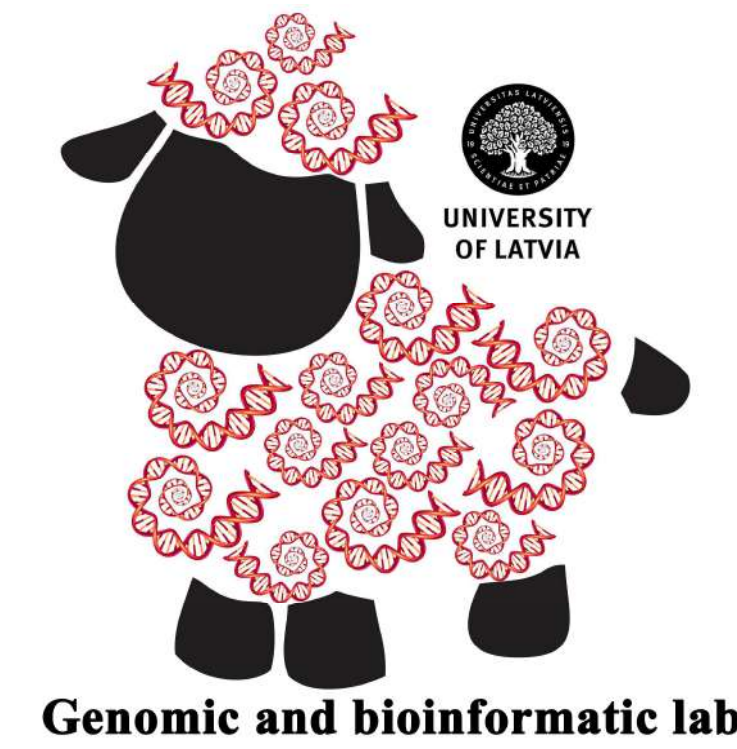


Data-Driven Genomic Analysis of Population Structure and Breed Differentiation of Latvian Dark-head Sheep



