

Original article

## Genomic diversity, within-breed structure, and autozygosity of Red Steppe cattle based on high-density SNP genotyping

**Alimsoltan A. Ozdemirov**

Federal Agrarian Scientific Center of the Republic of Dagestan, Makhachkala, Russia

e-mail: alim72@mail.ru

**Abstract.** The aim of this study was to provide an integrated population-genomic characterization of Red Steppe cattle using high-density SNP genotyping ( $n = 40$ ), with a sequential assessment of data quality, within-breed structure, and autozygosity inferred from runs of homozygosity (ROH). Sample-level quality control indicated a low proportion of missing genotypes: mean  $F\_MISS = 0.0009$  (0.0000–0.0098), corresponding to a mean call rate of 0.9991. Heterozygosity estimates were  $H_o = 0.3767$  and  $H_e = 0.3664$ ; the heterozygosity-based inbreeding coefficient (PLINK) averaged  $F = -0.0281$  (–0.0642–0.0868). Standardized heterozygosity identified outlier samples (A01, A08, A22). Structure analysis revealed within-breed heterogeneity in the PC1-PC2 space; according to a summary evaluation of ADMIXTURE model quality across  $K = 2-6$ , the lowest median metric was observed at  $K = 2$  (0.608340;  $N = 20$ ). ROH analysis showed pronounced inter-individual variation in autozygosity: total ROH length ( $\geq 1$  Mb) averaged 14.2505 Mb (median 12.9970 Mb; 0.0000–45.5073 Mb), with the highest values recorded for A20, A30, and A23. A genome-wide ROH coverage map (1-Mb windows) highlighted intervals with increased ROH overlap; the maximum overlap proportion reached 0.275 (11/40). Overall, the results provide a reproducible baseline for genomic monitoring of the herd and for downstream annotation of the identified ROH intervals.

**Keywords:** Red Steppe cattle, SNP genotyping, PCA, ADMIXTURE, heterozygosity, inbreeding, ROH, autozygosity

**For citation:** Ozdemirov A. A. Genomic diversity, within-breed structure, and autozygosity of Red Steppe cattle based on high-density SNP genotyping. *Agrarnyy nauchnyy zhurnal = Agrarian Scientific Journal*. 2026;(4):87–93. <https://doi.org/10.28983/asj.y2026i4pp87-93>.

### ЗООТЕХНИЯ И ВЕТЕРИНАРИЯ

Научная статья

УДК 636.2:575.17

<https://doi.org/10.28983/asj.y2026i4pp87-93>

## Геномное разнообразие, внутрипородная структура и аутозиготность коров красной степной породы по данным высокоплотного SNP-генотипирования

**Алимсолтан Ахмедович Оздемиров**

Федеральный аграрный научный центр Республики Дагестан, г. Махачкала, Россия

e-mail: alim72@mail.ru

**Аннотация.** Цель исследования заключалась в проведении интегрированной популяционно-геномной характеристики коров красной степной породы на основе высокоплотного SNP-генотипирования ( $n = 40$ ) с последовательной оценкой качества данных, внутрипородной структуры и аутозиготности, реконструированной по пробегам гомозиготности (ROH). Контроль качества на уровне образцов показал низкую долю пропусков генотипов: среднее значение  $F\_MISS = 0,0009$  (0,0000–0,0098), что соответствует среднему callrate 0,9991. Оценки гетерозиготности составили  $H_o = 0,3767$  и  $H_e = 0,3664$ ; коэффициент инбридинга на основе гетерозиготности (PLINK) в среднем равнялся  $F = -0,0281$  (–0,0642–0,0868). По стандартизированной гетерозиготности выявлены образцы-выбросы (A01, A08, A22). Анализ структуры обнаружил внутрипородную неоднородность в пространстве PC1–PC2; согласно сводной оценке качества модели ADMIXTURE при  $K = 2-6$ , наименьшее медианное значение метрики наблюдалось при  $K = 2$  (0,608340;  $N = 20$ ). Анализ ROH выявил выраженную межиндивидуальную вариабельность аутозиготности: суммарная длина ROH ( $\geq 1$  Мб) в среднем составила 14,2505 Мб (медиана 12,9970 Мб; 0,0000–45,5073 Мб), при этом наибольшие значения зарегистрированы у A20, A30 и A23. Карта геномного покрытия ROH (окна 1 Мб) выделила интервалы с повышенным перекрытием ROH; максимальная доля перекрытия до-





стигала 0,275 (11/40). Полученные результаты формируют воспроизводимую исходную основу для геномного мониторинга стада и последующей аннотации выявленных ROH-интервалов.

