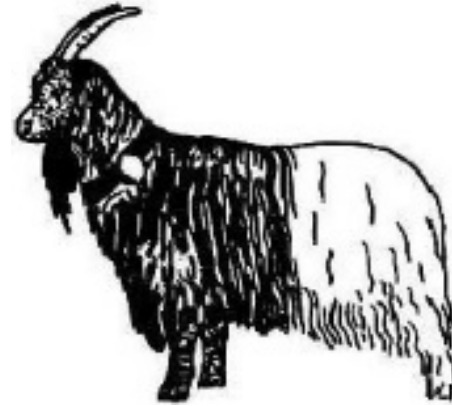


# Selektionssignaturen in Ziegen

Jan Henkel, Vidhya Jagannathan, Rashid Saif, Flurina Bertschinger,  
Corinne Schmocker, Erika Bangerter, Ursula Herren,  
Cord Drögemüller, Christine Flury, Tosso Leeb

# Genetics of depigmentation phenotypes (SNSF 31003A\_172964 / 1)

01.04.2017 – 31.03.2021



**Jan Henkel**



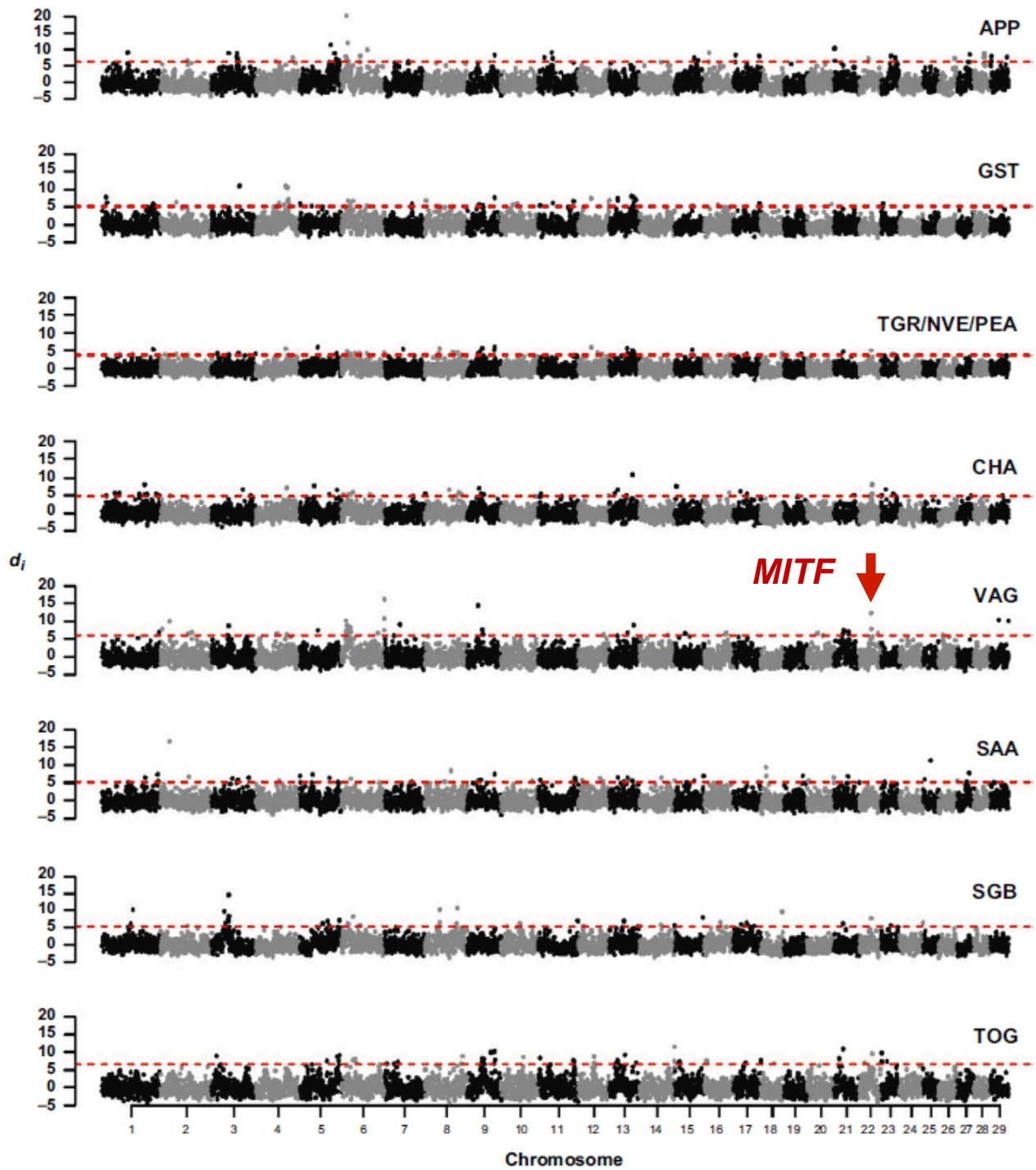


## Genetic diversity analyses reveal first insights into breed-specific selection signatures within Swiss goat breeds

A. Burren<sup>\*1</sup>, M. Neuditschko<sup>†1</sup>, H. Signer-Hasler<sup>\*</sup>, M. Frischknecht<sup>\*</sup>, I. Reber<sup>‡</sup>, F. Menzi<sup>‡</sup>,  
C. Drögemüller<sup>‡</sup> and C. Flury<sup>\*</sup>

<sup>\*</sup>School of Agricultural, Forest and Food Sciences HAFL, Bern University of Applied Sciences, Länggasse 85, 3052 Zollikofen, Switzerland.

<sup>†</sup>Swiss National Stud Farm, Agroscope Research Station, Les Longs-Prés, 1580 Avenches, Switzerland. <sup>‡</sup>Institute of Genetics, Vetsuisse Faculty, University of Bern, Bremgartenstrasse 109, 3001 Bern, Switzerland.







