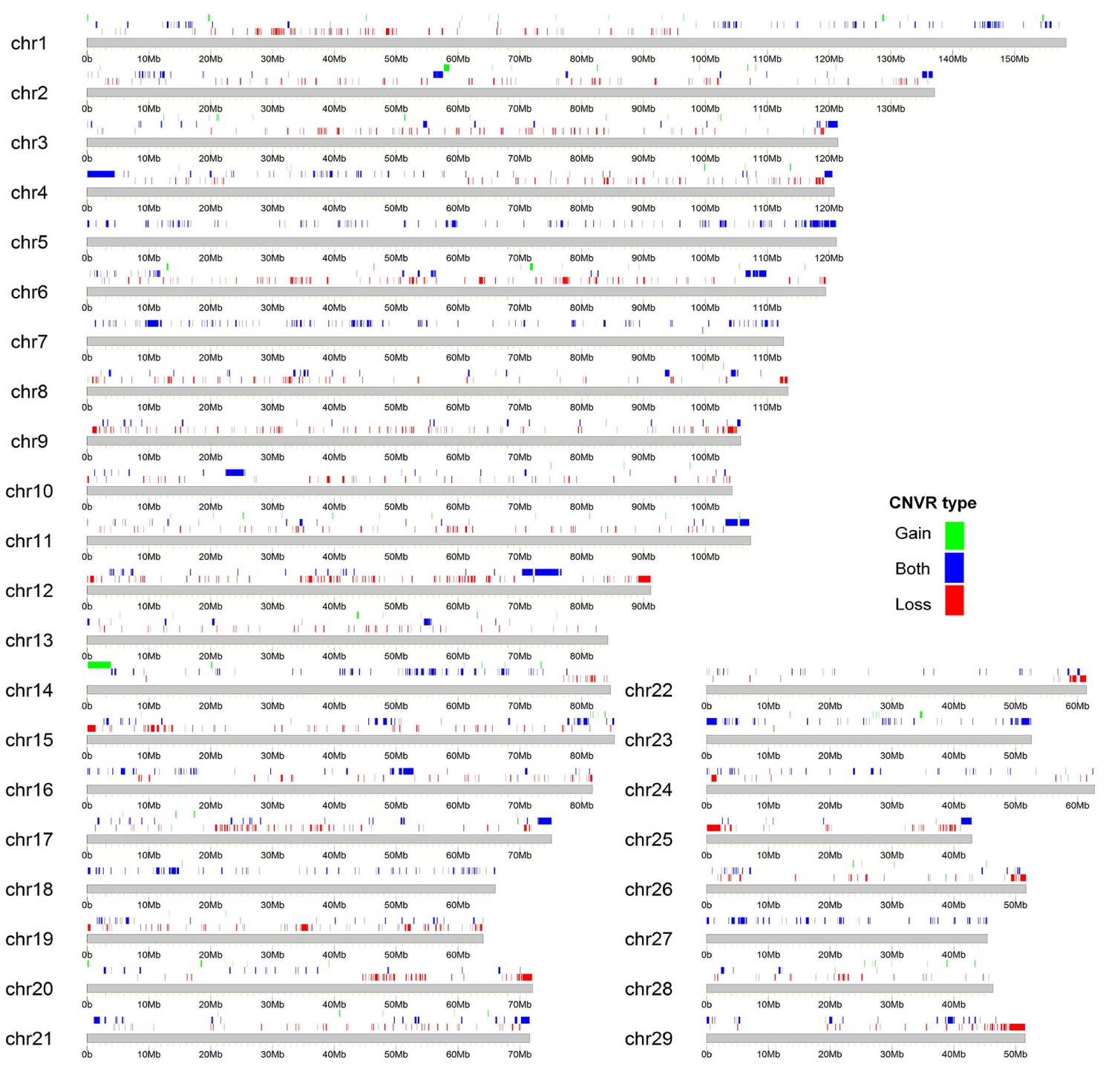
