

Supplemental Figure S4. Individual grouping inferred by *frappe* with A) K = 5 and **B) K = 6.** Each individual's genome is represented by a vertical bar composed of colored sections, where each section represents the proportion of an individual's ancestry derived from one of the K ancestral populations. Individuals are arrayed horizontally and grouped by population and continent of origin as indicated. Individual continental origin is labeled at the top.

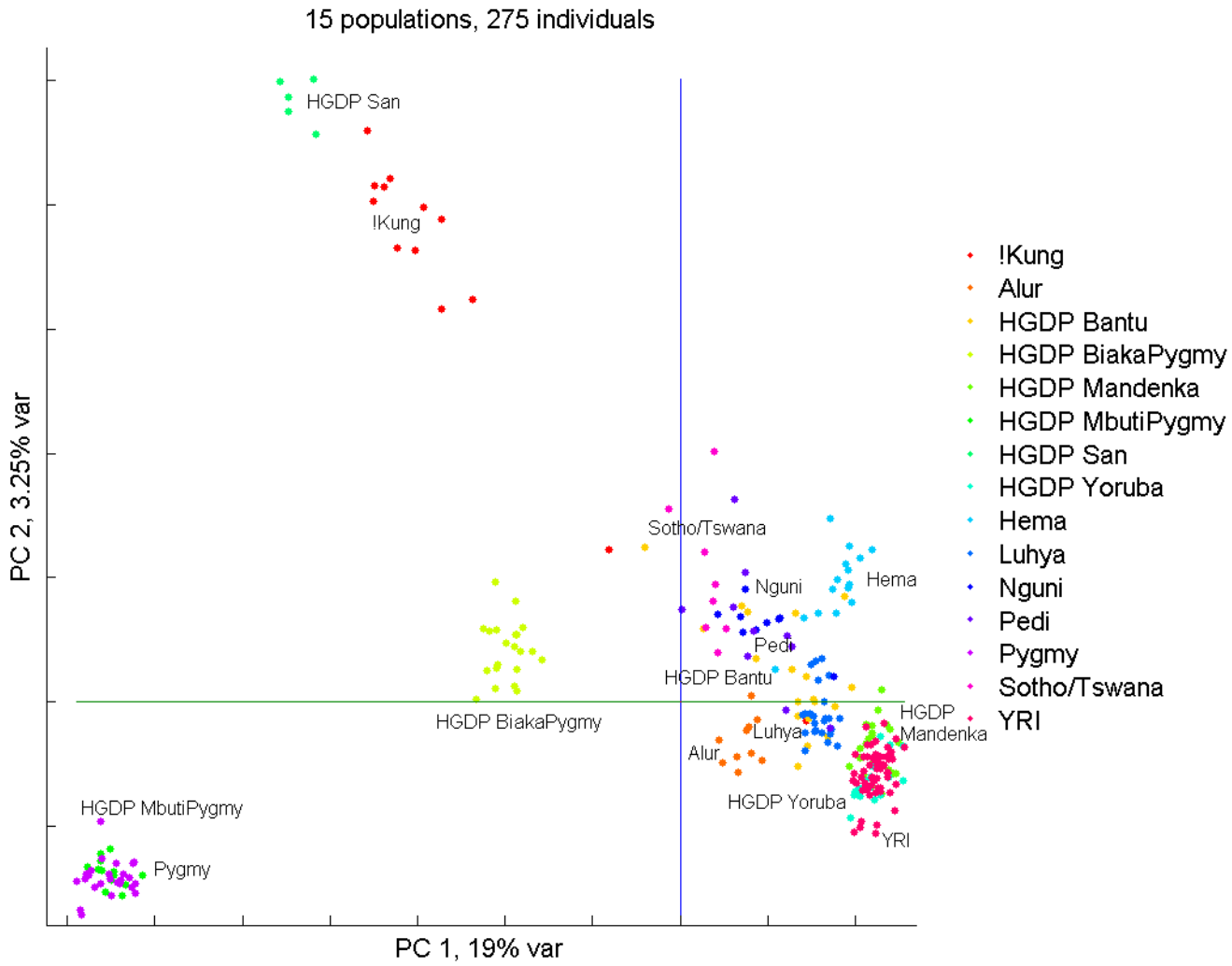