1 - Bezoar goat

2 - African Dwarf goat

3 - Boer goat

4 - Appenzeller goat

5 - Saanen goat



6 - Grisons Striped goat

7 - Peacock goat

8 - Nera Verzasca

9 - Capra Grigia

10 - St. Gallen Booted goat



11 - Toggenburger goat

12 - Chamois colored goat

13 - Valais Blacknecked goat



14 - Markhor

15 - Beetal

16 - Barbari

17 - Damani

18 - Kamori



19 - Dera Din Panah

20 - Teddy

21 - Pahari

22 - Pak Angora

23 - Nachi

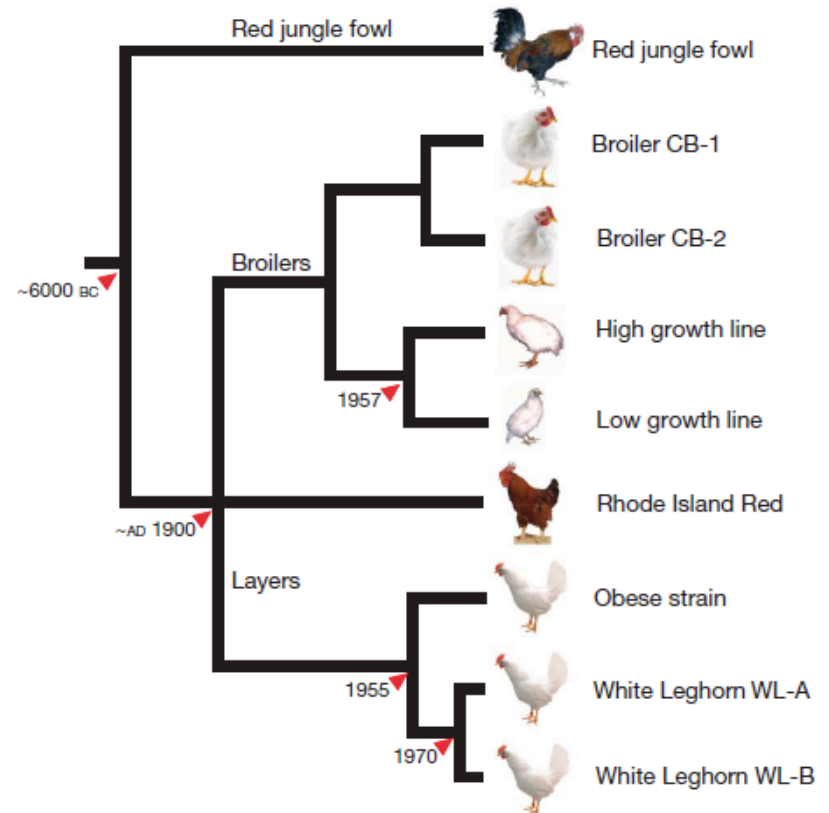


24 – Rajanpuri (Nukri)

## LETTERS

# Whole-genome resequencing reveals loci under selection during chicken domestication

Carl-Johan Rubin<sup>1\*</sup>, Michael C. Zody<sup>1,2\*</sup>, Jonas Eriksson<sup>1</sup>, Jennifer R. S. Meadows<sup>1</sup>, Ellen Sherwood<sup>3</sup>, Matthew T. Webster<sup>1</sup>, Lin Jiang<sup>1</sup>, Max Ingman<sup>4</sup>, Ted Sharpe<sup>2</sup>, Sojeong Ka<sup>5</sup>, Finn Hallböök<sup>5</sup>, Francois Besnier<sup>6</sup>, Örjan Carlborg<sup>6</sup>, Bertrand Bed'hom<sup>7</sup>, Michèle Tixier-Boichard<sup>7</sup>, Per Jensen<sup>8</sup>, Paul Siegel<sup>9</sup>, Kerstin Lindblad-Toh<sup>1,2</sup> & Leif Andersson<sup>1,6</sup>



