



Figure 1. Phylogenetic relationships among goat populations.

(a) A map depicting the locations of modern and ancient domestic samples analyzed in this study. (b) A maximum likelihood phylogenetic tree built using whole genomes of global modern samples. The branches are colored following the same color code used in map. (c) Principal component analysis (PCA) with modern globally distributed goats and ancient goats around the Fertile Crescent. (d) ADMIXTURE results for $k = 2$ and $k = 5$, which had the low cross-validation error.