**Additional File 2 for:**

**Signatures of selection and environmental adaptation across the goat genome post domestication.**

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**Figure S1**

Title: MDS plot of the breeds, grouped by production purpose: milk, meat and fiber groups

Description: group colors: milk = green, meat = red, fiber = blue; MDS and box plots of the first two components pre-filtering (upper) and MDS plots after filtering.

C:\Users\fbert\Downloads\MDS_HighResolution_Picture.tif

**Figure S2**

Title: Manhattan plot of the FLK results for the sub-continental group after filtering steps.

Description: Sub-geographical group names are reported on top of each plot. Chromosomes are alternates red and black.

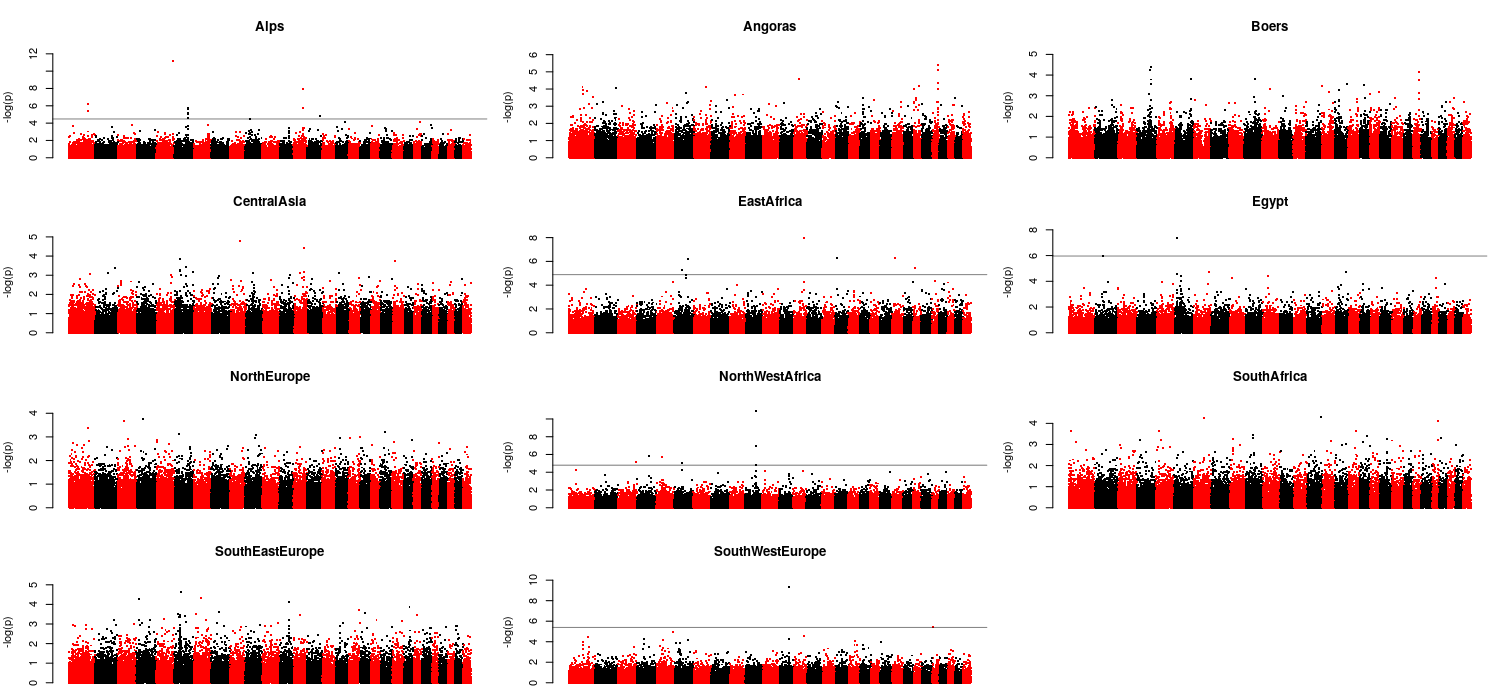


Figure S3

Title: Manhattan plot of the hapFLK results for the sub-continental group after filtering steps

Description: Sub-geographical group names are reported on top of each plot. Chromosomes are alternates red and black.

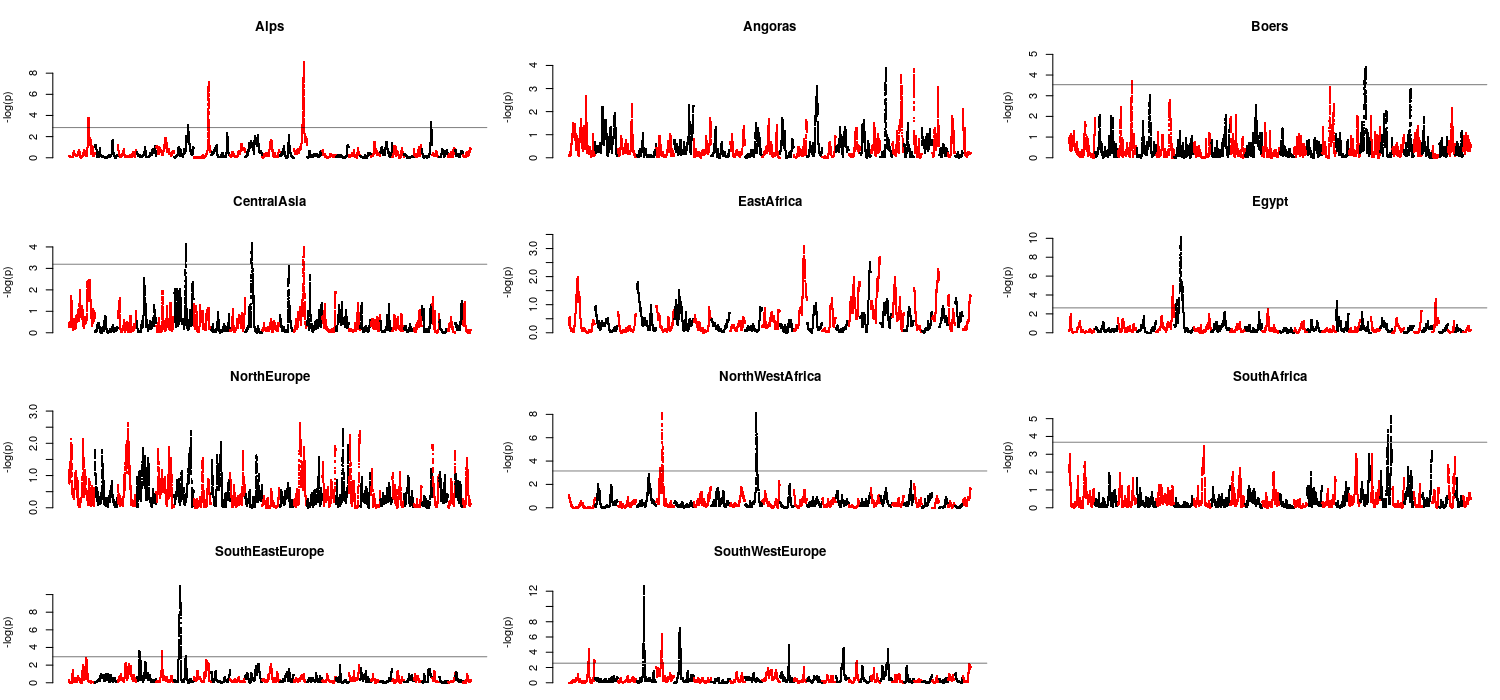


Figure S4

Title: Genomic distribution of FLK and hapFLK signals across population groups

Description: For each chromosome and each sub-continental group, the chromosomal position detected with at least one of the two approaches are detected.