**Ключевые слова:** красная степная порода, SNP-генотипирование, PCA, ADMIXTURE, гетерозиготность, инбридинг, ROH, аутозиготность

**Для цитирования:** Оздемиров А. А. Геномное разнообразие, внутривидовая структура и аутозиготность коров красной степной породы по данным высокоплотного SNP-генотипирования // Аграрный научный журнал. 2026. № 4. С. 87–93. <https://doi.org/10.28983/asj.y2026i4pp87-93>.

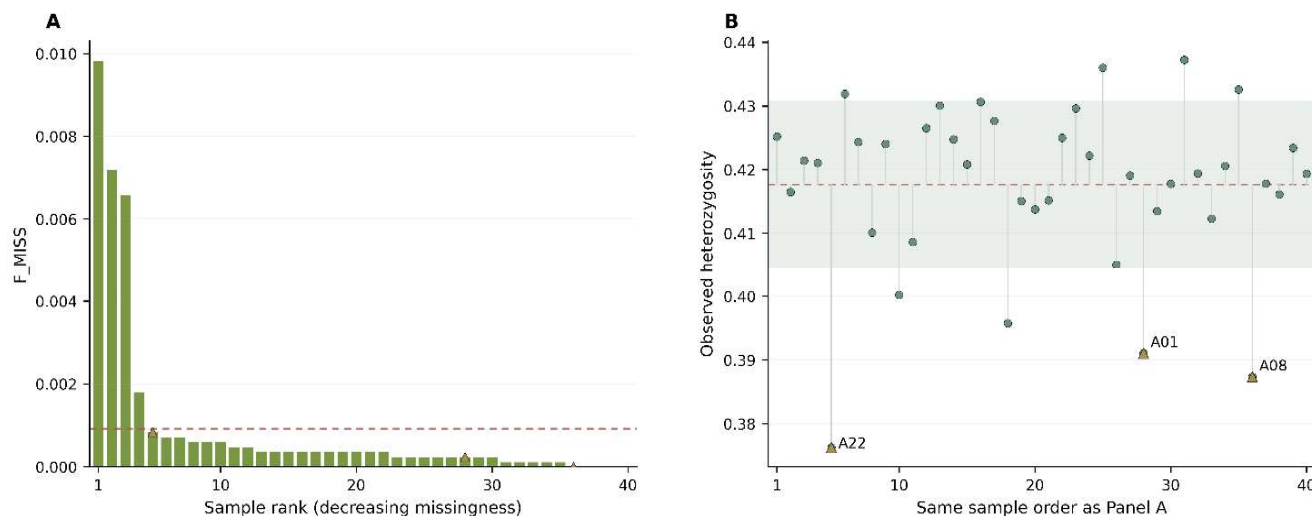
**Introduction.** The conservation and rational use of breed genetic resources increasingly relies on quantitative genetic indicators that describe a population not only in general terms, but through measurable parameters of diversity, relatedness, and within-breed heterogeneity. This is particularly important for local and regionally adapted breeds, because in populations of limited size and under uneven selection pressure across farms, changes in herd structure may accumulate gradually and become apparent at the level of genetic variability. Genetic monitoring based on marker panels has demonstrated that such approaches provide a reproducible basis for evaluating and comparing breed groups and for detecting within-breed differences [7, 13]. Over recent decades, high-density SNP arrays have become the main tool of population-genomic studies in farm animals, enabling simultaneous analysis of tens of thousands of markers across the genome. The development and adoption of 50K panels for cattle has substantially expanded the capacity to assess genomic diversity and breed structure at a genome-wide scale and has established a technological standard suitable for both research and applied tasks [1, 13]. Breed affiliation and within-breed heterogeneity in SNP data can be robustly described using both dimensionality-reduction methods and model-based ancestry estimation. In particular, principal component analysis (PCA) allows visualization and statistical detection of stratification in genotype data, whereas the ADMIXTURE model provides interpretable component profiles for a specified number of clusters. These approaches are widely used in cattle breed studies and have proven informative for distinguishing closely related breed groups and for revealing within-breed structure [5, 6, 9, 14, 15]. Beyond structure description, an important task is to translate genomic information into a selection-relevant framework. The concept of predicting genetic merit from dense genome-wide marker maps underpins modern genomic approaches in animal breeding, while standard software tools support reproducible data processing and the estimation of key population-genetic metrics from SNP data [8, 10]. Another major layer of genome-wide interpretation concerns autozygosity and inbreeding, which can be conveniently assessed through runs of homozygosity (ROH). ROH parameters quantify individual and population-wide burdens of homozygous segments, enable comparisons of autozygosity among animals, and help localize genomic regions that more frequently fall within ROH in a given cohort. Methodological aspects of ROH detection and the impact of SNP density on autozygosity estimates have been discussed in multiple studies and reviews, making the ROH approach a standard component of population-genomic analyses in livestock [3, 4, 11, 12]. In the present work, genomic diversity and within-breed organization of the studied cohort are evaluated from high-density SNP genotyping data through a sequential analysis of population structure (PCA/ADMIXTURE) and ROH-based autozygosity as complementary characteristics. This design yields a coherent description of population heterogeneity and inter-individual differences in homozygosity, providing a foundation for further monitoring and applied interpretation in a breeding context [6, 11, 12, 14].

