

# Analysis of excessive homozygous regions in Rhodesian Ridgeback dogs



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## Aim

Identification of excessively homozygous regions in Rhodesian Ridgeback dogs and to examine their potential influence on the population.

## Background

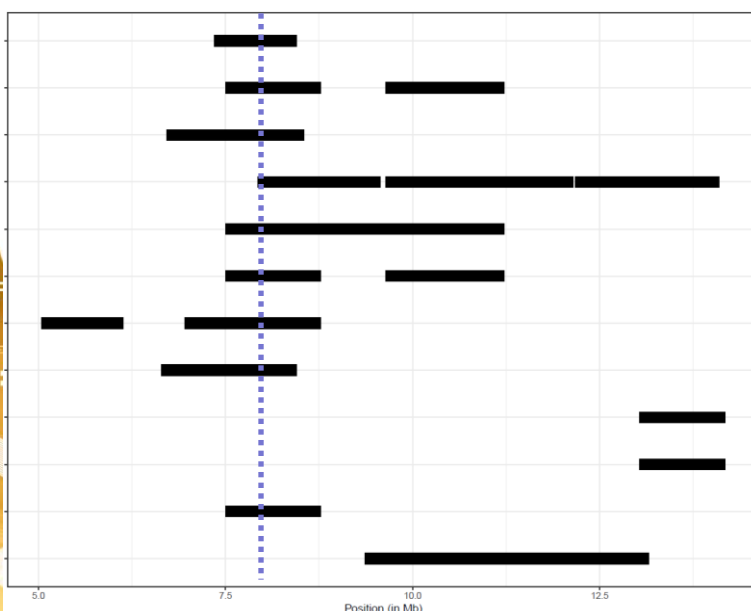
Runs of homozygosity (ROH) are continuous segments in the DNA-sequence of diploid organisms. Due to the high correlation with autozygosity, they can be implemented as a measurement for individual autozygosity. Through ROH detection the genetic relationships and inbreeding levels can be calculated, offering a better understanding of population structure and history.

## Animals, material and methods

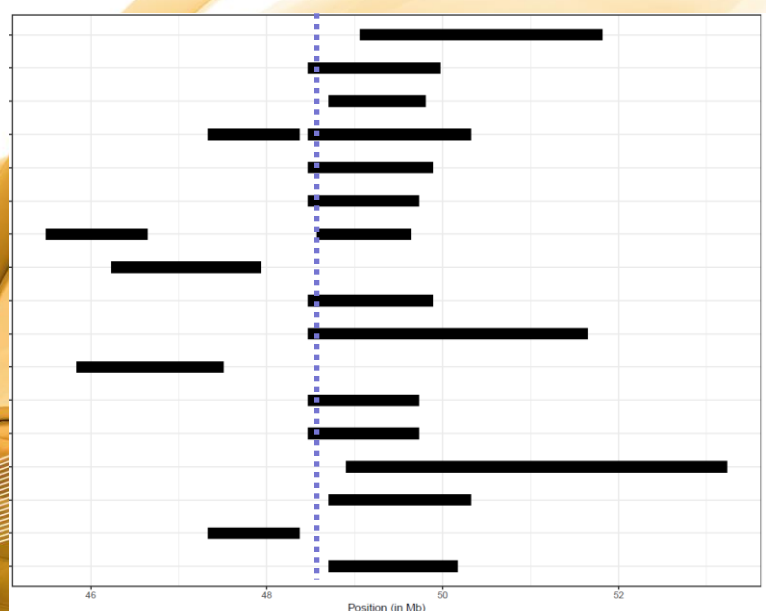
- Genotypes: 23 dogs (Illumina CanineHD 173,662 SNP)
- Quality control following Ferenčaković et al. (2013)
- Analysis with cgaTOH program (Zhang et al. 2013)
- ROH segment restrictions 1, 2, 4, 8 and 16 Mb
- ROH island segment overlaps in min. 50% of cases

## Results

Floppy ears CHR10: 7.89-8.04 Mb



Dorsal ridge genes CHR18: 48.41-48.49 Mb



## Conclusions

- Overlaps in Run of Homozygosity (ROH) islands are viable to be interpreted as signatures of selection
- Genes determining phenotypes characteristic for the breed found
  - Dorsal fur ridge (FGF4, ORAOV1 on chromosome 18)
  - Floppy ears (MSRB3 on chromosome 10)
  - Body size (HMGA2 on chromosome 10)
  - Muscling (MSTN on chromosome 37)
  - Various health related genes

