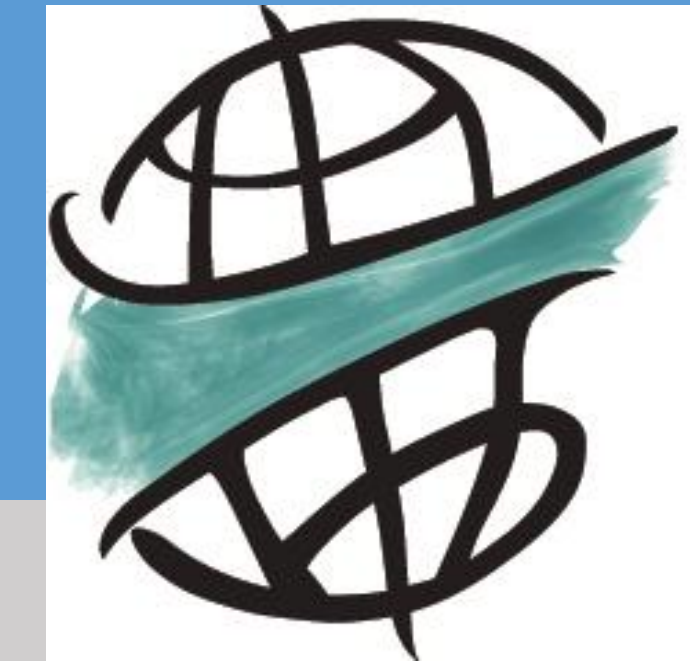


# A Marker- and Runs of Homozygosity-based Assessment of the Inbreeding Status of South African Beef Cattle Populations



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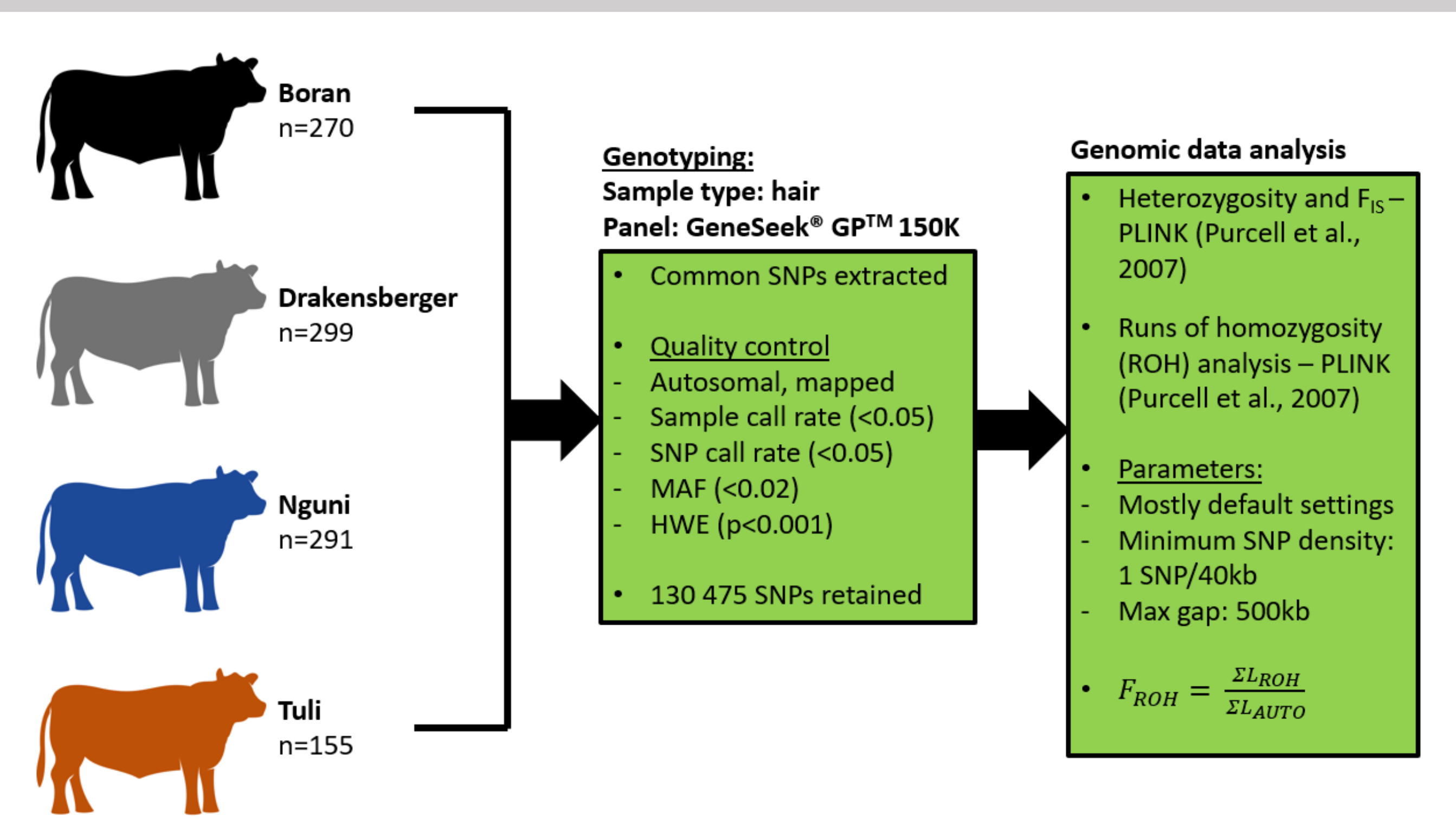
## Introduction