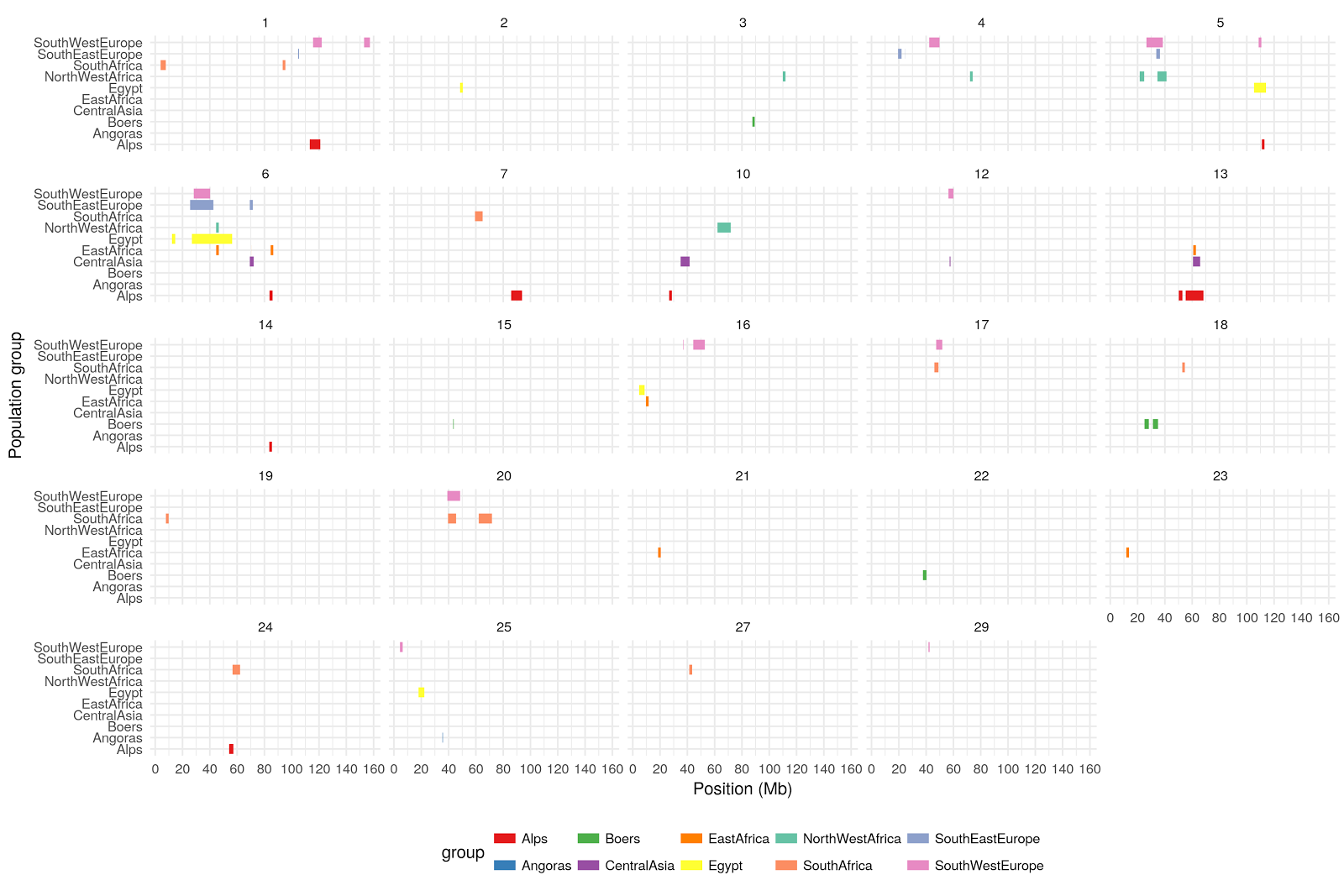


Figure S5

Title: Signatures of selection on chromosome 5 for the North western Africa, South eastern Africa and South western Africa groups.

Description: North western Africa (NWA): red; South eastern Europe (SEE): green; South western Europe (SWE): blue. The table (bottom-right) reported the genes within the region in which a signature was detected.

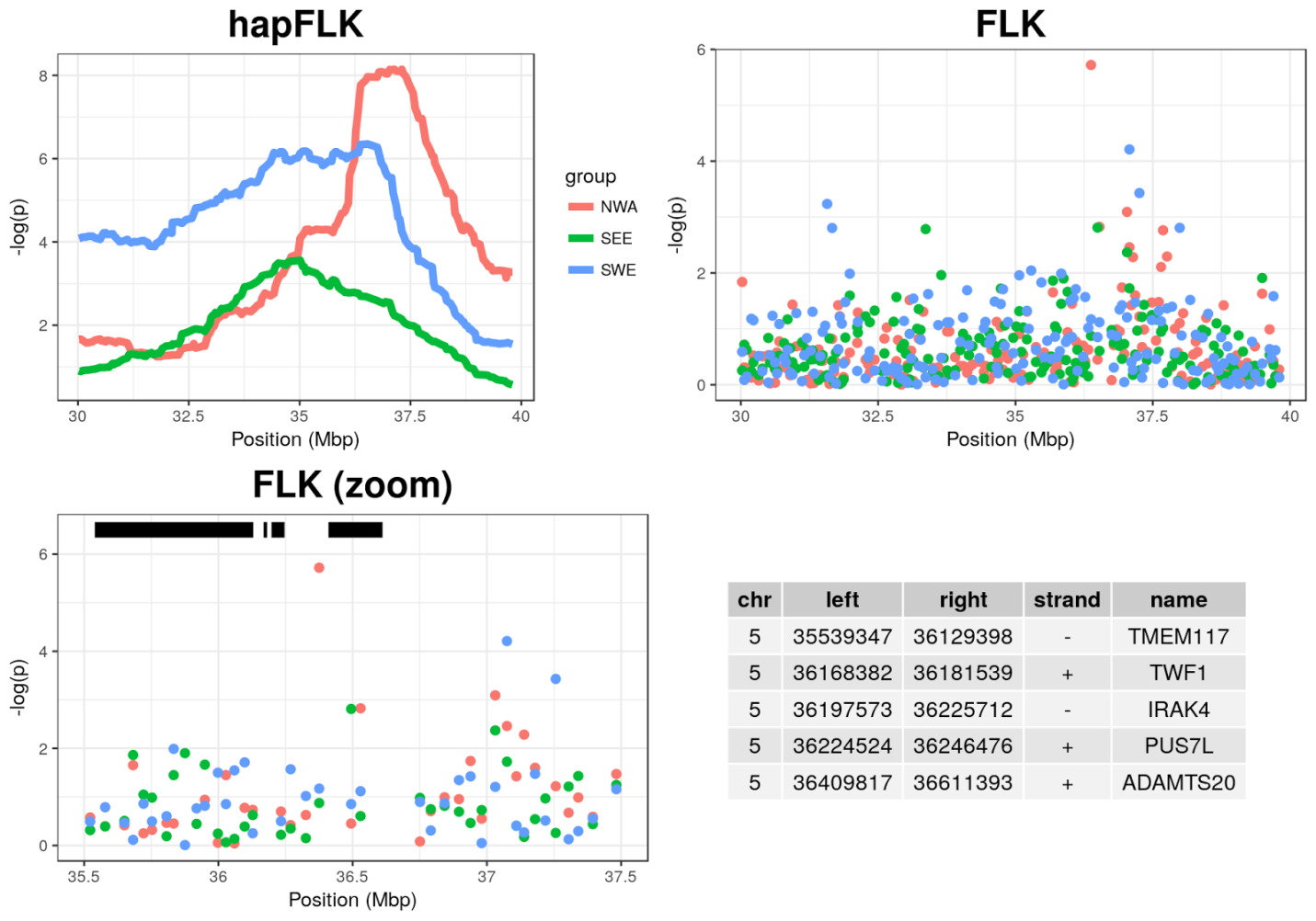


Figure S6

Title: Signatures of selection on chromosome 6 for the Central Asia, East Africa and South east Europe groups.

Description: Central Asia (CA): red; East Africa (EA): green; South east Europe (SEE): blue. The table (upper-right) reported the genes within the region in which a signature was detected.

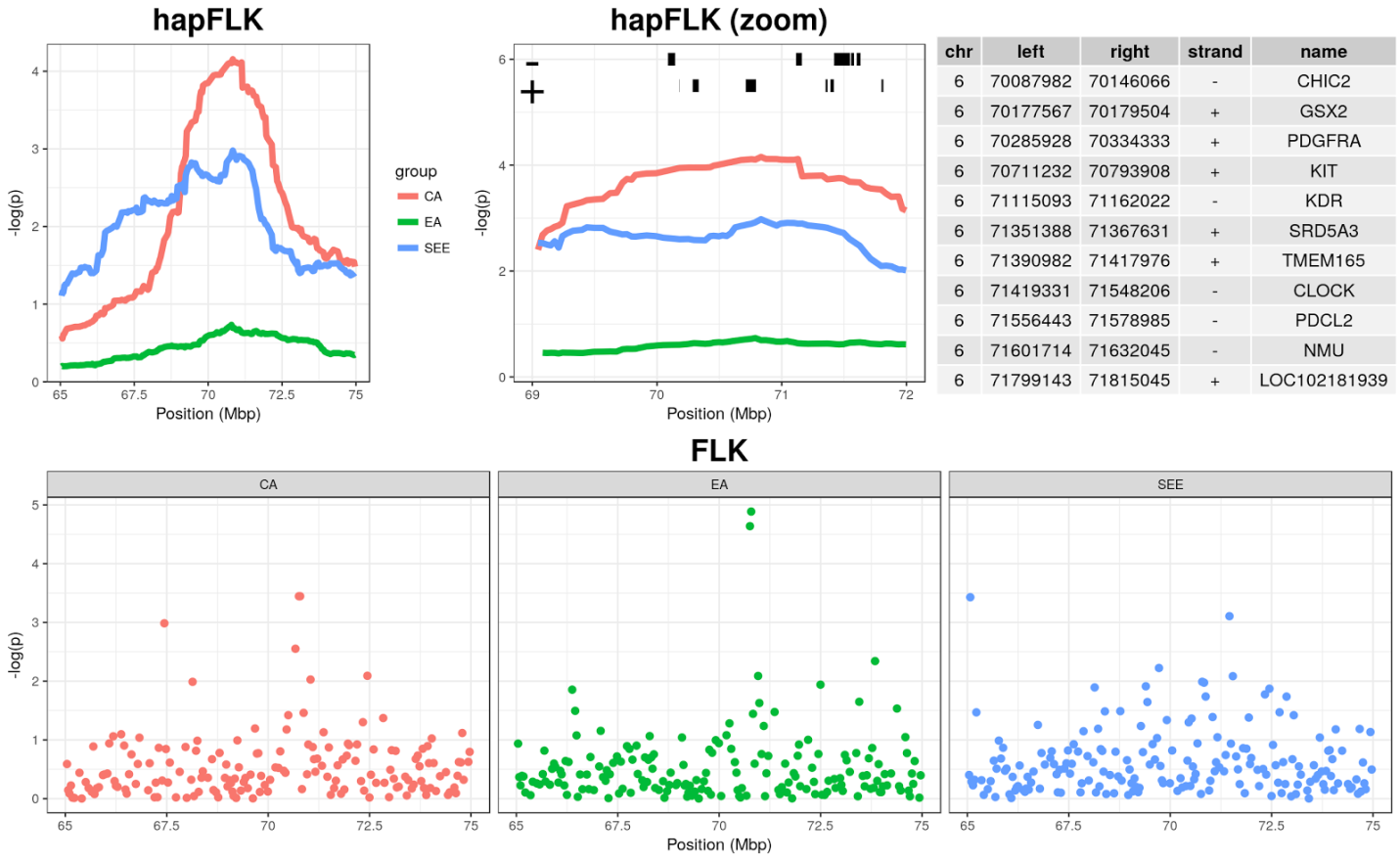


Figure S7

Title: Signatures of selection on chromosome 13 for the Alpines and Central Asia groups.

