

Supplemental Figures for:

Toward a more Uniform Sampling of Human Genetic Diversity: A Survey of Worldwide Populations by High-density Genotyping

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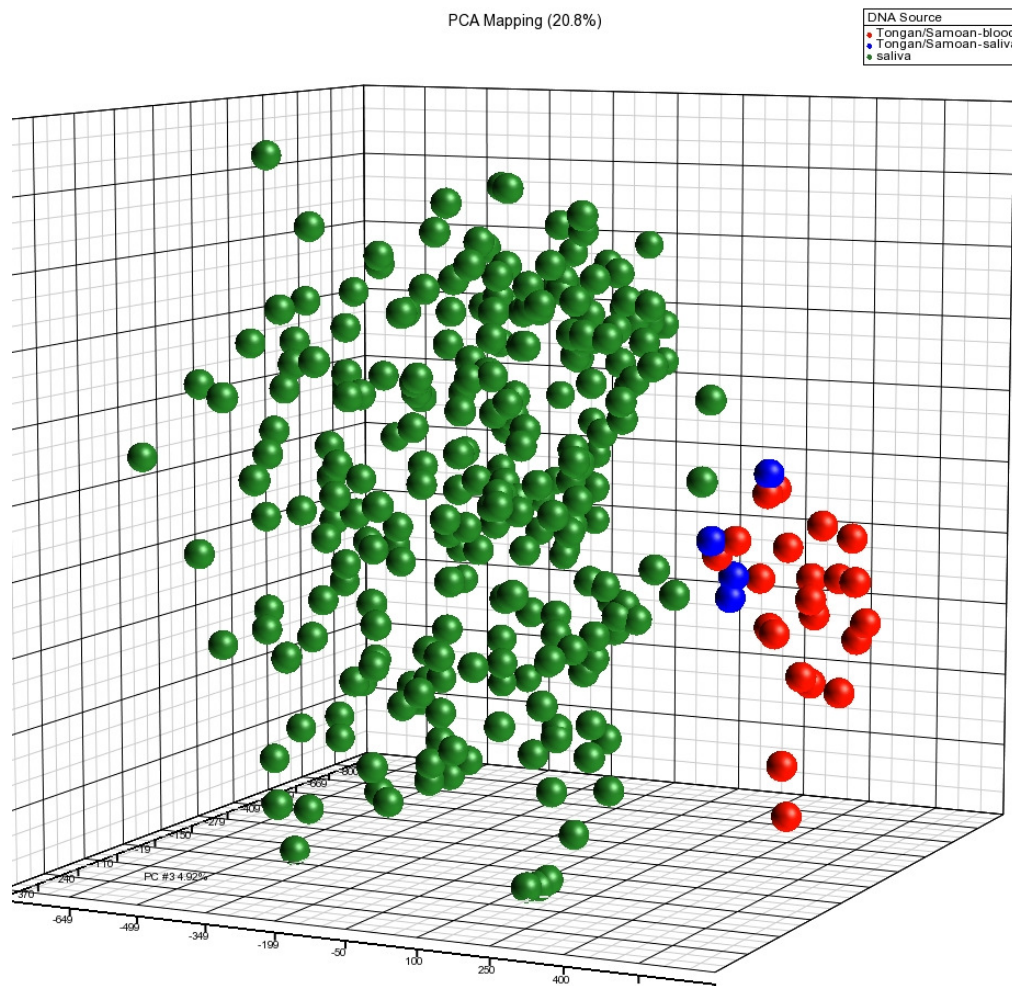
Supplemental Figure 1. PCA of blood vs saliva-derived DNA samples. PCA was performed in Partek Genomics Suite, using sample covariance as the dispersion matrix. For Tongan and Samoan samples, saliva-derived samples are in blue and blood-derived samples are in red. All other samples are saliva-derived and are in green.

Supplemental Figure 2. Bootstrap consensus tree of 40 populations. Populations are color-coded based on their continental origins. The hypothetical ancestral population is shown. Bootstrap value for each branch is shown.