- **Sanga cattle** (*Bos taurus africanus*) in South Africa (SA): local genetic resources with unique adaptive traits
- NB for **climate-smart, sustainable agriculture**
- **Boran**: Popular choice for crossbreeding in sub-tropical regions of SA (introduced to SA from Kenya and Uganda in late 1990's)
- **Drakensberger**: One of oldest breeds in SA (Breeders' Society since 1947)
- **Nguni**: Several ecotypes uniquely adapted to different agro-ecological zones (Breeders' Society since 1986)
- **Tuli**: Hardy and adaptable (Breeders' Society since 1970)
- All four breeds are well established in **seed stock** and **commercial livestock sectors** (+ smallholder and communal systems)
- Access to national **animal recording, genetic evaluation** and markets
- Data driven breeding objectives: can lead to **genetic erosion**
- May result in the failure of the population to adapt to new environmental challenges

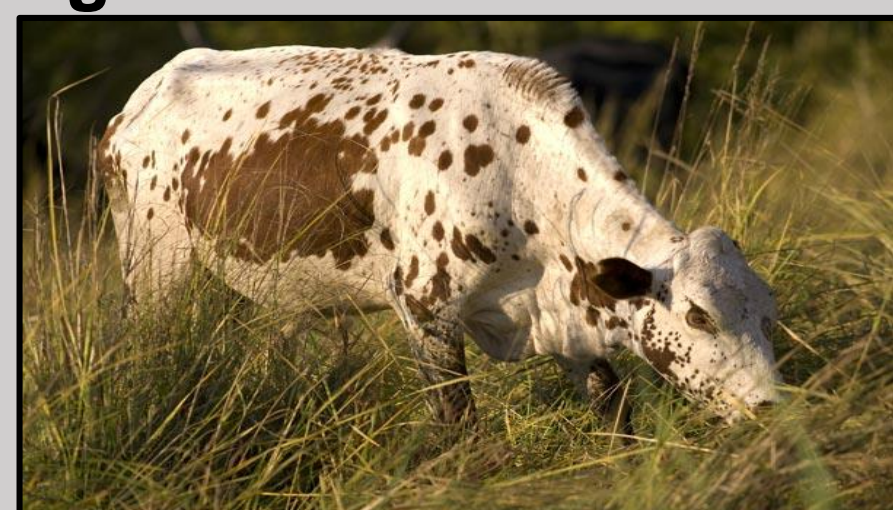
## Aim

To perform a genomic characterization and quantification of the inbreeding and runs of homozygosity (ROH) levels in four SA breeds.

## Materials & Methods



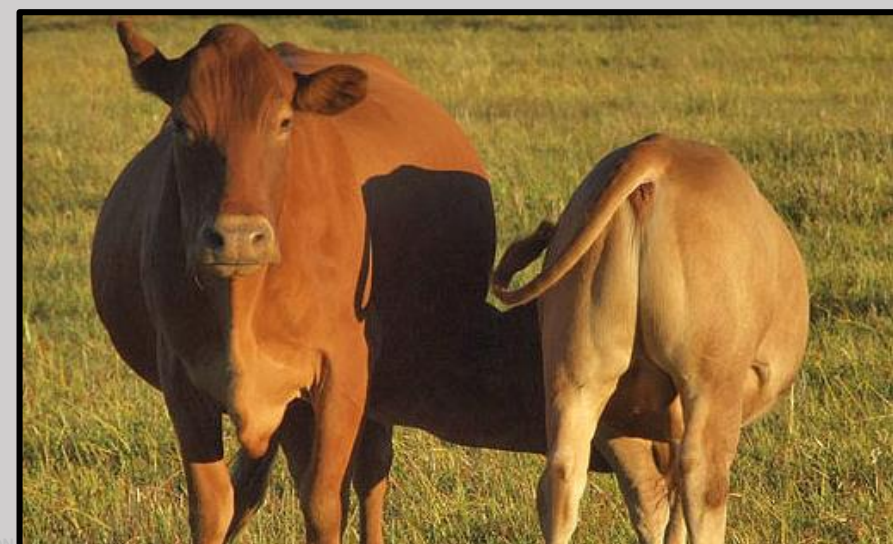
Nguni



Drakensberger



Tuli



Boran



## Results: Inbreeding coefficients

Table 1 Summary statistics of heterozygosity and inbreeding coefficients per breed

