CHARACTERIZATION OF MORPHOLOGY, GENOMIC DIVERSITY AND ENVIRONMENTAL ADAPTATION OF INDIGENOUS CATTLE POPULATIONS IN TIGRAY NATIONAL REGIONAL STATE, ETHIOPIA

A THESIS SUBMITTED

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THE SCHOOL OF GRADUATE STUDIES
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BY
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This is to certify that the dissertation prepared by Tsadkan Zegeye Kahsay entitled: “Characterization of Morphology, Genomic Diversity and Environmental Adaptation of Indigenous Cattle Populations in Tigray National Regional State, Ethiopia**”** submitted in partial fulfilment of the requirements for the Degree of Doctor of Philosophy in Applied Genetics complied with the regulations of the University and meets the accepted standards concerning originality and quality.

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DECLARATION

I, Tsadkan Zegeye Kahsay, hereby declare that this dissertation and its content is my own original work and any assistances or materials used during the course of this study are fully acknowledged.

January, 2024

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DEDICATION

This thesis is dedicated to the memory of my beloved late Grandmother Mrs. Alemash Weres Biru.

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LIST OF ABBREVIATIONS

AAF	Alternate Allele Frequency
ADMY	Average Dairy Milk Yield
AFC	Age at First Calving
AFLP	Amplified Fragment Length Polymorphism
AFM	Age at First Mating
AICc	Akaike Information Criterion corrected
AnGR	Animal Genetic Resources
AUC	Area Under the Receiving Operator Curve
BAM	Binary Alignment Map
BL	Body Length
BM	Beta Multiplier
bp	Base pair
BP	Biological Process
BQSR	Base Quality Score Recalibration
BWA	Burrows Wheeler Aligner
C	Categorical
CAAS	Chinese Academy of Agricultural Sciences
CC	Cellular Components
CD	Chest Depth
CI	Calving Interval
CL	Cultivated Land
CLR	Composite Likelihood Ratio
CMI	Crop Mask Irrigation
cmol/kg	Centimole/kilogram
CSA	Central Statistical Authority
CV	Cross Validation
DAGRIS	Domestic Animal Genetic Resources Information System

DAVID	Database for Annotation, Visualization, and Integrated Discovery
dbSNP	Single Nucleotide Polymorphism Database
DNA	Deoxyribonucleic Acid
DW	Dewlap Width
EBI	Ethiopian Biodiversity Institute
EDTA	Ethylenediaminetetraacetic acid
EL	Ear Length
ENM	Ecological Niche Modelling
FAO	Food and Agricultural Organization
FC	Combination of Feature Class
FDR	Functional Divergence Ratio
F_{HOM}	Inbreeding coefficient inbreeding coefficient using the “–het”
FL	Face Length
F_{ROH}	Inbreeding coefficient based on runs of homozygosity
F_{ST}	Genetic Distance
GAM	Generalized Additive Model
GATK	Genome Analysis Toolkit’s
Gb	Gigabase
gDNA	Genomic DNA
GDP	Gross Domestic Product
GFSAD	Global Food Security Analysis-Support Data
GO	Gene Ontology
GPS	Geographic Positioning System
GRRFAC	Genomic Reference Resource for African Cattle
GVCF	Genomic Variant Call Format
H	Hinge
HBC	Horn Base Circumference
HBS	Horn Base Spacing
HC	Hock Circumference

HCW	Hot carcass weight
HL	Horn Length
H_O	Observed Heterozygosity
Hp	Pooled Heterozygosity
HSD	Honest Significant Difference
HTS	Horn Tip Spacing
HW	Height at Withers
IBC	Institute of Biodiversity Conservation
iHS	Integrated Haplotype Score
ILRI	International Livestock Research Institute
Kb	Kilobase
KEGG	Kyoto Encyclopedia of Genes and Genomes
kg/m^3	Kilogram per cubic meter
km2	Square kilometters
KPa	kilopascals
L	Linear
L_{AUTO}	Length of the autosomal genome
LD	Linkage Disequilibrium
LDA	Linear Discriminant Analysis
LDD	Linkage Disequilibrium Decay
LL	Lactation Length
LMY	Lean Meat yield
L_{ROH}	Total length of ROH covering an individual
MST	Multivariate Statistical Tools
M	million
MAF	Minor allele frequency
masl	Meters above sea level
MaxEnt	Maximum Entropy Modelling
MAZT	Major Agroecological Zones of Tigray
Mb	Megabase

MC	Muzzle Circumference
MF	Molecular Function
ml	Milliliter
mm	Millimeter
MoA	Ministry of Agriculture
MVS	MaxEnt VariableSelection
ng/µl	Nanograms per microliter
NGS	Next-Generation Sequencing
NL	Neck Length
NSC	Number of Services per Conception
nSNPs	Number of Single Nucleotide Polymorphism
NZAGRC	New Zealand Agricultural Greenhouse Gas Research Centre
^oC	Degrees Celsius
P	Product
PC	Principal Component
PCA	Principal Components Analysis
PS	Perpetual Sheath
PW	Pelvic Width
Q	Quadratic
RAPD	Random Amplification of Polymorphic DNA
rEHH	Relative Extended Haplotype Homozygosity
RFLP	Restriction Fragment Length Polymorphism
RH	Rump Height
RL	Rump Length
ROH	Runs of Homozygosity
r_s	Spearman’s correlation
SBD	Soil Bulk Density
SC	Scrotal Circumference
SCaEC	Soil Cation Exchange capacity
SClC	Soil Clay Content

SDM	Spatial Distribution Models
SFS	Site Frequency Spectrum
SNNP	Southern Nations, Nationalities, and People’s
SOC	Soil Organic Content
SpH	Soil pH
SPSS	Statistical Package for the Social Sciences
SSaC	Soil Sand Content
SSiC	Soil Silt Content
SSRs	Simple Sequence Repeats
STMS	Sequence Tagged Microsatellite Sites
STRs	Short Tandem Repeats
T	Threshold
TAEC	Traditional Agro Ecology Category
TBT	Tail Base Thickness
Ti/Tv	Transitions to Transversions ratio
TL	Tail Length
UPGMA	Unweighted Pair Group Method with Arithmetic Mean
UTR	Untranslated Region
VCF	Variant Calling Format
VEP	Variant Effect Predictor
WGS	Whole Genome Sequencing
XP-EHH	Extended Haplotype Homozygosity
ZF_{ST}	Transformed value of the F_{ST}
ZHp	Transformed value of the Hp
π	Nucleotide Diversity

ABSTRACT

Ethiopia is the home of the largest cattle population in Africa and the fifth in the world. Cattle in Ethiopia are the primary agricultural entity serving fully or partially the livelihood of around 70% of the population. They are the most important generators of the agricultural GDP, contributing around 80% of the annual production of milk and meat. However, despite providing the majority of the livestock products in the country, Ethiopia's indigenous cattle genetic resource has yet to receive much attention. Breed identification and characterization still need to be completed, and an institutional framework for conservation and wise management of their genetic diversity needs to be established. The Tigray National Regional State, in the North of Ethiopia, is the fourth cattle-populated region, with about 8% of Ethiopia's cattle genetic resources. However, Tigray is one of the regions of Ethiopia where its animal genetic resources still need to be fully identified and characterized. This study aimed to undertake a comprehensive characterization of indigenous cattle populations in Tigray (Abergelle, Arado, Begait, Erob and Raya) involving their morphology, ecological niche suitability, genome-wide genetic diversity, and the genomic response of selection to the environmental challenges. Sampling sites were selected purposively to include a comprehensive representation of the indigenous cattle populations from their respective natural breeding areas. A total of 1650 matured cattle from the five populations were included to investigate the phenotypic description based on qualitative and quantitative traits. Data analysis was performed using chi-square involving crosstabs for the qualitative variability and multivariate discriminant analysis involving GLM, STEPDISC, CANDISC, DISCRIM, and Canonical discriminate function procedures of SAS for the quantitative variability. The stepwise discriminant analysis screened eighteen variables with a discriminant power for characterizing the female and thirteen for the male populations. High correct assignments to source populations were obtained for all populations except Abergelle and Erob, where around 30% of each shared morphologic similarity. The five populations were also clustered into four populations, with Abergele and Erob cattle overlapping. The environmental niche of each cattle population was characterized by the new approach applied to livestock, Environmental

Niche Modeling (ENM). From the sampling locations, thirty coordinates (4 to 7 per population) were collected using the Geographic Positioning System (GPS) and nine coordinates surrounding 1 kilometer of the initial sampling location were extracted using Google Earth Pro 7.3.1.4507. Finally, 300 coordinates were used to extract data (from thirty-three environmental predictors) for habitat suitability mapping and screening out of the main environmental variables. Four distinct habitat suitability maps were detected, except for the Arado and Erob cattle, with around 66% niche similarity. Six main environmental variables, temperature seasonality, soil bulk density, cultivated land, and annual, wettest and warmest quarter precipitations that could have a potential driving factor for morphological and genetic variability across the indigenous cattle in Tigray were sorted out. Next, the whole genome sequence data was followed to characterize the genome-wide genetic diversity, relatedness, and admixture of the same five cattle populations. A high number of genetic variants were detected, where around seven and thirty-four per cent of SNPs and indels were novel, respectively. The genome-wide average nucleotide diversity ranged from 0.0035 to 0.0036. The number of heterozygous SNPs was about 0.6 to 0.7 higher than homozygous SNPs. There was high variability in ROH records among and within animals of each population, with the lowest record in Arado (777.82) and the highest in Raya (1000.45). Similarly, the analysis of inbreeding revealed differences within and among populations, ranging up to 10% in some individuals of Begait and Raya populations. Only a fraction (0.01% SNPs and 0.22% to 0.27% indels) of the identified variants annotated for functional variability overlapped coding regions. The enrichment analysis of genes overlapped missense private SNPs screened 20 significant GO terms and KEGG pathways common or specific to each population. Out of the gens overlapped missense private SNPs, the genes *SCN4A*, *TAS1R2* and *KCNG4* related to body size and length were specifically detected in Begait cattle and genes *MMRN2* and *VWC2* related to meat quality were detected in Erob cattle supporting the morphological finding. The population structure revealed the ancestry background of the indigenous cattle in Tigray from Asian indicine (85.6% to 88.7%) and African taurine (11.3% to 14.1%) cattle, with very small European taurine introgression in some individuals. Finally, the positive signatures of adaptation of the cattle populations to the main environmental stressors were analyzed following two genomic scans (*Hp*) and (F_{ST}). Selective sweeps of the overlapped regions were analyzed using *Hp* and F_{ST} to retrieve the candidate protein-coding genes. Around 60% of the annotated selective sweeps regions overlapped with protein-coding genes, while the rest lacked genes. GO and KEGG pathways of the protein-coding genes overlapped selective sweep regions revealed enriched ($P < 0.05$) genes involved in adaptation to moisture-stressed lowlands (*HELB*, *HMGA2*, *IRAK3*, *LLPH*, *UCN2*, *LOC101902172*, *ADAMTS16*, *DDB1*, *ASIP*, *IL17B*, *SNAP29*) and moisture-stressed highlands (*NQO1*, *NEK6*, *LHX2*, *UCP*2, *UCP3* and *LCMT2*). This study shared detailed findings on the morphology, genetic and adaptive diversity of the indigenous cattle in Tigray. Diverse morphological and genomic diversity was observed in the Indigenous cattle in Tigray, indicating their importance as a genetic reservoir at regional and country levels. Moreover, the production type of the indigenous cattle in Tigray screened through the interlinking of morphological description and specific genes selected for production values provide insight into their breeding management.

Keywords: Body measurements, Discriminant function analysis, Habitat suitability, Multivariate analysis, Private missense variants, Selected environmental variables, Selective sweep regions, Indigenous cattle in Tigray.

CHAPTER 1. INTRODUCTION

1.1. Background and Justification

So far, around 1019 local cattle breeds have been recognized worldwide (FAO, 2015) and their population is now extended to 1.53 billion heads (FAOSTAT, 2023). However, in most developing countries, many animal genetic resources are non-descriptive due to the absence of detailed data about the population type, structure, and agroecological distribution. Apart to the limited identification and characterization, the genetic diversity of indigenous cattle genetic resource in most of the developing countries like Ethiopia are being threatened by different factors including unplanned crossbreeding which are happening even before the formal characterization, changes in husbandry or production environments, changes in producers' preference, weak or lack of Animal Genetic Resources (AnGR) management, globalization and climate change (Sansthan and KÖhler-Rollefson, 2005; FAO, 2009; FAO, 2015). Particularly, the changes in producers' preference for certain breeds or traits (Rege and Gibson, 2003; Tisdell, 2003) can lead to the loss of other essential traits for adaptation, disease resistance, fecundity, and fertility. The flow of genes between countries and the focus on similar breeding objectives due to globalization can result in the selection of the same cattle everywhere (Sheldon *et al*., 2008). Hence, this action can be ended in the long run with inbreeding and loss of genetic variation (Mwai *et al*., 2015; Eusebi *et al*., 2019). On top of this, the ever-changing climatic conditions resulting from global warming further challenge the AnGR by exerting an adverse effect on feed access and quality, water resources and disease incidences (Rojas-Downing *et al*., 2017).

Due to the above alarming conditions, there is currently a global concern for characterizing, improving, and conserving indigenous animal genetic resources (FAO, 2015; Eusebi *et al*., 2019). This is because the indigenous animal genetic resource, especially those in the tropical environment, have unique traits for adapting to such a challenging environment with recurrent drought, disease outbreaks, and shortage of quantity and quality feedstuffs (Mwai *et al*., 2015).

Ethiopia, the fifth cattle populated globally and the first in Africa has around 65.72 heads of cattle (FAOSTAT, 2023). Moreover, the country has been considered the center of zebu's first and second-wave introgression and gateway to the African content (Hanotte *et al*., 2002; FAO, 2007; Li *et al*., 2007; Ajmone-Marsan *et al*., 2010; Pitt *et al*., 2019). It has also been thought of as the center of the hybridization, origin and domestication of sanga cattle (Epstein, 1957; Ajmone-Marsan *et al*., 2010) that was formed from the interbreeding of zebu and humpless longhorn taurine stocks following the first introduction of zebu cattle into Africa (Epstein, 1957). Mukasa-Mugerwa (1989) and Rege (1999) indicated even the word sanga (which means ox or bull) had initially originated in Ethiopia.

Cattle in Ethiopia are the primary agricultural entity (Behnke and Fitaweke, 2011), serving fully or partially to the livelihood of nearly 70% of the population (FAO, 2019). They are the most important generator of the agricultural GDP (45%) in the country (Behnke and Fitaweke, 2011). Out of the total annual production of milk (3.8 billion liters of milk) (FAO and NZAGRC, 2017) and meat (one million tons) (Shapiro *et al*., 2015), cattle contribute 80% of the total product (Behnke and Fitaweke, 2011). Specifically, cows contribute to about 94.6% of the annual milk produced (CSA, 2017), from where the indigenous stocks in the hands of smallholder farmers with minimal production inputs, extensive management and poor health care facilities contribute 96% of it. However, despite serving the majority of the livestock products in the country (Workneh *et al*., 2003; FAO, 2007; Dereje and Kefelegn, 2016; EBI, 2016; Bekuma and Ketema, 2018), Ethiopia's indigenous cattle genetic resource has received little attention. Breed identification and characterization still need to be completed, and there needs to be an institutional framework for conservation and wise management of their genetic diversity (Zewdu *et al*., 2013; EBI, 2016).

1.2. Rationale of the Study

The Tigray National Regional State in the North of Ethiopia is an ancient center of civilizations (e.g, ancient pre-Aksumite Kingdom of Da'amat and Aksumite Kingdom of Axum) which were in trading contacts with the ancient civilizations of the Fertile Crescent and the Indus Valley (Finneran, 2007; Pagani *et al*., 2012). Accordingly, it had an important role in the introduction of livestock into the Horn of Africa (Helina and D'Andrea, 2017). It is the fourth most cattle-populated Ethiopian region, with about 8% of the country's cattle genetic resources (CSA, 2018). However, Tigray is one of the regions of Ethiopia where its animal genetic resources still need to be fully identified and characterized. Abergelle, Arado, Begait, Erob and Raya are the indigenous cattle in Tigray being reared in the Region. So far, these populations are not effectively characterized, with limited and fragmented works in the literature.

For instance, previous works to describe some of these populations morphologically were focused on a few of the qualitative and quantitative traits and reported on single trait-based analysis (Merha *et al*., 2007b; Dessalegn, 2009; Mulugeta and Berhan, 2015) without discriminating the combined effect of all measured traits and missed to show the morphological similarity and distinctiveness across the populations (Dossa *et al*., 2007; Yakubu *et al*., 2010). Hence, the indigenous cattle in Tigray need to be characterized morphologically incorporating multiple qualitative and quantitative traits and need to be addressed following the advanced multivariate statistical tools (Traore *et al*., 2008; Yakubu and Akinyemi, 2010; Birteeb *et al*., 2012; Aziz and Al-Haur, 2013) that have a higher power of evaluating all the quantitative traits and able to evaluate the variability within and among populations (Yakubu and Ibrahim, 2011).

Previously, there have been limited efforts to investigate the main ecological variables that have key roles in adaptive diversity in livestock (Gheyas *et al*., 2021). Livestock breeds were only characterized according to their place of origin or based on the morphological or phenotypic features without linking to the environmental variables that described their habitat (Sanarana *et al*., 2015; Matawork, 2017; FAO, 2018). Such approaches may fail to indicate the main environmental factors shaping adaptation. Recent studies tried to define non-descript indigenous chicken populations in Ethiopia (Fasil *et al*., 2021; Gheyas *et al*., 2021; Gebreslassie *et al*., 2022; Vallejo-Trujillo *et al*., 2022) using ecological niche modelling (ENM) and all recommended the boost importance of applying the model for other livestock breeds. Ecological niche modelling (ENM) or spatial distribution models (SDMs) are biological science models used for predicting the spatial distribution of species (Dicko *et al*., 2014) and identifying the main environmental variables that have a key role in shaping the adaptive nature of a species to a specific environment (Raxworthy *et al*., 2007). Such modelling tools are tremendously important (Graham *et al*., 2004), particularly in the tropics, where modelling has a crucial value for conservation (Anderson *et al*., 2002). For cattle, the only study conducted in Uganda reported the integration of environment with the Ugandan cattle adaptability to East Coast Fever (Vajana *et al*., 2018). This study is the first to characterize the indigenous cattle in Tigray's breeding niche or production environments following the detailed MaxEnt procedures of ENM.

Previous studies reported the genetic diversity of some of the indigenous cattle in Tigray populations using low-density molecular markers such as microsatellites, Y-chromosome markers or SNP arrays (Li *et al*., 2007; Merha *et al*., 2007a; Hailu *et al*., 2008; Merha *et al*., 2011; Zewdu *et al*., 2015). However, less dense molecular markers do not represent the complete genome sequence and couldn’t provide information on rare variants and their causal mutations. So, conserving rare variants may not be possible as they are inaccessible through less dense molecular markers (Eusebi *et al*., 2019). Particularly, SNP arrays could lead to incorrect results (Lachance and Tishkoff, 2013) due to the ascertainment biases (Nielsen *et al*., 2011; Pérez-Enciso *et al*., 2015) and inclusion of SNPs with high minor allele frequencies (Lencz *et al*., 2007).

The detection of all genetic variants in the genome is, therefore, an important step in finding mutant variants linked with complex traits in livestock species (Jiang *et al*., 2014; Das *et al*., 2015) and in the detailed investigation of large chromosome segments, including stretches of homozygous genomic regions (Bosse *et al*., 2012; Zhang *et al*., 2015b). Due to the recent advancement in next-generation sequencing (NGS) technology and sequence analysis tools, whole-genome-based characterization studies, less prone to breed ascertainment biases (Eusebi *et al*., 2019), are becoming the method of choice for genome diversity characterization (Shendure and Ji, 2008; Stafuzza *et al*., 2017). They are feasible tools to quickly, efficiently and accurately identify genetic variants (Shendure and Ji, 2008), including single nucleotide variants (SNPs and indels (Stafuzza *et al*., 2017). At the opposite of microsatellite and SNPs arrays, they provide a complete representation of the diversity of a genome and an entry point to the identification of candidate causative variants associated with Mendelian and quantitative traits (Jiang *et al*., 2014; Das *et al*., 2015). Therefore, the genome-wide genetic diversity, admixture, and relatedness of the indigenous cattle in Tigray and their genomic regions that pinpoint the signatures of adaptive selection for environmental stressors need to be investigated based on whole-genome sequence data.

This study could be the first to provide the detailed and comprehensive characterizations of the indigenous cattle in Tigray (Abergelle, Arado, Begait, Erob and Raya) involving their morphology, production environments, genome-wide genetic diversity and the genomic response of selection to the main environmental stressors. Moreover, as this study follows the recent methods and technologies, such as the Multivariate Statistical Tools (MST), Ecological Niche Modelling (ENM) and Next-Generation Sequencing (NGS) platform, it could clearly distinguish the morphologic and genetic variability as well as the regions specifically under strong positive selection, possibly indicate the adaptive diversity or production objective of each population. The detailed findings following this study might be used as a cornerstone for future cattle productivity improvement in the Region.

1.3. Objectives of the Study

General objective:

- To characterize the morphology, ecological niche suitability, genome-wide genetic diversity and the genomic response of selection to environmental factors in the indigenous cattle in Tigray (Abergelle, Arado, Begait, Erob and Raya).

Specific objectives:

- To characterize the morphological traits of the indigenous cattle in Tigray.
- To map the ecological niche suitability and screen the main environmental drivers of adaptation for the indigenous cattle in Tigray.
- To characterize the genetic diversity, relatedness and admixture of the indigenous cattle in Tigray.
- To detect genomic regions under positive selection in the indigenous cattle in Tigray in response to the main environmental drivers.

1.4. Research Questions

- ✓ How are the indigenous cattle in Tigray clustered based on morphological traits?
- ✓ How is the habitat suitability mapped and screened the main environmental factors determining the adaptive diversity of the indigenous cattle in Tigray?
- ✓ How are the indigenous cattle in Tigray clustered based on autosomal genetic variants (SNPs and indels)?
- ✓ How is the ancestral genetic background of the indigenous cattle in Tigray linked with European or African taurine and the Asian zebu reference cattle populations?
- ✓ How are the genomic responses of the indigenous cattle in Tigray concerning the main environmental drives of genomic selection?

1.5. Significance of the Study

This study is highly valuable for the academic or scientific community, policymakers, or society regarding the key findings reported in this thesis. It also reported the morphologic and genetic level similarity and distinctiveness of the indigenous cattle in Tigray, mapped their niche suitability and detected target regions under positive selection pressure for adapting their respective ecological niche. These findings can be used as a base for their conservation, breeding and selection strategies for improving their productivity and keeping their adaptive values. Moreover, the findings and procedures followed on the published and publishable manuscripts prepared could be used by the scientific or research communities for future research and scientific works.

CHAPTER 2. LITERATURE REVIEW

2.1. Cattle Domestication and Global Distribution

Domestication is the way of adapting wild plants and animals for human use. The domestication of animals and crop species contributed to the development of agriculture. The story of agriculture further contributed to the modification of the socio-cultural activity of human beings. For instance, feeding habits solely dependent on hunting wild animals were changed to rearing animals and planting crop species (Diamond, 2002; Vigne, 2008). The modern-day animals, including cattle, were, therefore, domesticated from their wild ancestors in a form to be utilized by human beings more effectively (Diamond, 2002; Mignon-Grasteau, 2005). The aurochs (Bos primigenius) reported to be the ancestor of modern cattle (*Bos taurus* and *Bos indicus*) were formerly widespread wild species from Northern tundra to both the Atlantic and Pacific coasts of Eurasia during the Pleistocene and Holocene (Zeuner, 1963) but extinct since 1627 A.D (Anno Domini, or "in the year of our lord) (Götherström *et al*., 2005).

As an indication of the origin and domestication of aurochs (*Bos Primigenius*), it was reported that the foremost fossil was found through archaeological findings 10,500 years ago in the Anatolian Fertile Crescent (Bradley and Magee, 2006). Different kinds of literature of previous studies had reported different domestication events of modern cattle. For instance, Bruford *et al*. (2003) reported three distinct initial domestication events of cattle from three distinct aurochs (*Bos Primigenius*) subspecies (*Bos primigenius primigenius*, *Bos primigenius africanus* and *Bos primigenius* nomadicus). *Bos primigenius primigenius*, which is believed to be the ancestor of humpless *Bos taurus* cattle of the Near East (Bradley *et al*., 1996; Bruford *et al.,* 2003; Bradley and Magee, 2006) was domesticated around 10,000 B.P. in the Near and Middle East (West Asia) (Wendorf and Schild, 1994). The *Bos primigenius* nomadicus, the ancestor of Bos taurus indicus (Bradley *et al*., 1996; Bruford *et al*., 2003; Ajmone-Marsan *et al*., 2010), was also domesticated around 9000 to 10,000 B.P (years Before the Present) or about 1500 years following the domestication of the *Bos primigenius primigenius* in the Indus Valley region of modern-day Pakistan (South Asia) (Grigson 1991; Loftus *et al*., 1994; Bradley *et al*., 1996; Bradley and Magee, 2006; Stock and Gifford, 2013). On the other hand, a hotspot of zebu mtDNA diversity from the Indian peninsula or South of the Himalayas indicated the domestication of *Bos taurus indicus* in India, followed by migrations toward Southwest Asia, China, and Southeast Asia (Lei *et al*., 2006; Lai *et al*., 2006; Chen *et al*., 2010). As a third domestication event, the *Bos primigenius africanus* or *Bos primigenius opisthonomous*, alternatively called African aurochs (Clutton-Brock, 1999), is believed to be the ancestor of humpless cattle of Northeast Africa (Bruford *et al*., 2003; FAO, 2007) was domesticated around 8,000-9,000 B.P. in the Northeastern part of the African continent (Wendorf and Schild, 1994). However, another study by Loftus *et al*. (1994) showed only one domestication center for the *Bos taurus taurus,* which was in the Fertile Crescent.

Next to the above three domestication centers, there was another (considered fourth) domestication center within Northeastern Asia (Mannen *et al*., 2004). However, there was uncertainty about whether it was domesticated independently or a simple introgression of local aurochs with cattle of the Near East (FAO, 2007). On top of the subspecies of cattle *Bos taurus* and *Bos indicus,* a third subspecies of cattle was reported *Bos javanicus* or the Balli cattle domesticated from Banteng (*Bos banteng* or *Bos javanicus*) in Indonesia (Southeast Asia) at 5500 BP (Nijman *et al*., 2003).

Recent molecular studies reported different stories from all the above cattle domestication stories. Through the analysis of the worldwide ancestry of 139 bovine breeds using the SNP array data, Decker *et al*. (2014) reported the formation of African taurine from the interbreeding of already domesticated Fertile Crescent taurine cattle and the wild African aurochs, supporting only two domestication events. Another molecular analysis using SNP array data from 180 populations involving about three thousand cattle samples collected from Africa, including two cattle populations from Ethiopia (Boran and Sheko), Europe, Asia and the Americas disproved the idea of a third domestication event in the Northeastern part of the African continent (today Egypt) and confirmed only two domestication events from two aurochs subspecies (*Bos primigenius primigenius* and *primigenius nomadicus*, respectively for taurine and indicine cattle) (Pitt *et al*., 2019) (Figure 1). It was, therefore, thought that the high variation being observed between the taurine cattle breeds from Africa and Eurasians or others may have resulted from the consequent hybridization of the already domesticated taurine cattle with the local aurochs therein (the Northeastern part of the African continent) at that moment (Decker *et al*., 2014; Pitt *et al*., 2019).

From the centers of domestication, present-day cattle were distributed worldwide through different dispersion methods. Ancient sea trading routes were vital to spreading cattle from the center of domestication to parts of the world. Earlier molecular genetic studies in cattle had revealed the introduction of zebu animals into Africa via an Indian Ocean corridor rather than overland through the Isthmus of Suez or the Sinai Peninsula (Hanotte *et al*., 2002; Freeman *et al*., 2006). On the other hand, archaeological and genetic information suggests that the spread of pastoralism in the Mediterranean basin followed terrestrial, coastal and maritime routes (Zilhão, 2001; Beja-Pereira *et al*., 2006).

Nowadays, the movement of livestock genotypes across the globe, especially cattle, is accelerating due to the development and marketing of high-yielding breeds, new breeding technologies, and the increasing demand for livestock products (FAO, 2007). They are also traded in the form of heifers, pregnant cows, bulls for meat, semen and embryos for breeding. This modern dispersion, essentially restricted to a few breeds that almost exclusively involve transfers from developed to developing countries, represents a significant threat to the conservation and utilization of indigenous farm animal genetic resources (AnGR) (FAO, 2007). For instance, in the 1990th, most of the world's semen trading was brought from a single breed (the Holstein-Friesian). Only one-third of semen trading came from other cattle breeds (Chupin and Schuh, 1993).

Different scholars (Hanotte *et al*., 2002; FAO, 2007; Li *et al*., 2007; Ajmone-Marsan *et al*., 2010; Pitt *et al*., 2019) indicated that Ethiopia was considered the center of cattle secondary domestication in African content. It was a center for zebu's first and second-wave introgression (Bruford *et al*. 2003; FAO, 2007). Ajmone-Marsan *et al*. (2010) showed

Ethiopia's hybridization and domestication of sanga cattle (Figure 1). Rege (1999) also supported this theory by tracing the origin of the word sanga back to Ethiopia. In the Ethiopian national language (Amharic), the word sanga means bull (Rege, 1999). In agreement with the earlier archaeological report (Mukasa-Mugerwa, 1989) that claimed the domestication of sanga cattle was limited to East Africa, Rege (1999) specified Ethiopia as the only origin of the sanga cattle (Rege, 1999). From Ethiopia, this sanga cattle type was distributed to other parts of the world (Epstein, 1957).

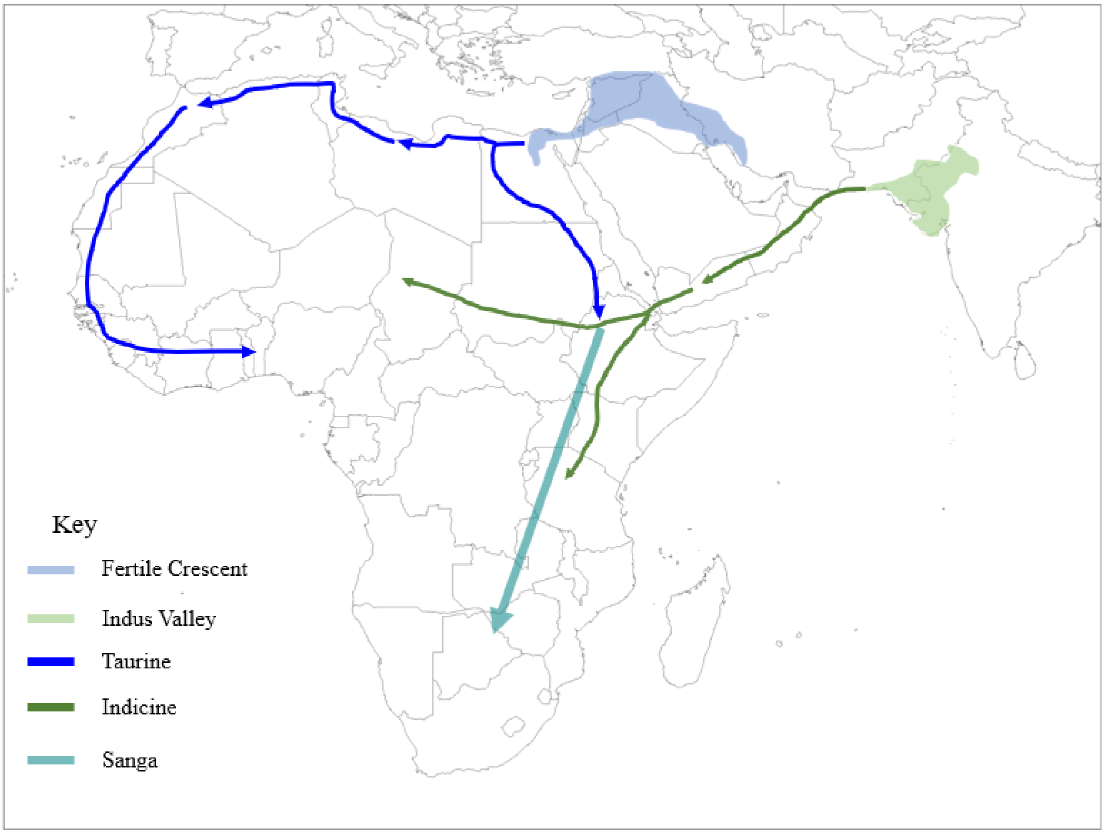


Figure 1. Showing the origin, domestication and migratory of taurine, indicine and the Sanga cattle.

2.2. Cattle Genetic Resource and their Genetic Diversity

Though the identification of cattle breeds, especially in the developing world, is not fully exploited, 1019 cattle breeds were recognized worldwide up to the year 2015 from the two major subspecies (*Bos taurus taurus* and *Bos taurus indicus*) (FAO, 2015). The worldwide cattle population grew to 1.53 billion heads, with the highest population coming from Brazil (224.6 million), second from India (193.17 million) and 65.72 head of cattle from Ethiopia, which is the highest record from Africa and fifth in the world (FAOSTAT, 2023).

However, the diversity of cattle genetic resources is being challenged by different risk factors (Figure 2) (Sansthan and KÖhler-Rollefson, 2005; FAO, 2009; FAO, 2015). Similarly, Tisdell (2003) reported different factors, including technology interference with the organic farm, commercialization targeting a single production trait, genetic admixture, continuous advancement in technology and biotechnology, political conflicts and natural disasters as the challenges for the present-day farm animal genetic resources. Some traits such as high milk production, milk fat content, milk fat percent, milk protein content and milk protein present in dairy products and some traits of meat yield and quality for beef cattle are extensively in selection (Tisdell, 2003).

Particularly, the preference for specific traits can lead to losing other essential traits for adaptation, disease resistance, fecundity, and fertility. In the long run, this action could cause a problem of reducing genetic diversity (Mwai *et al*., 2015; Eusebi *et al*., 2019). Generally, gene flow among countries and following similar breeding objectives can cause the global expansion of similar breeds (Sheldon *et al*., 2008) and end with inbreeding and loss of genetic variation.

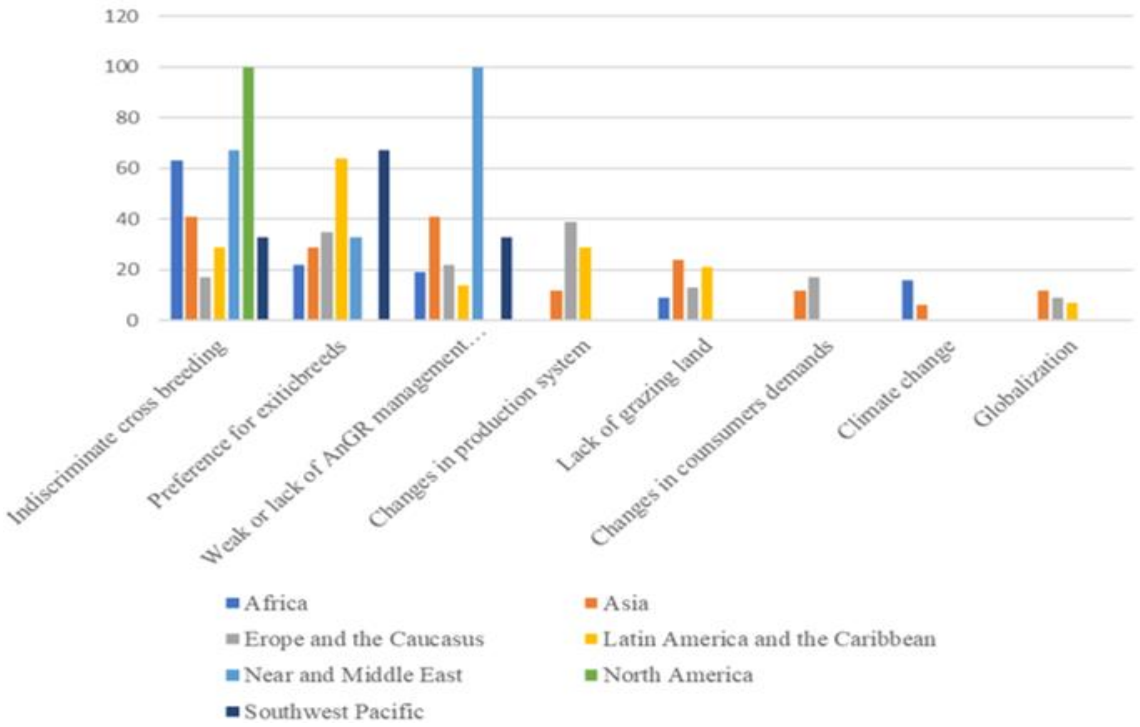


Figure 2. The proportion of different threats of AnGR reported in various regions of the world.

2.2.1. Ethiopian indigenous cattle genetic resource and their role for livelihood

In Ethiopia, livestock production is the backbone of household food security (Halderman, 2004). It is estimated to contribute about 25.3% of the total GDP (Shapiro *et al*., 2017), 45% of agricultural GDP, 23.8% of export earnings (Behnke and Fitaweke, 2011), and 31% of agricultural employment (Aleme and Lemma, 2015). Among the livestock sectors in Ethiopia, cattle production is one of the main agricultural activities, contributing to around 80% of the total livestock products (Behnke and Fitaweke, 2011).

The diversified agroecology and topography (EBI, 2016), its role as the center of secondary cattle diversification on the African continent (Hanotte *et al*., 2002; FAO, 2007; Li *et al*., 2007; Ajmone-Marsan *et al*., 2010; Pitt *et al*., 2019) might contributed for Ethiopia to have diversified and highest number of cattle populations where 98.24% are indigenous (CSA, 2018) and managed by smallholder farmers (Workneh *et al*., 2004; Rowlands *et al*., 2006;

EBI, 2016). Even if the production potential is subsistence (CSA, 2008), the indigenous stock contributes 96% of the total milk produced nationally. Only 4% comes from improved crosses and pure-grade exotic cattle reared by farmers in and around major cities of the country (FAO and NZAGRC, 2017).

Moreover, indigenous cattle genetic resources of Ethiopia can survive a wide variety of agro-ecological and environmental conditions with minimal production inputs, extensive management and poor healthcare facilities (Workneh *et al*., 2003; FAO, 2007; Dereje and Kefelegn, 2016; EBI, 2016; Amanuel and Hirpha, 2018). However, unlike all these intrinsic worth, Ethiopia's indigenous cattle genetic resource has yet to get much attention. Up to now, breed characterization and identification still need to be completed (EBI, 2016), and no information is available on the status and trend of cattle genetic resources (IBC, 2004; EBI, 2014). Moreover, the reproductive and productive performance of most of the local cattle is unknown (Habtamu *et al*., 2018). Only a few of the cattle populations identified so far (Table 1) (DAGRIS, 2007; EBI, 2016) have reported values for their productive and reproductive performance (Table 2).

Table 1. Indigenous cattle populations of Ethiopia recognized in DAGRIS.

Populations	Location	Purpose of production	References
Abergelle	Tigray	Draught power, meat, milk	DAGRIS, 2007; EBI, 2016
Afar	Afar	Meat, milk, skin and Hides	DAGRIS, 2007; EBI, 2016
Ambo	Oromiya	Draught power, meat, milk	DAGRIS, 2007; EBI, 2016
Arado	Tigray	Draught power, meat, milk	DAGRIS, 2007; EBI, 2016
Arsi	Oromiya	Draught power, meat, milk	DAGRIS, 2007; EBI, 2016
Bale	Oromiya	Draught power, meat, milk	DAGRIS, 2007; EBI, 2016
Begait	Tigray	Draught power, meat, milk	DAGRIS, 2007; EBI, 2016,
Begaria	Gambela	Draught power, meat, milk	DAGRIS, 2007; EBI, 2016
Borana	Oromiya	Draught power, meat, milk	DAGRIS, 2007; EBI, 2016
Fogera	Amhara	Draught power, meat, milk	DAGRIS, 2007; EBI, 2016
Gofa	South Ethiopia	Draught power, meat, milk	DAGRIS, 2007; EBI, 2016
Gojam Highland Zebu	Amhara	Draught power, meat, milk	DAGRIS, 2007; EBI, 2016
Guraghe	South Ethiopia	Draught power, meat, milk	DAGRIS, 2007; EBI, 2016
Hammer	South Ethiopia	Draught power, meat, milk	DAGRIS, 2007; EBI, 2016
Harar	Harar	Draught power, meat, milk	DAGRIS, 2007; EBI, 2016
Horro	Oromiya	Draught power, meat, milk	DAGRIS, 2007; EBI, 2016
Erob	Tigray	Draught power, meat, milk	DAGRIS, 2007; EBI, 2016
Jem-Jem	Oromiya	Draught power, meat, milk	DAGRIS, 2007; EBI, 2016
Jijiga	Somalia	Draught power, meat, milk	DAGRIS, 2007; EBI, 2016
Kereyu	Oromiya	Meat, milk	DAGRIS, 2007; EBI, 2016
Mursi	South Ethiopia	Draught power, meat, milk	DAGRIS, 2007; EBI, 2016
Nuer/Abigar	Gambela	Draught power, meat, milk	DAGRIS, 2007; EBI, 2016
Ogaden Zebu	Somalia	meat, milk	DAGRIS, 2007; EBI, 2016
Raya	Tigray	Draught power, meat, milk	DAGRIS, 2007; EBI, 2016
Sheko	South Ethiopia	Draught power, meat, milk	DAGRIS, 2007; EBI, 2016

DAGRIS Domestic Animal Genetic Resources Information System

Table 2. Reported productive and reproductive performances of indigenous cattle in Ethiopia.

Populations	ADMY	LL (M)	AFM (M)		AFC (M)	CI (M)	NSC (N)	Source
	Female	Female	Male	Female	Female	Female	Female	
Gofa cattle	2.1±0.2	9.3±0.9	36±0.8	40.8±0.8	56.4	15.3±4.6		Habtegiorgis *et al*., 2017
Mursi	2±0.6	7.8±2.4	43.2	40.8	55.2	14.5±4.5		Endashaw *et al*., 2015
Sheko			38.4	42	54			Takele, 2005
Boran	1.7±0.1	8	34.2	32.4-44.4	43.5±1.5	14.6±10	2.4±0.1	Aynalem *et al*., 2011
Fogera	1.98	8.1						Demelash *et al*., 2020
Bonga cattle	1.2	8.4±0.3	33.6 ± 0.1	34±0.1	45±0.1	21.77		Ebadu *et al*., 2017
Local cattle in Walmera distract	2±0.8	6.1±1.5			42.2±7.4	15±1	2±0.2	Amanuel and Hirpha, 2018
Local cattle in North Gondar	1.4±0.1	8.1±0.1		38.1±0.5	47.1±0.7	22.7±0.6	1.7±0.6	Bernabas Ayeneshet *et al*., 2018
Local cattle in Wolaita zone	2±0.1	10.8±0.5			47.1	19.9±0.8		Gebreegziabher and Tsegay, 2016
Local cattle in Awi zone	1.8							Fasil, 2006
Local cattle in Bure district	2							Adebabay, 2009
Local cattle in Gindeberet and Abuna	1.4±0.2							Bayissa *et al*., 2017
Local cattle in Dandi district						22		Belay *et al*., 2012
Afar	4±1	9±22			37±11	14±2		Merha *et al*., 2007b
Raya	3±1	7±17			41±10	15±3		Merha *et al*., 2007b
Arado	1.8±0.4	8±20			50±7	22±3		Merha *et al*., 2007b
Medeness	2.5±1	5.4±29			42±8	19±5		Merha *et al*., 2007b
Begait	5±0.5	6.8±32			38±5	16±2		Merha *et al*., 2007b
Fogera	2±0.7	5.3±24			44±6	20±4		Merha *et al*., 2007b

ADMY Average dairy milk yield, *LL* lactation length, *AFM* age at first mating, *AFC* age at first calving, *CI* calving interval, *NSC* number of services per conception, *M* month, *N* number.

2.3. Components of Indigenous Cattle Genetic Resource Characterization

The components of indigenous cattle or animal genetic resource characterization involve mainly three parts: the phenotypic, genetic and production system or environmental niche of the breed under characterization (FAO, 2011; FAO,12). However, in most developing countries, many animal genetic resources are non-descriptive due to the absence of detailed data about the population type, structure, and agroecological distribution. Identifying and recording animal genetic resources still needs to be completed, and it is always expected to find new breeds in these countries (Zewdu *et al*., 2008).

2.3.1. Phenotypic characterization

The phenotypic characterization describes the physical description, including qualitative traits such as coat color and its distribution pattern, colors for extremities including ear tip, tail switch, muscle, eyelid, horn and hoof color types. The qualitative part of physical characterization also includes conformation traits such as ear shape and orientation, hump size and location, face, rump and back profile, horn status, shape and orientation, navel width, and udder and teat size (FAO, 2012).

On the other hand, the quantitative part of the phenotypic characterization involves measuring and quantifying different body parties of an individual animal to describe the overall mean morphometrical description of the particular breed (FAO, 2012). Most of the traits to be included in the morphological characterization of cattle breeds involve height at withers (HW), body length (BL), pelvic width (PW), ear length (EL), tail length (TL), neck length (NL), hock circumference (HC), rump height (RH), rump length (RL), heart girth (HG), chest depth (CD), muzzle circumference (MC), dewlap width (DW), horn tip spacing (HTS), horn length (HL), horn base circumference (HBC), horn base spacing (HBS), Face length (FL), tail base thickness (TBT), perpetual sheath (PS), scrotal circumference (SC) (FAO, 2012). The analysis of the quantitative traits of farm animal genetic resources is advanced to multivariate statistical tools (Traore *et al*., 2008; Yakubu and Akinyemi, 2010; Birteeb *et al*., 2012; Aziz and Al-Haur, 2013) that have a higher power of evaluating all traits under investigation and able to see the actual variability within and among populations (Yakubu and Ibrahim, 2011). However, most studies tried to describe Ethiopian indigenous cattle following a single trait analysis (Table 3). Such univariate analysis based on single trait comparison could not explain the composite contribution of all measured quantitative morphological traits simultaneously (Dossa *et al*., 2007; Yakubu *et al*., 2010).

Table 3. Reported value of morphometric parameters for indigenous cattle in Ethiopia.

Populations	Sex	HW	BL	PW	HG	RL	EL	HL	MC	TL	HC	Source
Arsi	F	109	117		140		19	36		92		Yadeta and Yosef, 2020
	M	110	119		141		19	39		34		Yadeta and Yosef, 2020
Afar	F	116	125	38	146		20	61				Dereje *et al*., 2008
Abigar	F	114	122	35	143		18	45	39			Nakachew *et al*., 2018
	M	118	123	34	149		18	39	40			Nakachew *et al*., 2018
Arado	F	108	103	32	137		19	20				Dessalegn, 2009
	M	116	109	33	147		20	21				Dessalegn, 2009
Begait	F	132	128	40	160		18	21		98		Mulugeta and Berhan, 2015
	M	137	136	42	169		18	20		100		Mulugeta and Berhan, 2015
Bonga	F	101	111		135		17	22	38	29		Ebadu *et al*., 2017
	M	105	115		141		17	20	41	31		Ebadu *et al*., 2017
Fogera	F	124	107	37	149	39	24	14	38	84		Endalkachew *et al*., 2016
	M	129	112	38	162	40	25	16	42	89		Endalkachew *et al*., 2016
Goffa	F	107	107	37	135		20	27	27		29	Belay *et al*., 2017
	M	109	108	38	138		20	27		40	31	Belay *et al*., 2017
Mursi	F	105	115	35	134	18	18	27		72		Endashaw *et al*., 2015
	M	121	129	39	155	22	19	35		78		Endashaw *et al*., 2015
Sheko	F	99	110	34	137							Takele, 2005
	M	104	115	33	141							Takele, 2005
Ogaden Zebu	F	113	104	38	149		17	17	45		30	Fasil *et al*., 2014
	M	221	110	40	165		17	16	40		33	Fasil *et al*., 2014
Guraghe	F	105	99.6	32.6	130		16.5	18.6	36.2			Amine *et al*., 2024
	M	112	107	34.2	143.9		17.2	19.8	40.2			Amine *et al*., 2024
Jimma	F	104	101	32.6	124		16.3	19.9	36			Amine *et al*., 2024
	M	107	106	32.5	135.1		16.9	14.8	38.9			Amine *et al*., 2024
Indigenous cattle in South	F	106-115	112-124	32-38	135-146		17-20	16-60				Amine *et al*., 2008

Populations	Sex	HW	BL	PW	HG	RL	EL	HL	MC	TL	HC	Source
and North Wollo Zones												
	M	112-115	119-129	32-37	139-156		16-19	16-49				Dereje *et al*., 2008
Indigenous cattle in Awi, East and West Gojjam Zones	F	108.8	108.6	37.6	144.1		19.4	22.3	38.6	78.8		Fasil, 2006
	M	114.5	113.8	38.8	155.4		19.7	24	42	84		Fasil, 2006
Indigenous cattle in Gamo Goffa Zone	F	102.1	108.8	33.6	141.3	12.6	18.6	16	37.3	72.4	28.4	Chencha *et al*., 2013
	M	110.6	120.3	37	149.3	18.3	18.7	18.3	39	76.3	29.4	Chencha *et al*., 2013
Indigenous cattle in West Gojjam Zone	F	112.8	113.7	35.9	140.3		19.5	21.8	38.8	77.7		Andualem *et al*., 2016
	M	116.2	117	37	151.8		20.2	23.9	40	79.6		Andualem *et al*., 2016
Indigenous cattle in Hadiya Zone	F	99	102.3	29.4	136.9	29.6	16.6	17.9	36.7	81.7	28.4	Wondimu and Negassi, 2018
	M	107.6	109.7	39.9	145.7	32.9	18.2	20.5	38.9	84.4	33.5	Wondimu and Negassi, 2018

HW height at withers, *BL* body length, *PW* pelvic width, *EL* ear length, *TL* tail length, *HC* hock circumference, *RL* rump length, *MC* muzzle circumference horn length, *F* female, *M* male

2.3.1.1. Conventional way of production system characterization

There are various terminologies for cattle production systems based on different classification criteria. These include herd size (large, medium and small), feeding system (extensive, semi-intensive and intensive), commodity type (livestock only or livestock integrated with crop), herd movement (sedentary and transhumance), and production objective (dairy, beef and multipurpose). In a recent study by FAO (2018), four cattle production systems (mixed crop-livestock, pastoral/agro-pastoral, urban/peri-urban and commercial) are reported for each cattle production objective (dairy and beef).

Dairy production in the mixed crop-livestock system, mainly suited in Ethiopia's mid and high-altitude areas, accounts for about 65% of the milking cows in the country. Around 9.6 million farmers participate in this production system. The average herd size is four heads of animals per household, and the average daily milk yield is approximately 1.9 liters per individual cow (Figure 3) (Getachew *et al.*, 2010; FAO, 2018). However, apart from the low per-individual milk production, the gross contribution of milk offtake from this production system is very high, covering about 72% of the country's annual milk production. The rest collectively comes from the other dairy production systems (the pastoral/agro-pastoral system, urban/peri-urban and commercial) (FAO, 2018).

Unlike the dairy production system, Ethiopia has a limited intentional beef production system. Farmers consider it an immediate task for extra cash sources that can be performed within a short period. It is not the main farm activity in the mixed crop-livestock and pastoral/agro-pastoral production system. It is practiced as a permanent farm activity mainly in the commercial feedlot (commercial beef production system), followed by small-scale cattle fattening in urban and peri-urban areas (FAO, 2018). Especially in the commercial feedlot, young males are used in confined housing and stall-feeding systems for fattening, depending on the requirements of the export market (Matawork, 2017). Beef production in all the other production systems (mixed crop-livestock, the pastoral/agro-pastoral system, urban/peri-urban) mainly finishes old oxen (after completing their course of drafting or breeding) for about three to four months. In Ethiopia, particularly in Tigray, there is no whole routine involving cow to calf, calf to grower and grower to finisher stages of beef production (Matawork, 2017; FAO, 2018).

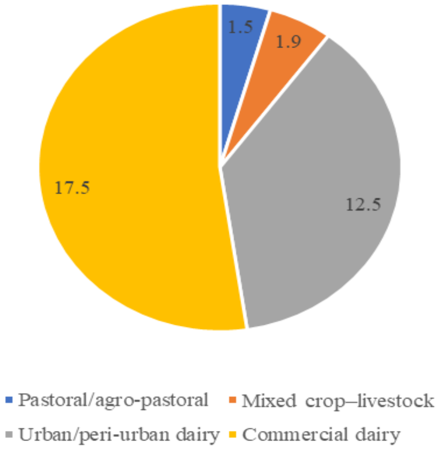


Figure 3. Average daily milk yield/cow (in liter) across different dairy production systems.

2.3.1.2. Environmental niche modelling-based habitat characterization

Models are essential tools to solve sophisticated phenomena in biological science, just as equations are applied to solve statistical or mathematical problems (Escobar, 2020). The models used in biological science include models used to predict the spatial distribution of species (Zimmermann *et al*., 2009; Kellermann *et al*., 2012; Dicko *et al*., 2014). These models are known by different terms, such as ecological niche modelling (ENM) (Peterson *et al*., 1999) and species distribution modelling (SDM) (Elith *et al*., 2006).

However, though they are expressed in different terms and used to solve different research problems that can produce various outcomes, they follow a similar protocol (Peterson, 2006). These procedures include modelling the geographical map of the species under investigation as grid cells, assigning the species under study as a dependent variable, collecting environmental variables for describing the characteristics of each cell, and finally, regularizing the importance of each environmental variable for measuring the range of suitability of each cell for the particular population under consideration (Hirzel *et al*., 2002; Raxworthy *et al*., 2007).

Ecological niche modelling has been extensively used for screening the distribution of wild species across a given habitat (Raxworthy *et al*., 2007; Meshgi *et al*., 2019; Fern *et al*., 2020; Su *et al*., 2021; Valencia-Rodríguez *et al*., 2021) and to accurately locate the prevalence of infectious diseases (Dicko *et al*., 2014; Ciss *et al*., 2019; Mwakapeje *et al*., 2019; Escobar, 2020; Muema *et al*., 2021). However, currently, it is being used to show the niche of other species, including livestock (Lozano-Jaramillo *et al*., 2019; Fasil *et al*., 2021; Gheyas *et al*., 2021; Gebreslassie *et al*., 2022; Vallejo-Trujillo *et al*., 2022). They efficiently show the main environmental contributors in determining the adaptive niche for a specific population (Soberón and Peterson, 2005; Meshgi *et al*., 2019). Moreover, they can predict the niche suitability of a particular species under investigation (Jiménez-Valverde *et al*., 2011), which can be a fundamental guideline for the area of livestock to facilitate and perform successful breed improvement whenever there is a need to improve an available breed through crossbreeding with an exotic breed or directly introducing the exotic breed to a new environment (Lozano-Jaramillo *et al*., 2019).

2.3.2. Methods of genetic diversity characterization reported in cattle and other farm animal genetic resources

Genetic diversity is described as the variability present within or across species, breeds, or individuals within a breed or species and across individuals within the same species (Woolliams and Oldenbroek, 2017). Keeping within or among breeds or cross-species diversity is mandatory to meet human beings' present and feature demands (FAO, 2015; Eusebi *et al*., 2019). Apart from gratifying the demands of human beings, conserving the within and among breeds diversity enables us to keep crucial traits such as disease resistance and adaptation, especially for the challenging tropical environments (Mwai *et al*., 2015; Eusebi *et al*., 2019).

The existing diversity of farm animal genetic resources (AnGR) has resulted from the long process of origins, domestication, management and environment (Gautier *et al*., 2010; FAO, 2011; Ajmone-Marsan *et al*., 2010; Purfield *et al*., 2012; FAO, 2015). The diversity of AnGR can be pronounced in DNA sequence variations due to nucleotide substitution (transition or transversion type), copy number variation, deletion or insertion, duplication or inversion of DNA fragments (Fulton, 2009).

Previously, within and among breeds, individuals and species, genetic diversity was assessed from the statistical inference of the pedigree records. However, this has drawbacks and limitations as it needs a careful data recording system for an extended period, perhaps from generation to generation (Eusebi *et al*., 2019). Mainly, it is impossible to think of it, especially in developing countries where their farming system is more expensive and where there is no experience of recording farm activities or keeping breeding histories of individual animals. Next, genetic diversities among populations of different breeds or species were analyzed by comparing blood groups or screening the various forms of the same enzymes or allozymes (Georges *et al*., 1990). Gradually, the genetic diversity studies based on biochemical, blood group, allozyme, and generally protein variability-based are expanded to detect variability on the DNA level (Robertson, 1994).