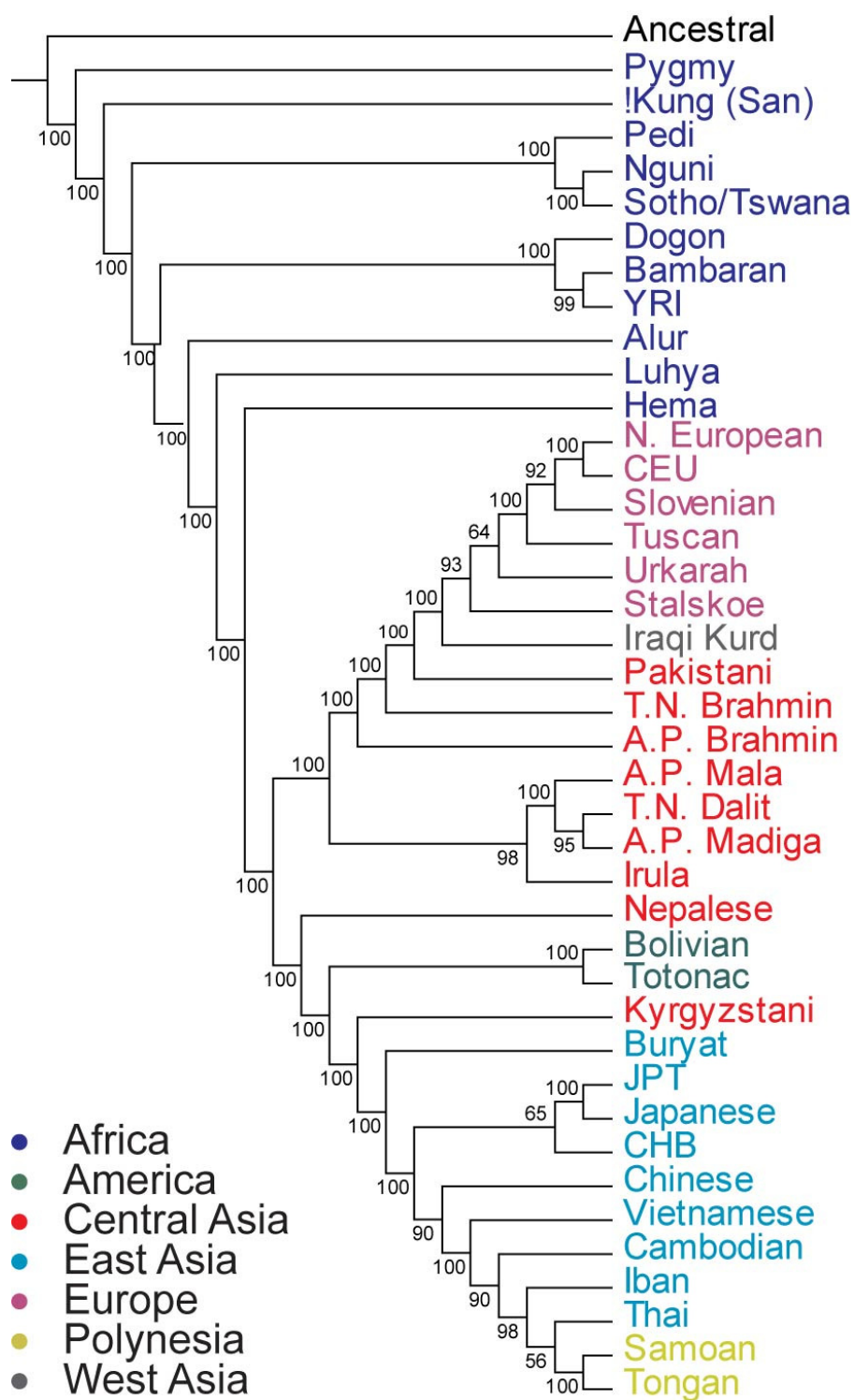
Supplemental Figure 3. Neighbour-joining tree of 80 populations. Populations are color-coded based on their continental origins. The hypothetical ancestral population is shown. Several populations in the HGDP panel were grouped together to improve the resolution. The modified group include: HGDP Bantu (Bantu Kenya, Herero, Nguni, Ovambo, Pedi, Sotho, and Tswana); HGDP N. Chinese (Oroqen, Daur, Hezhen, Mongola, Xibo, and Tu), HGDP S. Chinese (Dai, Lahu, Miao, Naxi, She, Tujia, Yi) and HGDP Han (Han and Han-NChina).

