Analysis of pedigree and marker based inbreeding coefficients in German Fleckvieh

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Introduction

➢ **Inbreeding coefficients can be based on:**

    ➢ **Pedigree information**

    ➢ **SNP marker information**

➢**For both sources of information different approaches can be used for the estimation of inbreeding coefficients**

Pedigree based inbreeding coefficients (1)

➢ **Classical inbreeding coefficient according to Sewall Wright (1922)**

- **Most common inbreeding concept in animal breeding**

- **However, did not take the age of the inbreeding into account**

Pedigree based inbreeding coefficients (2)

- **Ballou (1997)**

  - Ancestral inbreeding coefficient based on classical inbreeding coefficient of parents

- **Kalinowski et al. (2000)**

  - Splits classical inbreeding coefficients in two parts, i.e. "new" and "old" inbreeding

➢ **Marker based inbreeding coefficients (1)**

- ➢ **Estimation possible caused by massive genotyping of selection candidates**

- ➢ **Relationship between haplotypes within an individual**

- ➢ **Based on variance of diagonal of SNP derived GRM**

- ➢ **Based on SNP homozygosity (PLINK)**

Introduction

Aim of this study

➢ **Estimation of different pedigree based and marker based inbreeding coefficients**

➢ **Analysis of genome wide marker based inbreeding coefficients and chromosomal inbreeding coefficients**

Estimation of pedigree based inbreeding coefficients

> **Wrights inbreeding coefficients estimated with the method of Meuwissen and Luo (1992)**

> **Coefficients according to Ballou (1997) and Kalinowski et al. (2000) were estimated by gene dropping using the programme package GRAIN22**

Estimation of marker based inbreeding coefficients (1)

- Assume that possible genotypes of a SNP are:

  - $(1 - p_i)^2 + p_i(1 - p_i)F$

  - $2p_i(1 - p_i)(1 - F)$

  - $p_i^2 + p_i(1 - p_i)F$

- Define h_i as $2p_i(1 - p_i)$

Estimation of marker based inbreeding coefficients (2)

➢ **F_Gen1 is:**

➢ $F\_Gen1 = [x_i - E(x_i)]^2 / h_i - 1 = (x_i - 2p_i)^2 / h_i - 1,$

➢ **Where x_i is the number of copies of the reference allele for the ith SNP**

➢ **sampling variance of F_Gen1 depends on allele frequency**

Estimation of marker based inbreeding coefficients (3)

- ➢ **F_Gen2 is:**
  - ➢ **F_Gen2 = $[x^2_i - (1 + 2p_i)x_i + 2p^2_i] / h_i$**
  - ➢ **based on the correlation of uniting gametes as shown by Yang et al. (2010)**
- ➢ **Both marker based inbreeding coefficients were estimated with the software package GCTA (Yang et al., 2011)**

Fleckvieh bulls (Illumina 50 K)

