F_{ST} as an indicator of selective sweeps using admixed animals as a control

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Outline

- Use of local reduction of genetic variation in one of two breeds to reveal selective sweeps

Aim

- Use F_{ST} between Simmental (SIM) and Red Holstein Friesian (RHF) to reveal potential selective sweeps
- In swept regions check for accuracy in admixture

Materials and methods

37936 SNPs

101

87

305

Materials and methods- Software used

- PLINK

  QC: $mind > 0.1$

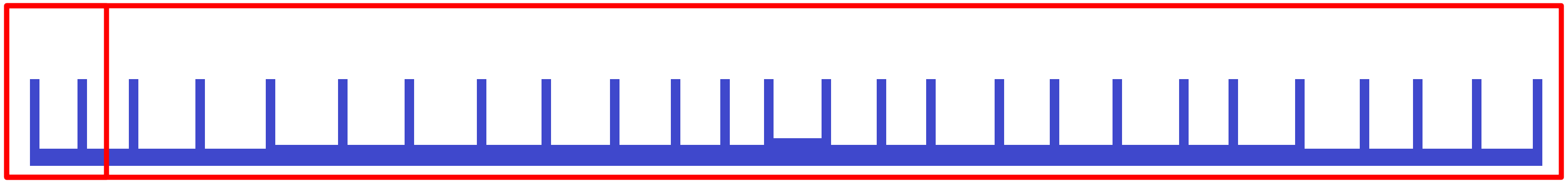
  $maf < 0.05$

  $geno > 0.1$

  $HWE > 10^{-5}$
- SAS genetics - F_{ST} calculation
- R - sliding windows

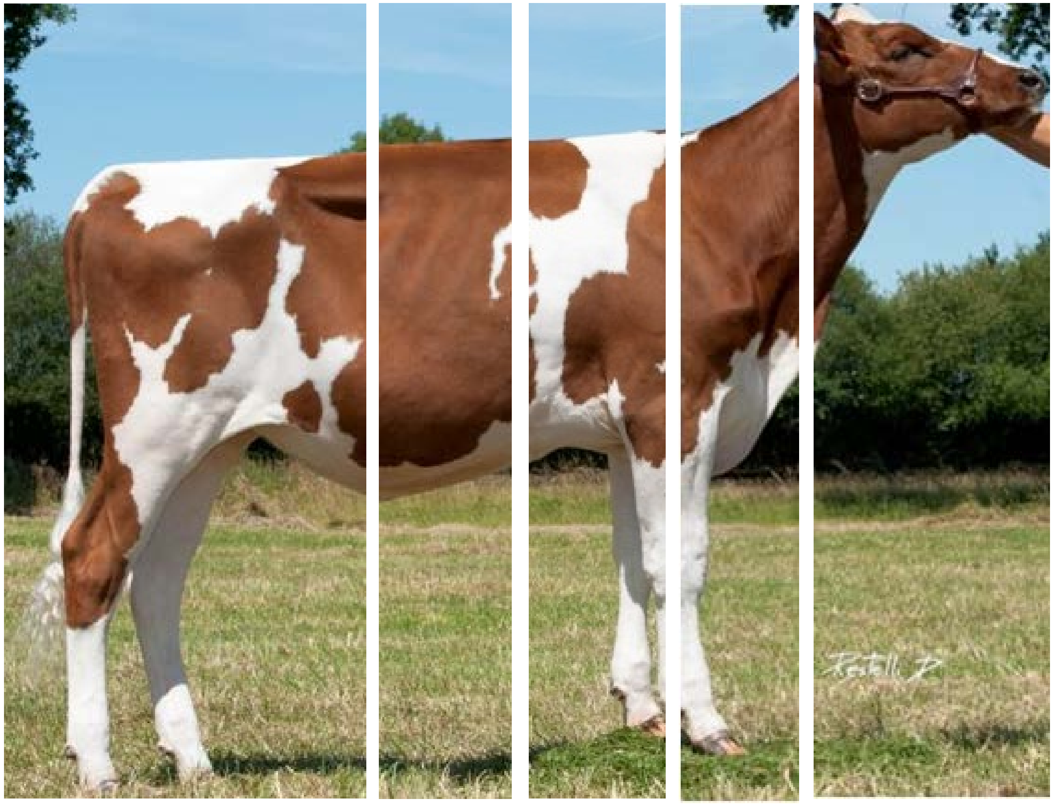
Methods

- Sliding windows of 2-20 consecutive SNPs
- Sliding windows of 250, 500 Kb and 1 Mb