Supplemental Figure 4: PCA of population structure. A) All individuals; B) Europe and West Asia; C) Africa; D) Eurasia, Polynesia, and America. PC3 and PC4 (A) or PC1 and PC2 (B, C, D) are shown. Each individual is represented by one dot and the color label corresponding to their regional origin (A) or population (B, C, D). The percentage of variance explained by each PC is shown on the axis.

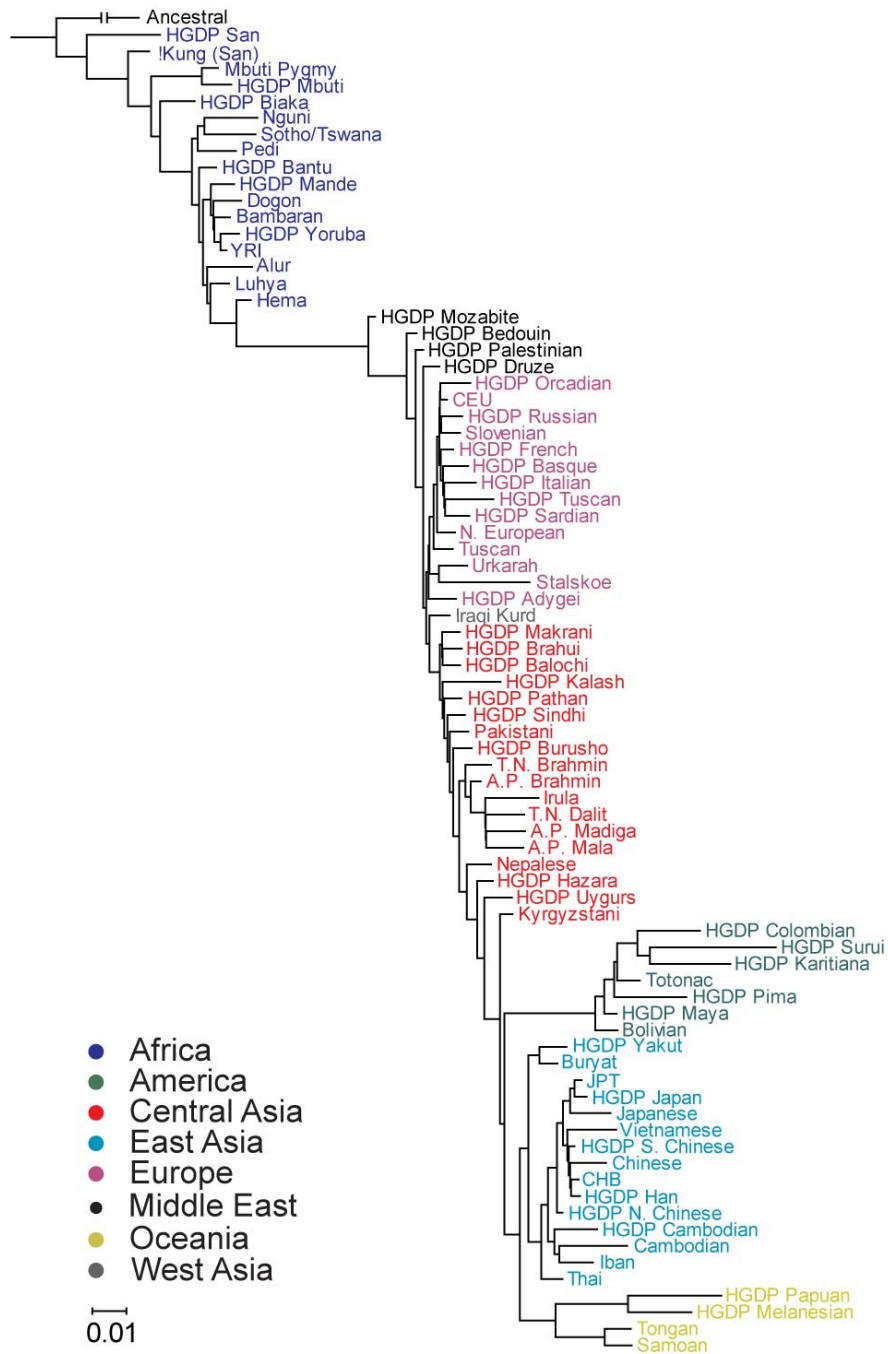
Supplemental Figure 5: PCA of genome-wide CNVs for all populations.



