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Corrigendum: Genome-wide survey reveals the genetic background of Xinjiang Brown cattle in China

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KEYWORDS

Xinjiang Brown cattle, specific-locus amplified fragment-sequencing, genetic structure, genetic diversity, candidate genes, ancestry proportion

A Corrigendum on Genome-wide survey reveals the genetic background of Xinjiang Brown cattle in China

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In the published article, there was an error in the legend for [Figure 4](#) as published. In the phrase “(B) Principal component analysis for the first two PCs of the 178 studied cattle”, 178 needs to be replaced with 177 in order to be consistent with the numbers in the text. The corrected legend appears below.

“Figure 4. Phylogenetic relationship and population structure of the Xinjiang Brown cattle-grazing type (XBG) cattle and the other three breeds evaluated in this study. (A) Neighbor-joining phylogenetic tree constructed from single-nucleotide variant data among four populations. (B) Principal component analysis for the first two PCs of the 177 studied cattle. (C) ADMIXTURE analysis with four presumed ancestral groups to two presumed ancestral groups (K = from 2 to 4).”

In the published article, there was an error in the legend for [Figure 5](#) as published. In the phrase “Ancestry proportion of the 130 XBG and 20 XBH individuals inferred using RFMix, as based on the reference panels of Kazakh and Brown Swiss cattle”, 130 needs to be replaced with 129, in order to be consistent with the numbers in the text. The corrected legend appears below.

“Figure 5. Ancestry proportion of the 129 XBG and 20 XBH individuals inferred using RFMix, as based on the reference panels of Kazakh and Brown Swiss cattle.”

In the published article, there was an error in the **Funding**. “National Agricultural Science and Technology Special Project of China (No. NK2022130302)” is a secret item and its number needs to be deleted. The correct **Funding** statement appears below.

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The authors apologize for these errors and state that this does not change the scientific conclusions of the article in any way. The original article has been updated.

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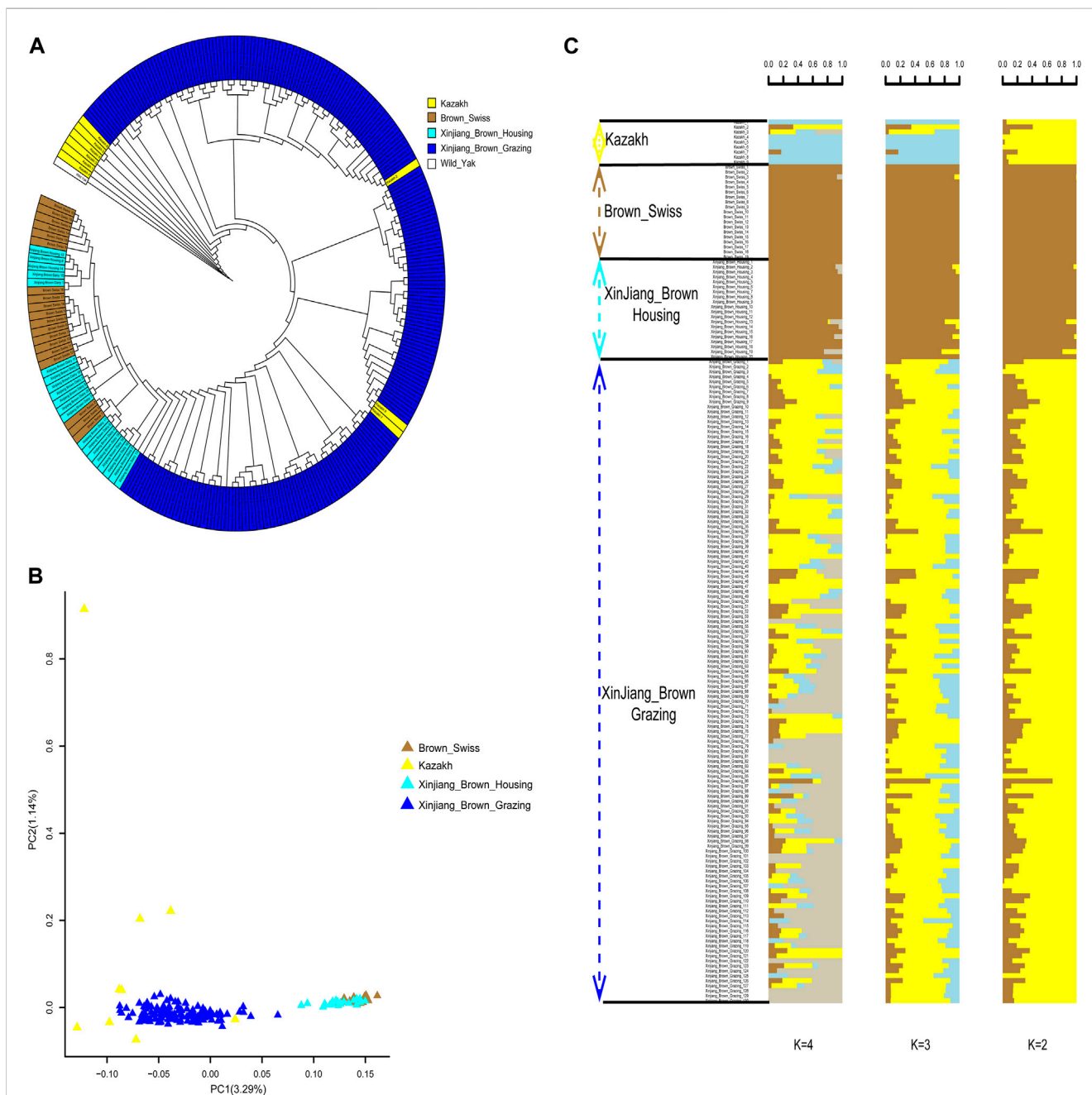