- 3,303 bulls

    - Call rate > 90%

    - MAF > 5%

    - Number of SNP vary between 32,619 and 36,134

    - Average number of SNP 35,956

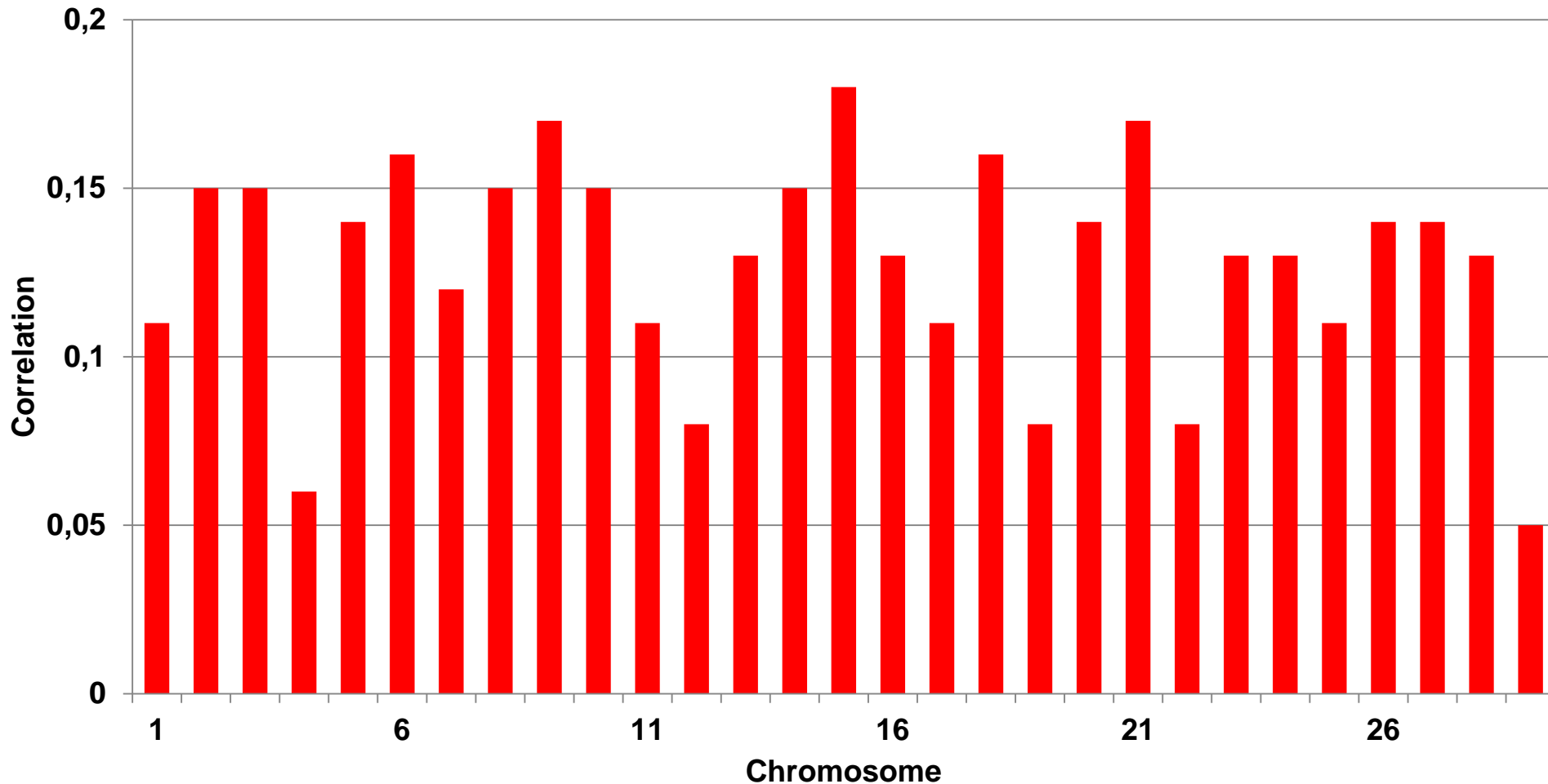**Correlation between pedigree based and marker based inbreeding coefficients**