Description: Alpines (Alps): red; Central Asia (CA): blue. The table (right) reported the genes within the region in which a signature was detected.

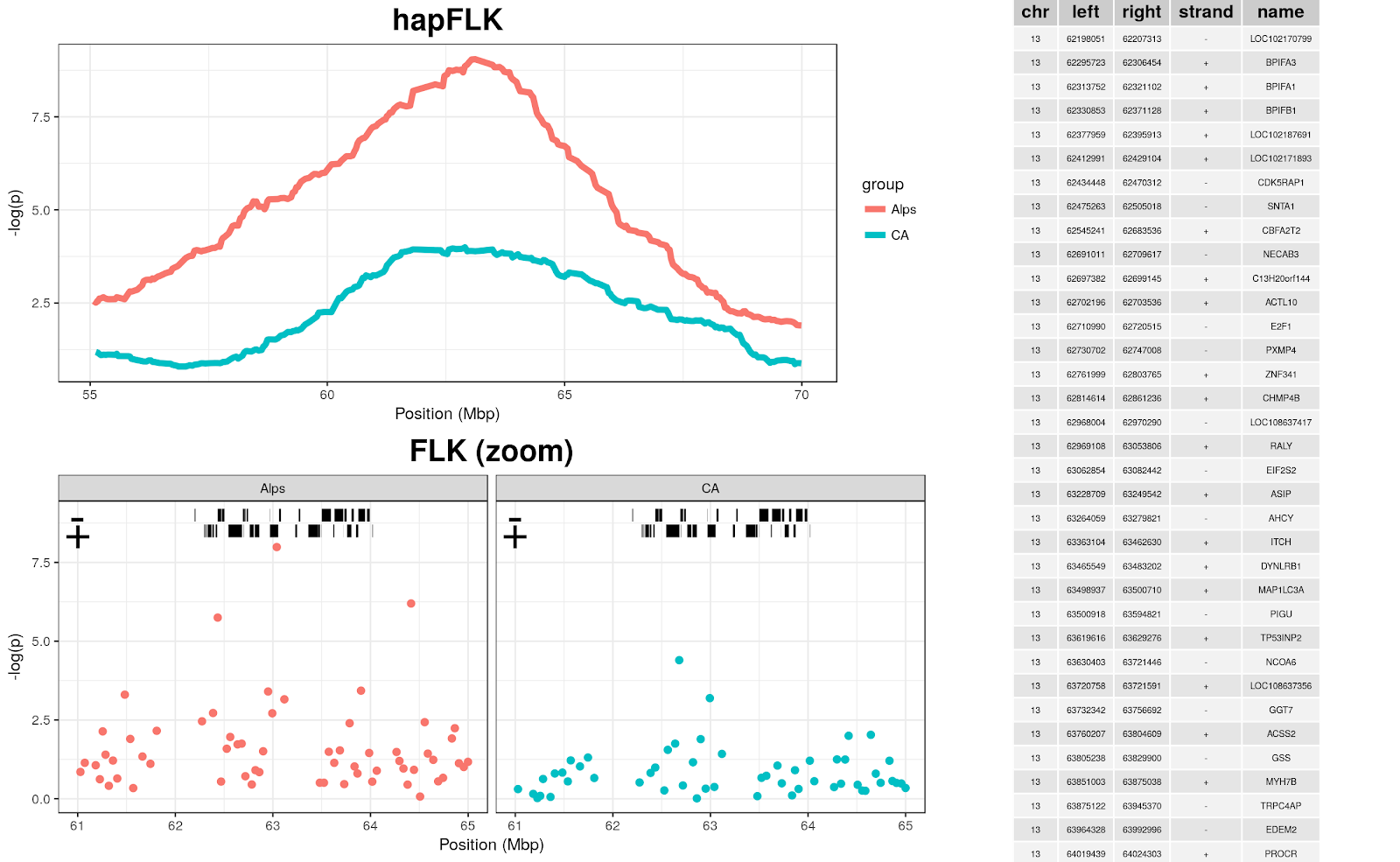


Figure S8

Title: Signatures of selection on chromosome 1 for the Alpines and South western Europe

Description: Alpines (Alps); red; South western Europe (SWE): blue. The table (bottom-right) reported the genes within the region in which a signature was detected.

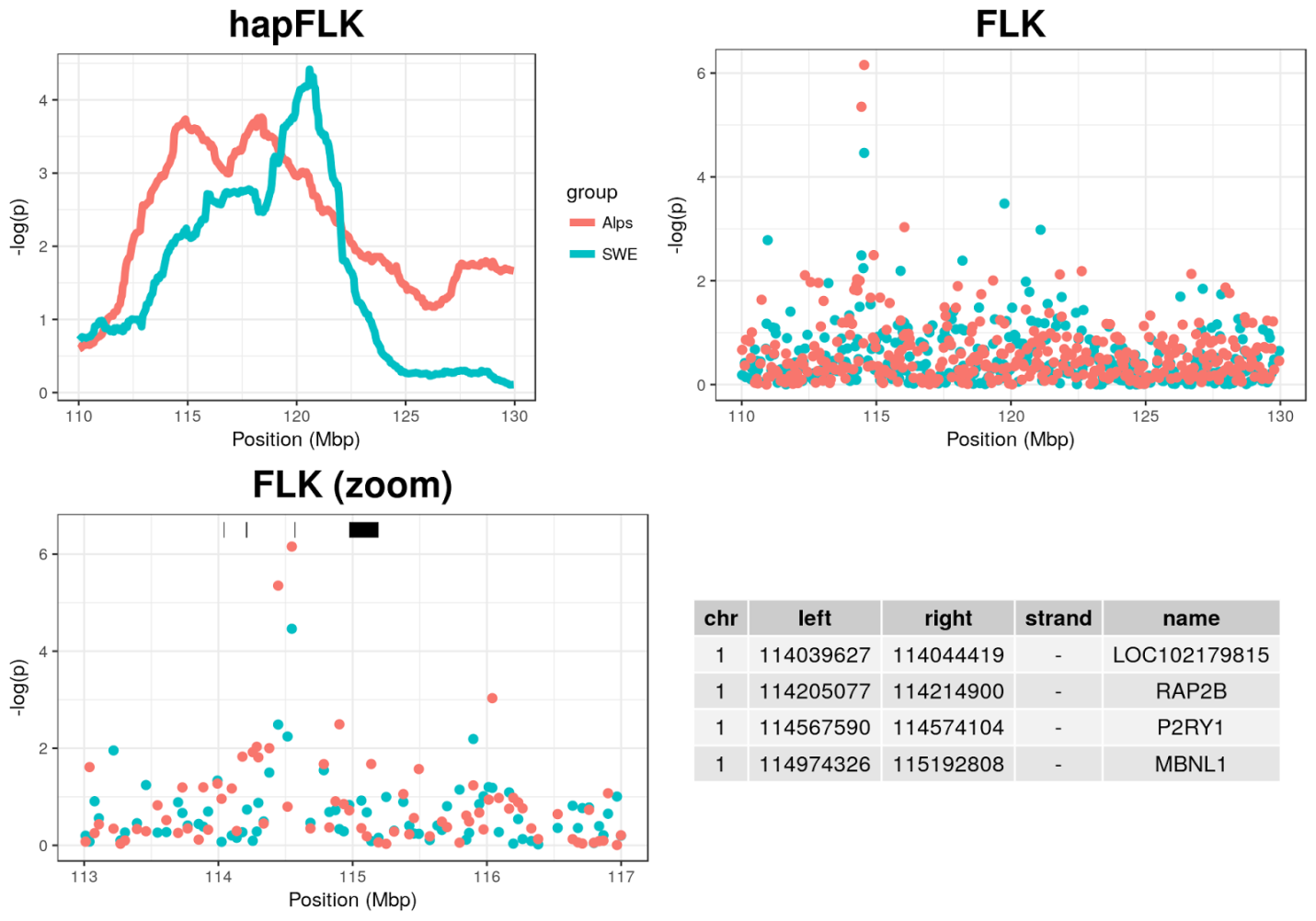


Figure S9

Title: FLK signals on CHI6 around the casein gene cluster. The cluster of unannotated genes between *YTHDC1* and *SULT1B1* consists of genes coding for glucuronosyltransferase enzymes.

Description: Alps; red; East Arica (EA): blue. The table (right) reported the genes within the casein cluster region.

