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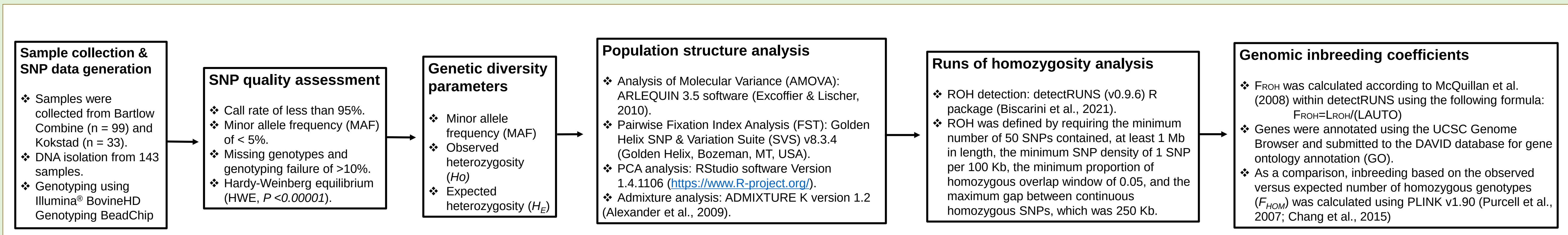
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INTRODUCTION

- ❖ A Sanga-type breed with *B. taurus* and *B. indicus* ancestry, Nguni cattle have shown resistance to diseases and harsh climatic conditions in Africa.
- ❖ Runs of homozygosity (ROH) are long continuous homozygous sections of the genome that are thought to have originated from a common ancestor due to their length.
- ❖ The frequency and length of ROH can be used for understanding the population genetic history, genomic inbreeding levels as well as the genetic structure of economical important traits and diseases. It is associated with gene expression and may present a major genetic component of phenotypic diversity.
- ❖ **Objective:** The aim of this study was to i) evaluate the genetic diversity and population structure of the Nguni populations in Bartlow Combine and Kokstad and, ii) investigate the levels of inbreeding in the two conservation herds using genome-wide ROHs.

