Climate Factors Drive the Local Adaptation of Old World Cattle

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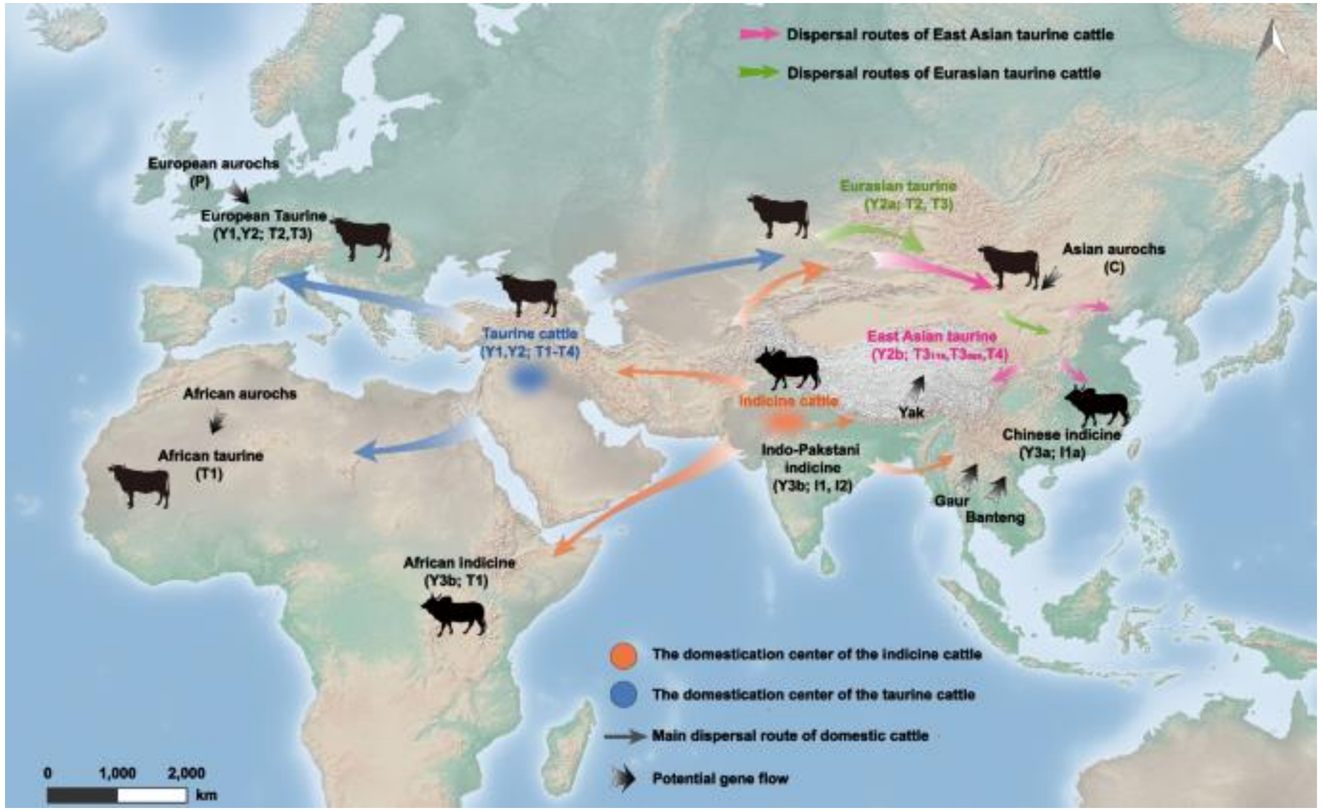
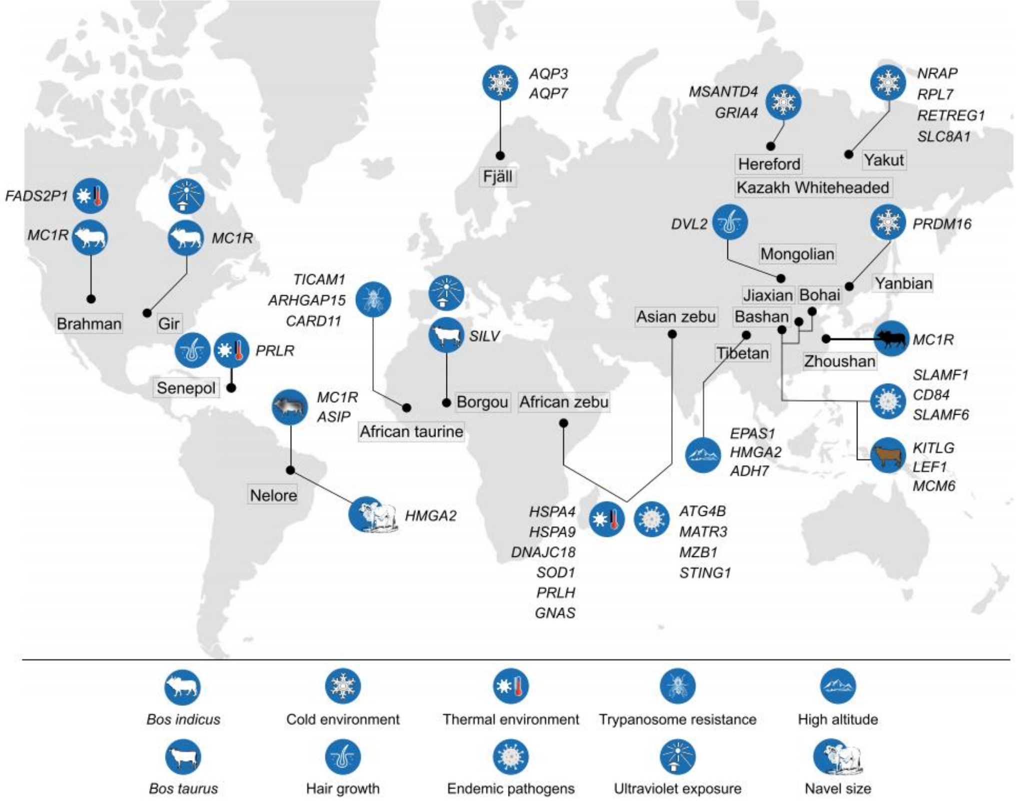
Background