Due to the development in molecular genetics, it is possible to assess the status of within or among breed diversity, even for the species in the developing world with no pedigree records (Sonesson *et al*., 2012). Out of the tools being used for detecting DNA level genetic diversity in cattle, generally in farm animal genetic resources where their merit and demerits described in Table 4 include Restriction Fragment Length Polymorphism (RFLP), Random Amplification of Polymorphic DNA (RAPD), Amplified Fragment Length Polymorphism (AFLP), Microsatellites, SNPs arrays based Single Nucleotide Polymorphism (SNPs) and Whole Genome Sequencing (WGS) based characterization.

Table 4. Advantages and disadvantages of molecular markers reported in detecting farm animal genetic diversity.

List[1]	Advantages	Disadvantages
RFLP	• First-generation molecular markers (Jiang, 2013; Yang *et al.*, 2013) • High consistency and reliability (Marty *et al.*, 2012, Yang *et al.*, 2013) • Co-dominance and so, can distinguish heterozygous from homozygous (Yang *et al.*, 2013) • Quick (Marty *et al.*, 2012) • Simple (Marty *et al.*, 2012; Jiang, 2013) • Good reproducibility (Habtamu *et al.*, 2011; Jiang, 2013)	• Low discriminatory power (Smith *et al.*, 2002) • Expensive, labor-intensive and time consuming (Smith *et al.*, 2002; Jiang, 2013; Yang *et al.*, 2013) • Low genotyping throughput (Jiang, 2013) • Difficult to automate (Jiang, 2013) • Hazardous (Jiang, 2013) • Low level of polymorphism (Yang *et al.*, 2013) • Requires large-sized DNA
RAPD	• Dominant markers (Jiang, 2013; Yang *et al.*, 2013) • Low cost (Hadrys *et al.*, 1992) • High-level polymorphism (Jiang, 2013) • Quick, simple and efficient (Hadrys *et al.*, 1992; Jiang, 2013) • Requires small sized DNA required and easy to automate (Kumar and Gurusubramanian, 2011, Jiang, 2013, Yang *et al.*, 2013) • Requires small sized DNA (Jiang, 2013)	• Poor reproducibility (Meunier and Grimont, 1993; Thangaraj *et al.*, 2011; Jiang, 2013; Yang *et al.*, 2013) • Poor reliability (Meunier and Grimont, 1993) • Dominant marker, so, cannot distinguish heterozygous from homozygous (Jiang, 2013; Yang *et al.*, 2013)
AFLP	• It solves the labour-intensive and time-consuming RFLP and the reliability problem of RAPD (Yang *et al.*, 2013) • Genetic stabile • Efficient, rapid, and cost effective (Vos *et al.*, 1995) • High discriminatory power (Tabit, 2016) • Requires small sized DNA (Jiang, 2013) • Good reproducible (Jiang, 2013)	• Dominant markers (Vos *et al.*, 1995), and so unable to distinguish homozygous from heterozygous (Paglia and Morgante, 1998) • Costly (Jiang, 2013) • Low polymorphic information content for bi-allelic markers (Jiang, 2013)

List[1]	Advantages	Disadvantages
STRs or SSRs or STMS	• Reproducibility (Jiang, 2013) • Co-dominant and can to distinguish homozygotes from heterozygotes (Jiang, 2013; Yang *et al*., 2013) • High polymorphism, co-dominant markers • High accuracy, high reproducibility, and different microsatellites can be multiplexed in PCR and Easily automated (Jiang, 2013, Yang *et al*., 2013) • Require very small-sized DNA (Jiang, 2013)	• During the occurrence of null-alleles, heterozygotes may be misclassified as homozygotes (Yang *et al*., 2013) • No information on functional trait biodiversity (Yang *et al*., 2013) • Labour-intensive and costly (Jiang, 2013) • Time-consuming, Labor-intensive for the marker development process and high start-up costs for automated detections (Jiang, 2013)
SNPs arrays	• Third generation molecular markers • Co-dominant markers (Jiang, 2013; Yang *et al*., 2013) • High genetic stability (Tsuchihashi and Dracopoli, 2002; Rege and Okey, 2006) • Excellent repeatability, and high accuracy (Tsuchihashi and Dracopoli, 2002). • Quick, high-throughput genotyping (Tsuchihashi and Dracopoli, 2002; Jiang, 2013). • Very easily automated (Jiang, 2013) • Amenable to high-throughput technology (Qiu *et al*., 2017)	• High costs for start-up marker development (Jiang, 2013) • Requires high-quality DNA and skill (Jiang, 2013, Rege and Okey, 2006)
WGS	• Easy and provides complete information by detecting all the variations within the genome (Yang *et al*., 2013).	• Needs advanced skill for data analysis (Yang *et al*., 2013).

[1] *AFLP* Amplified Fragment Length Polymorphism, *RAPD* Random Amplification of Polymorphic DNA, *RFLP* Restriction Fragment Length Polymorphism, *SSRs* Simple Sequence Repeats, *STMS* Sequence Tagged Microsatellite Sites, *STRs* Short Tandem Repeats, *SNP*, Single Nucleotide Polymorphism, *WGS* Whole Genome Sequencing.

2.4. Methods of Detecting Signature Selection Reported in Cattle and other Farm Animal Genetic Resources

The inimitable regions in a genome are brought down due to the selection of signatures (Jensen *et al*., 2016). A selective sweep is a condition where positively selected variables increase in a population (Bertolini *et al*., 2018). Selective sweeps can be categorized as hard or soft and comprehensive or fractional based on their source, nature, and mutation incidence. Hard-type selective seeps cause a rapid increase in the frequency of rare advantageous mutations to be fixed in the whole population (Saravanan *et al*., 2020) and finally reduce the genetic variability in the population (Pritchard *et al*., 2010). Soft-type selective sweeps cause multiple haplotypes carrying advantageous mutations to rise in frequency simultaneously. On the other hand, complete sweeps continue until beneficial mutations are fixed in a population, whereas in the case of partial sweeps, they do not proceed until fixation (Harris *et al*., 2018).

Due to the availability of next-generation technologies, it is possible to have population-wise sequence data. Hence, it is possible to screen regions of the genome subjected to selection pressure (Sabeti *et al*., 2007; Saravanan *et al*., 2020). The areas under selection are essential to show the evolutionary process and to identify regions enriched with genes tagged with a difference or linked with complicated diseases (Laland *et al*., 2010; Lappalainen *et al*., 2010; Gouveia *et al*., 2014) and traits of adaptation or economically essential traits (Cadzow *et al*., 2014; Zhao *et al*., 2015). These regions under immense selective pressure can be detected through different methods based on the type of selection signature to be investigated and the selection duration (Sabeti *et al*., 2006). 0

After the development of high throughput sequencing and SNP genotyping tools, there is a rapid transition from less dense molecular markers to SNP data and the development of different tools for detecting selection signatures from DNA sequence or SNP genotype data in the livestock populations (Qanbari and Simianer, 2014). The methods to detect regions under selective pressure (Table 5) are collectively used for within-population or among-population statistics (Saravanan *et al*., 2020).

2.4.1. Methods for detecting intrapopulation signatures of selection

These methods, which encompass site frequency spectrum, linkage disequilibrium, and reduced local variability (Weigand and Leese, 2018), are being used to screen for footprints of genomic selection by comparing genomic data within a population (Saravanan *et al*., 2020). Site frequency spectrum (SFS) is used to detect the selection of signatures within a population following the distribution of allele frequencies (Ronen *et al*., 2013). This method includes Tajima's D (Tajima, 1989), which compares the average number of the nucleotides ($\theta\pi$) and segregating sites (θs) (Carlson *et al*., 2005) by showing zero values absence of selection and negative value under beneficial selection (Saravanan *et al*., 2020). On the other hand, Fay and Wu's H statistic (Fay and Wu, 2000), which is part of SFS, detects recent positive selection based on ancestral allele (Cadzow *et al*., 2014), while a composite likelihood ratio test (CLR) (Lindsay, 1988) detects genomic imprints of beneficial selection across multiple sites in a population (Williamson *et al*., 2007).

Following the growth of genomic technologies involving haplotype phasing and imputation, there became a development of more advanced methods such as the linkage disequilibrium decay test (LDD) and, relative extended haplotype homozygosity (rEHH), and integrated haplotype score (iHS) test. All detect long homozygous regions with high-frequency haplotypes of soft or partial selective sweeps (Sabeti *et al*., 2002). In the two tests of the linkage disequilibrium method, rEHH detects genomic regions with a recent positive selection without considering ancestral alleles. In contrast, the iHS sees selection signatures by incorporating recombination and needs ancestral allele description and haplotype phasing, recombination map, genomic position and derived allelic information (Saravanan *et al*., 2020).

Reduced local variability methods include runs of homozygosity (ROH) (McQuillan *et al*., 2008) and pooled heterozygosity (*Hp*) (Rubin *et al*., 2010) tests that detect regions with reduced variability compared to the whole genome average. Since the individual's genome near the site under selection exhibit, a long ROH higher than the genome average runs of homozygosity can be used to detect signatures of selection (Forutan *et al*., 2018; Rebelato *et al*., 2018; Xie *et al*., 2019). Pooled heterozygosity (*Hp*) calculates the deviation of expected local heterozygosity depression in chromosomal windows from the average heterozygosity of the genome based on allele counts (Rubin *et al*., 2010).

2.4.2. Methods for detecting inter-population signatures of selection

Single-site population differentiation, including F_{ST} (Wright, 1949) and FLK (Bonhomme *et al*., 2010), detects genomic selection between populations. Wright's F_{ST} relies on quantifying the difference in allele frequency where a higher F_{ST} value shows the beneficial selection and a low value shows deleterious selection (Zhao *et al*., 2015). The fixation index (F_{ST}) might be overestimated as it considers unlimited population sizes; however, this could be fine if there are above 500 SNPs (Willing *et al*., 2012). It precisely distinguishes the variation undergoing selection (Saravanan *et al*., 2020). On the other hand, single-site population differentiation can also be calculated based on FLK or TFLK (which compares variance among populations) and based on a phylogenetic estimation of the population's kinship (F) matrix (Bonhomme *et al*., 2010).

Haplotype-based differentiation methods consider haplotype data across populations. They include cross-population extended haplotype homozygosity (XP-EHH) (Sabeti *et al*., 2007), which detects signatures of selection based on haplotype deference screening among populations, and a haplotype-based extension of the FLK statistic (hapFLK) (Fariello *et al*., 2013). The XP-EHH is a directional test, and a positive value shows the selection signature occurred in population one. In contrast, the negative value indicates the selection signature performed in the second population (Saravanan *et al*., 2020). The hapFLK test, uses haplotype data, and the hierarchical structure (Fariello *et al*., 2013).

Table 5. Methods of selection signature reported in cattle and other farm animal genetic resources.

Within population	Within population		Across populations		
Methods		Source	Methods		Source
Site frequency spectrum	Allele frequencies-based distribution in a population	Ronen *et al.*, 2013	Single site population differentiation		
• Tajima's D	Compares average number of θπ and θs	Carlson *et al.*, 2005	• F_{ST}	Based on the measure of differences in frequencies of alleles between populations.	Wright, 1949
• Fay and Wu's H	Detects recent positive selection mainly for non-ancestral alleles	Cadzow *et al.*, 2014	• FLK	Based on a phylogenetic estimation of the population's kinship (F) matrix.	Bonhomme *et al.*, 2010
• CLR	Detects signals of positive selection across multiple sites in a population	Williamson *et al.*, 2007			
Linkage disequilibrium	Based on long homozygous regions of no recombination	Sabeti *et al.*, 2002	Haplotype based differentiation	Uses haplotype information in multiple populations.	Saravanan *et al.*, 2020
• LDD	Compares average observed and expected allelic frequencies	Khan, 2019	• XP-EHH	Detects haplotype-difference between populations.	Sabeti *et al.*, 2007

Within population	Within population		Across populations		
• rEHH	Detect regions with the recent positive selection which do not need ancestral alleles description.	Sabeti *et al*., 2002	• hapFLK	Detects genomic signatures based on haplotype information and hierarchical structure of populations.	Fariello *et al*., 2013
• iHS	Measures how haplotypes are unusual around a variant.	Voight *et al*., 2006			
Reduced local variability	Detects genomic regions with reduced variability	Saravanan *et al*., 2020			
• ROH)	Detect selection signature by revealing long ROH near a target region	Forutan *et al*., 2018; Rebelato *et al*., 2018; Xie *et al*., 2019			
• *HP*	Detects local heterozygosity depression from genomic average	Saravanan *et al*., 2020			

CLR Composite likelihood ratio test, *LD* Linkage disequilibrium, *LDD* Linkage disequilibrium decay test, *rEHH* Relative extended haplotype homozygosity, *iHS* Integrated haplotype score, ROH Runs of homozygosity, *HP* Pooled heterozygosity, F_{ST} Fixation index, *XP-EHH* Extended haplotype homozygosity, *hapFLK* Haplotype-based extension of the FLK

2.6. Status of Genetic Characterization Studies in Ethiopian Indigenous Cattle

Most of the genetic characterization studies (Table 6) conducted in Ethiopian indigenous cattle populations have been relayed on low density markers such as microsatellite markers (Okomo-Adhiambo, 2002; Li *et al*., 2007; Merha *et al*., 2007a; Hailu et al., 2008; Zewdu *et al*., 2010; Merha *et al*., 2011; Shelema *et al*., 2023), Random Amplification of Polymorphic DNA (Fedlu *et al*., 2007), SNP markers such as Illumina Bovine 8K SNP BeadChip (Zewdu *et al*., 2012; Zewdu *et al*., 2013), 80K SNP bead chip (Dejenie et al., 2023); GeneSeek Genomic Profiler HD BeadChip (Zewdu *et al*., 2015), BovineHD BeadChip (800 K) (Selam *et al*., 2020). However, as they are brought from less dense molecular markers, they are prone to ascertainment biases (Nielsen *et al*., 2011; Pérez-Enciso *et al*., 2015) and they do not represent the complete genome sequence (Eusebi *et al*., 2019).Whole-genome sequence analyses on the other hand are less prone to ascertainment biases and can provide a complete representation of the diversity of a genome including causative variants linked to quantitative traits (Jiang *et al*., 2014; Das *et al*., 2015).

Recently, a few studies (Kim *et al*., 2020; Endashaw *et al*., 2022; Jang *et al*., 2022; Endashaw *et al*., 2023) have reported the whole genome characterization of Ethiopian indigenous cattle, making it the African country with the most significant number of cattle genome sequences available. However, there are still several main gaps in our knowledge of cattle populations from some geographic areas and those living in extreme environments yet to be characterized at the whole genome level (Zewdu *et al*., 2013; EBI, 2016). For instance, all the previous complete genome-based characterization studies on Ethiopian cattle populations (Kim *et al*., 2020; Endashaw *et al*., 2022; Jang *et al*., 2022) did not include any indigenous cattle in Tigray, except one population (Begait) (Endashaw *et al*., 2023).

Table 6. Genetic characterizations reported in Ethiopian indigenous cattle populations.

Population	Method	Reference
Abigar and Danakil, Sheko	18 autosomal microsatellite markers	Okomo-Adhiambo, 2002
Begait, Arado, Afar, Raya, Fogera,	5 Y-chromosome microsatellite analysis	Li *et al*., 2007
Horro, Sheko, Arsi, Abigar, Guraghe Highland	Random Amplification of Polymorphic DNA	Fedlu *et al.*, 2007
Begait, Arado, Afar, Raya, Fogera, Abergelle, Erob	20 autosomal microsatellite markers analysis	Merha *et al*., 2007a, Merha *et al*., 2011
Wegera, Dembia, Fogera	22 microsatellite markers	Zewdu *et al.*, 2010
Raya, Fogera, Arado, Begait, Guraghe, Ogaden, Sheko	GeneSeek Genomic Profiler HD BeadChip	Zewdu *et al*., 2015
Boran, Arsi, Ambo, Ogaden, Horro, Fogera, Raya, Danakil, African taurine, Sheko,	30 microsatellite loci autosomal microsatellite markers analysis	Hailu *et al*., 2008
Begait, Boran, Fogera	80K SNP bead chip (Gene Seek Genomic Profiler)	Dejenie *et al*., 2022
Boran, Arsi, Horro, Danakil	IlluminaBovine8KSNPBeadChip	Zewdu *et al*., 2013
Bale, Bagaria, Semien, Afar, Goffa, Boran, Mursi, Ogaden, Sheko,	HiSeq2500	Jang *et al.*, 2022
Ambo, Arsi, Boran, Danakil, Horro	Illumina Bovine 8K SNP BeadChip	Zewdu *et al*., 2012
Bonga, Jimma, and Keray	16 microsatellite loci autosomal microsatellite markers analysis	Shelema *et al*., 2023
Benishangul, Fogera, Gindeberet, Goffa, Nuer and Sheko	BovineHD BeadChip (800 K)	Selam *et al*., 2020
Ogaden, Boran	HiSeq2000	Kim *et al*., 2017
Arsi, Afar, Goffa, Boran, Fogera, Horro, Musri, Ogaden, Sheko	HiSeq2000	Kim *et al*., 2020
Abigar, Boran, Guraghe, Horro, Sheko	mitochondrial cytochrome b gene complete sequencing	Getinet *et al*., 2018
Bale, Choke, Semien, Afar, Boran, Ogaden, Arsi, Bagaria, Begait, Fogera, Goffa, Horro, Mursi, Sheko	Illumina NovaSeq 6000	Endashaw *et al*., 2022, Endashaw *et al*., 2023

CHAPTER 3. MATERIALS AND METHODS

3.1. Description of the Study Area

The study was conducted in Northern part of Ethiopia, Tigray National Regional State (Figure 4), which is located at 12°15' and 14°57' north latitude and 36°27' and 39°59' east longitude (Tagel *et al*., 2011). It shares borders primarily with Eritrea in the north, Sudan in the west and Amhara and Afar National Regional States from the south and east within the Ethiopian territory, respectively. The region is home to different agroecological zones, including cool sub-moist mid-highlands, tepid sub-moist mid-highlands, tepid moist mid-highlands, warm moist mid-highlands, warm semi-arid lowlands and warm sub-moist lowlands (MoA, 2001). It also has highly diversified landscapes, rainfall and variable temperature. The temperature ranges from 5 to 40°C (degrees Celsius).

The landscape extends from lowland plains in the range of 500 to 1500 meters above sea level (masl), highlands in the range of 2300 to 3200 masl, midlands and hills in the range of 1600-2200 masl and mountains up to an altitude range of 3935 masl (Kumasi and Asenso-Okyere, 2011). Tigray is recognized as one of the moister stressed areas in Ethiopia. It receives erratic rainfall with an annual range from 400 to 800 millimeter (mm), mainly acquired within three mounts (June, July and August) (Nyssen *et al*., 2009; Kumasi and Asenso-Okyere, 2011; Melaku, 2013). Tigray is Ethiopia's fourth most cattle-populated region, accounting for about eight percent of the country's cattle genetic resource, next to Oromiya, Amhara, and SNNP-Southern Nations, Nationalities, and People's Region (CSA, 2018).

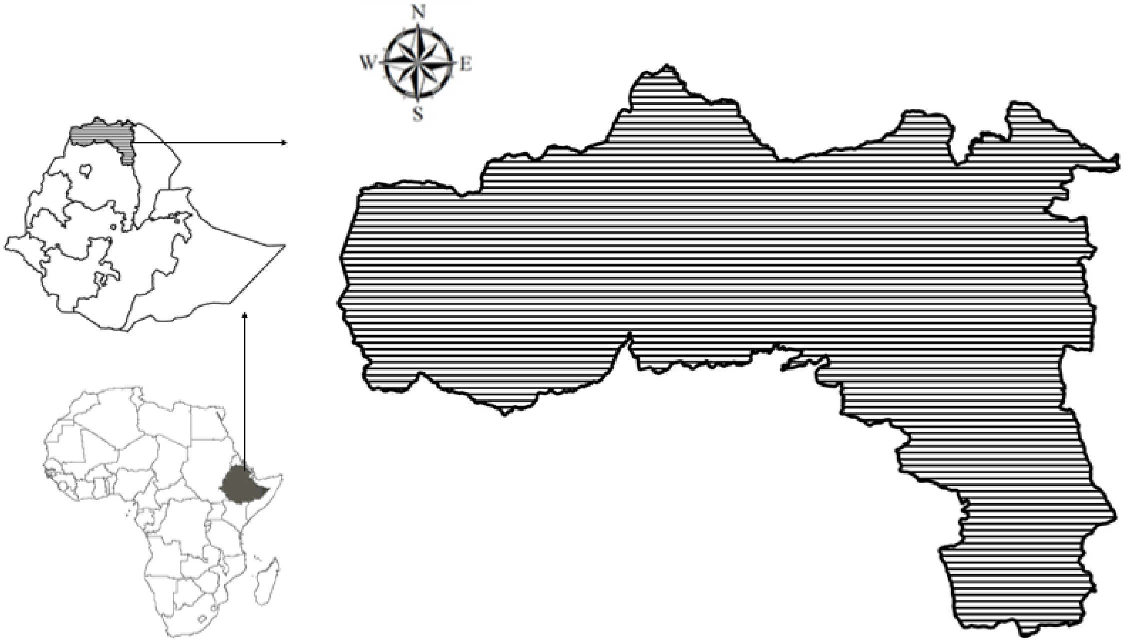


Figure 4. Physical map of the Tigray National Regional State

3.2. Sampling and Data Collection

3.2.1. Sampling and morphologic data collection

Firstly, the distributions of the indigenous cattle in Tigray (Abergelle, Arado, Begait, Erob and Raya) in the Tigray Region were screened through preliminary discussions with regional, zonal and district livestock expertise. Sampling sites were then selected purposively to include a comprehensive representation of the indigenous cattle in Tigray (Abergelle, Arado, Begait, Erob and Raya) of the Tigray Region from their respective natural breeding areas (Figure 5, Table 7 and Table S1).

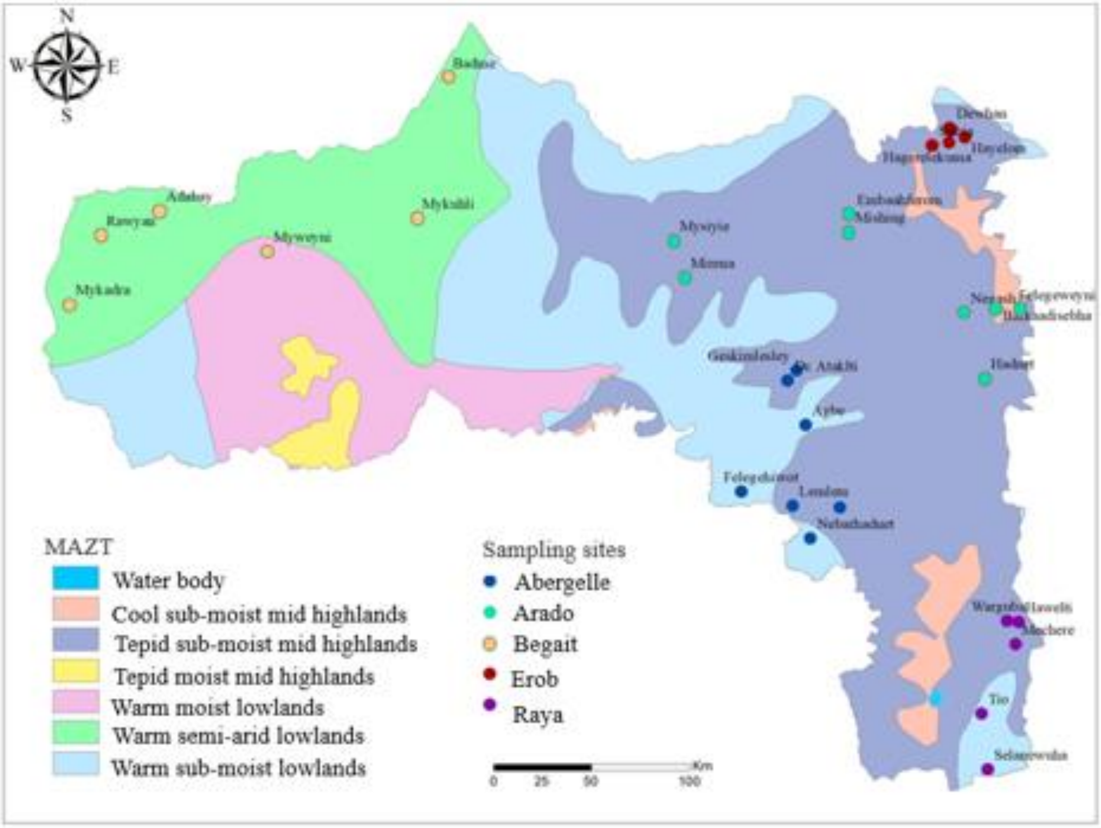


Figure 5. Agro-ecological map of Tigray National Regional State representing the sampling sites of the indigenous cattle in Tigray used for morphological characterization (MoA, 2001).

Table 7. Description of breeding areas for each study population across the Tigray National Regional State.

Population	Distribution	Agroecology	Altitude	Rainfall	Temperature	Landscape	Soil type
Abergelle	Southwestern	Tepid sub-moist mid-highlands	1595-1920masl	566-597mm	19.2-21.4°C	Mountainous and plateaus	•Campasols •Vertisols •Fluvisols
	Lower compartment of Southwestern	Warm sub-moist lowlands	1292-1479masl	195-628mm	21.4-28°C	Mountainous and plateaus	•Nitosols •Vertisols •Leptosols
Arado	Central and Eastern	Tepid sub-moist mid-highlands	2202-2487masl	508-567mm	17.2-19.2°C	Plains, mountains and plateaus	•Fluvisols •Campasols
	Eastern periphery	Cool sub-moist mid-highlands	2747masl	494-568mm	15.6-17.2°C	Mountains	•Humic-Andosols •Leptosols
Begait	Western and Southwestern	Warm semi-arid lowlands	633-1157masl	300-800mm	21- >28°C	Lowland plains	•Vertisols •fluvisols •leptisols
		Warm, moist lowlands	887masl	300-800mm	21-27°C	Lowland plains	•Cambisol
Erob	Northern peak	Tepid sub-moist mid-highlands		508-567mm	17.2-19.2°C	Mountainous	•Campasols •Vertisols •Fluvisols
Raya	Southeastern edge	Tepid sub-moist mid-highlands	1561-1980masl	566-597mm	19.2-1.4°C	Plains	•Campasols •Vertisols •Fluvisols
	Southern Tigray	warm sub-moist lowlands	1389-1448masl	195-628mm	21.4°C-28°C	Plains	•Nitosols •Vertisols •Leptosols
Source	Regional, zonal and district livestock expertise	MoA, 2001	Haftom *et al.*, 2019	Haftom *et al.*, 2019	Haftom *et al.*, 2019	Haftom *et al.*, 2019	MoA, 1998

The phenotypic characterization of sampled cattle was employed following the FAO guidelines (FAO, 2012). A total of 1650 (Table S1) matured cattle (300 females and 30 males from each of the five cattle populations) were recorded, excluding pregnant cows and castrated males from the sampling to leave out the effect mainly on heart girth and scrotal circumference measurements, respectively. The parameters recorded for each characteristic of color or conformation were evaluated through visual observation by the same person to avoid personal bias. The body measurements or quantitative morphological characters were measured with a measuring tape (centimeter) after making the animal stand appropriately on a levelled ground (Table 8).

Table 8. Qualitative and Quantitative variables recorded for describing the indigenous cattle in Tigray.

Qualitative Traits	**Description**
Coat color pattern	Plain, patchy, pied, spotted
Body parts color descriptions	Black, white, brown, red, etc.
Ear shape	Rounded, straight-edged
Ear orientation	Erect, lateral, drooping
Hump size	Absent, small, medium, large
Hump location	Thoracic, cervico-thoracic
Face profile	Straight, concave, convex ultra-convex
Rump profile	Flat, sloping, roofy
Horn status	Absent, present, scar
Horn shape	Straight, curved, lyre-shape, loose, stumps, polled
Horn orientation	Tips pointing laterally, upward, downward, forward, backward
Back profile	Straight, slopes up towards the rump, slopes down from withers, dipped (curved)
Navel flap width	Absent, small, medium, large
Udder size	Small, medium, large
Teat size	Rudimentary (hard to hold between thumb and index finger) Medium (can easily be held between thumb and index finger) Large (can be held between multiple fingers and thumb
Quantitative Traits	**Point of measurement (specification)**
Height at withers (HW)	The distance between the point of wither and ground

Body length (BL)	Length between point of shoulder and the pin bone
Heart girth (HG)	Circumference of the body behind the base of the hump to the point right behind the front legs
Chest depth (CD)	The distance from the back to the floor of the chest at the shallowest part of the chest
Neck length (NL)	Proximal end of cervical region to the distal end of the cranial region
Dewlap width (DW)	The widest part of the base of the neck vertically
Face length (FL)	Distance from poll to the end of muzzle
Horn length (HL)	Length from base to tip following its external curvature
Horn Tip spacing (HTS)	Distance between tip of one horn to the other
Horn base spacing (HBS)	The distance between the base of one horn and the other
Horn base circumference (HBC)	The circumference for the base of the horns
Muzzle circumference (MC)	Measured a little above the nostrils and around the point where the dewlap meets the chin
Ear length (EL)	length on the back side of ear from the root to the tip
Rump height (RH)	Distance between point of rump and ground
Rump length (RL)	The length of the rump
Pelvic width (PW)	Width between the two pins
Hock circumference (HC)	Circumference of the hock
Tail length (TL)	Length from the base of the tail to its pointed end without switch
Tail base thickness (TBT)	The circumference of base of the tail
Perpetual sheath (PS)	Widest part vertically from the base of the abdomen
Scrotal circumference (SC)	Recorded by pulling the testes firmly down into the lower part of the scrotum and placing a measuring tape around the widest point

3.2.2. Sampling and extraction of environmental predictors

From each sampling location, thirty coordinates (4 to 7 per population) were recorded using the Geographic Positioning System (GPS) during the sample collection for morphologic characterization (Figure 6 and Table S2). For habitat suitability characterization, nine coordinates surrounding 1 kilometer of the initial sampling location were added using Google Earth Pro 7.3.1.4507 (2016) following the procedures applied by Fasil *et al*. (2021), Gheyas *et al*. (2021), Gebreslassie *et al*. (2022) and Vallejo-Trujillo *et al*. (2022). Finally, 300 coordinates were used to extract the data (Table 9) for habitat suitability mapping of the indigenous cattle in Tigray given the highly diversified landscapes, variable rainfall and temperature ranges (Figure 7).

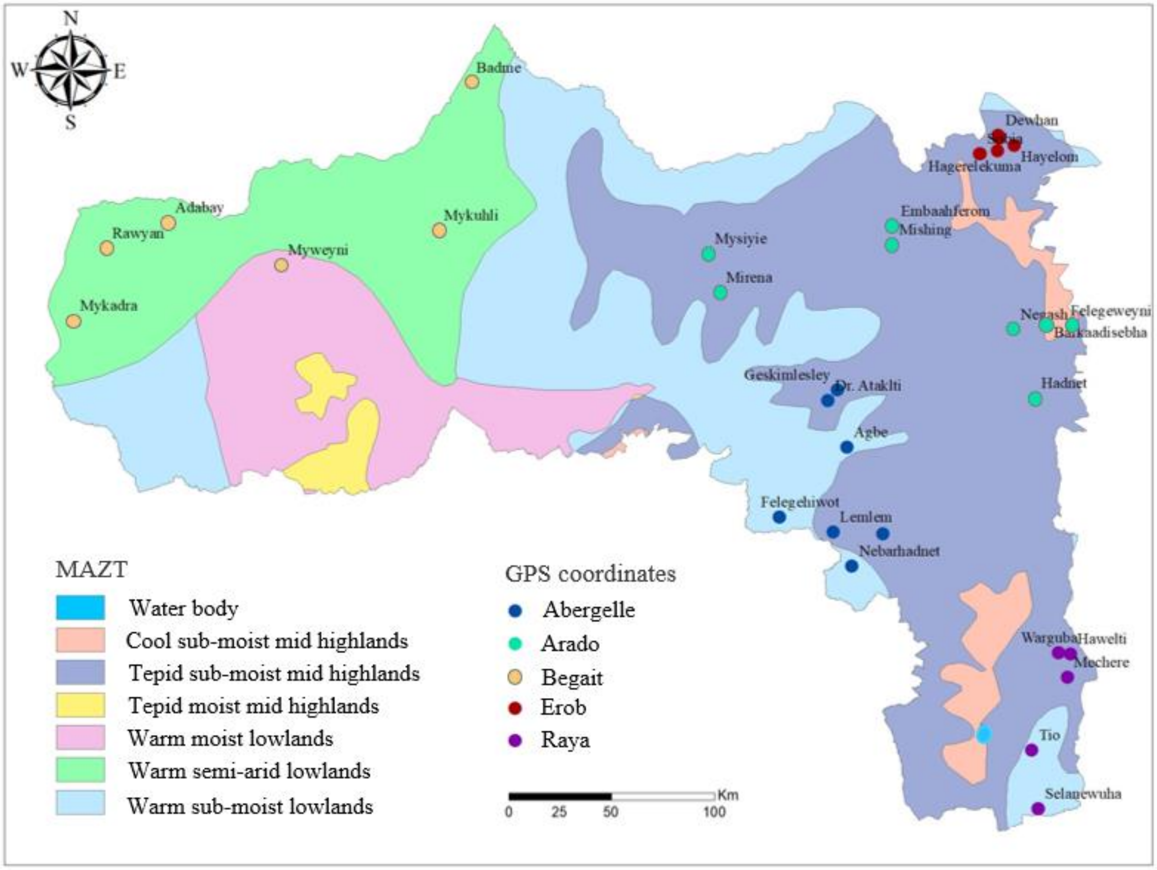


Figure 6. Sampling sites showing all the 30 coordinates taken using Geographic Positioning System (GPS) represented as a study area (MoA, 2001).

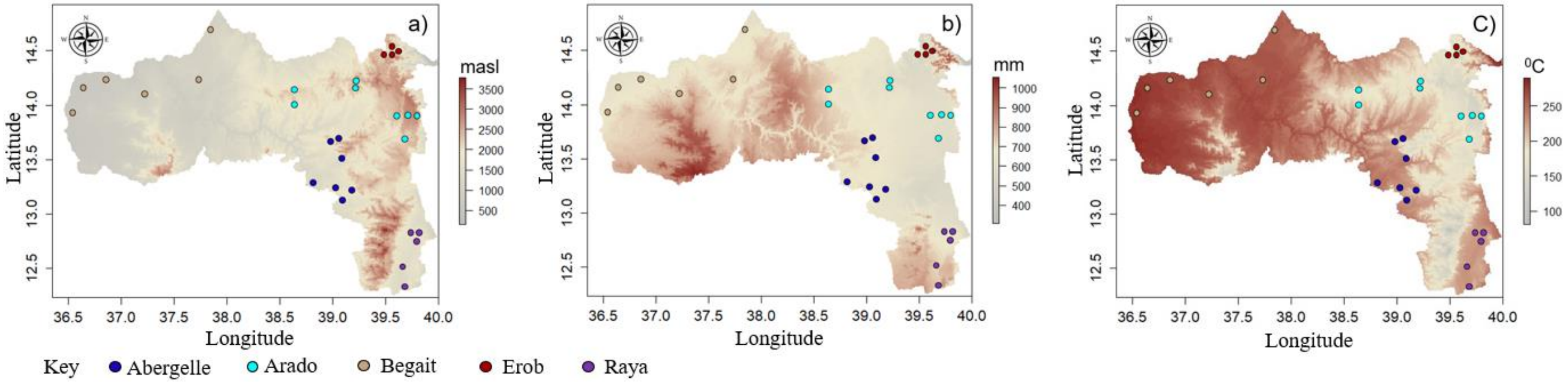


Figure 7. The Tigray map with sampling sites showing environmental variability.

Where: (a) showing the variation in altitude (meters above sea level, (b) showing the rainfall distribution (in millimeter) and (c) showing the temperature variation (in degrees Celsius).

Based on their important linkage to cattle productivity, biology, and agroecology in the Tigray Region, thirty-three environmental predictors were included for habitat suitability mapping, classification, and characterization (Table 9). Different sources were used to collect the data for environmental variables. The temperature and precipitation variables (bio1 to bio18) were extracted from the Global climate and weather data or WorldClim database (Fick and Hijmans, 2017) at a spatial resolution of 30 seconds around 1km^2, from data recorded for several years (1970-2000). The elevation data (bioelev), the water vapor pressure of the wettest month (WVP_07) and the water vapor pressure of the driest month (WVP_01) were also extracted from the WorldClim database considering their linkage with climatic variables. Seven soil characteristics, including soil pH, cation exchange capacity, soil bulk density, soil organic carbon, soil clay content, soil silt and soil sand content, were extracted from the SoilGrids1km v0.5.8 database (Hengl *et al*., 2014). Total cultivated land, grassland, forest coverage and crop mask irrigation layers were accessed using the 'Harmonized World Soil Dataset – Land Use and Land Cover with 30 arc-second rasters (Fischer *et al*., 2008). The Global Food Security Analysis-Support Data (Teluguntla *et al*., 2015) was used to obtain the crop dominance data.

Table 9. Thirty-three climatic and environmental variables used to characterize the habitat suitability of the indigenous cattle in Tigray.

Variables	Description	Units	Database
bio1	Annual mean temperature	^{0}C	WorldClim – Global Climate Data. http://www.worldclim.org/
bio2	Mean diurnal range (mean of monthly temperature)	^{0}C	
bio3	Isothermality (bio2/bio7) (*100)	^{0}C	
bio4	Temperature Seasonality	^{0}C	
bio5	Max temperature of warmest month	^{0}C	
bio6	Min temperature of coldest month	^{0}C	
bio7	Temperature annual range (bio5-bio6)	^{0}C	
bio8	Mean temperature of wettest quarter	^{0}C	
bio9	Mean temperature of driest quarter	^{0}C	
bio10	Mean temperature of warmest quarter	^{0}C	
bio11	Mean temperature of coldest quarter	^{0}C	
bio12	Annual precipitation	mm	
bio13	Precipitation of wettest month	mm	

Variables	Description	Units	Database
bio14	Precipitation of driest month	mm	
bio15	Precipitation seasonality	mm	
bio16	Precipitation of wettest quarter	mm	
bio17	Precipitation of driest quarter	mm	
bio18	Precipitation of warmest quarter	mm	
WVP_07	Water vapor pressure of the wettest month	KPa	
WVP_01	Water vapor pressure of the driest month	KPa	
bioelev	Meters above sea level	masl	
SoilpH	Soil pH	pH	Global gridded soil information.https://soilgrids.org/
SCaEC	Soil cation exchange capacity	cmol/kg	
SBD	Soil bulk density	kg/m^3	
SOC	Soil organic carbon	g/kg	
SClC	Soil clay content	%	
SSiC	Soil silt content	%	
SSaC	Soil sand content	%	
Forest_C	Forest cover	%	Harmonized World Soil Dataset http://www.fao.org/soils-portal/soil-survey/soil-maps-and-databases/harmonized-world-soil-database-v12/en/
Grass_C	Grass/Shrub Land cover	%	
CL	Cultivated land	%	
CMI	Crop irrigation coverage	%	
Crop_D	Crop dominance (major crops)	Category	Global Food Security Analysis-Support DATA https://croplands.org/

°C Annual temperature in degrees Celsius, *mm* millimeter, *masl* meters above sea level, *kg/m^3* kilogram per cubic metre, *cmol/kg* centimole/kilogram, *KPa* kilopascals, cmol/kg centimole/kilogram.

3.2.3. Blood sample collection and Ethical Clearance

Fifty-four whole blood samples were collected from the indigenous cattle in Tigray (11 Abergelle, 11 Arado, 11 Begait, 10 Erob, and 11 Raya cattle) (Figure 8) with good animal handling practice by a veterinary professional (DVM) during routine activities under the approval of the Ministry of Agriculture, Ethiopia. The whole blood was collected from the jugular vein of each animal by venipuncture with a 10ml (milliliter) vacutainer blood collection tube containing ethylenediaminetetraacetic acid (EDTA) as an anticoagulant. The blood was gently mixed with the EDTA and placed into an icebox containing ice. It was brought to the International Livestock Research Institute molecular laboratory facility (ILRI – Addis Ababa), where it was stored at -21°C (degree centigrade) until the extraction of the genomic DNA (gDNA).

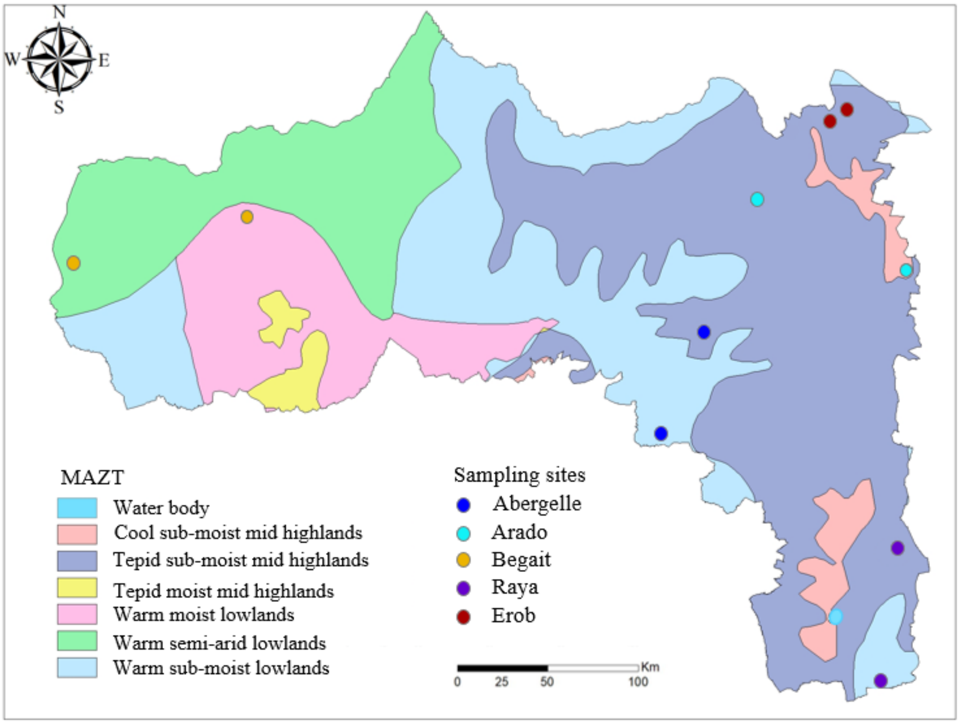


Figure 8. Agro-ecological map of Tigray Regional State representing the sampling sites of the indigenous cattle in Tigray used for blood sample collection ((MoA, 2001).

3.2.4. Sampling and population stratification for detecting signature selection

The procedures followed for the whole blood sample collection, handling and storing, gDNA extracting, quality checking and sequencing of the genomic DNA samples, checking the quality of the short sequence reads and mapping the sequence reads were extensively described in the materials and methods (section 3.2). Since signatures of natural selection mainly related to the environmental drivers of adaptation, the habitat grouping of the indigenous cattle in Tigray were used for both the *Hp* and F_{ST} detection of signature analysis following Gheyas *et al*. (2021) and Vallejo-Trujillo *et al*. (2022). As the Arado and Erob cattle populations overlapped in a similar breeding niche, one had to be selected for further signature analysis. The Arado cattle population was selected considering its wider habitat distribution compared to the Erob cattle population, which has a narrow geographical distribution (Figure 5).

Hence, the four populations (Abergelle, Arado, Begait and Raya) were considered for the selection signature analysis (Figure 9). Based on the contribution level of the six environmental variables (temperature seasonality (bio4), annual precipitation (bio12), wettest quarter precipitation (bio16), warmest quarter precipitation (bio18), cultivated land (Cl) and soil bulk density (SBD) in characterizing the environmental niche, each cattle population was grouped as high or low group under each environmental variable (Table 10).

Based on that, under the temperature seasonality, the Begait cattle, exposed to the highest (18.52 ± 1.46°C) temperature seasonality, were considered a high group for this particular environmental variable. In comparison, the Abergelle cattle exposed to relatively low variation temperature seasonality (15.24 ± 0.98°C) were considered as a low group. Three of the six environmental variables screened by the environmental niche modeling (ENM) (annual, wettest quarter and warmest quarter precipitations) were related to rainfall. The Raya and Arado cattle had the highest and lowest annual precipitation records; hence, they were categorized as high and low for this environmental variable, respectively. For the wettest quarter or the main rain season (June, July and August) of the Tigray Region (Nyssen *et al*., 2009; Kumasi and Asenso-Okyere, 2011; Melaku, 2013), the Begait cattle, had the highest record (513 ± 20.55mm) while the Raya cattle had the lowest rainfall record in the main rain season (337.88 ± 10.72mm). The Raya cattle, on the other hand, had the highest warmest season rainfall (bio18) record.

The other environmental variables selected by the ENM were cultivated land (CL) and soil bulk density. Both are mainly related to feed availability in an area. The land use for cultivation purposes (CL) is related to feed availability by affecting the land availability for grazing land. The SBD, directly correlated with water holding capacity and fertility of a particular soil (Arshad *et al*., 1996), can govern the type, quality and quantity of livestock feed resources in a specific area. In these environmental variables, the Arado and Begait cattle interchangeably had the highest and the lowest values for CL and SBD, respectively. The Arado cattle were distributed to the central tepid sub-moist mid-highlands and the eastern belts of the cool sub-moist midlands (Figure 5), with a characteristic of shortage of feed resulting from scarcity of grazing lands due to the allocation of most of the available land for food crops. Feed shortage resulting from the soil's infertility could also correlated with a soil type characteristic with low soil bulk density.

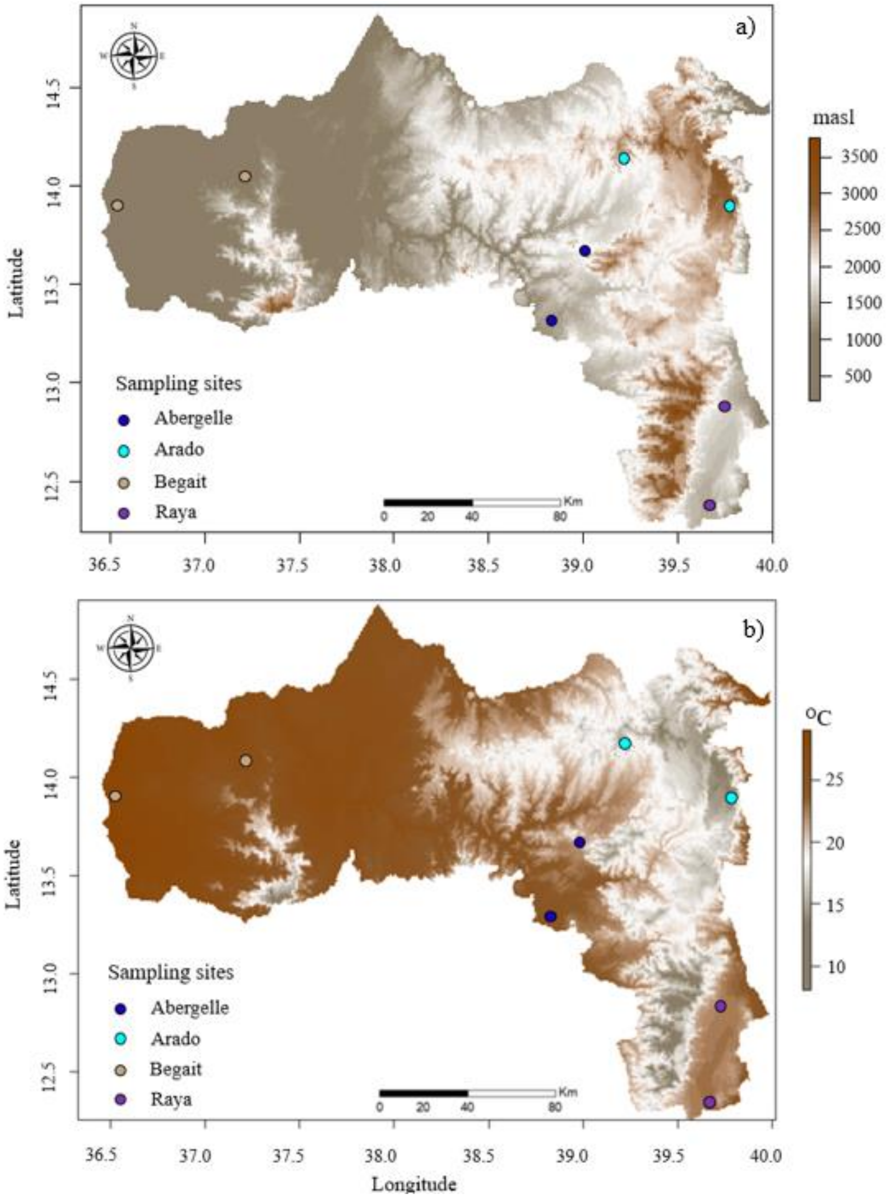


Figure 9. The Tigray regional map representing the sampling sites of the cattle populations used for detecting signature of selection.

Where: (a) shows variation in altitude (masl) and (b) variation in annual temperature.

Table 10. High and low populations clustered for the six selected environmental variables and their correlates, the annual temperature and elevation.

Environmental variables[1]	Populations[3]					
	Abergelle (n = 8)	Arado (n = 8)	Begait (n = 8)	Raya (n = 8)	High group	Low group
	Mean ± SD	Mean ± SD	Mean ± SD	Mean ± SD		
bio4	15.24 ± 0.98℃	15.44 ± 0.46℃	18.52 ± 1.46℃	17.62 ± 0.2℃	Begait	Abergelle
bio12	666.24 ± 22.19mm	621.5 ± 46.88mm	676.23 ± 31.56mm	677.92 ± 42.4mm	Raya	Arado
bio16	495.24 ± 34.12mm	411.79 ± 70.59mm	513 ± 20.55mm	337.88 ± 10.72mm	Begait	Raya
bio18	105.42 ± 18.71mm	125.19 ± 25.85mm	125.6 ± 35.74mm	187.18 ± 6.2mm	Raya	Abergelle
CL	27.42 ± 8.99%	34.99 ± 2.54%	21.73 ± 11.28%	32.97 ± 2.3%	Arado	Begait
SBD	1435.2 ± 26.49 kg/m^3	1413.4 ± 34.13 kg/m^3	1478.6 ± 22.18 kg/m^3	1423.9 ± 21.99 kg/m^3	Begait	Arado
Correlates[2]						
Annual temperature (°C)	22.44 ±15.62	16.62 ± 15.18	27.08 ± 8.18	22.77 ± 2.37	Begait	Arado
Elevation (masl)	1678.1 ± 243.04	2390.2 ± 230.87	838.22 ± 171.34	1532.5 ± 98.39	Arado	Begait

[1] *bio4* Temperature Seasonality in degrees Celsius, *bio12* Annual precipitation, *bio16* Precipitation of wettest quarter, *bio18* Precipitation of warmest quarter, *CL* Cultivated land, *SBD* Soil bulk density in kg/m^3 at depth.

[2] *masl* meters above sea level, *°C* Annual temperature in degrees Celsius.

[3] *n* number of samples *SD* Standard deviation.

3.3. Data Analysis

3.3.1. Morphologic data analysis

Before analyzing morphometric traits (body measurements), data was checked by box plots, Q-Q plots, stem-leaf, histograms and tests of normality to see if there are outliers and to confirm data normality (Tables S3 and S4). Multicollinearity was also checked before multivariate analysis using Pearson's correlation to see if multicollinearity or any pair of morphometric traits highly correlated with r > or is equal to 0.9 (Table S5).

The chi-square test of the procedure of SPSS version 25 (SPSS, 2017) was used to see the relation between population and the color characteristics and other qualitative physical traits. The statistical analyses were performed using SPSS version 25 (SPSS, 2017) for the data from categorical variables and the SAS procedure (SAS, 2009) for the data from quantitative variables.

The General linear model procedure of SAS (SAS, 2009) was used to assess the effect of populations on body measurements. Analysis was performed for males and females separately through the multiple univariate analyses of variance. Significant body measurement means were separated between populations using Tukey HSD at a probability level of 5%. The model employed was indicated below.

$$Yij = \mu + \alpha i + \epsilon ij$$

Where,

Yij	Measure of morphometric traits of each animal
μ	Overall mean
αi	i^{th} cattle population (i = Begait, Raya, Arado, Abergelle and Erob)
ϵij	Random error

The PROC discriminate procedure used the stepwise STEPDISC procedure to select morphological traits with more discriminate power. They were selected based on the level of significance $P < 0.05$ and partial R-square values ≥ 0.01. The CANDISC procedure was used for multivariate analysis to calculate Mahalanobis distances of the morphological traits and canonical functions that summarize variation between the five cattle populations. The DISCRIM procedure was applied to see the correct assignment of each animal to its population. Finally, the Canonical discriminate function analysis was performed to see the graphical representation of each cattle population.

3.3.2. Environmental data analysis

3.3.2.1. Distribution and association among parameters

First, the extracted data set, including all the 33 environmental variables, was checked for normality using the Kolmogorov-Smirnova and Shapiro-Wilk normality test. Further, the thirty-three environmental predictors were clustered into three, including climatic or precipitation-related variables (temperature variables = 11, bio1 to bio11; precipitation variables = 7 (bio12 to bio18); elevation variable (bioelev) = 1; and water vapor pressure variables = 2), vegetation and land use related variables (5) and soil type and characteristic related variables (7). Following that, the Principal Component Analyses (PCAs) were conducted separately for environmental variables under each cluster using the R package 'stats' and correlation test in R version 3.6.1 (R Development Core Team, 2019) for the three clusters. And then, the PCA and correlation results were plotted using the 'corrplot' of the R package.

3.3.2.2. Variables selection and model evluation for downstream analysis

Environmental variables that passed the correlation (< 0.6) and contribution (> 5%) thresholds were selected using the R-package of MaxEntVariableSelection (MVS) (Jueterbock *et al*., 2016). Next, the parameters for the model were set using the ENMeval in the R-package (Muscarella *et al*., 2014), which is a crucial step in controlling the model's overfitting and complication. This was done based on the different combinations of feature class (including linear (L), quadratic (Q), hinge (H), product (P), threshold (T) and categorical (C)) which is the transformed value of the original environmental variables and the regularization multiplier (beta multiplier), a model parameter that prevents model overfitting or complexity.

Next, the model with the best combination of feature class (FC) and beta multiplier (BM) was chosen following the least value for the Akaike Information Criterion corrected for small samples (AICc) (Akaike, 1974; Muscarella *et al*., 2014) that tested from 0.1 to 12 with steps of 0.5. AICc is used to identify which of the multiple models is most likely to be the best model for a given data set by assigning smaller values for the best mode (Galante *et al*., 2017). Finally, the selected model was evaluated by considering the values of the omission rate and the measure of Area Under the Receiving Operator Curve (AUC), which is regarded as a measure of the importance of the model. Large values of AUC indicate the model's fitness, while small values indicate the model's inefficiency (Ekelund, 2012).

3.3.2.3. Habitat suitability mapping, classification and characterisation

Having the best combination of feature class (FC = H) and beta multiplayer (BM = two), the finally selected environmental variables, test data (25% of the occurrence data) and training data (75% of the occurrence data), the environmental niche modelling (ENM) was analyzed in MaxEnt v3.4.1 (Phillips *et al*., 2006) for mapping the habitat suitability of the indigenous cattle in Tigray. The mapped habitat suitability was represented using cumulative habitat suitability (ranging from 0 to 100, indicating 0 as less suitable while 100 is highly suitable) and logistic output (ranging from 0 to 1, showing 0 as less suitable while one as highly suitable). The contribution of each selected environmental variable in predicting the model and characterizing the environmental niche for each cattle population was defined by the jackknife test and analysis of variable contributions of the MaxEnt v3.4.1 (Phillips *et al*., 2006), respectively.

To see the variation or similarity of the mapped environmental niches between each pair of populations within the indigenous cattle in Tigray, the Environmental Niche Modeling Tools (ENMTools) applied following the Perl software for the pairwise Pearson correlation and niche similarity statistic "niche overlap"(Warren *et al*., 2010). The pairwise Pearson correlation was analyzed ranging from -1 to 1 (where -1 shows the opposite; 0, no similarity; and +1 similar environmental niches) and the niche similarity statistic, ranging from 0 to 1 (where 0 indicates no overlap while 1, shows identical niches) (Warren *et al*., 2008).

Different clustering methods, including Unweighted pair group method with arithmetic mean (UPGMA), Complete linkage, Single linkage, and Ward, were tested to choose the best method with the highest value to be applied for the dendrogram. The Complete clustering method was then chosen for its highest value for correlation-based pairwise habitat suitability mapping comparison. The Ward clustering method was chosen in constructing the dendrogram and the heat map for the niche similarity-based pairwise habitat suitability mapping comparison.

