UNIKASSEL VERSITÄT | ÖKOLOGISCHE AGRARWISSENSCHAFTEN

Genomic characterization of a subsample of the Mangalica population in Germany

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Introduction

Mangalica pigs in Germany

- No official Herd book and more or less no pedigree information

- Three different types of Mangalica pigs
  - Blond Mangalica pig
  - Red Mangalica pig
  - Swallow-Bellied-Mangalica pig

- German breeders assume that Blond-, Red-, and Swallow-Bellied-Magalica pigs are different breeds.

Introduction

Mangalica pigs in Germany

- Number of breeders and animals
  - Approximately 325 people
  - Estimated number of animals around 650
  - Compared to 2012 the number of animals and breeders has been doubled

- Confirmed number of animals
  - 80 Blond Mangalica pigs
  - 97 Red Mangalica pigs
  - 120 Swallow-Bellied-Mangalica pigs
  - 31 Crosses

- Almost all animals are kept by hobby breeders

(Swallow-Bellied-Mangalica pig)

Introduction

Aim of this study

- To investigate the potential of genomic information in the German Mangalica pig population

(Red-Mangalica pig)

(Blond-Mangalica pig)

Materials and methods

Data

- 57 Mangalica pigs genotyped with a 70k SNP Chip

Data before & after quality filtering

	Before	**After**
Number of animals	57	50
Number of SNPs	62,543	34,066

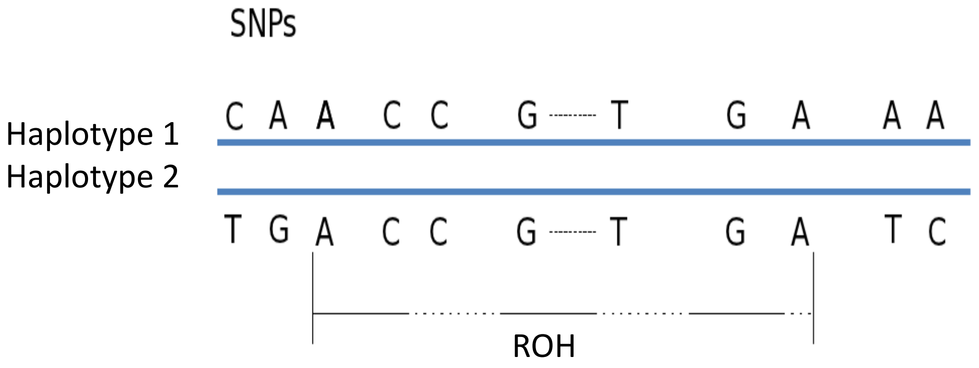
Autosomal SNPs
Individual call rate: > 90 %
SNP call rate: > 90 %
MAF: > 5 %
HWE: *P* ≤ 0.0001

- 10 Blond Mangalica pigs
- 20 Red Mangalica pigs
- 18 Swallow-Bellied-Mangalica pigs
- 2 Crossbreed animals

Materials and methods

Computations (Genomic inbreeding)

- Runs of homozygosity (ROH) definition (McQuillan et al., 2008)
  - 50 SNP-window
  - 1 het. SNP
  - 2 missing genotypes
  - Density of 1 SNP per 100 kb
  - Maximum gap of 1000 kb



- Chromosomal inbreeding were calculated separately for each chromosome
  - Relative to autosome length (F_{ROH_KA})
  - Relative to chromosome length (F_{ROH_KK})