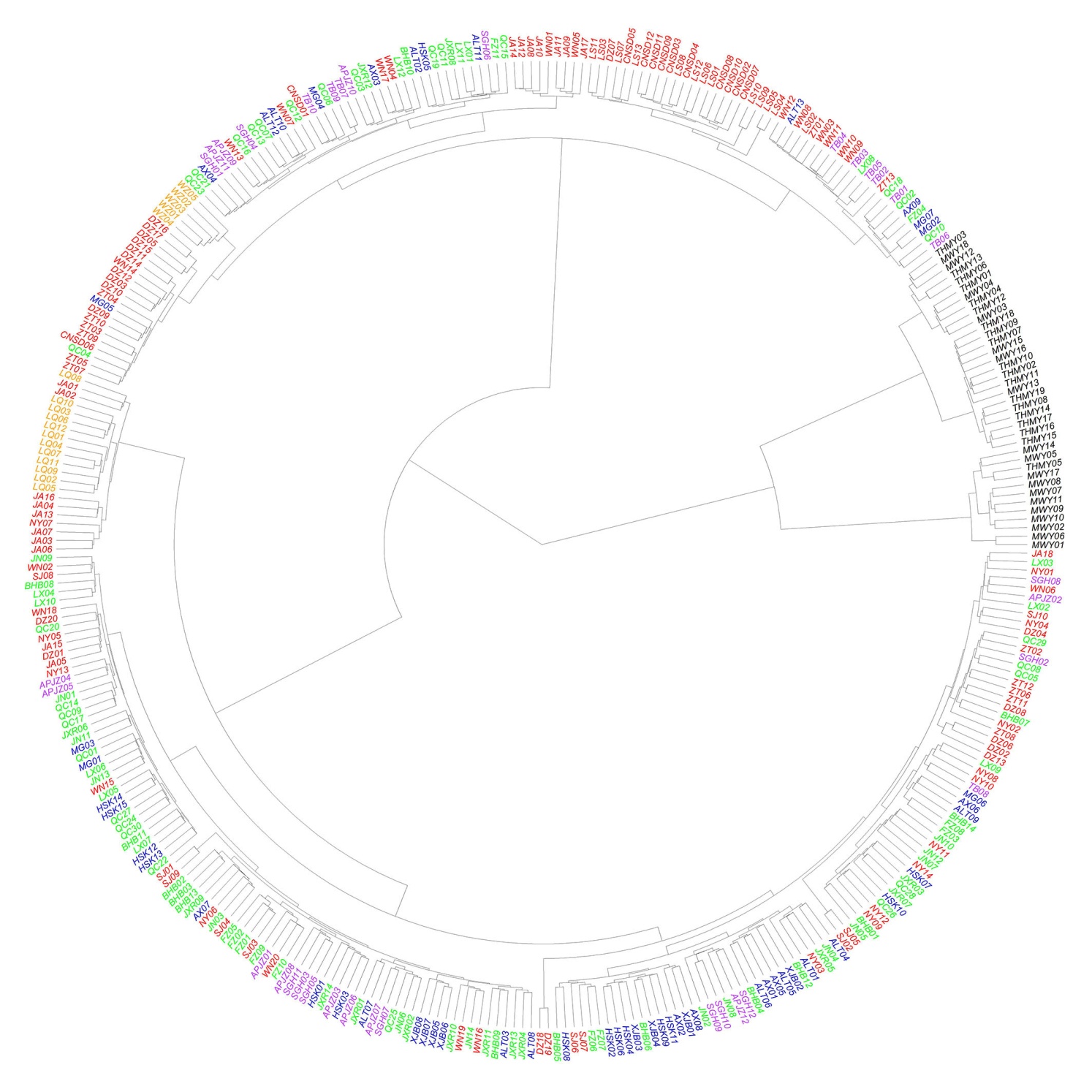
Supplementary Material