Further, a dendrogram and heat map-based approach was used to plot the variation and similarity among the habitat suitability for the indigenous cattle in Tigray. The graphical representation of dendrograms and heatmaps was plotted using 'ggplot2' and 'Reshape2 R-packages. Finally, the habitat classification was determined based on the two outputs (pairwise Pearson's correlation and niche similarity statistic) and a visual inspection of the suitability maps for each cattle population. And then, each habitat was characterized based on the environmental variables that significantly contributed to define the specific habitat.

3.3.2.4. Effect of Environmental predictors on phenotypic variability

Here, the main quantitative traits, which were selected in section 4.1.3 through stepwise discriminant analysis were integrated with the environmental variables selected using ENM. Based on partial R-squared values greater than 0.1 and the probability level for the

F statistic (*pr* > F) < 0.0001), ten morphological variables, including HW, HL, PW, MC, HG, HBC, NL, CD, BL, RH and eight morphological variables HG, DW, HW, HL, NL, BL, RH, PW were selected for the female and male cattle, respectively (Table S6). Following this, the prediction level of each of the six selected environmental variables (Cl, SBD, bio12, bio16, bio18 and bio4) on each of the phenotypic variables that had a solid discriminating ability were analyzed for female and male cattle populations, separately using Generalized Additive Model (GAM). Gam is a vital model to show the effect of non-leaner variables like the environmental variables on leaner quantitative variables like phenotypic traits by smoothing the relationship (Crawley, 2013).

The model was analyzed in R version 3.6.1 (R Development Core Team, 2019) using the R package “mgcv” involving the syntax “gam” (Wood, 2018) as follows:

$Y = X_i + S\,(E1, E2, E3, \ldots E6)$

Where: Y represented the response variable of the discriminant phenotypic trait, xi = 1, 2, 3, 4, 5 represented the cattle populations as affixed effect and S is the smoothing term and E1 to E6 represented the selected environmental variables.

3.3.3. Genomic data analysis

3.3.3.1. Genomic DNA extraction and quality checking

The blood and Tissue Kit of the Qiagen Dneasy was used to extract the gDNA samples. Extracted gDNA samples were evaluated for concentration and quality using a Nanodrop spectrophotometer (DeNovix-DS-11+spectrophotometer, USA) and 1% agarose gel electrophoresis. A minimum of 5µg of high-quality gDNA with a concentration > 50 nanograms per microliter (ng/µl) (Table S7) was used for whole-genome sequencing.

3.3.3.2. Library construction and sequencing

The gDNA samples were sent to the ILRI-CAAS Joint Laboratory of Livestock and Forage Genetic Resources in Beijing, P.R. China, which supervised the genome sequencing. Following the manufacturer's specifications, a paired-end DNA library was constructed for each of the 54 samples. The gDNA was sequenced on an Illumina HiSeq X10 platform.

3.3.3.3. Short read mapping and variant calling

The sequence reads were checked for quality using FastQC version 0.11.5. Following quality checking, paired-end reads (FASTAQ format) were aligned against the cattle reference genome assembly (ARS_UCD1.2, *Bos taurus*, Hereford breed) using the BWA version 0.7.17 (Li and Durbin, 2009). The mapped reads were sorted using samtools version 1.8 (Li *et al*., 2009) and converted to BAM formats using PICARD tools version 2.18.2. Duplicated reads were marked and removed using PICARD's MarkDuplicates command. Moreover, the percentages of reads mapped to the reference genome were computed from dedup_recal.bam file using the Genome Analysis Toolkit's (GATK, version 3.8-1-0-gf15c1c3ef) DepthOfCoverage "-ct 5 -ct 10 -ct 20 -ct 40".

The base quality score recalibration (BQSR) was performed using the GATK's BaseRecalibrator and the uniquely mapped reads for variant calling were selected using the GATK's HaplotypeCaller (McKenna *et al*., 2010). The genomic variants (GVCF files) generated from each sample were jointly analyzed using the GATK's GenotypeGVCFtool. Called variants (SNPs and indels) were separately subjected to variant filtration (GATK hard filter) setting MQ > 40, QD > 2.0, ReadPosRankSum > 8.0, MappingQualityRankSum > 12.5 and HaplotypeScore > 13 for SNPs and FS > 200.0, QD < 2.0, ReadPosRankSum < -20.0 and QUAL < 20) for indels. Only bi-allelic variants that meet the specified filtering criteria were selected for further analysis.

3.3.3.4. Variant statistics and annotation

The variant statistics (e.g., the total number of SNPs, total number of indels, and indels, indel length, and nucleotide substitution) were detected using VCF-stats command of VCFtools/0.1.14/Perl. The number of transitions and transversions, average ratios of transitions-to-transversions (Ti/Tv), and distribution of SNPs and indels at different allelic frequencies were analyzed using stats command and plot-VCF-stats of BCFtools/1.8 (Li *et al*., 2009). Moreover, SNPs and indels density across chromosomes were computed for each population using VCFtools version 0.1.15 and then averaged using R version 3.6.1 (R Development Core Team, 2019). Detected variants were checked based on the Ensembl cow gene database (ARS-UCD1.2) dbSNP *ver*150. Finally, the variants (SNPs and indels) were classified according to their potential function using the Ensembl Variant Effect Predictor tool (VEP, (https://www.ensembl.org/info/docs/tools/vep/index.html, *ver*109) and the genes overlapping private missense variants were functionally annotated by DAVID, version 6.8 (https://david.ncifcrf.gov/home.jsp). Significant Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways were selected based on different criteria including $P < 0.05$, Bonferroni < 0.05, FDR < 0.05 and fold enrichment > 1.

3.3.3.5. Genome-wide nucleotide diversity and heterozygosity

The genome-wide nucleotide diversity (π) was analyzed for each population using VCFtools version 0.1.15 in 20kb windows with a 10kb sliding step (with the –window -pi 20000 –window-pi-step 10000 option) (Danecek *et al*., 2011). The numbers of non-reference heterozygous and homozygous variants (SNPs and indels) were analyzed using the VCF-stats command of VCFtools/0.1.14/Perl. Further, the observed heterozygosity (H_O) was calculated following the command "–het" in PLINK version 1.9 (Purcell *et al*., 2007).

3.3.3.6. Runs of homozygosity and genomic inbreeding

The runs of homozygosity (ROH) were detected using PLINK version 1.9 (Purcell *et al*., 2007) by setting a sliding window of 50 SNPs (--homozyg-window-snp 50), one possible heterozygous genotype (--homozyg-window-het 1), two missing genotypes (--homozyg-window-missing 2), a minimum SNP density of 1 SNP every 50 kb (--homozyg-density 50), a minimum number of 100 SNPs (--homozyg-snp100), a minimum length of 100 kb (--homozyg-kb 100), a maximum gap of 1Mb between consecutive homozygous SNPs (--homozyg-gap 1000), and the presence of the SNP in a least five homozygous reads (--homozyg-window-threshold 0.05).

The genomic inbreeding value for each cattle was calculated by dividing the sum of ROHs length by the total length of the genome ($F_{ROH} = L_{ROH}/L_{AUTO}$), following McQuillan *et al*. (2008), Zhang *et al*. (2015a), Addo *et al*. (2019) and Guo *et al*. (2019a), considering, the autosomal genome length of (ARS_UCD1.2). An alternate inbreeding coefficient (F_{HOM}) was also calculated for each animal using the "–het" command in PLINK version 1.9 (Purcell *et al*., 2007), following Addo *et al*. (2019).

3.3.3.7. Genetic relationship

Publicly available genome sequences of 15 cattle populations (Table S8) from six reference groups were added to the dataset for genetic relationship and differentiation analyses. These included African sanga (Afar and Ankole, crosses between African zebu and longhorn humpless taurine), African zenga (Fogera and Horro, crosses between African zebu and sanga), African zebu (Ethiopian Boran and Kenana), African taurine (Muturu and N'Dama), European taurine (Angus and Holstein), Asian zebu (Bhagnari, Cholistani, Dhanni, Sahiwal and Tharparkar). The VCFs of all the reference populations were generated from their raw sequence reads by applying the same procedures mentioned above and subsequently merged with the indigenous cattle in Tigray.

The merged dataset included 164 cattle genomes and 42,766,398 raw SNPs variants. It was pruned using PLINK version 1.9 (Purcell *et al.*, 2007) by setting different filtering and quality control thresholds, such as "–mind 0.25 –geno 0.1 –maf 0.05 –indep-pairwise 50 10 0.5 –set-missing-var-ids C@P". Where –mind 0.25 = individual sample to be removed following 25% or more missing genotype data, --geno 0.1 = variants to be removed due to 10% of missing genotype data, --maf 0.05 = variants to be removed due to minor allele frequency less than 0.05, --indep-pairwise 50 10 0.5 = SNPs with pairwise r^2 values higher than 0.5 in sliding windows of 50 SNPs moving stepwise with ten SNPs at a time across the genome and set-missing-var-ids C@P = missing IDs set. After applying the quality control and filtering thresholds, the pruned final data set including 3,695,054 SNPs and 164 animals was converted to plink.fam, plink.bin, and plink.bed file using the flag "–make-bed" in PLINK version 1.9 (Purcell *et al.*, 2007).

3.3.3.7.1. Principal component analysis

The LD pruned dataset of 3,695,054 SNPs and 164 individuals was used for principal component analysis (PCA). To calculate pca.egenvel and pca.egenvec, the flag "plink –pca" was used at a default parameter, for the first 20 principal components (PCs). Then, the proportions of variances explained by the eigenvector were computed by dividing each egenvel by the total sum of all egenvels (1 to 20) and expressing it as a percentage. Finally, the two first PCs were plotted against each other using the ggplot2 package in R version 3.6.1 (R Development Core Team, 2019) to illustrate the population clustering.

3.3.3.7.2. Genetic admixture analysis

Using the same LD pruned dataset (3,695,054 SNPs), the ADMIXTURE version 1.3.0 software (Alexander *et al*., 2009) was used to determine the optimal number of clusters (K) and to describe individual ancestry. A cross-validation procedure was performed using the program's flag "-cv" for K = 1 to K = 10. The K with the lowest cross-validation error was taken as the recommended number of clusters for the dataset. The cross-validation error

(CV) value for each K (1 to 10) and the cluster assignments were plotted using R version 3.6.1 (R Development Core Team, 2019).

3.3.3.7.3. Genetic differentiation

The genetic distance (F_{ST}) between pairs of populations (Weir and Clark Cockerham, 1984) was analyzed using VCFtools version 0.1.15 in 100 kb windows with a 50 kb sliding step (with the –window-pi 100000 –window-pi-step 50000 option) (Purcell *et al*., 2007). The pairwise weighted F_{ST}-based heat map with a dendrogram was plotted in R version 3.6.1 (R Development Core Team, 2019).

3.3.4. Detection of selection signature regions and annotation

3.3.4.1. Populations clustering based on environmental category

As, three inbreed individuals detected in Raya cattle (section 4.2); they were omitted and also, three individuals were removed randomly from Abergelle, Arado and Begait, from the signature analysis to avoid sample size biasness. Totally, 32 samples were analyzed considering eight individuals from each population. Following different filtering criteria (--mind 0.25 --geno 0.1 --maf 0.05 --indep-pairwise 50 10 0.5 --set-missing-var-ids C@P) the total number of SNPs accounted in the data set of the four populations used to analysis the signature selection was 2493773. Having the 2493773 SNPs, and 32 individuals, the principal component analysis was computed using the flag “plink --pca” at a default parameter (PCA) to see the populations clustering. Keeping the first 20 PCA components, the proportions of variances explained by the eigenvector were computed by dividing each egenvel by the total sum of all egenvels (1-20) and expressed it as a percentage. Finally, the top two principal components (PCs) were plotted on R version 3.6.1 (R Development Core Team, 2019).

3.3.4.2. Detection of selective sweep regions

A genomic scan using the pooled heterozygosity (*Hp*) approach was conducted for all the cattle populations categorized under the high and low groups to detect candidate regions under positive selection. Further, a fixation index (F_{ST})of the high-group populations against the low groups was applied following the average value for each of the six environmental variables in each population's respective ecological niche (Table 10).

Pooled heterozygosity (*Hp* analysis), a signature analysis within a given population, is among the methods used to detect selection signatures based on the reduced local variability (Weigand and Leese, 2018). It detects regions with reduced variability compared to the whole genome average by calculating the deviation of expected local heterozygosity depression in chromosomal windows from the average heterozygosity of the genome based on allele counts (Rubin *et al.*, 2010). The regions under selection using the *Hp* analysis were detected using in 100 kb windows with a 50 kb sliding step. The *Hp* transformed (*ZHp*) values were calculated following the equation $ZHp = (Hp - \mu Hp)/\sigma Hp$). Where: *Hp* represented the *Hp* record in each window, μHp represented the mean value of *Hp* and σ is the standard deviation of the *Hp.*

The F_{ST} analysis (Wright, 1949) used to detect genomic selection between populations was analyzed using VCFtools version 0.1.15 (Purcell *et al.*, 2007) in a 100 kb overlapping bin windows with a 50 kb sliding step. The standardized weighted ZF_{ST} values were calculated using the equation $ZF_{ST} = (F_{ST} - \mu F_{ST})/\sigma F_{ST}$). Where: F_{ST} represented the F_{ST} record in each window, μF_{ST} represented the mean value of F_{ST} and σF_{ST} is the standard deviation of the F_{ST}.

After running the signature analysis (F_{ST} or *Hp),* the number of outlier windows were selected, putting certain criteria (number of SNPs and values for *ZHp* and ZF_{ST}). The significant windows under the *Hp* or F_{ST} analysis were the extreme low and extreme top 1% selective windows having at least 20 SNPs, respectively. Neighboring windows were merged and changed to Bed format using BEDTools. Overlapping selective sweep regions resulting from the *Hp* and F_{ST} analysis were then screened using BEDTools intersect, version 0.2.29 (intersect—bedtools 2.30.0 documentation) and were used for downstream analysis.

3.3.4.3. Annotation of selective sweep regions and functional enrichment analysis of genes under selection

Candidate genes were detected by annotating the selective sweep regions using the Ensembl cow genes database 109, *Bos taurus* (ARS-UCD1.2) (https://www.ensembl.org/biomart). Retrieved genes were then functionally annotated by DAVID, version 6.8 (https://david.ncifcrf.gov). Significant ($P < 0.05$) Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways were selected based on different criteria, including $P < 0.05$.

CHAPTER 4. RESULTS

4.1. Phenotypic Characterization of the Indigenous Cattle Populations in Tigray

4.1.1. Qualitative traits variations among cattle populations

4.1.1.1. Coat color variety and abundance

The color characteristics were significantly associated with population ($P < 0.001$). The predominant within-population coat color for Raya, Arado, Abergelle and Erob cattle populations were light red and brown with a plain coat pattern, while Begait has black with white, light black with white and dark grey with a mainly patchy coat color pattern. Black ear tip and tail switch, dark brown muzzle, brown eyelid, as well as very light olive-green horn and grey hoof were the dominant color of the sampled populations, except for Begait cattle, which show blackish muzzle and eyelid in most of the animals, with dark grey horn (Table 11 and Figure 10).

Table 11. Frequencies (in percentage) and chi-square test of each level of color characteristics assessed in the indigenous cattle populations in Tigray.

Traits	Variety	Populations					
		BG	RAY	AR	ABR	ER	*Overall*
		%	%	%	%	%	%
Coat color	Black	4.2	1.5	7.9	7.6	7.9	5.9
	White	1.5	0.9	1.2	1.8	1.8	1.5
	Brown	0	18.5	17.3	16.4	15.5	13.5
	Dark grey	21.5	0.6	0	0	0	4.4
	Light red	0.0	33.9	37.9	37.9	41.8	30.3
	Black and white	24.2	7.6	3.9	4.2	3.9	8.8
	White and spotted black	4.8	0	0	0	0	1
	Dark brown and white	1.8	7	10	9.7	9.7	7.68
	Dark red and white	0	10.3	1.8	1.8	2.4	3.3
	Light black and white	24.8	10	6.4	4.5	6.4	10.24
	Light red and white	0	7.3	13.6	16.1	10.6	9.5
	Light black and brown	17	2.4	0	0	0	3.9
		$X^2 = 1067.09$, $P< 0.001$					
Coat color pattern	Plain	22	47	69	54	55	50
	Pied	26	25	12	3	2	13
	Patchy	44	22	17	39	38	32
	Spotted	8	5	2	4	5	5

Traits	Variety	Populations					
		BG	RAY	AR	ABR	ER	*Overall*
		%	%	%	%	%	%
		X^2 = 286.13, *P* < 0.001					
Ear tip color	Black	92	52	52	50	46	58
	White	1	1	1	2	2	1
	Brown	7	41	35	35	36	31
	Dark red	0	6	12	13	16	10
		X^2 = 215.88, *P* < 0.001					
Tail switch color	Black	97.9	51.8	49.7	46.4	48.2	58.8
	White	1.5	1.2	0.3	2.4	2.4	1.6
	Brown	0.6	37.6	39.7	42.1	44.2	32.8
	Dark red	0	9.4	10	9.1	5.2	6.7
	Grey	0	0	0.3	0	0	0.1
		X^2 = 286.47, *P* < 0.001					
Muzzle color	Black	69.1	4.2	8.2	5.8	7.0	19
	Dark brown	10.9	76.7	73.3	88.7	76.6	65
	Reddish	0	19.1	18.5	5.5	16.4	12
	Dark grey	20	0	0	0	0	4
		X^2 = 1094.54, *P* < 0.001					
Eyelid color	Black	65	4	8	6	0	16.4
	Grey	24	0	0.3	0	0	4.8
	Brown	11.5	77	73	89	82	66.5
	Reddish	0	19	18	5	18	12
		X^2 =1178.43, *P* < 0.001					
Horn color	Black	5	2	4	5	6	4
	very light olive green	37	45	51	50	49	46.6
	Dark grey	45	15	13	12	10	19
	Very light red	0	11	9	8	9	7.4
	Whitish grey	13	27	23	25	26	23
		X^2 = 206.72, *P* < 0.001					
Hoof color	Grey	89	75	57	61	61	69
	Light black	11	2	9	1	2	5
	Very light red	0	23	34	38	37	26
		X^2 = 221.23, *P* < 0.001					

BG Begait, *RAY* Raya, *AR* Arado, *ABR* Abergelle, *ER* Erob.

Figure 10. Pictorial representation of the indigenous cattle in Tigray.

Where: (a) Begait, (b) Raya, (c) Abergelle, (d) Arado and (e) Erob.

4.1.1.2. Body conformation variations among cattle populations

All the body conformation traits (Table 12) showed statistically significant association with population ($P < 0.001$). The majority of the cattle had small, erected, thoracic hump. The exception is the Raya cattle, which shows a small cervico-thoracic oriented hump. The majority of males of all cattle populations had a medium-sized hump compared to the females where it was small-sized. However, 13.3% of Arado and 16.7% of Erob males had large hump sizes. Most Begait cattle had round-shaped ear tips erected forward, concave faces, a sloppy rump, a back profile slopped up towards the rump, and a curved horn shape oriented forward. Begait cattle's females mainly had large navel flaps and large udder with long teats. Lateral ear with a straight tip, flat face and rump profile, straight back profile and curved horn shape which was oriented upward, small navel flap and small udder with medium-sized teats were the characteristics of all the other populations, except the Raya cattle that had round ear tip and convex face profile and the Arado cattle that also had rounded ear tip (Table 12).

Table 12. Frequencies (%) and chi- square test of each level of body conformation or appearance traits assessed in the indigenous cattle populations in Tigray.

Traits	Varity	Populations					
		BG	RAY	AR	ABR	ER	*Overall*
		%	%	%	%	%	%
Ear shape	Round edged	58.5	61.5	57.3	48.2	29.4	51
	Straight edged	41.5	38.5	42.7	51.8	70.6	49
		$X^2 = 89.88, P < 0.001$					
Hump size (Female)	Absent	5	7	0	0	0	2.4
	Small	95	93	99.3	98.7	97.7	96.7
	Medium	0	0	0.7	1.3	2.3	0.9
		$X^2 = 70.92, P < 0.001$					
Hump size (Male)	Small	10	43.3	10	33.3	3.3	20
	Medium	90	56.7	76.7	66.7	80	74
	Large	0	0	13.3	0	16.7	6
		$X^2 = 34.43, P < 0.001$					
Hump location	Thoracic	92.1	5.2	96.1	100	97.6	78.2
	Cervico- thoracic	3.3	88.5	1.2	0	0.3	18.7
	Absent	4.5	6.4	2.7	0	2.1	3.2
		$X^2 = 1385.72, P < 0.001$					
Face profile	Flat	11	11	95	99	97.2	62.6
	Concave	76	4	2	0.3	0.3	16.4
	Convex	13	85	3	0.7	2.4	20.9
		$X^2 = 2184.58, P < 0.001$					

Traits	Varity	Populations					
		BG	RAY	AR	ABR	ER	*Overall*
		%	%	%	%	%	%
Rump profile	Flat	8	88	88	98	96	75.9
	Sloping	52	11	12	0	0	14.7
	Roofy	40	1	0	2	4	9.4
		$X^2 = 1081.19$, $P < .001$					
Horn shape	Straight	5	1	8	4	3	4.1
	Curved	95	93	92	96	97	94.5
	Lyre	0	5	0	0	0	1
	Spiral	0	1	0	0	0	0.4
		$X^2 = 96.58$, $P < 0.001$					
Horn orientation	Upward	25.2	100	64.2	94.5	83.3	73.5
	Forward	67.9	0	26.7	1.8	9.7	21.2
	Lateral	4.5	0	9.1	3.6	7	4.8
	Downward	2.4	0	0	0	0	0.5
		$X^2 = 721.61$, $P < 0.001$					
Back profile	Straight	37	71	85	90	89	74.4
	Slops up to wards Rump	58	27	15	10	11	24.2
	Slops down from Withers	5	2	0	0	0	1.4
		$X^2 = 351.65$, $P < 0.001$					
Navel flap width	Absent	0	14	3	1	0	3.7
	Small	9	50	90	91	93	66.5
	Medium	42	36	7	8	7	20
	Large	49	0	0	0	0	9.8
		$X^2 = 1086.52$, $P < 0.001$					
Udder size	Small	3	61	57	95	94	62
	Medium	44	37	43	5	6	27
	Large	53	2	0	0	0	11
		$X^2 = 1050.39$, $P < 0.001$					
Teat size	Rudimentary	0.0	28.7	37.3	34	41	28.2
	Medium	38.3	56.3	60.7	66	59	56.1
	Long	61.7	15	2	0	0	15.7
		$X^2 = 670.98$, $P < 0.001$					

BG Begait, *RAY* Raya, *AR* Arado, *ABR* Abergelle, *ER* Erob.

As for the findings of the field observations and measurements, there were four types of Raya cattle horns, locally called Geraro, Korsuma, Genbo and Tulu (Figure 11a-d). Geraro (Figure 11a) is a type of horn that opens upward with a wide tip, and it was commonly observed in the area. Sometimes, the space between the horns' tips extends up to 80cm. Korsuma (Figure 11b) was the next most common horn type. This type of horn has tips pointing backwards. Next was Genbo (Figure 11c), a kind of horn wide at the center and then narrow at its tips (narrow upper interval). The least abundant horn type was the Tulu type (Figure 11d). This horn type had a large base circumference, and its tips pointed to the front.

Figure 11. The different horn types observed in the Raya cattle population: Geraro (a), Tulu (b), Korsuma (c) and Genbo (d).

4.1.3. Morphometric variation among cattle populations

Begait cattle had consistently higher ($P < 0.001$) for most of the body measurements (around 11) compared to the other four cattle populations. The morphological trait values for the Raya cattle were the second-largest for most morphological traits. However, the Raya cattle had larger values for specific characteristics such as muzzle circumference, dewlap width, horn length, horn base circumference and upper horn spacing measurements. The Arado cattle were in the third position for most body measurements, preceding

Abergelle and Erob. The latter two had similar linear body measurements except for some traits such as tail length and body length, for which the measured value of the Abergelle cattle was significantly (*P* < 0.001) more significant compared to the Erob cattle. On the other hand, height at wither was larger for Erob cattle compared to the Abergelle cattle (Tables 13 and 14).

Table 13. Average values (cm) (mean ± SD) of body measurements for female cattle populations.

Traits	Populations					Prob > F
	Begait (n=300)	Raya (N=300)	Arado (N=300)	Abergelle (N=300)	Erob (N=300)	
HW	125.23 ± 5.03^{a}	114.00 ± 5.44^{b}	104.84 ± 4.2^{c}	88.99 ± 3.44^{e}	90.54 ± 2.95^{d}	<.0001
BL	125.14 ± 4.71^{a}	114.15 ± 4.79^{b}	92.46 ± 6.14^{c}	90.84 ± 6.22^{d}	85.4 ± 6.07^{e}	<.0001
PW	42.32 ± 3.26^{a}	32.19 ± 2.63^{b}	29.29 ± 1.83^{c}	27.47 ± 2.85^{d}	26.84 ± 0.91^{e}	<.0001
EL	21.97 ± 1.91^{a}	17.57 ± 1.6^{b}	17.12 ± 2.16^{c}	16.05 ± 1.6^{d}	15.69 ± 1.53^{d}	<.0001
TL	98.00 ± 5.57^{a}	89.58 ± 5.89^{b}	77.25 ± 9.91^{c}	70.75 ± 8.37^{d}	66.16 ± 11.55^{e}	<.0001
NL	49.75 ± 2.57^{a}	43.72 ± 3.09^{b}	37.51 ± 2.64^{c}	36.44 ± 1.77^{d}	36.19 ± 1.67^{d}	<.0001
HC	34.62 ± 1.43^{a}	30.16 ± 2.38^{b}	28.92 ± 1.25^{c}	28.72 ± 1.64^{cd}	28.41 ± 2.6^{d}	<.0001
RH	135.1 ± 4.74^{a}	118.53 ± 5.78^{b}	112.31 ± 4.86^{c}	110.79 ± 4.21^{d}	110.43 ± 4.46^{d}	<.0001
RL	25.86 ± 1.87^{a}	24.36 ± 2.39^{b}	20.73 ± 2.8^{c}	18.46 ± 1.71^{d}	18.58 ± 1.82^{d}	<.0001
HG	158.23 ± 8.19^{a}	145.06 ± 4.24^{b}	134.62 ± 4.39^{c}	134.48 ± 3.92^{c}	134.31 ± 3.73^{c}	<.0001
CD	68.78 ± 3.61^{a}	54.88 ± 3.09^{b}	54.65 ± 2.31^{b}	53.37 ± 3.36^{c}	53.32 ± 3.55^{c}	<.0001
MC	36.46 ± 1.66^{b}	37.3 ± 2.08^{a}	36.14 ± 2.19^{b}	29.99 ± 2.58^{c}	29.71 ± 1.8^{c}	<.0001
DW	16. 36 ± 1.34^{b}	22.32 ± 3.67^{a}	16.98 ± 1.48^{b}	16.36 ± 1.7^{b}	16.39 ± 1.09^{b}	<.0001
HTS	37.07 ± 5.68^{bc}	60.12 ± 18.06^{a}	38.94 ± 10.68^{b}	38.49 ± 5.94^{bc}	36.22 ± 5.34c	<.0001
HL	23.63 ± 6.82^{b}	62.76 ± 11.11^{a}	21.29 ± 7.03^{c}	24.67 ± 3.65^{b}	23.91 ± 3.64^{b}	<.0001
HBC	17.54 ± 2.3^{c}	29.16 ± 5.24^{a}	17.53 ± 2.72^{c}	18.84 ± 2.35^{b}	18.65 ± 2.23^{b}	<.0001
HBS	16.10 ± 1.26^{a}	16.02 ± 2.85^{a}	14.62 ± 1.34^{c}	14.53 ± 0.63^{c}	14.34 ± 0.9^{c}	<.0001
FL	42.33 ± 3.73^{a}	41.68 ± 2.43^{ab}	41.24 ± 3.62^{bc}	40.75 ± 3.72^{c}	40.98 ± 3.9^{2bc}	<.0001
TBT	19.00 ± 1.28	18.90 ± 1.56	18.88 ± 1.37	18.86 ± 1.36	18.83 ± 1.33	0.611

Means within a row not bearing a common superscript letter significantly differ (*P* < 0.05), *Prob > F* probability value, *HW* height at withers, *BL* body length, *PW* pelvic width, *EL* ear length, *TL* tail length, *NL* neck length, *HC* hock circumference, *RH* rump height, *RL* rump length, *HG* heart girth, *CD* chest depth, *MC* muzzle circumference, *DW* dewlap width, *HTS* horn tip spacing, *HL* horn length, *HBC* horn base circumference, *HBS* horn base spacing, *FL* Face length, *TBT* tail base thickness, *SD* Standard deviation.

Table 14. Average values (cm) (mean ± SD) of body measurements for male cattle populations.

Traits	Populations					Prob > F
	Begait (N=30)	Raya (N=30)	Arado (N=30)	Abergelle (N=30)	Erob (N=30)	
HW	130.42 ± 3.37^{a}	116.74 ± 5.71^{b}	109.45 ± 5.55^{c}	89.72 ± 4.08^{e}	93.58 ± 2.65^{d}	<.0001
BL	127.96 ± 4.92^{a}	118.34 ± 6.45^{b}	99.81 ± 4.67^{c}	91.47 ± 7.38^{d}	87.05 ± 6.17^{e}	<.0001
PW	41.84 ± 2.87^{a}	32.56 ± 2.7^{b}	28.77 ± 1.76^{c}	26.95 ± 2.8^{d}	26.46 ± 0.99^{d}	<.0001
EL	21.66 ± 1.96^{a}	18.62 ± 1.57^{b}	18.63 ± 1.73^{b}	17.16 ± 1.7^{c}	15.58 ± 1.63^{c}	<.0001
TL	98.84 ± 6.74^{a}	88.91 ± 6.97^{b}	76.21 ± 9.45^{c}	74.51 ± 7.59^{c}	71.35 ± 12.12^{d}	<.0001
NL	52.68 ± 1.6^{a}	44.45 ± 3.44^{b}	41.94 ± 1.66^{c}	38.51 ± 1.18^{d}	37.28 ± 1.62^{d}	<.0001
HC	34.83 ± 1.73^{a}	33.32 ± 2.55^{a}	29.38 ± 1.56^{c}	29.20 ± 2.24^{c}	29.07 ± 2.81^{c}	<.0001
RH	136.52 ± 3.51^{a}	121.14 ± 6.37^{b}	113.65 ± 5.87^{c}	113.91 ± 3.19^{c}	113.24 ± 4.47^{c}	<.0001
RL	25.96 ± 2.01^{a}	25.02 ± 1.96^{b}	21.37 ± 2.56^{c}	18.04 ± 1.69^{d}	18.42 ± 1.63^{d}	<.0001
HG	172.09 ± 4.71^{a}	152.81 ± 2^{b}	140.56 ± 3.03^{c}	136.95 ± 3.38^{d}	138.86 ± 3^{d}	<.0001
CD	73.59 ± 2.81^{a}	60 ± 1.98^{b}	55.61 ± 2.44^{c}	53.74 ± 3.67^{c}	53.53 ± 4.82^{c}	<.0001
MC	38.69 ± 1.3^{b}	40.1 ± 1.59^{a}	37.06 ± 2.09^{c}	32.86 ± 2.14^{d}	32.44 ± 1.19^{d}	<.0001
DW	16.83 ± 0.89^{c}	26.36 ± 2.32^{a}	17.29 ± 1^{b}	16.88 ± 1.31^{c}	16.88 ± 1.53^{c}	<.0001
HTS	37.64 ± 5.79^{b}	57.17 ± 13.61^{a}	41.38 ± 12.46^{b}	38.01 ± 5.08^{b}	36.58 ± 4.9^{b}	<.0001
HL	25.86 ± 6.8^{b}	61.9 ± 11.66^{a}	19.88 ± 5.42^{c}	24.96 ± 3.75^{b}	23.98 ± 3.14^{bc}	<.0001
HBC	17.53 ± 2.23^{bc}	28.04 ± 4.36^{a}	16.76 ± 2.6^{c}	18.52 ± 1.77^{bc}	19.31 ± 2.14^{c}	<.0001
HBS	16.43 ± 1.21^{a}	16.09 ± 2.45^{a}	14.7 ± 1.16^{b}	14.55 ± 0.59^{b}	14.49 ± 0.75^{c}	<.0001
FL	46.25 ± 2.83^{a}	44.22 ± 1.62^{a}	44.04 ± 3.67^{a}	44.03 ± 3.91^{a}	43.99 ± 3.91^{a}	0.037
TBT	19.34 ± 1.39	19.26 ± 1.74	19.19 ± 1.41	19.16 ± 1.31	19.12 ± 1.21	0.978
PS	13.83 ± 1.63^{a}	13.9 ± 1.76^{a}	12.83 ± 1.67^{ab}	12.32 ± 1.74^{b}	12.23 ± 2.22^{b}	<.0001
SC	37.45 ± 0.82^{a}	37.01 ± 0.74^{a}	34.96 ± 0.8^{b}	34.93 ± 0.98^{b}	34.94 ± 0.77^{b}	<.0001

Means within a row not bearing a common superscript letter significantly differ ($P < 0.05$), *Prob > F* probability value, *HW* height at withers, *BL* body length, *PW* pelvic width, *EL* ear length, *TL* tail length, *NL* neck length, *HC* hock circumference, *RH* rump height, *RL* rump length, *HG* heart girth, *CD* chest depth, *MC* muzzle circumference, *DW* dewlap width, *HTS* horn tip spacing, *HL* horn length, *HBC* horn base circumference, *HBS* horn base spacing, *FL* Face length, *TBT* tail base thickness, *PS* perpetual sheath, *SC* scrotal circumference, *SD* Standard deviation.

Eighteen body measurements were found to be significant (partial R-square = 0.9036 to 0.0118, F-value = 3503.73 to 4.4) in discriminating the female cattle populations (Table 15). At the same time, thirteen variables ranged from partial R-square = 0.9401 to 0.0893 and F-value = 569.05 to 3.26, which were mainly important in differentiating the male cattle populations (Table 16).

Table 15. Summary of stepwise selection of body measurements for the female cattle population.

Variable entered	Partial R-Square	F-value	*Pr* > F	Wilk's lambda	*Pr* < lambda	ASCC	*Pr* > ASCC
HW	0.9036	3503.73	<.0001	0.0964	<.0001	0.2259	<.0001
HL	0.8224	1729.18	<.0001	0.0171	<.0001	0.4296	<.0001
PW	0.4885	356.43	<.0001	0.0088	<.0001	0.5041	<.0001
MC	0.3833	231.80	<.0001	0.0054	<.0001	0.5637	<.0001
HG	0.2905	152.59	<.0001	0.0038	<.0001	0.5887	<.0001
HBC	0.2429	119.50	<.0001	0.0029	<.0001	0.6002	<.0001
NL	0.2247	107.91	<.0001	0.0023	<.0001	0.6115	<.0001
CD	0.1744	78.59	<.0001	0.0019	<.0001	0.6183	<.0001
BL	0.1111	46.44	<.0001	0.0017	<.0001	0.6237	<.0001
RH	0.1014	41.91	<.0001	0.0015	<.0001	0.6271	<.0001
DW	0.0996	41.08	<.0001	0.0013	<.0001	0.6299	<.0001
HTS	0.0788	31.73	<.0001	0.0012	<.0001	0.6323	<.0001
TL	0.0734	29.38	<.0001	0.0011	<.0001	0.6381	<.0001
RL	0.0512	19.99	<.0001	0.0011	<.0001	0.6390	<.0001
HC	0.0433	16.76	<.0001	0.0010	<.0001	0.6408	<.0001
EL	0.0360	13.81	<.0001	0.0010	<.0001	0.6414	<.0001
TBT	0.0276	10.49	<.0001	0.0010	<.0001	0.6421	<.0001
HBS	0.0118	4.40	0.0015	0.0010	<.0001	0.6428	<.0001

Pr > F the probability level for the F statistic, *Pr < lambda* based on the F approximation to Wilks' lambda, *Pr > ASCC* based on the F approximation to Pillai's trace, *HW* height at withers, *HL* horn length, *PW* pelvic width, *MC* muzzle circumference, *HG* heart girth, *HBC* horn base circumference, *NL* neck length, *CD* chest depth, *BL* body length , *RH* rump height, *DW* dewlap width, *HTS* horn tip spacing, *TL* tail length, *RL* rump length, *HC* hock circumference, *EL* ear length, *TBT* tail base thickness, *HBS* horn base spacing.

Table 16. Summary of stepwise selection of body measurements for male cattle population.

Variable entered	Partial R-Square	F-value	*Pr* > F	Wilk's lambda	*Pr* < lambda	ASCC	*Pr* > ASCC
HG	0.9401	569.05	<.0001	0.0599	<.0001	0.2350	<.0001
DW	0.8716	244.28	<.0001	0.0077	<.0001	0.4529	<.0001
HW	0.7117	88.25	<.0001	0.0022	<.0001	0.5762	<.0001
HL	0.5091	36.81	<.0001	0.0011	<.0001	0.6019	<.0001
NL	0.3143	16.16	<.0001	0.0007	<.0001	0.6343	<.0001
BL	0.2847	13.93	<.0001	0.0005	<.0001	0.6630	<.0001
RH	0.2445	11.25	<.0001	0.0004	<.0001	0.6898	<.0001

PW	0.1843	7.80	<.0001	0.0003	<.0001	0.6963	<.0001
MC	0.1319	5.20	0.0006	0.0003	<.0001	0.7051	<.0001
EL	0.1286	5.02	0.0008	0.0002	<.0001	0.7204	<.0001
CD	0.1186	4.54	0.0018	0.0002	<.0001	0.7244	<.0001
HBC	0.1108	4.17	0.0032	0.0002	<.0001	0.7308	<.0001
SC	0.0893	3.26	0.0138	0.0002	<.0001	0.7319	<.0001

Pr > F the probability level for the F statistic, *Pr < lambda* based on the F approximation to Wilks' lambda, *Pr > ASCC* Average squared canonical correlation based on the F approximation to Pillai's trace, *HG* heart girth, *DW* dewlap width, *HW* height at withers, *HL* horn length, *NL* neck length, *BL* body length, *RH* rump height, *PW* pelvic width, *MC* muzzle circumference, *EL* ear length, *CD* chest depth, *HBC* horn base circumference, *SC* scrotal circumference.

The analysis of Mahalanobis distances between each pair of indigenous cattle populations in Tigray revealed the highest pair-wise morphological distance between Begait and Abergelle (male cattle or Erob (female cattle). On the other hand, the closest morphological distance was obtained between Abergelle and Erob cattle populations (Table 17).

Table 17. Mahalonobis distances among the indigenous cattle populations in Tigray

Populations	Populations				
	Begait	Raya	Arado	Abergelle	Erob
Begait		128.08	137.65	208.56	217.62
Raya	236.93		79.38	119.99	127.40
Arado	262.07	129.50		23.30	24.39
Abergelle	434.03	200.46	42.58		0.82
Erob	424.22	197.32	43.76	3.99	

Above diagonal values represented the pair-wise distance among female and below diagonal among male cattle.

The highest proportions of the total cumulative variances for female and male cattle populations were expressed by the first and second canonical variables, accounting for 95.9% and 96.37% in the female and male cattle populations, respectively (Tables 18 and 19). Traits with high canonical coefficients in can 1 or 2 (canonical structure) were the main contributors in characterizing the cattle populations. For the female cattle population, height at withers, neck length, and pelvic width in can 1, horn length, horn base circumference, and horn tip spacing in can 2 were the highest contributing variables (Table 18). For the male cattle population, heart girth, neck length, height at withers, pelvic width, and chest depth were among the variables that have high canonical coefficients in can 1, while dewlap width, horn length and horn base circumference were among the variables that have high canonical coefficients in can 2 (Table 19).

Table 18. Total canonical structure, eigenvalue and percent of total variance of female cattle populations based on body measurements.

Variable	Can1	Can2	Can3	Can4
HW	0.94683*	0.07544	-0.21364	-0.16641
BL	0.87740	0.14823	-0.04676	0.20668
HG	0.85990	-0.10283	0.23354	-0.06510
MC	0.67563	0.31329	-0.53704	0.12129
NL	0.91202*	-0.01868	0.16475	-0.03567
CD	0.78040	-0.43010	0.10951	-0.03566
HC	0.73091	-0.24386	0.13932	0.07097
DW	0.18259	0.73137	0.02693	-0.06231
RH	0.86044	-0.22815	0.15780	-0.02805
RL	0.81004	0.15846	-0.03682	-0.09967
PW	0.89703*	-0.23920	0.08325	0.07054
HTS	0.18249	0.66008*	0.03926	0.15755
HBS	0.41308	0.14103	0.08029	0.08885
HL	0.26214	0.90090*	0.21041	-0.04213
HBC	0.16459	0.81709*	0.20050	-0.03900
EL	0.75593	-0.25888	-0.00001	0.12110
TBT	0.04042	-0.01017	-0.00209	0.02450
TL	0.81063	0.09926	-0.03813	0.34917
EV	30.5292	10.5487	1.6892	0.0652
PV	0.7128	0.2463	0.0394	0.0015
CV	0.7128	0.9590	0.9985	1.0000

*Main contributors, *EV* Eigen value, *PV* proportion of variation, CV cumulative variance, *HW* height at withers, *BL* body length, *HG* heart girth, *MC* muzzle circumference, *NL* neck length, *CD* chest depth, *HC* hock circumference, *DW* dewlap width, *RH* rump height, *RL* rump length, *PW* pelvic width, *HTS* horn tip spacing, *HBS* horn base spacing, *HL* horn length, *HBC* horn base circumference, *EL* ear length, *TBT* tail base thickness, *TL* tail length.

Table 19. Total canonical structure, eigenvalue and percent of total variance of male cattle population based on body measurements.

Variable	Can1	Can2	Can3	Can4
HW	0.93842*	0.095663	-0.23141	-0.17007
BL	0.812104	0.21469	-0.19597	0.214847
HG	0.959233*	-0.0503	0.205829	-0.07902
MC	0.709166	0.436736	-0.36378	0.022482
NL	0.939073*	-0.0735	-0.04989	0.137046
CD	0.902652*	-0.16121	0.146932	0.058374
DW	0.235176	0.931658*	-0.00721	-0.00714
RH	0.855782	-0.12379	0.234458	0.095098
PW	0.923107*	-0.10327	0.107706	0.084112
HL	0.235498	0.897937*	0.174964	0.060537
HBC	0.086817	0.830058*	0.214928	-0.06686

SC	0.757717	0.259201	0.202978	0.042321
EL	0.723624	-0.09568	-0.19764	0.344147
EV	61.64	17.1	2.59	0.38
PV	0.7544	0.2093	0.0316	0.0047
CV	0.7544	0.9637	0.9953	1.0000

* Main contributors, *EV* Eigen value, *PV* proportion of variation, CV cumulative variance, *HW* height at withers, *BL* body length, *HG* heart girth, *MC* muzzle circumference, *NL* neck length, *CD* chest depth, *DW* dewlap width, *RH* rump height, *PW* pelvic width, *HL* horn length, *HBC* horn base circumference, *SC* scrotal circumference, *EL* ear length.

The assignments of individual animals to source population based on morphological resemblance revealed that all of the Begait and Raya cattle individuals were classified correctly to their respective groups. Females (98.33%) and male (100%) Arado cattle individuals were also correctly assigned to their source populations. However, individuals were mis assigned between the Abergelle and Erob cattle populations (Tables 20 and 21). The canonical discriminate function representations (Figures 12 and 13) also revealed an overlap between Abergelle and Erob cattle populations.

Table 20. Percent (%) of individual female cattle classified into five morphological groups.

Populations	Populations					
	Begait	Raya	Arado	Abergelle	Erob	Total
Begait	100	0	0	0	0	100
Raya	0	100	0	0	0	100
Arado	0	0	98.33	0.67	1	100
Abergelle	0	0	0.61	69.09	30.3	100
Erob	0	0	0.3	32.73	66.97	100
Priors	0.2	0.2	0.2	0.2	0.2	1
Error Rate	0	0	0.0166	0.3091	0.3303	0.1312

Table 21. Percent (%) of individual male indigenous cattle in Tigray classified into five morphological groups.

Population	Populations					
	Begait	Raya	Arado	Abergelle	Erob	Total
Begait	100	0	0	0	0	100
Raya	0	100	0	0	0	100
Arado	0	0	100	0	0	100
Abergelle	0	0	0	73.33	26.67	100
Erob	0	0	0	20	80	100
Priors	0.2	0.2	0.2	0.2	0.2	1
Error Rate	0	0	0	0.2667	0.2	0.0933

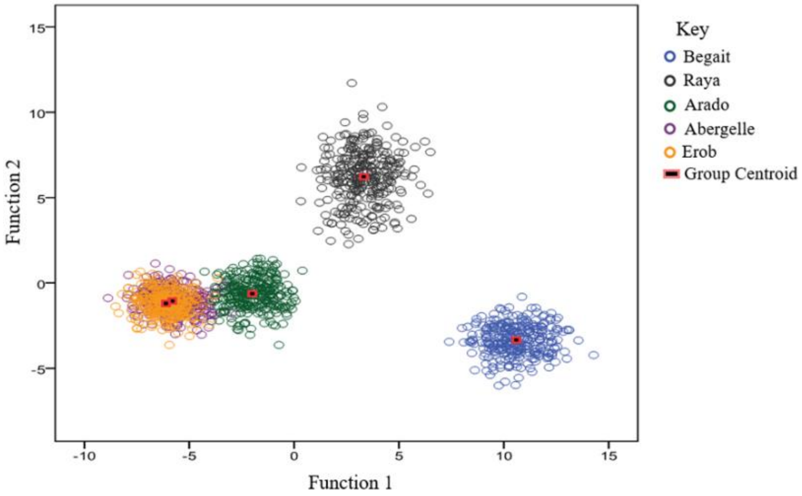


Figure 12. Canonical discriminate function of female cattle.

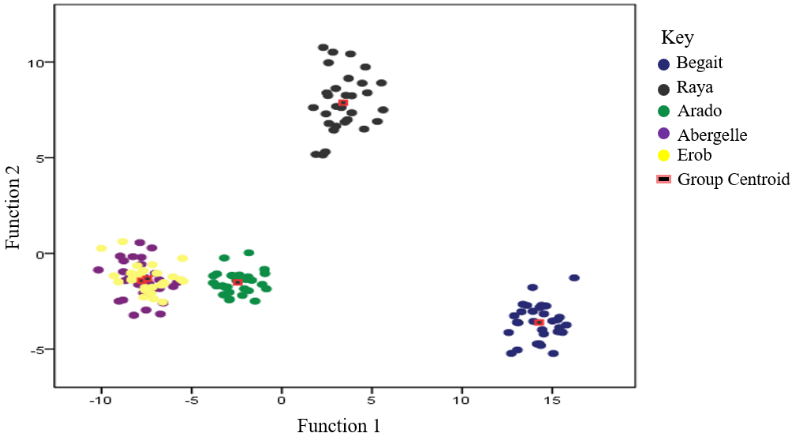


Figure 13. Canonical discriminate function of male cattle.

4.2. Habitat Suitability Mapping, Characterization and Identification of Key Ecological Variables Driving the Adaptive Diversity of the Indigenous Cattle in Tigray

4.2.1. Correlation and PCA based association of environmental variables

4.2.1.1. Correlation based association

None of the environmental variables was normally distributed. They had a Shapiro-Wilk value of 0.377 to 0.984, with *P*-values ranging from 0.001 to 0.002, except SBD with *P*= 0.2 (Table S9). Accordingly, the analysis result from Spearman's correlation (r_s) for the 33 environmental variables (a = climatic and precipitation-related variables, b = soil variables, c = vegetation and land use) are presented in Figure 14.

Spearman's correlation (r_s) among the temperature variables (bio1 to bio11) revealed, except with bio3 (isothermality) where weakly to strong and negatively correlated (r_s = -0.32 to -0.77), all were moderate to very strong (r_s > 0.51 to 0.99) and positively correlated with each other. On the other hand, they had a very weak to moderate correlation (≥ r_s -4 to < 4) with the precipitation variables, except some variables bio2, bio5, and bio9 had a strong ($r_s \approx 0.6$) correlation with one or two of the precipitation variables. The elevation (meters above sea level) (bioelev) was strong to very strong correlated with most of the temperature variables. Both the water vapor at the wettest (July) and driest months (January) were strongly correlated with each of the temperature variables (r_s = 0.6 to 0.98) and with elevation (r_s = -0.85 and -0.98). However, they are weakly correlated with most precipitation variables (Figure 14a and Table S10).

Spearman's correlation among the environmental variables under the soil cluster showed the soil cation exchange capacity positively and strongly ($r_s \approx 0.71$) correlated with soil clay content. It strongly but negatively ($r_s \approx -0.70$) correlated with the soil sand content. However, the soil clay content was very strongly and negatively ($r_s \approx -0.94$) correlated with the soil sand content. Similarly, it was strongly but positively ($r_s \approx 0.62$) correlated with the soil silt content. Other soil variables, such as soil bulk density, organic carbon, and pH, did not have strong or very strong correlations with each other or with the other soil-related variables (Figure 14b and Table S11).

The Spearman's correlation, among the five environmental variables under the vegetation and land use cluster, the land use for agricultural purposes (cultivated land) was negatively and strongly ($r_s \approx -0.85$) correlated with grass/shrub land (a land cover used for grazing of the indigenous cattle in Tigray) (Figure 14c and Table S12).

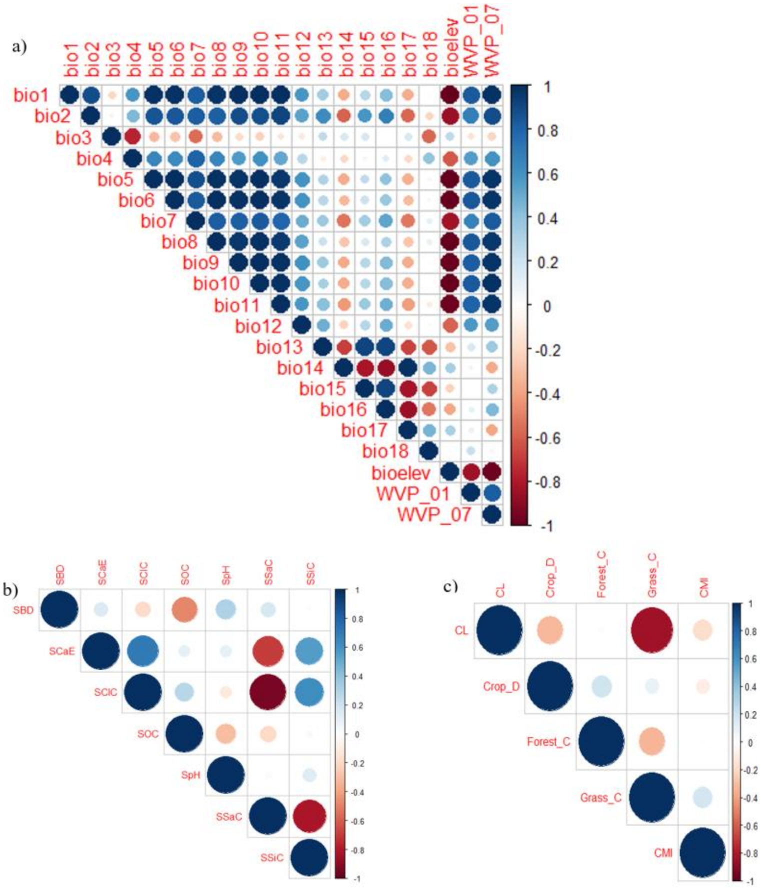


Figure 14. Correlation of the thirty-three environmental variables.

Where: a = climatic variables (*bio1-bio11* temperature related variables, *bio12 - 18* precipitation variables, *bioelev* elevation, *WVP_01* Water vapor pressure of the driest month (January is the driest month in Tigray, *WVP_07* Water vapor pressure of the wettest month (July is the wettest month in Tigray); b = soil variables (*SSaC* Soil sand content, *SOC* Soil organic content, *SSiC* Soil silt content, *SBD* Soil bulk density, *SClC* Soil clay content, *SCaEC* Soil cation exchange capacity and *SpH* Soil pH); c = vegetation and land use variable (*Grass_C* Grass land cover, *CMI* Crop mask irrigation, *CL* Cultivated land, *Fores_C* Forest cover, *Crop_D* Crop dominance).

4.3.1.2. PCA based association of environmental variables

Based on the data from the 33 environmental variables, the distribution and clustering of the site coordinates of the indigenous cattle in Tigray are presented in each cluster's Principal Component Analysis (PCA) plots in Figure 15 (a = soil variables, b = vegetation and land use, and c = temperature and precipitation related variables). The environmental variables under each cluster were well expressed by the first two Principal Components (PC1 and PC2), explaining over 67% of the total variance. However, each population's category was different across the three ecological clusters.

Based on the soil-related environmental cluster, most of the site coordinates for Abergelle and Erob cattle populations were clustered in the same category, while most of the Raya cattle were in the other category, as explained by PC1 exerting 46.1% of the total variance. The site coordinates for Arado or Begait cattle were not distinguished; they were somewhat irregularly distributed across the soil PCA plot showing three subgroups for the Arado cattle and almost four subgroups for the Begait cattle (Figure 15a). This shows the heterogeneity of soil type and characteristics across the breeding areas for the Arado and Begait cattle populations, which indirectly determines the variety and nature of cattle feed type and distribution grown in the area. Based on vegetation and land use environmental cluster, the site coordinates for the Abergelle cattle showed two sub-clusters, as explained by PC1 (43.8%). Only the site coordinates for the Raya cattle showed homogeneity. They were grouped close to each other while all the rest showed heterogeneity, with relatively the site coordinates for the Arado cattle grouped partly with Raya, Abergelle and Erob (Figure 15b).

More importantly, the weather and climatic variables (Figure 15c) clustered the cattle populations in different groups explaining a combined effect of around 79.6%. Accordingly, the Arado and Erob cattle site coordinates were mainly cultured together (Figure 15c, red and blue dots encircled in a purple-bordered circle), except for some individuals of the Arado cattle site coordinates distantly from the group. The Raya cattle site coordinates were clustered in the second quadrant of the PCA plot (Figure 15c, yellow dots encircled within the yellow-bordered circle). The Abergelle cattle site coordinates were closely grouped to each other in the third coordinate of the PCA plot (Figure 15c, green dots encircled in a green bordered circle). Those Begait cattle site coordinates were also closely grouped in the third quadrant of the weather and climatic variables PCA plot (Figure 15c, black dots encircled within a black-bordered circle) but distantly placed from the cluster for Abergelle cattle.

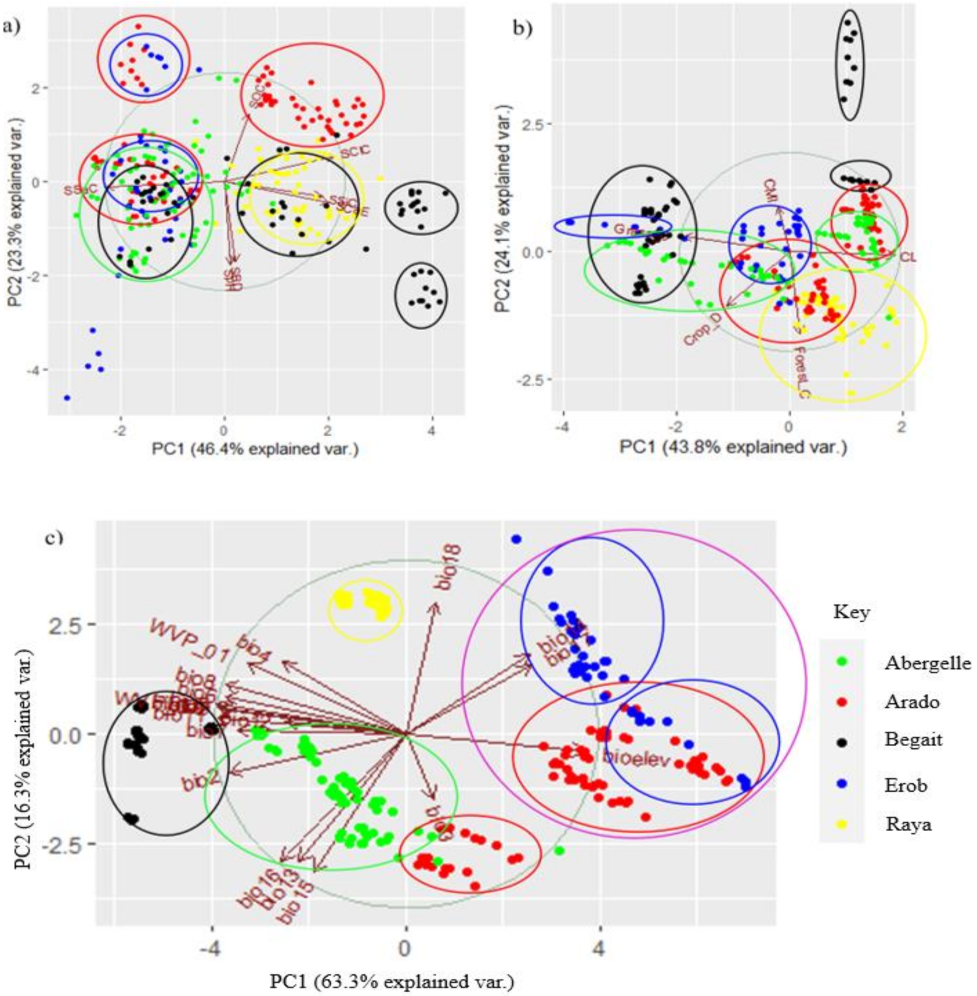


Figure 15. Principal Component Analysis (PCA) plots of the environmental variables.