**Material and methods.** The study material comprised Red Steppe cows ( $n = 40$ ) genotyped using a high-density SNP array of the BovineSNP50 class (~50,000 markers). Sample identifiers were unified to the Paper-ID format (A01-A40) and matched to the original Sample\_ID values to ensure consistent reporting. Quality control was performed using per-sample genotype missingness (F\_MISS) and call rate ( $1 - F\_MISS$ ). Genomic diversity was assessed using observed and expected heterozygosity ( $H_o$ ,  $H_e$ ) and the heterozygosity-based inbreeding coefficient (F, PLINK); an LD-pruned marker set was additionally used and outliers were identified based on standardized heterozygosity. Within-breed structure was examined by principal component analysis (PCA; PC1–PC2 visualization) and by the model-based approach ADMIXTURE across  $K = 2-6$ ; for each  $K$ , 20 runs were performed and model quality was compared using aggregated statistics (median, p25-p75, min-max). Autozygosity was quantified from runs of homozygosity (ROH, PLINK): total ROH length was calculated at minimum-length thresholds of 1, 2, 4, 8, and 16 Mb and decomposed into length classes (1-2, 2-4, 4-8, 8-16,  $\geq 16$  Mb). The genomic distribution of ROH was characterized using ROH coverage in 1-Mb windows as the proportion of individuals ( $n = 40$ ) whose ROH overlapped a given window; windows with the highest coverage were highlighted as candidate intervals for downstream annotation.

**Results.** This section presents the results of the genomic analysis of Red Steppe cattle, moving from genotyping quality control and heterozygosity assessment to within-breed structure

(PCA/ADMIXTURE) and ROH-based autozygosity. This sequence first verifies the technical reliability of the dataset and then supports biological interpretation on a consistent basis.

To evaluate whether deviations in individual heterozygosity could be attributed to differences in genotyping completeness, we summarized sample-level missingness and observed heterozygosity in a combined QC-oriented figure (Figure 1A,B). By displaying both metrics in the same sample order, the figure allows direct comparison between data completeness and heterozygosity profiles across the 40 genotyped animals.



Panel A shows per-sample missingness ( $F\_MISS$ ) for the 40 genotyped individuals, ranked from highest to lowest missingness. Panel B shows observed heterozygosity for the same individuals in the identical sample order, allowing direct visual comparison between genotyping completeness and heterozygosity profiles. Circles denote all samples, whereas triangles indicate standardized heterozygosity outliers identified in the LD-pruned dataset. The dashed reference lines indicate the cohort mean for each metric; in Panel B, the shaded band represents mean  $\pm$  SD. Outlier samples are labeled according to the manuscript sample IDs (A01, A08, and A22).

**Figure 1 – Integrated sample-level quality control profile of Red Steppe cattle genotypes**

**Рисунок 1 – Интегрированный профиль контроля качества генотипирования образцов красной степной породы**

The combined QC profile indicates that heterozygosity outliers are not concentrated among samples with the highest missingness, arguing against a simple missingness-driven technical explanation for their deviation. Overall, missingness remained low across the cohort, whereas heterozygosity showed greater between-sample variation, supporting the interpretation that the detected outliers are more likely to reflect biological rather than purely technical differences.

Following the assessment of genotyping quality and heterozygosity, we examined within-breed structure using principal component analysis (PCA). The distribution of animals in the space of the first two principal components (PC1 and PC2) is shown in Figure 2.

Within-breed heterogeneity is evident in the PC1-PC2 space. A subset of animals forms a compact central group, whereas several individuals are shifted relative to the main point cloud. Coloring by F quartiles reflects variation in the inbreeding coefficient within the cohort. Standardized heterozygosity outliers are marked separately and remain within the overall PC1-PC2 distribution.

For a complementary model-based assessment of genetic structure, ADMIXTURE was applied across a range of K values and model fit was compared. Summary statistics of the ADMIXTURE model-quality metric as a function of the number of components K are presented in Figure 3; the median, interquartile range, and range across runs are shown.

The lowest median model-quality metric was observed at  $K = 2$  (0.608340,  $N = 20$ ). With increasing numbers of components, the median increased ( $K = 3$ : 0.629950;  $K = 6$ : 0.859720). Across-run variability was more pronounced at higher K values (most notably at  $K = 5-6$ ).