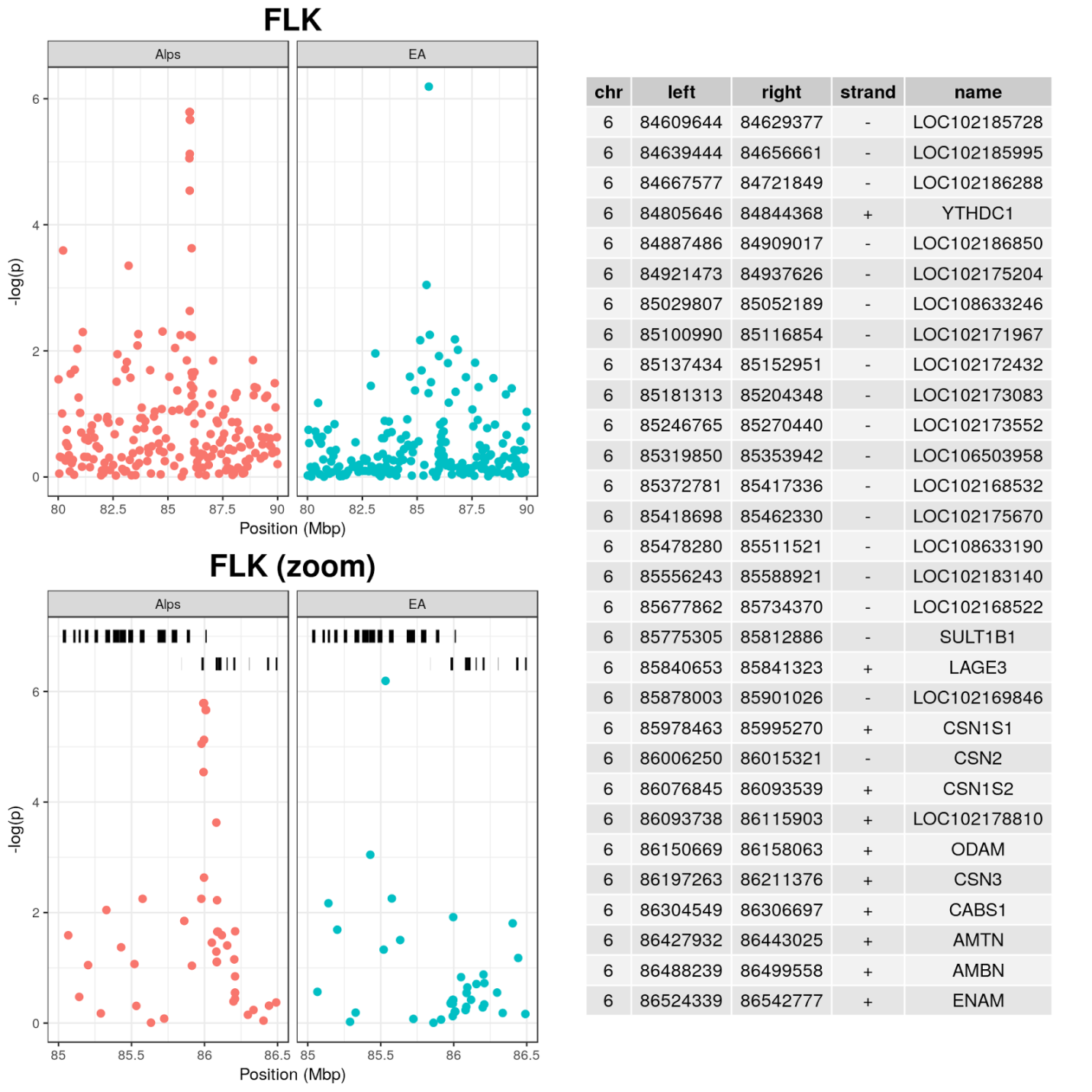


Figure S9. Selection signature, on CHI12 in the CA and SWE groups.

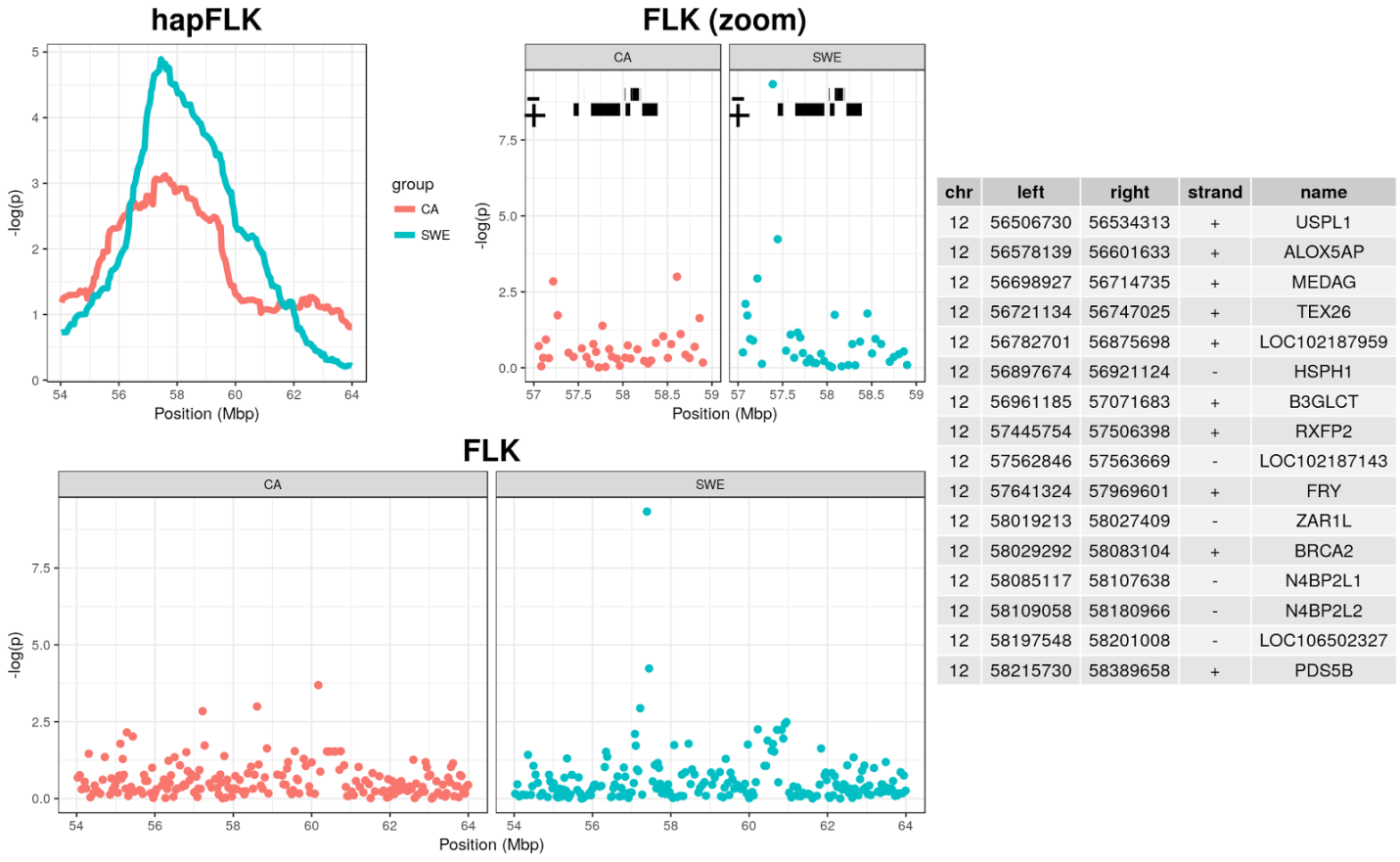


Figure S10

Title: Signatures of selection on chromosome 6 for the Egypt, South eastern Europe and South western Europe groups.

Description: Egypt (Egypt): red; South eastern Europe (SEE): green; South western Europe (SWE): blue. The table (bottom-right) reported the genes within the region in which a signature was detected.

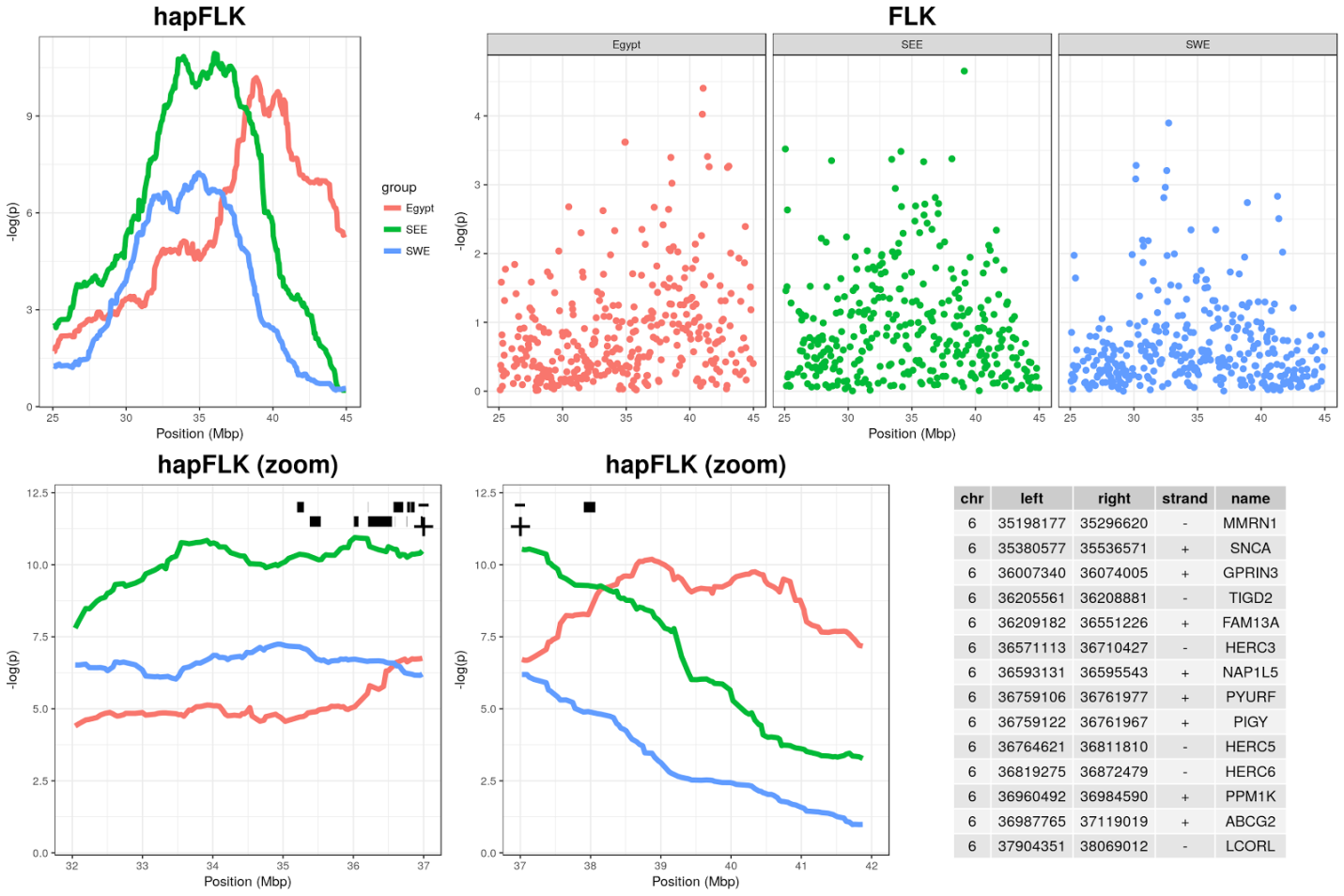


Figure S11

Title: Signatures of selection on chromosome 12 for the Central Asia and South western Europe