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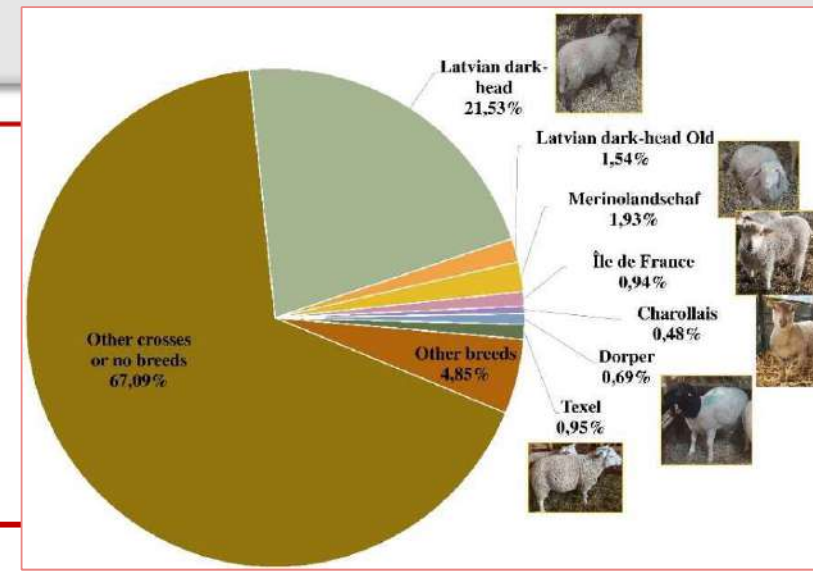
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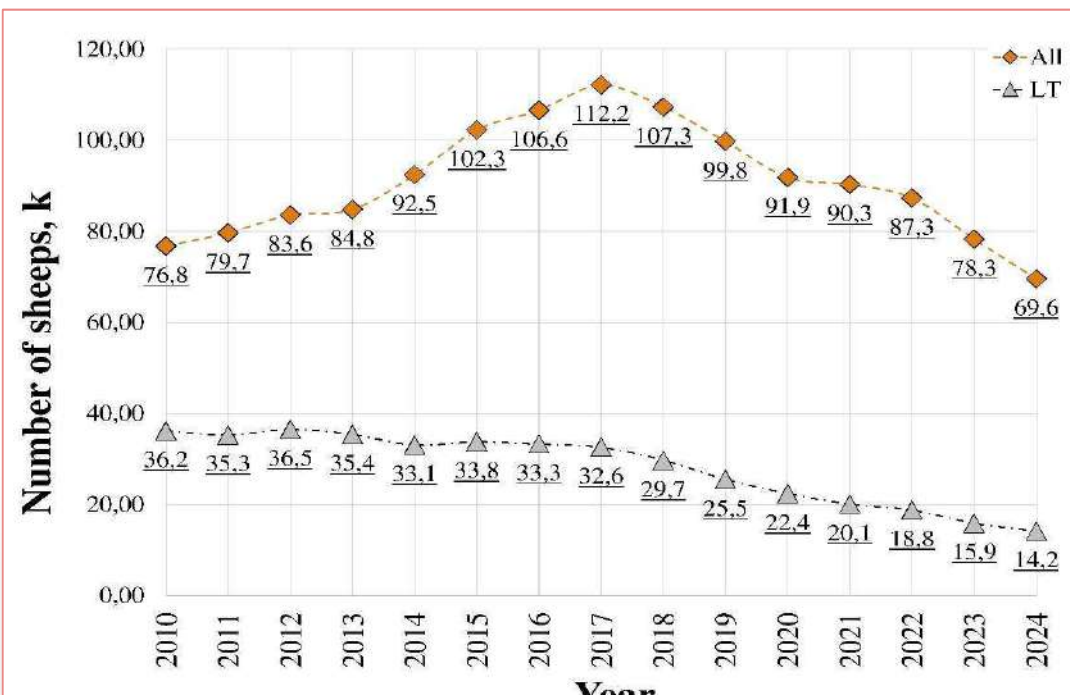