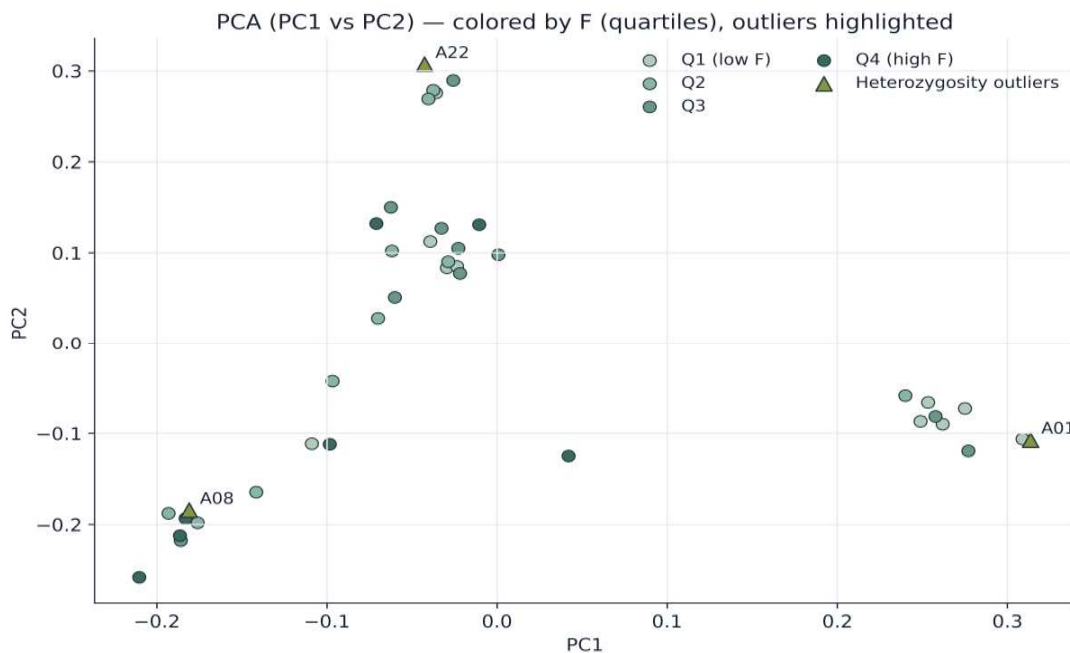
To quantify autozygosity in each animal, runs of homozygosity (ROH) were computed and total ROH length was decomposed into length classes. The composition of total ROH length by length class for each sample (A01-A40) is shown in Figure 4 as a stacked bar chart.

Total ROH length ( $\geq 1$  Mb) averaged 14.25 Mb (median 12.997 Mb) and ranged from 0.00 to 45.51 Mb. The largest total ROH values were observed in A20 (45.51 Mb), A30 (45.29 Mb), and A23 (40.13 Mb), whereas the minimum (0.00 Mb at the  $\geq 1$  Mb threshold) was recorded for A16, A29, and





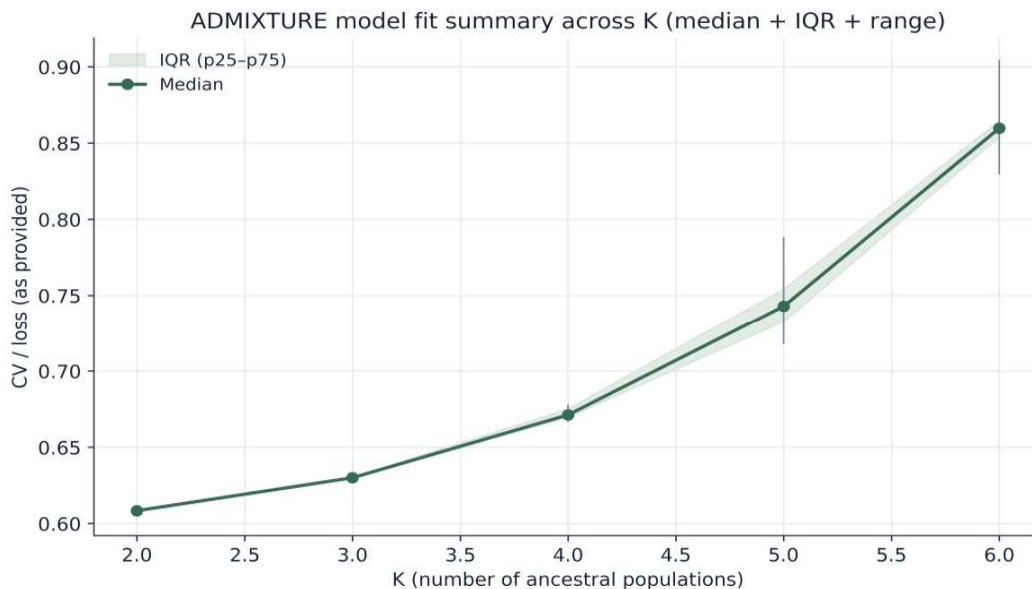
A26. Based on mean contributions of length classes, the largest contribution came from 8-16 Mb segments (mean 6.47 Mb), followed by 4-8 Mb (3.00 Mb) and  $\geq 16$  Mb (2.43 Mb); contributions from 2-4 Mb (1.98 Mb) and 1-2 Mb (0.37 Mb) were smaller.