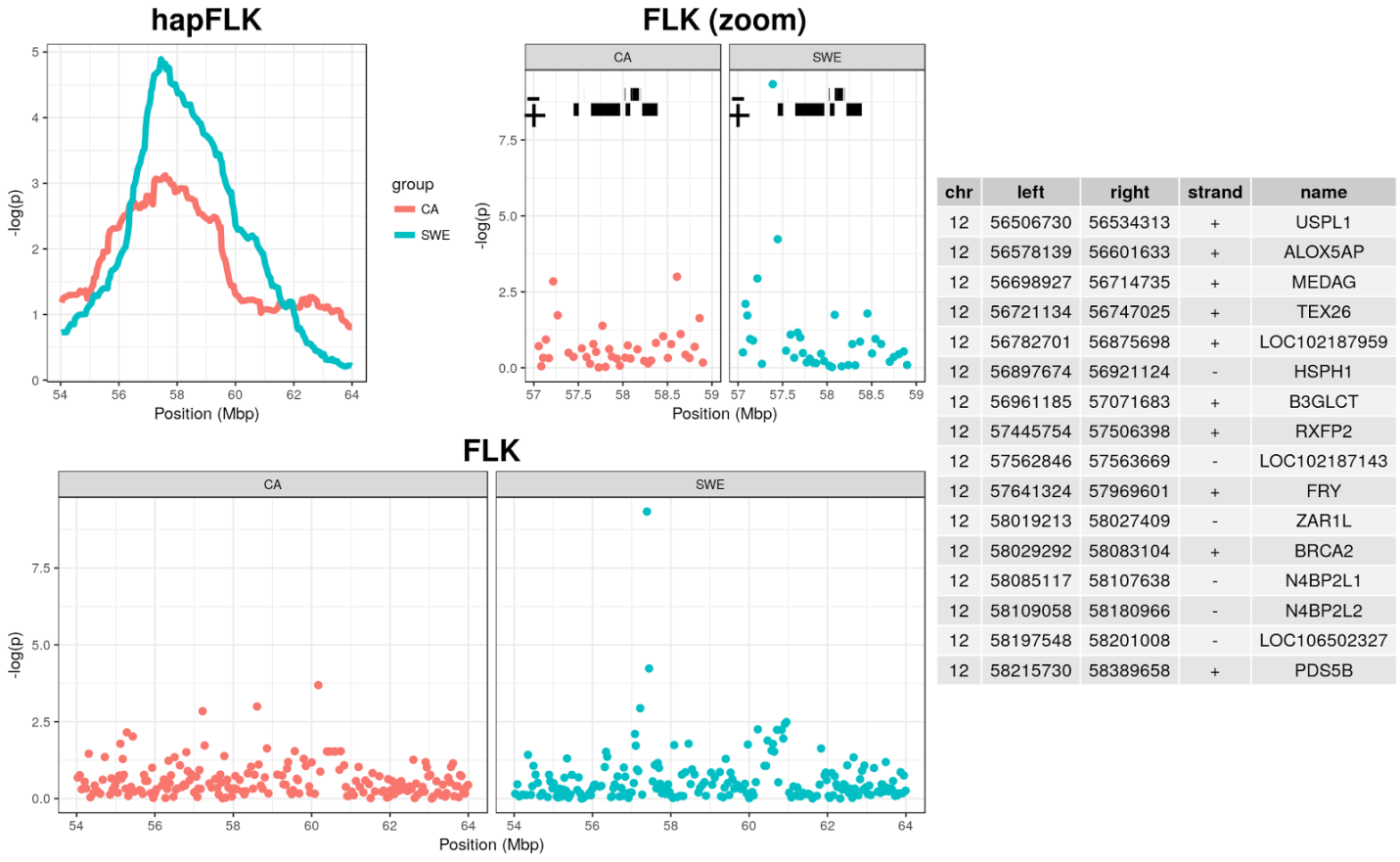
Description: Central Asia (CA); red; South western Europe (SWE): blue. The table (right) reported the genes within the region in which a signature was detected.

Figure S12

Title: ROH, *F*ST and XP-EHH results for the group of “meat-producing” goat breeds

Description: Analysis types showed with different plot colors, within the most external squared-based circle, where each color represent a chromosome (chromosome number outside the squares): green (external) = ROH; blue (middle) = Fst; violet (internal): XP-EHH. For the three analyses, the regions above the threshold are marked in red.

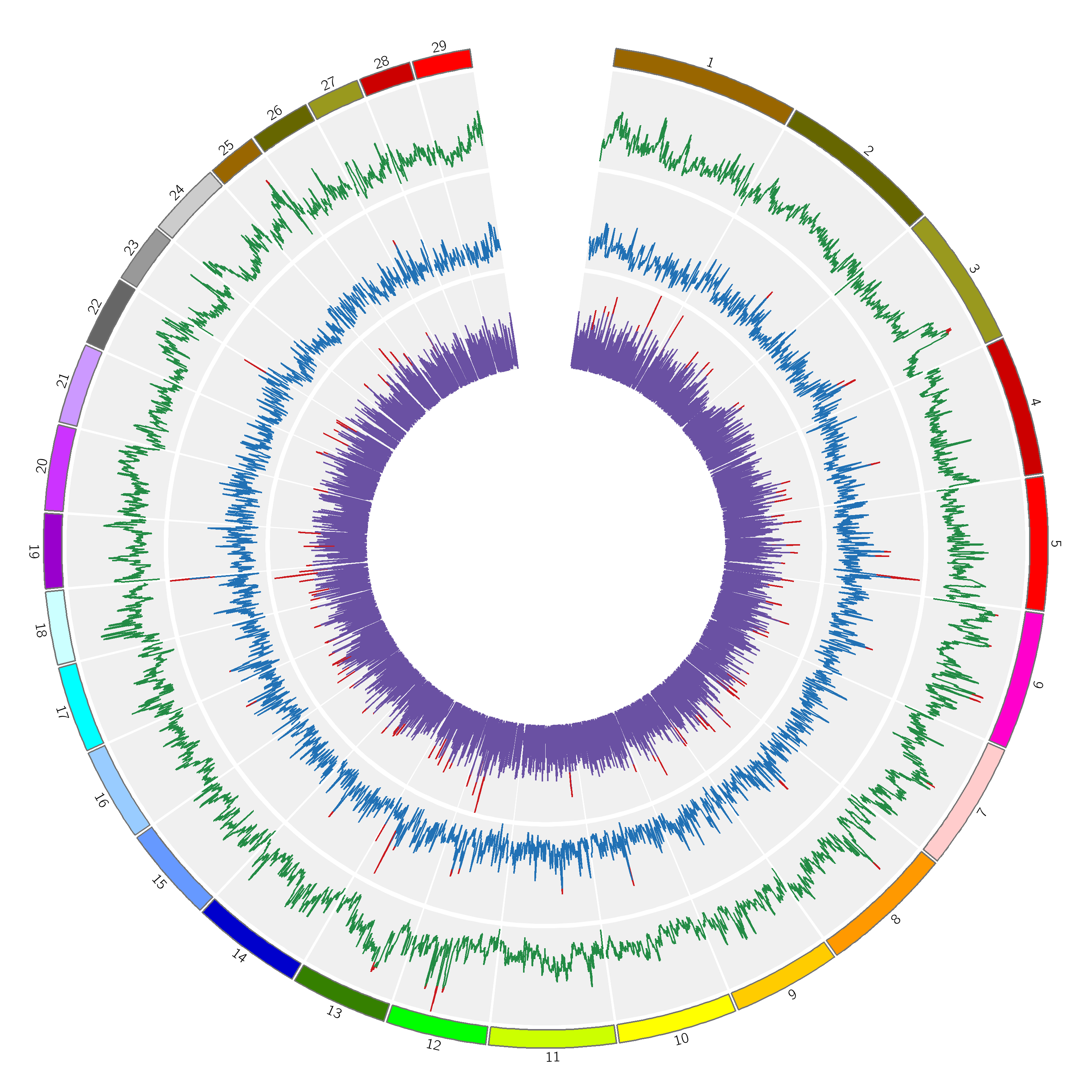


Figure S13

Title: ROH, *F*ST and XP-EHH results for the group of “milk-producing” goat breeds

Description: Analysis types showed with different plot colors, within the most external squared-based circle, where each color represent a chromosome (chromosome number outside the squares): green (external) = ROH; blue (middle) = Fst; violet (internal): XP-EHH. For the three analyses, the regions above the threshold are marked in red.