	F_Gen1	F_Gen2
F_Gen1	1.00	0.56
F_Gen2	0.56	1.00

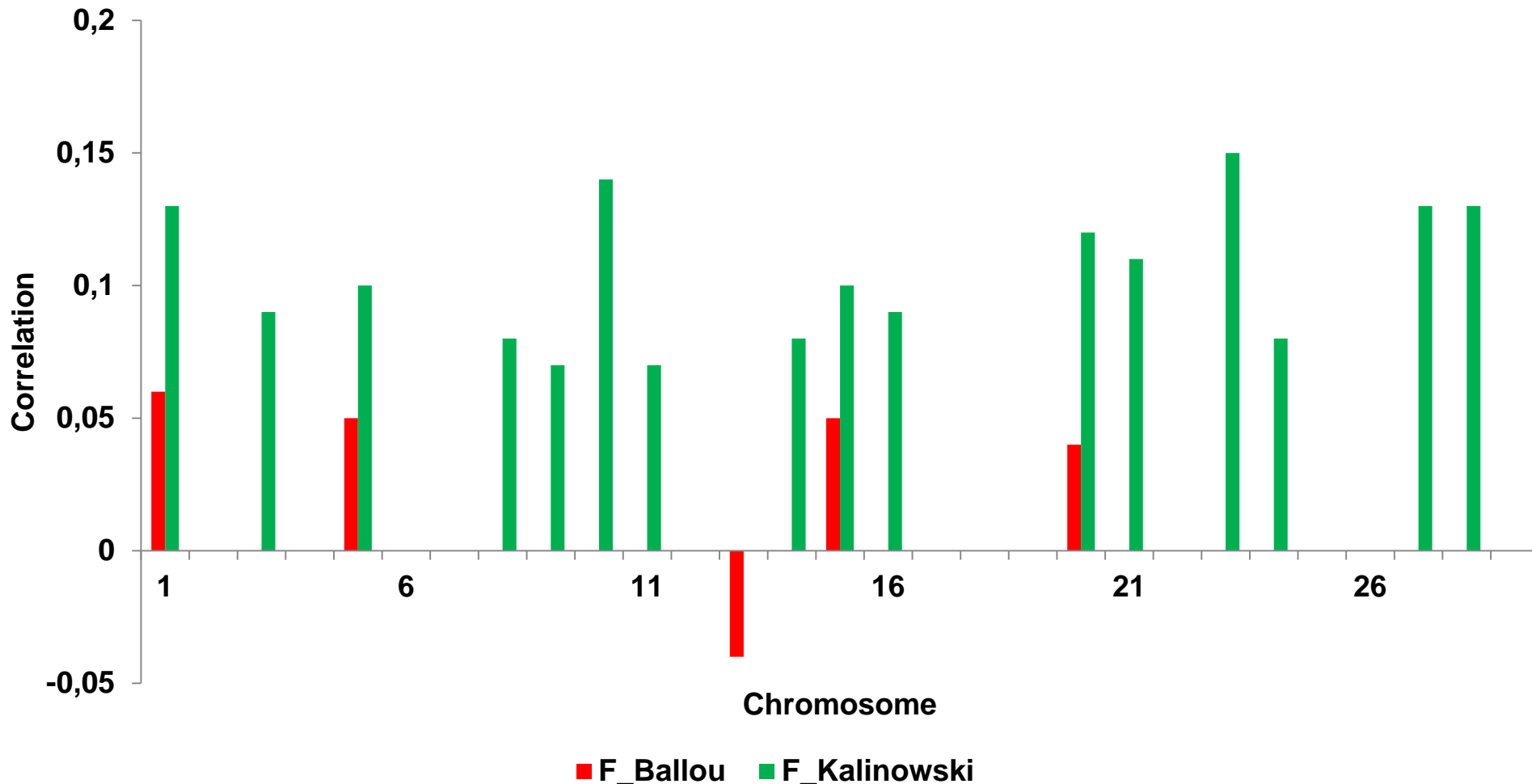|	F_Wright	F_Ballou	F_new	F_old
F_Gen1	0.09	n.s.	n.s.	n.s.
F_Gen2	0.45	0.04	0.26	0.26

Results

Correlation between Wright's inbreeding coefficient and chromosomal inbreeding coefficients

Results

Correlation between ancestral inbreeding coefficients and chromosomal inbreeding coefficients

Material and methods

Fleckvieh bulls and cows (High density)

- ➢ 866 bulls and 1,996 cows

  - ➢ Call rate > 90%

  - ➢ MAF > 5%

  - ➢ Number of SNP vary between 526,693 and 582,880

  - ➢ Average number of SNP 578,982 in bulls

  - ➢ Average number of SNP 567,074 in cows

Correlation between pedigree based and marker based inbreeding coefficients for HD genotyped FV bulls and cows

Bulls	F_Gen1	F_Gen2
F_Gen1	1.00	0.76
F_Gen2	0.76	1.00

Cows	F_Gen1	F_Gen2
F_Gen1	1.00	0.74
F_Gen2	0.74	1.00

Bulls	F_Wright	F_Ballou	F_new	F_old
F_Gen1	0.17	n.s.	0.17	0.15
F_Gen2	0.40	n.s.	0.40	0.22

Holstein Friesian bulls (50 K)