PC1 and PC2 denote the first and second principal components, respectively; the x-axis represents PC1 and the y-axis represents PC2. Point color corresponds to quartiles of the F coefficient estimated in PLINK (QC set). Standardized heterozygosity outliers are highlighted separately, and labels indicate sample IDs (A01–A40) for the marked points.

**Figure 2 – PCA (PC1–PC2) colored by quartiles of the F coefficient (PLINK)**

**Рисунок 2 – Анализ главных компонент (PC1-PC2) с окраской по квантилям коэффициента F (PLINK)**

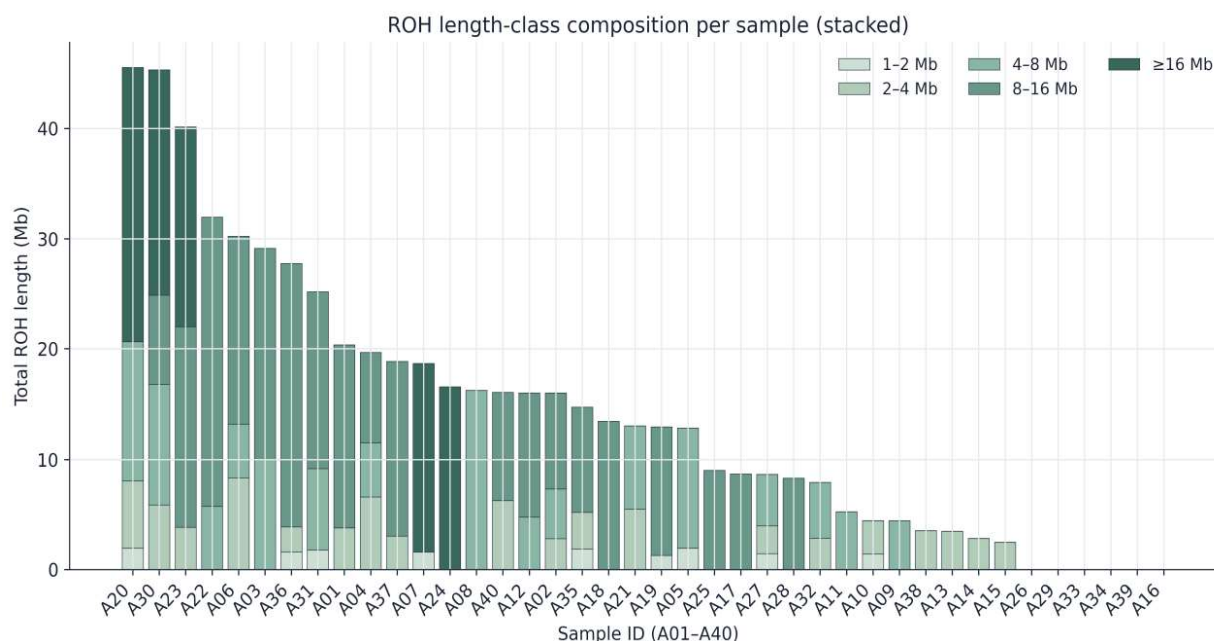


Note: K is the assumed number of ancestral components; X-axis: K; Y-axis: model-quality metric (CV error/loss); line: median; band: interquartile range (p25-p75); whiskers: min-max.

**Figure 3 – Summary of ADMIXTURE model quality across K (median, interquartile range, and range)**

**Рисунок 3 – Сводка качества модели ADMIXTURE при различных K (медиана, межквартильный размах и полный диапазон)**

After decomposing ROH by length classes, we summarized the results into a single integral indicator per animal - total ROH length at the  $\geq 1$  Mb threshold. Total ROH length ( $\geq 1$  Mb) per sample is shown in Figure6; samples are ordered in decreasing value and the top 10 are highlighted.



Note: ROH are runs of homozygosity; length classes: 1-2, 2-4, 4-8, 8-16, and  $\geq 16$  Mb; X-axis: samples (A01-A40, ordered by total ROH length); Y-axis: total ROH length (Mb); colored segments: contribution of each length class; bar height: total ROH length ( $\geq 1$  Mb) per sample.