$$F_{ROH\_KA} = \frac{\sum L_{ROH\_K}}{L_{AUTO}}$$

Relative to autosomal length

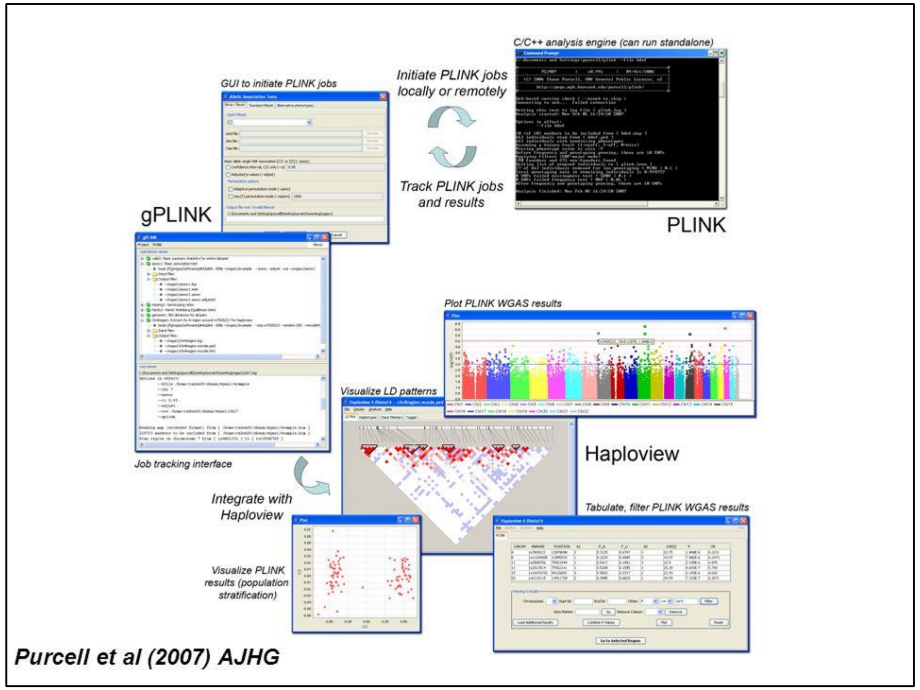
$$F_{ROH\_KK} = \frac{\sum L_{ROH\_K}}{L_{AUTO\_K}}$$

Relative to chromosomal length

Materials and methods

Computations (Relatedness and admixture)

- Population structure analysis in PLINK software (Purcell et al., 2007)
  - Multidimentional Scaling (MDS)
  - Admixture