Methods

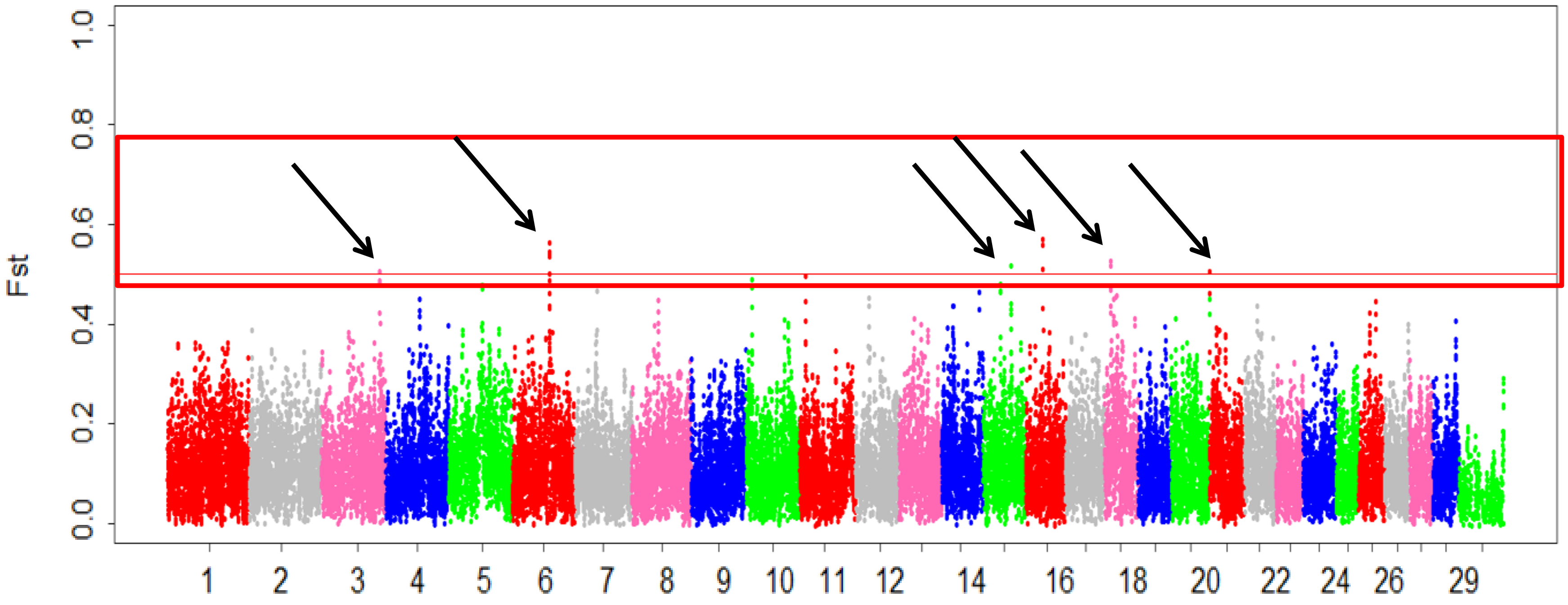
Crosses divided into groups: 0-0.50 RHF



- 0.50-0.60 RHF
- 0.60-0.70 RHF