Where: a = soil variables (*SSaC* Soil sand content, *SOC* Soil organic content, *SSiC* Soil silt content, *SBD* Soil bulk density, *SClC* Soil clay content, *SCaEC* Soil cation exchange capacity and *SpH* Soil pH), b = vegetation and land use variables (Grass_C Grass land cover, *CMI* Crop mask irrigation, *CL* Cultivated land, *Fores_C* Forest cover, *Crop_D* Crop dominance) and c = climatic variables (*bio1-bio11* temperature related variables, *bio12-18* precipitation variables, *bioelev* elevation *WVP_01* Water vapor pressure of the driest month (January is the driest month in Tigray, *WVP_07* Water vapor pressure of the wettest month (July is the wettest month in Tigray).

4.2.2. Selection of contributing variables for model building and prediction

The MaxEntVariableSelection (MVS) screened six environmental variables jointly contributed about 74.98% of the total contribution from all the 33 environmental variables for model building. Based on the contribution (>5%) (Figure 16a) and correlation (<0.6) (Figure 16b) thresholds, cultivated land from vegetation and land use variables, soil bulk density from soil-related variables, and four variables from temperature and precipitation-related variables, including annual precipitation (bio12), precipitation of the wettest quarter (bio16), precipitation of the warmest quarter (bio18) and temperature seasonality (bio4) were selected for further analysis.

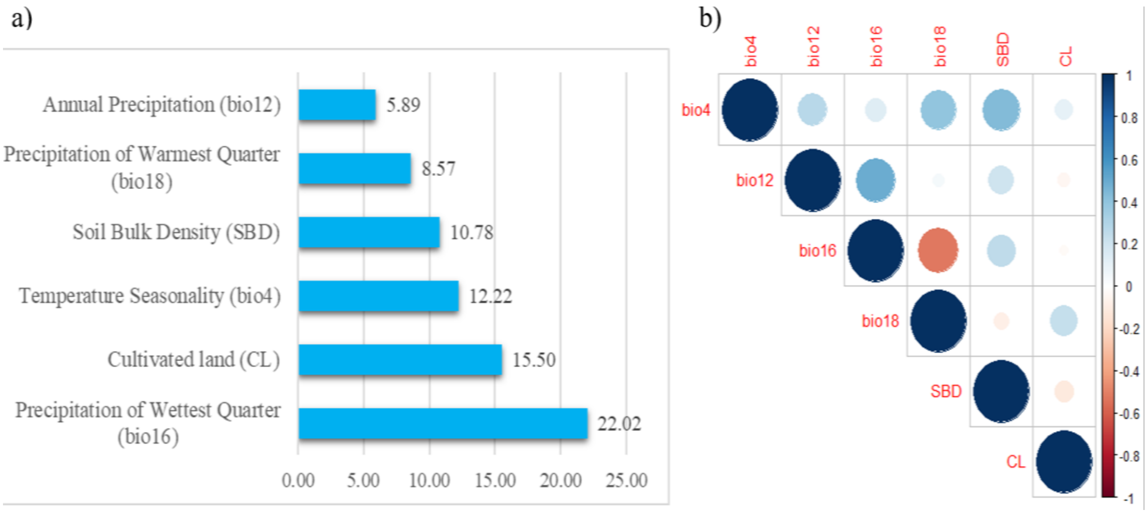


Figure 16. Uncorrelated environmental variables selected using MaxEntVariableSelection (MVS).

Where: (a) contribution (5%) threshold and (b) correlation (< 0.6) threshold.

On the other hand, the finally selected variables used for model building were also evaluated for their contribution in predicting the model performance based on the Jackknife analysis, where each variable can show important information on its own (Figure 17a-c). The environmental variable with the highest gain, when used in isolation in all the tests (jackknife of regularized training gain, jackknife of test gain and jackknife of AUC presented in Figure 17a, b and c, respectively), was the precipitation of the wettest quarter (bio16), which therefore appears to have the most useful information by itself. Thus, precipitation of the wettest quarter (bio16) was the environmental variable that decreases the gain the most when omitted, which therefore appeared to have the most information that can’t be represented in the other variables. Next to bio16 (precipitation of the wettest quarter), the environmental variables with the highest gain, when used in isolation, were the annual precipitation (bio12) and precipitation of the warmest quarter (bio18). Interestingly, the jackknife of AUC values of each environmental variable showed a high contribution and predictability (AUC > 0.6) (Figure 17c and Figure S1), revealing a very high probability of modelling the habitat suitability for the cattle populations under consideration.

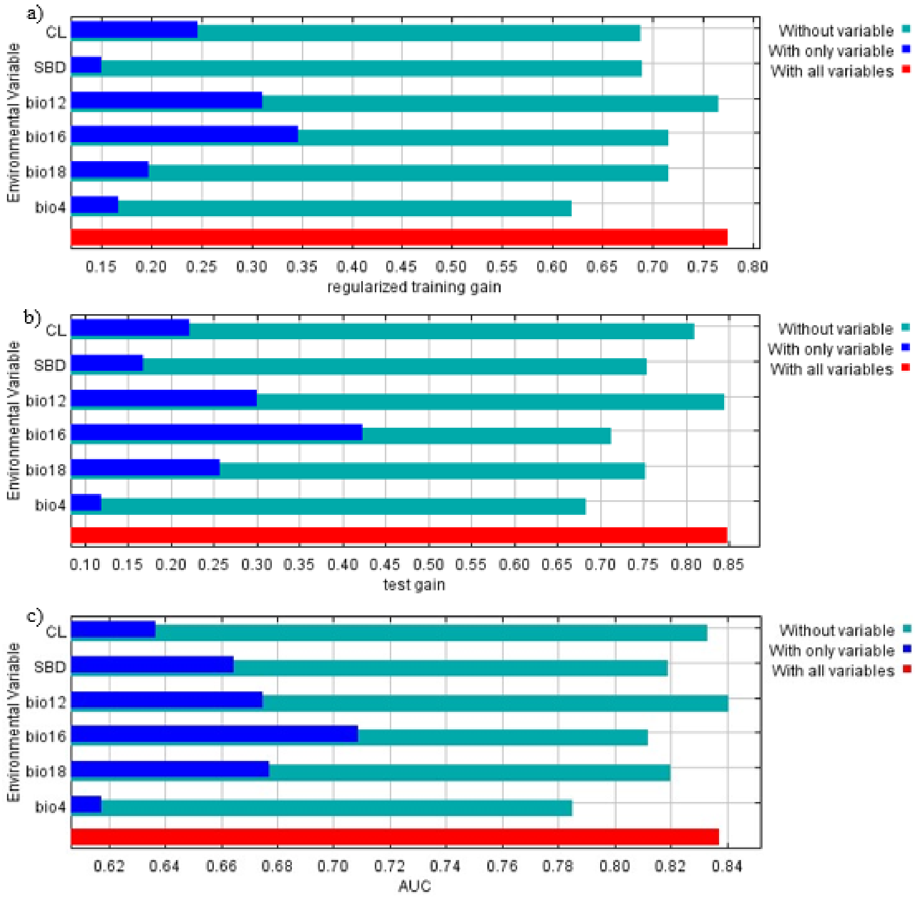


Figure 17. Jackknife plots for the indigenous cattle in Tigray.

Where: (a) Jackknife of regularized training gain (b) Jackknife of test gain and (c) Jackknife of AUC gains based upon the three scenarios including without variable, with only variable and with all variable. Blue bar shows contribution of a specific environmental variable when comparing with all environmental variables (Red bar).

4.2.3. Model (ENM) performance evaluation

Of all the total 192 alternatives produced (Table S13), the model with the best combinations of feature class (FC = hinge (H)) out of the 15 combinations (L, Q, P, H, LQ, LP, LH, QP, QH, PH, LQP, LQH, LPH, QPH, LQPH) and beta multiplier (BM = 2) out of the 25 runs (0.1 to 12 runs with a step of 0.5) was selected (Figure 18a) following its highest test value of AUC (Area Under the Receiving Operator Curve = 0.8659) and its minimum AICc values (Akaike Information Criterion corrected for small samples = 6533.1).

Further, the selected model produced low omission rates (false negativity) on both the test and training data and closely matched the predicted line (black color straight line), exhibiting a high success rate (Figure 18b and Figure S2). Similarly, the area under the receiving operating curve for test and training data showed 81.8 to 98%, which was an excellent model prediction power (Figure 18c and Figure S3).

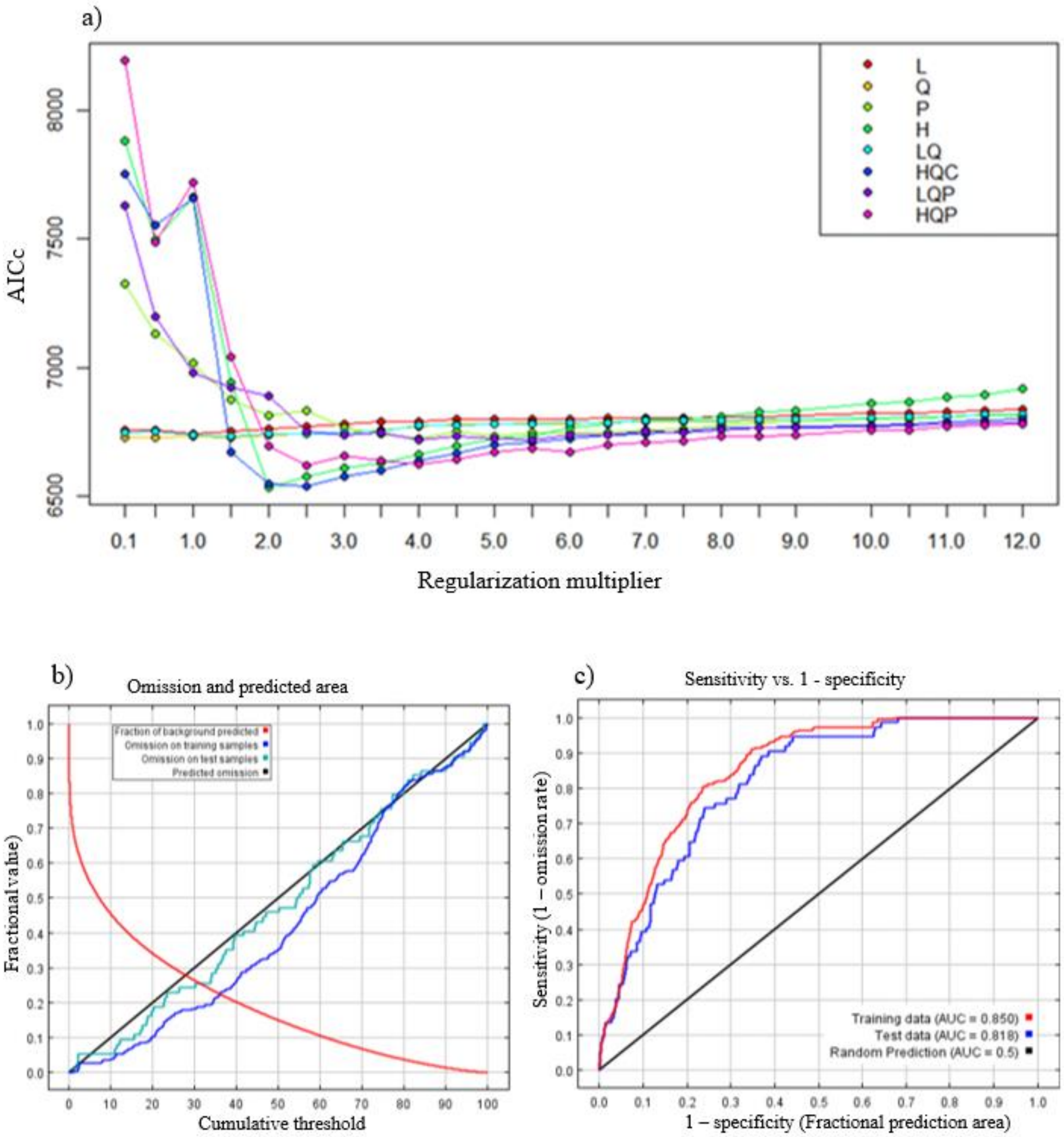


Figure 18. AICc values, Omission rates and predicted areas and MaxEnt Receiver Operating Curve for training and test data.

Where: (a) AICc values for analyzed feature combinations using different beta-multipliers where light-green colored showed the best combination of FC and BM (b) Omission rates and predicted areas of the cumulative threshold on test and training data (c) MaxEnt Receiver Operating Curve for training and test data. “The red (training) line shows the “fit” of the model to the training data. The blue (testing) line indicates the fit of the model to the testing data, and is the real test of the model’s predictive power (Phillips, 2005).

4.2.4. Habitat suitability mapping, classification and characterisation

4.2.4.1. Habitat suitability mapping

The MaxEnt analysis using the best-selected model with FC (Hinge) and BM (two) along with the finally selected six environmental variables and all the combined data (300 occurrence data) mapped the cumulative habitat suitability for the indigenous cattle populations adapted in the Tigray Region. The cumulative habitat suitability (Figure 19) revealed most parts of the Tigray Region were shown to be suitable for the region's indigenous cattle production.

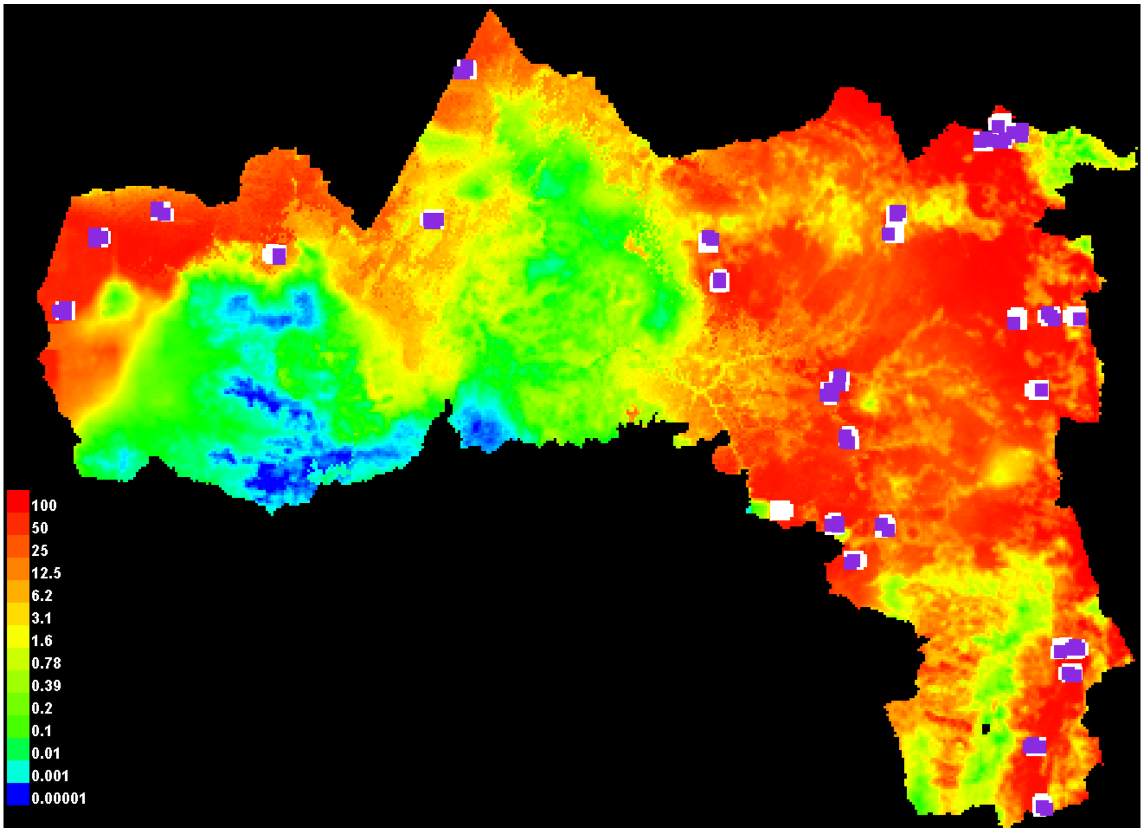


Figure 19. Overall suitability mapping (cumulative output) a representation of the MaxEnt model for the indigenous cattle in Tigray.

Where: Warmer colors show areas with better predicted conditions. White dots show the presence locations used for training, while violet dots show test locations.

The MaxEnt application at a population level, using the best-selected model with FC (Hinge) and BM (two) along with the finally selected six environmental variables, predicted the habitat suitability maps of individual populations (Abergelle, Arado, Begait, Erob and Raya) across the Tigray Region's landscape and estimated the contribution of each environmental variable in the niche of each population (Figure 20 and Table S14).

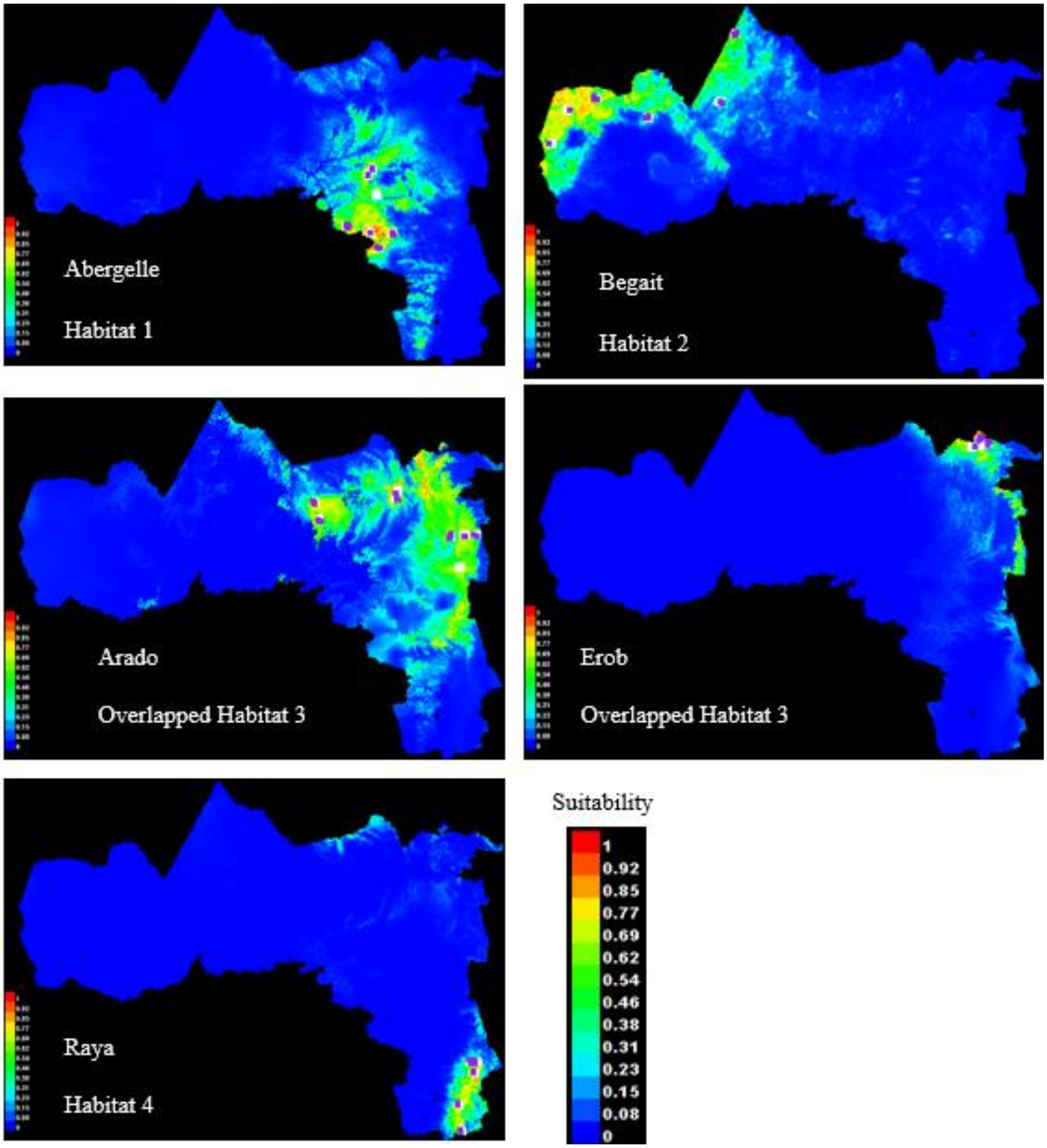


Figure 20. Suitability maps (logistic output) representing each individual cattle population.

Where: Warmer (red, orange, and yellow) colors show areas with better predicted conditions.

4.2.4.2. Pairwise comparison of models for Habitat suitability classification

The Complete clustering method showed the highest value (Complete ≈ 0.46) (Figure S4a), and it was applied to produce the dendrogram for the correlation-based pairwise habitat suitability mapping comparison (Figure S5). The correlation-based pairwise suitability mapping comparison showed correlation levels < 0.6 (Table S15a) with no overlap between each breeding niche.

For the niche similarity-based pairwise habitat suitability mapping comparison, the Ward clustering method showed the highest recorded (≈ 0.35) (Figure S4b). The niche similarity-based pairwise suitability mapping comparison showed around 66% niche overlap between the habitat suitability of the Arado and Erob cattle populations (Table S15b). The habitat suitability maps for individual cattle populations (Figure 20), along with the dendrogram resulted from the niche similarity-based comparison, revealed four different environmental niches for the indigenous cattle in Tigray (Abergelle, Begait, Raya and Arado-Erob) (Figure 21).

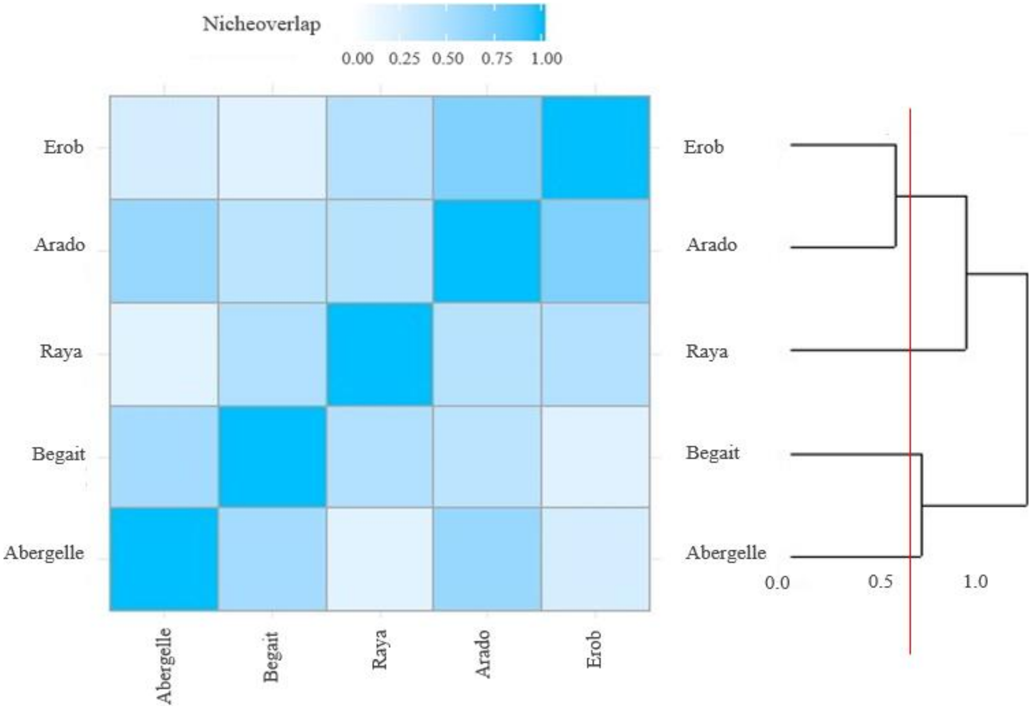


Figure 21. Heatmap and dendrogram of niche overlap statistic between suitability maps among populations.

4.2.4.3. Habitat suitability characterisation

Table 22, represents the characteristics of the four environmental niches, including the environmental niche for Abergelle, Begait, Raya and Arado-Erob cattle populations. The Abergelle cattle environmental niche was characterized by five of the six finally selected environmental variables, including temperature seasonality (bio4 = 32.7%), annual precipitation (bio12 = 10.2%), precipitation of the wettest quarter (bio16 = 24.7%), precipitation of warmest quarter (bio18 = 14.6%) and cultivated land (13.3%). But, it was mainly shaped by the temperature seasonality and precipitation of the wettest quarter; each jointly contributed about 57.4% of the role in characterizing the habitat suitability. The Begait cattle environmental niche was shaped by the temperature seasonality and soil bulk density which jointly contributed about 89.6%. The Raya cattle habitat was characterized by four (bio4, bio16, bio18 and soil bulk density) of the six finally selected environmental variables. However, it was mainly shaped by precipitations of the wettest and warmest quarters followed by soil bulk density which combinedly contributed about 95.6%.

Finally, as the Arado and Erob cattle populations showed mainly overlapped (60%) environmental niches, their environmental niches were categorised as similar characterized by precipitations of the wettest and warmest quarters, temperature seasonality and cultivated land. The only source of difference between the two (Arado and Erob cattle environmental niches) was the annual precipitation (bio12), which had a significant contribution (15.2%) in shaping the Arado cattle environmental niche. In contrast, it has an under-threshold contribution (2.4%) in characterizing the Erob cattle breeding niche. On the other hand, temperature seasonality (bio4) was the only common variable which has a significant contribution (> 5%) values in characterizing the environmental niches of all five cattle populations (Table 22).

Table 22. Major contributing agro-ecological variables by potential environmental niche.

Grouping based on habitat similarity	Population	Major contributor parameters among environmental niches (%)[1]	Within group possible source of differentiation
1	Abergelle	bio4 (32.7%), bio12 (10.2%), bio16 (24.7%), bio18 (14.6%), CL (13.3%) and SBD (4.6)	
2	Begait	bio4 (6.1%), bio12 (0.2%), bio16 (2.7), bio18 (2.2), CL (5.2%), and SBD (83.5%)	
3	Raya	bio4 (5.6%), bio12(0.5), bio16 (35.3%), bio18 (47%), CL (0.4) and SBD (11.3%)	
4	Arado	bio4 (39%), bio12 (10.5), bio16 (10.5%), bio18 (9.9%), CL (25.3%) and SBD (0.2)	bio12
	Erob	bio4 (23.2%), bio12 (2.4%), bio16 (60.6%), bio18 (6.1%) and CL (0)	

[1]*bio4* Temperature seasonality, *bio12* Annual precipitation, *bio16* Precipitation of the wettest quarter, *bio18* Precipitation of the warmest quarter, *Cl* Cultivated land, *SBD* Soil bulk density.

4.2.5. Effect of enviromental variables on perdicting the phenotypic variability among the indigenous cattle in Tigray

The environmental variables, precipitation of wettest quarter (bio16) and precipitation of warmest quarter (bio18) showed significant ($P < 0.05$ to 0.001) contributions in predicting all the ten main quantitative phenotypic variables which were used in determining the phenotypic variability among the female cattle populations. Next, the temperature seasonality (bio4), annual precipitation (bio12) and cultivated land had a significant contribution in predicting eight of the ten quantitative phenotypic variables (HW, PW, MC, HG, NL, CD, BL, RH) in the female cattle populations. The soil bulk density showed a significant contribution in predicting the height at withers (HW) and Neck length (NL) variability of the female cattle populations exclusively (Table 23).

In the male cattle populations, the only environmental variable that significantly affected all eight quantitative phenotypic variables was precipitation of the warmest quarter (bio18). The temperature seasonality (bio4) and precipitation of the wettest quarter (bio16) each had a significant effect in differentiating six of the eight quantitative phenotypic traits of the male cattle (Table 24).

Table 23. Quantitative traits predicted with Generalized Additive Model (GAM) in the Tigray female indigenous cattle in Tigray

Trait[1]	Fixed effects	MaxEnt selected environmental variables (Random effects) [2]						df[3]	AIC[4]	R-sq.(adj)[5]	Deviance explained
		bio4	bio12	bio16	bio18	Cl	SBD				
HW	Population	***	***	***	***	***	***	51.3211	9007.293	0.891	89.4%
HL	Population			**	***			18.22378	10128.61	0.834	83.6%
PW	Population	***	***	***	***	***		44.34111	7161.018	0.823	82.8%
MC	Population	***	***	***	***	*		33.34346	6588.468	0.814	82%
HG	Population	***	***	***	***	***		43.18291	9338.727	0.75	75.7%
HBC	Population			*	***			20.91263	7756.52	0.66	66.4%
NL	Population	***	***	***	***	***	***	47.77921	7060.845	0.814	82%
CD	Population	***	**	***	***	***		36.28513	7932.718	0.751	75.7%
BL	Population	***	**	***	***	**		41.41779	9577.736	0.758	76.4%
RH	Population	***	***	***	***	**		37.34588	9183.156	0.764	76.9%

Significant codes: '***' = 0.001; '**' = 0.01; '*' = 0.05

[1] *HW* height at withers, *HL* horn length, *PW* pelvic width, *MC* muzzle circumference, *HG* heart girth, *HBC* horn base circumference, *NL* neck length, *CD* chest depth, *BL* body length, *RH* rump height

[2] *bio4* Temperature seasonality, *bio12* Annual precipitation, *bio16* Precipitation of the wettest quarter, *bio18* Precipitation of the warmest quarter, *Cl* Cultivated land, *SBD* Soil bulk density

[3] *df* degrees of freedom

[4] *AIC* Akaike information criterion

[5] *R-sq.(adj)* R-square adjusted

Table 24. Quantitative traits predicted with Generalized Additive Model (GAM) in the Tigray male indigenous cattle in Tigray.

Trait[1]	Fixed effects	MaxEnt selected environmental variables (Random effects) [2]						df[3]	AIC[4]	R-sq.(adj)[5]	Deviance explained
		bio4	bio12	bio16	bio18	CL	SBD				
HG	Population	***		**	***			27.87002	888.2457	0.899	91.7%
DW	Population				***			15.60944	561.8175	0.873	88.5%
HW	Population	***	***	***	***	**		41.6876	919.8617	0.914	93.7%
HL	Population				***			13.02604	1022.77	0.83	84.3%
NL	Population	***		***	***		*	29.03163	697.1818	0.852	88%
BL	Population	***		***	*			29.48829	988.9535	0.73	78.2%
RH	Population	***		***	***			22.49216	938.7785	0.744	78.1%
PW	Population	***		*	***			21.86788	724.4198	0.833	85.6%

Significant codes: '***' = 0.001; '**' = 0.01; '*' = 0.05

[1] *HG* heart girth *DW* dewlap width, *HW* height at withers, *HL* horn length, *NL* neck length, *BL* body length, *RH* rump height, *PW* pelvic width

[2] *bio4* Temperature seasonality, *bio12* Annual precipitation, *bio16* Precipitation of the wettest quarter, *bio18* Precipitation of the warmest quarter, *Cl* Cultivated land, *SBD* Soil bulk density

[3] *df* degrees of freedom

[4] *AIC* Akaike information criterion

[5] *R-sq.(adj)* R-square adjusted

4.3. Genome-wide Diversity and Admixture of the Indigenous cattle in Tigray

4.3.1. Mapping and variant detection

The number of paired-sequence reads for each animal ranged from 200,684,387 to 289,752,799, with a mapping rate of 99.61% to 99.79% to the reference genome (ARS_UCD1.2). The average sequencing depth among populations ranged from 10.13 X (Erob cattle) to 10.64 X (Begait cattle). Furthermore, over 88% of the bases were covered with at least five reads, and 39% to 42% were covered with at least ten reads (Table 25).

Table 25. Summary results on sequencing and mapping of sequence reads across the genome of the indigenous cattle in Tigray.

Sample[1]	Total reads	MR (%)[2]	PPR[3]	MD (X)[4]	5_b (%)[5]	10_b (%)[6]	20_b (%)[7]	40_b (%)[8]
ABR02	223701820	99.78	97.7	10.13	88.8	38.2	1.1	0.4
ABR 07	225383302	99.78	97.39	9.98	85.9	35.2	1.1	0.4
ABR 10	211853306	99.74	97.7	9.51	84.6	31.6	0.9	0.3
ABR 11	265608575	99.78	97.54	11.66	92.4	52.9	1.7	0.4
ABR 12	206914185	99.77	97.64	9.22	83.3	29.0	0.9	0.3
ABR 13	267674295	99.76	97.61	11.65	91.9	51.4	1.8	0.5
ABR 14	258784661	99.78	97.46	11.31	91.9	50.0	1.5	0.4
ABR 15	254717248	99.77	97.66	11.44	90.9	50.8	1.7	0.4
ABR 16	219354788	99.77	97.6	9.74	85.4	33.2	0.9	0.4
ABR 21	224258471	99.75	97.61	10.06	88.5	38.2	1.1	0.4
ABR 29	215860301	99.74	97.6	9.72	87.1	33.8	1.0	0.4
Average	234010087	99.77	97.59	10.40	88.25	40.39	1.25	0.39
AR01	268732515	99.72	97.52	11.74	92.3	52.7	1.8	0.5
AR05	207962334	99.77	97.6	9.45	86.2	31.5	0.9	0.4
AR 06	225872374	99.78	97.57	10.02	88.3	37	1	0.4
AR 10	228945045	99.73	97.61	10.19	88.1	38.9	1.0	0.3
AR 11	242935153	99.61	97.39	10.69	89.1	42.6	1.2	0.4
AR 13	272318578	99.77	97.73	11.94	92.4	53.9	1.9	0.5
AR 23	236874813	99.74	97.53	10.67	89.7	42.4	1.3	0.4
AR 24	269700129	99.74	97.6	11.56	92.3	52.4	1.7	0.4
AR 30	260181861	99.74	97.57	11.46	91.3	51.9	1.8	0.4
AR31	200684387	99.73	97.64	9.12	84.1	27.8	0.8	0.4
AR32	207542739	99.79	97.60	9.40	84.6	31.0	0.9	0.4
Average	238340903	99.74	97.58	10.57	88.95	42.01	1.30	0.41
BG 01	241159107	99.76	97.71	10.64	89.9	43	1.3	0.4

Sample[1]	Total reads	MR (%)[2]	PPR[3]	MD (X)[4]	5_b (%)[5]	10_b (%)[6]	20_b (%)[7]	40_b (%)[8]
BG 02	224954591	99.79	97.73	9.97	87.4	35.4	1.0	0.4
BG 05	289752799	99.72	97.53	12.29	93.3	58.1	2.2	0.5
BG 07	207478671	99.74	97.69	9.26	85.0	29.6	0.8	0.3
BG 13	220949139	99.77	97.53	9.98	86.5	34.7	1.0	0.4
BG 15	238733623	99.74	97.76	10.57	88.8	42.7	1.2	0.4
BG 17	266767650	99.69	97.53	11.37	91.4	49.0	1.7	0.5
BG 19	279123320	99.72	97.43	12.02	92.7	55.2	2.1	0.5
BG 20	216099482	99.68	97.55	9.70	86.1	32.8	0.9	0.4
BG 21	223640202	99.77	97.7	9.91	87.6	35.6	1.0	0.4
BG 31	248420836	99.72	97.77	11.28	91.8	49.6	1.5	0.4
Average	241552675	99.74	97.63	10.64	89.14	42.34	1.34	0.42
ER 01	282881666	99.71	97.43	12.27	92.3	57.3	2.3	0.4
ER04	200721988	99.67	97.55	9.30	85.8	30.9	0.9	0.4
ER 06	212690117	99.73	97.73	9.53	86	31.8	0.9	0.4
ER 07	226350254	99.68	97.19	10.14	87.2	38.3	1.1	0.4
ER 10	227694454	99.76	97.72	10.17	88.6	38.1	1.1	0.4
ER 11	224425333	99.75	97.51	9.93	88.0	36.7	1.1	0.4
ER13	215739659	99.71	97.27	9.83	86.6	35.7	1.0	0.4
ER 15	260329447	99.74	97.58	11.65	92.3	53.0	1.8	0.4
ER 17	212074051	99.77	97.43	9.56	85.2	32.4	0.9	0.4
ER 18	202140293	99.75	97.58	8.88	82.4	25.7	0.8	0.3
Average	226504726	99.73	97.50	10.13	87.44	37.99	1.19	0.39
RAY 05	205800875	99.74	97.55	9.19	82.3	27.9	0.8	0.3
RAY 06	201381053	99.77	97.43	9.09	82.3	28.1	0.9	0.3
RAY11	288609469	99.71	97.44	12.69	93.7	61.9	2.7	0.5
RAY 17	251020395	99.74	97.66	11.13	91.3	47.9	1.5	0.4
RAY 19	235906893	99.77	97.45	12.02	92.7	55.2	2.1	0.5
RAY 21	218822571	99.78	97.57	9.86	87.6	35.6	1.0	0.4
RAY 22	213692973	99.69	97.41	9.7	87.2	34.5	1.0	0.4
RAY 23	203433032	99.71	97.53	9.20	83.9	28.5	0.9	0.4
RAY 25	276489917	99.74	97.62	11.83	92.6	54.9	2.0	0.5
RAY 26	201246838	99.71	97.72	9.12	84.6	28.7	0.8	0.3
RAY 30	203685341	99.74	97.51	9.26	84.7	29.6	0.9	0.4
Average	208571680	90.67	97.54	10.28	87.54	39.35	1.33	0.40

[1] *ABR* * Abergelle, *RA** Arado cattle, *BG* * Begait, *ER* * Erob, and *RAY* * Raya

[2] *MR* Total numbers of reads mapped to the *ARS-UCD1.2* reference genome.

[3] *PPR*Percentage of both mates of a read pair that were properly mapped to the same chromosome.

4*MD* Mean sequence depth

[5] *5_b* Percentage of the genome with bases covered by at least 5 reads.

[6] *10_b* Percentage of the genome with bases covered by at least 10 reads.

[7] *20_b* Percentage of the genome with bases covered by at least 20 reads.

[8] *40_b* Percentage of the genome with bases covered by at least 40 reads.

Variant calling and filtration combining the indigenous cattle in Tigray resulted in the detection of around 36 million (M) SNPs (n = 36,003,573) and 3.7M indels (n = 3,703,659) (Table S16b). The number of SNPs detected per individual sample ranged from 12 to 13M (Table S16a Table S9a). The number of SNPs at population level ranged from 28M to 29M, of which 7% were novel (Table 25). Around 1.1 to 1.2M indels were detected in each individual cattle (Table S16a), while the number of indels in each population ranged from 2,755,496 (Erob) to 2,905,857 (Arado). Of these, around 34% were novel (Table 26).

Except for Erob cattle, the number of private SNPs across individual samples ranged from 32,245 to 81,933, and the number of private indels ranged from 5,276 to 14,182 (Figure 22). Among Erob cattle, four samples (ER06, ER17, ER13 and ER10) had fewer private variants (9,929 to 11,526 SNPs and 2,675 to 2,870 indels) compared to the remaining indigenous cattle in Tigray samples. At the population level, 571,535, 634,275, 583,831, 433,013 and 569,013 private SNPs were detected for Abergelle, Arado, Begait, Erob and Raya cattle populations, respectively.

Table 26. Variant statistics (SNPs and indels) across the genome of the indigenous cattle in Tigray.

Variables	Populations				
	Abergelle	Arado	Begait	Erob	Raya
N	11	11	11	10	11
SNPs					
Novel (%)	2135111 (7.22)	2138760 (7.2)	2091767 (7.23)	1999834 (7.13)	2161976 (7.36)
Known	27428853	27574364	26840780	26045211	27231606
Total	29563964	29713124	28932547	28045045	29393582
Indels					
Novel (%)	985169 (34.11)	991807 (34.13)	968237 (34.22)	938479 (34.06)	1003423 (34.6)
Known	1902736	1914050	1861562	1817017	1896421
Total	2887905	2905857	2829799	2755496	2899844

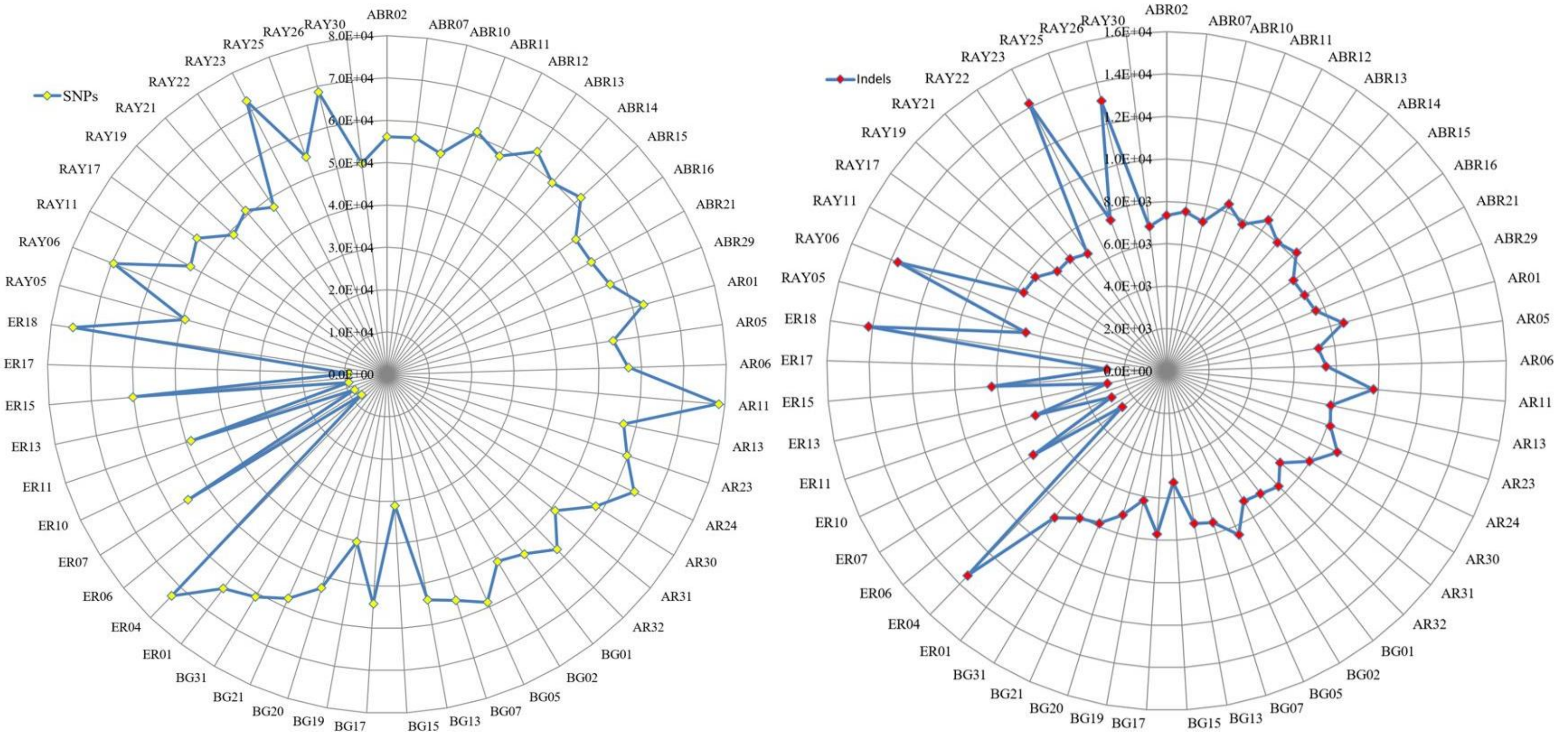


Figure 22. The distribution of private SNPs and indels across samples for each population.

Where: ABR* for Abergelle, AR* for Arado, BG* for Begait, ER* for Erob and RAY* for Raya cattle.

4.3.2. Genetic variants density and allele frequencies

The densify of genome-wide SNPs ranged from 11.27 ± 7.69 to 11.94 ± 7.88 SNPs/kb and of indels from 1.08 ± 1.34 to 1.17 ± 1.41 indels/kb across the five indigenous cattle in Tigray (Tables S17 and S18). Chromosomes 23, 27 and 28 had the highest density of variants (13 to 14 SNPs/kb and 1.3 to 1.4 indel/kb), while chromosomes 19, 13, 3 and 11 had the lowest ones (10 to 11 SNPs/kb and < 1.1 indels/kb). The chromosome-wise distributions of variants (SNPs and indels) were proportional to the length of the chromosomes (Tables S19 and S20). As expected, large chromosomes had more variants than small ones (Figure 23a-d). However, the density of variants (SNPs/kb or indel/kb) was higher on small chromosomes than large ones.

Across the indigenous cattle in Tigray, the average alternate (non-reference) allele frequencies of SNPs and indels were 0.32 and 0.28 to 0.3, respectively. The proportion of SNPs with mean alternate allele frequency (AAF) < 0.5 ranged from 77% to 79% and the proportion of SNPs with mean AAF > 0.9 was around 4%. The proportion of indels with mean alternate allele frequency (AAF) < 0.5 ranged from 78% to 80% (Table S21). However, most of the variants (SNPs and indels) had frequencies of 10% or less (Figure 24). Allele frequencies of private SNPs ranged from 0.05 to 0.55, of which 67% (Erob cattle) to 83% (Arado cattle) of these SNPs had an allele frequency of 0.05 (Figure 25).

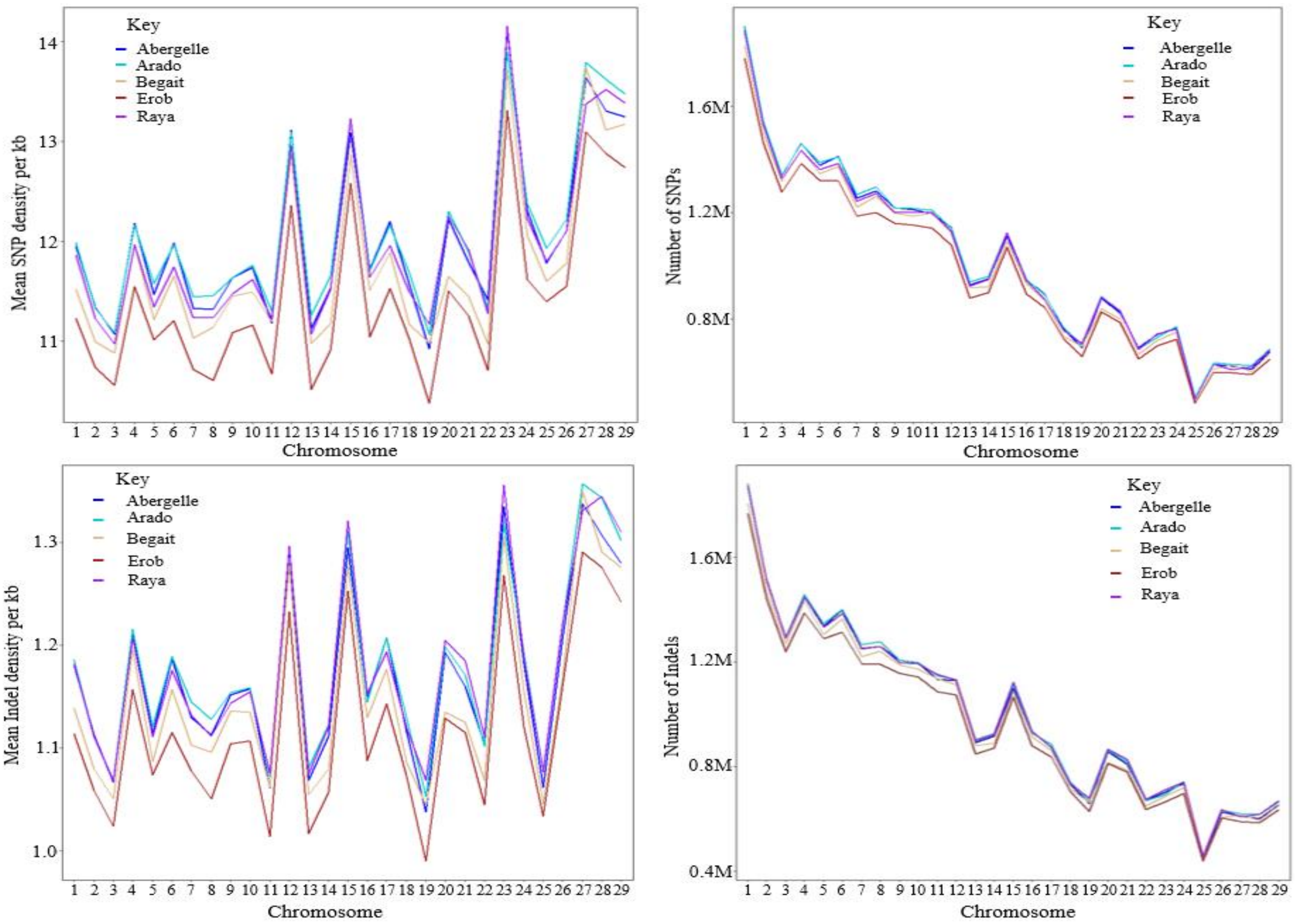


Figure 23. Mean variants density across 1kb window for indigenous cattle in Tigray chromosomes.

Where: (a) Mean SNPs density (b) mean indel density, (c) SNPs distribution across the chromosomes

and (d) Indels SNPs distribution across the chromosomes.

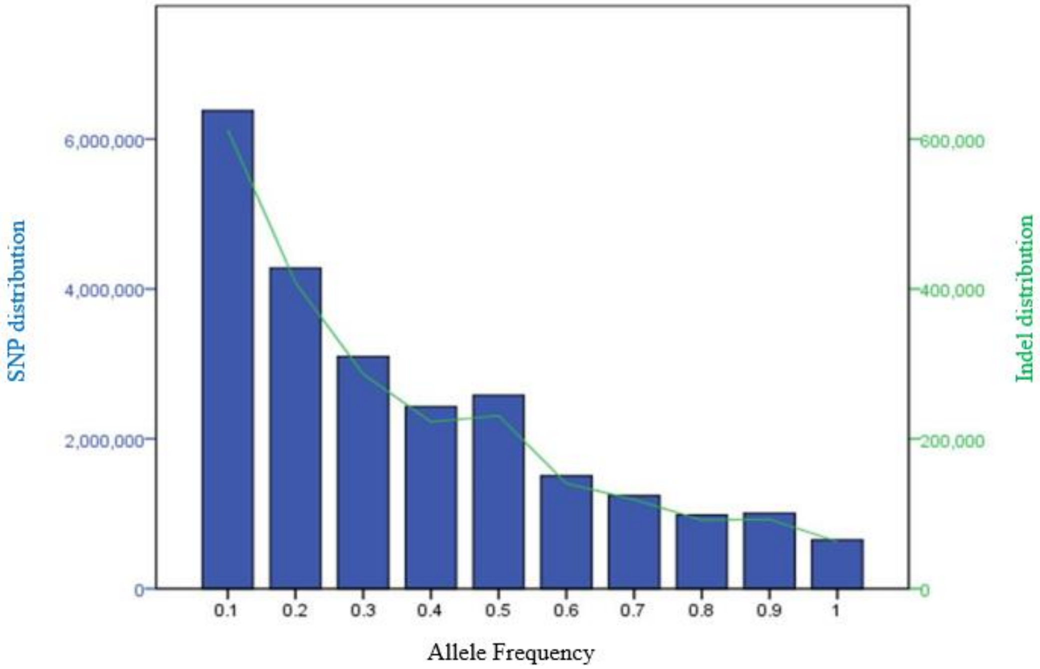


Figure 24. Distribution of the variants based on allele frequency (blue bars represent SNPs and the green line represents indels).

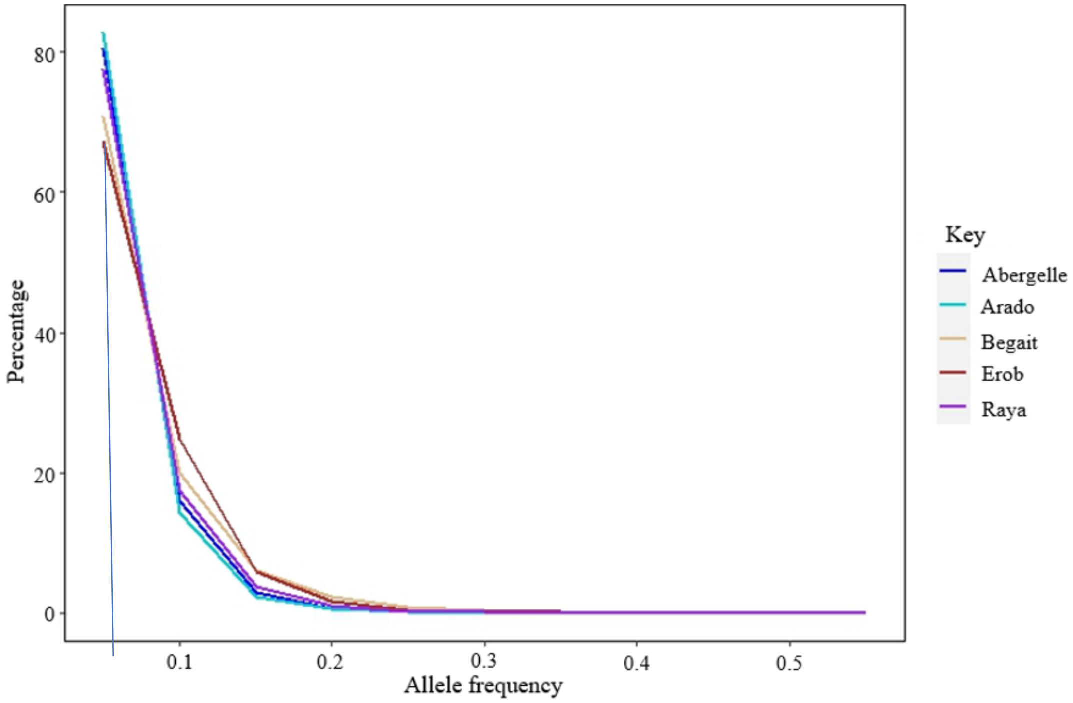


Figure 25. Allele frequency of private SNPs, where each color line represents a cattle population.

4.3.2. Nucleotide substitution and indel length distribution

The transitions-to-transversions (Ti/Tv) ratio was around 2.35 (Table 27). It supported a high sequencing accuracy for all samples. Across all the samples, the highest number of nucleotide substitutions were recorded for the bases Cytosine to Thymine (C > T) and the bases Guanine to Adenine (G > A) and the least number of nucleotide substitutions for the bases Adenine to Thymine (A > T) and Thymine to Adenine (T > A) (Table 27 and Figure S6a). The number of insertions was about 0.33 to 0.35 times higher than deletions. Furthermore, the length of indels ranged from -28bp (deletion, Abergelle) to +23 bp (insertion, Begait). Almost 50% of the indels had a length of 1 bp, while the majority of indels were less than 5bp (85.52% in Abergelle, 85.47% in Arado, 85.46% in Begait, 85.53% in Erob and 85.45% in Raya cattle). Only around 14% of the total indels had lengths greater than or equal to 6bp (Table 28 and Figure S6b).

Table 27. Numerical distribution of nucleotide substitution across the genome of the indigenous cattle in Tigray.