➢**2,528 bulls**

➢**Call rate > 90%**

➢**MAF > 5%**

➢**Number of SNP vary between 41,988 and 44,170**

➢**Average number of SNP 44,008**

Results

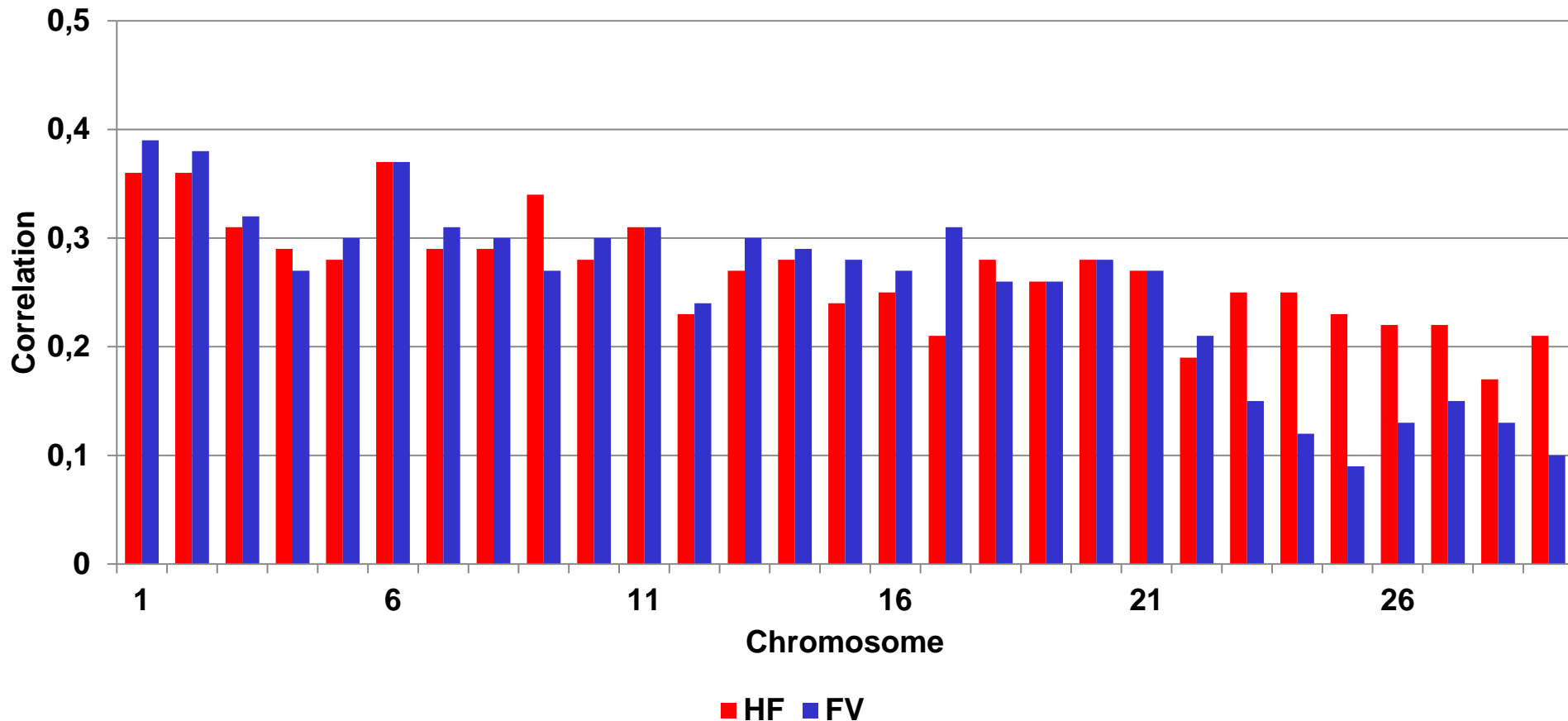**Correlation between pedigree based and marker based inbreeding coefficients (HF)**