- 0.70-0.80 RHF
- 0.80-1 RHF

Based on STRUCTURE analysis

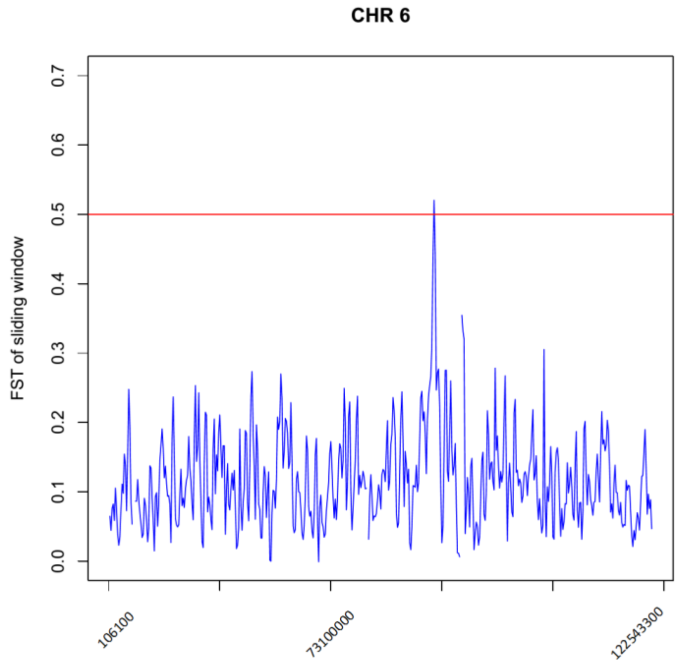
Results