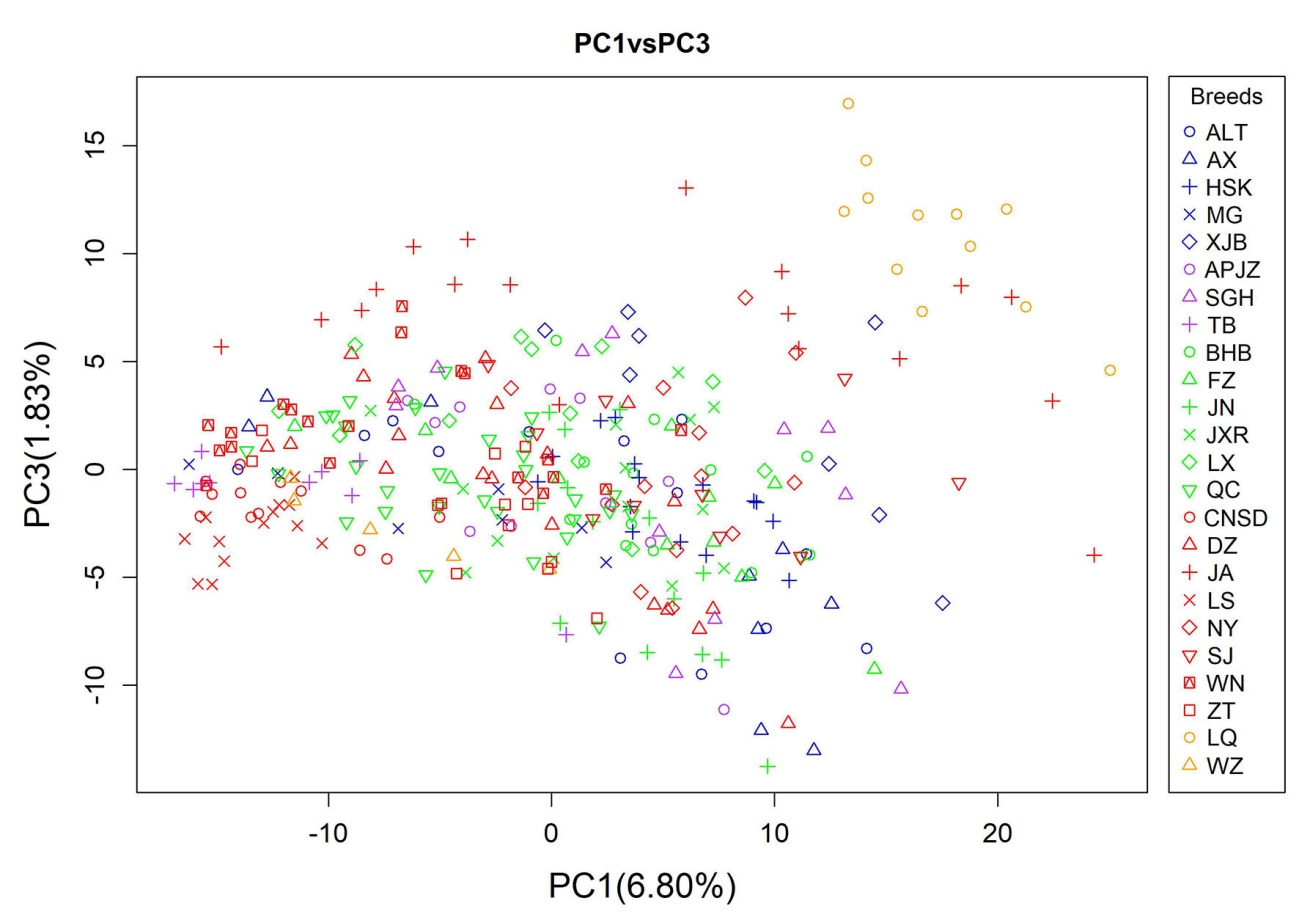
# Supplementary Figures

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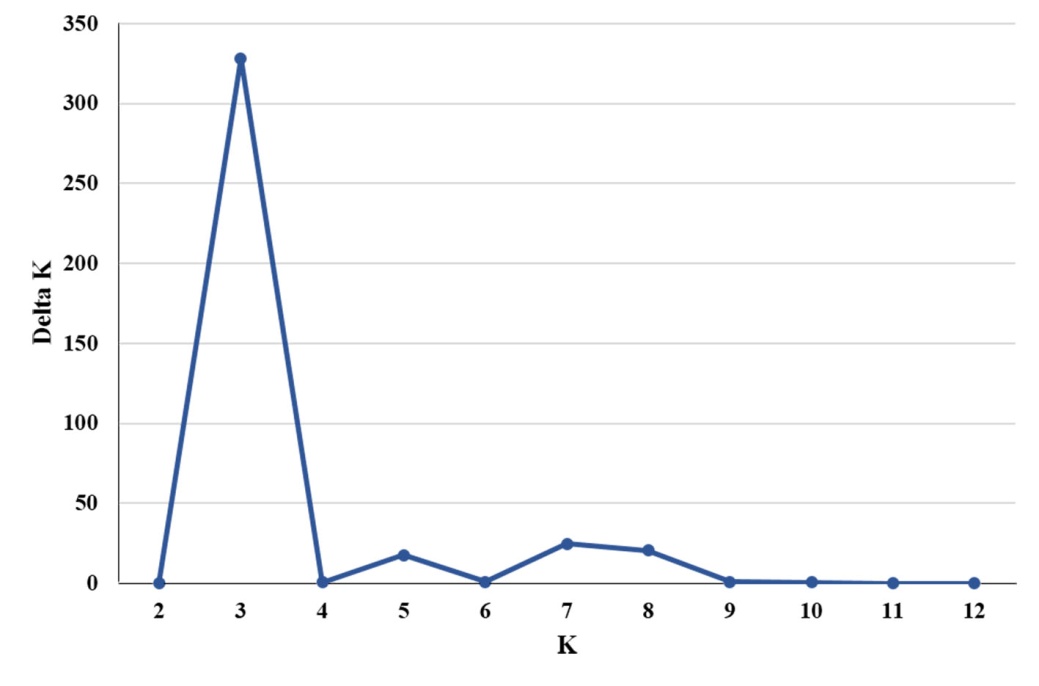
**Figure S1.** Genomic distribution of CNVRs in 318 Chinese indigenous cattle.



**Figure S2.** Neighbor-joining clustering map of 318 Chinese indigenous cattle and 37 yaks.

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**Figure S3.** Principal component analysis (PCA) based on CNVs of animals assessed, with colors and shapes representing specific breeds. PC3 described 1.97% of the total variation, separated LQ and partial JA from other cattle breeds.



**Figure S4.** DeltaK values for K=2 to K=12. The DetaK value of K=3 is the largest. Accordingly, the best K value is the number of three.