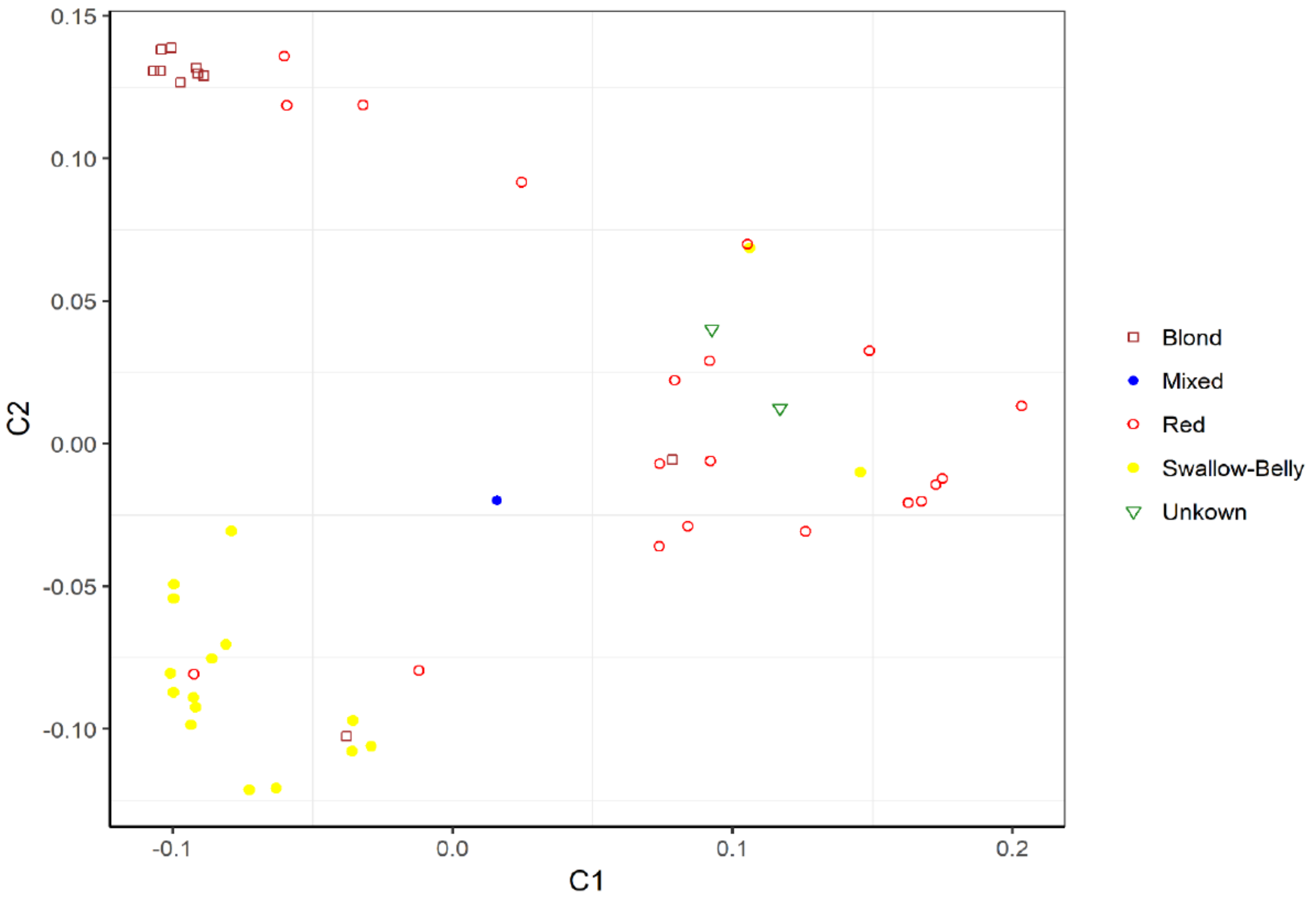


Purcell et al (2007) AJHG

Results and discussion

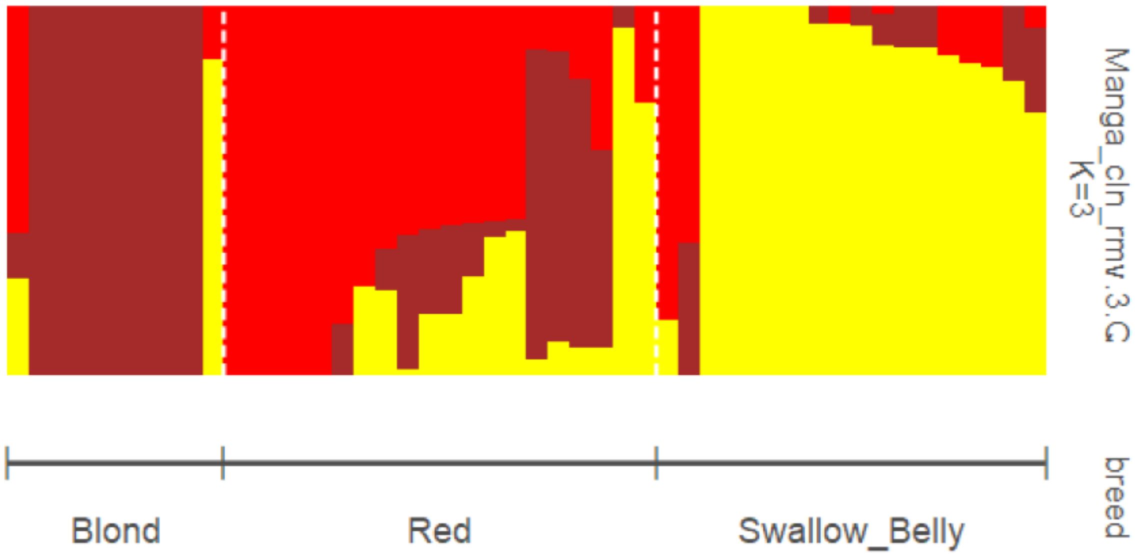
Population structure (Relatedness)