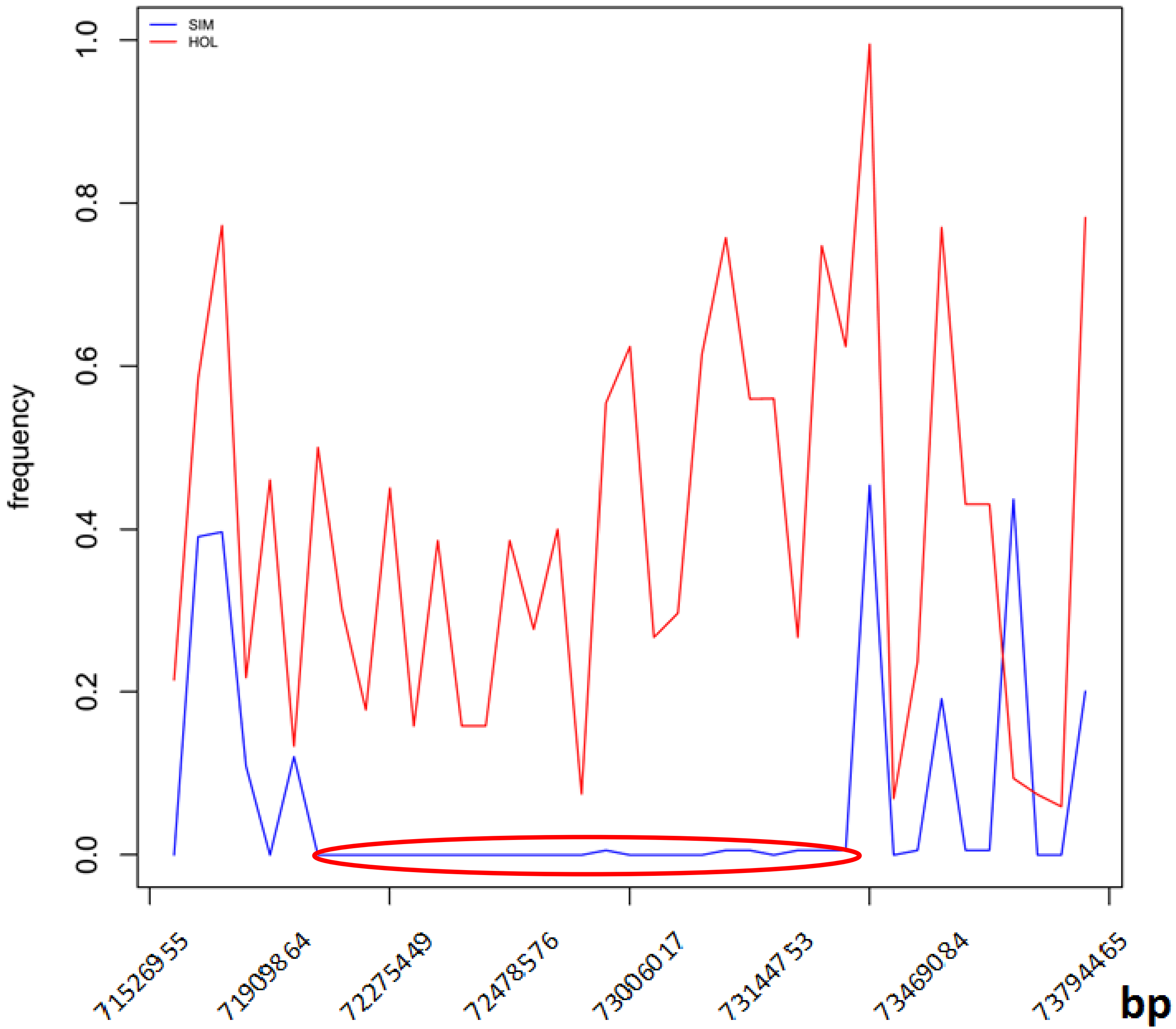
Manhattan plot of Win5 F_{ST}

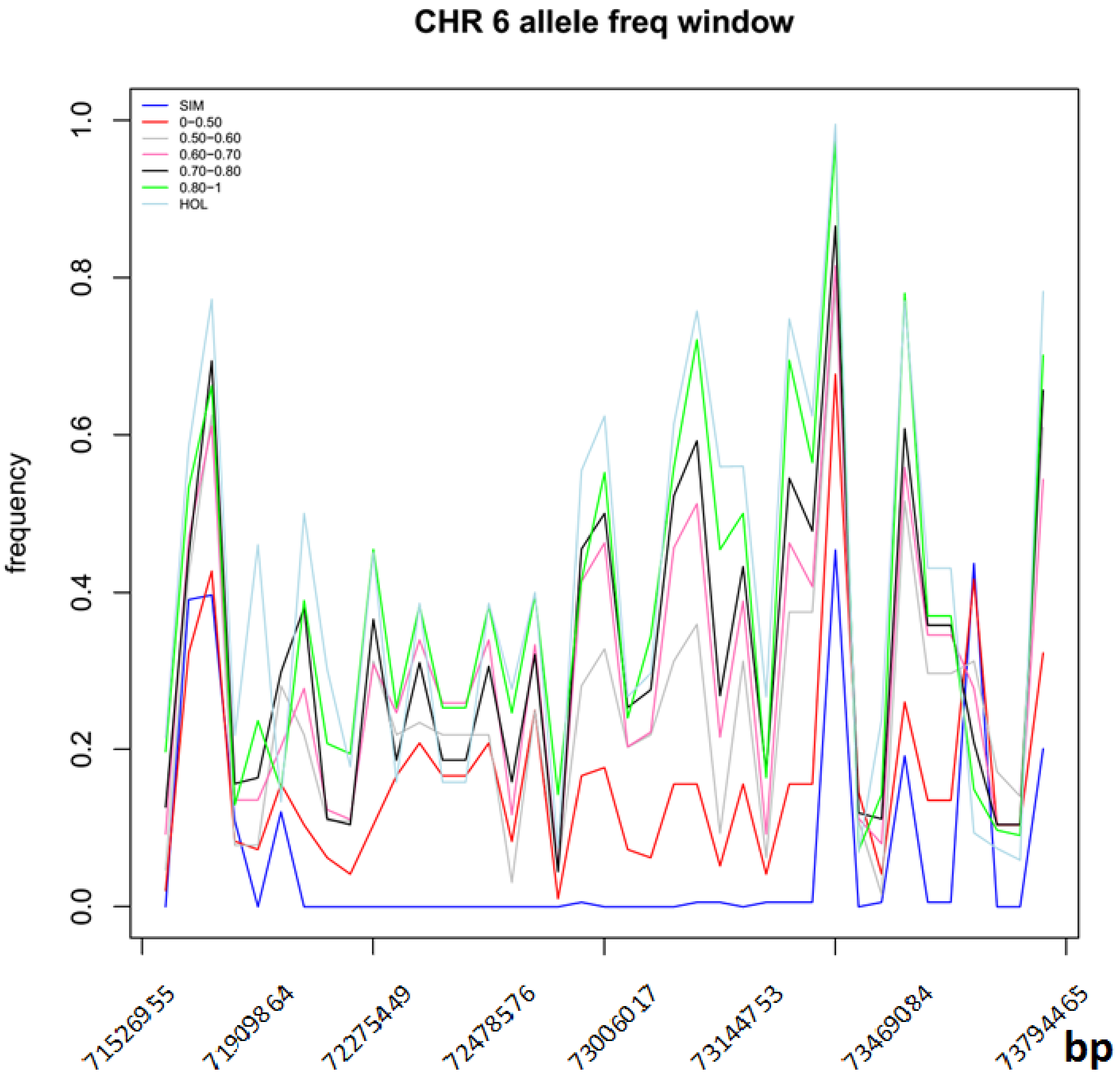
Results