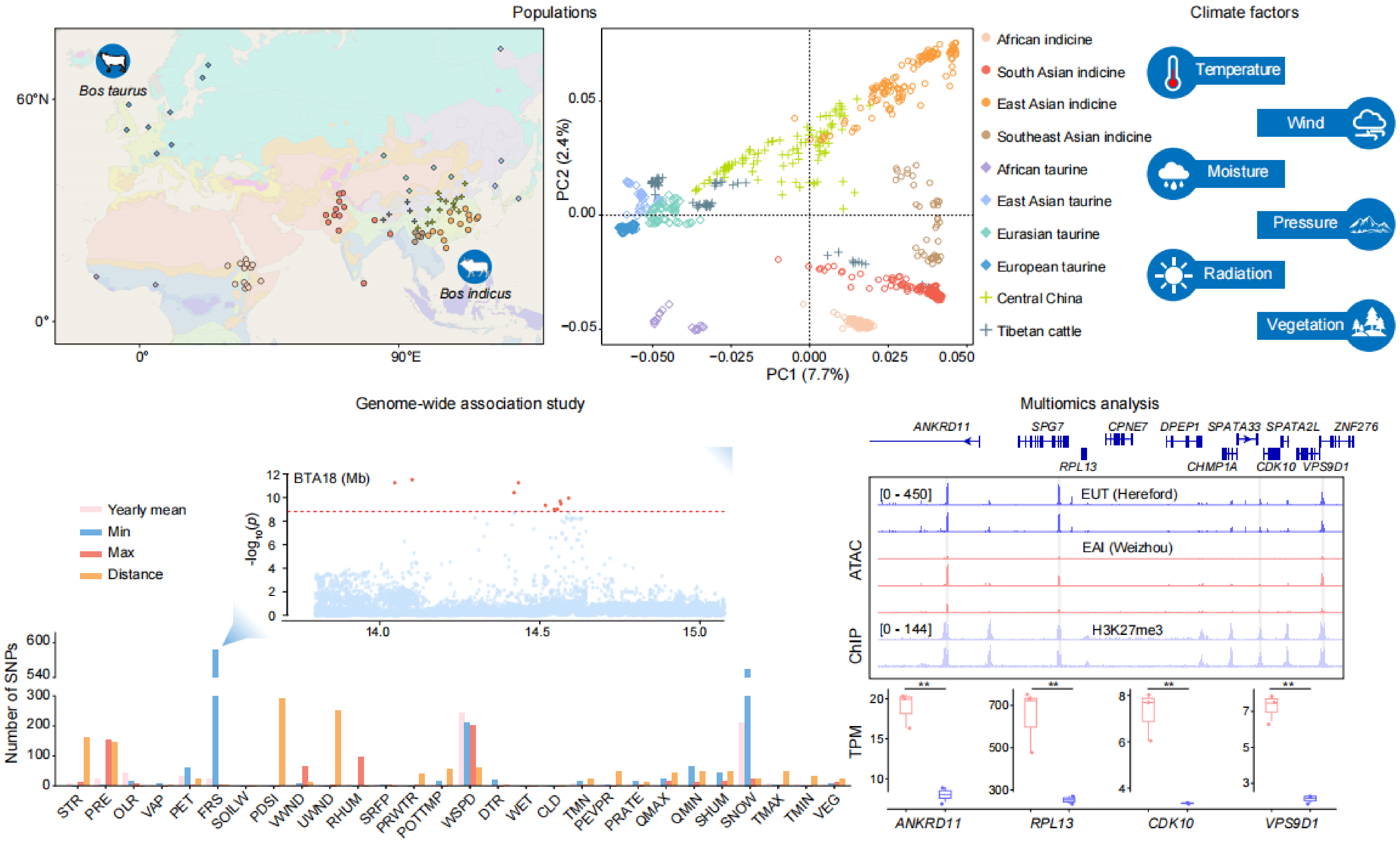
(*Xia et al.* 2023)