FIGURE 4 Phylogenetic relationship and population structure of the Xinjiang Brown cattle-grazing type (XBG) cattle and the other three breeds evaluated in this study. **(A)** Neighbor-joining phylogenetic tree constructed from single-nucleotide variant data among four populations. **(B)** Principal component analysis for the first two PCs of the 177 studied cattle. **(C)** ADMIXTURE analysis with four presumed ancestral groups to two presumed ancestral groups (K = from 2 to 4).

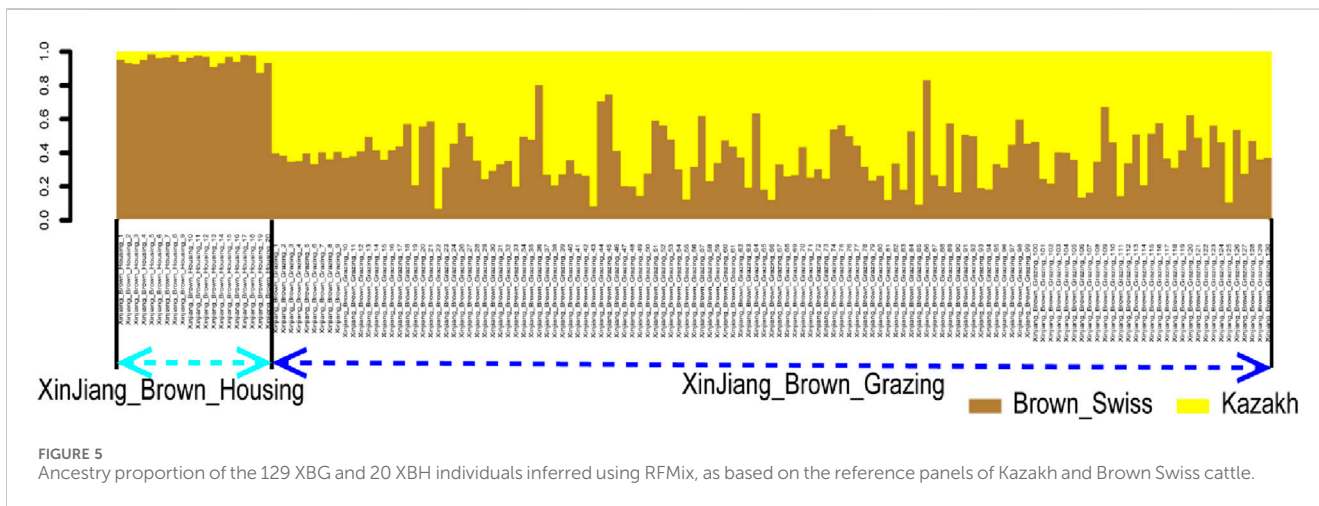


FIGURE 5 Ancestry proportion of the 129 XBG and 20 XBH individuals inferred using RFMix, as based on the reference panels of Kazakh and Brown Swiss cattle.