	F_Gen1	F_Gen2
F_Gen1	1.00	0.72
F_Gen2	0.72	1.00

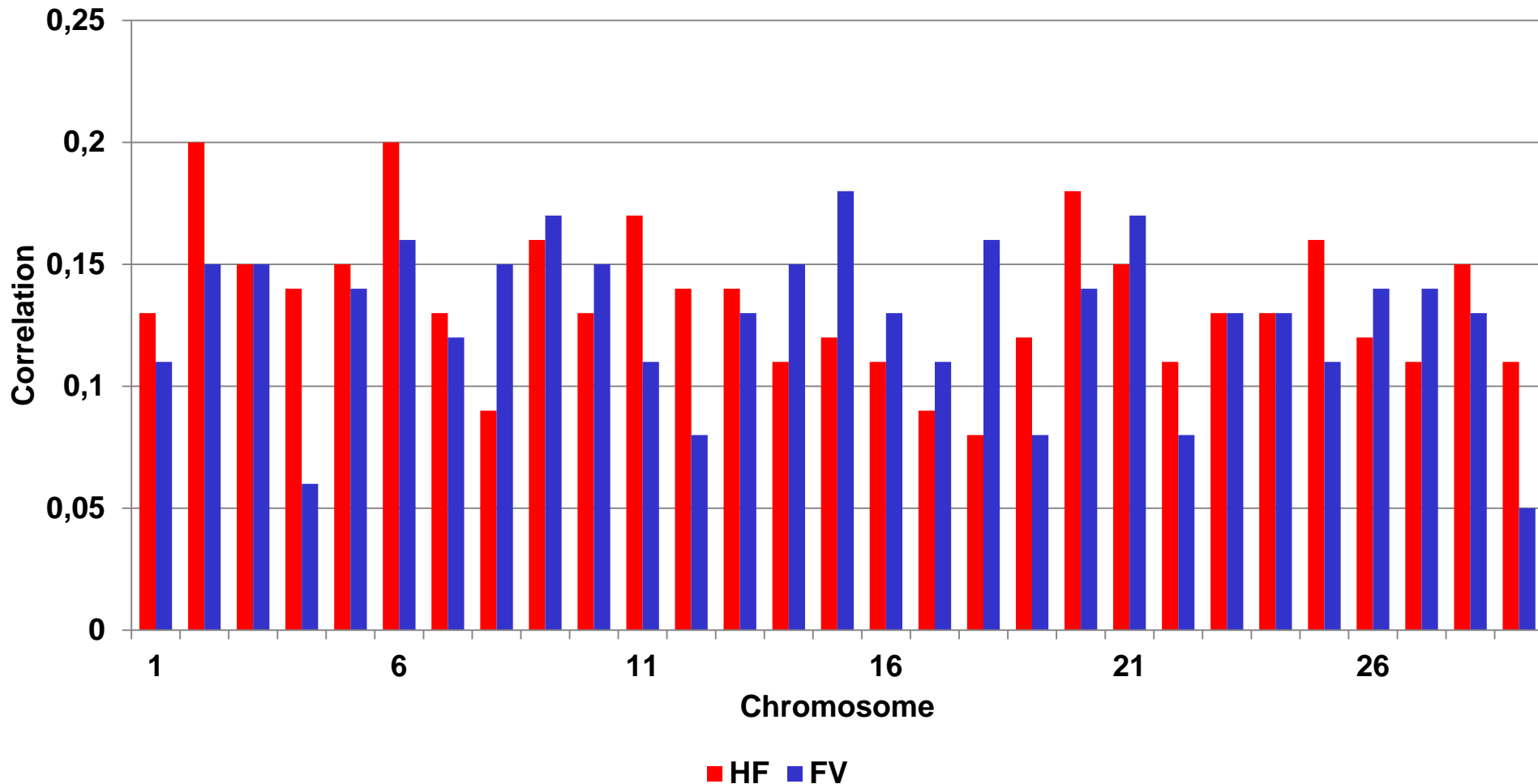| BTA	F_Wright	F_Ballou	F_new	F_old
F_Gen1	0.12	- 0.19	n.s.	n.s.
F_Gen2	0.54	0.07	0.40	0.40