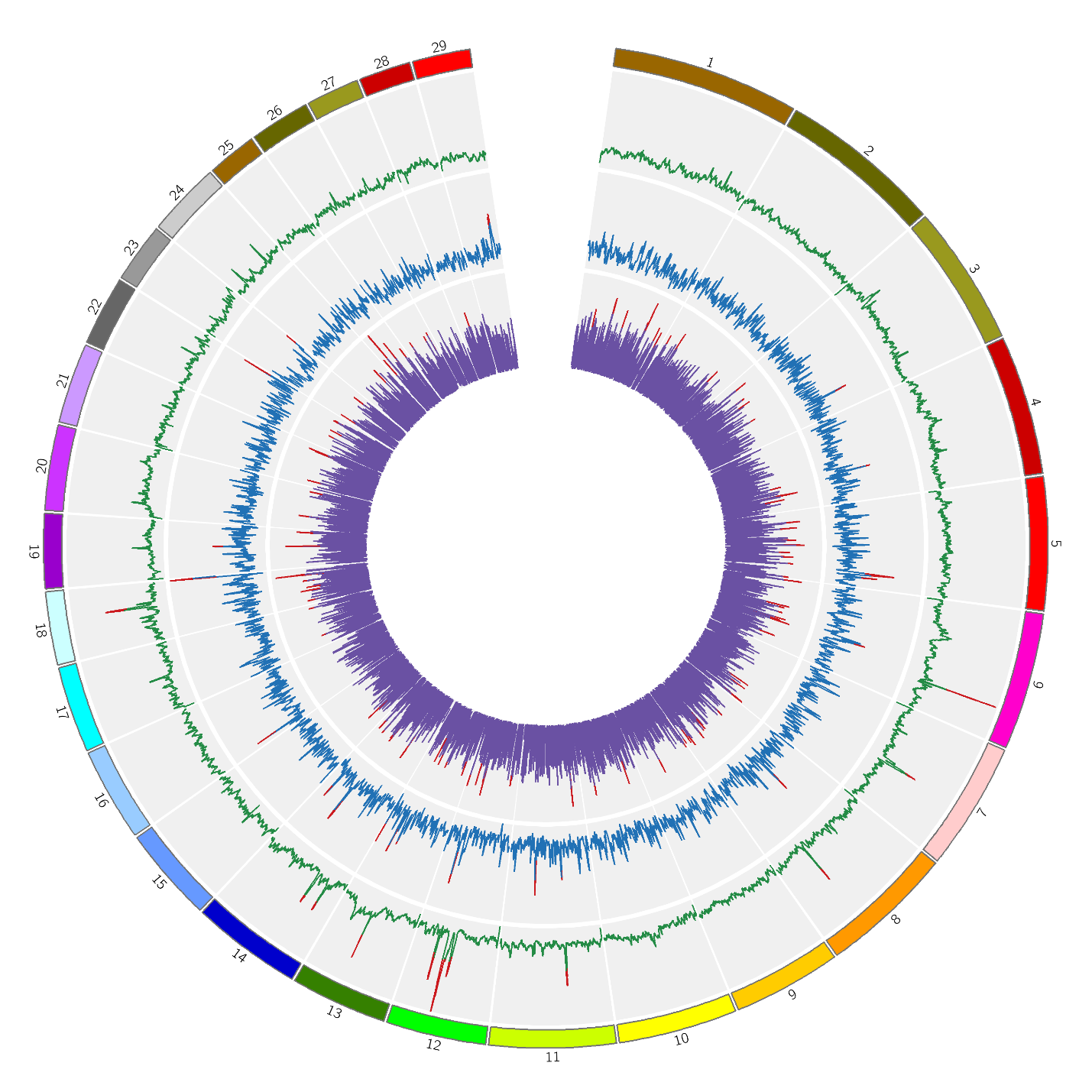


Figure S14

Title: CDA for the region on chromosome 25 detected for the group of “meat-producing” goat breeds.

Description: (a): LONG and (b) SHORT: (b). Left: CDA plot. Right: Correlation value of the SNPs used for the analyses for CAN1 and CAN2.

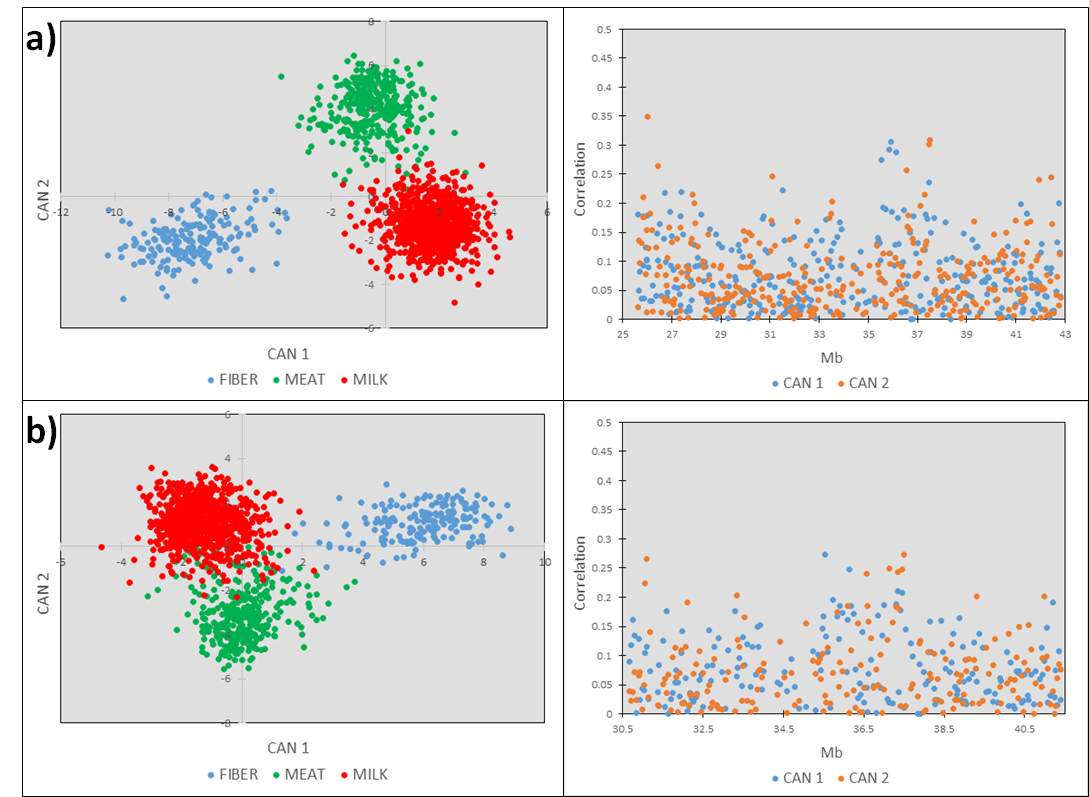


Figure S15

Title: CDA for the region on chromosome 25 detected for the group of “meat-producing” goat breeds.

Description: (a): LONG and (b) SHORT: (b). Left: CDA plot. Right: Correlation value of the SNPs used for the analyses for CAN1 and CAN2.

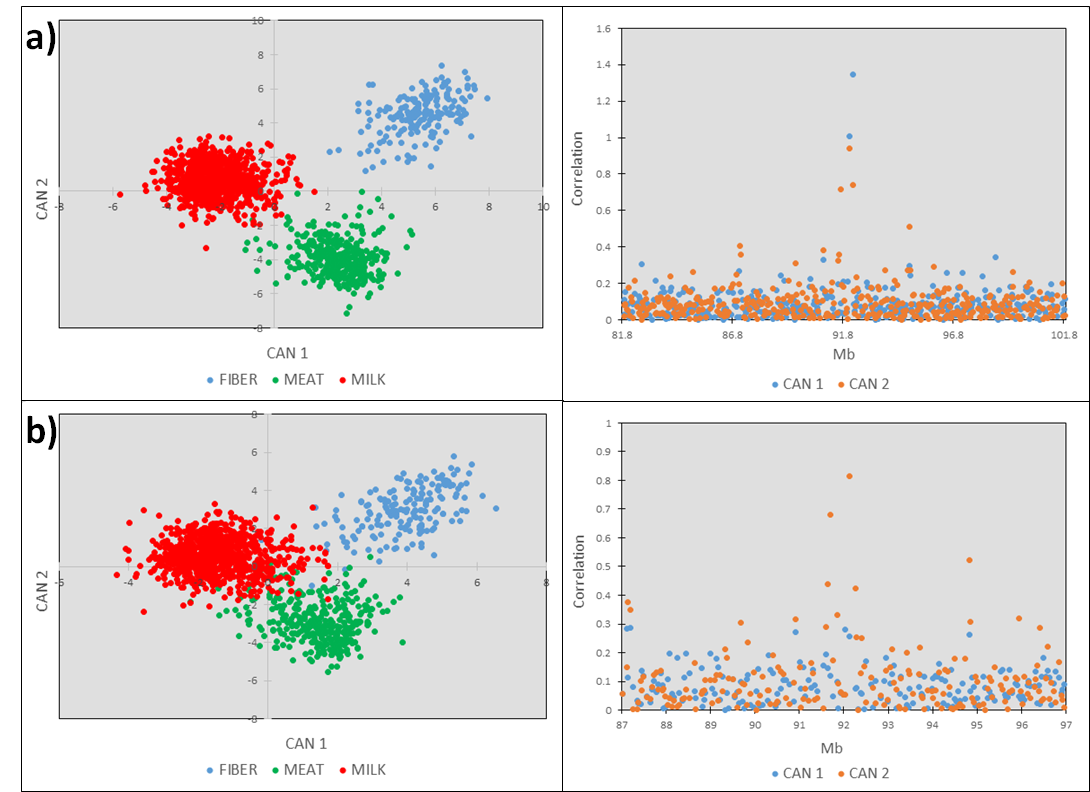


Figure S16

Title: CDA for the region on chromosome 25 detected for the group of “milk-producing” goat breeds.

Description: (a): LONG and (b) SHORT: (b). Left: CDA plot. Right: Correlation value of the SNPs used for the analyses for CAN1 and CAN2.



Figure S17

Title: MDS plot of breeds considered for the panel of coat colors

Description: Breed codes and subdivision based on the coat color pattern are indicated in the right part of the plot.