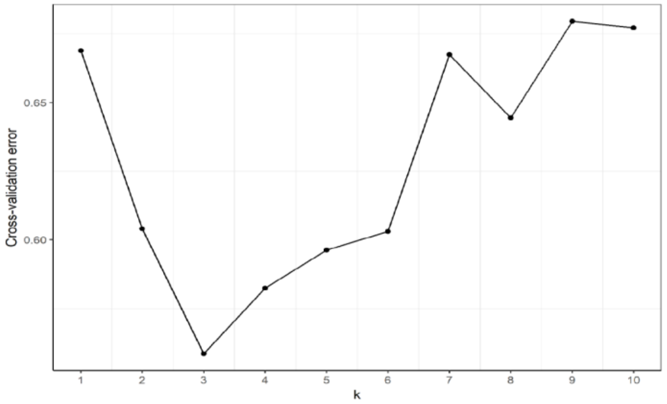
- Two different clusters (Blond-Mangalica pigs and Swallow-Belly-Mangalica pigs
- No cluster for Red Mangalica pigs (only 5 individuals cluster together)
- Probably several animals assumed to be pure Red-Mangalica pigs are crossbreed animals



Results and discussion

Population structure (Admixture)



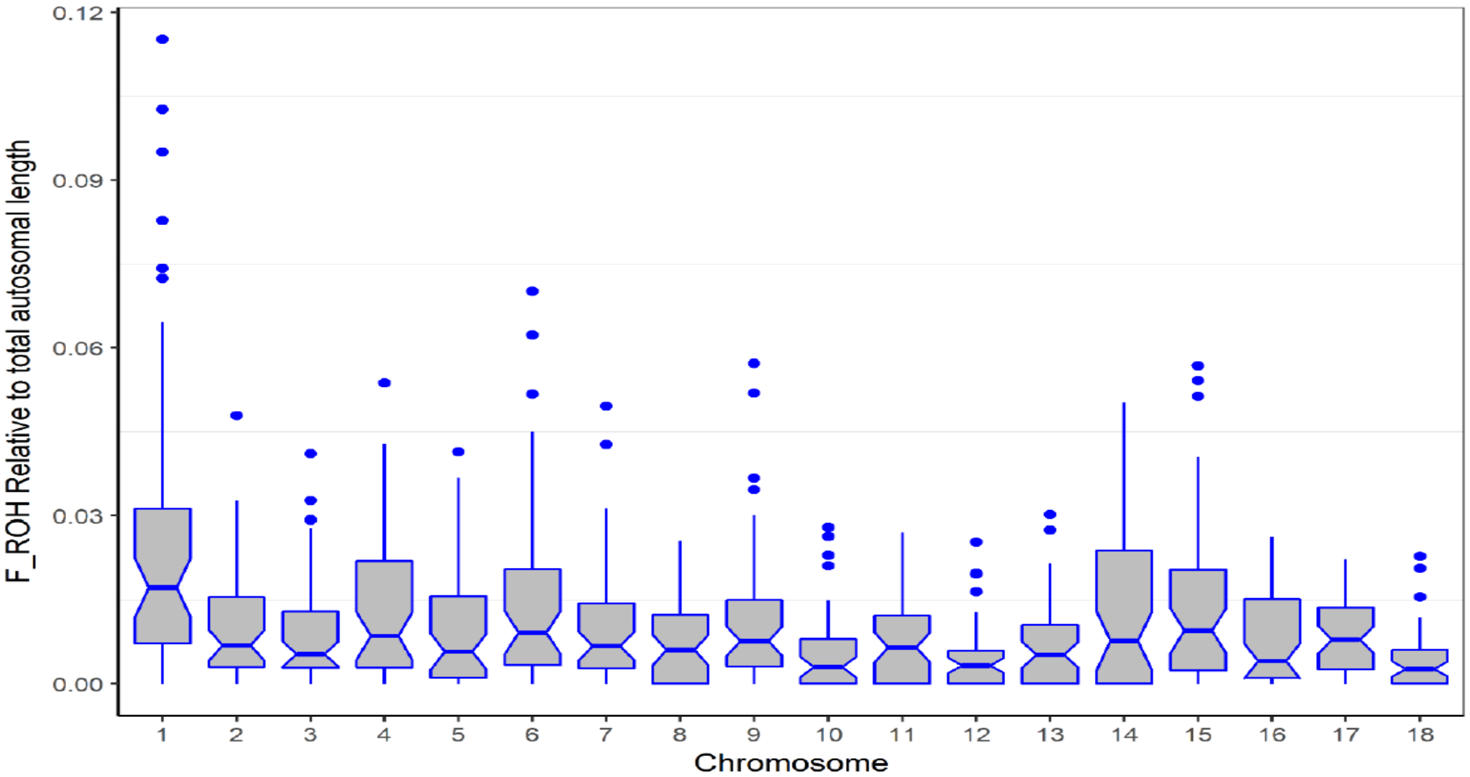


- Admixture results showed that three different clusters (k) are optimal for the data (smallest cross-validation error)
- Confirm the MDS results (again only 5 Red-Mangalica pigs were not influenced by another cluster)

