



# Genomic inbreeding based on runs of homozygosity in the regional German horse breed Schleswig Coldblood

## Project motivation / Introduction

- Schleswig Coldblood horse (origin in Northern Germany and Southern Denmark) was formerly used in agriculture and forestry
  - due to the mechanization of these sectors the breed was threatened with extinction at the mid-1970s
- today only approx. 180 breeding animals; closed studbook
  - listed as endangered livestock breed (category phenotypic conservation population)
  - some influence of three allowed breeds, namely Jutlander and, to a lesser extent, Boulonnais and South German Coldblood

**objective:** using genome-wide SNP genotypic data of a large sample of all living Schleswig Coldblood horses for characterizing the population structure and assess

- genomic inbreeding
- monitoring of genetic diversity



## Conclusion

**moderate mean genomic inbreeding** ( $F_{ROH}$  of 10.0%) and no clear trend over the years in the Schleswig Coldblood horse population

at least one longer ROH (10Mb) in most of the sampled horses  
 ➤ indication of **relevance of recent inbreeding** to be monitored

results of pedigree structure analyses as basis of new tools for **support of mating planning** and **improved breed management**



## Results

**Table 1:** Mean  $F_{ROH}$  with standard deviation (std.), minimum and maximum for 219 Schleswig Coldblood horses, determined with 2,000 kb as length of DNA stretches considered as ROH across all sampled horses and within subgroups defined by years of birth.

birthyear	N	mean	std.	minimum	maximum
< 2000	10	0.1006	0.0334	0.0379	0.1551
2000-2004	17	0.1023	0.0360	0.0382	0.1625
2005-2009	25	0.0988	0.0406	0.0051	0.1598
2010-2014	52	0.0870	0.0383	0.0011	0.1722
2015-2019	47	0.1106	0.0361	0.0140	0.1733
> 2019	68	0.1022	0.0369	0.0165	0.1994
all	219	0.0999	0.0378	0.0011	0.1994

ROH = run of homozygosity,  $F_{ROH}$  = genomic inbreeding coefficient based on ROH (McQuillan<sup>[b]</sup>)

Note from analyses with alternative settings:

202 of the 219 sampled horses (92,2%) had at least one very long ROH of 10,000kb

## Material and methods

85K SNP genotypes of **219 Schleswig Coldblood horses** were used to determine **runs of homozygosity (ROHs)** with **PLINK** software<sup>[a]</sup> and the following functions / settings:

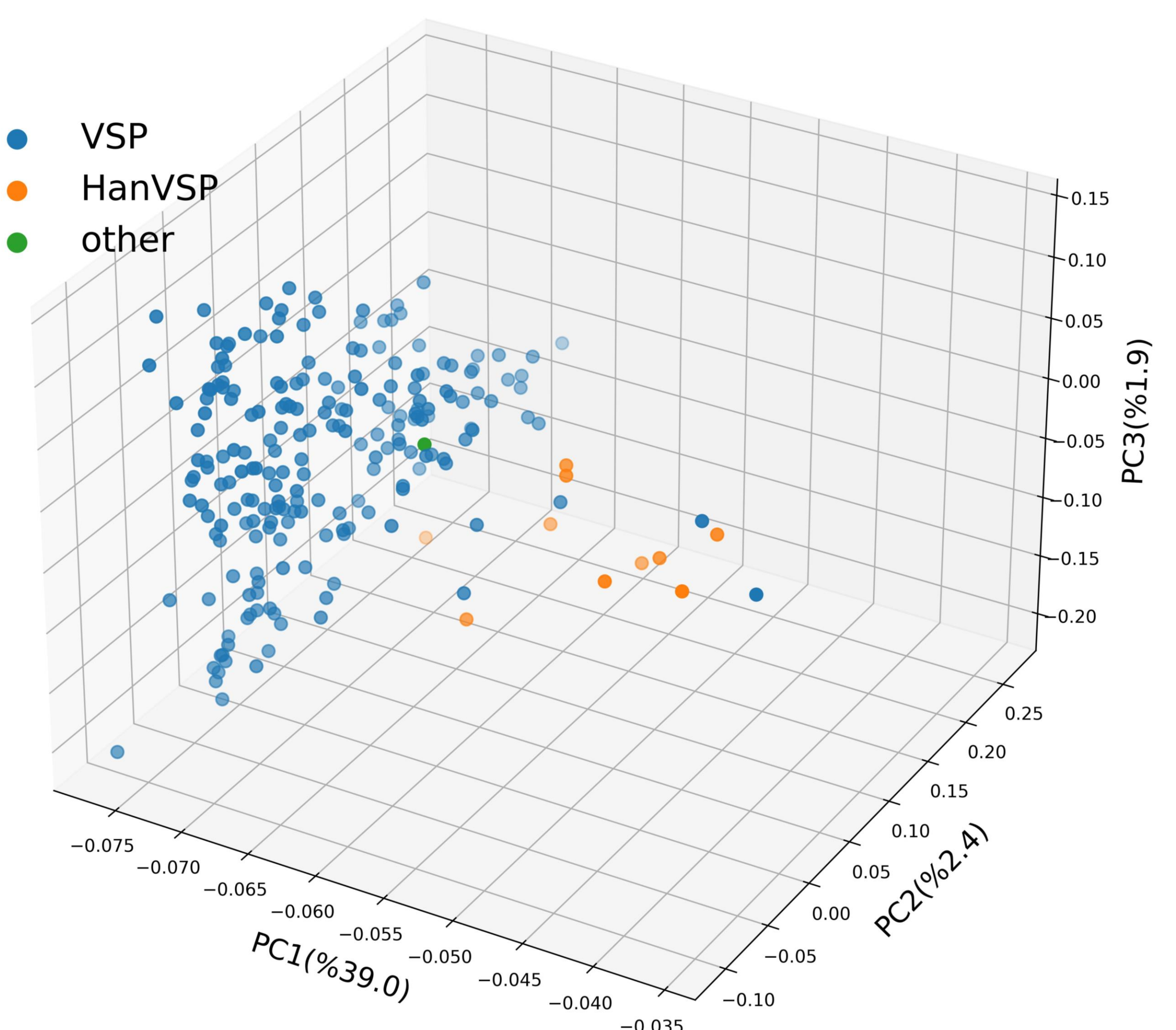
- homozyg
- homozyg-window-kb (2,000 vs 10,000)
- homozyg-snp 25 (minimum number of SNPs in one ROH)
- homozyg-window-het 0 (no heterozygotes allowed in ROH)

**N = 57,286 quality controlled autosomal SNPs** entered the analyses

calculation of **genomic inbreeding** for each individual and each scenario (different window sizes) according to McQuillan<sup>[b]</sup>:

$$F_{ROH} = \frac{\text{total length of all ROH}}{\text{autosomal genome length covered by SNPs}}$$

afterwards: **mean  $F_{ROH}$**  over all horses for each scenario (Table 1)



**Figure 1:** Principal component plot from all genotyped Schleswig Coldblood horses (N=219); PC1 (PC2, PC3) = Vector to the 1st (2nd, 3rd) principal component

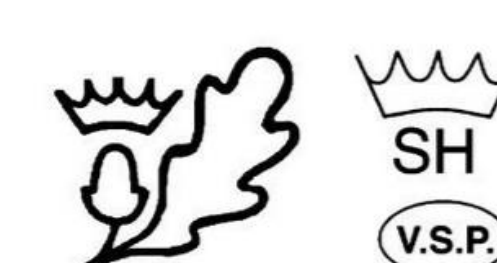
**Registered breeds in the pedigree of horses as indicated in Figure 1:**

VSP = Schleswig Coldblood  
 HanVSP = Hanoverian Coldblood with Schleswig origin  
 other = other coldblood breed

## Literature / Acknowledgements

- [a] Purcell, S., et al. (2007): PLINK: a toolset for whole-genome association and population-based linkage analysis. Am. J. Hum. Genet. 81, 559-575.  
 [b] McQuillan, R., et al. (2008): Runs of homozygosity in European populations. Am. J. Hum. Genet. 83, 359-372.

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