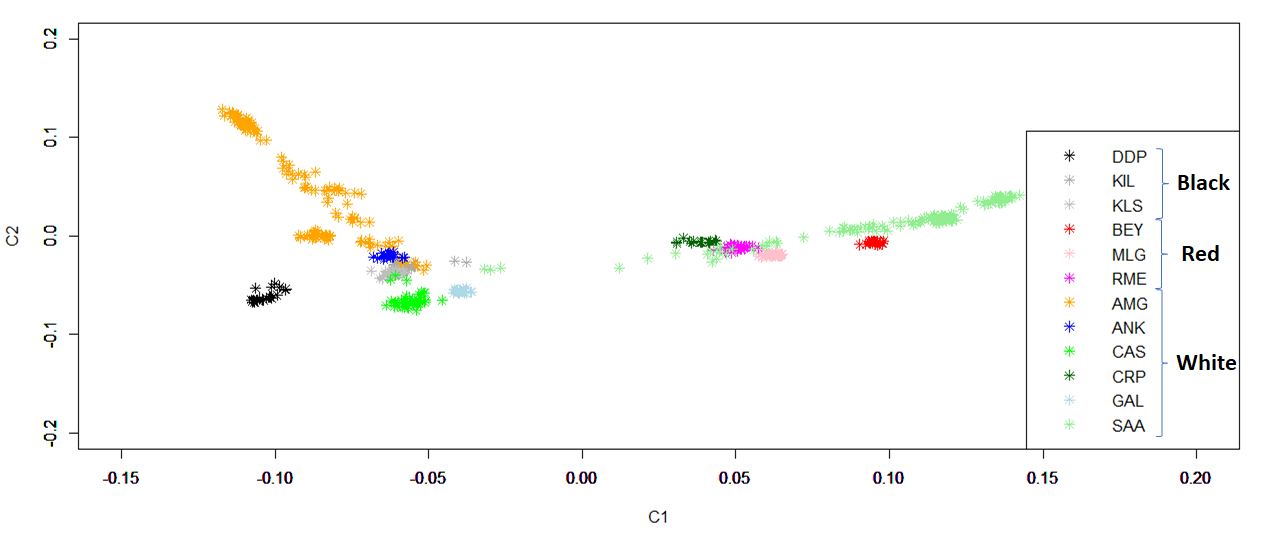


Figure S18

Title: CDA for the region on chromosome 18 near the *MC1R* gene detected for the group of coat color breeds.

Description: (a): LONG and (b) SHORT: (b). Left: CDA plot. Right: Correlation value of the SNPs used for the analyses for CAN1 and CAN2.

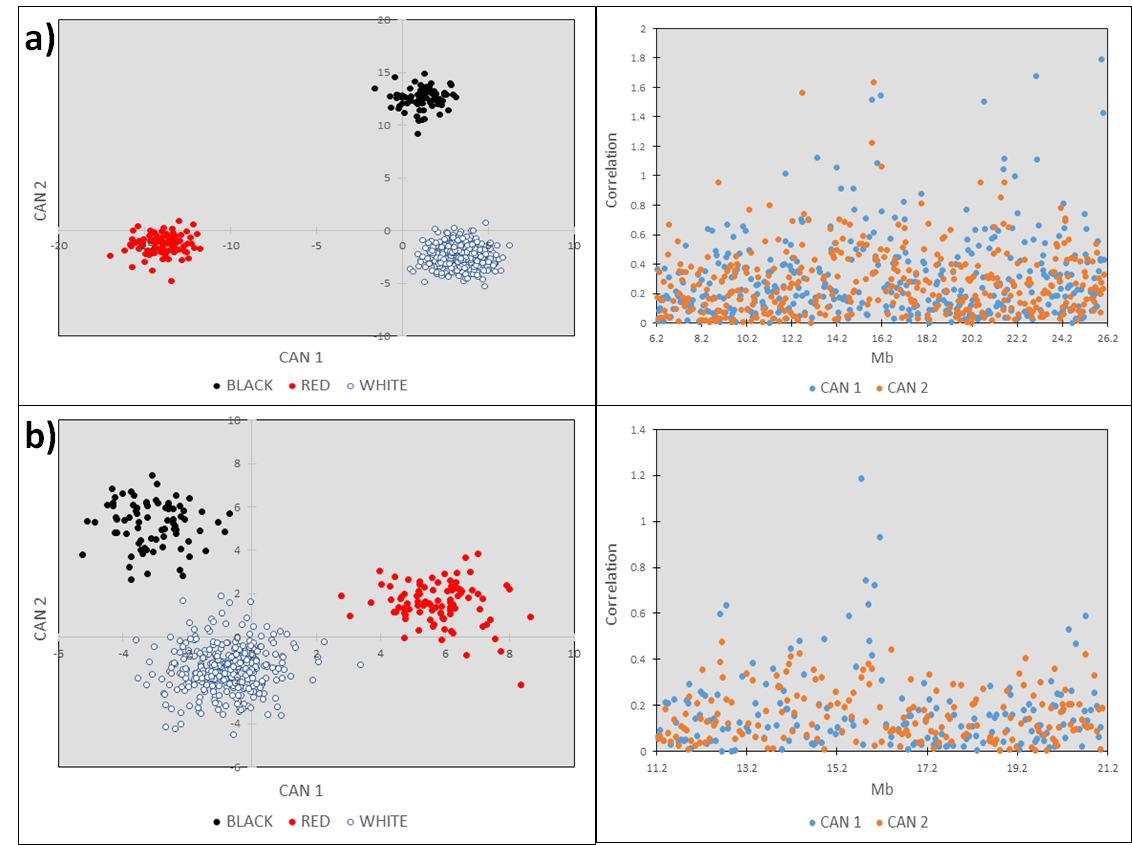


Figure S19

Title: CDA for the region on chromosome 13 near the *ASIP* gene detected for the group of coat color breeds.

Description: (a): LONG and (b) SHORT: (b). Left: CDA plot. Right: Correlation value of the SNPs used for the analyses for CAN1 and CAN2.

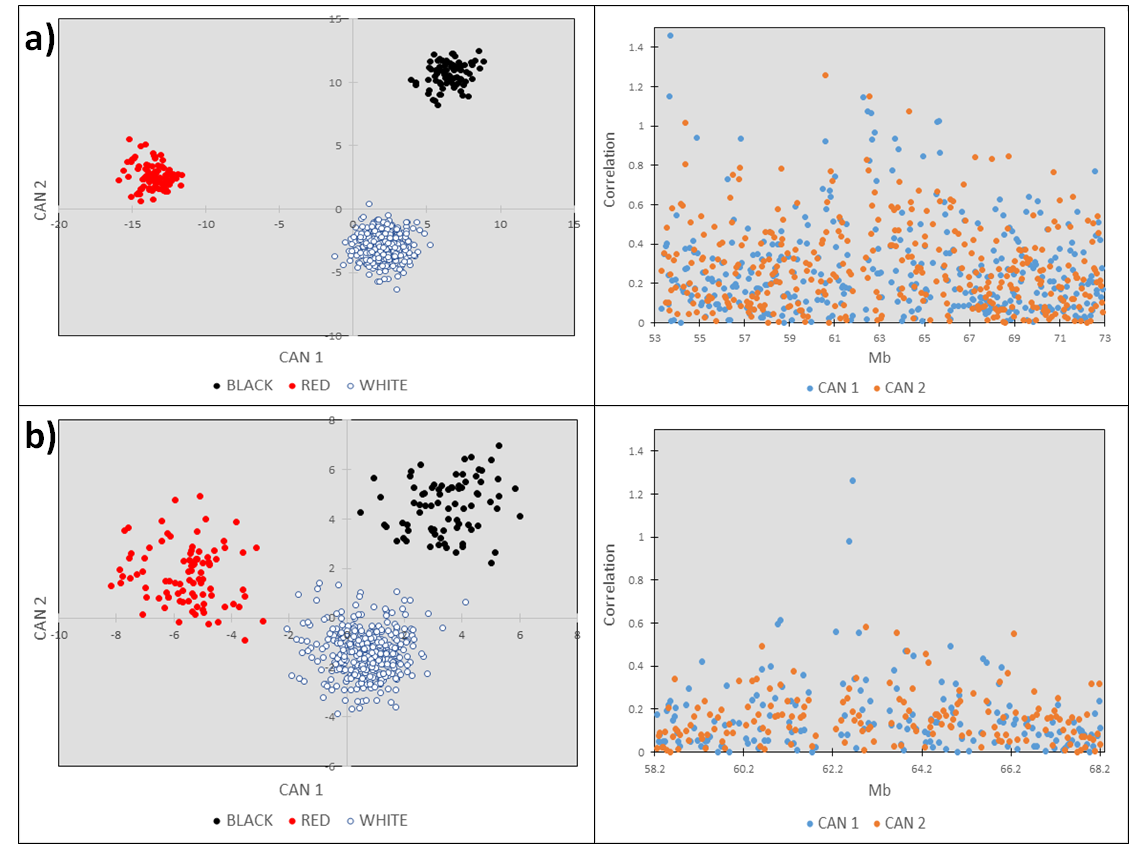


Figure S20

Title: CDA for the region on chromosome 5 near the *ADAMTS20* gene detected for the group of coat color breeds.

Description: (a): LONG and (b) SHORT: (b). Left: CDA plot. Right: Correlation value of the SNPs used for the analyses for CAN1 and CAN2.