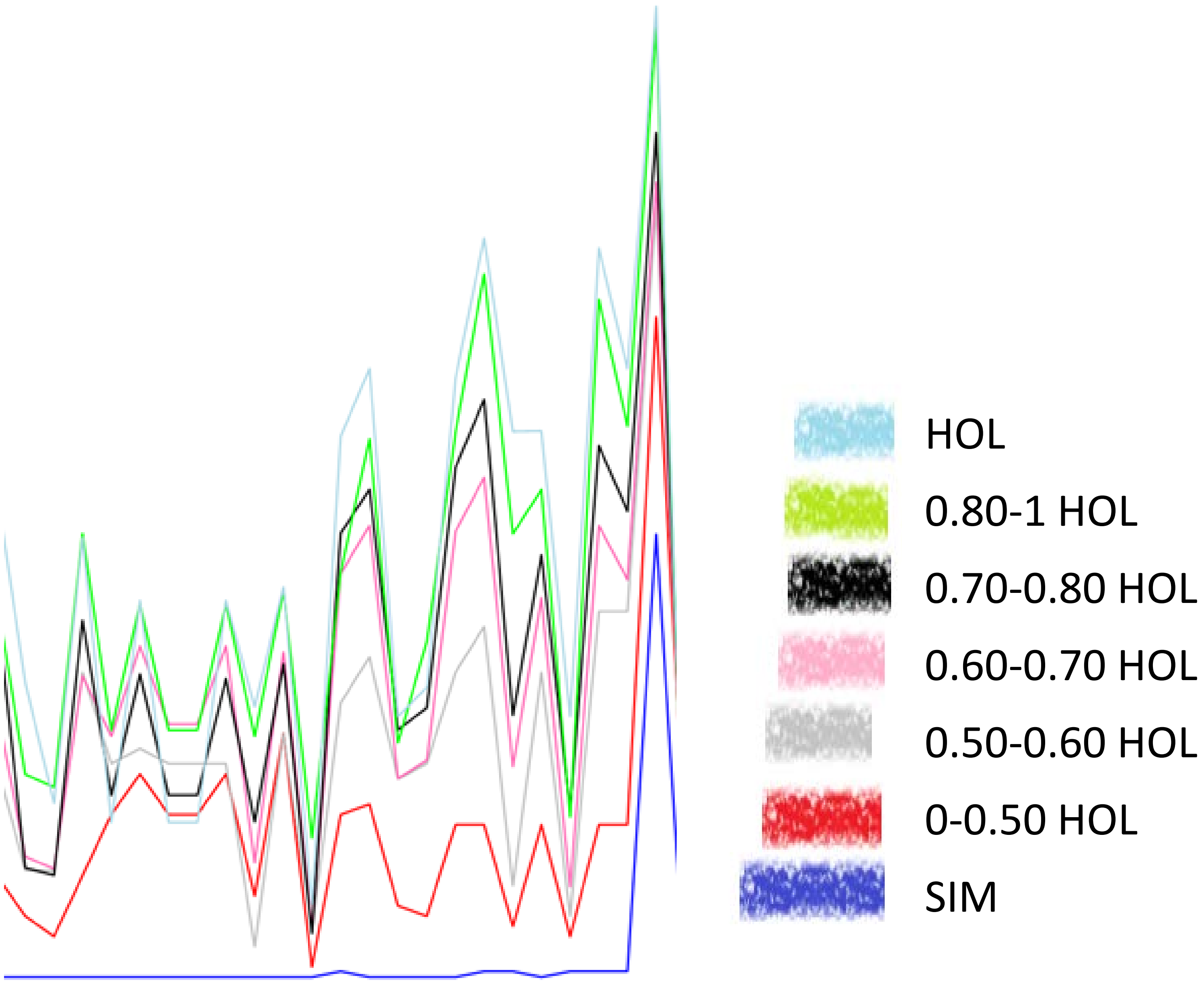
- The top signal - chromosome 6, 2.6 Mb
- 22 of which were fixed in SIM