INTRODUCTION: Sheep in Latvia and Latvian Dark-head breed

The Latvian Dark-head (*Latvijas tumšgalve*; LT) is the only sheep breed developed in Latvia, is fully adapted to local climatic conditions, and carries significant cultural, ecological, and socio-economic value. The growing dominance of commercially optimised breeds threatens indigenous genetic resources, underscoring the need for advanced genomic monitoring and data-driven conservation strategies.



LT was created by crossing local Latvian sheep with Shropshire and Oxfordshire rams imported from Sweden and England. The first pedigree or breeder's book for LT rams was issued in 1939.



In 2001, the Sheep Breeders Association officially began operating in Latvia and is authorised to carry out selection work in sheep breeding, including the Latvian dark-head.

Therefore, genetic studies on LT are crucial for conserving its diversity and informing future breeding programs.



AIM

This study aimed to evaluate the genetic diversity of the Latvian Dark-head breed and compare it with that of other dominant sheep breeds in Latvia.



MATERIAL and METHODS

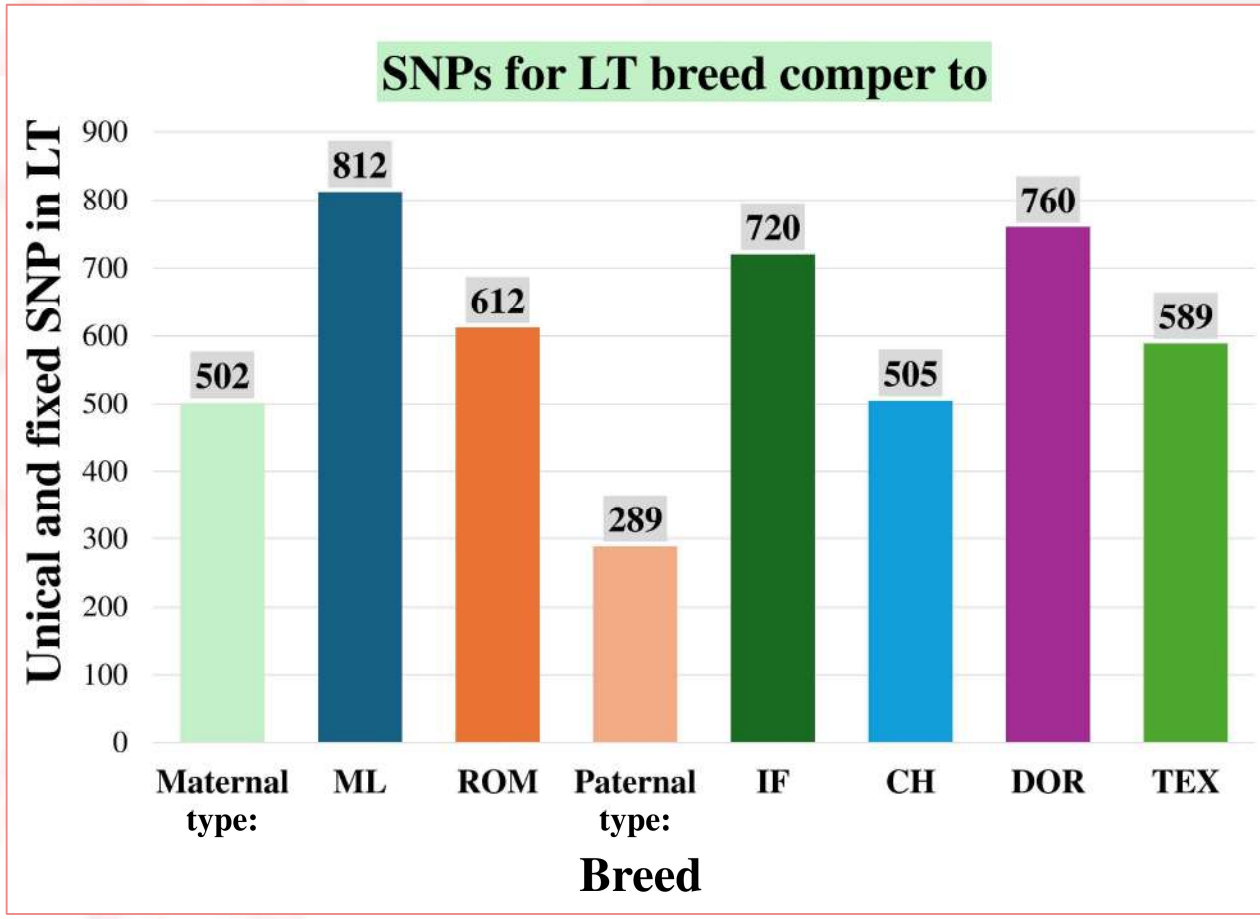