Results

Correlation between marker based genome wide inbreeding coefficient and chromosomal inbreeding coefficients
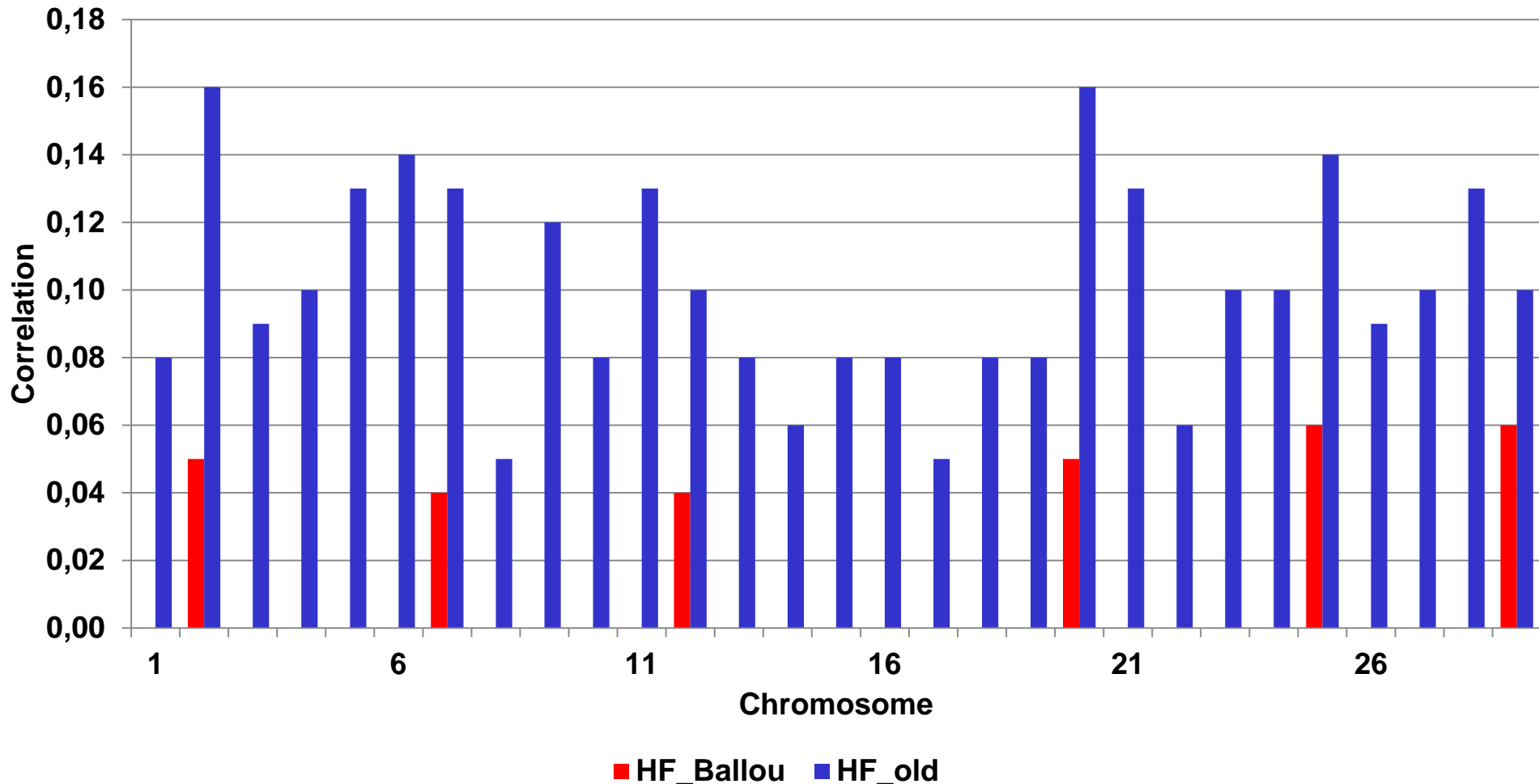
Results

Correlation between Wright's inbreeding coefficient and chromosomal inbreeding coefficients

Results

Correlation between ancestral inbreeding coefficients and chromosomal inbreeding coefficients

Conclusion

➢ **Inbreeding is not equally distributed across the genome**

➢ **Correlations between genome wide and chromosomal inbreeding coefficients are similar in Fleckvieh and Holstein Friesian**

➢ **Correlations between marker based inbreeding coefficients and pedigree based inbreeding coefficients are higher in Holstein Friesian**

Conclusion

➢ **Ballous concept of ancestral inbreeding failed in both populations**

➢ **Kalinowskis concept of old and new inbreeding showed moderate correlations to marker based inbreeding coefficients**