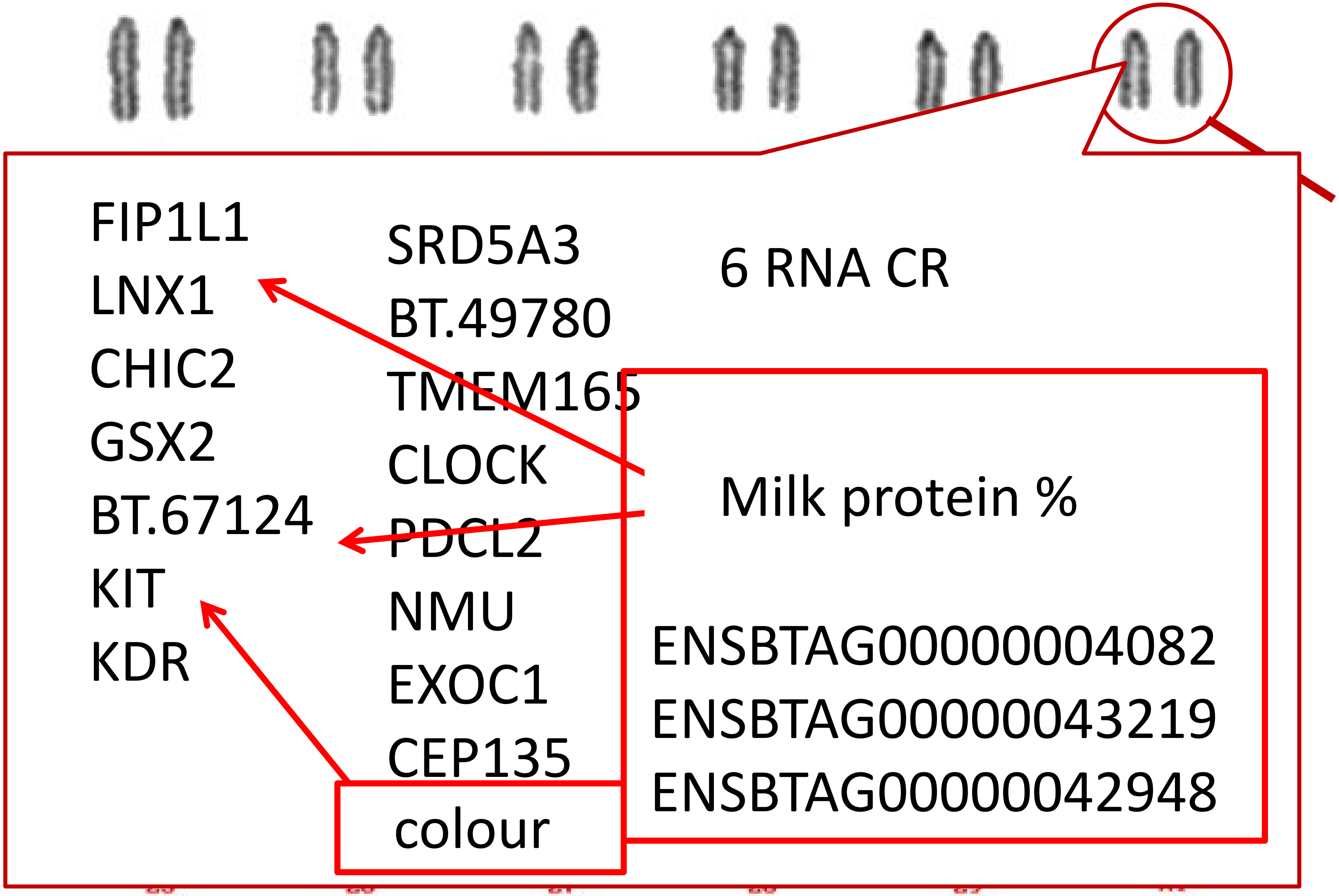
CHR 6 allele freq window




CHR 6 allele freq window
SIM
0−0.50
0.50−0.60
0.60−0.70
0.70−0.80
0.80−1
HOL
frequency
0.0
0.2
0.4
0.6
0.8
1.0
71526955
71909864
72275449
72478576
73006017
73144753
73469084
73794465
bp


HOL
0.80-1 HOL
0.70-0.80 HOL
0.60-0.70 HOL
0.50-0.60 HOL
0-0.50 HOL
SIM

Genes in region of CHR 6



FIP1L1
LNX1
CHIC2
GSX2
BT.67124
KIT
KDR

SRD5A3
BT.49780
TMEM165
CLOCK
PDCL2
NMU
EXOC1
CEP135

6 RNA CR

Milk protein %

ENSBTAG00000004082
ENSBTAG00000043219
ENSBTAG00000042948

colour

Conclusion

- Results indicate a selective sweep in SIM in region of CHR 6
- Good concordance of the admixture levels with allele frequencies
- In the swept region of chromosome 6, a total of 17 protein coding genes and 6 RNA coding regions were found
- The KIT gene responsible for coat color patterns in SIM

Further research

- KIT- indication of different expression of coat color pattern?
- Other breeds?
- Other genes

Thank you for attention