Nucleotide substitution[1]	Population[2]				
	ABR (N = 11)	AR (N = 11)	BG (N = 11)	ER (N = 10)	RAY (N = 11)
A > C	1163650	1168200	1139306	1108539	1159447
A > G	4617218	4636061	4534566	4418513	4595475
A > T	879988	884155	860290	835000	876229
C > A	1230556	1237089	1202191	1164066	1224922
C > G	1135067	1141536	1110983	1075914	1129324
C > T	5744637	5777051	5608171	5411407	5700535
G > A	5767713	5800307	5629465	5431403	5724353
G > C	1137839	1144012	1114739	1079326	1131548
G > T	1233745	1241488	1206275	1167903	1229929
T > A	884513	889825	865341	839132	881259
T > C	4607940	4626324	4523999	4408324	4584911
T > G	1161098	1167076	1137221	1105518	1155650
TS/TV	2.349	2.349	2.35	2.349	2.345

[1] A > C = substitution of Adenine by Cytosine, A > G = Adenine by Guanine, A > T = Adenine by Thymine, C > A = Cytosine by Adenine, C > G = Cytosine by Guanine, C > T = Cytosine by Thymine, G > A = Guanine by Adenine, G > C = Guanine by Cytosine G > T = Guanine by Thymine, T > A = Thymine by Adenine, T > C = Thymine by cytosine and T > G = Thymine by Guanine

[2] *ABR* Abergelle, *AR* Arado, *BG* Begait, *ER* Erob, *RAY* Raya

Table 28. Distribution of insertions and deletions across the genome of the indigenous cattle in Tigray.

Description	ABR	AR	BG	ER	RAY
1bp	1451722	1460409	1422733	1386758	1455869
2bp	455489	458417	446212	435726	459339
3bp	256672	257672	250611	244393	257419
4bp	201403	202424	196866	190997	201212
5 bp	104354	104799	102026	98806	104213
≥ 6bp	418265	422136	411351	398816	421792
1bp (%)	50.27	50.26	50.28	50.33	50.21
≤ 5bp (%)	85.52	85.47	85.46	85.53	85.45
≥ 6bp (%)	14.48	14.53	14.54	14.47	14.55
Maximum insertion	20	20	23	21	21
Maximum deletion	-28	-27	-27	-27	-27
Insertion	1655574	1666501	1618905	1572964	1663890
Deletion	1232331	1239356	1210894	1182532	1235954
Insertion/Deletion	1.34	1.34	1.34	1.33	1.35

ABR Abergelle, *AR* Arado, *BG* Begait, *ER* Erob, *RAY* Raya, *bp* base pair

4.3.3. Functional distribution of genetic variants (SNPs and indels)

The annotation of the SNPs showed that around 59.5% of them were in the intergenic regions. Around 76% of annotated SNPs were in introns, 7% in upstream of genes, 7.2% in downstream of genes, 0.5% in 3’ untranslated region (UTR), 0.2% in 5’ UTR and 0.11% in non-coding transcript exon. The number of SNPs in the coding regions (stop gain, stop lost and stop retained, start lost, missense and synonymous SNPs, and coding sequences) was approximately 0.01% in all populations (380,309 in Abergelle, 383,116 in Arado, 373,578 in Begait, 361,55 in Erob and 380,299 in Raya cattle) (Table 29 and Figure S7), of which around 17%-18% had deleterious effects (Figure S8).

Around 57%, 77%, 7.4%, 8%, 0.6%, 0.2% and 0.1% of the indels were in intergenic regions, introns, upstream of genes, downstream of genes, 3’ UTR, 5’ UTR and non-coding transcript exons, respectively. The total numbers of indels located within the coding regions (stop gain, stop lost, stop retained, start lost, start retained, frameshifts, inframe insertions, inframe deletions, protein-altering variants and coding sequences) ranged from

0.22% (Raya cattle, 6,414) to 0.27% (Erob cattle, 7,462) (Table 30). Among the indels located in the coding regions, 63.20%, 63.39%, 62.65%, 63.48% and 77.6% resulted in codon frameshifts (codon alteration), of which 0.81%, 0.84%, 0.98%, 0.84% and 0.88% may affect protein functions in Abergelle, Arado, Begait, Erob, and Raya cattle populations, respectively (Figure S9).

Table 29. Population level summary of annotation of SNPs in the genome of the indigenous cattle in Tigray.

All consequences	Abergelle	Arado	Begait	Erob	Raya
Number of samples	11	11	11	10	11
Bi-allelic variants processed	29563964	29713124	28932547	28045045	29393582
Splice donor variant	707	684	693	672	690
Splice acceptor variant	439	452	442	429	435
Stop gained	1682	1748	1706	1648	1765
Stop lost	245	238	237	239	243
Start lost	397	406	382	373	413
Missense variant	149334	150764	146883	141733	149448
Splice region variant	40755	41135	39987	38861	40791
Synonymous variant	228481	229776	224200	217399	228249
Stop retained variant	169	183	169	160	180
Coding sequence variant	1	1	1	1	1
Mature miRNA variant	123	125	121	120	125
5_prime UTR variant	49794	49766	48751	46913	50016
3_prime UTR variant	137652	138671	135235	131341	137754
Non-coding transcript exon variant	31400	31309	30515	29622	31084
Intron variant	22387867	22473356	21940886	21255569	22194958
Non-coding transcript variant	502772	505660	496259	476848	500512
Upstream gene variant	2074721	2090124	2042625	1979084	2075740
Downstream gene variant	2111713	2121229	2070242	2007161	2104907
Intergenic variant	17584768	17682416	17197428	16677542	17502131

Table 30. Population level summary of annotation of indels in the genome of the indigenous cattle in Tigray.

All consequences	Abergelle	Arado	Begait	Erob	Raya
Number of samples	11	11	11	10	11
Bi-allelic variants processed	2887905	2905857	2829799	2755496	2899844
Transcript ablation	4	5	5	5	5
Splice donor variant	248	240	236	206	227
Splice acceptor variant	232	234	215	208	221
Stop gained	57	61	64	62	61
Frameshift variant	4788	4875	4688	4737	4977
Stop lost	28	28	28	24	25
Start lost	42	39	41	34	38
Inframe insertion	825	834	815	799	853
Inframe deletion	1565	1578	1561	1540	1781
Protein altering variant	39	41	46	40	44
Splice region variant	3797	3913	3805	3716	3952
Stop retained variant	17	17	21	22	20
Start retained variant	13	14	13	13	12
Coding sequence variant	202	204	206	191	206
Mature miRNA variant	12	16	13	16	17
5 prime UTR variant	4855	4835	4842	4647	4985
3 prime UTR variant	16000	16025	15703	15327	16165
Non-coding transcript exon variant	2439	2440	2409	2321	2441
Intron variant	2237586	2246670	2192419	2135981	2239005
Non-coding transcript variant	47834	48290	47388	45827	48017
Upstream gene variant	214934	216603	211424	205980	217097
Downstream gene variant	230871	232624	227186	220614	232751
Intergenic variant	1642232	1653813	1607488	1565117	1648903

4.3.4. Enrichment analysis of the genes overlapping private SNPs

A separate analysis of the private SNPs for each population showed 1,455, 1,809, 1,470, 1,203, and 1,701 private missense SNPs for Abergelle, Arado, Begait, Erob and Raya cattle populations, respectively, of which 97.9% (Erob) to 98.9% (Raya) were in coding regions. The remaining ones overlapped with splice regions. Of the missense SNPs in the coding regions, 33.1%, 34.4%, 52.7%, 64.8% and 58.1% had deleterious effects in Abergelle, Arado, Begait, Erob and Raya cattle populations, respectively (Figure 26).

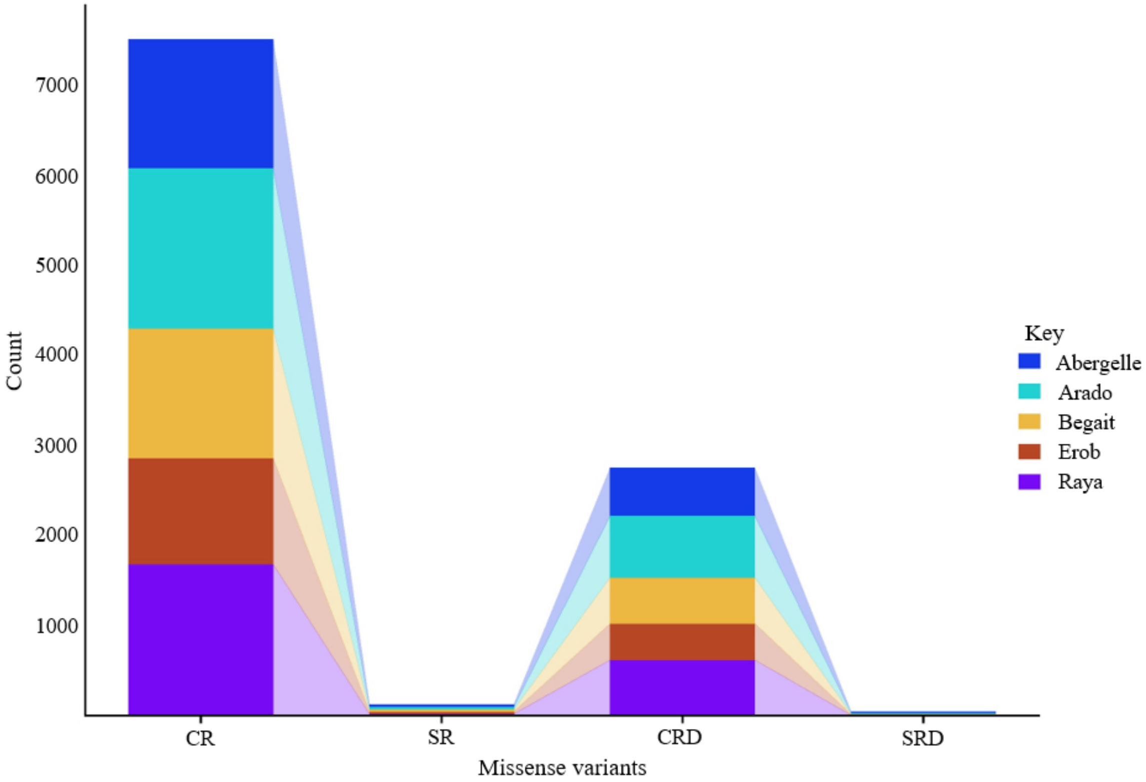


Figure 26. Private SNPs with missense effects overlapping coding and splicing regions.

Where, CR represents the number of missense SNPs overlapping coding regions, SR represents the number of missense SNPs overlapping splice regions, CRD represents the number of missense SNPs overlapping coding regions with deleterious effects, and SRD represents the number of missense SNPs overlapping splice regions with deleterious effects**.**

Functional enrichment analysis of the genes overlapping private SNPs in coding regions identified 16, 12, 16, 6 and 10 significant ($P < 0.05$, Bonferroni < 0.05, FDR < 0.05 and fold enrichment >1) GO terms of biological process (BP), cellular component (CC), molecular function (MF) and KEGG pathways in Abergelle, Arado, Begait, Erob and Raya cattle populations, respectively (Figure 27). Out of the enriched terms, the top three most significant ones ($P = 1.6 \times 10^{-5}$ to 6.8×10^{-67}, Bonferroni = 1.65×10^{-2} to 7.5×10^{-64}, FDR= 8.3×10^{-3} to 7.5×10^{-64} and fold enrichment = 2.3 to 4.3) were olfactory receptor activity (GO:0004984), olfactory transduction (bta04740) and odorant binding (GO:0005549). These were common to all populations.

Within populations, the enrichment analysis further identified many population specific genes associated with the aforementioned three most significant terms. Around 11% (Erob cattle) to 17% (Abergelle cattle) of the genes were associated with olfactory receptor activity, 13% (Erob cattle) to 18% (Abergelle cattle) with olfactory transduction, and 3% (Erob cattle) to 6% (Abergelle cattle) with odorant binding.

Eleven genes, including *OR4F73*, *OR1L21*, *OR5AN1*, *OR9S29*, *OR9M1D*, *OR2H20*, *OR4X16*, *OR5AK29*, *OR6C4*, *OR8B1AU* and *OR9S40*, were commonly enriched in the three shared GO terms. Six GO terms (GO:0004871~signal transducer activity, GO:0004872~receptor activity, GO:0004888~transmembrane signalling receptor activity, GO:0038023~signaling receptor activity, GO:0060089~molecular transducer activity, GO:0099600~transmembrane receptor activity) with related molecular functions were enriched in four populations (Abergelle, Arado, Begait and Raya cattle). A total of 41 genes were over represented in all the six GO terms. Interestingly, two significant GO terms of the cellular component associated with an integral component of the plasma membrane (GO:0005887) and the intrinsic component of the plasma membrane (GO:0031226) were only enriched in Begait cattle. Two GO terms of the cellular component (GO:0005578) related with proteinaceous extracellular matrix and extracellular matrix component (GO:0044420) were significantly enriched only in the Erob cattle.

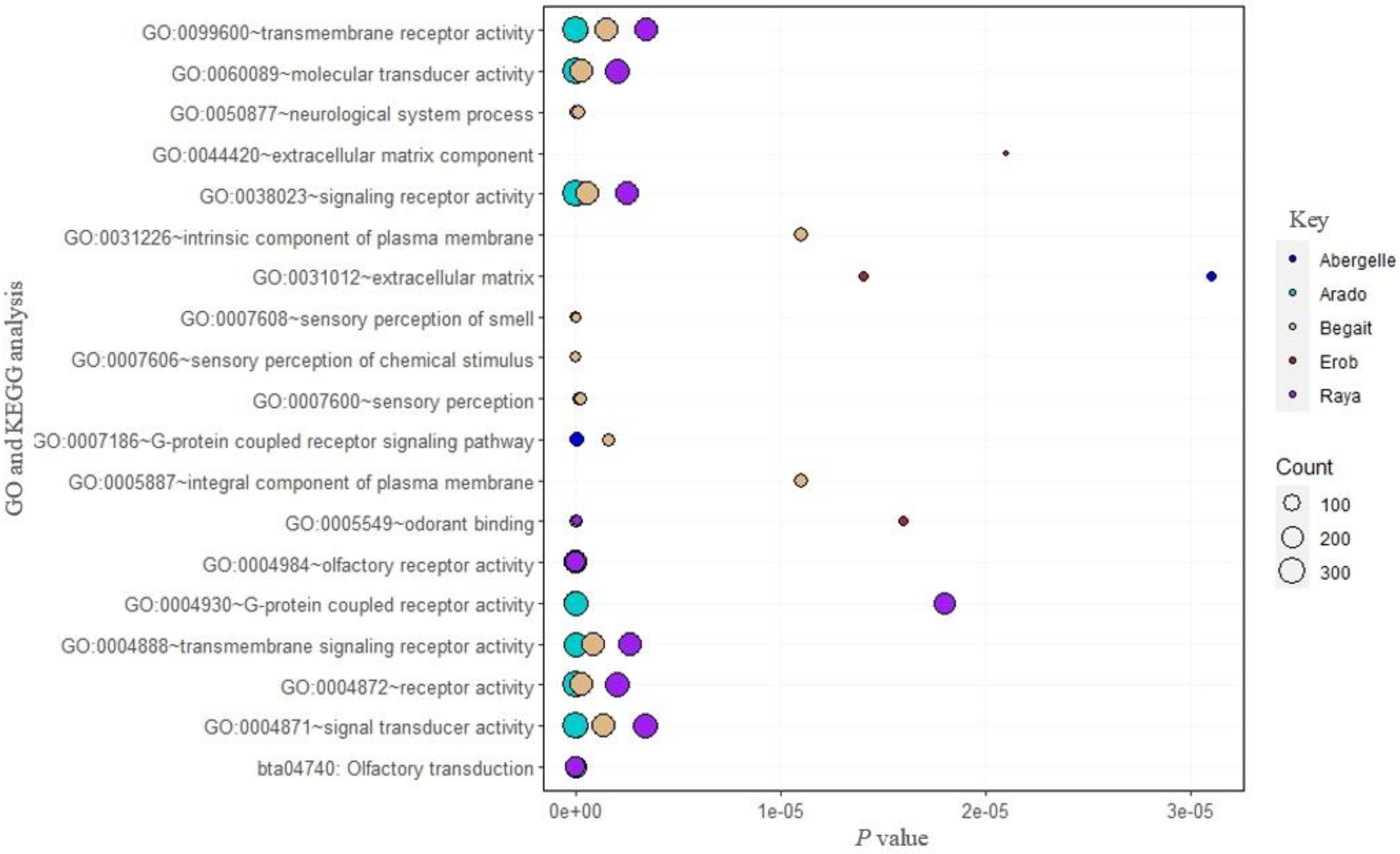


Figure 27. Gene Ontology (GO) and Kyoto encyclopedia of Genes and Genomes (KEGG) pathway terms in the indigenous cattle in Tigray. Where: the size of the circles represents how large the number of genes represented in a specific GO or KEGG pathway term and the level of significance, while each colored circle represents a population.

4.3.5. Heterozygosity and Nucleotide diversity

The average non-reference heterozygous variants (SNPs and indels) were around 0.6 to 0.7 times higher than the corresponding homozygous variants (Table S22). At the individual level, the ratio of heterozygous to the homozygous SNPs ranged from 1.39 to 1.89, and of the indels from 1.39 to 1.84 (Figure 28). The mean observed heterozygosity (H_O) was the highest in Arado cattle (0.302 ± 0.010) but the lowest in Raya cattle (0.278 ± 0.016) (Table S22). Besides, the average genome-wide nucleotide diversity (π) ranged from 3.5 ± 1.77 x 10^{-3} (Raya) to 3.57 ± 1.76 x 10^{-3} (Arado) (Figure 29 and Table S22).

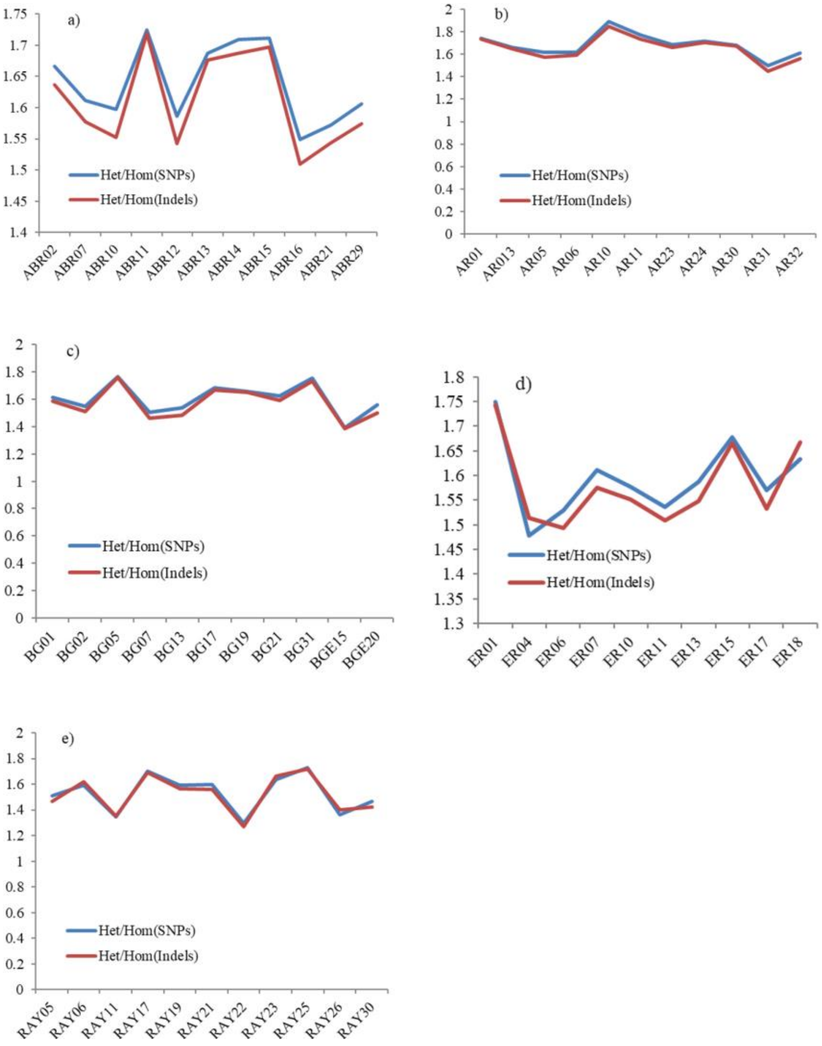


Figure 28. Distribution of heterozygous-to-homozygous variants among individual samples. (a) Abergelle (b) Arado, (c) Begait, (d) Erob (d) and (e) Raya.

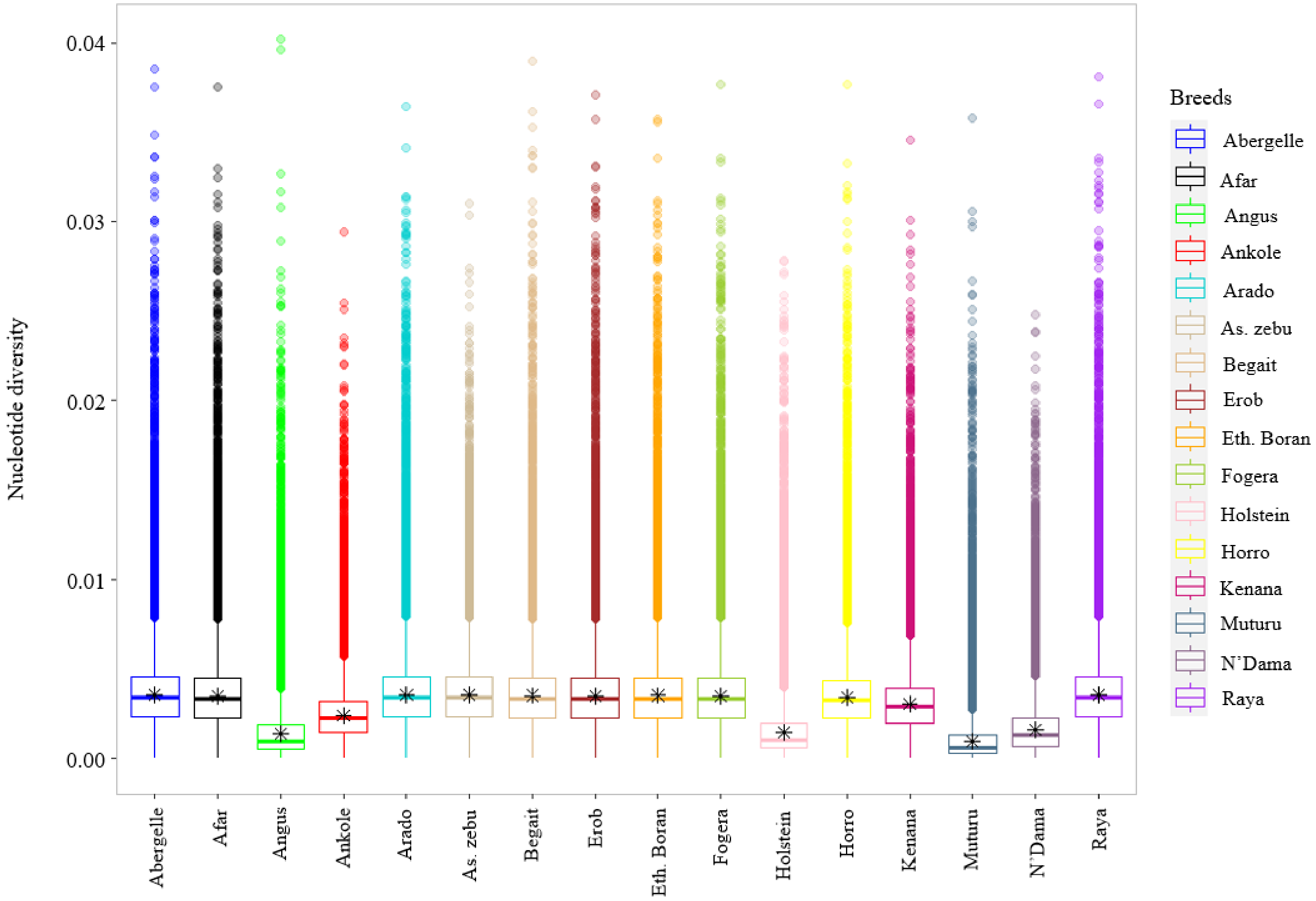


Figure 29. Box plot for nucleotide diversity, where each colored box plot represents a cattle population.

4.3.6. Runs of homozygosity and genomic inbreeding

4.3.6.1. Abundance and length of ROH in the indigenous cattle in Tigray compared to major cattle groups

The average number and length of ROH segments varied considerably within and among populations (Figure 30, Table 31 and Table S23). The within population average number of ROHs for the indigenous cattle in Tigray ranged from 777.82 (Arado cattle) to 1000.45 (Raya cattle), and the within population average sum of the length of ROHs ranges from 122.01 megabase (Mb) (Arado cattle) to 163.88Mb (Raya cattle). The average number of ROHs and the average sum of the length of ROHs in the indigenous cattle in Tigray were higher than the ones recorded in Asian zebu, African zebu from Sudan (Kenana), African taurine (Muturu and N'Dama) and African sanga from Uganda (Ankole). But they were much lower compared to European taurine cattle (Holstein and Angus). However, in general, all the indigenous cattle in Tigray had close ROH profiles with the other cattle populations originating from Ethiopia (Afar, Eth.Boran, Fogera and Horro) (Table 31).

Table 31. ROH statistics in the genome of the indigenous cattle in Tigray compared to reference cattle populations.

Population	No w/o ROH[1]	No w/ ROH[2]	Total No. of ROH[3]	Avg. No. of ROH segments (min-max)[4]	Avg ROH segment lengths in Mb (min-max)[5]
Abergelle	0	11	9131	830.09 (748-907)	130.13 (112.92-148.83)
Arado	0	11	8556	777.82 (706-861)	122.01 (108.02-135.65)
Begait	0	11	10003	909.36 (767-1504)	148.9 (121.14-266.71)
Erob	0	10	8371	837.1 (727-1099)	131.92 (110.40-177.46)
Raya	0	11	11005	1000.45 (703-1662)	163.88 (105.87-297.29)
Eth.Boran	0	10	8937	893.7 (734-1259)	143.94 (113.6-210.41)
Kenana	0	10	4624	462.4 (150-1657)	73.79 (20.24-298.06)
Fogera	0	9	7817	868.56 (571-1353)	124.5 (84.47-234.48)
Horro	0	11	8508	773.45 (618-1334)	121.74 (91.91-228.27)
Ankole	0	10	2299	209 (6-423)	31.16 (0.78-58.99)
Afar	0	10	7441	744.1 (649-918)	115.21 (95.06-146.82)
Holstein	0	10	22124	2212.4 (1827-2710)	432.61 (325.89-547.33)

Population	No w/o ROH[1]	No w/ ROH[2]	Total No. of ROH[3]	Avg. No. of ROH segments (min-max)[4]	Avg ROH segment lengths in Mb (min-max)[5]
Angus	0	10	22999	2299.9 (1374-2670)	439.31 (264.38-553.70)
Muturu	0	10	6755	675.5 (40-1590)	94.88 (4.79-232.72)
N'Dama	0	10	6870	687 (194-969)	94.49 (23.67-133.10)
Asian zebu	1	9	1292	143.56 (0-704)	20.39 (113.57-103.09)

[1] Number of animals without ROH

[2] Number of animals with ROH

[3] Total number of ROH across each population

[4] Average number of ROH segments (Minimum to maximum)

[5] Average ROH segment length in megabyte (Minimum to maximum)

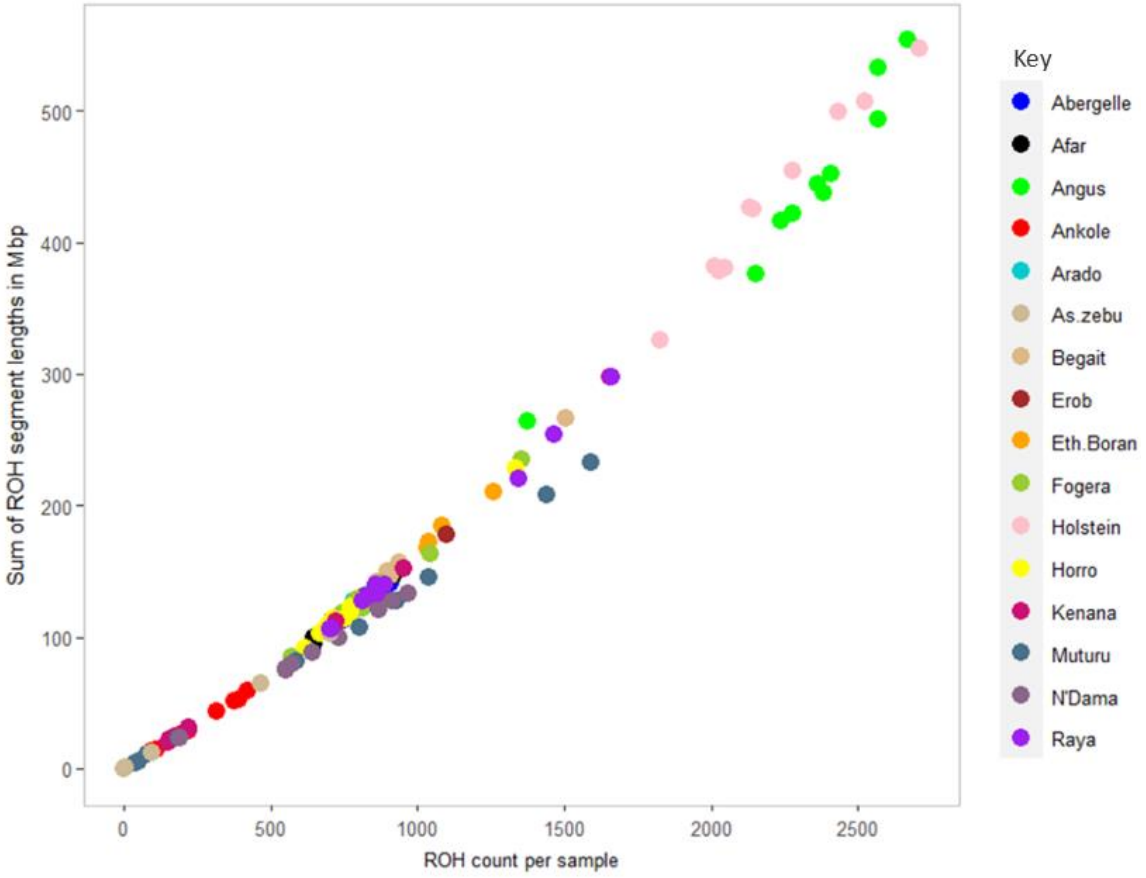


Figure 30. ROH profile of each animal across all cattle, including comparative populations.

Where: individual color and circle represent a cattle population and individuals, respectively.

4.3.6.2. Distribution of ROH based on segment length categories

The number of ROH across length categories (0.1-0.25Mb, > 0.25-0.5Mb, > 0.5-1Mb and > 1Mb) varied among populations. ROH in the length category of 0.1-0.25Mb accounted for 90% to 92% of the total ROH. For the length categories > 0.25-0.5Mb and > 0.5-1Mb, ROH frequencies were about 7% to 10% and 0.2% to 0.4%, respectively (Tables 32 and 33). ROH >1Mb were only found in Begait and Raya cattle (BG15, RAY11, RAY22 and RAY26) (Table S23). In the length categories 0.1-0.25Mb, the indigenous cattle in Tigray had more ROH when compared to Holstein and Angus, but they were less than the African sanga from Uganda (Ankole), African taurine (Muturu and N'Dama) and the Asian zebu. Above the 0.25Mb length category, the indigenous cattle in Tigray had more ROH when compared to Ankole, Muturu, N'Dama and Asian zebu, but they were less than Angus and Holstein (Tables 32 and 33).

Table 32. Abundance of ROH across different ROH segment length categories (0.1-0.25Mb, > 0.25-0.5Mb, > 0.5-1Mb and >1Mb).

Populations[1]	0.1-0.25Mb		> 0.25-0.5Mb		> 0.5-1Mb		> 1Mb	
	Count	%	Count	%	Count	%	Count	%
ABR	8440	92.4	670	7.3	21	0.2	0	0
AR	7875	92	665	7.8	16	0.2	0	0
BG	8964	89.6	994	9.9	44	0.4	1	0.01
ER	7680	91.7	669	8	22	0.3	0	0
RAY	9947	90.3	1010	9.2	45	0.4	3	0.04
Eth.Boran	8094	90.6	815	9.1	28	0.3	0	0
KEN	4204	90.9	394	8.5	25	0.5	1	0
FOG	7118	91.1	678	8.7	21	0.3	0	0
HOR	7850	92.3	632	7.4	24	0.3	2	0
ANK	2249	97.8	50	2.2	0	0	0	0
AFR	6865	92.3	565	7.6	11	0.1	0	0
HOL	17821	80.6	3828	17.3	436	2	39	0.2
AAN	18819	81.8	3762	16.4	392	1.7	26	0.1
MUT	6528	96.6	223	3.3	4	0.1	0	0
NDA	6678	97.2	192	2.8	0	0	0	0
As. zebu	1236	95.7	56	4.3	0	0	0	0

[1]*ABR* Abergelle, *AR* Arado, *BG* Begait, *ER* Erob, *RAY* Raya, *Eth.Boran* Ethiopian Boran, *KEN* Kenana, *FOG* Fogera, *HOR* Horro, *ANK* Ankole, *AFA* Afar, *HOL* Holstein, *ANG* Angus, *MUT* Mururu, *NDA* Ndama, *As. zebu* Asian zebu.

Table 33. Average genomic size covered with ROH across different length categories (0.1-0.25Mb, > 0.25-0.5Mb, > 0.5-1Mb and > 1Mb).

Populations	0.1-0.25Mb	> 0.25-0.5Mb	> 0.5-1Mb	> 1Mb
	Mb (%)	Mb (%)	Mb (%)	Mb (%)
Abergelle	109.1 (83.84)	19.76 (15.19)	1.26 (1)	0 (0)
Arado	101.7 (83.35)	19.4 (15.9)	0.92 (1)	0 (0)
Begait	115.9 (77.84)	29.21 (19.62)	2.59 (1.74)	1.2 (0.81)
Erob	109.06 (82.68)	21.41 (16.23)	1.44 (1)	0 (0)
Raya	126.09 (76.94)	29.78 (18.26)	4.81 (2)	3.2 (1.95)
Eth.Boran	115.89 (80.51)	26.17 (18.18)	1.89 (1)	0 (0)
Kenana	59.21 (80.25)	12.88 (17.46)	1.59 (2)	0.1 (0.14)
Fogera	112.54 (81.36)	24.31 (17.57)	1.48 (1)	0 (0)
Horro	101.92 (83.72)	18.24 (14.98)	1.38 (1)	0.2 (0.16)
Ankole	29.63 (95.11)	1.52 (4.89)	0 (0)	0 (0)
Afar	96.48 (83.74)	18.02 (15.64)	0.71 (1)	0 (0)
Holstein	267.28 (61.78)	130.96 (30.27)	29.7 (7)	4.68 (1.08)
Angus	282.03 (64.2)	127.85 (29.1)	26.38 (6)	3.05 (0.69)
Muturu	87.74 (92.48)	6.9 (7.27)	0.24 (0)	0 (0)
N'Dama	88.77 (93.94)	5.72 (6.06)	0 (0)	0 (0)
Asian zebu	18.42 (90.33)	1.97 (9.67)	0 (0)	0 (0)

4.3.6.3. Genomic positions under runs of homozygosity and inbreeding across the indigenous cattle in Tigray

The chromosome-wise distributions of the number and length of ROH and the incidence of SNPs on ROH were different across the five indigenous cattle in Tigray, except for the Abergelle and Erob cattle (Figure 31a-c and Tables S24-26). At the population level, the mean genomic inbreeding coefficient was the smallest in Arado ($F_{ROH} = 0.047 \pm 0.004$ and $F_{HOM} = 0.043 \pm 0.035$) but the highest in Raya cattle ($F_{ROH} = 0.064 \pm 0.025$ and $F_{HOM} = 0.07 \pm 0.054$) (Table S27). One Begait cattle (BG15 with $F_{ROH} = 0.103$ and $F_{HOM} = 0.107$) and three Raya cattle (RAY11 with $F_{ROH} = 0.114$ and $F_{HOM} = 0.12$, RAY22 with $F_{ROH} = 0.099$ and $F_{HOM} = 0.168$, and RAY26 with $F_{ROH} = 0.088$ and $F_{HOM} = 0.111$) showed strong genomic inbreeding values based on both methods (Figure 31d and Table S28).

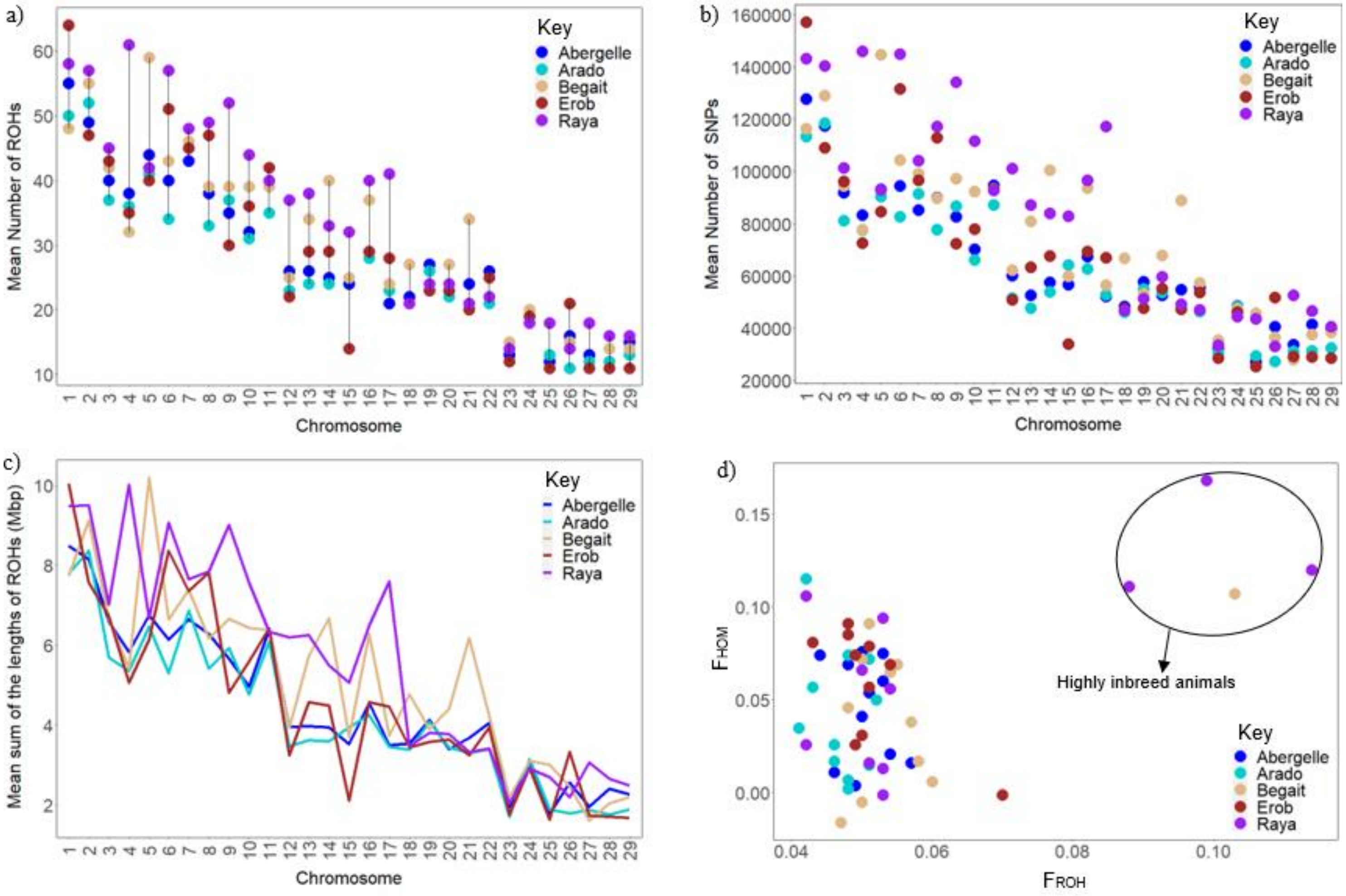


Figure 31. Genomic positions under runs of homozygosity (ROH) and inbreeding coefficients (F_{ROH} and F_{HOM}).

Where: (a) Chromosome-wise mean number of ROH across cattle populations. (b) Chromosome-wise mean sum of ROH lengths across cattle populations. (c) Incidence of SNPs on ROH across each autosome among individual animals of each cattle population (where each circle represents an individual within a population and each color represents a population). (d) Inbreeding coefficients (F_{ROH} and F_{HOM}) among individual animals of each cattle population (where each circle represents an individual within a population and each color represents a population).

4.3.7. Population structure and genetic admixture

The PCA showed the presence of six potential clusters of populations (Figure 32). PC1 and PC2 explained 32.27% and 12.33% of the total variation, respectively (Figure 32 and Figure S10). PC1 separated Ankole and taurine cattle (African and European) from Asian zebu, Kenana and all the cattle from Ethiopia, including the indigenous cattle in Tigray (Abergelle, Arado, Begait, Erob and Raya). PC2 divided the European taurine cattle and Asian zebu from the Ankole and African taurine cattle (Figure 32). Combining PC1 and PC2 illustrated that the indigenous cattle in Tigray (Abergelle, Arado, Begait, Erob and Raya), including all the cattle from Ethiopia (Afar, Fogera, Horro, and Ethiopian Boran) were close to the Asian zebu and the African sanga (Ankole).

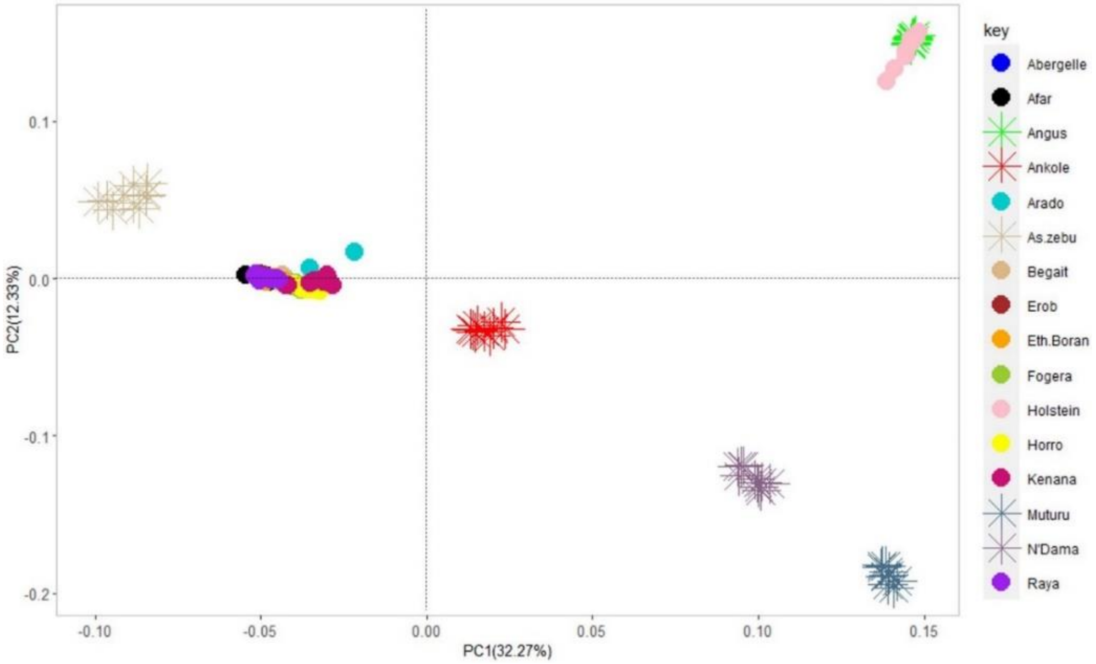


Figure 32. Principal component analysis plot (PC1 and PC2) of the indigenous cattle in Tigray and representatives of different cattle groups.

Where: African sanga (Afar and Ankole, crosses between African zebu and longhorn humpless taurine), African zenga (Fogera and Horro, crosses between African zebu and sanga), African zebu (Ethiopian Boran and Kenana), African taurine (Muturu and N’Dama), European taurine (Angus and Holstein) and Asian zebu (Bhagnari, Cholistani, Dhanni, Sahiwal and Tharparkar).

PC1 and PC2 for the indigenous cattle in Tigray and other Ethiopian cattle representing three cattle groups; African zebu (Ethiopian Boran), African sanga (Afar) and African zenga (Fogera and Horro) jointly accounted for 15.34% of the total variation, of which the Begait and Erob cattle were separated from the other populations (Figure 33a). The PC1 (6.09%) of the five indigenous cattle in Tigray alone separated Begait cattle from the other four indigenous cattle in Tigray, while PC2 (5.23%) divided Raya and Begait from the other four indigenous cattle in Tigray (Figure 33b).

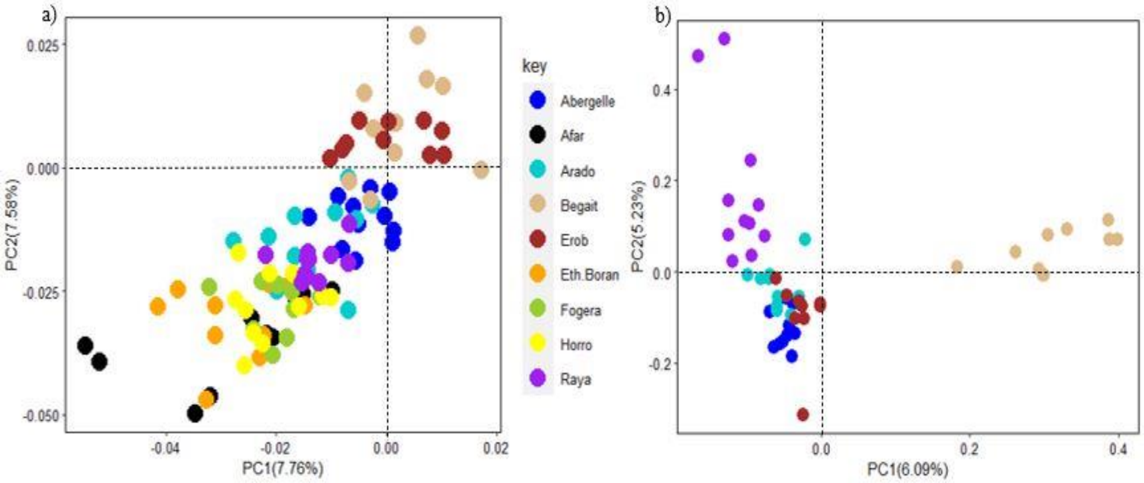


Figure 33. Principal component analysis plot (PC1 and PC2) of the indigenous cattle in Tigray with other Ethiopian cattle.

Where: the three cattle groups represented African zebus (Ethiopian Boran), African sanga (Afar) and African zenga (Fogera and Horro). (b) Principal component analysis plot (PC1 and PC2) for the indigenous cattle in Tigray alone (Abergelle, Arado, Begait, Erob and Raya).

As indicated by the lowest cross-validation error (0.51) (Figure 34), the admixture analysis suggested three ancestral sources. At K = 3, the taurine ancestry for the indigenous cattle in Tigray was shown to be mainly shared with the African taurine, except for some individuals in Arado (n = 3) and Begait (n = 2) cattle having 0.1 to 1.8% of European taurine ancestry (Figure 35). In each population, the African taurine ancestry ranged from 11.3% (Erob cattle) to 14.1% (Begait cattle) and, accordingly, the indicine ancestry from 85.6% (Arado cattle) to 88.7% (Erob cattle) (Figure S11). More interestingly, as the number of potential ancestries increased, the indigenous cattle in Tigray local ancestry appeared. At K = 7 and K = 10, both Erob and Begait cattle showed some unique local ancestries (Figure 36).

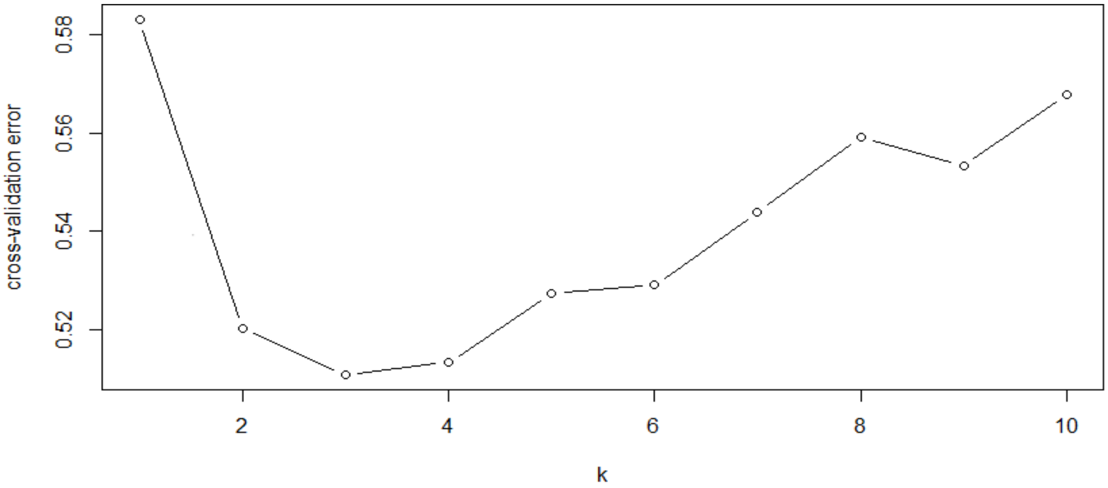


Figure 34. Cross-validation errors of different k values used for admixture analysis.

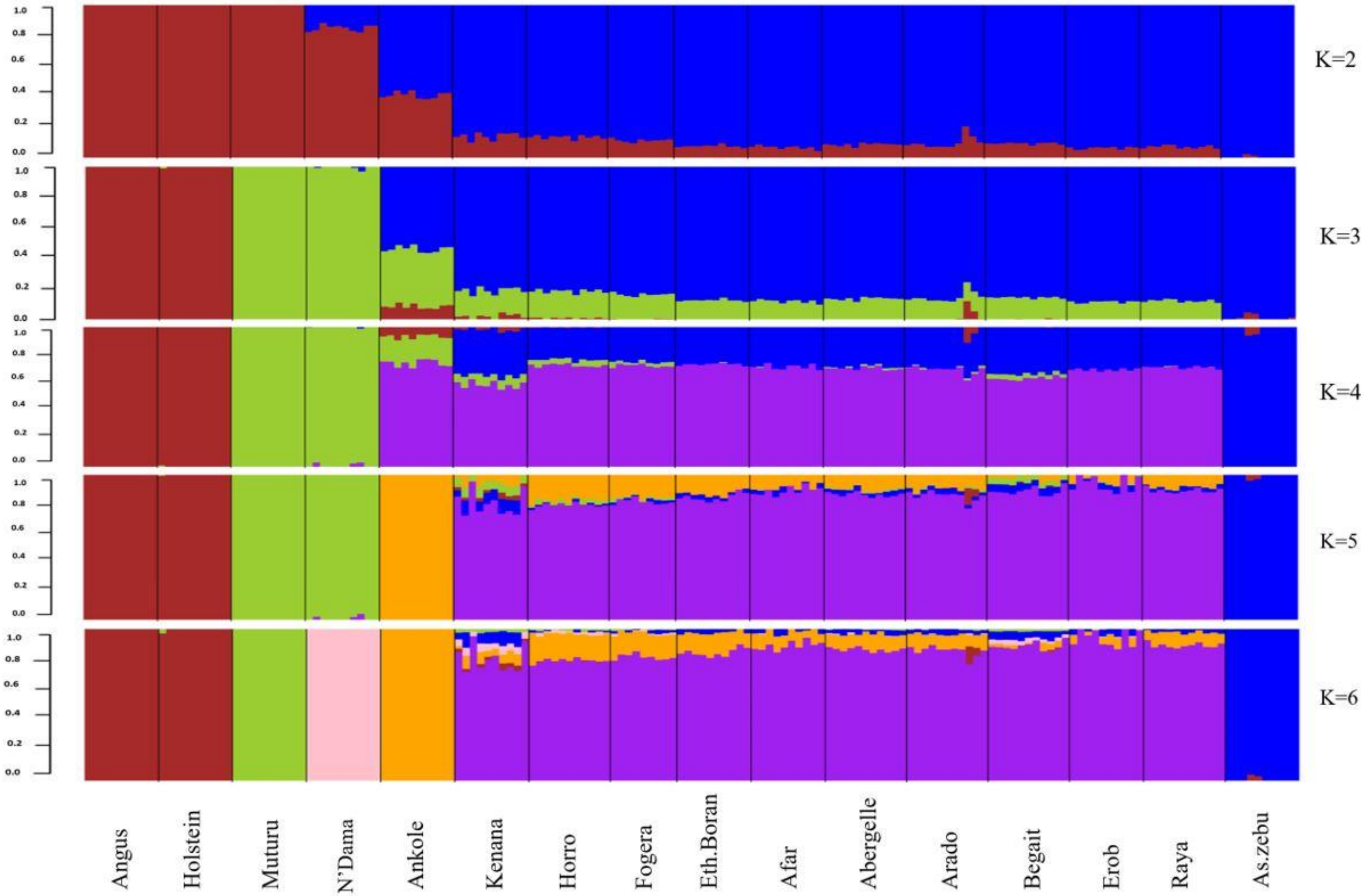


Figure 35. Admixture K = 2 to K = 6, where the black lines separate the populations.

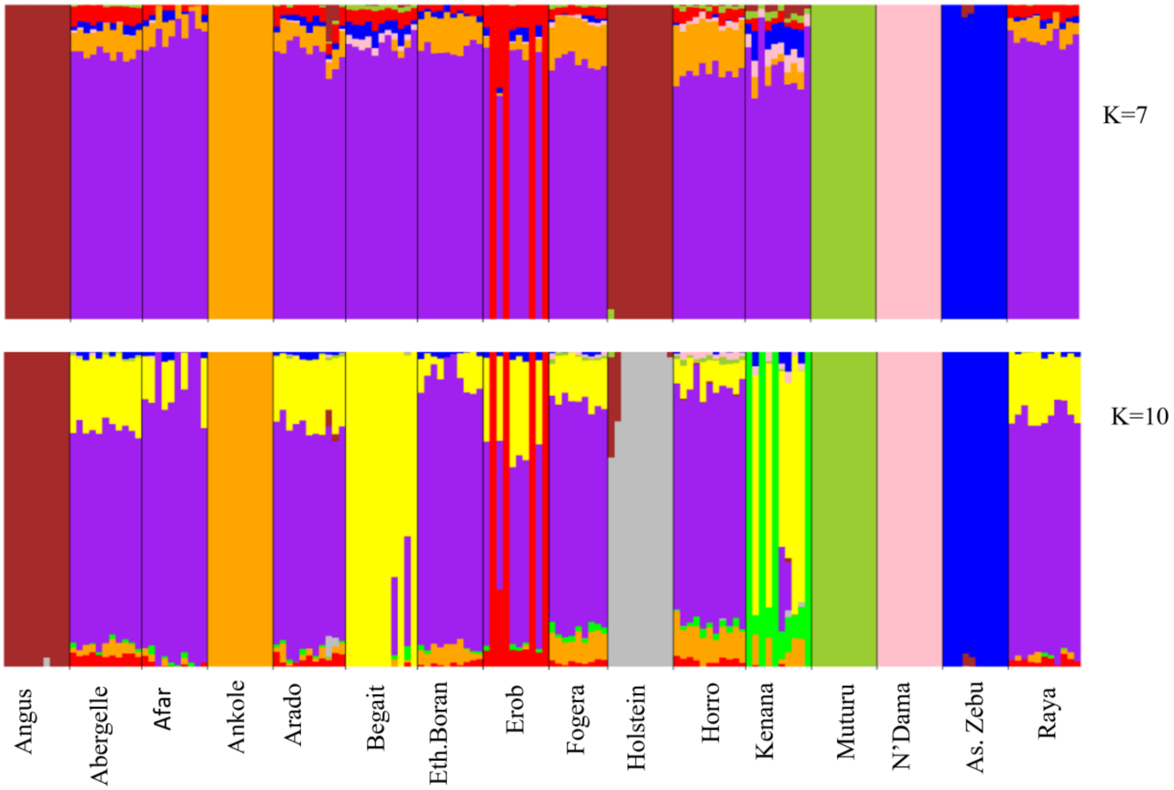


Figure 36. Admixture k = 7 and k = 10 showing unique local ancestry for Erob and Begait cattle, respectively

Where: the colors represent each K population cluster and black lines separate the populations labeled below the figure.

4.3.8. Population Genetic differentiation

Genetic differentiation (F_{ST}) across the indigenous cattle in Tigray ranged from 0.07 to 0.08 with Asian zebu, 0.084 to 0.108 with Ankole (African sanga originating from Uganda), 0.236 to 0.264 with N'Dama (African taurine), 0.328 to 0.36 with Muturu (African taurine) and 0.300 to 0.335 with the European taurine cattle (Angus and Holstein) (Table 34). Two groups observed among the indigenous cattle in Tigray for the F_{ST} estimates with other Ethiopian cattle populations, with higher genetic differentiation ($F_{ST} \approx 0.02$ and $F_{ST} \approx 0.02$) for Begait and Erob cattle from Ethiopian Boran, Fogera and Horro cattle than for Abergelle, Arado and Raya cattle ($F_{ST} \approx 0.01$) (Table 34).