**Figure 4 – Composition of total ROH length by length class (stacked bars) for each sample (A01-A40)**

**Рисунок 4 – Структура суммарной длины ROH по классам длины (столбики с накоплением) для каждого образца (A01–A40)**

Across animals, total ROH length ( $\geq 1$  Mb) averaged 14.25 Mb (median 12.997 Mb) and ranged from 0.00 to 45.51 Mb. The highest total ROH burden was observed in A20 (45.51 Mb), A30 (45.29 Mb), and A23 (40.13 Mb), whereas no ROH segments  $\geq 1$  Mb were detected in A16, A29, or A26. In terms of mean class contributions, 8–16 Mb segments accounted for the largest share of total ROH burden (6.47 Mb on average), followed by 4–8 Mb (3.00 Mb) and  $\geq 16$  Mb (2.43 Mb), whereas 2–4 Mb (1.98 Mb) and 1–2 Mb (0.37 Mb) segments contributed less. Because cumulative ROH burden per animal is already reflected by the overall bar height and sample ordering in the ROH length-class composition plot, a separate ranked plot of total ROH length is not required.

In addition to total ROH burden per animal, we assessed the genomic distribution of ROH to identify regions that were most frequently encompassed by homozygous tracts in the cohort. Genome-wide ROH coverage is shown in Figure 5 as the proportion of individuals ( $n = 40$ ) whose ROH overlap a given 1-Mb window; windows with the highest coverage are highlighted.

ROH coverage varied across genomic windows and remained low across most of the genome, whereas a limited number of windows showed elevated overlap among animals in the cohort. The maximum observed coverage was 0.275 (11/40), and the next highest windows reached 0.250 (10/40) and 0.225 (9/40). These peaks indicate genomic regions that recurrently fall within ROH across individuals and therefore represent candidate segments for further functional or comparative interpretation.

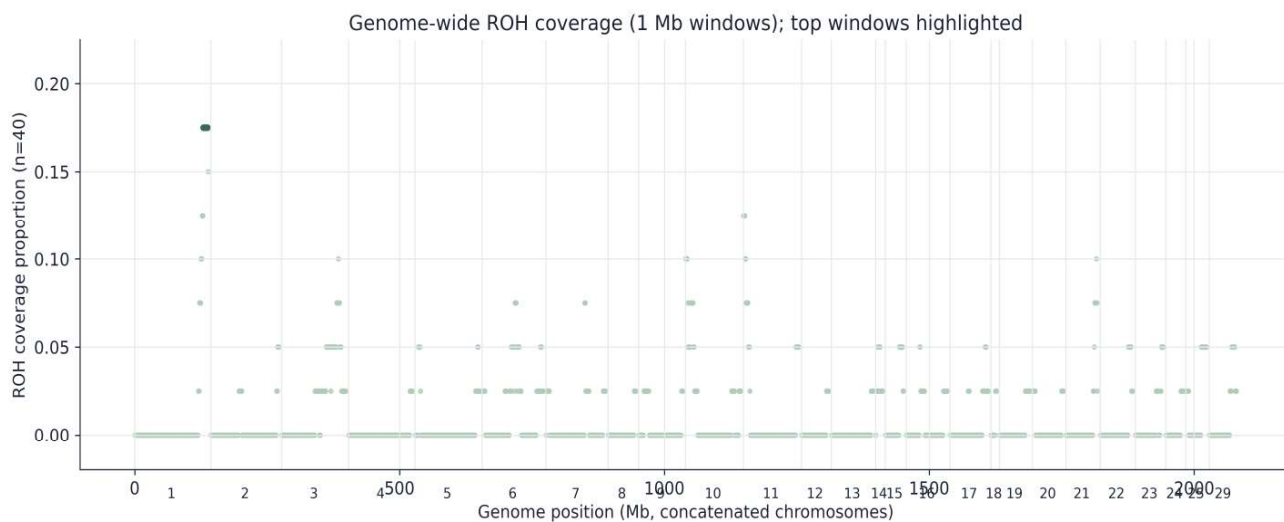
For interpreting the results, it is reasonable to follow the sequence of genomic signals—from the reliability of the input data and quality-control outcomes, to indications of within-breed heterogeneity, and finally to ROH-based autozygosity parameters and their genomic distribution. This order is methodologically justified because inferences about structure and ROH are valid only in the absence of systematic biases driven by genotyping quality.

First, the consistently high genotyping quality across samples is notable: missingness is low throughout the cohort and the mean call rate is close to 1. This reduces the likelihood that the observed heterozygosity and inbreeding patterns are technical artifacts associated with poor-quality samples. Against this background, the Ho/He relationship and the distribution of the PLINK F coefficient indicate moderate variability without evidence of a cohort-wide heterozygosity collapse. At the same time, the identification of individual samples as standardized-heterozygosity outliers (A01, A08, A22) is of practical interest: provided that call rate is comparable, such cases typically warrant targeted checks at the sample level (identity, provenance, repeatability) and careful comparison with PCA and ROH results. Importantly,





heterozygosity outlier status is neither an error nor proof of a single specific scenario; rather, it is a marker that can increase the informativeness of downstream analyses and help focus interpretation.