Results and discussion

Genomic inbreeding (F_{ROH_KA})

- Chromosomal inbreeding relative to autosomal length

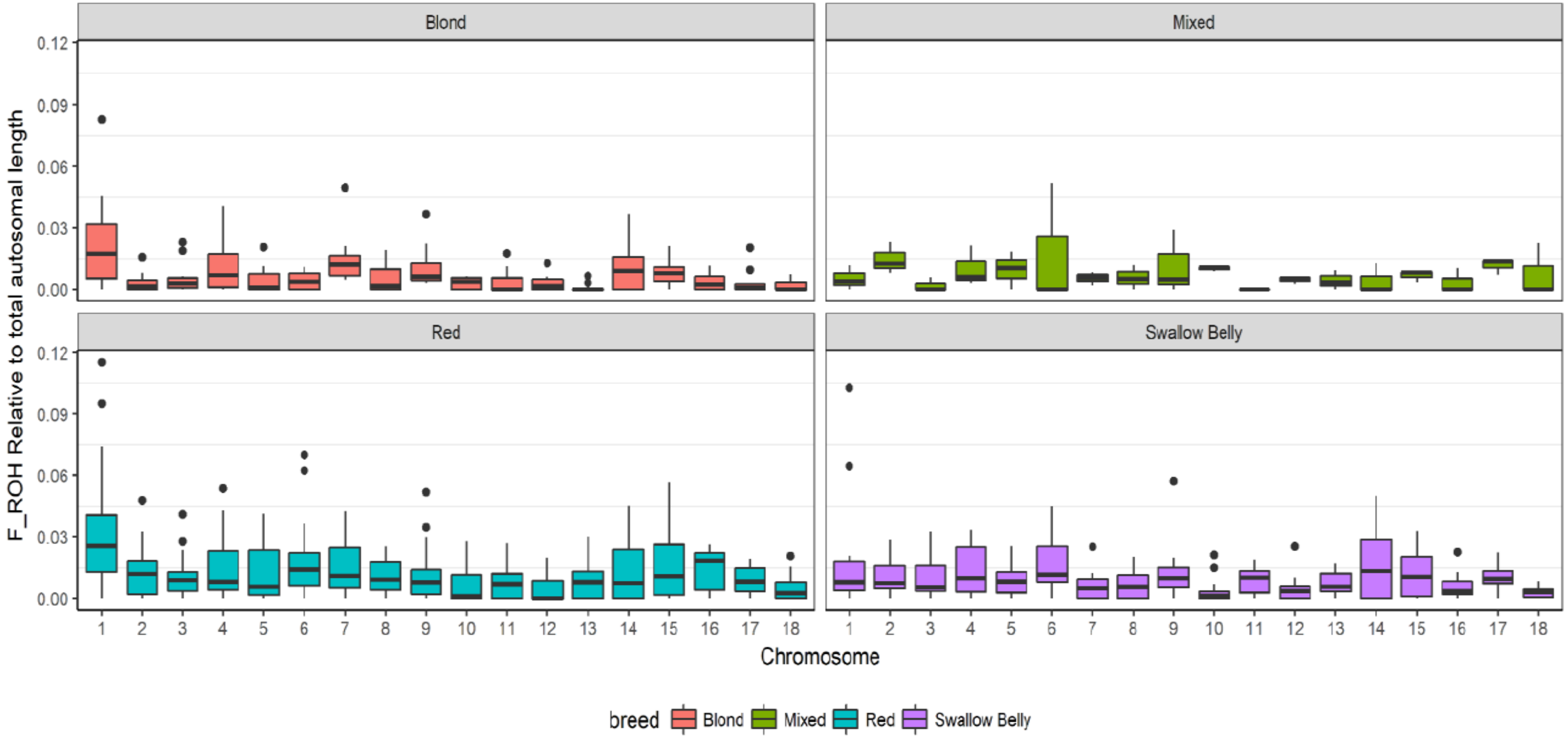


- Inbreeding level varied across chromosomes
- Highest mean *F* Chr. 1, Chr. 6 & Chr. 14