Overall, the heat map and dendrogram (Figure 37 and Table 34) generated from pairwise weighted F_{ST} values among the indigenous cattle in Tigray and the indigenous cattle in Tigray against other cattle populations (African sanga, African zenga, African zebu, Asian zebu, African and European taurine cattle) showed two main genetic clades: One comprising the taurine group with two sub-clusters African and European) and another including the Asian zebu and other non-taurine African origin populations (including the indigenous cattle in Tigray). This was consistent with the PCA and admixture analysis results.

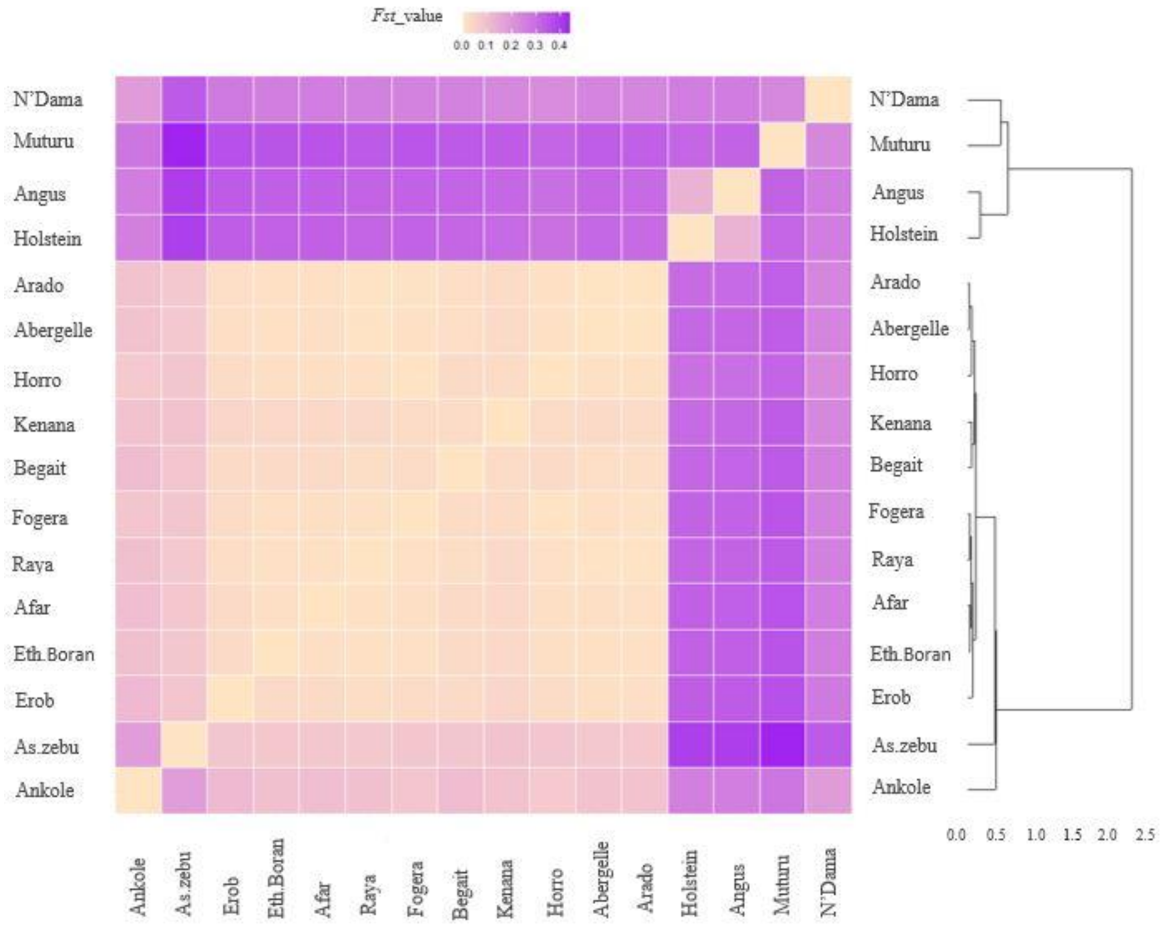


Figure 37. Heat map and dendrogram based on pairwise weighted F_{ST} values.

Where: the deep color indicates higher pairwise population differentiation while lighter color lower population differentiation.

Table 34. Population differentiation (F_{ST}) among the indigenous cattle in Tigray and with representative groups of cattle populations.

	ABR	AR	BG	ER	RAY	Eth.Boran	KEN	FOG	HOR	ANK	AFA	HOIL	ANG	MUT	NDA	As. zebu
ABR	0.000	0.001	0.016	0.014	0.003	0.010	0.025	0.006	0.007	0.086	0.012	0.307	0.309	0.333	0.241	0.070
AR		0.000	0.015	0.015	0.002	0.009	0.024	0.006	0.007	0.084	0.010	0.300	0.303	0.328	0.236	0.070
BG			0.000	0.026	0.018	0.025	0.023	0.022	0.025	0.101	0.026	0.312	0.315	0.338	0.246	0.077
ER				0.000	0.017	0.024	0.037	0.022	0.023	0.108	0.026	0.332	0.335	0.360	0.264	0.080
RAY					0.000	0.010	0.029	0.009	0.011	0.092	0.010	0.314	0.317	0.340	0.248	0.070
Eth.Boran						0.000	0.030	0.011	0.011	0.091	0.013	0.322	0.325	0.352	0.255	0.074
KEN							0.000	0.023	0.023	0.087	0.031	0.304	0.307	0.335	0.233	0.084
FOG								0.000	0.003	0.079	0.013	0.319	0.322	0.349	0.246	0.076
HOR									0.000	0.069	0.014	0.290	0.292	0.315	0.221	0.078
ANK										0.000	0.096	0.253	0.255	0.276	0.183	0.178
AFA											0.000	0.326	0.328	0.355	0.257	0.074
HOL												0.000	0.125	0.312	0.259	0.393
ANG													0.000	0.320	0.261	0.396
MUT														0.000	0.235	0.435
NDA															0.000	0.338
As. zebu																0.000

[1] *ABR* Abergelle, *AR* Arado, *BG* Begait, *ER* Erob, *RAY* Raya, *Eth.Boran* Ethiopian Boran, *KEN* Kenana, *FOG* Fogera, *HO*R Horro, *ANK* Ankole, *AFA* Afar, *HOL* Holstein, *ANG* Angus, *MUT* Mururu, *NDA* N'dama, *As. zebu* Asian zebu.

4.4. Detecting Signature of Selection in the Indigenous cattle in Tigray

Principal component analysis plot (PC1 and PC2) of around 2.49M SNPs from the cattle (Abergelle, Arado, Begait and Erob) used for selection signature analysis distinguished the Begait cattle from the other three through the first principal component (PC1 = 5.45%). In comparison, PC2 (5.3%) separated the Raya and Begait from the rest (Figure 38).

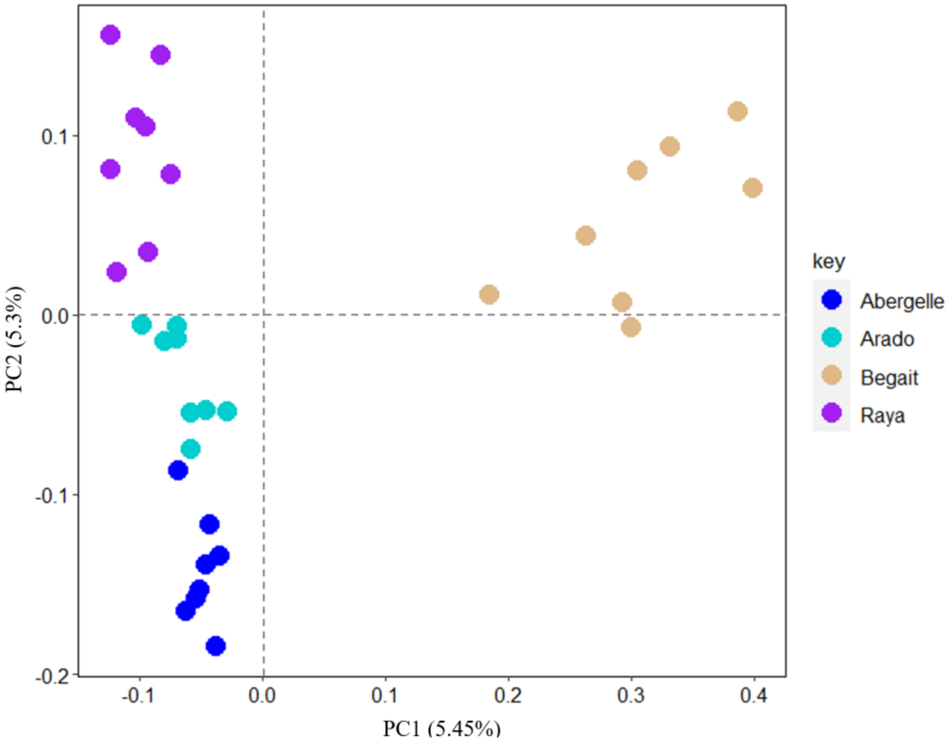


Figure 38. Clustering of the indigenous cattle in Tigray populations used for signature analysis.

4.4.2. Detection of signature of selection based on Hp analysis

The genome-wide autosomal *Hp* analysis for each cattle screened around 49733 selective windows with approximately a mean value of *Hp* = 0.34. The standardized *Hp* values (*ZHp*) for the Abergelle cattle ranged from -7.39 to 3.46. For Arado, Begait and Raya cattle, the record of the standardized *Hp* values varied from -7.35 to 3.70, -7.31 to 3.56 and -7.86 to 3.68, respectively. The regions of lowest diversity for Abergelle, Arado, Begait and Raya cattle were recorded at chromosomes 2, 5, 2 and 12 with *Hp* = 0.048 and *ZHp* = -7.385, *Hp* = 0.051 and *ZHp* = -7.349, *Hp* = 0.046 and *ZHp* = -7.31 and *Hp* = 0.024 and *ZHp* = -7.856, respectively (Table 35, Figure 39a - d and Tables S29-S32).

Out of the total windows under the regions of positive selection, 497 of them were found under the low 1% standardized *Hp* values expected to be under strong positive selection (Tables S29-S32). The windows in the extreme low 1% for Abergelle, Arado, Begait and Erob had *ZHp* threshold values of -2.96, -2.905, -2.951 and -2.982 respectively (Table 35 and Figure 39a - d). After merging adjacent windows, 256, 258, 257 and 230 selective sweep regions were obtained for Abergelle, Arado, Begait and Raya cattle populations, respectively. The size of the selective sweep regions varied from the shortest size 0.1Mb to the largest 1.3Mb, 1.3Mb, 0.6Mb and 0.7Mb size in Abergelle, Arado, Begait and Raya cattle, respectively (Tables S29-S32).

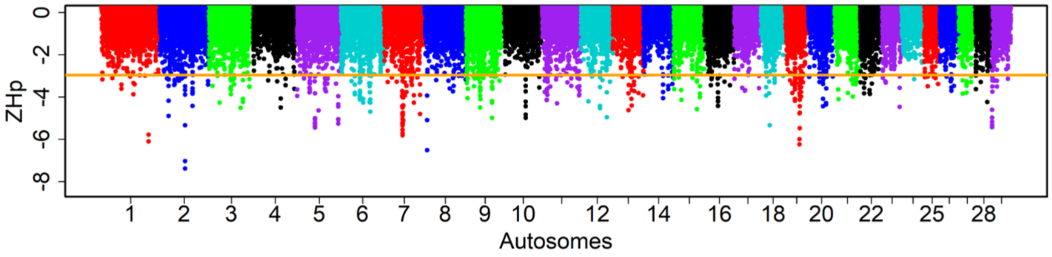
Of the total 256, 258, 257 and 230 selective sweep regions obtained for Abergelle, Arado, Begait and Raya cattle populations (Table 35), respectively, the list of overlapping selective sweep regions screened through the BEDTools intersect between a pair of cattle populations categorized as high or low groups under each environmental variable were presented in Tables S33-S35. Accordingly, most of the selective sweep regions detected as regions of low diversity in each cattle population were unique to a respective population. Only around 22.9% to 28.7% were screened to be shared candidate regions of reduced diversity between each pair of cattle populations.

Table 35. *Hp* analysis basic statistics in each cattle population.

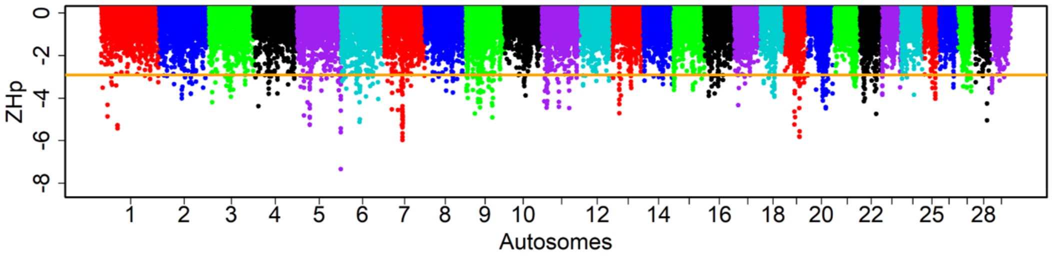
Description	Populations			
	Abergelle	Arado	Begait	Raya
Total number of windows	49733	49732	49732	49734
Number of windows with 20 and above SNPs	49715	49713	49713	49715
Min *Hp*	0.048	0.051	0.046	0.024
Max *Hp*	0.475	0.485	0.483	0.488
Mean *Hp*	0.339	0.339	0.340	0.340
Min *ZHp*	-7.385	-7.349	-7.314	-7.856

Max *ZHp*	3.459	3.701	3.55	3.683
Low 1% windows	497	497	497	497
Low 1% Min *ZHp*	-7.385	-7.349	-7.314	-7.856
Low 1% Max *ZHp*	-2.960	-2.905	-2.951	-2.982
Number of selective sweep regions after merging adjacent windows	256	258	257	230

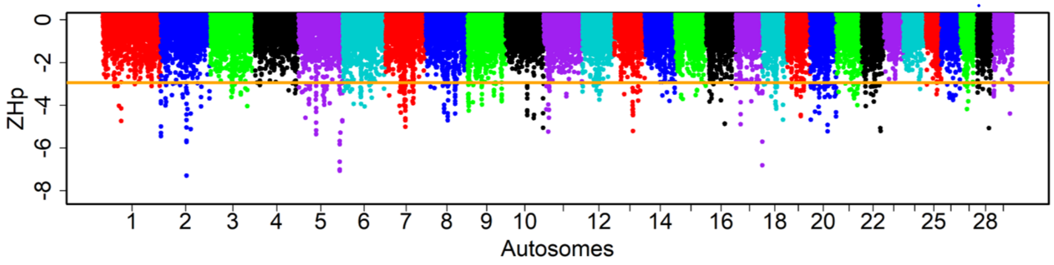
a) Abergelle



b) Arado



c) Begait



d) Raya

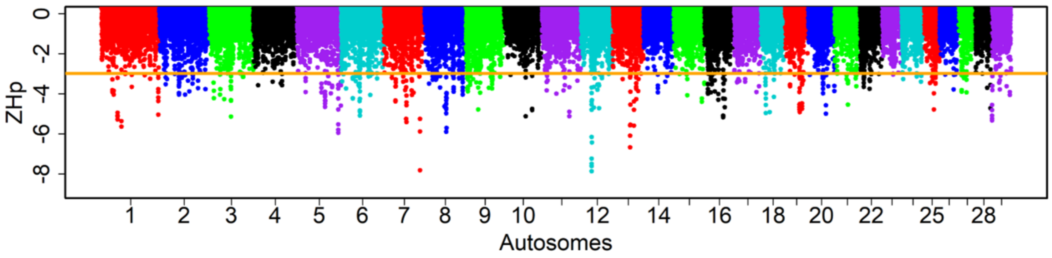


Figure 39. The Distribution of *ZHp* scores across the genome of each indigenous cattle in Tigray (a = Abergelle, b = Arado, c = Begait and d = Raya).

4.4.3. Detection of signature of selection based on F_{ST} analysis

The F_{ST} statistics detected from the fixation index (F_{ST}) between each pair of the indigenous cattle in Tigray (including Abergelle vs. Begait, Abergelle vs. Raya, Arado vs. Begait, Arado vs. Raya and Begait vs. Raya cattle populations) as categorized high or low group in each environmental variable (Table 10) were represented in Table 36 and Tables S36-S40. A total of 49761 windows were obtained from each F_{ST} analysis. Among the groups of F_{ST} analysis, both the minimum (-0.449) and the maximum (0.516) values were recorded between Begait and Raya (Table 36).

Around 497 windows were recorded in the top 1% F_{ST} analysis detected in each group. The F_{ST} values in the top 1% windows ranged from 0.147 in the annual precipitation group (Arado and Raya) to 0.516 in the precipitation of the wettest quarter group (Begait and Raya). On the other hand, the transformed value of the F_{ST} (ZF_{ST}) in the top 1% outlier windows ranged from 3.482 between the Arado and Raya cattle (in the annual precipitation) to 9.965 between Begait and Abergelle (in the temperature seasonality group). The region of high genetic differentiation between Abergelle and Begait cattle (temperature seasonality group) was located at chromosome 5 (Max F_{ST} = 0.510 and Max ZF_{ST} = 9.965) (Table 36 and Figure 40). For annual rainfall (Arado and Raya), precipitation of the wettest quarter (Begait and Raya), precipitation of the warmest quarter (Abergelle and Raya), cultivated land or soil bulk density (Arado and Begait), the regions of high differentiation were located on chromosomes 11 (Max F_{ST} = 0.382 and Max ZF_{ST} = 8.954) (Table 36 and Figure 41a), chromosome 19 (Max F_{ST} = 0.516 and Max ZF_{ST} = 9.574) (Table 36 and Figure 41b), chromosome 3 (Max F_{ST} = 0.384 and Max ZF_{ST} = 8.654) (Table 36 and Figure 41c) and chromosome 2 (Max F_{ST} = 0.491 and Max ZF_{ST} = 9.559) (Table 36 and Figure 42).

Table 36. F_{ST} analysis basic statistics among the indigenous cattle in Tigray grouped based on environmental variables.

Description[1]	bio4	bio12	bio16	bio18	CL and SBD
Populations[2]	ABR and BG	AR and RAY	BG and RAY	ABR and RAY	AR and BG
Total number of windows	49761	49761	49761	49761	49761
Min F_{ST}	-0.219	-0.323	-0.449	-0.387	-0.370
Max F_{ST}	0.510	0.382	0.516	0.384	0.491
Mean F_{ST}	0.008	-0.003	0.010	-0.001	0.008
SD F_{ST}	0.050	0.043	0.053	0.044	0.050
Min ZF_{ST}	-4.509	-7.437	-8.695	-9.474	-7.480
Max ZF_{ST}	9.965	8.954	9.574	8.654	9.559
Top1% windows	497	497	497	497	497
Top1% Min F_{ST}	0.188	0.147	0.198	0.155	0.188
Top1% Max F_{ST}	0.510	0.382	0.516	0.384	0.491
Top1% Min ZF_{ST}	3.568	3.481	3.557	3.510	3.565
Top1% Max ZF_{ST}	9.965	8.954	9.574	8.654	9.559
Regions after merging adjacent windows	217	139	156	153	152

[1] *bio4* Temperature Seasonality in degrees Celsius, *bio12* Annual precipitation, *bio16* Precipitation of wettest quarter, *bio18* Precipitation of warmest quarter, *CL* Cultivated land, *SBD* Soil bulk density

[2] *ABR* and *BG* Abergelle and Begait, *AR* and *RAY* Arado and Raya, *BG and RAY* Begait and Raya, *ABR* and *RAY* Abergelle and Raya, *AR* and *BG* Arado and Begait.

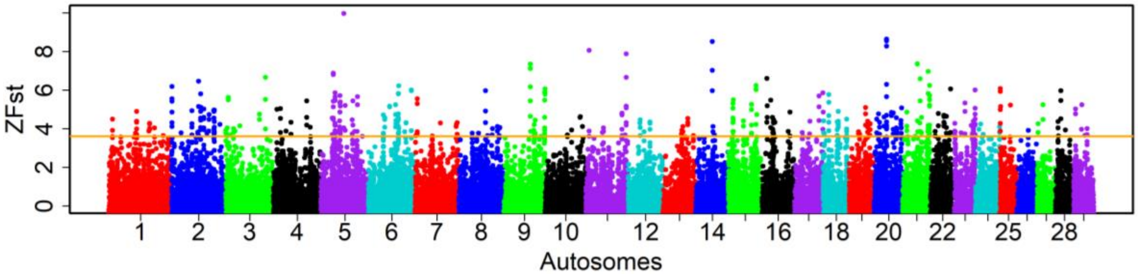
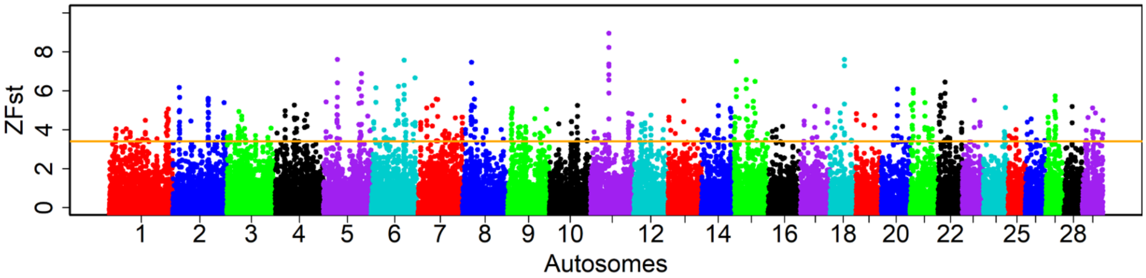
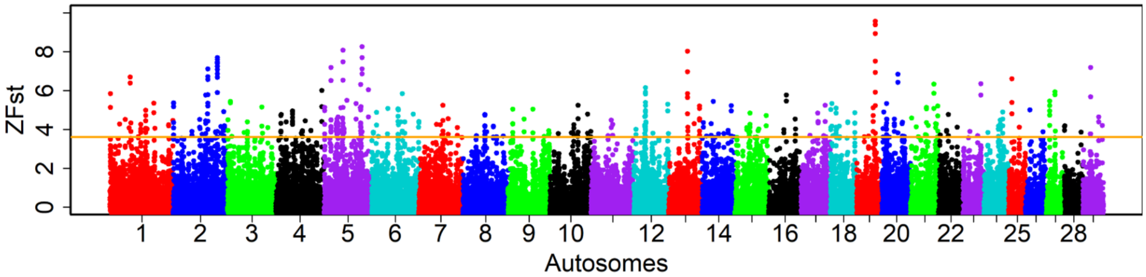


Figure 40. The Distribution of ZF_{ST} score following the analysis of F_{ST} between the high (Begait) and low (Abergelle) group populations for temperature seasonality (bio4).

a) Annual precipitation



b) Precipitation of wettest quarter



c) Precipitation of warmest quarter

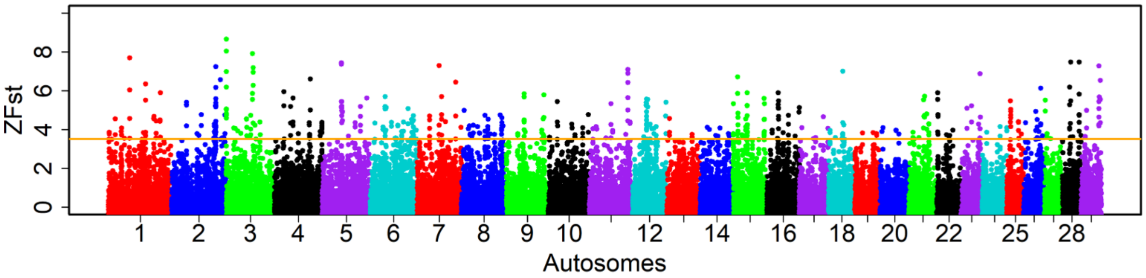


Figure 41. The Distribution of ZF_{ST} scores following the analysis of F_{ST} between the high and low group populations for Rainfall related environmental variables.

Where: (a) The Distribution of ZF_{ST} score following the analysis of F_{ST} between the high (Raya) and low (Arado) group populations for annual precipitation (bio12); (b) The Distribution of ZF_{ST} score following the analysis of F_{ST} between the high (Begait) and low (Raya) group populations for wettest quarter precipitation (bio16); (c) The Distribution of ZF_{ST} score following the analysis of F_{ST} between the high (Raya) and low (Abergelle) group populations for warmest quarter precipitation (bio18).

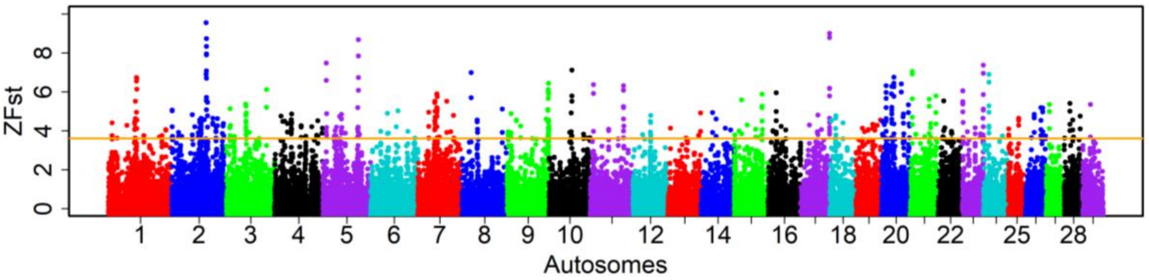


Figure 42. The Distribution of ZF_{ST} scores following the analysis of F_{ST} between the high and low group populations for CL or SBD related variables.

Where: Arado cattle were the high group for cultivated land (CL) and low group for soil bulk density (SBD) while the Begait cattle high group for soil bulk density (SBD) and low group for cultivated land (CL).

4.4.4. Annotation of selective sweep regions and functional enrichment analysis of retrieved genes

The collections of selective sweep regions common to F_{ST} analysis and to one or both of the high or low groups detected through the pooled heterozygosity (*Hp*) under each environmental factor were considered the strongest evidence for further detection of protein codding candidate genes (Figure 43). Accordingly, 30 selective sweep regions for the temperature seasonality (Abergelle and Begait), 53 for annual precipitation (Arado and Raya), 49 for precipitation of the wettest quarter (Begait and Raya) and 47 for precipitation of the warmest quarter (Abergelle and Raya) for rainfall related environmental factors and 51 for the cultivated land and soil-related environmental variables were annotated based on Ensemble cow genes 109 (ARSUCD1.2) (Figure 43). Out of the total regions annotated, 60% (18), 49.1% (26), 59.2%) (29), 53.2% (25) and 47.1% (24) selective sweep regions overlapped protein codding candidate genes in temperature seasonality, annual precipitation, precipitation of the wettest quarter, precipitation of the warmest quarter and in cultivated land or soil bulk density, respectively. Around 71, 61, 65, 73 and 66 protein-coding genes were detected for the cattle grouped under temperature seasonality, annual precipitation, precipitation of the wettest quarter, precipitation of the warmest quarter and cultivated land or soil bulk density, respectively (Tables 37-41 and Table S41). Collectively, 17.45 Megabase pairs (1.95Mb (bio4), 4.95Mb (bio12), 2.9Mb (bio16), 3.1Mb (bio18), 4.55Mb (CL or SBD)) of the annotated selective sweep regions were missed from carrying protein-coding genes (Tables S42-47).

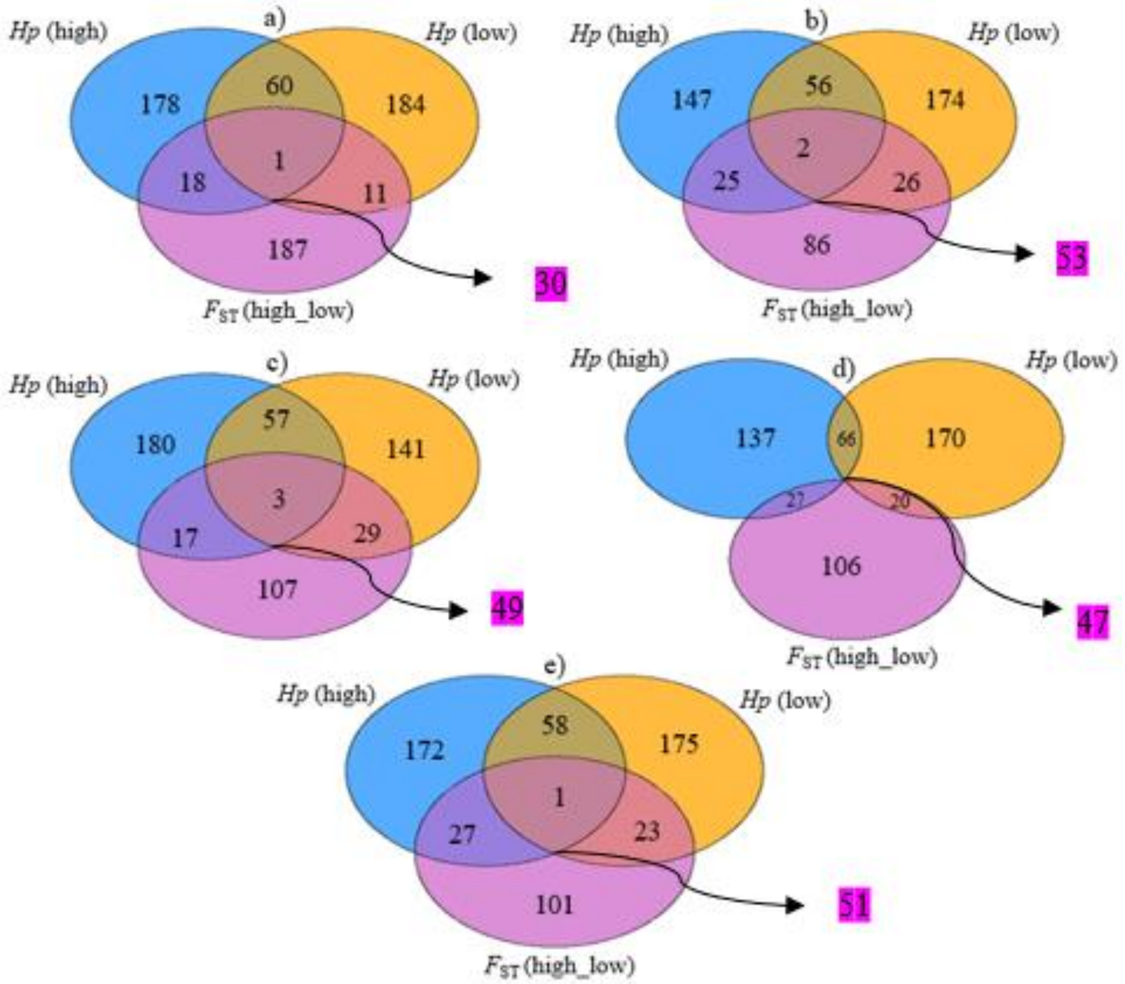


Figure 43. Venn diagram showing common regions among *Hp* (high) and *Hp* (low) groups and common regions of F_{ST} between (high and low groups) with *Hp* (high) or *Hp* (low) for each environmental variable.

Where: (a) temperature seasonality, (b) annual precipitation, (c) precipitation of the wettest quarter, (d) precipitation of the warmest quarter and (e) cultivated land or soil bulk density.

4.4.4.1. Bio4 selective sweep regions overlapped protein codding genes

Out of the 71 protein-coding genes under the temperature seasonality (bio4), about 35.2% (21) were concentrated in a 0.35Mb selective sweep region at chromosome 25 (Table 37). This region contains functionally enriched genes ($P < 0.05$) including *TMEM204* (F_{ST} = 0.203 - 0.267 and ZF_{ST} = 3.872 - 5.14), *EME2* (F_{ST} = 0.203-0.267 and ZF_{ST} = 3.872 - 5.14), *NME3* (F_{ST} = 0.203 - 0.267 and ZF_{ST} = 3.872 - 5.14), *HAGH* (F_{ST} = 0.203 - 0.267 and ZF_{ST} = 3.872 - 5.14) all were under strong positive selection towards the low group (Abergelle cattle). Further, five protein coding genes, including *NFATC3* (F_{ST} = 0.192 - 0.206 and ZF_{ST} = 3.65 - 3.935), *P2RX6* (F_{ST} = 0.207 - 0.303 and ZF_{ST} = 3.955 - 5.854), *SLC26A6* (F_{ST} = 0.199 - 0.313 and ZF_{ST} = 3.791 - 6.059), *UCN2* (F_{ST} = 0.199 - 0.313 and ZF_{ST} = 3.791 - 6.059), *ADAMTS16* (F_{ST} = 1.98 - 0.231 and ZF_{ST} = 3.766 - 4.426) (*UCK1* with F_{ST} = 0.219 - 0.225 and ZF_{ST} =4.189 - 4.314) in the high group (Begait) were significantly enriched (Table S48) in different GO and KEGG pathways.

Particularly, both the genes *UCK1* (in Begait) and *NME3,* under positive selection in the Abergelle, were solely involved in many gene ontologies (GO) biological processes (BP) such as CTP biosynthetic process (GO:0006241), pyrimidine ribonucleoside triphosphate biosynthetic process (GO:0009209), CTP metabolic process (GO:0046036) and pyrimidine ribonucleoside triphosphate metabolic process (GO:0009208). Other genes (*P2RX6* and *SLC26A6)* were involved in three gene ontology (GO) cellular components (CC), including the intrinsic component of the nuclear inner membrane (GO:00312290), integral component of nuclear inner membrane (GO:0005639) and nuclear membrane part (GO:0044453) (Table S48).

Table 37. Overlap of *Hp* and F_{ST} detected regions and corresponding protein codding genes in the groups (high group, Begait and Low group, Abergelle) for temperature seasonality.

Chr	Start	End	Direction	nSNPs	Min. F_{ST}	Min. ZF_{ST}	Max. F_{ST}	Max. ZF_{ST}	Overlapping protein codding genes
2	350001	700000	high	521-683	0.253	4.862	0.319	6.184	*ENSBTAG00000040536*
3	100550001	100750000	high	564-672	0.209	3.982	0.285	5.509	*PRDX1, MMACHC, ENSBTAG00000017029 (A0A3Q1MV06_BOVIN), TESK2*
5	28700001	28850000	high	948	0.194	3.688	0.194	3.688	*SLC11A2, ENSBTAG00000049198 (A0A3Q1M0M7_BOVIN)*
5	48250001	48800000	low	399-598	0.252	4.847	0.268	5.169	*MSRB3, LEMD3, WIF1*
5	57950001	58100000	low	702-1481	0.211	4.03	0.51	9.965	*OR6C202*
11	101450001	101800000	high	653-817	0.219	4.189	0.225	4.314	*FAM78A, PLPP7, PRRC2B, POMT1, UCK1, PRRT1B*
12	29500001	29750000	low	407-591	0.191	3.626	0.224	4.285	*ENSBTAG00000053332*
17	62950001	63150000	high	391-734	0.23	4.415	0.266	5.119	*UNC119B, ACADS, SPPL3*
17	72350001	72500000	high	591-602	0.207	3.955	0.303	5.854	*LRRC74B, P2RX6, SLC7A4, TUBA3C, MZT2B, SMPD4, ENSBTAG00000031018, MED15*
18	35500001	35650000	high	210-221	0.192	3.651	0.206	3.935	*NFATC3, PLA2G15, SLC7A6*
18	35650001	35750000	high	308	0.226	4.336	0.226	4.336	*SLC7A6OS, PRMT7, SLC7A6*
19	26600001	26700000	high	407	0.195	3.715	0.195	3.715	*ZMYND15, CXCL16, MED11, PELP1, ARRB2*
20	30650001	31200000	low	403-969	0.208	3.979	0.227	4.348	*ENSBTAG00000033187*
20	67600001	67850000	high	1221-1314	0.198	3.766	0.231	4.426	*ICE1, ADAMTS16*
21	10500001	10700000	low	342-612	0.204	3.882	0.216	4.128	*NR2F2*
22	51200001	51350000	high	443-455	0.199	3.791	0.313	6.059	*NCKIPSD, CELSR3, SLC26A6, TMEM89, UQCRC1, UCN2*
23	47600001	47750000	low	911-882	0.2	3.807	0.209	3.995	*ENSBTAG00000054759*
25	1100001	1450000	low	791-859	0.203	3.872	0.267	5.14	*UNKL, C25H16orf91, CCDC154, CLCN7, PTX4, TELO2, IFT140, TMEM204, CRAMP1, JPT2, MAPK8IP3, ENSBTAG00000052060, NME3, MRPS34, EME2, SPSB3, NUBP2, IGFALS, HAGH, FAHD1, MEIOB*

nSNPs number of Single Nucleotide Polymorphism, *Min.*F_{ST} minimum F_{ST} value, *Min.*ZF_{ST} standardized F_{ST} value, Max.F_{ST} maximum F_{ST} value, Max. $ZF_{ST,}$ standardized F_{ST} value.

4.4.4.2. Bio12, bio16 and bio18 selective sweep regions overlapped protein codding genes

Twenty-two functionally enriched genes ($P < 0.05$) were found to be under strong selection in the annual rainfall group (bio 12) (Table S49). The gene *CTNNB1* (F_{ST} = 0.95 - 0.95 and ZF_{ST} = 4.606 - 4.606), which was under strong positive selection in the low group (Arado cattle) was the most frequently enriched in 12 gene ontology (GO) biological processes, two cellular components including beta-catenin destruction complex (GO:0030877) and transcription factor complex (GO:0005667), and one Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway (bta05225, Hepatocellular carcinoma).

Three candidate genes in the low group for annual precipitation (Arado cattle), including *LHX2* (F_{ST} = 0.171 - 0.186 and ZF_{ST} = 4.032 - 4.386), *LCMT2* (F_{ST} = 0.155 - 0.171 and ZF_{ST} = 3.679 - 4.036) and *NEK6* (F_{ST} = 0.151 - 0.16 and 3.568 - 3.777) were involved in four and above GO terms biological processes. Other candidate genes including *NFAT5*, *NFE2L1*, *NQO1* and *RASL11B*, were significantly enriched in at least one GO or KEGG pathway in the low group (Arado cattle). Candidate genes under strong positive selection in the high group (Raya cattle) such as *CDKN2B* (F_{ST} = 0.192 - 0.197 and ZF_{ST} = 4.521 - 4.653), *DDB1* (F_{ST} = 0.164 - 0.164 and ZF_{ST} = 3.879 - 3.879) and *ATF7IP* (F_{ST} = 0.181 - 0.229 and ZF_{ST} = 4.263 - 5.382) were significantly involved each in four related GO terms (Table 38 and Table S49).

Apart from the annual rainfall, two other rainfall-related environmental factors were the main rainfall season (bio16) and the warmest season (bio18) of the Tigray Region. The genes *HELB* (F_{ST} = 0.207 - 0.211 and ZF_{ST} = 3.72 - 3.8), *HMGA2* (F_{ST} = 0.28 - 0.36 and ZF_{ST} = 5.14 - 6.54) under strong selection in the Begait cattle or high group for the wettest quarter (bio16) and low group (Raya cattle) including *SHLD1* and *PCNA* (F_{ST} = 0.26 - 0.31 and ZF_{ST} = 4.8 - 5.64) were involved in several gene ontology (GO) biological processes related with damage repair and regulation of DNA damage stimulus. In addition, these genes and two other genes (*IRAK3*, *TKFC*) under strong selection in the high group

(Begait cattle) and one (*IL17B*) in the low group (Raya cattle) were significantly (*P* = 0.038713) involved in the regulation of stress response (GO:0080134). Genes including *PAX3* in the high group and *ASIP*, *ATF7IP*, *CDKN1C*, *DDB1*, and *RXFP2* in the low group were particularly involved in two GO terms of the biological processes, including positive regulation of cellular biosynthetic process (GO:0031328) and positive regulation of biosynthetic process (GO:0009891) (Table 39 and Table S50).

Several of the genes (*FANCG, WAPL, VCP, STOML2, CTCF, ACD, ATP12A, UNC13B, DPEP2, NRN1L, DPEP3, PSMB10, NUTF2, PARD6A, CENPJ*) significantly enriched (*P* < 0.05) in different GO terms of biological process, cellular components or molecular functions were under strong positive selection in the high group for bio18 or warmest quarter precipitation (Raya cattle). Some important genes, under strong selection in the low group (Abergelle) (*CSF1R* and *PHLDA2*) and high group (*SLC22A18*) populations for bio18, were mainly involved in enzyme binding (GO:0019899). Moreover, four genes (*LOC782699*, *G3X800_BOVIN*, *G5E622_BOVIN* and *G5E6C5_BOVIN)* overlapped a 0.1Mb selective sweep at chromosome 8 were under strong selection specifically in the low group (Abergelle). These genes were involved in many GO terms of the biological process related with reproduction organ and reproduction activities development (Table 40 and Table S51).

Table 38. Overlap of *Hp* and F_{ST} detected regions and corresponding protein codding genes in the groups (high group, Raya and Low group, Arado) for annual precipitation.

Chr	Start	End	Direction	nSNPs	Min. F_{ST}	Min. ZF_{ST}	Max. F_{ST}	Max. ZF_{ST}	Overlapping protein codding genes
1	83500001	83600000	high	525	0.148	3.503	0.148	3.503	*KLHL6*
5	34250001	34600000	low	413-509	0.15	3.55	0.184	4.347	*ARID2*
5	91900001	92050000	high	971-1092	0.149	3.54	0.152	3.592	*RERGL*
5	95250001	95550000	high	496-670	0.181	4.263	0.229	5.382	*PLBD1, ENSBTAG00000054625, ATF7IP*
6	68400001	68600000	low	535-1097	0.183	4.323	0.225	5.286	*RASL11B*
6	86300001	86400000	high	656	0.154	3.637	0.154	3.637	*DCK*
7	21250001	21450000	both	404-500	0.153	3.621	0.188	4.448	*LINGO3, PEAK3, OAZ1, DOT1L, PLEKHJ1, SF3A2, AMH, JSRP1, AP3D1*
7	60850001	60950000	high	278	0.158	3.732	0.158	3.732	*CSNK1A1*
8	21850001	22100000	high	451-559	0.192	4.521	0.197	4.653	*CDKN2B*
8	59650001	59800000	both	282-294	0.164	3.876	0.169	3.985	*RUSC2, FAM166B*
10	55000001	55200000	low	596-675	0.16	3.793	0.186	4.399	*RAB27A, RSL24D1*
11	45950001	46400000	low	500-535	0.193	4.547	0.314	7.361	*TTL, POLR1B, CHCHD5, SLC20A1*
11	94950001	95300000	low	435-971	0.171	4.032	0.186	4.386	*LHX2*
11	95300001	95450000	low	589-880	0.151	3.568	0.16	3.777	*NEK6*
12	29100001	29300000	high	224-539	0.17	4.011	0.184	4.338	*RXFP2*
13	17900001	18000000	low	722	0.161	3.802	0.161	3.802	*PDSS1, ENSBTAG00000048553*
15	1500001	1700000	high	555-663	0.173	4.096	0.183	4.325	*ANKRD49, AASDHPPT, KBTBD3*
16	36250001	36350000	low	650	0.176	4.156	0.176	4.156	*DPT*
18	12850001	13050000	high	523-619	0.157	3.713	0.174	4.119	*FBXO31, MAP1LC3B, ZCCHC14*
18	36600001	36900000	low	661-546	0.158	3.731	0.162	3.843	*ENSBTAG00000052086 (NFE2L1 (A0A3Q1MA42_BOVIN)), NFAT5, NQO1, NOB1*
20	40900001	41000000	low	769	0.155	3.665	0.155	3.665	*NPR3*
21	55000001	55150000	low	756-757	0.155	3.679	0.171	4.036	*TGM7, LCMT2, ADAL, ZSCAN29*
22	13750001	13850000	low	542	0.195	4.606	0.195	4.606	*CTNNB1*
23	29850001	30000000	high	1896-1699	0.174	4.1	0.234	5.516	*OR2J1, OR2W1D, OR2W1, OR2AD1, OR2AD1B*
27	23900001	24200000	low	680-1355	0.17	4.018	0.176	4.156	*TRMT9B*
29	39800001	39900000	high	475	0.164	3.879	0.164	3.879	*DDB1, TKFC, CYB561A3, TMEM138, TMEM216, ENSBTAG00000053752*

nSNPs number of Single Nucleotide Polymorphism, *Min.*F_{ST} minimum F_{ST} value, *Min.*ZF_{ST} standardized F_{ST} value, Max.F_{ST} maximum F_{ST} value, Max. $ZF_{ST,}$ standardized F_{ST} value.

Table 39. Overlap of *Hp* and F_{ST} detected regions and corresponding protein codding genes in the groups (high group, Begait and low group, Raya) for the wettest quarter precipitation.

Chr	Start	End	Direction	nSNPs	Min. F_{ST}	Min. ZF_{ST}	Max. F_{ST}	Max. ZF_{ST}	Overlapping protein codding genes
2	350001	550000	high	548	0.226	4.079	0.294	5.366	*ENSBTAG00000040536*
2	110200001	110800000	high	598-722	0.216	3.896	0.322	5.891	*ENSBTAG00000051776 (A0A3Q1MGV2_BOVIN), PAX3, ENSBTAG00000053079, SGPP2*
2	126400001	126550000	low	373	0.204	3.663	0.204	3.663	*ARID1A*
4	12550001	12700000	low	806-906	0.200	3.587	0.238	4.306	*PON3*
5	47350001	47700000	high	520-950	0.207	3.718	0.211	3.802	*HELB, ENSBTAG00000053419, IRAK3, ENSBTAG00000052954, TMBIM4, LLPH*
5	47700001	47950000	high	400-496	0.281	5.135	0.356	6.535	*HMGA2*
5	91900001	92050000	low	851-1030	0.217	3.906	0.239	4.329	*RERGL*
5	95250001	95550000	low	452-656	0.214	3.865	0.373	6.864	*PLBD1, ENSBTAG00000054625, ATF7IP*
6	15850001	15950000	high	535	0.203	3.640	0.203	3.640	*ENSBTAG00000049691*
7	57400001	57550000	low	298-317	0.203	3.640	0.205	3.693	*RBM27, POU4F3*
7	60550001	60650000	low	573	0.246	4.457	0.246	4.457	*ENSBTAG00000048563*
7	60650001	60850000	low	383-466	0.208	3.745	0.217	3.906	*AFAP1L1, ENSBTAG00000052766, GRPEL2, PCYOX1L, IL17B*
7	96450001	96600000	low	354-475	0.205	3.692	0.226	4.086	*ENSBTAG00000003118, LIX1*
8	59650001	59750000	both	227	0.215	3.871	0.215	3.871	*ENSBTAG00000011402*
8	83950001	84050000	high	811	0.201	3.616	0.201	3.616	*OGN, OMD*
9	39900001	40050000	high	564-747	0.215	3.872	0.249	4.521	*CDC40*
12	28800001	29500000	low	278-603	0.228	4.125	0.273	4.968	*RXFP2*
13	47200001	47500000	low	434-542	0.264	4.800	0.308	5.642	*SLC23A2, TMEM230, PCNA, CDS2*
13	47900001	48050000	low	692-894	0.217	3.915	0.227	4.107	*SHLD1*
13	63600001	63700000	low	345	0.237	4.292	0.237	4.292	*ASIP*
16	37550001	37700000	low	365-422	0.212	3.819	0.220	3.977	*KIFAP3*
19	46400001	46500000	low	976	0.211	3.801	0.211	3.801	*ENSBTAG00000051312(Histone H2B (G3MXG7_BOVIN))*
19	46500001	46900000	both	661-841	0.286	5.224	0.322	5.905	*EFCAB3, METTL2A*
20	4500001	4600000	low	776	0.268	4.883	0.268	4.883	*DUSP1*
20	11750001	12050000	high	923-973	0.207	3.728	0.237	4.300	*ENSBTAG00000034170*
21	57900001	58100000	both	390-724	0.278	5.073	0.344	6.324	*ENSBTAG00000053789*
25	26650001	26750000	low	608	0.227	4.106	0.227	4.106	*ITGAL, ENSBTAG00000048731, ENSBTAG00000052789, ENSBTAG00000043974, ENSBTAG00000051451, ZNF688*
29	39800001	39950000	low	420-449	0.241	4.375	0.255	4.640	*DDB1, TKFC, CYB561A3, TMEM138, ENSBTAG00000053752, TMEM216, CPSF7, SDHAF2*
29	48650001	48750000	low	791					*PHLDA2, SLC22A18, CDKN1C*

nSNPs number of Single Nucleotide Polymorphism, *Min.*F_{ST} minimum F_{ST} value, *Min.*ZF_{ST} standardized F_{ST} value, Max.F_{ST} maximum F_{ST} value, Max. $ZF_{ST,}$ standardized F_{ST} value.

Table 40. Overlap of *Hp* and F_{ST} detected regions and corresponding protein codding genes in the groups (high group, Raya and low group, Abergelle) for the warmest quarter precipitation.

Chr	Start	End	Direction	nSNPs	Min. F_{ST}	Min. ZF_{ST}	Max. F_{ST}	Max. ZF_{ST}	Overlapping protein coding genes
2	126400001	126500000	high	295	0.158	3.562	0.158	3.562	*ARID1A*
2	133450001	133600000	low	755-901	0.167	3.775	0.210	4.742	*UBR4*
3	29200001	29300000	low	976	0.173	3.918	0.173	3.918	*SYT6*
3	59700001	59800000	high	289	0.161	3.631	0.161	3.631	*ENSBTAG00000053100, SAMD13*
3	65700001	65900000	low	1051-1074	0.246	5.545	0.260	5.860	*ADGRL4*
4	40550001	40750000	low	1080-1166	0.163	3.682	0.192	4.331	*GNAT3*
4	88300001	88400000	low	744	0.165	3.740	0.165	3.740	*ENSBTAG00000031958*
5	48400001	48800000	low	239-461	0.193	4.353	0.209	4.710	*LEMD3, WIF1*
5	95300001	95550000	high	445-426	0.173	3.913	0.187	4.223	*ENSBTAG00000054625, ATF7IP*
6	37200001	37650000	low	576-1084	0.174	3.931	0.229	5.164	*NCAPG, DCAF16, LCORL*
7	61200001	61450000	low	721-790	0.164	3.705	0.211	4.763	*SLC26A2, HMGXB3, CSF1R*
7	96450001	96600000	high	306-486	0.208	4.695	0.286	6.439	*ENSBTAG00000003118, LIX1*
8	7250001	7350000	low	215	0.221	4.982	0.221	4.982	*ENSBTAG00000025954(LOC782699), ENSBTAG00000035768(G5E622_BOVIN), ENSBTAG00000008678(G3X800_BOVIN), ENSBTAG00000039873(G5E6C5_BOVIN)*
8	59250001	59400000	high	435-470	0.155	3.510	0.173	3.900	*PHF24, DNAJB5, C8H9orf131, VCP, FANCG, PIGO, STOML2, FAM214B*
8	59450001	59600000	high	351-657	0.160	3.614	0.209	4.719	*UNC13B*
11	96450001	96800000	low	415-493	0.196	4.432	0.222	4.999	*PBX3*
12	36400001	36700000	high	421-520	0.187	4.220	0.198	4.470	*CENPJ, RNF17, ATP12A*
18	35100001	35250000	high	237-267	0.156	3.516	0.156	3.535	*RIPOR1, CTCF, CARMIL2, ACD, PARD6A, ENKD1, C18H16orf86*
18	35350001	35500000	high	218-219	0.164	3.706	0.166	3.755	*NUTF2, EDC4, NRN1L, PSKH1, PSMB10, LCAT, SLC12A4, DPEP3, DPEP2, DDX28*
20	4500001	4600000	high	763	0.172	3.892	0.172	3.892	*DUSP1*
23	47600001	47700000	low	786	0.179	4.033	0.179	4.033	*ENSBTAG00000054759*
25	9450001	9750000	low	471-968	0.184	4.146	0.218	4.929	*TVP23A, CIITA, DEXI*
26	42650001	42850000	high	697-1000	0.188	4.241	0.190	4.284	*ENSBTAG00000055162(A0A3Q1LWX0_BOVIN), ENSBTAG00000051599(A0A3Q1MIK6_BOVIN), ENSBTAG00000023846, ENSBTAG00000023845, PSTK, IKZF5, ENSBTAG00000048256*
28	41150001	41350000	high	458-742	0.211	4.765	0.258	5.821	*WAPL, OPN4*
29	48600001	48800000	high	700-741	0.193	4.352	0.246	5.554	*ENSBTAG00000048649, NAP1L4, PHLDA2, SLC22A18, CDKN1C*

nSNPs number of Single Nucleotide Polymorphism, *Min.*F_{ST} minimum F_{ST} value, *Min.*ZF_{ST} standardized F_{ST} value, Max.F_{ST} maximum F_{ST} value, Max. ZF_{ST}, standardized F_{ST} value.

4.4.4.3. CL and or SBD selective sweep regions overlapping protein codding genes

For the group under cultivated land or soil bulk density, a 0.4Mb length located at chromosome 17 was the gene-rich region overlapping 20 protein-codding genes (Table 41 and Table S41). It included significantly ($P < 0.05$) enriched genes such as *PI4KA* (F_{ST} = 0.21-0.21 and ZF_{ST} = 3.98 - 3.98) and *CRKL* (F_{ST} = 0.21- 0.21 and ZF_{ST} = 3.98 - 3.98), both were under strong positive selection in the low group for cultivated land or high group for soil bulk density (Begait cattle). The gene *CRKL* was involved in two important GO terms and one KEGG pathway of biological processes such as cranial skeletal system development (GO:1904888) and spermatogenesis (GO:0007283) and one KEGG pathway (bta05163, Human cytomegalovirus infection while *PI4KA* gene was involved in GO term of a cellular component (GO:0005737, cytoplasm) (Table S52).

Different protein-coding genes in the genome of the Begait cattle including *AIFM3*, *NPM1*, *BTRC*, *NDUFS4*, *ICE1*, *RFX6*, *LOC101902172* (*ENSBTAG0000003417*), *SNAP29*), overlapped different selective sweep regions (Table 41 and Table S41) were significantly enriched in different GO and KEGG pathways (Table S52). For instance, the genes *AIFM3* and *NDUFS4* were involved in a very important molecular function, the oxidoreductase activity (GO:0016651).

Genes in the interferon beta-3 family (*LOC112447877*, *LOC112447878* and *LOC100848709*), interferon alpha-H (*LOC783912*) and interferon omega-1 (*LOC523509*) overlapped a 0.15Mb selective sweep at chromosome 8 were the most frequently appeared genes (in Begait) in several GO and KEGG pathways including the biological processes of the cytokine-mediated signaling pathway (GO:0019221) and defense response to viruses (GO:0051607), the molecular function of cytokine activity (GO:0005125), KEGG pathways of Human cytomegalovirus infection (bta05163), JAK-STAT signaling pathway (bta04630) and Cytokine-cytokine receptor interaction (bta04060). In addition, these genes (*LOC112447877*, *LOC112447878* and *LOC100848709*, *LOC783912*, *LOC523509*), along with a gene (*ENSBTAG00000033806* (*LOC613401*)) under strong positive selection in the

Arado cattle, were significantly enriched in KEGG pathway (bta04217, Necroptosis) (Table 41 and Tables S41 and S52).

Candidate protein-coding genes in the Arado cattle, including *HSPD1*, *UCP2*, *UCP3*, *CTNNB1*, *COQ10B*, *BOLL*, *SF3B1*, *PAWR*, *HSPE1*, *DNAJB13*) were significantly enriched in different GO and KEGG pathways. Especially the three genes *HSPD1*, *UCP2*, and *UCP3* were involved in an important biological process related to response to cold (GO:0009409). The *HSPD1*, with *HSPE1* and *DNAJB13* genes, were engaged in an essential molecular function called chaperone binding. Moreover, the genes *UCP2* and *UCP3* were involved in a critical biological process (badly needed in same areas as the Arado cattle are adapted) called adaptive thermogenesis (GO:1990845). *UCP2* and *UCP3* were also involved in related biological processes and cellular components, including mitochondrial transmembrane transport (GO:1990542), mitochondrial transport (GO:0006839) and mitochondrial inner membrane (GO:0005743) and in oxidative phosphorylation uncoupler activity (GO:0017077), a GO term of the molecular function (Table S52).

Table 41. Overlap of *Hp* and F_{ST} detected regions and corresponding protein codding genes in the groups (high group, Arado and Low group, Begait) for cultivated land (CL).