(*Xia et al.* 2023)

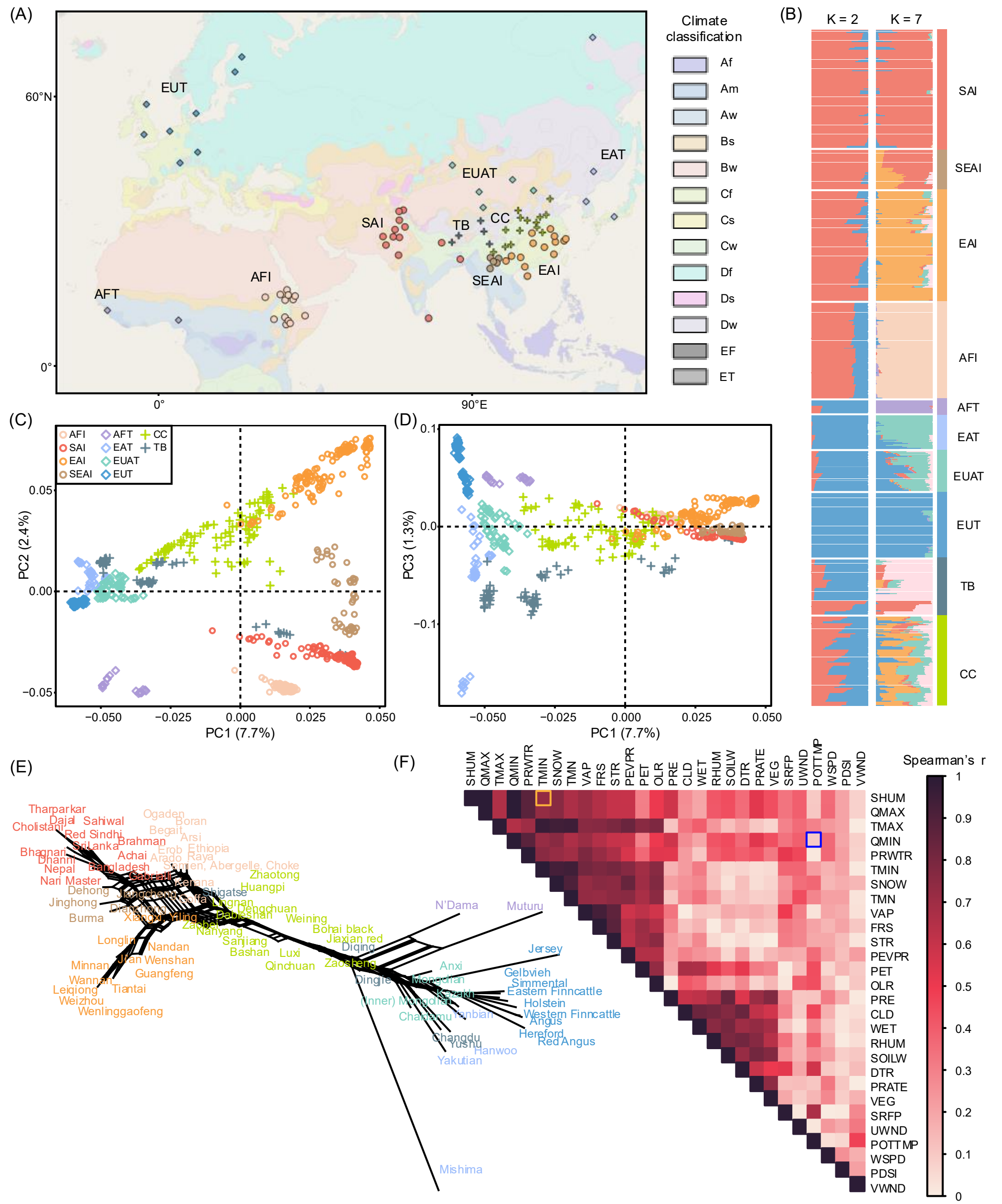
- ➢ Climate driven adaptive evolution
- ➢ Limitations of existing studies
- ➢ Climate adaptive differentiation of domestic cattle

