# ABSTRACT

There is limited genetic information available in most African goat populations. However, improvements in genomic technologies have enabled easy and effective analysis of different genetic parameters. This study used Single Nucleotide Polymorphism (SNP) data of four goat genotypes from Kenya; Galla (n = 12), Alpine (n = 28), Saanen (n = 24) and Toggenburger (n = 30). After SNP quality control, 48808 SNPs that were available for analysis. Runs of homozygosities (ROHs) were detected to analyse the distribution and inbreeding coefficients. Across the genotypes, 348 ROHs were detected with the highest number observed in Toggenburger and lowest in Galla. ROHs that described recent inbreeding were observed in Alpine. The highest mean sum of ROH was observed on the long ROHs category (>16 Mb) which have a negative effect on animals performance. Distribution of ROHs per chromosome was breed-specific without a clear pattern across the genotype. Furthermore, 32 genomic regions with the high frequency of ROHs were detected. Sixteen genes (missense and synonymous) were identified to determine their effects on animal performance. High inbreeding coefficient values were observed in all exotic genotypes suggesting continuous use of few breeding bucks. Toggenburg was found to be the most inbred genotype with the highest breeding coefficient of 0.68 compared to other genotypes. To maintain and improve the genetic diversity in Kenya, these findings will be useful for the strategic implementation of genetic improvement and conservation programs to ensure continual contribution to food security.