MATERIALS & METHODS



RESULTS AND DISCUSSION

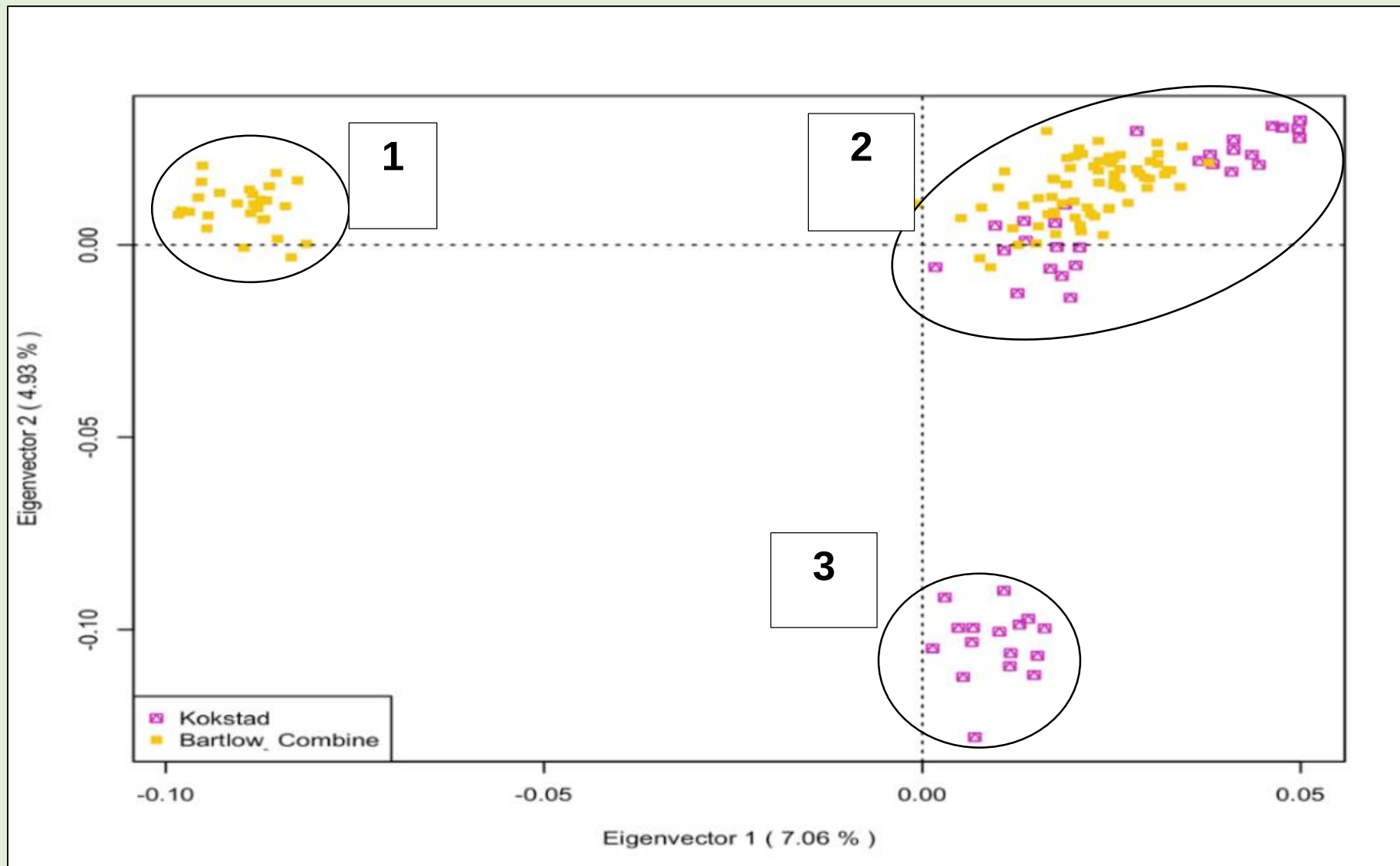


Figure 1. PCA-based clustering of Bartlow Combine and Kokstad Nguni cattle populations.

- ❖ The Principle Component Analysis (PCA) analysis clearly shows the genetic differentiation between the two populations (Figure 1).
- ❖ At $K = 5$, pure and admixed individuals are observed in the Nguni herds. Thus, the two herds had a shared ancestor.
- ❖ AMOVA revealed a low genetic variation (2.42%) among populations, while (97.60%) of total variation corresponds to the differences among samples within populations.
- ❖ A low pairwise F_{ST} (0.0242) value was reported between the two Nguni cattle populations.

Table 1. Population-wise mean of sum of ROH within each ROH length category, the sum of ROH (in Mb) was calculated per animal and averaged population-wise.

Class	Bartlow Combine	Kokstad
0-6 Mb	1.67	1.57
6-12 Mb	7.62	7.29
12-24 Mb	13.36	14.76