Results and discussion

Genomic inbreeding (F_{ROH_KA})

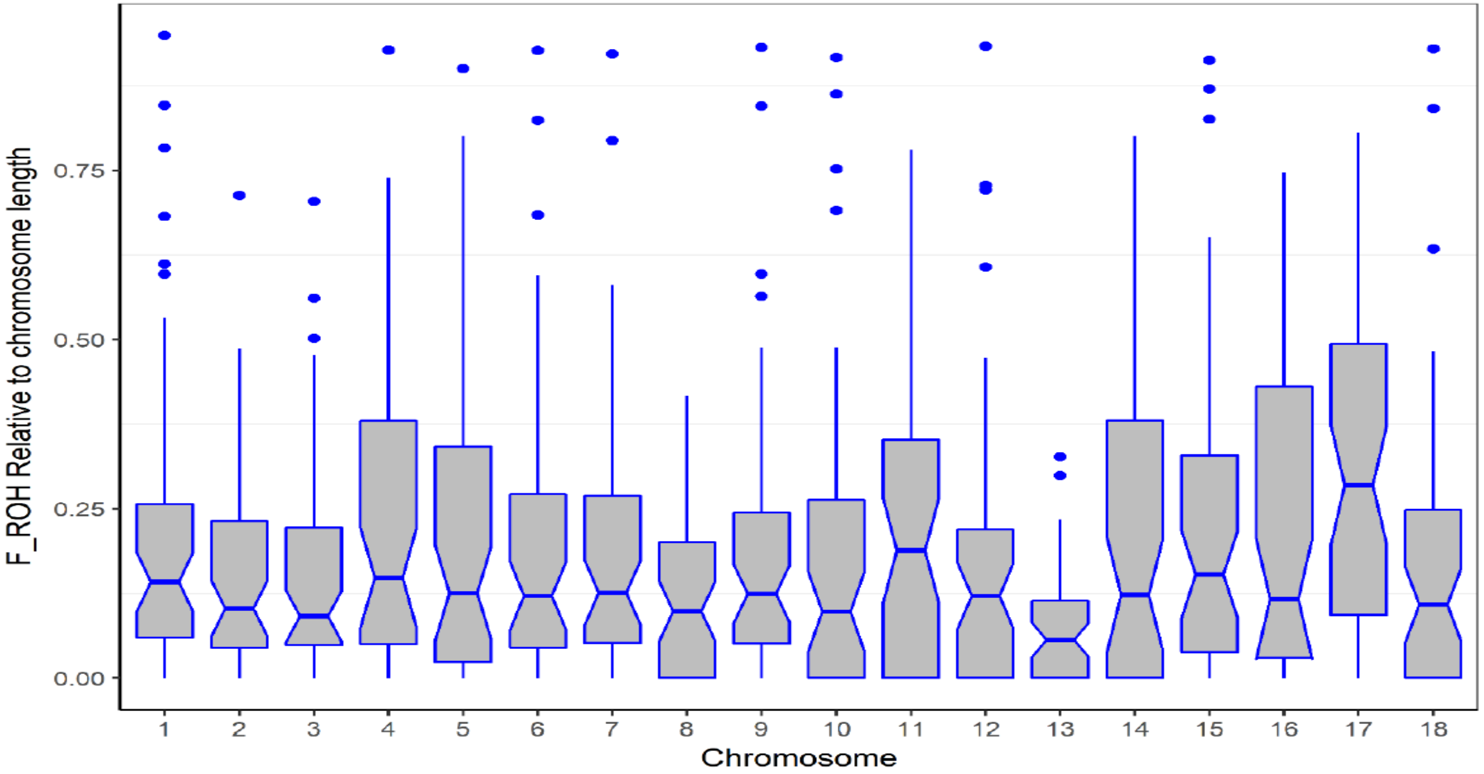
- Compared across breeds (autosomal length)



Results and discussion

Genomic inbreeding (F_{ROH_KK})