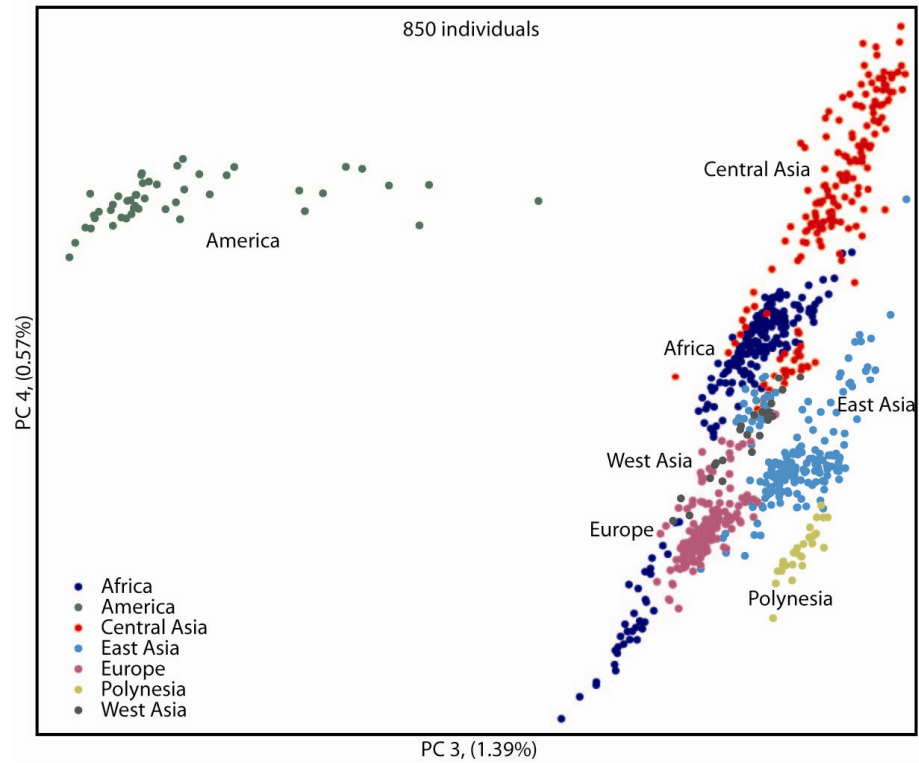
Supplemental Figure 1



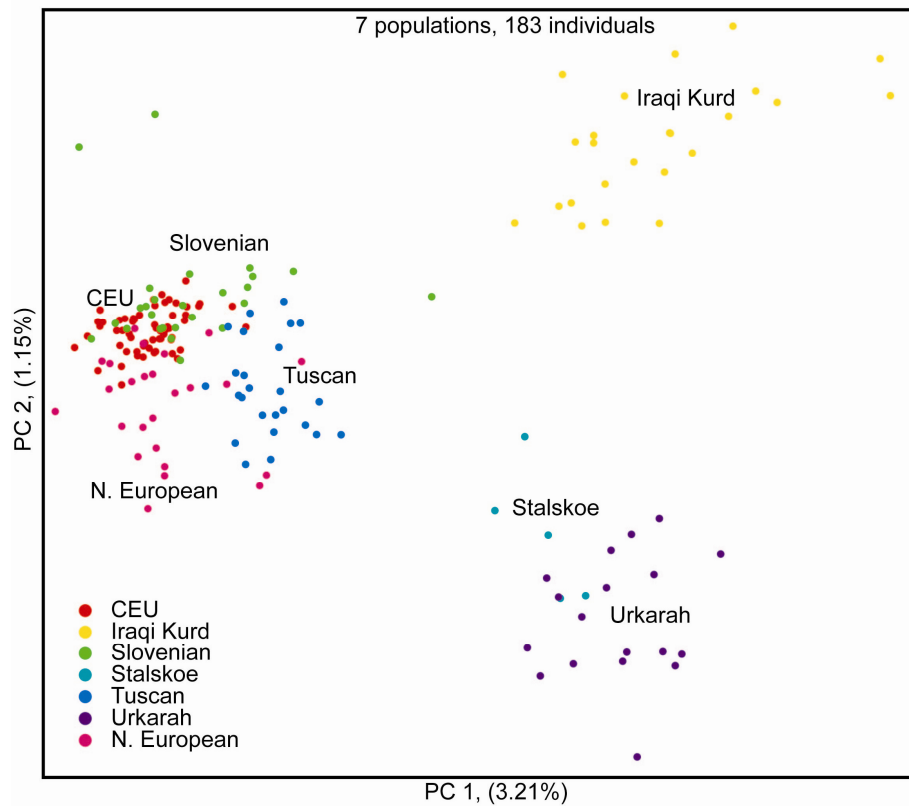
Supplemental Figure 2