Supplemental Figure S1



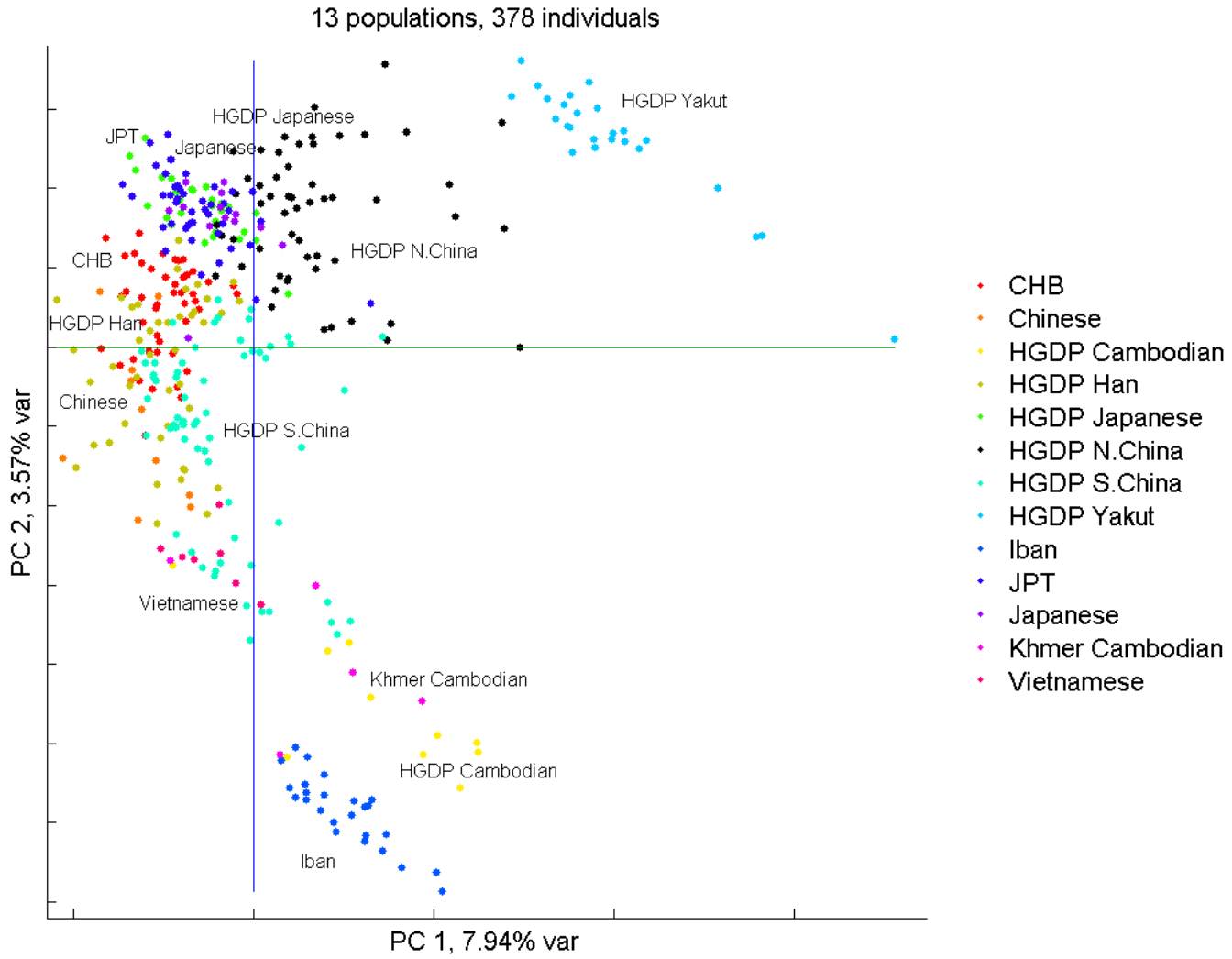
Supplemental Figure S2



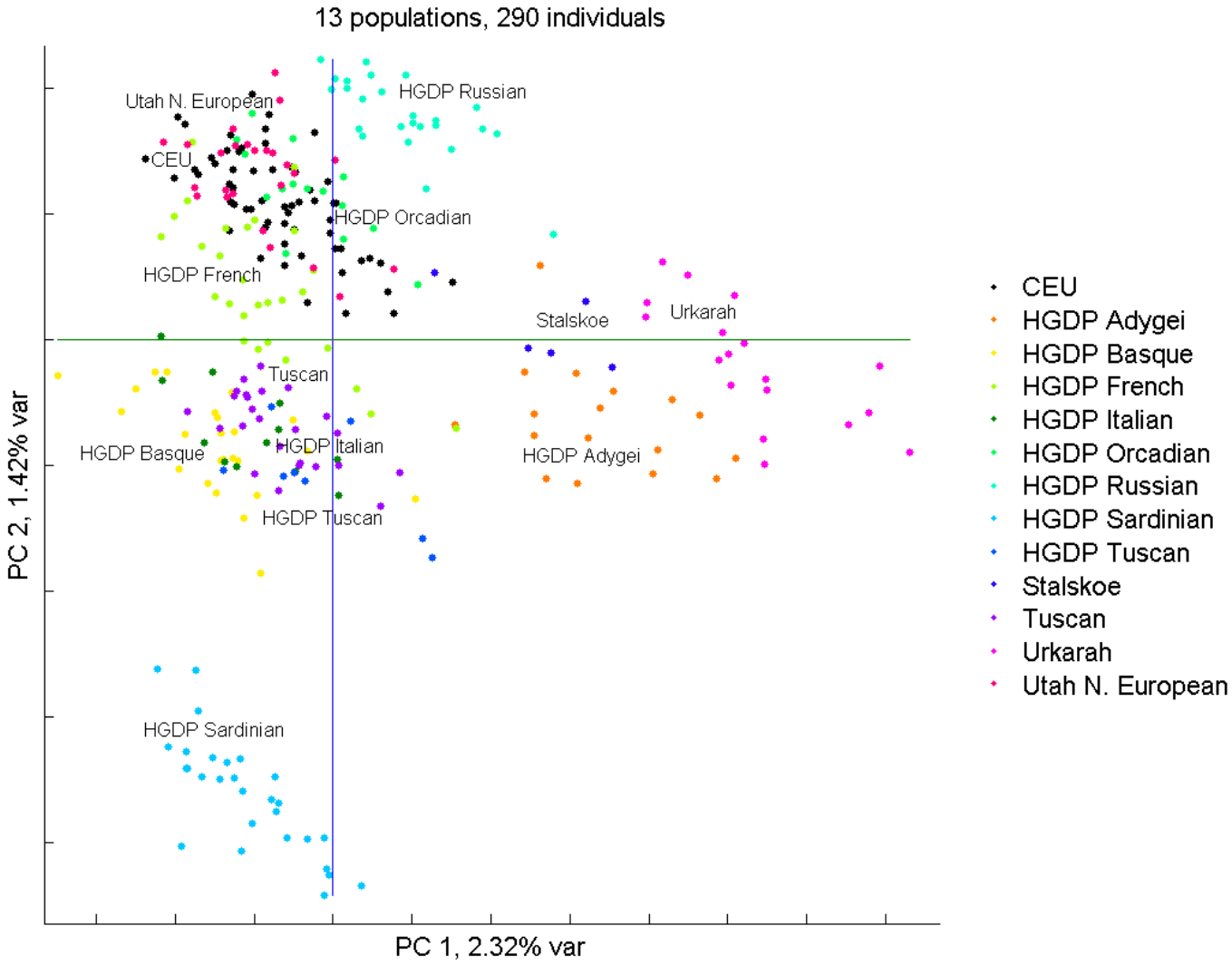
Supplemental Figure S3A