Note: Genome-wide ROH coverage was calculated in non-overlapping 1-Mb windows as the proportion of animals ( $n = 40$ ) with at least one ROH overlapping a given window. The x-axis shows concatenated genomic position with chromosome boundaries, and the y-axis shows window-level ROH coverage across the cohort. Windows with the highest coverage are high lighted.

**Figure 5 – Genome-wide ROH coverage (1-Mb windows)**

**Рисунок 5 – Геномное покрытие ROH по всему геному (окна 1 Мб)**

Turning to structure, PCA captures within-breed heterogeneity despite all animals originating from a single herd. In population-genetic terms, this means that the cohort is not fully described by a single compact cluster without internal organization: individual shifts are present and the PC1–PC2 distribution is compatible with substructure. Coloring points provide an additional layer of information by F quartiles, which illustrates how variation in relative homozygosity/inbreeding relates to position in principal-component space. If these signals align, they strengthen the case for genuine internal heterogeneity; if they diverge, they suggest that structure and autozygosity may reflect different aspects of the herd's genetic organization.

The ADMIXTURE model-quality summary across  $K$  shows the minimum at  $K = 2$  within  $K = 2$ -6; the difference between  $K = 2$  and  $K = 3$  is present but remains moderate relative to the overall increase at higher  $K$ . Pragmatically, within this cohort, simpler structure models fit better than more subdivided ones, and higher  $K$  values show increased across-run instability. Nevertheless, biological interpretation of  $K$  requires not only a model-quality metric but also individual ancestry profiles (Q matrices) and, ideally, external context (origin, lines, sires), because the metric alone does not define the meaning of components. The most informative result block relates to ROH, because runs of homozygosity provide a direct and interpretable measure of autozygosity. The cohort shows pronounced inter-individual variation in total ROH length ( $\geq 1$  Mb), ranging from 0 to 45.5 Mb with a mean of about 14.25 Mb and a median of about 13.0 Mb. This range highlights that, even within a single herd, individual animals may differ substantially in autozygosity. Decomposing ROH into length classes adds interpretive depth: the presence of long segments (notably 8–16 Mb and  $\geq 16$  Mb) distinguishes animals with a higher concentration of long ROH, whereas a predominance of shorter classes shifts the profile toward more fragmented autozygosity. Importantly, this spectrum is not reducible to a single number and supports viewing autozygosity as a multi-component characteristic, which is useful for herd monitoring and between-animal comparisons.

The spatial dimension also deserves attention, namely genome-wide ROH coverage and candidate ROH-enriched regions. The 1-Mb window coverage map shows that most of the genome has low ROH overlap across the cohort, but a small number of windows reach higher values, including 0.275 (11/40), 0.250 (10/40), and 0.225 (9/40). Such peaks can be treated as candidate intervals of increased ROH coverage, i.e., regions that fall within ROH more frequently in a subset of animals. At the same time, it is essential to maintain an appropriate level of evidence: increased ROH coverage alone is not proof of selection or functional relevance. In a strict academic framework, these peaks are best viewed as a starting point for subsequent steps, including robustness checks under alternative ROH settings, gene annotation and comparison with known QTL/candidate regions, and, ideally, validation in independent cohorts of the same breed or related populations. Only after such checks should stronger claims be considered.

Finally, it is appropriate to state the main limitations and the practical scope of interpretation. The sample size ( $n = 40$ ) provides a clear and reproducible baseline for QC parameters, PCA, and ROH metrics, but limits the granularity of conclusions about population structure and especially about the nature of ROH-enriched regions. In addition, without extended information on pedigree and sires, the interpretation of within-breed stratification necessarily remains cautious and requires confirmation in independent material. Nevertheless, the current result set has clear practical value because it establishes a reproducible framework for genomic herd monitoring, including transparent QC, marking individual heterozygosity features, structure description, and quantitative autozygosity assessment. Thus, the study provides a foundation for expanding the cohort, deepening interpretation, and when phenotypes and pedigrees are available—moving from descriptive population genomics to selection-oriented evaluation models and management of genetic risks.

### Conclusions.

SNP genotyping data were of high quality:  $F_{\text{MISS}} = 0.0009$  (0.0000–0.0098) and mean call rate = 0.9991; heterozygosity estimates were  $H_o = 0.3767$  and  $H_e = 0.3664$ , and mean  $F$  (PLINK) = -0.0281 (-0.0642–0.0868). Standardized-heterozygosity outliers were identified (A01, A08, A22).