Chr	Start	End	Direction	nSNPs	Min. F_{ST}	Min. ZF_{ST}	Max. F_{ST}	Max. ZF_{ST}	Overlapping protein codding genes
2	400001	550000	low	658	0.263	5.048	0.263	5.048	*ENSBTAG00000040536*
2	85900001	86550000	high	377-526	0.264	5.080	0.356	6.898	*ENSBTAG00000012171, SF3B1, COQ10B, HSPD1, HSPE1, MOB4, RFTN2, MARS2, BOLL*
2	126400001	126500000	high	271	0.202	3.851	0.202	3.851	*ARID1A*
3	100550001	100700000	low	626-681	0.271	5.200	0.317	6.113	*PRDX1, MMACHC, ENSBTAG00000017029*
4	31550001	31700000	high	337-552	0.206	3.925	0.228	4.361	*ENSBTAG00000033806(LOC613401)*
4	66150001	66350000	high	470-480	0.192	3.647	0.223	4.255	*MTURN, PLEKHA8, FKBP14*
5	9100001	9300000	high	490-894	0.207	3.951	0.340	6.585	*PAWR, ENSBTAG00000048833*
6	68450001	68550000	high	745	0.262	5.022	0.262	5.022	*RASL11B*
8	23050001	23200000	low	761-1150	0.295	5.687	0.361	6.991	*ENSBTAG00000051881 (LOC783912) interferon alpha-H, ENSBTAG00000053037 (LOC523509) interferon omega-1, ENSBTAG00000053413, IFNB3 (LOC100848709) (ENSBTAG00000055306), IFNB3 (LOC112447877) (ENSBTAG00000049948) interferon beta-3, IFNB3 (LOC112447878) (ENSBTAG00000055103) interferon beta-3*
9	33650001	33800000	high	657-837	0.192	3.639	0.221	4.227	*RFX6*
10	55050001	55250000	high	471-610	0.207	3.947	0.256	4.906	*RSL24D1*
11	46150001	46250000	high	1053	0.210	4.007	0.210	4.007	*TTL*
15	1500001	1600000	high	609	0.199	3.777	0.199	3.777	*ANKRD49, AASDHPPT*
15	53350001	53500000	high	626-805	0.193	3.670	0.213	4.070	*DNAJB13, UCP2, UCP3*
17	43600001	43750000	high	738-913	0.200	3.802	0.250	4.801	*GUCY1A1*
17	72150001	72550000	low	841	0.209	3.979	0.209	3.979	*ENSBTAG00000047538, HIC2, ENSBTAG00000030927, PI4KA, SERPIND1, SNAP29, CRKL, AIFM3, LZTR1, THAP7, TUBA3E, LRRC74B, P2RX6, SLC7A4, TUBA3C, MZT2B, SMPD4, ENSBTAG00000031018, MED15, KLHL22*
20	3100001	3250000	low	802-822	0.197	3.748	0.199	3.783	*NPM1*
20	11700001	12050000	low	886-894	0.234	4.486	0.241	4.610	*ENSBTAG00000034170 (LOC101902172)*
20	25150001	25600000	low	485-570	0.191	3.626	0.271	5.209	*NDUFS4*
20	67600001	67750000	low	872-1239	0.257	4.933	0.277	5.329	*ICE1*
21	47300001	47500000	low	606-817	0.202	3.850	0.291	5.612	*MIPOL1*
22	13700001	13900000	high	778-794	0.210	3.994	0.210	4.006	*CTNNB1*
26	22100001	22400000	low	389-548	0.205	3.898	0.206	3.915	*BTRC, POLL, DPCD, ENSBTAG00000053939*
26	50500001	50600000	low	915	0.196	3.725	0.196	3.725	*ENSBTAG00000049317*

nSNPs number of Single Nucleotide Polymorphism, *Min.*F_{ST} minimum F_{ST} value, *Min.*ZF_{ST} standardized F_{ST} value, Max.F_{ST} maximum F_{ST} value, Max. $ZF_{ST,}$ standardized F_{ST} value.

CHAPTER 5. DISCUSSION

5.1. Morphological Variation of Indigenous Cattle in Tigray

Most of the indigenous cattle in Tigray studied here showed diverse morphological characteristics different from those previously described and reported in other Ethiopian cattle. Similarly, some morphological traits observed in other Ethiopian cattle populations were not found in the population examined here.

For example, the light red and brown coat colors distributed as a plain pattern were also frequently observed in other Ethiopian cattle from different regions (Andualem *et al*., 2016), while the black with white coat color distributed mainly as a patchy coat pattern has been reported in Mursi cattle found in Southwestern Ethiopia (Endashaw *et al*., 2015). Grey coat color was reported for Ogaden cattle in Southeastern Ethiopia (Fasil *et al*., 2014). However, the white coat color, the dominant coat color in Boran cattle in Eastern Ethiopia (Gillooly *et al*., 2001), was not common in the populations studied here. The horn type and structure (Geraro, Korsuma, Genbo and Tulu) observed in Raya cattle, the curved in (convex) face profile observed in Raya cattle, the curved out (concave) face profile, roofy back profile, large udder and teat size observed in Begait cattle. Unlike the quantitative traits directly linked to animal genetic resources' production and service functions (AnGR), qualitative characteristics are linked with adaptive importance (FAO, 2012). Hence, the variation of the qualitative traits across the populations could indicate the population's exposure to different environmental stresses.

Similar to the study of Wondimu and Negassi (2018), who examined Southern Ethiopia indigenous cattle in Tigray, pelvic width, chest girth, hock circumference, height at wither, and muzzle circumference were among the main discriminating variables. Height at wither, body length, ear length, tail length without switch and face length were also reported as important discriminant quantitative traits of indigenous cattle populations in the Northeast States of India (Pundir *et al*., 2015), which agrees with the findings of this study except for the face length which was not a discriminating variable in this study. However, considering the main discriminant parameters related to body frame size (e.g. height at wither, height at rump, body length, chest depth and heart girth), the Begait cattle in this study was the largest of all populations reported so far in Ethiopia, while the Raya population was similar in size to most other Ethiopian cattle populations. Arado, Abergelle and Erob were the smallest populations described so far in Ethiopia (Fasil, 2006; Dereje *et al*., 2008; Chencha *et al*., 2013; Fasil *et al*., 2014; Endashaw *et al*., 2015; Andualem *et al*., 2016; Belay *et al*., 2017; Nakachew *et al*., 2018; Wondimu and Negassi, 2018). This variation could result from genetic, environmental, management, husbandry practices or the genotype by environment interaction. Knowing the body frame of cattle could have implications for cattle production objectives. For instance, the aim of cattle fattening and dairy production directly depends on understanding the cattle fame size. For a short-term fattening with a small-scale production objective, cattle with a small framed body size are predominantly preferred as they early reach physiological maturity, the growth stage when fattening begins. On the other hand, large-framed cattle are preferred over small-framed cattle for long-term fattening programs with large-scale production objectives (McKiernan *et al*., 1998) and breed selection for sustaining dairy production (Addis and Godadaw, 2015).

In this study, most individuals of both sexes were correctly assigned to their source population except Abergelle and Erob. These values were higher than the ones reported in other studies for Ethiopian cattle. In Chencha *et al*. (2013), 63.5% of animals from the Gamo zone in Southern Ethiopia were correctly classified as highland and lowland indigenous cattle populations. Dereje *et al*. (2008) reported the overall classification hit rate of 55.2 % and 60.1% for Northeastern Ethiopia's female and male cattle populations. Fasil (2006) reported 80.85% and 79.90% of the overall correct classification for male and female cattle populations in the East and West Gojjam zones (Amhara region). However, the results of this study were similar to those of Wondimu and Negassi (2018), who obtained 90% of the correct assignment for the highland and lowland male cattle populations of the Hadya zone (Southern Ethiopia) except the Abergelle with Erob which showed around 30% individuals miss assigned across each other. This was further confirmed through the canonical discriminate function analysis, which showed an overlap between Abergelle and Erob cattle populations. This might indicate the possibility that the two populations (Abergelle and Erob) have been distributed from a common ancestral population to geographically different parts of the Tigray region.

5.2. Habitat Suitability Variation of the Indigenous cattle in Tigray and the screened key Ecological Variables

The MaxEnt program was extensively applied in the spatial distribution and suitability maps of different wildlife animals or plants (Raxworthy *et al*., 2007; Meshgi *et al*., 2019; Fern *et al*., 2020; Su *et al*., 2021; Valencia-Rodríguez *et al*., 2021), epidemiological studies of different prevalence diseases of wildlife or domestic animals (Cardoso-Leite *et al*., 2014; Dicko *et al*., 2014, Ciss *et al*., 2019; Mwakapeje *et al*., 2019; Escobar, 2020; Muema *et al*., 2021) and even modelling the impact of climate change in the future generation of species (Jeschke and Strayer, 2008). Currently, it is being used to predict the niche similarity mapping of domesticated animals like chickens (Lozano-Jaramillo *et al*., 2019; Fasil *et al*., 2021; Gheyas *et al*., 2021; Gebreslassie *et al*.2022; Vallejo-Trujillo *et al*., 2022). It was also used in identifying the main environmental variables that influence the adaptive diversity of a particular species to specific agroclimatic and biogeographical circumstances (Meshgi *et al*., 2019).

A species' biological existence, productivity and reproduction rely on climatic and non-climatic aspects (O'Donnell and Ignizio, 2012). Changes in the climatic predictors including the annual mean temperature (bio1), mean diurnal range of temperature (bio2), isothermality (bio3), temperature seasonality (bio4), the maximum temperature of the warmest month (bio5), minimum temperature of the coldest month (bio6), annual temperature range (bio7), mean temperature of the wettest (bio8), driest (bio9), warmest (bio10) and coldest (bio11) quarters, annual precipitation (bio12), precipitation of the wettest (bio13) and driest (bio14) months, precipitation seasonality (bio15), precipitation of the wettest (bio16), driest (bio17), warmest (bio18) quarters were reported to affect the physiology of the species and its distributions across a specific environment (O'Donnell and Ignizio, 2012, Gheyas *et al*., 2021; Gebreslassie *et al*. 2022; Vallejo-Trujillo *et al*., 2022). Moreover, elevation, the water vapor pressure of the driest and wettest months, and soil-related variables, including soil pH, soil cation exchange capacity, soil bulk density, soil organic carbon, soil clay content, soil silt content, soil sand content and soil total available water capacity, and vegetation and land use variables including forest cover, grass/shrub land, cultivated land and major crops cultivated in a specific area are also stated to be the essential factors in determining the agroecological variation of a particular landscape and have a very important linkage with livestock biology like chicken in Ethiopia (Gheyas *et al*., 2021; Vallejo-Trujillo *et al*., 2022).

In this section, the ecological niche for the indigenous cattle in Tigray were mapped, classified and characterized using the Maximum Entropy (MaxEnt) program of the ecological niche modeling (ENM). The analysis of the 33 environmental variables (Table 8) following the MaxEnt program screened six uncorrelated environmental variables, which significantly contributed in building and predicting the model appropriate for mapping the habitat suitability of the indigenous cattle in Tigray. The set of the selected environmental variables included soil bulk density, cultivated land, annual precipitation (bio12), precipitation of the wettest (bio16) and warmest (bio18) quarters and temperature seasonality (bio4). They all showed a significant prediction power (> 0.6), low omission rate (false negativity), high values (81.8 to 98%) of AUC for the training and test data, and jackknife analysis (> 60%) that make them the key determinants of adaptive diversity among the Tigray populations.

The soil bulk density significantly contributes in defining the soil's quality and productivity (Arshad *et al*., 1996). This can further shape the productivity and type of the grazing and foraging species and the crop types that could be grown in a particular soil type, which can directly relate to cattle feed variety, quantity, quality, and distribution. The cultivated land selected in this study was strongly and negatively ($r_s \approx -0.85$) correlated with grass/shrub land. In Tigray, generally Ethiopia, grass/shrub land is used for grazing the indigenous cattle in Tigray and contributes nearly 80% of the cattle feed, especially under smallholders (Endashaw *et al*., 2015; Addisu *et al*., 2016; Gashu *et al*., 2017; Denbela and Yidinachachew, 2018). This crucial environmental variable (cultivated land) is directly or indirectly linked with feed availability, type and volume of cattle feed. For instance, there is a critical shortage of cultivated land for crop production in areas like Tigray, where the landscape is mostly mountainous and hills (Kumasi and Asenso-Okyere, 2011). Mostly, the landless youngsters made to own land for cultivation at the expense of grazing land for livestock. In such circumstances, livestock production, primarily cattle, which need a relatively large volume of feed for maintenance, production, and reproduction, is in danger of population size reduction. Some farmers in Tigray are replacing their large ruminants with small ruminants or chickens due to the shortage of grazing areas. On the other way, cultivated land is linked with cattle positively or negatively depending on the purpose it is being used for. Suppose farmers used it to produce crops essential in delivering quality and quantity of crop residues for cattle. In that case, it is positively linked with increasing cattle productivity. However, cattle production can be negatively affected if the cultivated land is used to produce crops with less quantity or quality crop residues (Homann-Kee Tui *et al*., 2004; Tadesse *et al*., 2010).

Among the six important environmental variables selected, three variables, including precipitation of the wettest and warmest quarters and temperature seasonality (bio4)) are related to season variation. Tigray is located in the drier northern part of Ethiopia. It belongs to the African drylands in the Sudano-Sahelian region, where moisture stress is an issue (Kumasi and Asenso-Okyere, 2011). This could be the reason why total and seasonal precipitations acquired in the Tigray Region were the crucial factors in the first place in shaping the habitat or adaptive diversity of the indigenous cattle in Tigray. Similarly, seasonal and total precipitation were reported to be more important environmental variables compared to monthly precipitations in predicting the habitat suitability of other animals like toed sloths (*Bradypus*) mammal (Phillips, 2005). Precipitation of the warmest and coldest seasons and temperature seasonality were also reported as the most important variables associated with habitat suitability in Ethiopian indigenous chickens (Fasil *et al*., 2021). The amount of precipitation distribution acquired in a given area was reported to have high predicting power in determining the habitat suitability of wild mammals (Phillips, 2005) and domesticated animals' (Fasil *et al*., 2021; Gheyas *et al*., 2021; Gebreslassie *et al*., 2022; Vallejo-Trujillo *et al*., 2022) consistent to the finding of this study. This could be due to the tremendous influence of rainfall distribution in controlling the long-term forage production of an area (Liu *et al*., 2021) which directly influences the species distribution due to its direct relation to feed quantity and quality for the animals available in an area.

Most of the key environmental variables (bio4, bio12, bio16, bio18 and Cl) had a significant contribution in predicting most (eight out of ten) of the quantitative phenotypic variables that have the highest power indiscriminating the female indigenous cattle in Tigray (Table 31). However, only three of them (bio4, bio16 and bio18) had a significant contribution in predicting most (six of the eight) quantitative phenotypic variables that have the highest discriminant power in determining the phenotypic variability of the male indigenous cattle in Tigray (Table 32). This indicates that the MaxEnt selected environmental variables influence the phenotypic variability and have different prediction power for female and male cattle phenotypic traits. Likewise, MaxEnt selected environmental variables related to temperature and precipitation were previously reported to trigger phenotypic variability in indigenous chicken populations of Ethiopia (Fasil *et al*., 2021).

5.3. Genome-wide Diversity and Level of Admixture in the Indigenous Cattle in Tigray

This is the first report on whole-genome-sequence-based characterization of the genetic diversity, relatedness, and admixture of the indigenous cattle in Tigray. Abundance, distribution and functional description of SNPs and indels, genome-wide nucleotide diversity (π), heterozygosity (H_O), runs of homozygosity (ROH) and genomic inbreeding coefficient were used to evaluate the intra-population genetic diversity. The pairwise population differentiation (F_{ST}), PCA and admixture analysis were employed to assess the inter-population differentiation and relationship among the indigenous cattle in Tigray and between the indigenous cattle in Tigray and other representatives of different cattle groups (African sanga, African zenga, African and Asian zebu, and African and European taurine).

The high variation in abundance of genetic variants (SNPs and indels) within and across the indigenous cattle in Tigray illustrated their rich genetic diversity. The substantial number of novel variants (SNPs and indels) found in the indigenous cattle in Tigray (Table 22) further indicate their importance as a reservoir of genetic diversity previously uncharacterized. Interestingly, many novel indels (around 34%) were detected compared to novel SNPs. However, it should be emphasized that indels have been given so far, less attention in cattle genomic analyses (Stafuzza *et al.*, 2017) despite being part of the essential drivers of phenotypic and genetic diversity (Iqbal *et al.*, 2019). Most of the whole genome analyses on African cattle were based on SNPs (Kim *et al.*, 2017; Tijjani *et al.*, 2019; Kim *et al.*, 2020; Endashaw *et al.*, 2022; Jang *et al.*, 2022; Mauki *et al.*, 2022; Endashaw *et al.*, 2023), while this study is the first to report indels for Ethiopian cattle.

5.3.1. Genetic "functional" variability in the Indigenous Cattle in Tigray

A substantial number of novel variants (SNPs and indels) were detected in each population, where around 20% of them were missense private variants. Further analysis of the missense private variants overlapping codding regions identified several GO terms and KEGG pathways shared by different populations or population-specific. The two most significant GO terms of the molecular function (the olfactory receptor activity and odorant binding) and one most significant KEGG pathway (olfactory transduction) present in all the indigenous cattle in Tigray were associated with olfaction or odor recognition. An efficient olfactory reception is an important fitness mechanism for adaptation, including food and water search behavior and reproduction (Kour *et al.*, 2022). Odor recognition influences food intake, identification and preference (Soria-Gómez *et al.*, 2014).

The GO terms of the cellular component related to integral component of the plasma membrane (GO:0005887) and its subtype intrinsic component of the plasma membrane (GO:0031226) were only found in Begait cattle. In these GO terms, several important genes were found to be associated with morphology, production, reproduction, feed efficiency, immune response and environmental adaptation. For example, *Sodium Voltage-Gated Channel Alpha Subunit 4* (*SCN4A*) (Cai *et al.*, 2019) and *Taste receptor type 1 member*

2 (*TAS1R2*) (Zhang *et al.*, 2012) genes were reported to be associated with body height in cattle. *Potassium Voltage-Gated Channel Modifier Subfamily G Member 4* (*KCNG4*) gene was found to be related to morphometric traits like rump height, body length and chest depth in goats (Easa *et al.*, 2022). *Fms-related tyrosine kinase 4* (*FLT4*) gene was relevant to production and growth in cattle (Keogh *et al*., 2019). *Gamma-aminobutyric acid type A receptor subunit gamma1* (*GABRG1*) was implicated in milk yield (Pedrosa *et al.*, 2021). The genes *Protocadherin 8* (*PCDH8*) (Taussat *et al*., 2020) and *Solute Carrier Family 26 Member 3* (*SLC26A3*) (Kern *et al*., 2016) in Begait cattle were associated with feed efficiency and the gene *protocadherin 18* (*PCDH18*) was related to the immune system and adipogenesis (de Lima *et al*., 2020). *Dual oxidase 2* (*DUOX2*) gene was important for thyroid hormones production and for innate immunity (Maruo *et al.*, 2016), *MFSD2 Lysolipid Transporter B, Sphingolipid* (*Mfsd2b*) gene was reported to be important in S1P transport activity (Kobayashi *et al.*, 2018) which is essential for various cellular functions (Spiegel and Milstien, 2011; Cyster and Schwab, 2012). *Integrin Subunit Alpha 5* (*ITGA5*) involved in different inflammation and immune response functions (such as bacterial invasion of epithelial cells, phagosome and human papillomavirus infection (Wang *et al.*, 2021c). *Neuropeptide FF Receptor 1* (*NPFFR*) (Moulédous *et al*., 2010) and *Hydroxytryptamine Receptor 7* (*HTR7*) (Hedlund *et al.*, 2003) genes were important in body temperature regulation. Last but not least, *Potassium Voltage-Gated Channel Modifier Subfamily V Member 2* (*Kcnv2*) was reported to be associated with visual adaptation in a changing lighting condition environment (Hölter *et al.*, 2012).

Two significant GO terms of the cellular component (GO:0005578~proteinaceous extracellular matrix and GO:0044420~extracellular matrix component) were explicitly enriched in Erob cattle. Genes such as *Multimerin 2* (*MMRN2*), *Von Willebrand factor C domain containing 2* (*VWC2*) and *Laminin subunit gamma 1* (*LAMC1*) were important in these GO terms. *MMRN2* was associated with a meat quality trait called meat juiciness (Leal-Gutiérrez *et al.*, 2019). Similarly, *VWC2* was considered as a candidate gene for intramuscular fat content, one of the most important meat quality traits in beef cattle (Halli *et al.*, 2022). *VWC2* also reported to be associated to feed efficiency in pigs (Wang *et al.*, 2015). *LAMC1* was involved in different inflammation and immune response pathways, including prion diseases (bovine spongiform encephalopathy), amoebiasis and toxoplasmosis in cattle. Moreover, *LAMC1* was important to regulate temperature variation in cattle (Flori *et al.*, 2019).

Six molecular function GO terms relevant to intra or extra-cellular activity were significantly enriched in four of the indigenous cattle in Tigray (Abergelle, Arado, Begait and Raya), in which a few genes such as *Cadherin EGF LAG seven-pass G-type receptor 1* (*CELSR1*), *Gamma-aminobutyric acid type A receptor rho3 subunit* (*GABRR3*), *Plexin A2* (*PLXNA2*) and *Toll-like receptor 6* (*TLR6*) were identified in Abergelle, Arado and Raya cattle, while the gene *Macrophage stimulating 1 receptor* (*MST1R*) was overrepresented in the six GO terms (in Abergelle, Arado, Begait and Raya). *CELSR1* (Guo *et al.*, 2019b) was found to be overexpressed following in vitro treatment of lipopolysaccharide, a cause of the endometrium inflammation (Sheldon *et al.*, 2010), supporting its importance in immune response. In a significantly enriched GO terms in Abergelle, Arado and Raya cattle, *TLR6* was found to be an important candidate gene for bovine tuberculosis resistance (Song *et al.*, 2014). Several studies (Zhang *et al.*, 2009; Seabury *et al.*, 2010; Fisher *et al.*, 2011; Elmaghraby *et al.*, 2018; Maurić Maljković *et al.*, 2023) have reported the importance of toll-like receptor genes for immunity, disease resistance and adaptive immune responses, including mastitis, the most economically important disease in dairy cattle (Elmaghraby *et al.*, 2018; Maurić Maljković *et al.*, 2023). Other genes *Macrophage stimulating 1* (*MST1*) relevant to oxidative stress (Xiao *et al.*, 2011), *Plexin A2* (*PLXNA2*) for cattle temperament (Gutiérrez-Gil *et al.*, 2008) and *Gamma-aminobutyric acid type A receptor subunit rho3* (*GABRR3*) for fertility such as sperm motility (Hering *et al*., 2014) were also detected in the six GO terms (Abergelle, Arado and Raya cattle).

The presence of missense variants in genes involved in olfaction may be attributed to the adaptation of the indigenous cattle in Tigray to the dry agroecological landscape in the region, a characteristic of the Sudano-Sahelian ecology with heat and water stress as an issue (Nyssen *et al.*, 2009; Kumasi and Asenso-Okyere, 2011; Melaku, 2013). In addition, the regional landscape is mainly composed of mountains and hills (Kumasi and Asenso-Okyere, 2011) with limited grazing resources. As a result, the indigenous cattle in Tigray are strongly adapted to feed shortage, as evidenced by the overrepresentation of genes associated with the olfactory and sensory perception of smell to differentiate the edible from non-edible or palatable from non-palatable browse plant species.

5.3.2. Genetic diversity, population genetic structure and relationships

There was a high genome-wide nucleotide diversity (π) across all indigenous cattle in Tigray, comparable with the values observed in Asian indicine cattle but higher than those in taurine cattle (Muturu, N'Dama, Angus and Holstein) (Figure 29) and indicine-taurine admixed ($\pi = 2.9\times10^{-3}$ for Jiaxian Red) cattle (Xia *et al.*, 2021). Similarly, the observed heterozygosity (H_O), an important indicator of genetic variability in domestic animals (Zhang *et al.*, 2018), ranging from 0.278 to 0.302 among the indigenous cattle in Tigray was similar with other indicine but higher than African and European taurine cattle.

The comparison of the ROH distribution pattern between the indigenous cattle in Tigray and showed different patterns of ROH as compared to Asian zebu, African taurine (N'Dama and Muturu), African sanga (Ankole), African zebu (Kenana) and European-taurine (Angus and Holstein) cattle groups included in this study. As expected from their high genomic diversity, the number and cumulative length of ROH were smaller in the indigenous cattle in Tigray compared with previous reports for taurine cattle (Purfield *et al.*, 2012; Xia *et al.*, 2021) and indicine-taurine admixed cattle outside Ethiopia (Xia *et al.*, 2021). However, the number and length of ROHs observed in the indigenous cattle in Tigray were similar to the one reported for other Ethiopian populations included in this study (Horro, Fogera, Borana, Afar). It suggests common breeding history among Ethiopian cattle populations, while PCA and admixture results suggest close genetic relationships among the Ethiopian cattle as recently showed in a genome analysis study including 14 Ethiopian indigenous cattle in Tigray (Endashaw *et al.*, 2023).

Inbreeding coefficients were far lower in the indigenous cattle in Tigray than those reported in other cattle populations, particularly the Danish dairy cattle breeds (Zhang *et al.*, 2015a), with an inbreeding coefficient five times higher at a population level. An inbreeding coefficient below 5%, as observed for nearly all animals in this study (F_{ROH}), is generally considered to have no consequence on an individual's fitness (Slate *et al.*, 2004). Therefore, the level of inbreeding in the indigenous cattle in Tigray is within an acceptable range to accommodate within-population improvement of their productivity despite some individuals within the Begait and Raya cattle with intense inbreeding.

Taurine ancestry was generally low in the indigenous cattle in Tigray relative to other African-humped cattle (Kim *et al.*, 2020). This is particularly expected for cattle populations geographically close to the entry points of Asian indicine cattle into Africa. Historic factors associated with the arrival and admixture of cattle in the Horn of Africa, including the Tigray Region, likely shaped today's genome diversity of the indigenous cattle in Tigray. As an ancient center of civilization, the Tigray Region probably witnessed the early arrival of taurine cattle, followed by late introductions of indicine cattle in several migration waves, which continuously enriched the genome landscape of the indigenous cattle in Tigray. While the findings of this study indicated a large proportion of indicine background in the indigenous cattle in Tigray (above 85%), a proportion of African taurine ancestry was still found in their genomes. Moreover, unique local ancestries were observed in Erob ($K = 7$) or Begait ($K = 10$) poured into all non-taurine African cattle (Figure 36). Hence, the rich genetic variation in modern the indigenous cattle in Tigray might be a legacy of multiple introductions, admixture and dispersion of cattle across the Horn of Africa.

Moreover, a closer relationship was observed between Begait and Kenana cattle (a Sudanese cattle) than with other the indigenous cattle in Tigray. Begait cattle are typically found near the Sudanese border in the Western and Northwestern Tigray areas. Therefore, gene flow from Begait cattle to Sudanese cattle is possible or vice versa. The close morphological relationship between Erob and Abergelle cattle observed (in section) is not supported by the genetic relationship analysis with the two populations here clearly separated (e.g., F_{ST}-based dendrogram, Figure 28).

5.4. Detecting Signature of Selection in the Indigenous cattle in Tigray

The part of this study, which characterizes the respective ecological niche for each cattle population in section 4.2, has identified six major environmental factors related to heat, moisture and feed stress. These factors are supposed to be the driving forces behind adaptive diversity in the indigenous cattle in Tigray. The signals left on the genome landscape of the indigenous cattle in Tigray, which hold the secret to surviving these key environmental stressors, were detected using two autosomal genomic scans, the pooled heterozygosity (*Hp* analysis) and fixation index (F_{ST} analysis).

Several important genes related to adaptation to heat stress, feed stress, disease resistance or immune response, as well as genes indicating the productive value or reproductive performance, were under strong positive selection in one or the other cattle populations (Abergelle, Begait and Raya) adapted to the moisture stressed lowlands of the Tigray National Regional State. On the other hand, several important genes related to cold stress adaptation, feed stress and disease resistance or immune response were under strong selection in the cattle population; Arado adapted to the moisture-stressed highlands of the Tigray National Regional State.

5.4.1. Identified genes and their implication for adaptation to moisture stressed lowlands

Genes such as *DNA Helicase B* (*HELB*), *High mobility group AT-hook 2* (HMGA2), *Interleukin-1 receptor-associated kinase 3* (*IRAK3*) and *Long-term synaptic facilitation factor* (*LLPH*) under strong positive selection in the Begait cattle were reported to be important for adaptation to the tropical environments with a primary heat stress (Naval-Sánchez *et al.,* 2020). The *ENSBTAG00000034170* (*LOC101902172*) gene under strong positive selection in the Begait cattle was also reported to be important for heat tolerance in cattle (Buaban *et al*., 2022). *Paired box gene 3* (*PAX3*) gene, which is important for spotting white phenotype colors (Hauswirth *et al*., 2012), was under strong selection in Begait cattle; this is particularly characteristic of coat color of this population reported in section 4.1 of this study. Interestingly, these spotting white phenotype coat colors are also very important for heat stress regulation in cattle (Anzures-Olvera *et al*., 2019).

A gene called *Urocortin-2* (*UCN2*), which was under strong selection in Begait, is essential for both feed and heat stress adaptation through its capability to suppress food intake, hold the gat from being empty by delaying metabolic activity related digesting. As well as this gene (*UCN2*) is very important to reduce the heat stress pressure by decreasing heat-induced edema (https://www.uniprot.org/uniprot/Q96RP3). Other genes important for feed stress adaptation detected in Begait cattle include *ADAM Metallopeptidase with Thrombospondin Type 1 Motif 16 (ADAMTS16)* (Sahana *et al.*, 2013; Higgins *et al*., 2018) and *Synaptosome associated protein 29*(*SNAP29*) (Chakraborty *et al*., 2020). Mainly, the *SNAP29* gene interacts with cytidine triphosphate synthetase (CTPS) along the cytokeratin network that links the cytokeratin to the regulation of metabolism by compartmentalizing metabolic enzymes during nutrient deficiency (Chakraborty *et al*., 2020). It (*SNAP29*) regulates membrane fusion essential to complete autophagy (enables cells to survive stress from the external environment, such as nutrient deprivation, as well as internal stresses like accumulation of damaged organelles and pathogen invasion) (Legakis and Klionsky, 2006*)* and supporting cell division (Morelli *et al*., 2021).

Several genes related to immune repose were under strong positive selection in Begait cattle. These include the *Purinergic Receptor P2X6* (*P2RX6)* gene reportedly involved in the biological regulation of immune T cells and phagocytes (Chen *et al*., 2022). The *Triokinase And FMN Cyclase* (*TKFC*) gene reported to regulate innate antiviral immunity where its deficiency leads to impaired innate immunity in response to viral illness (Wortmann *et al*., 2020). Three genes in the interferon beta-3 family (*LOC112447877*, *LOC112447878* and *LOC100848709*) and two other genes in the interferon alpha-H (*LOC783912*) and in the interferon omega-1 (*LOC523509*), significantly enriched in several GO and KEGG ($P < 0.05$) were involved in codding Interferon proteins that are crucial in defending the bodies against viruses or foreign cells (Pestka and Baron, 1981). The *Adaptor Protein* (*CRKL*) gene also regulates the contents of immunoglobulins in colostrum and serum (Lin *et al.*, 2022).

In addition to the detection of genes linked with the adaptation importance of its ecological niche, such as heat stress, feed stress and immune response, very crucial candidate genes that can indicate its productive value, fertility and growth performances were specifically under strong positive selection in Begait cattle. The genes with product type or value include, *Beta-Transducin Repeat Containing E3 Ubiquitin Protein Ligase* (*BTRC*) gene reportedly related to mammary gland development, milk production (Yao *et al*., 2023) and encodes proteins in the ubiquitin-proteasome pathway along the lactation (Wickramasinghe *et al*., 2011). *Uridine-cytidine kinase 1* (*UCK1*) gene controls lactation persistency in cattle (Do *et al*., 2017). *Metabolism of Cobalamin Associated C* (*MMACHC*) gene regulates vitamin B-12 content in bovine milk (Rutten *et al*., 2013). Moreover, the genes with fertility and growth performances in Begait cattle include *Solute Carrier Family 26 Member 6* (*SLC26A6*) (Lu *et al*., 2016) and *Phosphatidylinositol 4-kinase alpha* (*PI4KA*) (Rocha *et al*., 2023) that regulates embryo development during pregnancy. Moreover, the *SLC26A6* gene regulates fertility traits regarding scrotal circumference and sperm motility (Sweett *et al*., 2022). *Interactor of Little Elongation Complex ELL Subunit* 1 (ICE1) gene also controls overall male fertility in cattle (Wei *et al*., 2018). *Regulatory Factor X6* (*RFX6*) gene relates with having large birth weight (Cole *et al*., 2014). *Nucleophosmin* (*NPM1*) gene encodes a multifunctional nucleolar phosphoprotein that plays a key role in controlling various aspects of cell growth and homeostasis and as a candidate gene for growth traits in cattle (Huang *et al*., 2010).

An important gene called *Agouti Signaling Protein (ASIP)* linked to coat color and skin pigmentation (Norris, 2008; Hubbard *et al*., 2010; Wang *et al*., 2016; Purfield *et al*., 2017; Guo *et al*., 2019a) was under strong selection in the Raya cattle. This gene is essential for preventing skin damage from excessive exposure to heat and sun, and hence it has been considered an innate sunscreen to fight ultraviolet (UV) (Ali *et al*., 2018). This gene (*ASIP*) is also essential for feed efficiency, particularly in obesity in beef steers (Kern *et al*., 2016). *Relaxin Family Peptide Receptor 2* (*RXFP2*), a vital gene known for its impact on horn status, was explicitly under strong positive selection in the Raya cattle. It (*RXFP2*) has been suggested to be critical for developing the horns of goats and cattle and important to determine the size and presence of the horns of wild and domestic sheep (Randhawa *et al*., 2014; Randhawa *et al*., 2016; Gutiérrez-Gil *et al*., 2017). Apart from the role of size and presence of horns, the *RXFP2*gene was also reported to control horn type, development, and morphology (Pan *et al*., 2018; Ahbara *et al*., 2019; Liu *et al*., 2020). It (*RXFP2*) is a receptor for the relaxin and insulin-like factor 3 proteins that impact horn status and size depending on its biochemical interaction with testosterone. The strong selection of the specific gene (*RXFP2*) was correlated with the morphology of the Raya cattle, which was observed to have a variety of horns in size, shape and circumferences (Figure 10). The presence of horn varieties distinct from the other populations and a gene for horn performance particularly under selection in the Raya cattle can be directly linked to its adaptive variation as horns have the physiological importance of thermoregulation. The anatomical association of Horns' cores with the nasal heat exchange; made them to be crucial in preventing water loss by cooling air. Furthermore, horns play a role in grooming and self-care, allowing cattle to remove debris, itchiness, and parasites, thus contributing to cattle comfort and overall welfare (Dhaka *et al*., 2023).

Three genes, including *DNA damage-binding protein 1 (DDB1), Interleukin 17 B (IL17B)* and *Casein Kinase 1 Alpha 1 (CSNK1A1)* related to feed efficiency, were strongly selected in the Raya cattle. *DDB1* was reported to be associated with feed efficiency in cattle and other animals like domestic fowl and pigs (Leung-Pineda *et al*., 2009; Connor *et al*., 2010; Fox *et al*., 2012; Ribeiro *et al.,* 2012). It (*DDB)* was also reported to be important in residual feed intake (Seabury *et al.,* 2017) and to have a pleiotropic effect on growth and carcass quality traits in Rubia Gallega cattle (Martinez-Castillero*et al*., 2021). *IL17B* was reported to be over-expressed in cattle receiving low-energy diets (Linde, 2018). *CSNK1A1* relates to lipid metabolism (the degradation of lipids to satisfy the metabolic needs of the body (e.g., energy production)) in cattle (Li *et al*., 2022), probably during time of feed shortage.

The genes related to immune response that were under strong positive selection in the Raya cattle included *Proliferating cell nuclear antigen* (*PCNA*), *Interleukin 17 B* (*IL17B*, *Dual specificity phosphatase 1*(*DUSP1*), *Pleckstrin homology-like domain, family A, member 2 PHLDA2, FA Complementation Group G* (*FANCG*), *Valosin-containing protein* (*VCP*) and *WAPL Cohesin Release Factor* (*WAPL*) genes. *PCNA* has a crucial modulator of inflammatory responses (Wang *et al*., 2021b) and negatively regulates Toll-like receptor signaling pathways involved in innate host defense (Nguyen *et al*., 2020). *IL17B* prevents autoimmunity in African Kenana cattle (Pappu *et al.,* 2008). It (*IL17B*) has also an anti-inflammatory cytokine effect in the *IL-17* family (Reynolds *et al*., 2015) that play vital roles in the pathogenesis of inflammatory bowel disease (Zhang *et al.,* 2023). *DUSP1* associates with mitogen-activated protein kinase (MAPK) signaling pathway (Campos *et al*., 2019) and considered a key regulator of the immune response through its role in the dephosphorylation and inactivation of mitogen-activated protein kinases (MAP kinases) (O'Gorman *et al*., 2009). *FANCG* is important in maintaining the genome, in DNA repair (Castellanos *et al.,* 2014) and in protecting the 17 mitochondria from oxidative stress (Bose *et al*., 2020). *PHLDA2* and *WAPL* were also reported to be associated with immune modulation (Sigdel *et al*., 2021) and with "cohesin's DNA releasing factor, regulating 3D chromatin architecture in cattle (Sun *et al*., 2021) respectively. *VCP* that belongs to the type II AAA (ATPases associated with diverse cellular activities) family and involved in ubiquitinated protein degradation that particularly controls several immunity related functions including degradation, autophagy, lysosomal clearance and mitochondrial quality control (Scarian *et al*., 2022) and disrupting the VCP disease (a disease affecting muscle, bone and brain (Ju *et al*., 2009)

Apart the genes detected for ecological adaptive importance mentioned above, several genes related to meat production and quality traits were under strong selection in Raya cattle including *CCCTC-Binding Factor* (*CTCF*)*, Adrenocortical dysplasia* (*ACD*)*, Neuritin 1 Like* (*NRN1L*)*, Dipeptidase 3 (DPEP3), Proteasome 20S Subunit Beta 10* (*PSMB10*)*, Nuclear transport factor 2* (*NUTF2*)*, Par-6 family cell polarity regulator alpha* (*PARD6A*) and *Solute Carrier Family 12 Member 4* (*SLC12A4*) related (Marín-Garzón *et al*., 2021) which agrees with its historical meaning, and could further indicate the production value of the Raya cattle as meat type breed.

Ended out of the genes detected in cattle populations inhabited the moisture stressed low lands of the Tigray National Regional State, few of them particularly related to reproductive performance and immune importance were under strong positive selection in Abergelle cattle. These included, *Hydroxy acyl glutathione Hydrolase* (*HAGH*) gene that involves in sperm motility, sperm morphology and post-testicular sperm maturation (Wang *et al*., 2021a). *Nucleoside diphosphate kinase 3* (NME3) gene that regulates energy requirements in neural development (Chen *et al*., 2018). *Essential Meiotic Structure-Specific Endonuclease Subunit 2* (*EME2*) gene important in DNA damage repair and maintaining genomic stability (Loyau *et al*., 2016). *Colony stimulating factor 1 receptor* (*CSF1R*) gene essential to provide instructions for making a protein called the colony-stimulating factor 1 receptor (*CSF-1* receptor). The signaling pathways stimulated by the *CSF-1* is important in cellular process like growth, division and maturation. It (*CSF1R*) gene plays an integral role in the differentiation and survival of macrophages (Achkova and Maher, 2016).

The presence of relatively few genes under strong selection in Abergelle cattle compared to the Begait and Raya cattle, where a lot of genes were detected to be under strong selection, particularly for heat stress, feed stress and genes that indicate the production value or type of the two population, Begait as milk breed and Raya as meat type breed can show the ease of natural selection pressure being exerted in Abergelle cattle showing the environmental variability within the broad category of the moisture stressed lowlands of the Tigray National Regional State. Further, the lack of genes being selected to indicate the productive value of the Abergelle cattle can show that this population (Abergelle) was not specifically selected for its milk or meat production.

5.4.2. Identified genes and their implication for adaptation to moisture stressed highlands

The Tigray highlands (Figure 9), where the Arado cattle were sampled, are different from most of the central Ethiopian highlands, which are ordinarily situated at high altitudes and receive plenty of rainfalls (with around 1088.65mm wet season rainfall) (Gheyas *et al*., 2021). The former is geographically high altitude but moisture-stressed and receives only around 620mm of annual rainfall. Under this category, essential genes, which are linked to its ecological niche, including *NADH Quinone Dehydrogenase 1* (*NQO1*), *NIMA Related Kinase 6* (*NEK6*), *LIM Homeobox 2* (*LHX2*), *uncoupling protein 2* (*UCP2*), *uncoupling protein 3* (*UCP3*) were strongly under selection for cold-related stress adaptation in Arado. The *NQO1* gene improves the H2O2 (Hydrogen peroxide) induced oxidative stress in cattle (Sun *et al*., 2019). It (*NQO1*) can also be involved in xenobiotic metabolism (Kern *et al*., 2016) to recognize chemical substances foreign to animal life. The genes *NEK6*, *UCP2* and *UCP3* are essential for adaptive response to hypoxia in cattle (De Donato *et al*., 2015; Ghoreishifar *et al*., 2020), a low oxygen content at the tissue level to meet the cells' metabolic needs. More importantly, *UCP2* and *UCP3* are crucial to uncoupling ATP production from mitochondrial respiration, and the uncoupling function leads to energy dissipation in the form of heat (Kowalewska-Łuczak *et al*., 2018). They (*UCP2* and *UCP3*) are also essential in adaptive thermogenesis (GO:1990845), a metabolic process where the body burns calories to produce heat. *UCP2* can further be expressed in a wide variety of tissues, including white adipose tissue, skeletal muscle and immune system tissues, affecting the production of reactive oxygen in different species (Schrauwen *et al*., 2002). *LHX2* is essential for secondary hair follicle development (Geng *et al*., 2014; Han *et al*., 2021), a crucial adaptive philology for animals adapted to cold environments. Moreover, a gene called *Leucine Carboxyl Methyltransferase 2* (*LCMT2*) related to feed tress adaptation was significantly under positive selection in Arado. It (*LCMT2*) was reported to be inversely changed in response to withdrawal with the body weight change (Gao *et al*., 2020).

However, five genes related to heat stress were under strong selection in Arado. These include *heat shock protein family D (Hsp60) member 1* (*HSPD1*), *heat shock protein family E (Hsp10) member 1 (HSPE1), Catenin Beta 1 (CTNNB1), DnaJ Heat Shock Protein Family (Hsp40) Member B13 (DNAJB13)* and *Coenzyme Q10B (COQ10B)* genes. *CTNNB1* exhibited the highest expression at 41°C after 24 h to 48 h of differentiation. However, it showed the lowest expression at 41°C after differentiation over five days (Guo *et al*., 2016), showing the importance of managing heat stress. *HSPE1* was reported to be essential for heat adaptation in Gyr cattle (Peripolli *et al*., 2018) and for regulating metabolic activity and survival in Humped cattle, adapted to hot environments (Kumar *et* *al*., 2015). *DNAJB13* was also reported to instruct heat shock proteins (Freitas *et al*., 2021) and *COQ10B* to regulate heat stress responses in cattle (Lee *et al.,* 2020). The presence of genes under strong positive selection, important for heat stress adaptation in the cattle population adapted to the moisture-stressed highlands, may indicate the correlations of some genes in different environmental challenges (Gheyas *et al*., 2021) or else these genes may have pleiotropic effect (affecting more than one characters simultaneously) or a condition when a gene affects the expression of several responses even if they may not be trait related (Vallejo-Trujillo *et al*., 2022). For instance, *HSPD1* was significantly enriched in different GO and KEGG pathways (Table S52). It *(HSPD1)* was significantly enriched in response to cold (GO:0009409), in response to Tuberculosis (bta05152) and in response to lipid and atherosclerosis (bta05417). Moreover, *HSPD1* and the other two *HSPE1* and *DNAJB13* were engaged in an essential molecular function called chaperone binding (GO:0051087) (Table S52), important in governing protein folding stress and recognizing in binding nonnative proteins and preventing unspecific aggregation (Beissinger and Buchner,1998). The *COQ10B* gene was important for cellular respiration (GO:0045333) and spermatogenesis (GO:0007283) (Table S52).

Several genes related to adaptive immunity and different multifunctional responses were under strong positive selection in Arado. These include *Nuclear Factor of Activated T Cells 5* (*NFAT5*) gene important for survival of immune cells and resisting inflammatory diseases (Lee *et al*., 2019). *RAS Like Family 11 Member B* (*RASL11B*) gene important to regulate the infection of an acute *Escherichia coli* strain in bovine mastitis infection (Dego *et al*., 2012). *ENSBTAG00000033806* (*LOC613401*) gene was significantly enriched in the pathway for necroptosis (bta04217), a very important function in initiating innate immunity (Yu *et al*., 2021). Expression of the *Nuclear factor erythroid 2-related factor 1* (*NFE2L1*) gene regulates antioxidant defense system and synthesis of proteasome enzymes (Lisse *et al*., 2016). It (*NFE2L1*) also reported protects from ferroptosis by sustaining proteasomal activity (Kotschi *et al*., 2022). *Pro-apoptotic WT1 regulator* (*PAWR*) involves in immune response (Endashaw *et al*., 2023). Genes *Splicing factor SF3B1* (*SF3B1*) and *AT-rich interaction domain 2* (*ARID2*) involve in cellular metabolism (Connor *et al*., 2010) and neuromuscular process (Shin *et al*., 2014). Particularly, *ARID2* is very essential to resist *Mycobacterium avium subspecies paratuberculosis,* Johne's disease in cattle (Brito *et al*., 2018). Johne's disease not only affects the health of the cattle up to death but also associates with other health problems such as lameness, mastitis and affects the overall cattle productivity by triggering poor productivity and reduced product efficiency (Orpin *et al*., 2020). It (*ARID2*) also important in making a protein involved with chromatin remodeling that is important for metabolic programming (Diniz *et al*., 2021). Moreover, it (*ARID2*) has a gene pleiotropy or expression abundance in sperm, a test for functional variants for the fertility of tropical bulls (Porto-Neto *et al*., 2023). Further all, the gene *Boule homolog* (*BOLL*) is important in the spermatogenesis of cattle-yak and yak (Mipam *et al*., 2023), and its deficiency was reported to cause a spermatogenic arrest and sperm maturation failure in many species (Nosková *et al*., 2020).

More importantly, the detection of genes that have a pleiotropic effect and genes that control multiple functions in the cattle population (Arado) that is adapted to moisture-stressed highlands in the Tigray National Regional State indicates the adaptation, maintenance, growth, productivity and reproduction performance of cattle populations in the glob that inhabited similar agroecological zones and the evolution and stability of their genomic landscape depended on the involvement of genes with specific or several functions and the interaction among them. Moreover, similar to that of the Abergelle cattle, no genes were strongly selected for specific production values (meat or milk) in the Arado cattle.

CHAPTER 6. CONCLUSIONS AND RECOMMENDATIONS

6.1. Conclusions

Through the comprehensive characterization of the morphology, ecological niche suitability, genome-wide genetic diversity, and the genomic response of selection to the environmental challenges of the indigenous cattle in Tigray (Abergelle, Arado, Begait, Erob and Raya), this study came up with the following key findings:

- The morphological characterization revealed the highest morphological distance between Begait and Erob or Abergelle and the shortest between Abergelle and Erob. It further discriminated into four different clusters of populations except for the Abergele and Erob cattle, which overlapped each other.
- The morphological valuation of the indigenous cattle in Tigray with previously reported indigenous cattle populations across different parties of Ethiopia exhibited diverse morphological characteristics different from those previously described and documented Ethiopian cattle populations. Similarly, some morphological traits observed in other Ethiopian cattle populations were not found in the population examined here. For instance, the diversified horn type and structure (Geraro, Korsuma, Genbo and Tulu) identified in this study were not reported. The convex (curved in) shaped face profile of the Raya cattle and the concave (curved out) face and roofy rump profile, large-sized navel flap, udder and teat of the Begait cattle were unique to the studied cattle populations compared to most of the indigenous cattle populations studied so far in different parts of Ethiopia. Besides, the white coat color, described in other parties of Ethiopia, was not common in the indigenous cattle in Tigray. As for the body frame parameters reported here (e.g., height at wither, height at rump, body length, chest depth and heart girth), the Begait cattle population in this study was the largest of all previously reported cattle populations in Ethiopia. In contrast, the Raya population was similar in size to most other Ethiopian cattle populations, while Arado, Abergelle and Erob were the smallest populations described so far in Ethiopia.

- The environmental niche characterization of the indigenous cattle in Tigray revealed distinct habitat suitability except for the Arado and Erob cattle, with around 66% niche similarity. It further sorted out six main environmental variables that could have a potential driving factor for the morphological and genetic variability observed among the indigenous cattle in Tigray. Based on the contribution level of the six environmental variables in characterizing the ecological niche for each population, four clusters of habitats were obtained, including Abergelle, Begait, Raya and an overlapped habitat for Arado and Erob. Moreover, the selected environmental variables significantly predicted the phenotypic differentiation among populations.
- The whole genome sequence-based characterization revealed high variation in genetic variants (SNPs and indels) within and across the indigenous cattle in Tigray, illustrating their rich genetic diversity. It also showed a substantial number of novel variants (SNPs and indels) in the indigenous cattle in Tigray, indicating their importance as a reservoir of genetic diversity previously uncharacterized. Around 1.5% to 2.1% of the total variants found to be private to respective populations; they might serve as important diagnostic markers. The analysis of the private variants further supported the morphological findings, particularly in the Begait cattle (which had the largest body size), a finding in agreement with the missense variants within genes linked to morphometric traits. Significantly enriched ($P < 0.05$) genes like *SCN4A* and *TAS1R2* associated with body height and *KCNG4* with traits like rump height, body length and chest depth were detected only in the Begait cattle. *MMRN2* and *VWC2* associated with meat juiciness and intramuscular fat content, one of the most essential meat qualities were also detected only in Erob cattle (where a relatively high number of Erob males were observed with large hump sizes, a trait known for meat quality), findings in agreement with the morphological findings. On the other side, all the indigenous cattle in Tigray shared highly significant GO and pathway terms associated with the sensory perception of smell expressed through overrepresented genes in the olfactory family with the olfactory and sensory perception of smell, mainly to search and differentiate feedstuffs. The length and

incidence of ROHs and genomic inbreeding coefficient analyses screened inbreed individuals in Raya and Begait cattle.

- Further, the relationship analysis of the whole genome sequence data showed a low taurine ancestry, with more than 85% coming from the indicine ancestry in the indigenous cattle in Tigray. Moreover, the indigenous cattle in Tigray, particularly the Erob and Begait cattle, manifested a unique local ancestry and shared with all non-taurine African cattle, including the population from other parts of Ethiopia (Afar, Fogera, Horro and Eth. Boran). This result was accompanied by the historical value of the Tigray Region as the ancient center of civilization in trading contacts with the ancient civilizations (the Fertile Crescent and Indus Valley) and a previous report which showed the earliest Archeological evidence indicating the Tigray national region state as a livestock routine, the whole genome sequence characterization findings of this study probably witnessed the early arrival of taurine cattle, followed by late introductions of indicine cattle in several migration waves, continuously enriched the genome landscape of the indigenous cattle in Tigray. The dendrogram based on genome-wide pairwise genetic differentiation analysis clustered the same five cattle populations into four groups, which is different from the morphologic clustering, where the Abergelle and Erob populations were separately grouped in a distinct genetic clade.
- The detection of signature selection in the indigenous cattle in Tigray resulted in many candidate genes putatively under selection in each population, revealing the importance of identifying key environmental variables before adaptation studies. For instance, no common genes were identified putatively under positive selection in the populations Abergelle and Raya even if they are traditionally categorized under similar agroecological zones (tepid sub-moist mid-highlands and warm sub-moist lowlands); the adaptive selection analysis supported ENM based habitat stratification. Important genes for adaptation to heat stress (*HELB*, *HMGA2*, *IRAK3*, *LLPH*, *UCN2* and *LOC101902172*) and feed stress (*ADAMTS16*, *DDB1*, *ASIP*, *IL17B*, *SNAP29*) were detected in one or the other cattle populations, Begait or Raya, linked to their ecological niche (moisture stressed lowlands of the Tigray Region). Further,

important genes were obtained for adaptation to cold stress (*NQO1*, *NEK6, LHX2*, *UCP*2 and *UCP3*) and feed stress (*LCMT2*) in the population (Arado) inhabited to the moisture-stressed highlands, a characteristic of its ecological niche.

- Several genes were detected that linked with the morphological findings. For instance, the gene *PAX3*, which has the functional importance of spotting white phenotype colors, was under strong positive selection in the Begait cattle; this is particularly characteristic of the coat color of the Begait cattle reported in the morphological finding. Two genes, *UCK1* and *BTRC*, important for lactation persistency, milk yield, and mammary gland development, were under strong selection in Begait, specifically characterized by a well-developed large udder and teat size in morphology. The gene *RXFP2*, known for its impact on horn status, type, development and morphology, was also under strong positive selection in the Raya cattle, a characteristic of horn diversity of the Raya cattle reported in the morphological finding. In addition, various genes (*CTCF, ACD, NRN1L, DPEP3, PSMB10, NUTF2, PARD6A* and *SLC12A4*) related to meat traits were under strong selection in the Raya cattle. However, no genes were detected to be under strong selection for any production values (milk or meat) neither in the Abergelle nor Arado cattle.

6.1. Recommendations

- In this analysis, the ARS-UCD1.2 taurine breed was used as a reference genome for aligning the genome of indigenous cattle in Tigray. However, the findings of this study revealed they are predominantly an indicine background, so further works should also consider re-analysis based on indicine reference genome to minimize subspecies ascertainment SNP biases.
- Long ROH and an intense inbreeding (>10%) were detected in a few Begait and Raya cattle, possibly resulting from consanguineous mating. So, these two populations may need special attention to maintain their within-population genetic diversity by creating farmers' awareness of breeding management.
- Apart from the low or highlands adaptation, the detection of several genes under strong

selection for feed tress in the indigenous cattle in Tigray detected by the signature selection analysis strongly agrees with the finding of several genes commonly over-represented in the indigenous cattle in Tigray detected by the functional analysis of private variants respective to each population are important pave showing the importance of considering feed efficiency traits; a critical adaptive diversity in the indigenous cattle in Tigray.

- The large body size, large teat, and well-developed and large udder size observed in the Begait cattle and the essential genes linked with body size, lactation persistency, milk yield, and mammary gland development detected explicitly in the Begait cattle and the genes associated with meat yield and quality traits specifically detected in the Raya cattle could pinpoint the imperative direction of a future selection for upgrading the two populations as milk and meat type breeds, respectively and conservation for the Abergelle and Arado for non-specialized multipurpose breeding objectives.
- The discriminant morphometric traits screened in the indigenous cattle in Tigray were strongly influenced by the main environmental variables selected by ENM. Some were also supported by the genomic analysis (for instance, in the Begait and Raya cattle), a possibility of these traits to be a preference for farmers too; so, farmers' preference should also be considered during conservation, breeding improvement and selection in the indigenous cattle in Tigray.
- The morphological and genomic diversity in the indigenous cattle in Tigray, for instance, the discrete morphological features observed in the Begait and Raya cattle and unique local ancestors observed in the Begait and Erob cattle which were not common in other Ethiopian cattle populations included in this study could reveal the importance of the indigenous cattle in Tigray as a reservoir of genetic diversity at a country level.
- Overall, the findings of this study strongly supported the effectiveness of ENM-based characterization of a particular species’ habitat to come up with an adequate characterization of its adaptive diversity, so adopting the detailed procedures followed in this study could improve similar research works in livestock species.