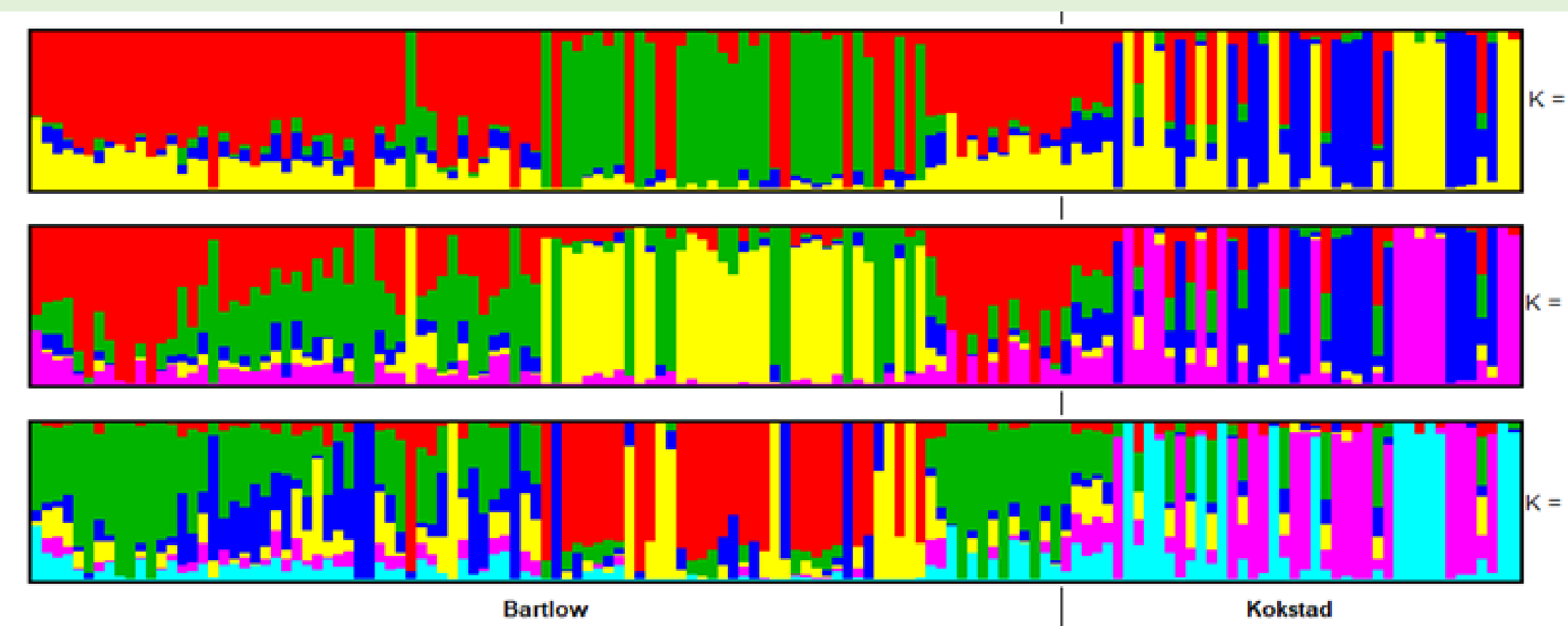


Figure 2. Admixture plot of population clustering based on Kokstad and Bartlow Combine herds with extrapolated K values varying from 4 to 6. The number of ancestral populations K is represented by one vertical line with K -coloured segments.