Highlights



Populations
Bos taurus
Bos indicus
60°N
0°
0°
90°E
PC2 (2.4%)
PC1 (7.7%)
0.05
0.00
-0.05
-0.050
-0.025
0.000
0.025
0.050
African indicine
South Asian indicine
East Asian indicine
Southeast Asian indicine
African taurine
East Asian taurine
Eurasian taurine
European taurine
Central China
Tibetan cattle
Climate factors
Temperature
Wind
Moisture
Pressure
Radiation
Vegetation
Genome-wide association study
Yearly mean
Min
Max
Distance
BTA18 (Mb)
-log10(p)
14.0
14.5
15.0
Number of SNPs
STR PRE OLR VAP PET FRS SOILW PDSI WND UWND RHUM SRFP PRWTR POTTMP WSPD DTR WET CLD TMN PEVPR PRATE QMAX QMIN SHUM SNOW TMAX TMIN VEG
Multiomics analysis
ANKRD11
SPG7
RPL13
CPNE7
DPEP1
CHMP1A
SPATA33
CDK10
SPATA2L
VPS9D1
ZNF276
[0 - 450]
EUT (Hereford)
EAI (Weizhou)
ATAC
[0 - 144]
H3K27me3
ChIP
TPM
ANKRD11
RPL13
CDK10
VPS9D1

The genomic genetic characteristics and climate conditions



(A) Geographic distribution of cattle breeds/populations worldwide. Sampling locations of the 85 breeds/populations shown are: African indicine (AFI), African taurine (AFT), European taurine (EUT), East Asian taurine (EAT), Tibetan cattle (TB), Eurasian taurine (EUAT), South Asian indicine (SAI), Southeast Asian indicine (SEAI), Central China (CC), and East Asian indicine (EAI).