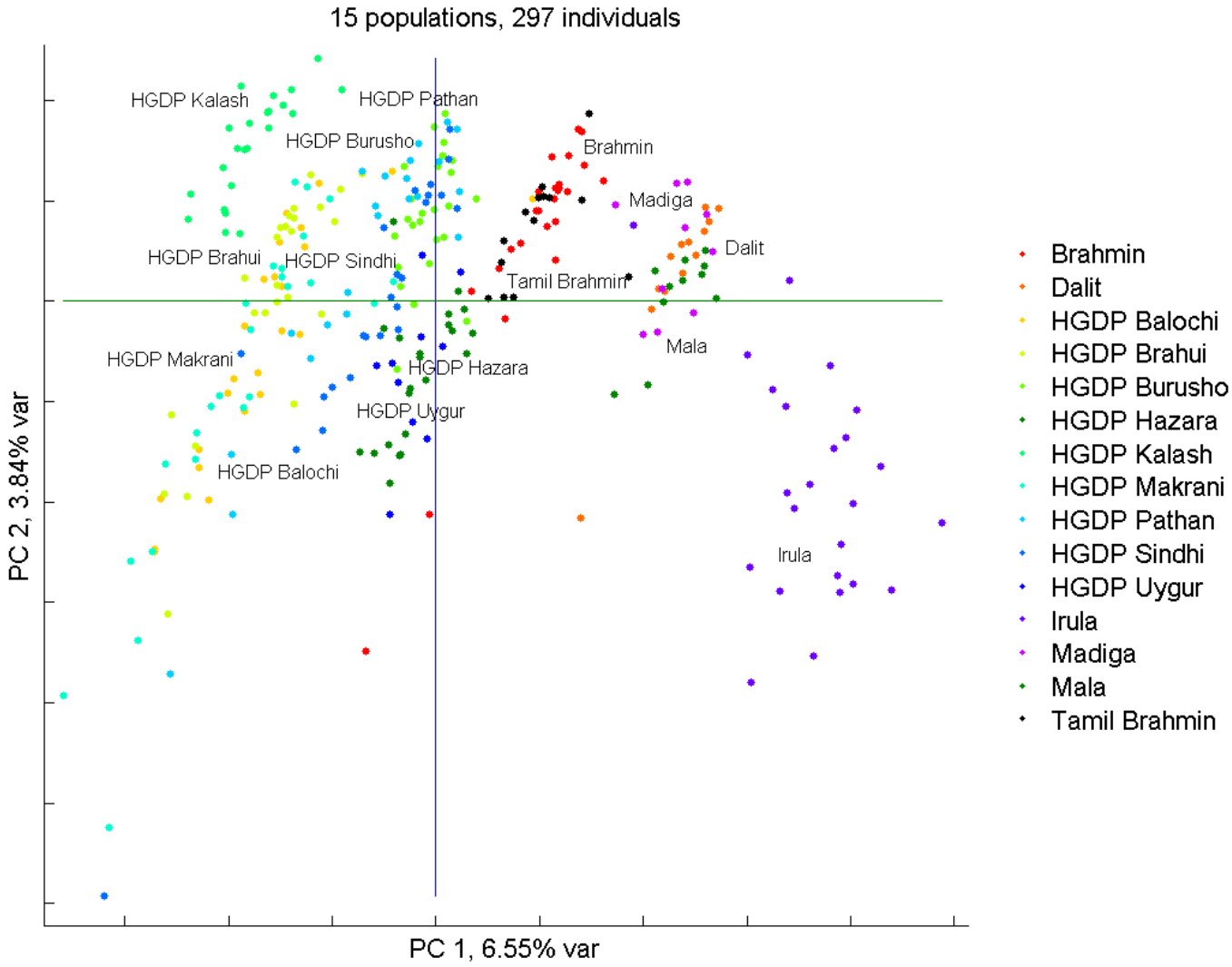
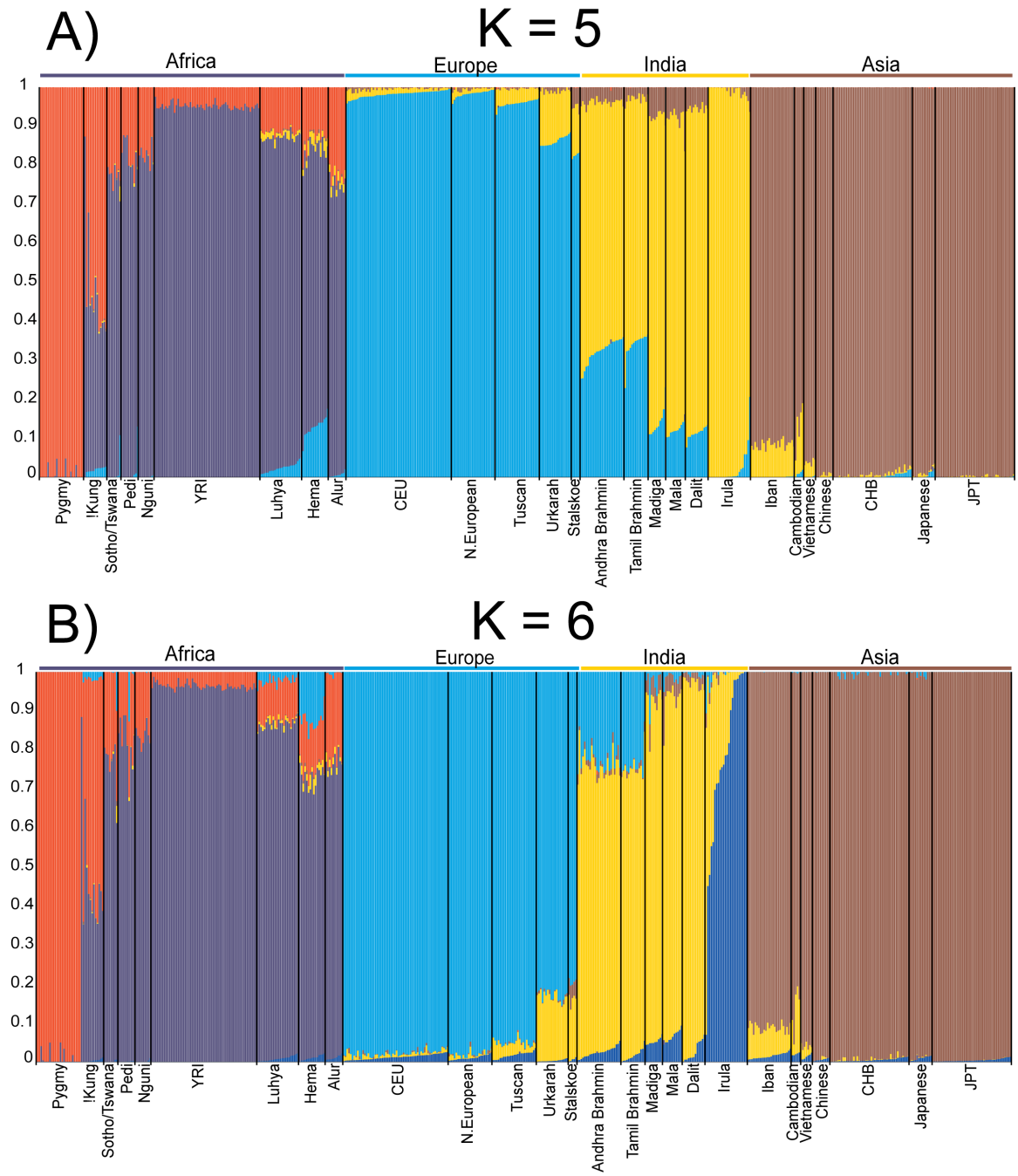
Supplemental Figure S3B



Supplemental Figure S3C



Supplemental Figure S3D



Supplemental Figure S4