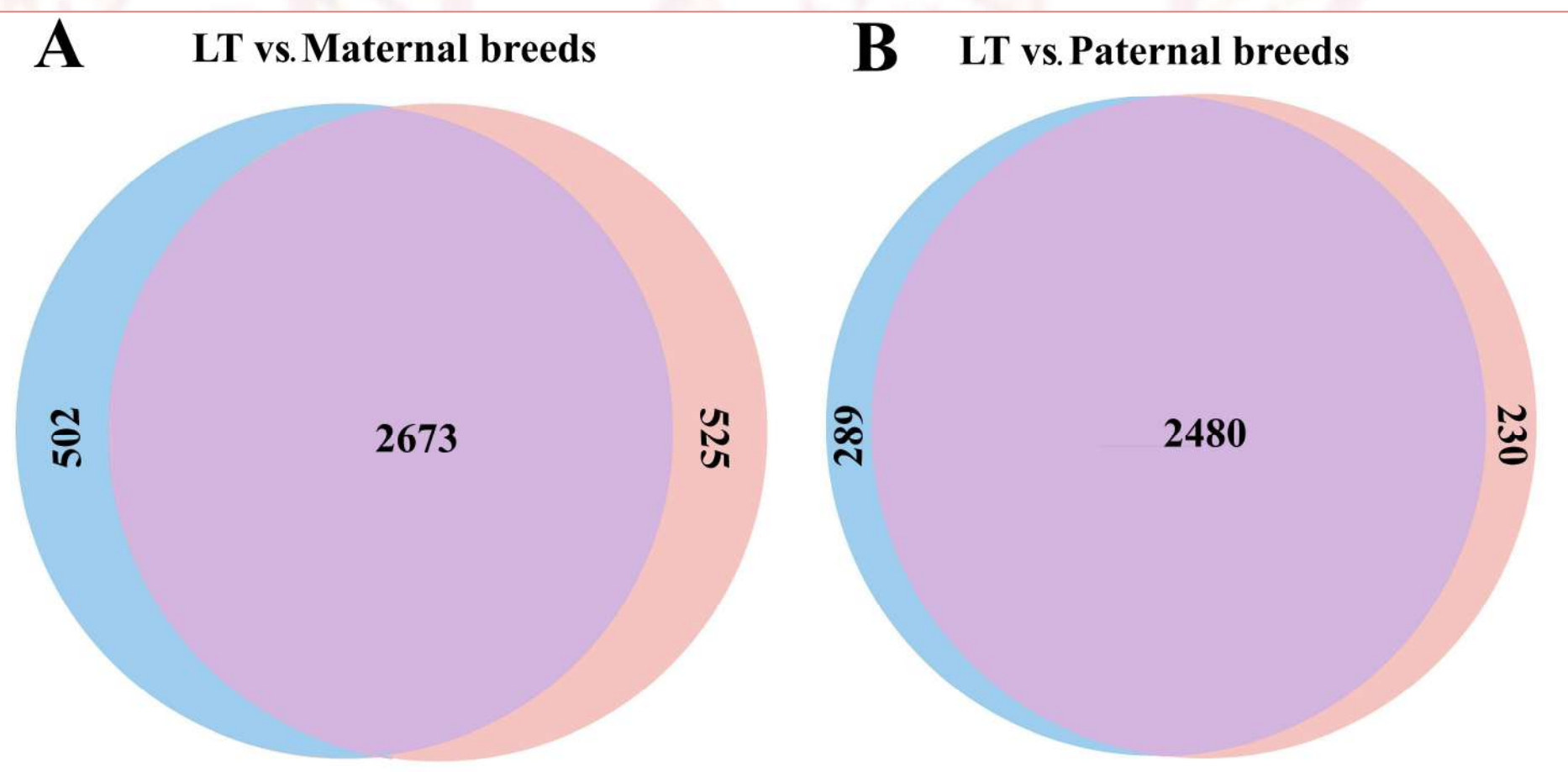
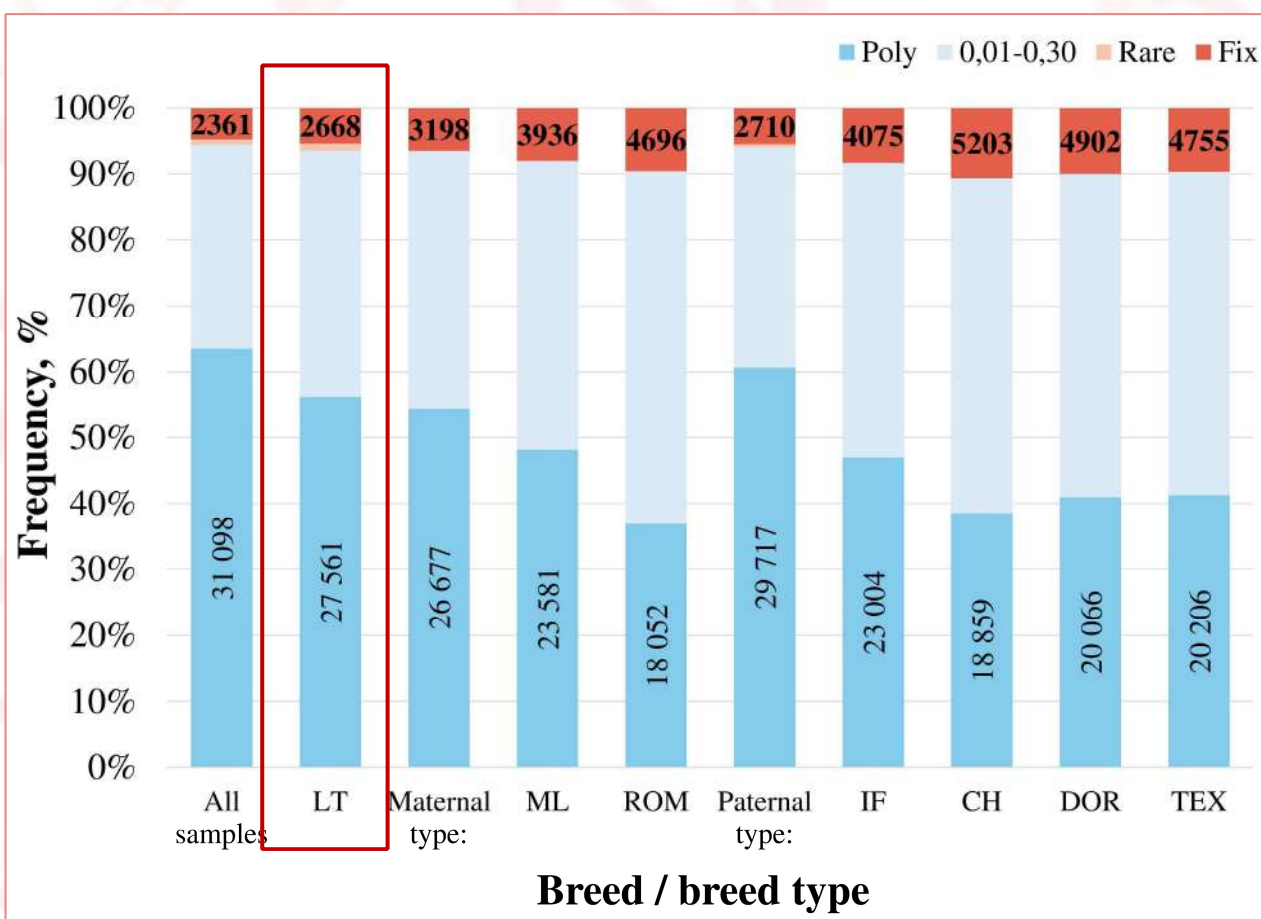
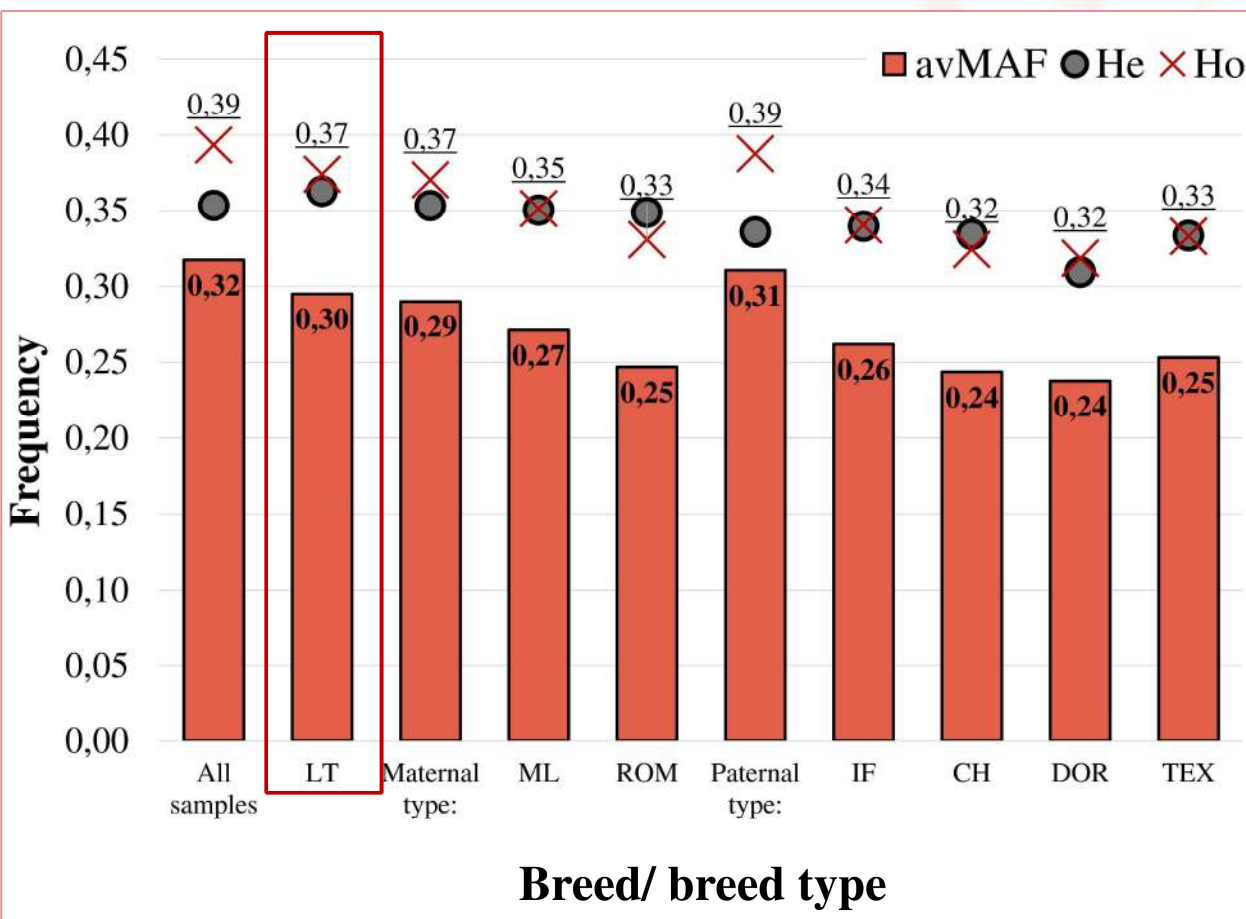
Breed	Breed type	Samples	Total by type
Latvian dark-head (LT)	Maternal	135	135
Merinolandschaf (MLS)	Maternal	26	38
Romanova (ROM)	Maternal	12	
Île de France (IF)	Paternal	33	88
Charollais (CH)	Paternal	14	
Dorper (DOR)	Paternal	15	
Texel (TEX)	Paternal	22	
Oxford Down (OX)	Paternal	4	