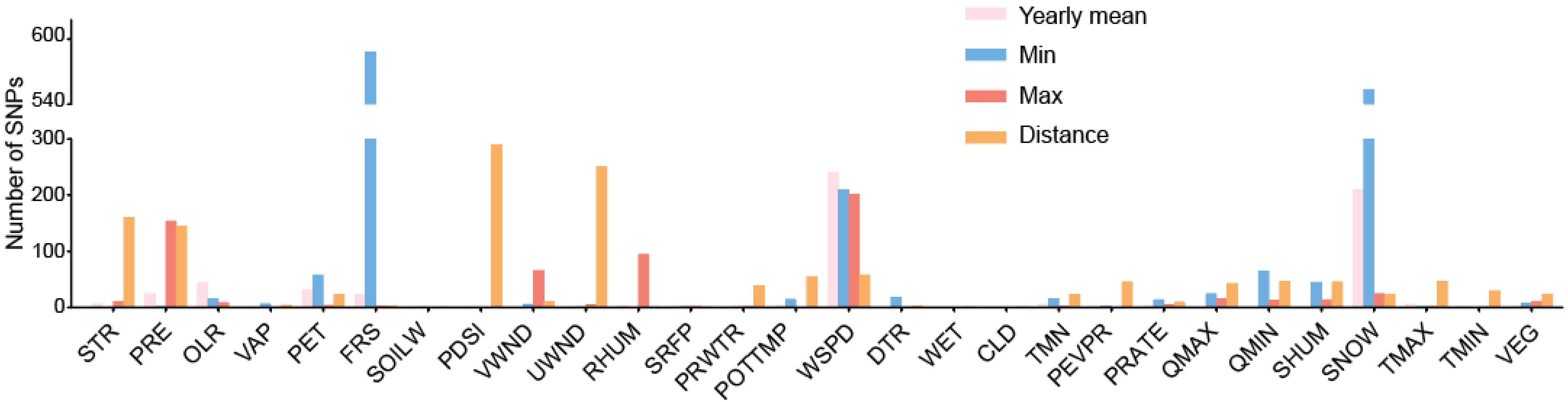
(B) Admixture analysis of cattle populations showing ancestry proportions at $K = 2$ and $K = 7$.

(C) Principal component analysis (PCA) of all 744 cattle, illustrated by PC1 vs. PC2 and (D) PC1 vs. PC3. The colors reflect the geographic regions of the samples.

(E) Phylogenetic network showing the relationships among the breeds identified using SplitsTree4.

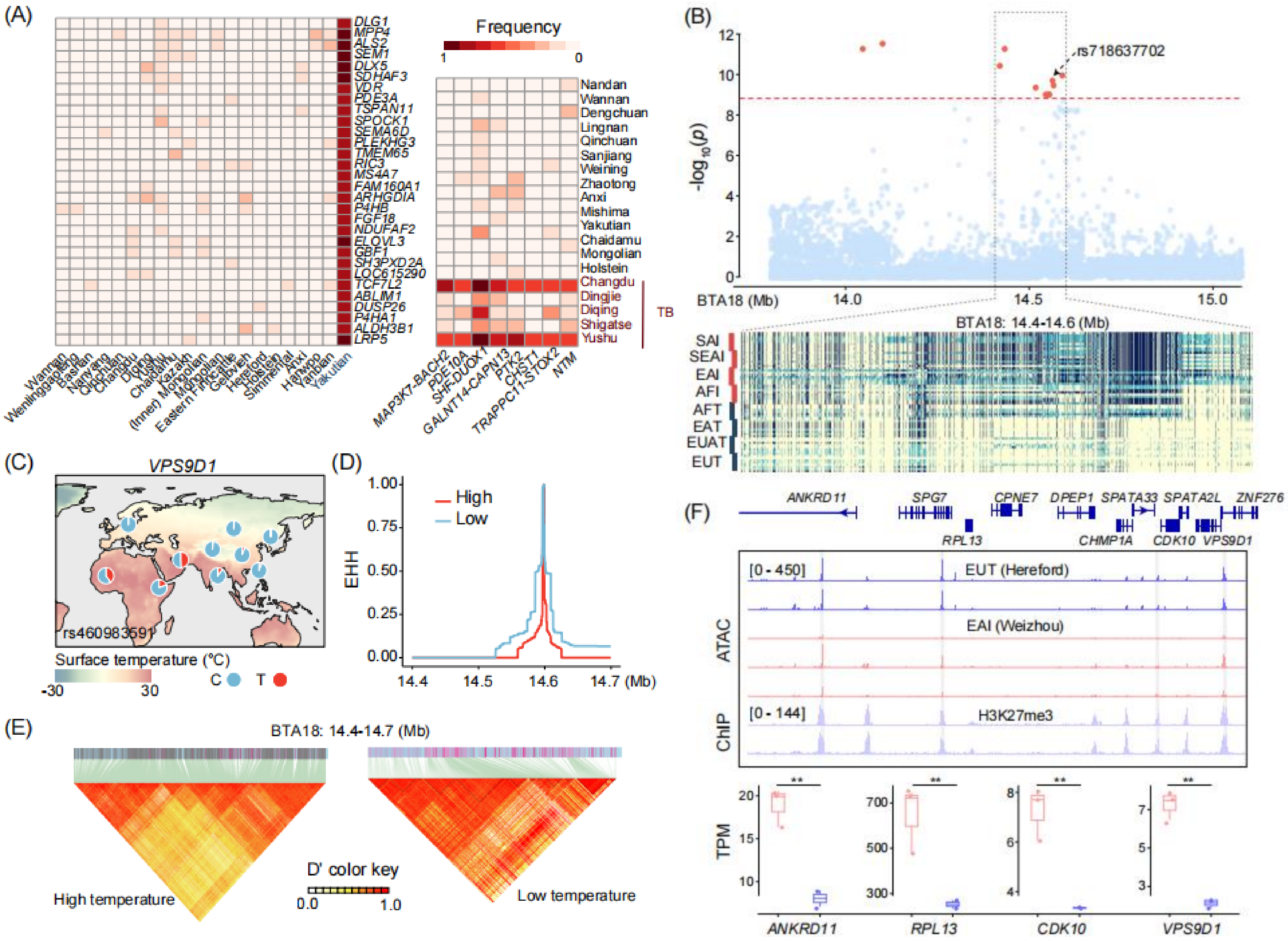
(F) Heatmap showing the absolute values of Spearman's rank correlation coefficients for the annual mean values of the 28 climate factors.