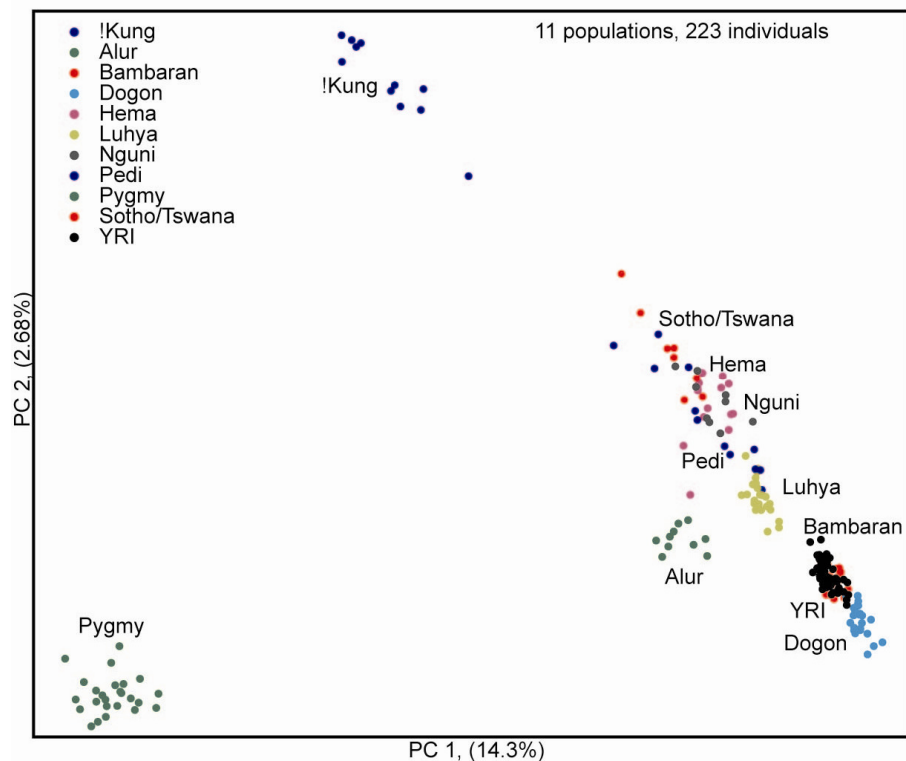
Supplemental Figure 3



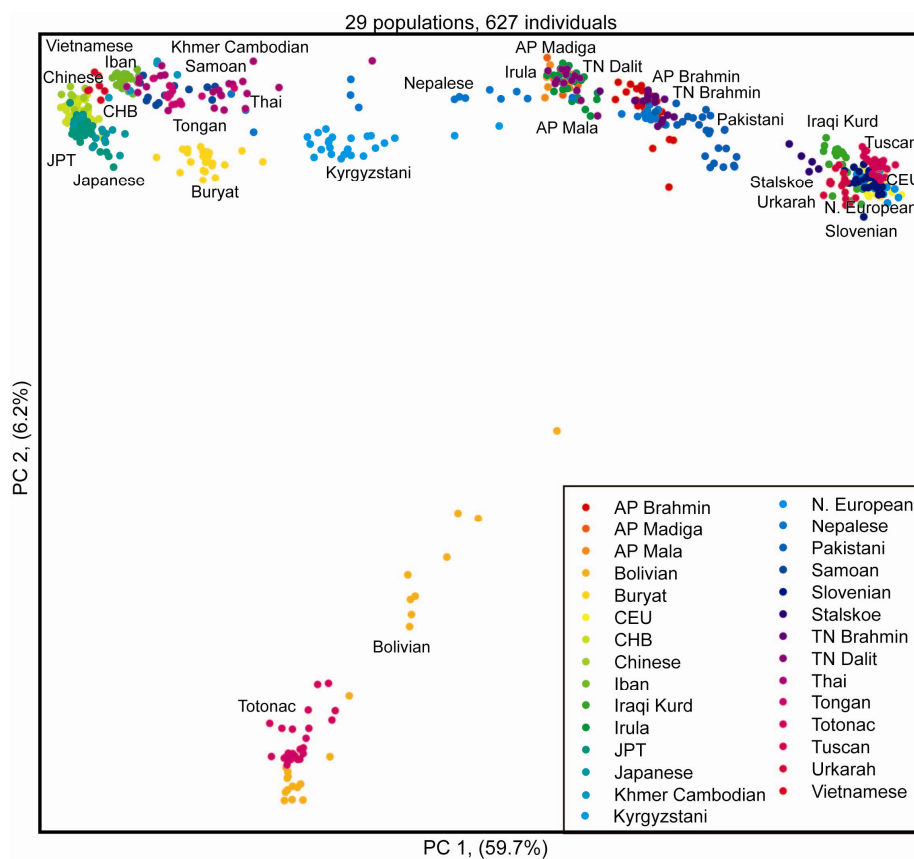
Supplemental Figure 4A