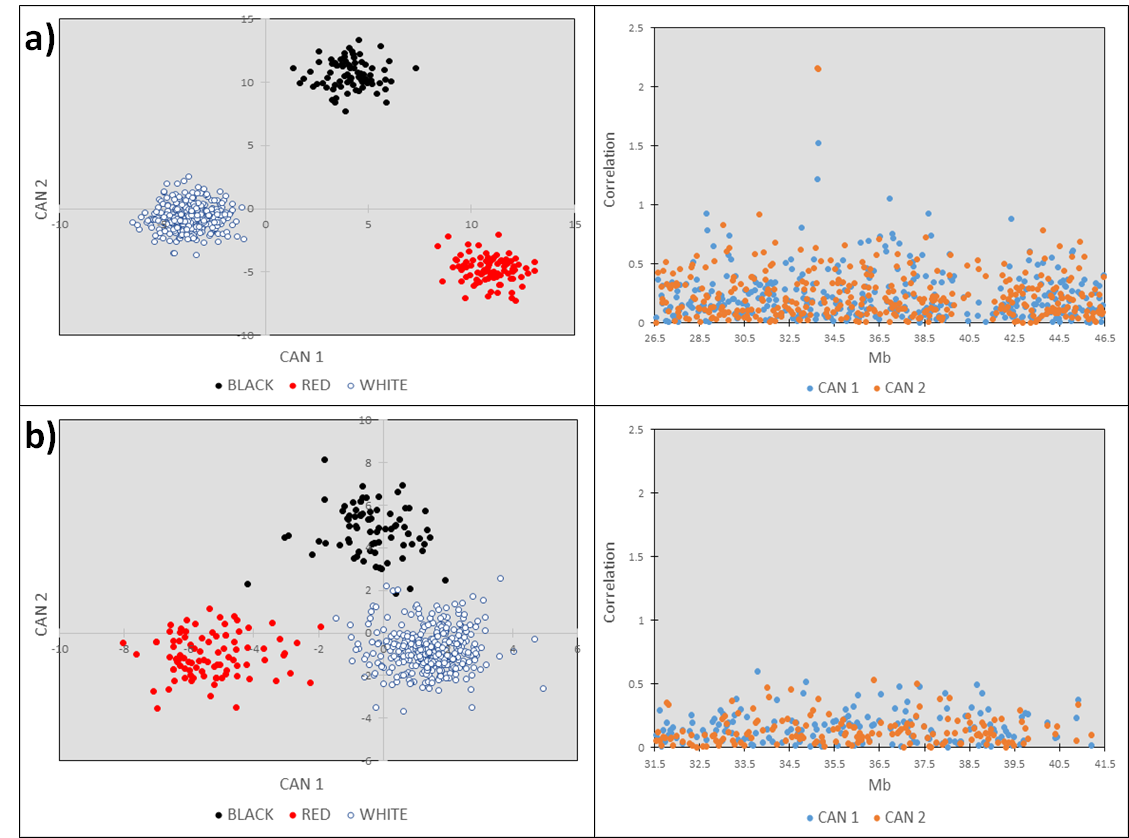


Figure S21

Title: MDS plot of the filtered dataset considering components 1 and 2. Animals are colored based on the Köppen group: Tropical (green), Dry (red), Temperate (orange), Continental (blue)

Description: Animals are color-coded based on the Köppen classification of groups: Tropical (green), Dry (red), Temperate (orange), Continental (blue).

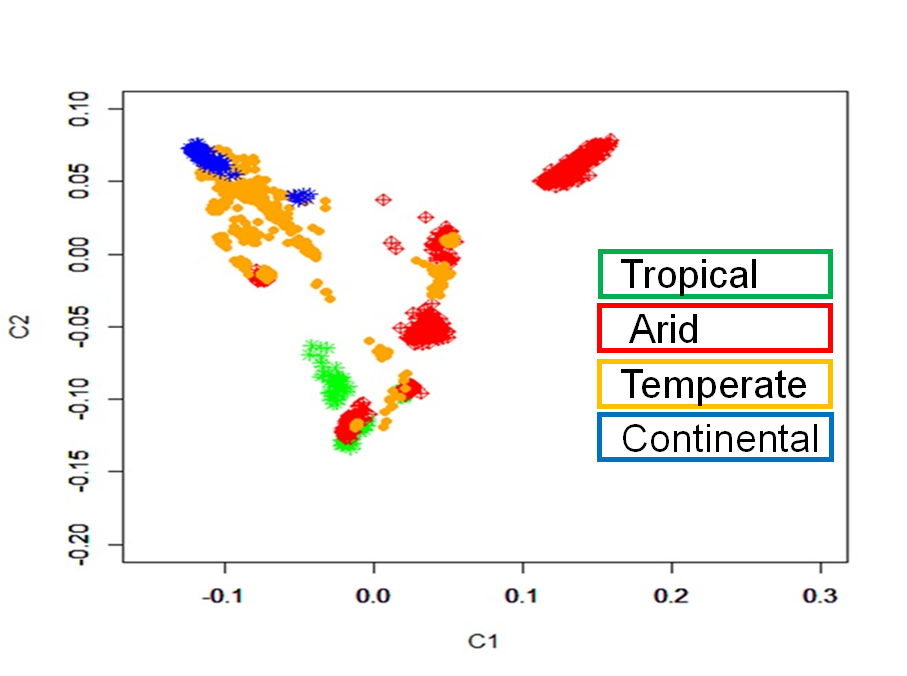


Figure S22

Title: *F*ST plot of the comparison of the Dry group vs. the other groups.

Description: The threshold line in red represents the 0.995 of the percentile distribution (*F*ST = 0.398).

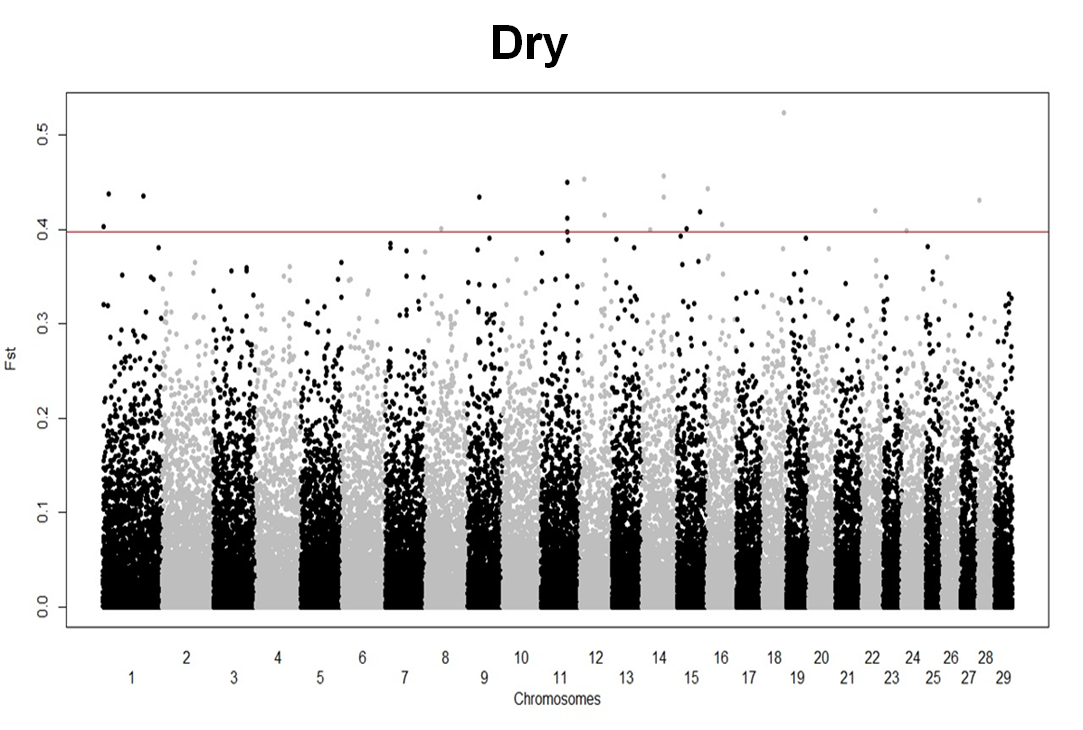


Figure S23

Title: *F*ST plot of the comparison of the Temperate group vs. the other groups.

Description: The threshold line in red represents the 0.995 of the percentile distribution (*F*ST = 0.320).

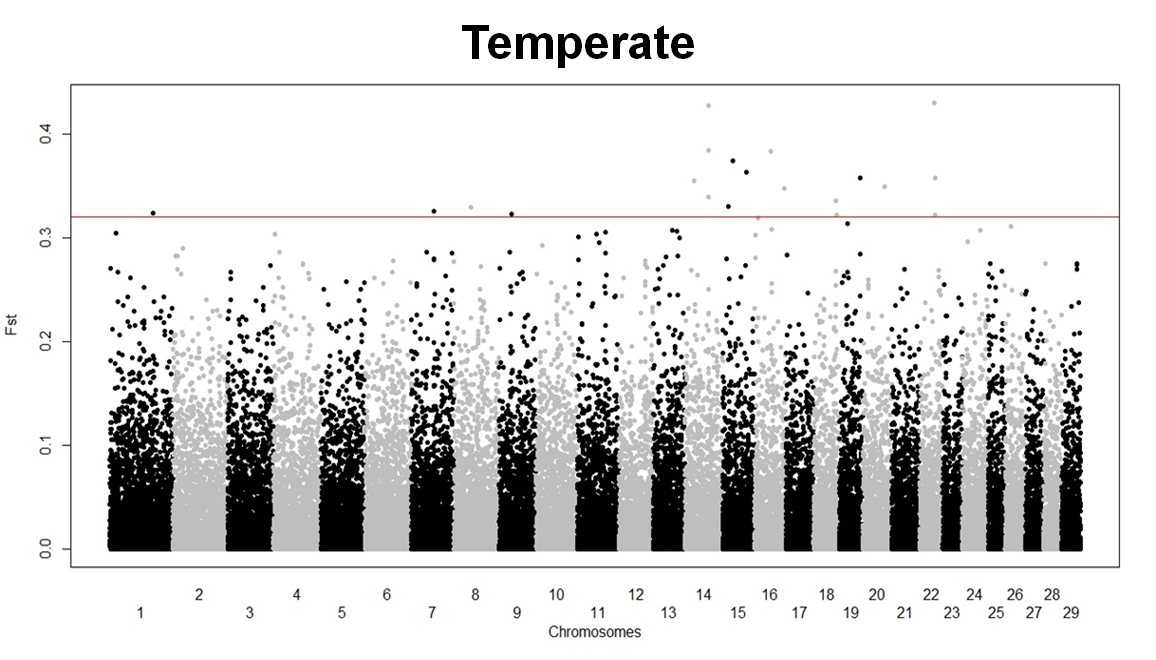


Figure S24

Title: *F*ST plot of the comparison of the Continental group vs. the other groups.

Description: The threshold line in red represents the 0.995 of the percentile distribution (*F*ST = 0.507).