Identification of genomic variations related to climate adaptability



- We combined three models (GEMMA, LFMM, and BayPass) to control for population structure interference.
- A total of 3,165 SNPs significantly associated with 28 climate variables were identified.
- Over 50% of the SNPs are located in intronic regions, while the enrichment of SNPs in exonic regions is relatively low.
- The number of SNPs associated with snow cover and frost frequency is the highest (1,269), while the signals associated with wet day frequency and cloud cover are very limited.

The population geographical distribution of genetic variations related to temperature adaptation



(A) Frequencies of group-specific substitutions in adaptive genes in Yakutian and Tibetan cattle.

(B) Associations of genetic variants with FRS on *Bos taurus* autosome (BTA) 18, and haplotype structures for the candidate regions.

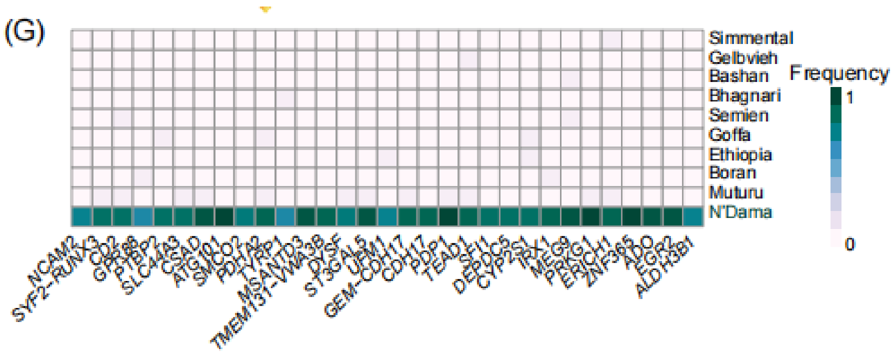
(C) Geographical distributions of the allele frequency of rs460983591 in global cattle groups.

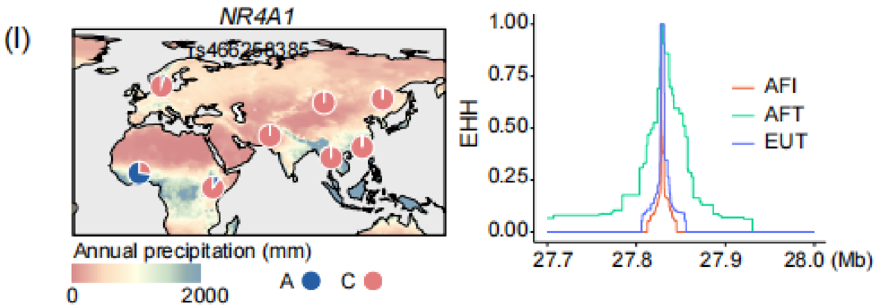
(D) Decay of extended haplotype homozygosity (EHH) around rs472613982 in groups of cattle that survived at different ambient temperatures.