# Experiment design

**24 pools with 12 animals each**

**PCR free libraries**

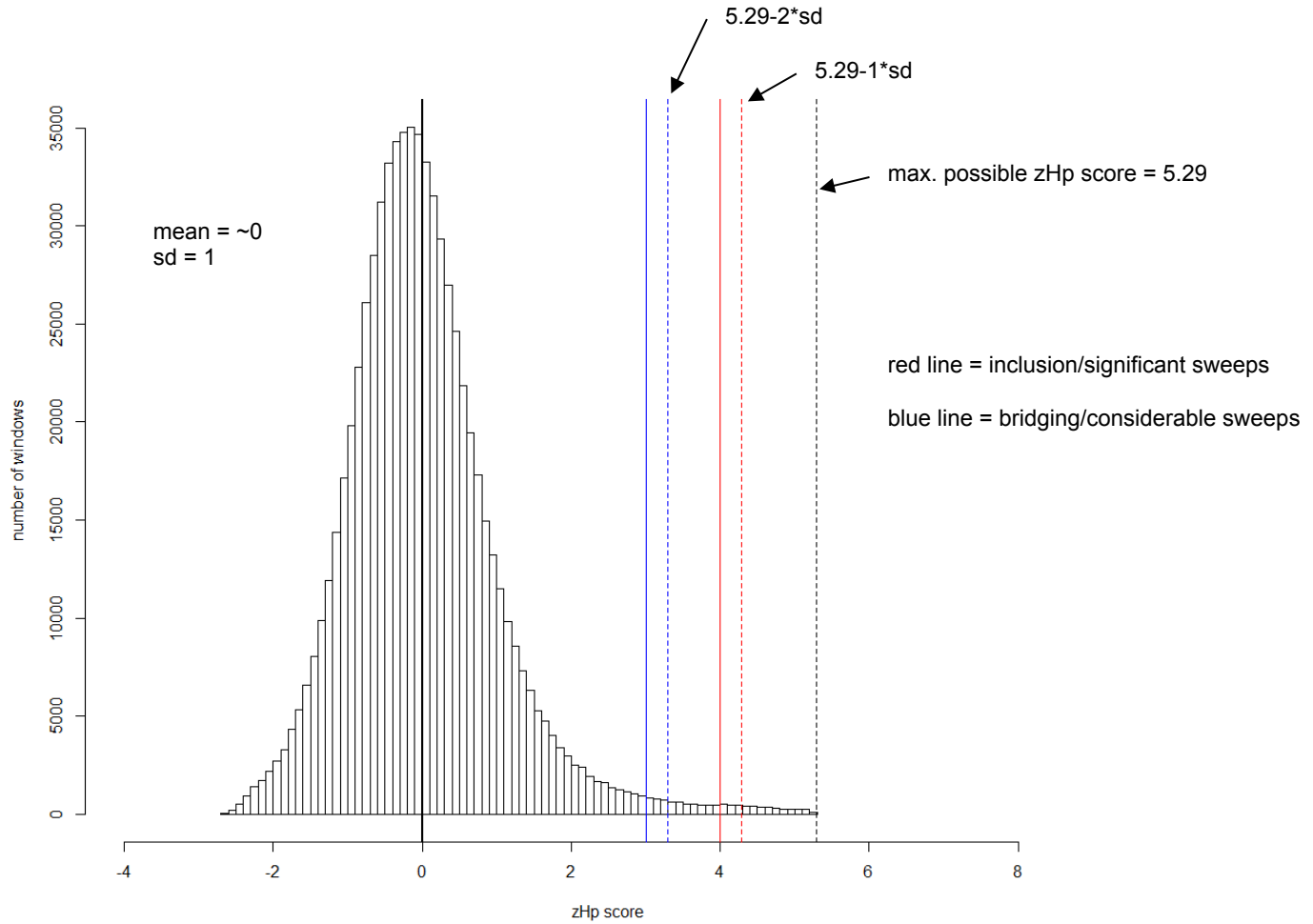
**1 lane per pool**

**~24x coverage = 1x coverage per chromosome**



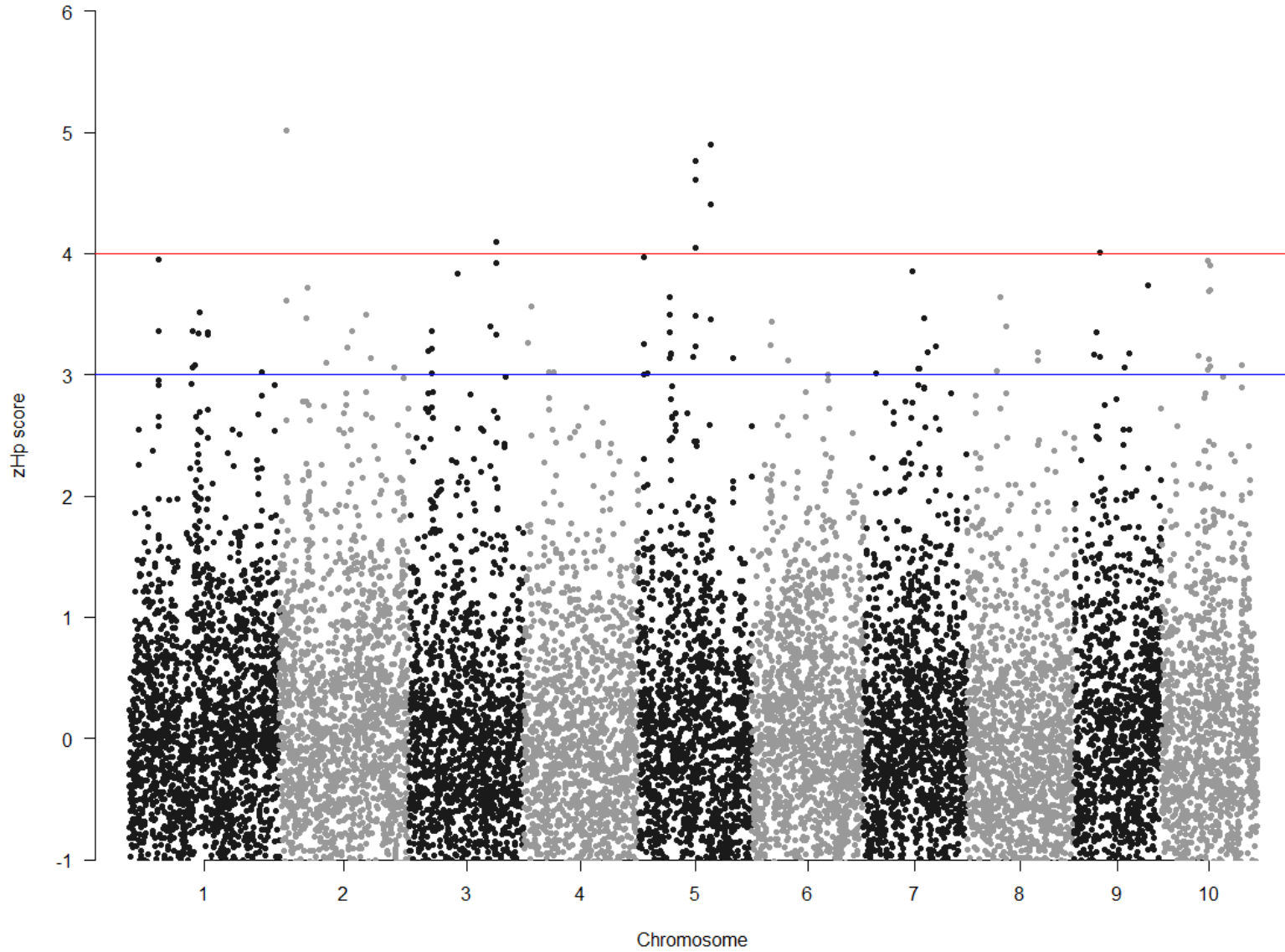
We will count the numbers of reads corresponding to the most and least frequently observed allele ( $n_{maj}$  and  $n_{min}$ , respectively) in each breed pool. Pooled heterozygosity ( $H_p$ ) for each window will be calculated by scoring  $H_p = 2\sum n_{maj} \sum n_{min} / (\sum n_{maj} + \sum n_{min})^2$ , where  $\sum n_{maj}$  and  $\sum n_{min}$  are the sums of  $n_{maj}$  and  $n_{min}$  for all SNVs in the window. Then the individual  $H_p$  will be transformed into a Z-score  $ZH_p$  as follows:  $ZH_p = (H_p - \mu H_p) / \sigma H_p$ .