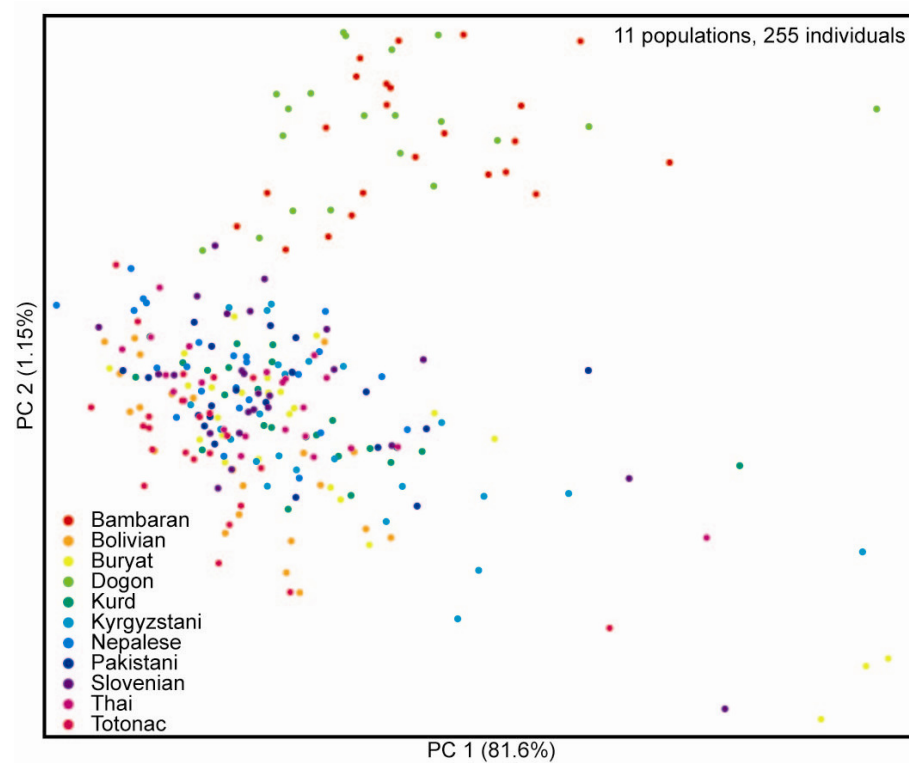
Supplemental Figure 4B



Supplemental Figure 4C



Supplemental Figure 4D



Supplemental Figure 5