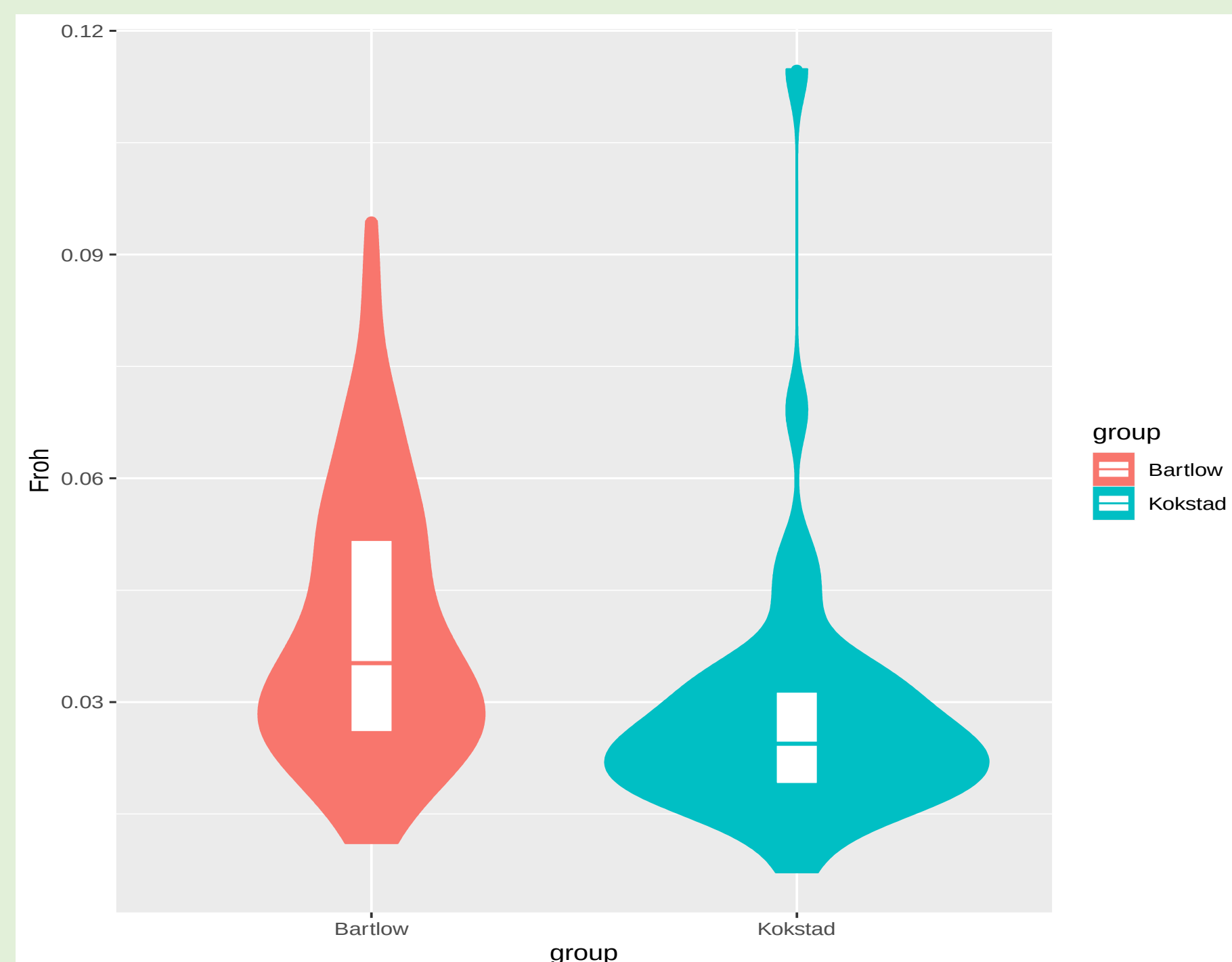


Figure 4. Genomic inbreeding levels based on ROHs estimated for Bartlow Combine and Kokstad Nguni cattle populations.