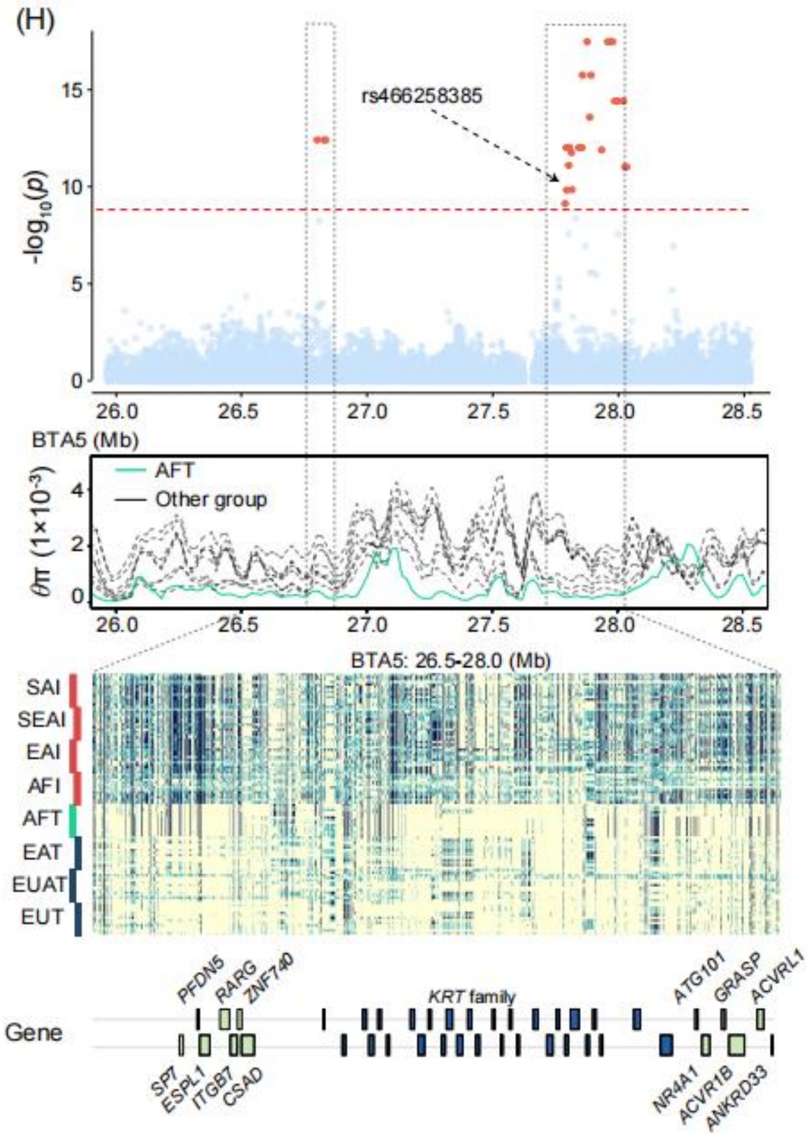
(E) Linkage disequilibrium block of the groups of cattle living at different ambient temperatures.

(F) The regulatory effects of candidate functional variants on BTA18 (14.4–14.6 Mb). Gene expression levels (TPM, Transcripts Per Million) in Hereford (EUT, cold-adapted, blue; $n = 2$) and Weizhou (EAI, heat-adapted, red; $n = 3$) cattle skeletal muscle obtained from RNA-seq are shown.