zHp distribution/150kb\_window - all 21 pools  
filtered

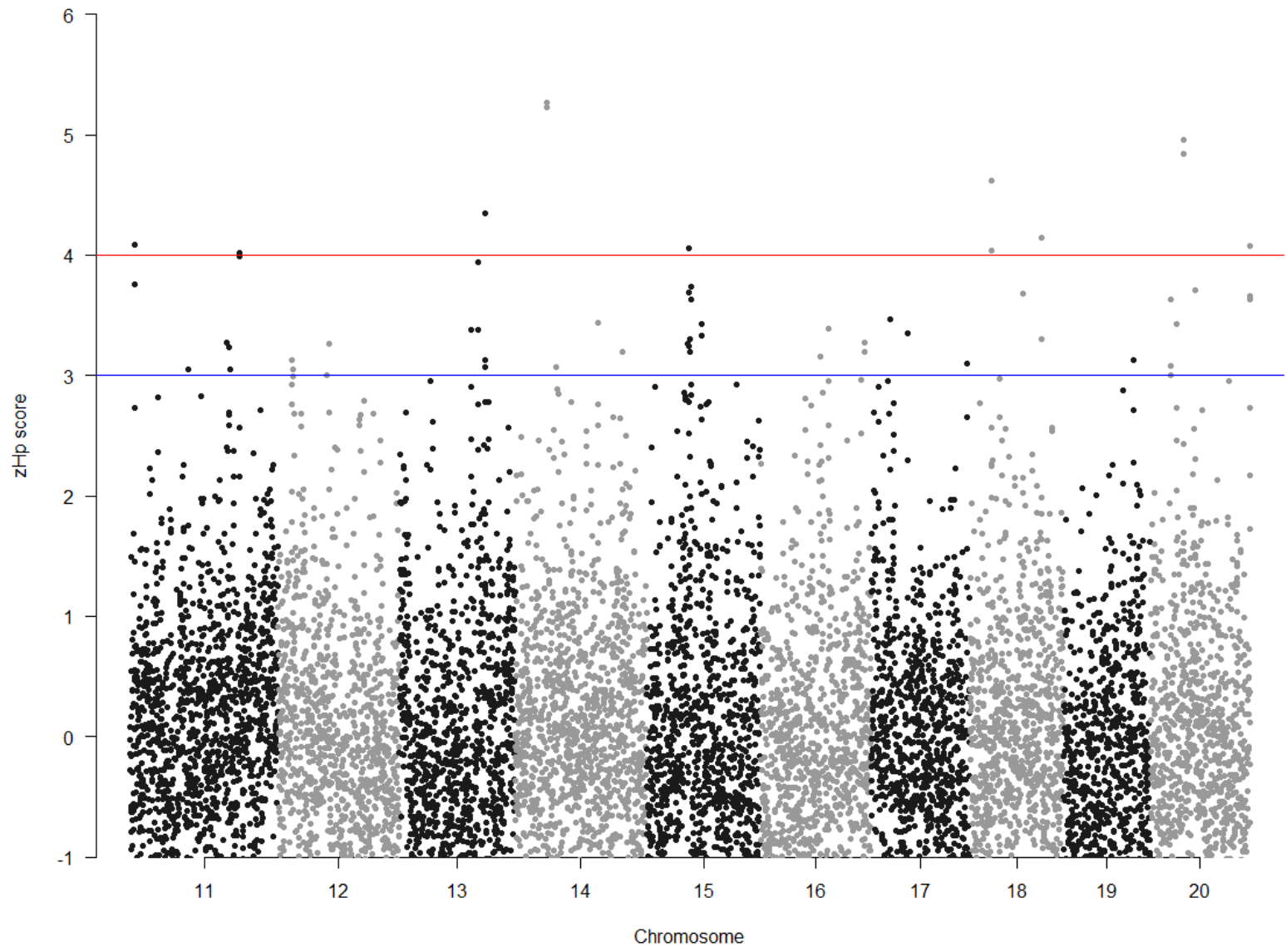




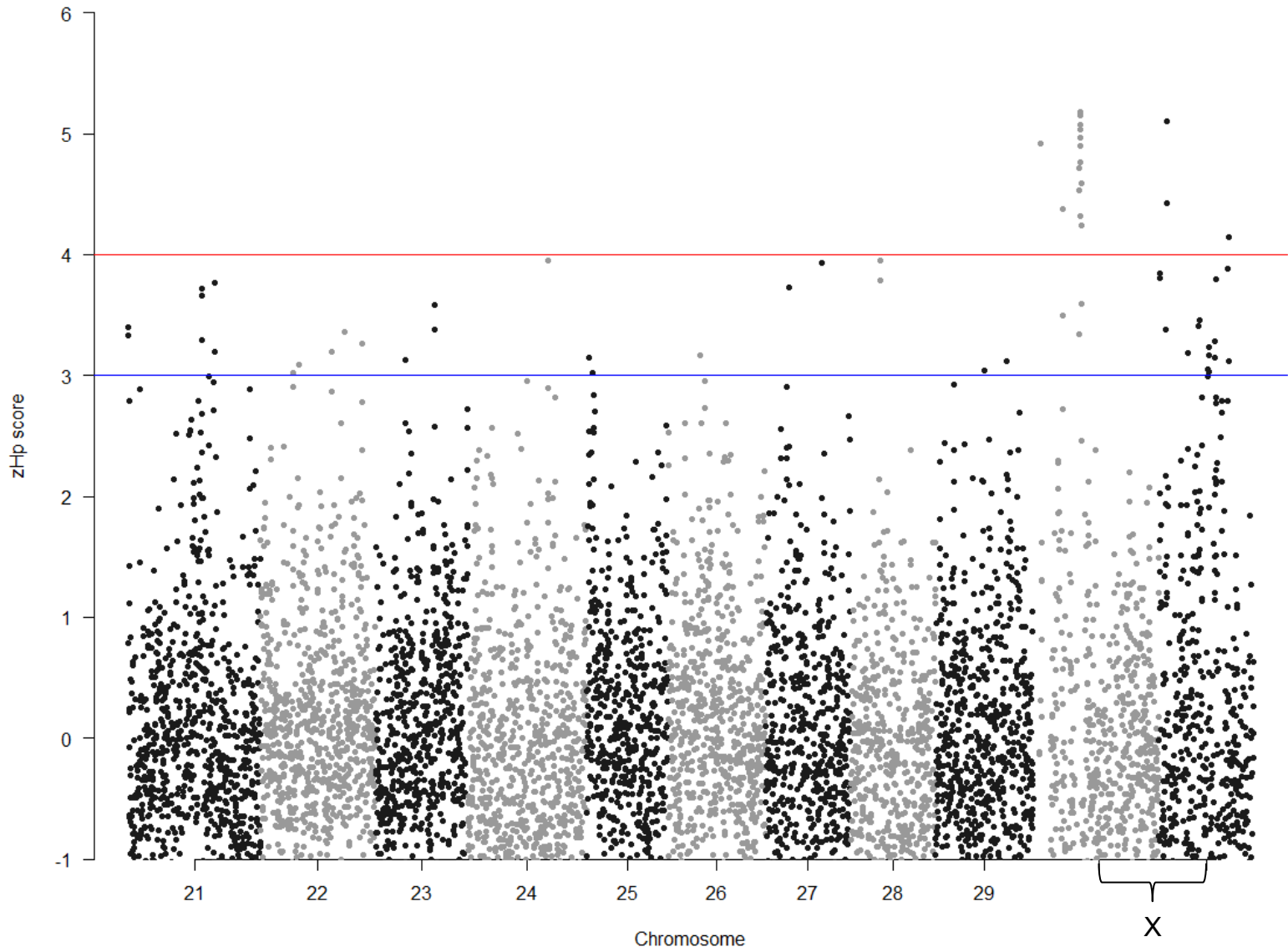
# Saanenziege, 150 kb window, chr. 1-10



# Saanenziege, 150 kb window, chr. 11-20



# Saanenziege, 150 kb window, chr. 21-X



# Zusammenfassung

- **illumina Pool-seq Daten für 20 Ziegenrassen & Bezoar**
- **Technische Artefakte (Sequenzfehler) sind eine grosse Herausforderung**
- **Datenanalyse sehr rechenintensiv**
- **Viele Signale für potentielle Selektionssignaturen**

## Nächste Schritte

- **Überprüfung Pool-seq Daten mittels Sequenzierung von 24 Einzeltieren**
- **Identifizierung von kausalen Varianten**

# illumina NovaSeq 6000 in Bern

ca. CHF 1'000.- pro Genom