- Chromosomal inbreeding relative to chromosomal length

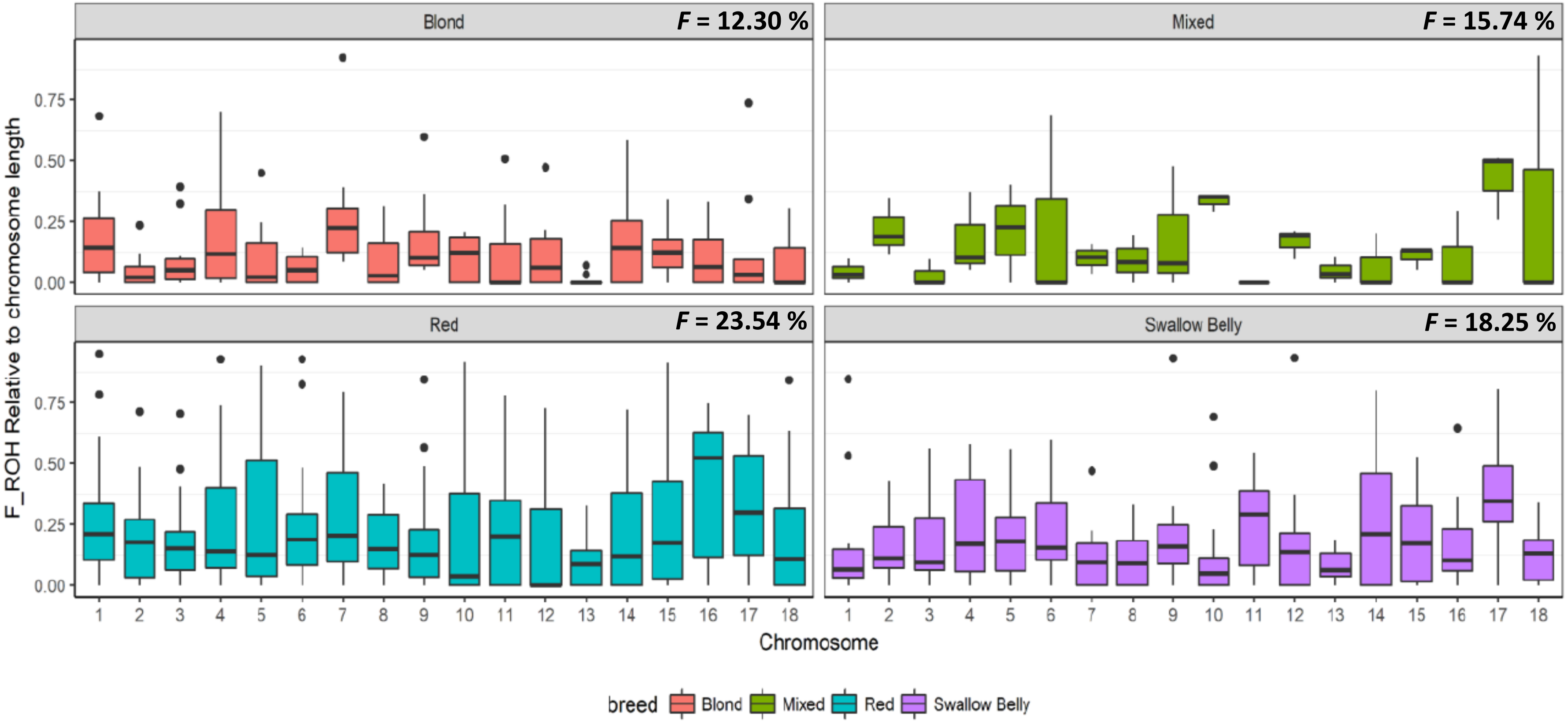


- Variation in inbreeding across chromosome captured better with $\mathbf{F_{ROH\_KK}}$

Results and discussion

Genomic inbreeding (F_{ROH_KK})

- Compared across breeds (chromosomal length)



Conclusion

- DNA extraction from hair samples works unexpected well
- SNP information has the potential to be implemented in Mangalica pig breeding in Germany
- Breeders have to cover the costs for generating SNP information
- Results of this study must be confirmed with larger data sets and additional breeds

Thank you for your attention