The population geographical distribution of genetic variations related to moisture adaptability





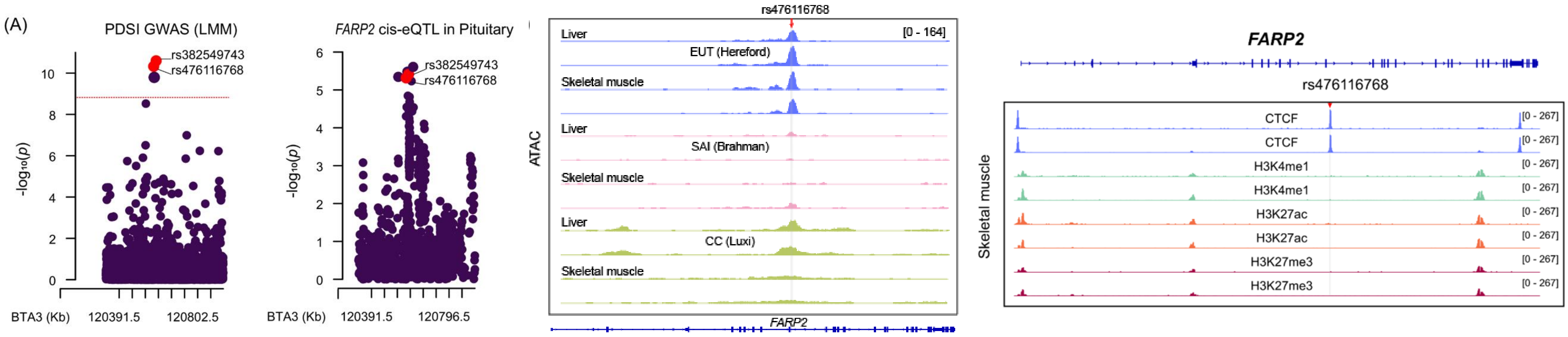


(G) Frequencies of lineage-specific substitutions in adaptive genes of N'Dama cattle.

(H) Associations of genetic variants with PRE on BTA5 based on the LMM model. Selective sweep signals based on the $\theta\pi$ of the cattle groups are plotted. Haplotype structures for significant regions.

(I) Geographical distributions of the allele frequencies of rs466258385 in NR4A1 across global cattle groups. Decay of EHH around rs466258385 in AFT, AFI, and EUT.

Overlap with eQTLs



eQTLs of the *FARP2* gene in the pituitary gland and GWAS loci of the PDSI in cattle on BTA3

Chromatin accessibility at the rs476116768 locus in the *FARP2* gene, profiled by ATAC-seq in skeletal muscle and liver of Hereford (EUT, blue; n = 2), Brahman (SAI, pink; n = 2), and Luxi (CC, green; n = 2) cattle.。

Chromatin profiles at the *FARP2* insulator variant rs476116768 visualized of Hereford

Summary

- **Systematic Analysis:** A multi-omics integration framework was successfully constructed and applied, systematically revealing the genetic and regulatory basis of cattle adaptation to diverse climates.
- **Key Mechanisms Discovered:**
  - Elucidated the differential contributions of coding and non-coding region variations in adaptation.
  - Found evidence of convergent evolution, such as general evolution of the *PTK2* gene in high-altitude species.
- **Important Genetic Resources:** Identified key candidate genes, such as *CDK10* (cold tolerance) and *FARP2* (drought resistance), providing precise targets for molecular breeding design.

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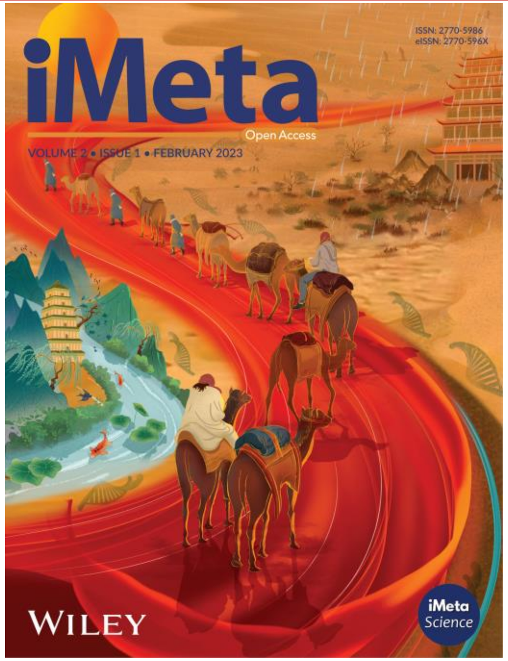

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