Population-structure analysis indicated within-breed heterogeneity: PCA revealed stratification of the cohort, and within  $K = 2$ –6 the lowest median ADMIXTURE model-quality metric was observed at  $K = 2$  (0.608340,  $N = 20$ ).

ROH analysis showed inter-individual variation in autozygosity: total ROH length ( $\geq 1$  Mb) averaged 14.2505 Mb (median 12.9970 Mb; 0.0000–45.5073 Mb), with the highest values observed in A20, A30, and A23.

Genome-wide ROH coverage analysis (1-Mb windows) identified regions with increased ROH overlap in the cohort; the maximum was 0.275 (11/40), supporting the definition of candidate consensus ROH regions for downstream annotation.

*The article was prepared within the framework of the implementation of the topic of the state assignment of the Federal State Budgetary Scientific Institution Federal Scientific Center of the Republic of Dagestan “Improving the breeding and productive qualities of regionalized breeds of dairy and beef cattle, sheep based on genomic selection methods and DNA technologies”, Пер. № в ЕГИСУ НИОКТР 122023400294-0.*

### REFERENCES / СПИСОК ЛИТЕРАТУРЫ

1. Alexander D. H., Novembre J., Lange K. Fast model-based estimation of ancestry in unrelated individuals. *Genome Research*. 2009;19(9):1655–1664. DOI:10.1101/gr.094052.109.
2. Development and characterization of a high density SNP genotyping assay for cattle / L. K. Matukumalli et al. *PLoS ONE*. 2009;4(4):e5350. DOI:10.1371/journal.pone.0005350.
3. Estimates of autozygosity derived from runs of homozygosity: empirical evidence from selected cattle populations / M. Ferencaković et al. *Journal of Animal Breeding and Genetics*. 2013;130(4):286–293. DOI:10.1111/jbg.12012.
4. Estimating autozygosity from high-throughput information: effects of SNP density and genotyping errors / M. Ferencaković et al. *Genetics Selection Evolution*. 2013;45:42. DOI:10.1186/1297-9686-45-42.
5. Gautier M., Laloë D., Moazami-Goudarzi K. Insights into the genetic history of French cattle from dense SNP data on 47 worldwide breeds. *PLoS ONE*. 2010;5(9):e13038. DOI:10.1371/journal.pone.0013038.
6. Genome-wide SNP analysis clearly distinguished the Belarusian Red cattle from other European cattle breeds / N. A. Zinovieva et al. *Animal Genetics*. 2021;52(5):720–724. DOI:10.1111/age.13102.
7. Investigation of the Genetic Diversity of Dagestan Mountain Cattle Using STR-Markers / V. V. Volkova et al. *Diversity*. 2022;14(7):569. DOI:10.3390/d14070569.
8. Meuwissen T. H. E., Hayes B. J., Goddard M. E. Prediction of total genetic value using genome-wide dense marker maps. *Genetics*. 2001;157(4):1819–1829. DOI:10.1093/genetics/157.4.1819.
9. Patterson N., Price A. L., Reich D. Population structure and eigenanalysis. *PLoS Genetics*. 2006;2(12):e190. DOI:10.1371/journal.pgen.0020190.
10. PLINK: A Tool Set for Whole-Genome Association and Population-Based Linkage Analyses / S. Purcell et al. *The American Journal of Human Genetics*. 2007;81(3):559–575. DOI:10.1086/519795.
11. Runs of homozygosity and population history in cattle / D. C. Purfield et al. *BMC Genetics*. 2012;13:70. DOI:10.1186/1471-2156-13-70.
12. Runs of homozygosity: current knowledge and applications in livestock / E. Peripolli et al. *Animal Genetics*. 2017;48(3):255–271. DOI:10.1111/age.12526.
13. The Bovine HapMap Consortium. Genome-wide survey of SNP variation uncovers the genetic structure of cattle breeds. *Science*. 2009;324:528–532. DOI:10.1126/science.1167936.
14. Whole-genome SNP analysis elucidates the genetic structure of Russian cattle and its relationship with Eurasian taurine breeds / A. A. Sermyagin et al. *Genetics Selection Evolution*. 2018;50:37. DOI:10.1186/s12711-018-0408-8.
15. Worldwide patterns of ancestry, divergence, and admixture in domesticated cattle / J. E. Decker et al. *PLoS Genetics*. 2014;10(3):e1004254. DOI:10.1371/journal.pgen.1004254.

*The article was submitted 01.07.2025; approved after reviewing 29.08.2025; accepted for publication 03.09.2025.*

*Статья поступила в редакцию 01.07.2025; одобрена после рецензирования 29.08.2025; принята к публикации 03.09.2025.*