- Basic indices of genetic diversity: percentage of polymorphic markers, observed/expected heterozygosity (H_o / H_e), and Minor Allele Frequency (MAF)
- A comparative analysis to identify fixed SNPs ($MAF=0$) in the LT breed and/or its related breed types. The bootstrapping approach was used for the LT population in the comparison.
- Principal component analysis (PCA) and structure analysis (Genetic admixture) and Genetic admixture analysis

Genotyping of SNP of the GeneSeek® Genomic Profiler™ Ovine 50K array – 48,981 SNPs after quality control



RESULTS

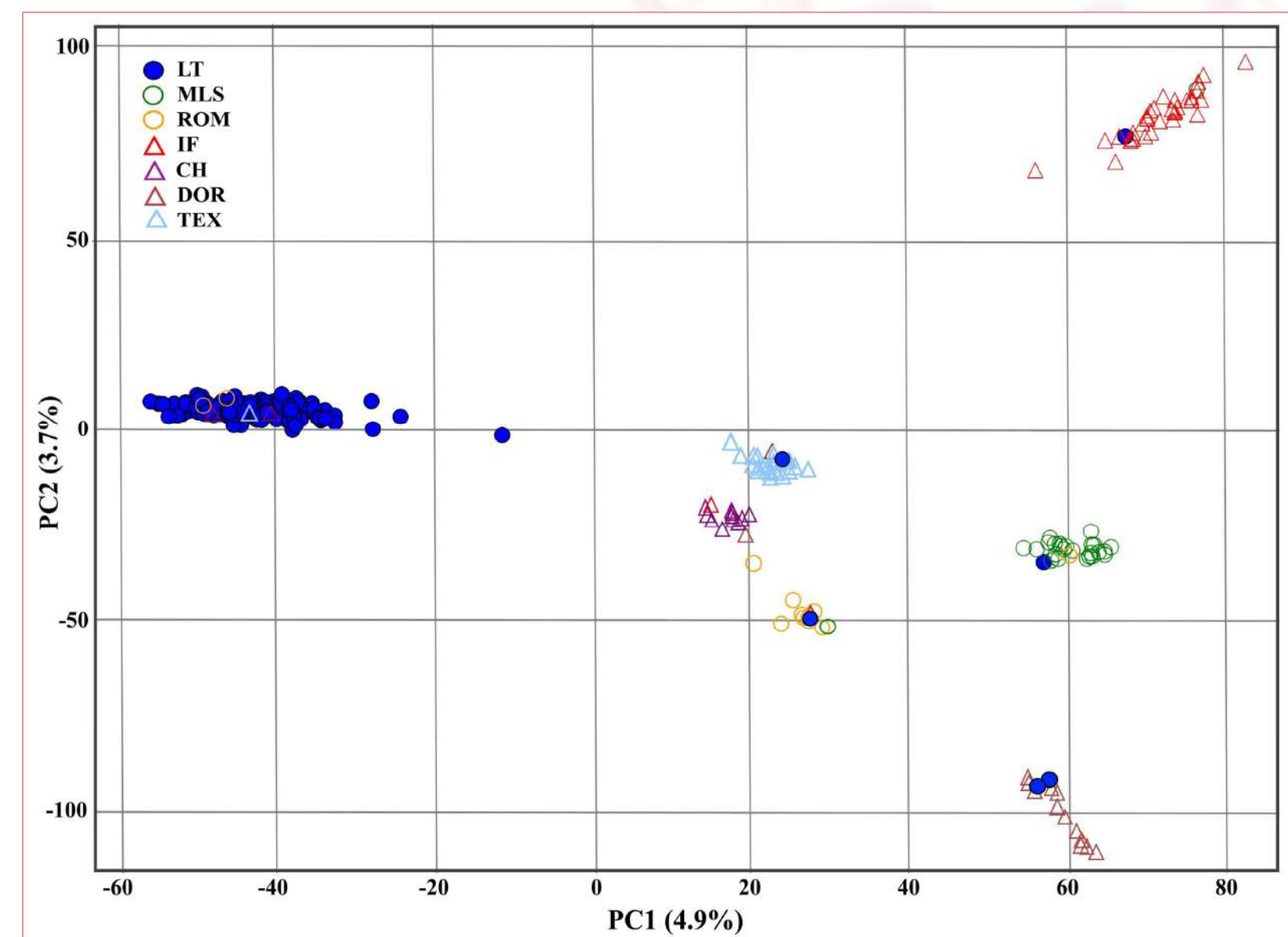


In the Latvian dark-head breed samples:

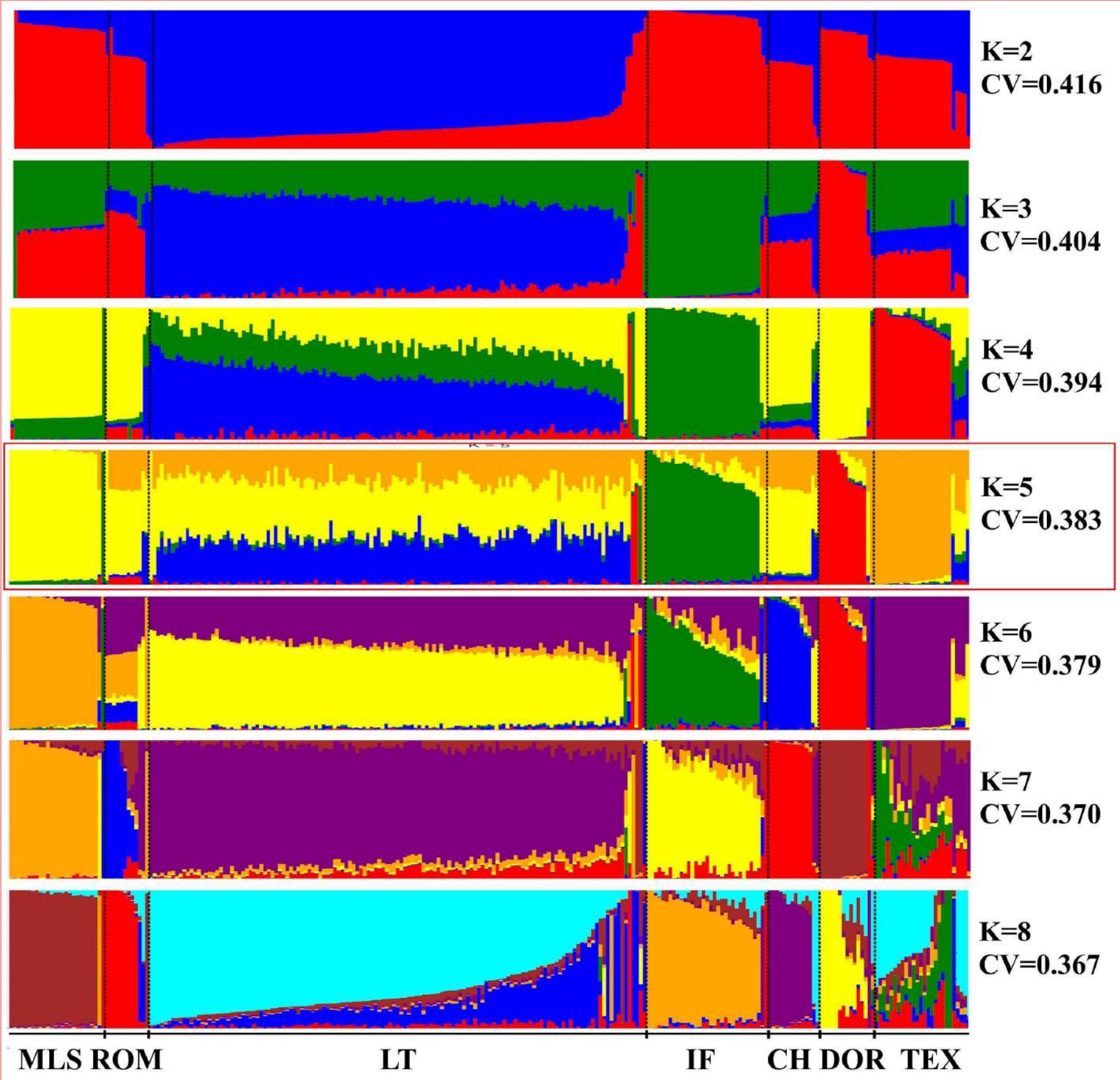
- 27'561 (56.27%) SNPs highly polymorphic ($MAF 0.3 - 0.5$)
- 3'169 (5.66%) SNPs rare ($MAF < 0.01$)
- 2'668 (5.45%) SNPs fixed ($MAF = 0$)

Compared to maternal- or paternal-type breeds, the LT breed was differentiated by 502 (15.81% of fixed SNPs in LT) and 289 (10.44%) unique fixed SNPs.

From all fixed SNPs, from 289 (10.83%) to 812 (30.43%) SNPs were unique to the LT breed compared to others.



F_{ST}	
Breed	vs. LT
Maternal type:	
ML	0.228
ROM	0.233
Paternal type:	
IF	0.223
CH	0.232
DOR	0.332
TEX	0.240



At the initial level of analysis ($K = 2$), LT and other breeds had different genetic component distributions. The LT breed had three primary components when the cluster number was increased to $K = 5$, with one of these components being quite low in other breeds. Cross-validation error improved only little after $K = 5$, where the curve elbowed.

While the 99% of LT breed is clearly segregated by PC1, it is positioned relatively close to the TEX, CH, and ROM breeds on the PC2 axis.

Latvian dark-head breed shows high or very high genetic differentiation from other breeds.



CONCLUSION

Fixed SNPs enable the detection of distinct genetic traits and interbreed differences, AI-assisted ancestry inference, and precision breeding applications. The Ovine50K platform, along with computational genomic analysis, enables the identification of breed-specific markers at scale. It also helps create tools for selection and genetic monitoring for the Latvian national sheep breed. The results provide a basis for future machine learning methods to evaluate sheep genetics and inform decisions in sustainable animal breeding.

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