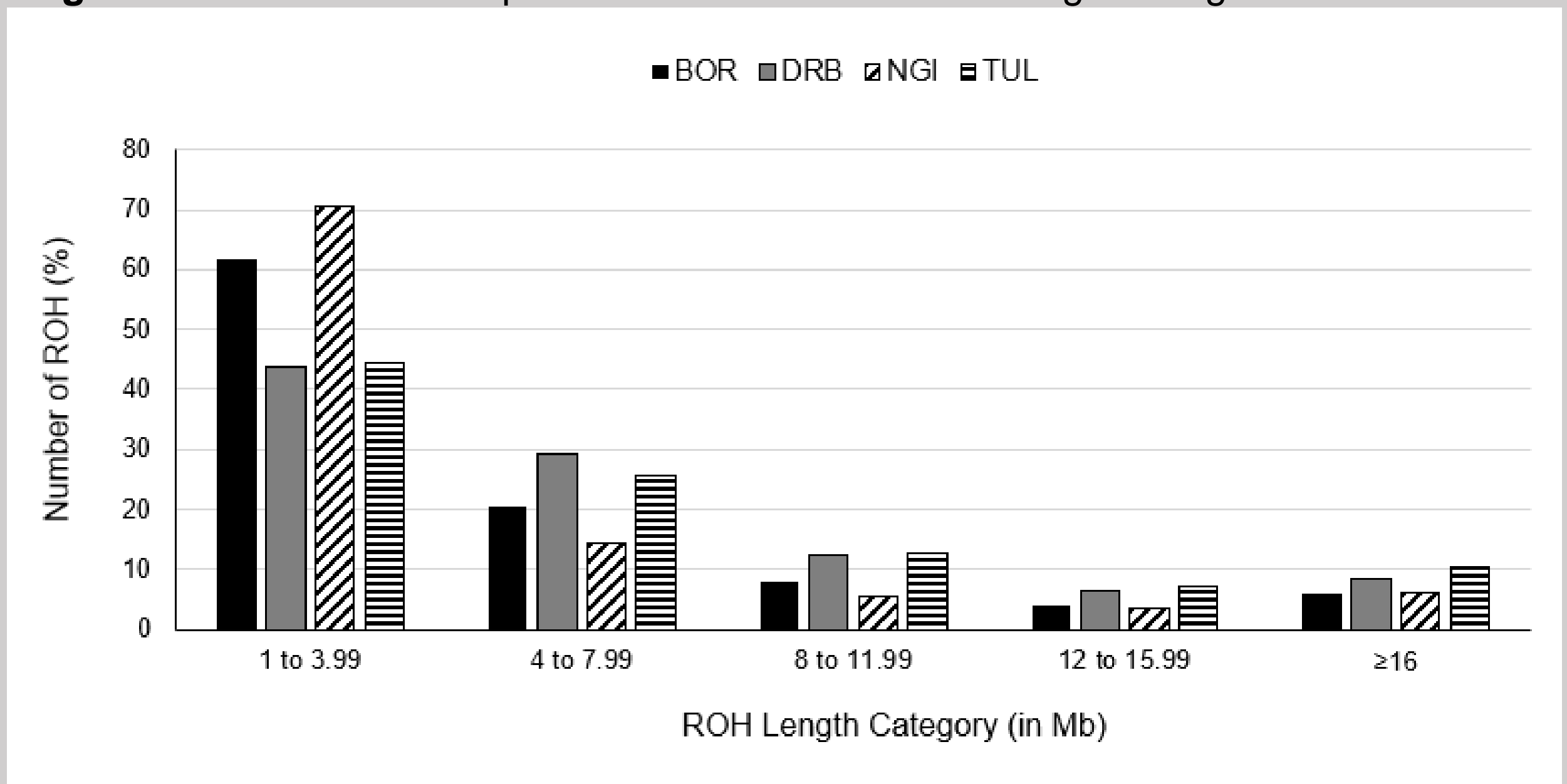
Breed	H <sub>E</sub>	H <sub>O</sub>	F <sub>IS</sub>	F <sub>ROH</sub>
BOR	0.294	0.296	-0.005	0.002
DRB	0.347	0.342	0.015	0.003
NGI	0.319	0.311	0.026	0.002
TUL	0.331	0.332	-0.002	0.003

BOR= Boran, DRB= Drakensberger, NGI= Nguni, TUL= Tuli

## Results: ROH descriptive statistics

- **2 015 ROH** segments identified in total (range: 3 235 for the Nguni to 4 723 for the SA Boran).

Fig 1 The number of ROH per breed within the defined length categories



## Discussion and conclusion

- Moderate heterozygosity was indicated, and diversity losses ( $H_O < H_E$ ) and gains ( $H_O > H_E$ ) supported inbreeding coefficients ( $F_{IS}$ ).
- The ROH profiles of the cattle populations in this study are indicative of more **distant ancestral effects**.
- Frequency of long ROH is **currently low** (ROH>16Mb range: 5.89% in BOR to 10.31% in TUL), however, **caution** should be taken when pipelines for genomic selection (GS) are implemented for these breeds.
- An increase in the frequency of long ROH (as a result of GS) have proven to **enhance deleterious variation**.
- The breeds are generally in a **healthy genetic condition (in terms of inbreeding levels)**, even though they are subjected to directional selection.

## References

- Purcell *et al.* (2007). PLINK: a tool set for whole-genome association and population-based linkage analyses. *Am J Hum Genet.* 81(3), 559-575.