➢ **Higher marker densities and allele frequency independent estimates showed positive effects**
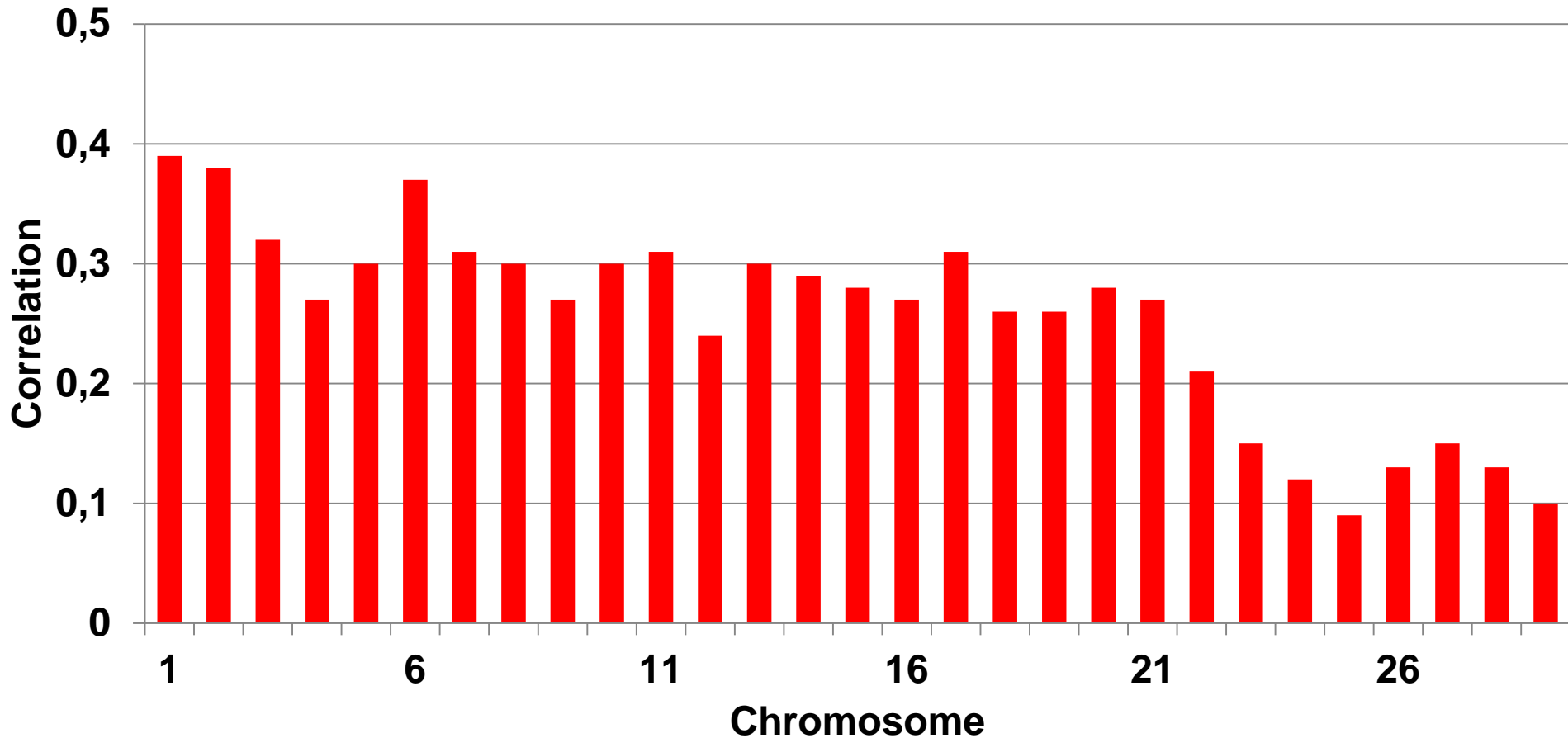
Thanks for your attention

Results

Correlation between marker based genome wide inbreeding coefficient and chromosomal inbreeding coefficients

Results

Correlation between Kalinowskis "new" inbreeding and chromosomal inbreeding coefficients