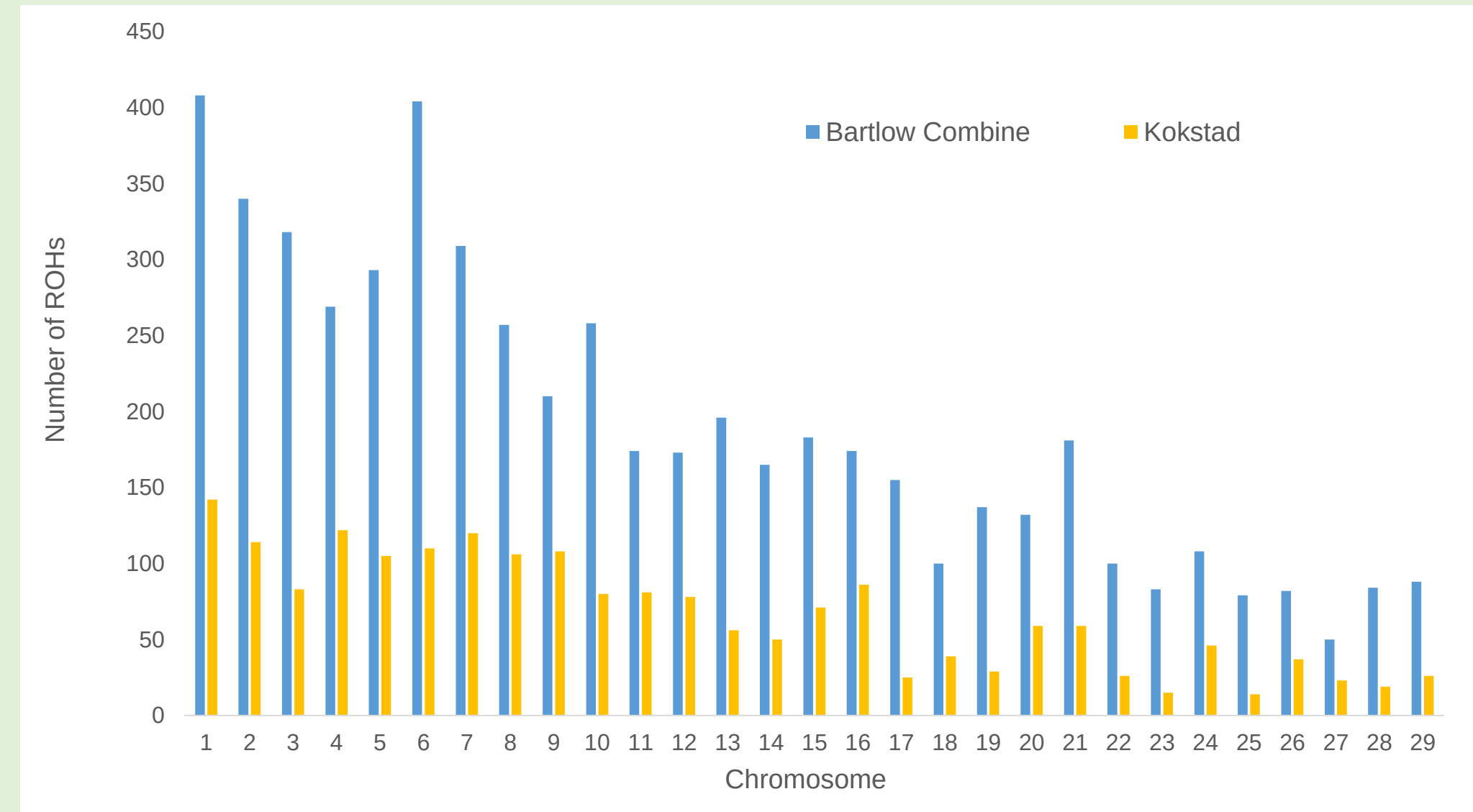


Figure 3. The number of runs per chromosome of the Bartlow Combine and Kokstad conservation populations. The bars exhibit the total number of ROH per chromosome identified in the 143 Nguni cattle animals.

- ❖ A total of 5 510 and 1 929 ROHs were detected in Bartlow Combine and Kokstad Nguni cattle animals, respectively (Figure 3).
- ❖ Overall, Bartlow Combine had higher number of ROHs in all chromosomes compared to the Kokstad Nguni population.
- ❖ The highest number of runs was observed in the 0–6 Mb (5 415, 1 915 ROHs), followed by 6–12 Mb (89, 12 ROHs) and lastly, 12–24 Mb category (6, 2 ROHs) in Bartlow Combine and Kokstad Nguni cattle populations, respectively.
- ❖ The highest ROH mean was observed in high ROH classes for both populations, 13.36 Mb and 14.76 Mb in category 12–24 Mb in Bartlow Combine and Kokstad populations, respectively (Table 1).
- ❖ Lengths of ROH were further used to estimate inbreeding coefficient (F_{ROH}), shown in Figure 4; inbreeding coefficient (F_{ROH}) was highest in Kokstad (0.11) compared to Bartlow Combine (0.09) population.
- ❖ Average F_{HOM} values of -0.02 ± 0.04 and -0.04 ± 0.05 were reported in Bartlow Combine and Kostad conservation populations, respectively.
- ❖ High (0.85) and moderate (0.64) correlation was observed between F_{ROH} vs F_{HOM} in Bartlow Combine and Kokstad conservation populations, respectively.

CONCLUSIONS

- ❖ The genetic diversity parameters used in the present study revealed that Bartlow Combine and Kokstad Nguni cattle had similar genetic diversity.
- ❖ The population structure analysis revealed that there is a low genetic variation among populations and high genetic variation among samples within populations.
- ❖ This emphasizes the importance of increasing the diversity of purebred breeds through management strategies demonstrated in this study.
- ❖ The study showed that both Nguni cattle populations had the highest frequency and length of short ROH (0–6 Mb), indicating higher ancient inbreeding in both Nguni populations.
- ❖ This study highlights the potential to use the SNP genotype data to assess population genomic parameters such as levels of inbreeding in conservation flocks and has provided information on the identification and assessment of runs of homozygosity.