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8. SUPPLEMENTARY FILES

8.1. List of Publications

1. Multivariate characterization of phenotypic traits of five native cattle populations from Tigray, Northern Ethiopia. http://doi.org/10.1007/s11250-021-02652-z
2. Genome-wide diversity and admixture of five indigenous cattle populations from the Tigray region of northern Ethiopia. http://doi.org/10.3389/fgene.2023.1050365

8.2. Supplementary Figures

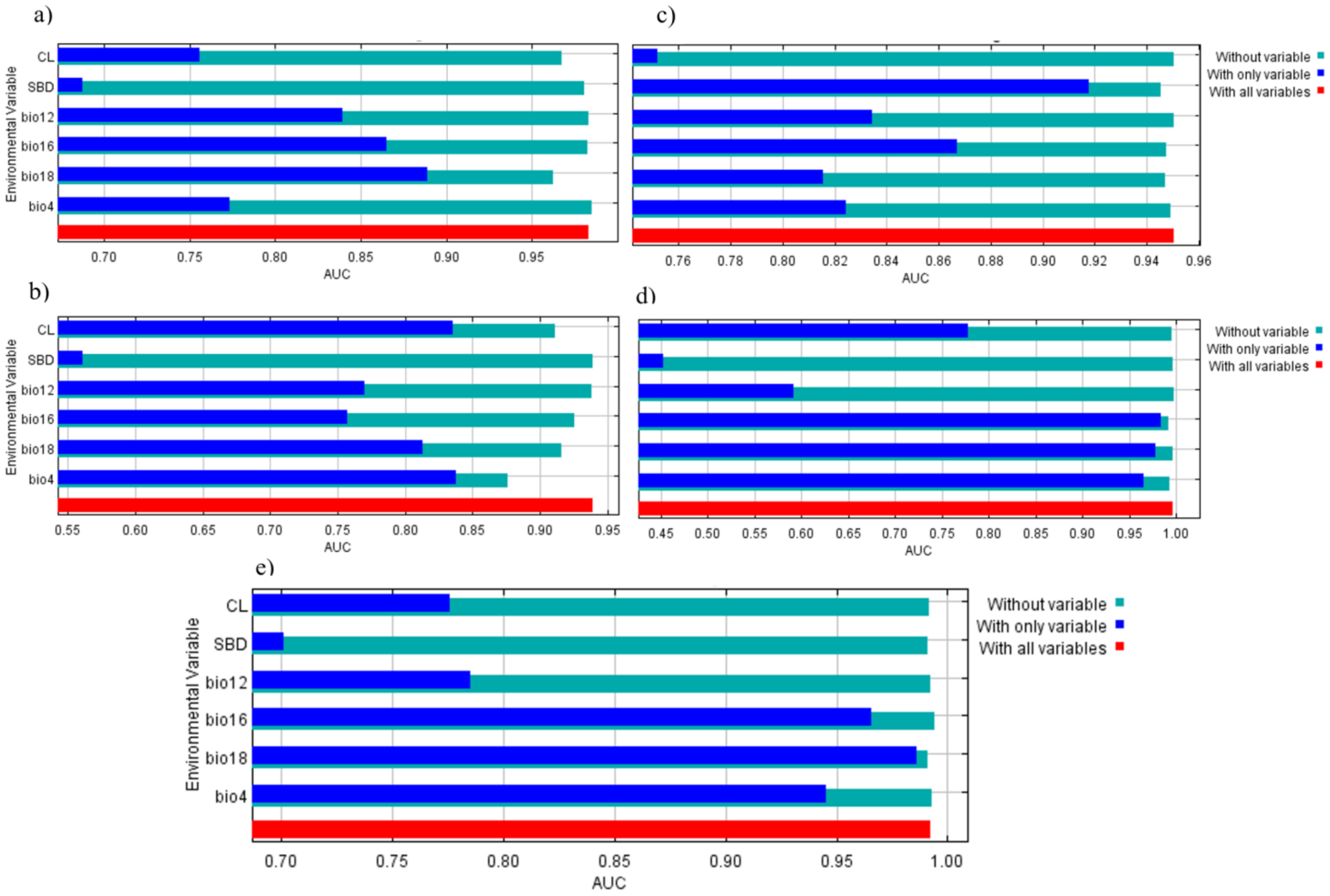

Figure S1. Jackknife of AUC for each indigenous cattle population of the Tigray region. Abergelle cattle (a), Arado cattle (b), Begait cattle (c), Erob cattle (d) and Raya cattle (e).

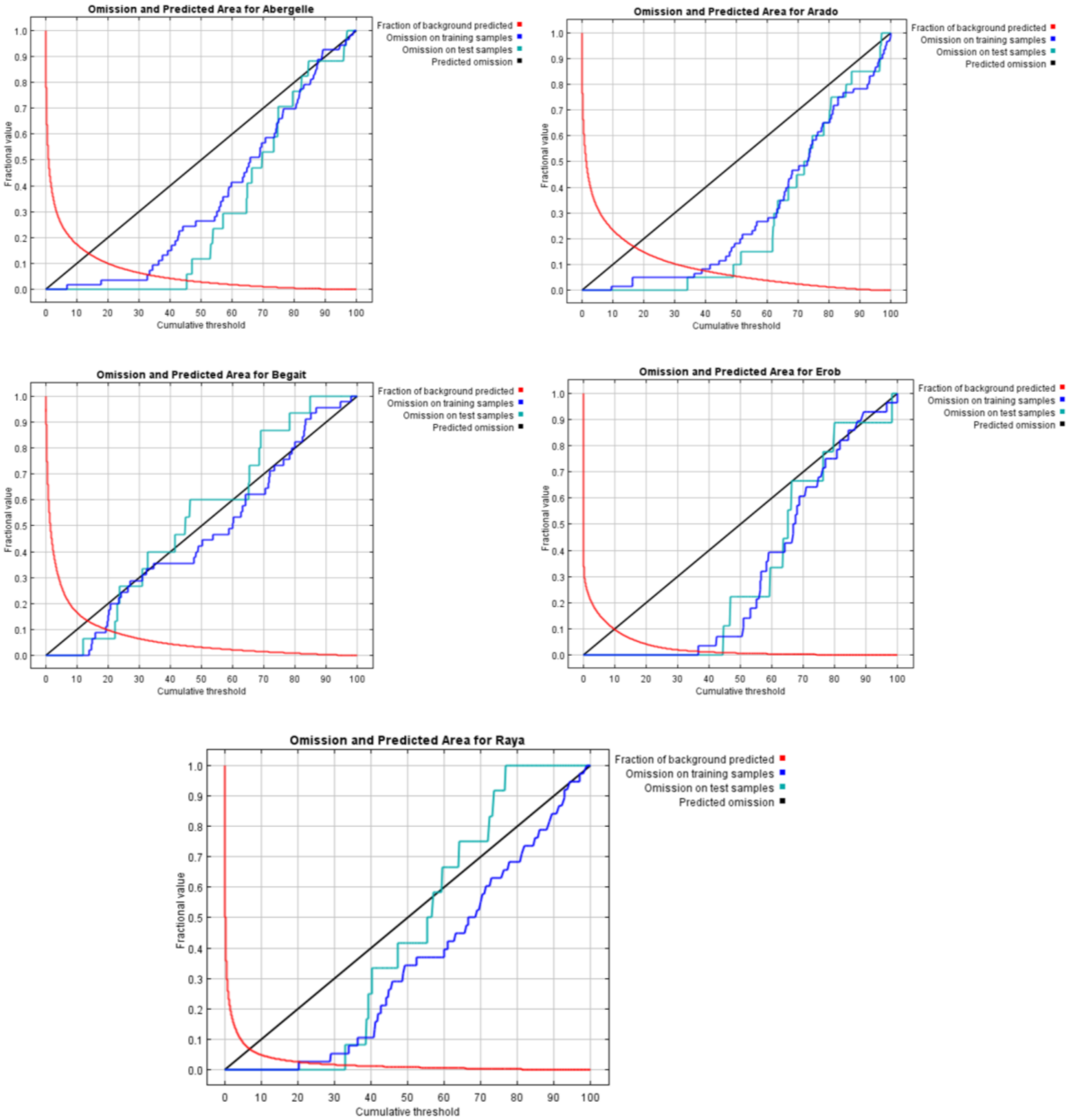

Figure S2. Omission rate and predicted area as a function of the cumulative threshold (Abergelle, Arado, Begait, Erob and Raya).

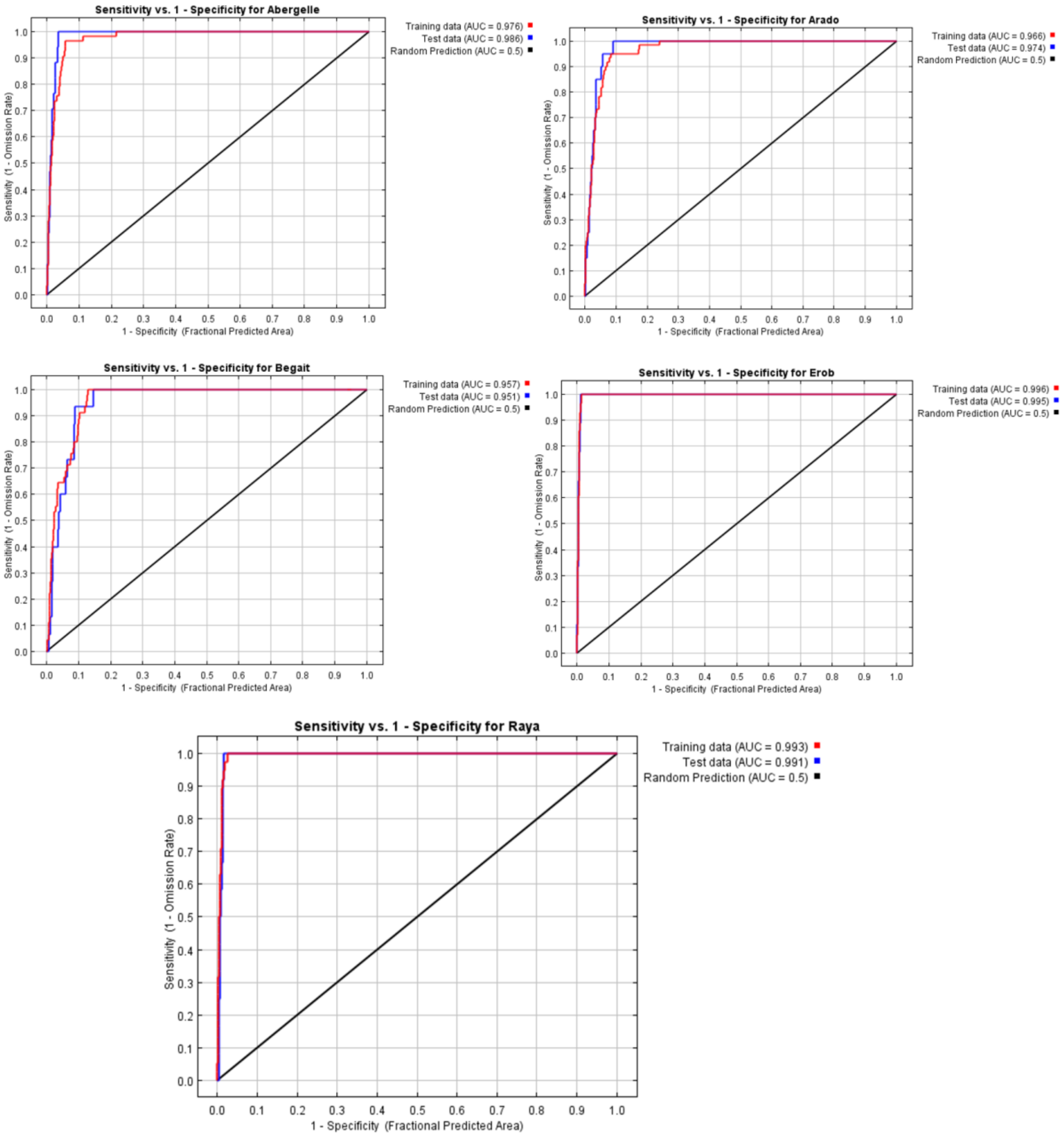

Figure S3. Area **U**nder the Receiving Operator **C**urve for training and test data for individual population (Abergelle, Arado, Begait, Erob and Raya).

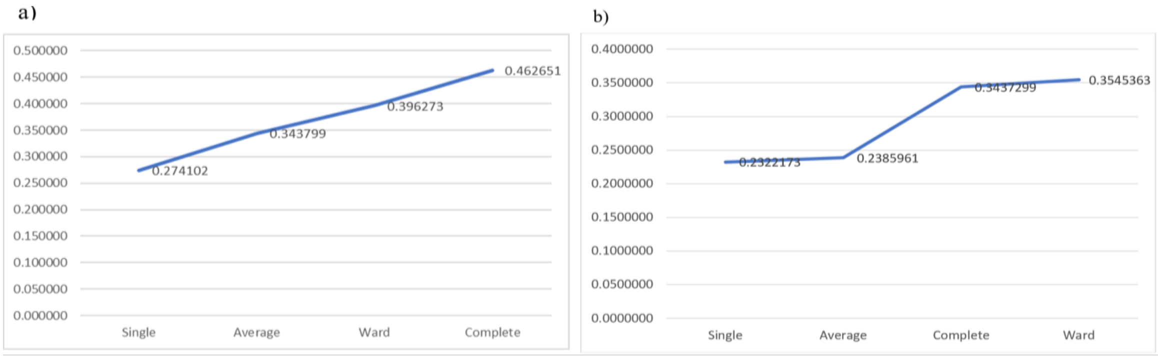

Figure S4. The agglomerative coefficients for clustering methods. (a) For correlation and (b) niche overlapping.

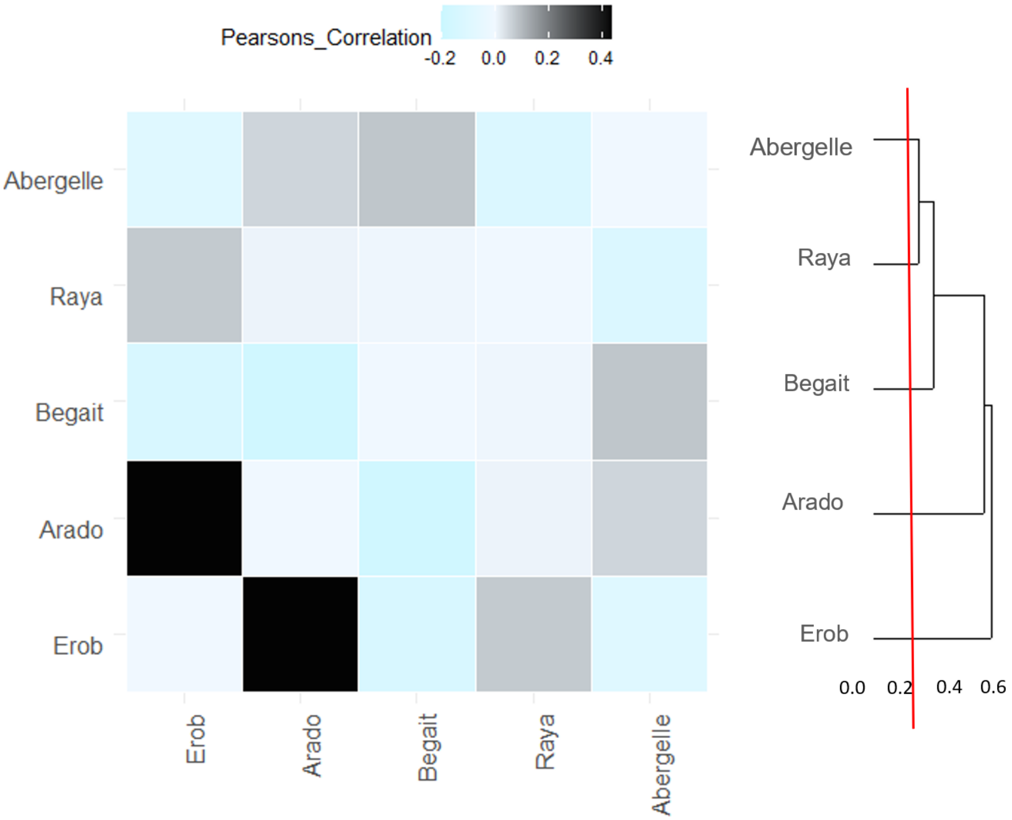

Figure S5. Dendrogram and heatmap of pairwise Pearson correlation test between suitability maps for individual populations (Correlation based Pairwise comparison of models for environmental niche definition.

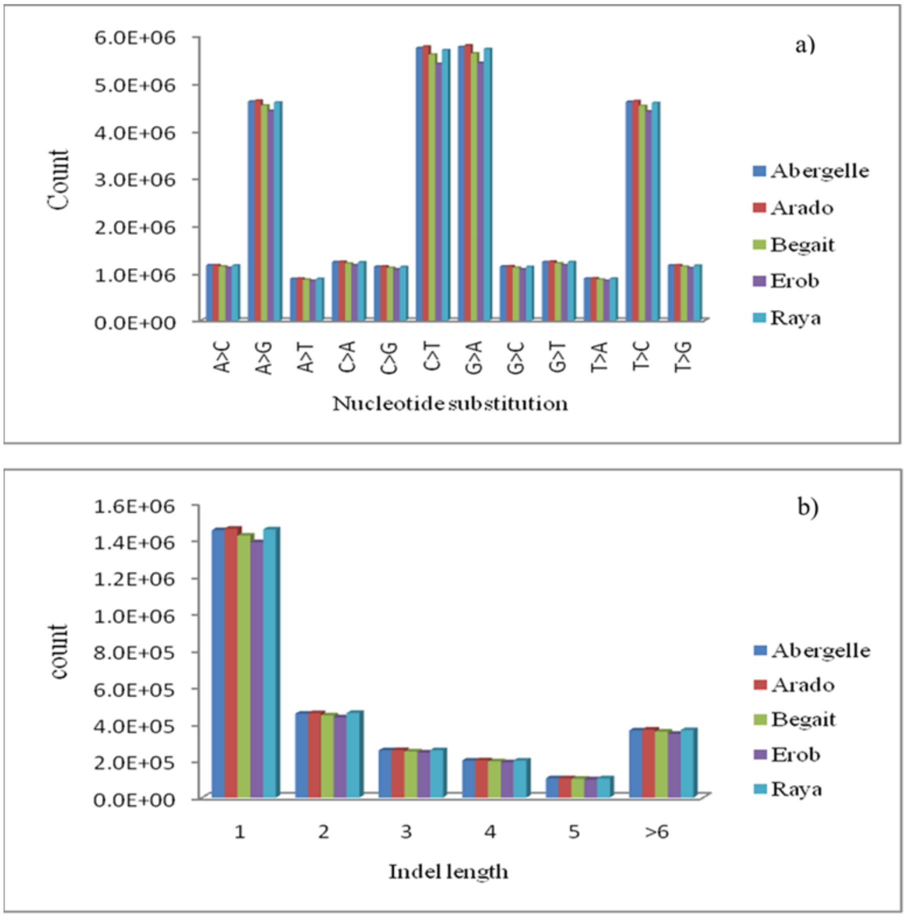

Figure S6. (a) Status of nucleotide substitution (A > C = substitution of Adenine by Cytosine, A > G = Adenine by Guanine, A > T = Adenine by Thymine, C > A = Cytosine by Adenine, C > G = Cytosine by Guanine, C > T = Cytosine by Thymine, G > A = Guanine by Adenine, G > C = Guanine by Cytosine G > T = Guanine by Thymine, T > A = Thymine by Adenine, T > C = Thymine by cytosine and T > G = Thymine by Guanine) across the indigenous cattle in Tigray and (b) Distribution of indel length across the genome of indigenous cattle in Tigray.

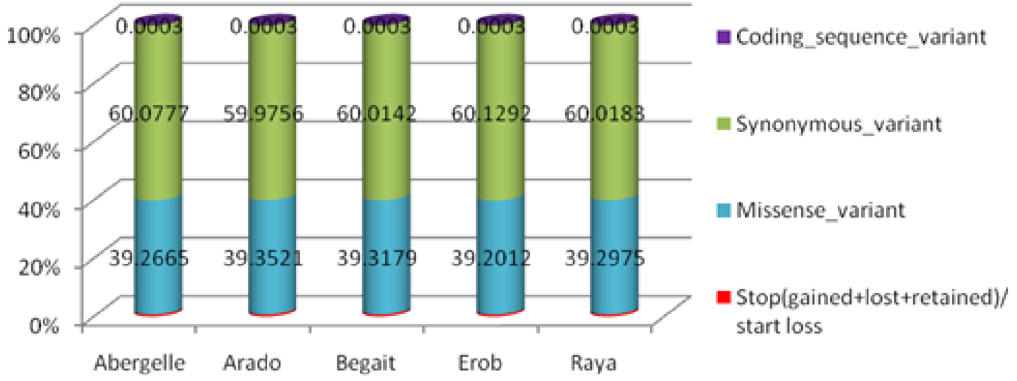

Figure S7. Showing the polymorphism consequences.

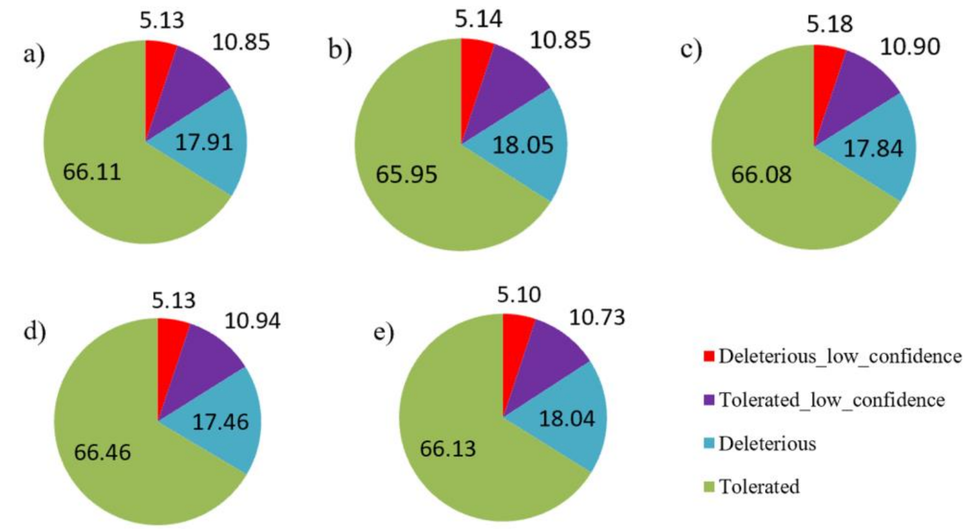

Figure S8. VEP based SIFT analysis for amino acid altering SNPs (%). (a) Abergelle, (b) Arado, (c), Begait, (d) Erob and (e) Raya.

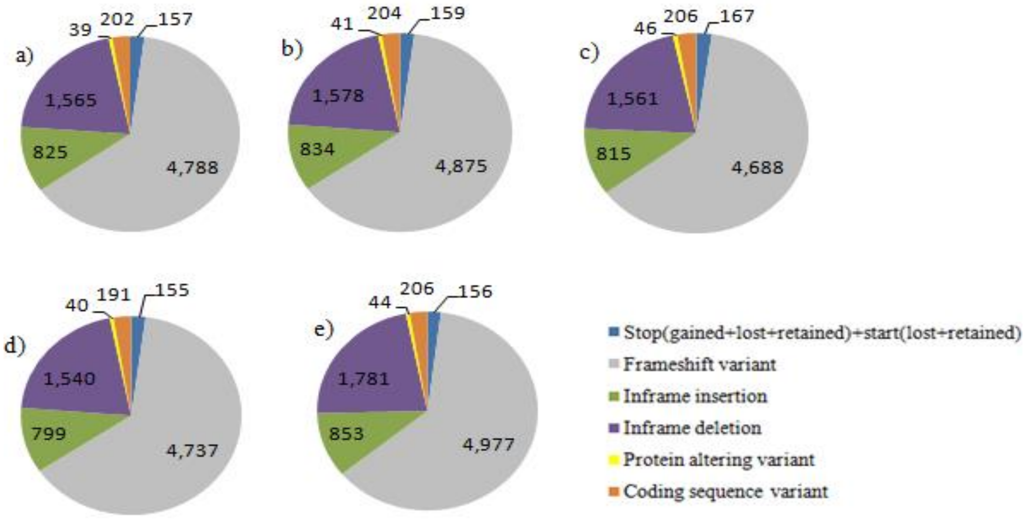

Figure S9. Indels with coding consequence. (a) Abergelle (b) Arado (c) Begait (d) Erob and (e) Raya.

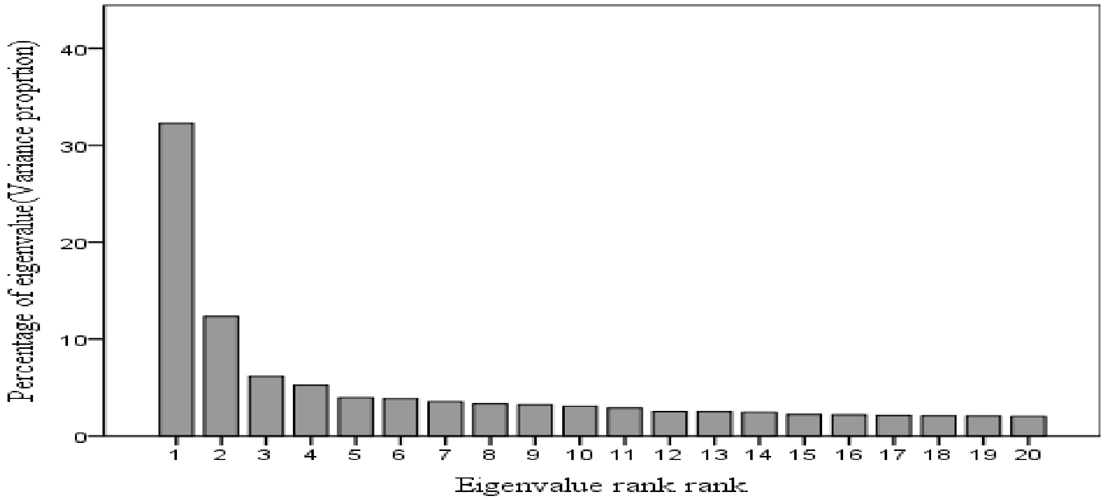

Figure S10. Proportion of variance explained by each principal component (1 to 20).

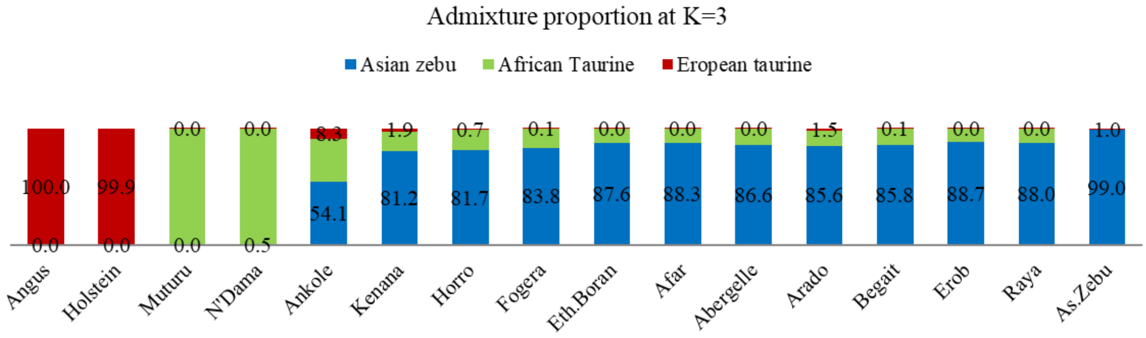

Figure S11. Indicine and taurine ancestry proportion (%) at K = 3 based on the Q (ancestry fractions) = 3.

8.2. Supplementary Tables

Table S1. Details of sampling sites and sample size for morphologic characterization of the indigenous cattle in Tigray.

	Sampling site	Sampled population	Sample size
1	Dr. Ataklti	Abergelle cattle	46
2	Geski mlesley	Abergelle cattle	46
3	Agbe	Abergelle cattle	46
4	Nebar hadnet	Abergelle cattle	46
5	Felege hiwot	Abergelle cattle	54
6	Lemlem	Abergelle cattle	46
7	Metkel limat	Abergelle cattle	46
8	Hadnet	Arado cattle	41
9	Negash	Arado cattle	42
10	Barka Adisebha	Arado cattle	42
11	Felegeweyni	Arado cattle	42
12	Mishing	Arado cattle	41
13	Emba ahferom	Arado cattle	41
14	Mirena	Arado cattle	41
15	Mysiyie	Arado cattle	40
16	Adabay	Begait cattle	55
17	Rawyan	Begait cattle	55
18	Mykadra	Begait cattle	55
19	Myweyni	Begait cattle	55
20	Mykuhli	Begait cattle	55
21	Badme	Begait cattle	55
22	Sobia	Erob cattle	80
23	Hayelom	Erob cattle	80
24	Dewhan	Erob cattle	85
25	Hagere Lekuma	Erob cattle	85
26	Warguba	Raya cattle	66
27	Mechere	Raya cattle	66
28	Hawelti	Raya cattle	66
29	Tio	Raya cattle	66
30	Selen wuha	Raya cattle	66
Total			1650

°C Annual temperature in degrees, *masl* meters above sea level, *mm* millimeter.

Table S2. Description of sampling sites used for suitability mapping of the indigenous cattle in Tigray.

Sampling site	Breeding area for	Latitude	Longitude	AT (°C)[1]	AR (mm)[2]	Elevation (masl)[3]
Dr. Ataklti	Abergelle cattle	13.658838	38.999575	21.7	703	1861
Geskimlesley	Abergelle cattle	13.692862	39.029837	21	690	1920
Agbe	Abergelle cattle	13.507318	39.061078	23.7	652	1479
Felegehiwot	Abergelle cattle	13.280274	38.840258	24.5	660	1292
Lemlem	Abergelle cattle	13.231711	39.015414	22.8	675	1646
Nebarhadnet	Abergelle cattle	13.118852	39.075798	22.9	654	1595
Metkellimat	Abergelle cattle	13.225166	39.176874	22.1	636	1752
Hadnet	Arado cattle	13.665492	39.669864	17.3	589	2272
Negash	Arado cattle	13.890208	39.602561	16.7	603	2355
Barkaadisebha	Arado cattle	13.803985	39.709430	15.9	598	2487
Felegeweyni	Arado cattle	13.902062	39.791273	14.4	601	2747
Mishing	Arado cattle	14.165556	39.207444	16.9	593	2323
EmbaAhferom	Arado cattle	14.234983	39.201965	16.3	579	2423
Mirena	Arado cattle	14.011558	38.646797	18.9	701	2072
Mysiyie	Arado cattle	14.136803	38.610493	17.9	699	2202
Adabay	Begait cattle	14.238897	36.851468	27.2	654	721
Rawyan	Begait cattle	14.154573	36.650330	28	644	633
Mykadra	Begait cattle	13.918810	36.544534	28	686	688
Myweyni	Begait cattle	14.099845	37.221322	26.6	712	887
Mykuhli	Begait cattle	14.212909	37.728453	26.4	720	1050
Badme	Begait cattle	14.733869	37.807847	27.24	683.2	1157
Sobia	Erob cattle	14.462218	39.492260	18.2	619	2130
Hayelom	Erob cattle	14.412668	39.505405	15.7	532	2567
Dewhan	Erob cattle	14.511637	39.556432	19.3	683	1932
Hagerelekuma	Erob cattle	14.495475	39.535967	19	708	1980
Warguba	Raya cattle	12.839231	39.748865	22.4	641	1651
Mechere	Raya cattle	12.758637	39.777378	22.8	655	1561
Hawelti	Raya cattle	12.850892	39.771827	22.6	631	1612
Tio	Raya cattle	12.521997	39.662444	23.1	715	1448
Selanewuha	Raya cattle	12.331403	39.682325	23	737	1389

[1] *AT* Annual temperature *in* degrees Celsius (*°C*)

[2] *AR* Annual rainfall in millimeter (*mm)*

[3] *masl* meters above sea level

Table S3. Tests of normality for female cattle populations’ quantitative traits.

Tests of normality for female cattle population quantitative traits							
breed name		Kolmogorov-Smirnov[a]			Shapiro-Wilk		
		Statistic	df	Sig.	Statistic	df	Sig.
Body height at withers	Begait	.049	300	.076	.993	300	.186
	Raya	.040	300	.200*	.992	300	.124
	Arado	.031	300	.200*	.995	300	.510
	Abergelle	.031	300	.200*	.995	300	.402
	Erob	.033	300	.200*	.995	300	.439
Body length	Begait	.039	300	.200*	.992	300	.110
	Raya	.036	300	.200*	.995	300	.388
	Arado	.028	300	.200*	.996	300	.608
	Abergelle	.036	300	.200*	.994	300	.266
	Erob	.039	300	.200*	.994	300	.230
Heart girth	Begait	.044	300	.200*	.991	300	.064
	Raya	.043	300	.200*	.995	300	.424
	Arado	.029	300	.200*	.995	300	.498
	Abergelle	.035	300	.200*	.995	300	.529
	Erob	.029	300	.200*	.994	300	.269
Muzzle circumference	Begait	.033	300	.200*	.994	300	.296
	Raya	.027	300	.200*	.995	300	.374
	Arado	.036	300	.200*	.994	300	.231
	Abergelle	.044	300	.200*	.991	300	.052
	Erob	.045	300	.200*	.997	300	.815
Neck length	Begait	.033	300	.200*	.996	300	.659
	Raya	.028	300	.200*	.996	300	.638
	Arado	.053	300	.044	.992	300	.120
	Abergelle	.034	300	.200*	.995	300	.399
	Erob	.034	300	.200*	.995	300	.466
Chest depth	Begait	.027	300	.200*	.996	300	.669
	Raya	.043	300	.200*	.994	300	.279
	Arado	.035	300	.200*	.996	300	.557
	Abergelle	.038	300	.200*	.994	300	.292
	Erob	.053	300	.041	.993	300	.167
Hock circumference	Begait	.038	300	.200*	.996	300	.562
	Raya	.039	300	.200*	.995	300	.446
	Arado	.030	300	.200*	.996	300	.584
	Abergelle	.029	300	.200*	.996	300	.741
	Erob	.044	300	.200*	.993	300	.219
Dewlap measurement	Begait	.035	300	.200*	.995	300	.366
	Raya	.040	300	.200*	.993	300	.141
	Arado	.040	300	.200*	.994	300	.351
	Abergelle	.043	300	.200*	.991	300	.051
	Erob	.031	300	.200*	.995	300	.425
Face measurement	Begait	.036	300	.200*	.996	300	.565
	Raya	.048	300	.090	.991	300	.051
	Arado	.043	300	.200*	.994	300	.260
	Abergelle	.032	300	.200*	.992	300	.098
	Erob	.043	300	.200*	.994	300	.250
Rump height	Begait	.036	300	.200*	.992	300	.106
	Raya	.035	300	.200*	.995	300	.396
	Arado	.035	300	.200*	.996	300	.555
	Abergelle	.033	300	.200*	.992	300	.096
	Erob	.035	300	.200*	.992	300	.082
Rump length	Begait	.038	300	.200*	.993	300	.153
	Raya	.046	300	.200*	.994	300	.283
	Arado	.026	300	.200*	.994	300	.241

Tests of normality for female cattle population quantitative traits							
breed name		Kolmogorov-Smirnov[a]			Shapiro-Wilk		
		Statistic	df	Sig.	Statistic	df	Sig.
	Abergelle	.040	300	.200*	.994	300	.314
	Erob	.050	300	.065	.992	300	.091
Pelvic width	Begait	.037	300	.200*	.995	300	.447
	Raya	.041	300	.200*	.995	300	.405
	Arado	.043	300	.200*	.995	300	.374
	Abergelle	.028	300	.200*	.996	300	.570
	Erob	.038	300	.200*	.993	300	.214
Upper horn spacing	Begait	.022	300	.200*	.996	300	.579
	Raya	.029	300	.200*	.996	300	.596
	Arado	.036	300	.200*	.992	300	.123
	Abergelle	.029	300	.200*	.995	300	.445
	Erob	.026	300	.200*	.994	300	.251
Lower horn spacing	Begait	.039	300	.200*	.993	300	.159
	Raya	.032	300	.200*	.995	300	.415
	Arado	.035	300	.200*	.996	300	.682
	Abergelle	.021	300	.200*	.995	300	.502
	Erob	.028	300	.200*	.994	300	.324
Horn length	Begait	.033	300	.200*	.992	300	.100
	Raya	.050	300	.070	.994	300	.245
	Arado	.026	300	.200*	.995	300	.502
	Abergelle	.042	300	.200*	.994	300	.313
	Erob	.032	300	.200*	.995	300	.356
Horn circumference at base	Begait	.029	300	.200*	.995	300	.400
	Raya	.033	300	.200*	.996	300	.548
	Arado	.042	300	.200*	.996	300	.547
	Abergelle	.036	300	.200*	.996	300	.718
	Erob	.036	300	.200*	.995	300	.408
Ear size	Begait	.038	300	.200*	.996	300	.673
	Raya	.038	300	.200*	.996	300	.569
	Arado	.041	300	.200*	.993	300	.188
	Abergelle	.040	300	.200*	.993	300	.216
	Erob	.045	300	.200*	.996	300	.618
Tail thickness at the base	Begait	.035	300	.200*	.997	300	.791
	Raya	.029	300	.200*	.996	300	.555
	Arado	.037	300	.200*	.995	300	.534
	Abergelle	.039	300	.200*	.992	300	.128
	Erob	.055	300	.028	.989	300	.027
Tail size	Begait	.036	300	.200*	.996	300	.617
	Raya	.048	300	.091	.993	300	.139
	Arado	.039	300	.200*	.994	300	.254
	Abergelle	.031	300	.200*	.998	300	.933
	Erob	.035	300	.200*	.994	300	.253
*. This is a lower bound of the true significance.							
a. Lilliefors Significance Correction							

Table S4. Tests of normality for male cattle populations' quantitative traits.

Tests of normality for male cattle population quantitative traits							
Breed name		Kolmogorov-Smirnov[a]			Shapiro-Wilk		
		Statistic	df	Sig.	Statistic	df	Sig.
Body height at withers	Begait	.097	30	.200*	.984	30	.921
	Raya	.089	30	.200*	.969	30	.513
	Arado	.130	30	.200*	.938	30	.081
	Abergelle	.129	30	.200*	.965	30	.403
	Erob	.131	30	.196	.968	30	.499
Body length	Begait	.136	30	.161	.934	30	.062
	Raya	.106	30	.200*	.964	30	.384
	Arado	.134	30	.179	.963	30	.367
	Abergelle	.157	30	.058	.950	30	.167
	Erob	.083	30	.200*	.980	30	.836
Heart girth	Begait	.104	30	.200*	.985	30	.929
	Raya	.083	30	.200*	.979	30	.791
	Arado	.092	30	.200*	.961	30	.324
	Abergelle	.100	30	.200*	.986	30	.952
	Erob	.138	30	.152	.972	30	.588
Muzzle circumference	Begait	.169	30	.029	.944	30	.118
	Raya	.124	30	.200*	.972	30	.604
	Arado	.072	30	.200*	.982	30	.887
	Abergelle	.122	30	.200*	.948	30	.151
	Erob	.152	30	.073	.957	30	.255
Neck length	Begait	.121	30	.200*	.965	30	.402
	Raya	.150	30	.082	.968	30	.488
	Arado	.105	30	.200*	.956	30	.251
	Abergelle	.131	30	.199	.973	30	.621
	Erob	.112	30	.200*	.968	30	.498
Chest depth	Begait	.117	30	.200*	.977	30	.732
	Raya	.091	30	.200*	.986	30	.954
	Arado	.108	30	.200*	.967	30	.471
	Abergelle	.084	30	.200*	.983	30	.903
	Erob	.121	30	.200*	.954	30	.213
Hock circumference	Begait	.106	30	.200*	.947	30	.138
	Raya	.116	30	.200*	.947	30	.137
	Arado	.129	30	.200*	.945	30	.123
	Abergelle	.102	30	.200*	.958	30	.272
	Erob	.161	30	.047	.937	30	.074
Dewlap measurement	Begait	.094	30	.200*	.983	30	.902
	Raya	.072	30	.200*	.983	30	.906
	Arado	.109	30	.200*	.969	30	.511
	Abergelle	.132	30	.195	.955	30	.226
	Erob	.101	30	.200*	.968	30	.488
Face measurement	Begait	.091	30	.200*	.971	30	.573
	Raya	.147	30	.096	.962	30	.342
	Arado	.123	30	.200*	.955	30	.224
	Abergelle	.155	30	.064	.948	30	.145
	Erob	.103	30	.200*	.962	30	.339
Rump height	Begait	.154	30	.067	.940	30	.093
	Raya	.116	30	.200*	.946	30	.130
	Arado	.102	30	.200*	.957	30	.255
	Abergelle	.101	30	.200*	.978	30	.763
	Erob	.133	30	.184	.933	30	.057
Rump length	Begait	.149	30	.086	.957	30	.259
	Raya	.069	30	.200*	.983	30	.888
	Arado	.087	30	.200*	.973	30	.623
	Abergelle	.114	30	.200*	.928	30	.043
	Erob	.142	30	.126	.954	30	.220
Pelvic width	Begait	.095	30	.200*	.966	30	.446
	Raya	.108	30	.200*	.971	30	.566

Tests of normality for male cattle population quantitative traits							
Breed name		Kolmogorov-Smirnov[a]			Shapiro-Wilk		
		Statistic	df	Sig.	Statistic	df	Sig.
	Arado	.106	30	.200*	.988	30	.976
	Abergelle	.085	30	.200*	.982	30	.867
	Erob	.085	30	.200*	.940	30	.091
Upper horn spacing	Begait	.078	30	.200*	.990	30	.993
	Raya	.147	30	.098	.963	30	.359
	Arado	.096	30	.200*	.972	30	.581
	Abergelle	.122	30	.200*	.951	30	.177
	Erob	.128	30	.200*	.957	30	.260
Lower horn spacing	Begait	.111	30	.200*	.985	30	.932
	Raya	.097	30	.200*	.967	30	.453
	Arado	.086	30	.200*	.970	30	.545
	Abergelle	.077	30	.200*	.980	30	.835
	Erob	.105	30	.200*	.966	30	.435
Horn length	Begait	.108	30	.200*	.937	30	.073
	Raya	.118	30	.200*	.970	30	.550
	Arado	.117	30	.200*	.966	30	.440
	Abergelle	.107	30	.200*	.973	30	.621
	Erob	.075	30	.200*	.965	30	.402
Horn circumference at base	Begait	.109	30	.200*	.976	30	.702
	Raya	.118	30	.200*	.975	30	.669
	Arado	.106	30	.200*	.946	30	.132
	Abergelle	.162	30	.044	.940	30	.089
	Erob	.121	30	.200*	.977	30	.750
Preputial length male	Begait	.197	30	.004	.933	30	.060
	Raya	.082	30	.200*	.992	30	.997
	Arado	.133	30	.186	.971	30	.556
	Abergelle	.110	30	.200*	.987	30	.967
	Erob	.180	30	.014	.947	30	.141
Scrotal circumference in bulls	Begait	.141	30	.133	.946	30	.130
	Raya	.128	30	.200*	.983	30	.891
	Arado	.122	30	.200*	.967	30	.469
	Abergelle	.100	30	.200*	.969	30	.523
	Erob	.101	30	.200*	.960	30	.316
Ear size	Begait	.106	30	.200*	.981	30	.860
	Raya	.107	30	.200*	.966	30	.446
	Arado	.130	30	.200*	.971	30	.580
	Abergelle	.128	30	.200*	.942	30	.102
	Erob	.093	30	.200*	.984	30	.910
Tail thickness at the base	Begait	.115	30	.200*	.972	30	.603
	Raya	.151	30	.080	.968	30	.491
	Arado	.110	30	.200*	.966	30	.426
	Abergelle	.115	30	.200*	.968	30	.475
	Erob	.140	30	.138	.964	30	.395
Tail size	Begait	.105	30	.200*	.947	30	.138
	Raya	.126	30	.200*	.960	30	.313
	Arado	.082	30	.200*	.980	30	.813
	Abergelle	.161	30	.046	.962	30	.341
	Erob	.111	30	.200*	.974	30	.648
*. This is a lower bound of the true significance.							
a. Lilliefors Significance Correction							

Table S5. Pearson’s correlations among measurements of the indigenous cattle in Tigray.

	HW	BL		PW	EL	TL	NL	HC	RH	RL	HG	CD	MC	DW	HTS	HL	HBC	HBS	FL	TBT	PS
HW		.83**		.80**	.63**	.76**	.82**	.64**	.76**	.77**	.75**	.68**	.71**	.23	.20	.28	.18	.38*	.16	.05	
BL	.77**			.74**	.64**	.71**	.77**	.60**	.71**	.70**	.71**	.62**	.64**	.25	.24	.34*	.25	.37*	.15	.03	
PW	.82**	.70**			.73**	.69**	.81**	.71**	.81**	.66**	.78**	.78**	.51**	.00	.02	.04	-.02	.33*	.13	.06	
EL	.68**	.58**		.65**		.58**	.68**	.61**	.69**	.55**	.65**	.68**	.43*	-.04	-.01	-.03	-.06	.28	.12	.05	
TL	.70**	.65**		.68**	.55**		.70**	.58**	.66**	.64**	.66**	.57**	.58**	.22	.21	.28	.19	.34*	.10	.03	
NL	.86**	.74**		.86**	.71**	.71**		.66**	.78**	.71**	.78**	.72**	.54**	.15	.15	.24	.16	.38*	.13	.16	
HC	.65**	.53**		.63**	.46*	.60**	.66**		.68**	.55**	.66**	.67**	.36*	-.03	-.02	.01	-.03	.27	.08	.03	
RH	.76**	.63**		.81**	.62**	.65**	.80**	.58**		.65**	.80**	.76**	.45*	.01	.01	.06	-.01	.33*	.14	.04	
RL	.81**	.74**		.69**	.58**	.62*	.72*	.61**	.61**		.67**	.56**	.58**	.25	.23	.37*	.23	.39*	.13	.05	
HG	.84**	.73**		.89**	.64**	.72**	.88**	.70**	.84**	.74**		.71**	.46*	.08	.09	.17	.09	.33*	.13	.03	
CD	.78**	.70**		.83**	.65**	.67**	.85**	.60**	.80**	.63**	.79**		.37*	-.14	-.10	-.14	-.18	.25	.12	.05	
MC	.76**	.72**		.57**	.50*	.59**	.63**	.57**	.49*	.72**	.59**	.53**		.32*	.29	.35*	.28	.28	.09	.03	
DW	.31*	.34*		.14	.07	.25	.17	.35*	.10	.41*	.19	.08	.58**		.46*	.64**	.61*	.16	.04	-.01	
HTS	.20	.28		.04	.03	.09	.09	.17	.02	.26	.07	.01	.38*	.63*		.60**	.51**	.13	.03	-.01	
HL	.26	.38*		.15	.03	.27	.17	.36*	.07	.44*	.20	.09	.48*	.82**	.58**		.74*	.23	.03	.02	
HBC	.12	.24		.03	-.09	.16	.03	.19*	.03	.26	.07	-.03	.37*	.75**	.51**	.78**		.17	.02	.02	
HBS	.46*	.41*		.45*	.36*	.37*	.44*	.36*	.40*	.50*	.48*	.44*	.44*	.26	.09	.22	.16		.05	.02	
FL	.18	.13		.22	.31*	.20	.23	.24	.26	.19	.28	.23	.09	-.04	-.01	-.05	-.05	.05		.01	
TBT	.05	.02		.07	.13	.02	.21	.08	.04	.05	.05	.05	.03	.05	.10	.03	.09	.07	.22		
PS	.35*	.2		.31*	.21	.20	.34*	.33*	.25	.25	.30*	.22	.34*	.23	.20	.24	.14	.12	.07	-.01	
SC	.65**	.62**		.66**	.51**	.63**	.68**	.57**	.69**	.63**	.74**	.65**	.61**	.44*	.27	.40	.30*	.39*	.21	.13	.30*

Values with**= Significant ($P < 0.01$), * =significant($P < 0.05$) *HW* height at withers, *BL* body length, *PW* pelvic width, *EL* ear length, *TL* tail length, *NL* neck length, *HC* hock circumference, *RH* rump height, *RL* rump length, *HG* heart girth, *CD* chest depth, *MC* muzzle circumference, *DW* dewlap width, *HTS* horn tip spacing, *HL* horn length, *HBC* horn base circumference, *HBS* horn base spacing, *FL* Face length, *TBT* tail base thickness, *PS* perpetual sheath, *SC* scrotal circumference.

Where: Above diagonal show correlation values for female and below diagonal for male cattle populations.

Table S6. Selected morphometric traits for predicting the effect of main environmental variable on phenotypic variability of the indigenous cattle in Tigray.

Variable entered	Partial R-Square	F-value	Pr> F	Wilk's lambda	Pr< lambda	Average Squared Canonical Correlation	Pr> ASCC
Female							
HW	0.9036	3503.73	<.0001	0.0964	<.0001	0.2259	<.0001
HL	0.8224	1729.18	<.0001	0.0171	<.0001	0.4296	<.0001
PW	0.4885	356.43	<.0001	0.0088	<.0001	0.5041	<.0001
MC	0.3833	231.80	<.0001	0.0054	<.0001	0.5637	<.0001
HG	0.2905	152.59	<.0001	0.0038	<.0001	0.5887	<.0001
HBC	0.2429	119.50	<.0001	0.0029	<.0001	0.6002	<.0001
NL	0.2247	107.91	<.0001	0.0023	<.0001	0.6115	<.0001
CD	0.1744	78.59	<.0001	0.0019	<.0001	0.6183	<.0001
BL	0.1111	46.44	<.0001	0.0017	<.0001	0.6237	<.0001
RH	0.1014	41.91	<.0001	0.0015	<.0001	0.6271	<.0001
Male							
HG	0.9401	569.05	<.0001	0.0599	<.0001	0.2350	<.0001
DW	0.8716	244.28	<.0001	0.0077	<.0001	0.4529	<.0001
HW	0.7117	88.25	<.0001	0.0022	<.0001	0.5762	<.0001
HL	0.5091	36.81	<.0001	0.0011	<.0001	0.6019	<.0001
NL	0.3143	16.16	<.0001	0.0007	<.0001	0.6343	<.0001
BL	0.2847	13.93	<.0001	0.0005	<.0001	0.6630	<.0001
RH	0.2445	11.25	<.0001	0.0004	<.0001	0.6898	<.0001
PW	0.1843	7.80	<.0001	0.0003	<.0001	0.6963	<.0001

Pr > F the probability level for the F statistic, *Pr < lambda* based on the F approximation to Wilks' lambda, *Pr > ASCC* based on the F approximation to Pillai's trace, *HW* height at withers, *HL* horn length, *PW* pelvic width, *MC* muzzle circumference, *HG* heart girth, *HBC* horn base circumference, *NL* neck length, *CD* chest depth, *BL* body length , *RH* rump height, *DW* dewlap width, *HTS* horn tip spacing, *TL* tail length, *RL* rump length, *HC* hock circumference, *EL* ear length, *TBT* tail base thickness, *HBS* horn base spacing.

Table S7. Extracted gDNA quality reports collected from indigenous cattle in Tigray.

Sample[1]	Sex	Population	Concentration in ng/uL	260/280	260/230
ABR02	F	Abergelle	65.729	1.8	2.28
ABR07	F	Abergelle	127.176	1.8	1.93
ABR10	M	Abergelle	105.025	1.75	2.16
ABR11	M	Abergelle	219.777	1.81	1.81
ABR12	F	Abergelle	50.37	1.75	1.92
ABR13	M	Abergelle	53.963	1.77	1.79
ABR14	F	Abergelle	61.672	1.76	1.84
ABR15	F	Abergelle	51.138	1.77	1.65
ABR16	M	Abergelle	55.075	1.89	2.19
ABR21	M	Abergelle	61.815	1.84	1.9
ABR29	F	Abergelle	62.386	1.78	1.77
AR01	F	Arado	55.65	1.77	1.8
AR05	F	Arado	53.691	1.83	1.83
AR06	F	Arado	74.482	1.74	2.05
AR10	M	Arado	62.199	1.85	2.37
AR11	M	Arado	60.315	1.81	1.96
AR13	F	Arado	89.223	1.83	2.05
AR23	F	Arado	86.414	1.75	2.15
AR24	F	Arado	83.777	1.77	1.97

AR30	F	Arado	71.169	1.79	2.1
AR31	F	Arado	51.697	1.78	1.87
AR32	M	Arado	66.633	1.81	1.97
BG01	F	Begait	59.349	1.75	2.19
BG02	F	Begait	58.854	1.75	1.98
BG05	F	Begait	54.813	1.79	1.74
BG07	F	Begait	51.566	1.77	1.75
BG13	F	Begait	98.864	1.77	2.07
BG15	M	Begait	157.242	1.8	2.06
BG17	F	Begait	58.33	1.77	1.99
BG19	F	Begait	59	1.7	2.02
BG20	F	Begait	59.508	1.76	2.11
BG21	F	Begait	171.389	1.79	1.9
BG31	F	Begait	78.96	1.78	2.11
ER01	M	Erob	92.316	1.78	2.11
ER04	F	Erob	73.308	1.77	2.02
ER06	M	Erob	174.752	1.83	2
ER07	M	Erob	64.94	1.81	2.48
ER10	F	Erob	100.854	1.87	2.29
ER11	F	Erob	330.196	1.74	1.94
ER13	F	Erob	209.48	1.8	2.04
ER15	F	Erob	96.342	1.82	1.94
ER17	M	Erob	417.424	1.81	1.95
ER18	F	Erob	249.471	1.85	2.04
RAY05	M	Raya	55.058	1.73	2.07
RAY06	M	Raya	53.533	1.77	2.03
RAY11	F	Raya	101.287	1.84	2.44
RAY17	F	Raya	337.08	1.83	2.14
RAY19	F	Raya	59.713	1.79	1.93
RAY21	F	Raya	52.713	1.73	2.07
RAY22	F	Raya	116.279	1.85	1.84
RAY23	F	Raya	62.256	1.75	2.12
RAY25	F	Raya	53.595	1.76	2.05
RAY26	F	Raya	87.681	1.78	1.83
RAY30	F	Raya	57.642	1.75	2.01

[1] ABR* Abergelle, RA* Arado cattle, BG * Begait, ER* Erob and RAY * Raya cattle.

Table S8. Description of publicly available data for reference populations used in this study.

Breed	Acronym	Land of origin	Number	Bio-project accession numbers
Afar	AFR	Ethiopia	10	PRJNA574857
Angus	AAN	Canada	10	PRJNA574857
Ankole	ANK	Uganda	10	PRJNA176557
Bhagnari (Asian zebu)	TBG	Pakistan	2	PRJNA312138
Cholistani (Asian zebu)	CHO	Pakistan	2	CNP0000189
Dhanni (Asian zebu)	DHA	Pakistan	2	CNP0000189
Eth.Boran	BOR	Ethiopia	10	CNP0000189
Fogera	FOG	Ethiopia	9	PRJNA574857
Holstein	HOL	Canada	10	PRJNA574857
Horro	HOR	Ethiopia	11	PRJNA176557
Kenana	KEN	Sudan	10	PRJNA574857
Muturu	MUT	Nigeria	10	PRJNA312138
N’Dama	NDA	Guinea	10	PRJNA386202
Sahiwal (Asian zebu)	SHW	Pakistan	2	PRJNA312138
Tharparkar (Asian zebu)	THP	Pakistan	2	CNP0000189
Total sample			110	

Table S9. Tests of Normality for each of the 33 environmental variables under considered for mapping and characterization of the environmental niches for the indigenous cattle in Tigray.

Environmental variables	Kolmogorov-Smirnov			Shapiro-Wilk		
	Statistic	df	Sig.	Statistic	df	Sig.
bio1	0.112	300	0	0.952	300	0
bio2	0.144	300	0	0.93	300	0
bio3	0.191	300	0	0.908	300	0
bio4	0.127	300	0	0.915	300	0
bio5	0.117	300	0	0.939	300	0
bio6	0.142	300	0	0.949	300	0
bio7	0.111	300	0	0.949	300	0
bio8	0.142	300	0	0.933	300	0
bio9	0.113	300	0	0.962	300	0
bio10	0.105	300	0	0.947	300	0
bio11	0.115	300	0	0.956	300	0
bio12	0.066	300	0.003	0.984	300	0.002
bio13	0.135	300	0	0.942	300	0
bio14	0.129	300	0	0.898	300	0
bio15	0.191	300	0	0.89	300	0
bio16	0.172	300	0	0.885	300	0
bio17	0.127	300	0	0.911	300	0
bio18	0.154	300	0	0.929	300	0
Elevation (bio elevation)	0.07	300	0.001	0.967	300	0
WVP_01	0.103	300	0	0.962	300	0
WVP_07	0.151	300	0	0.942	300	0
CL	0.21	300	0	0.8	300	0
Crop_D	0.31	300	0	0.759	300	0
Forest_C	0.08	300	0	0.975	300	0
Grass_C	0.206	300	0	0.816	300	0
CMI	0.242	300	0	0.801	300	0
Soil bulk density	0.043	300	.200*	0.984	300	0.002
Soil cation exchange capacity	0.147	300	0	0.839	300	0
Soil clay content	0.086	300	0	0.968	300	0
Soil organic content	0.102	300	0	0.835	300	0
Soil sand content	0.149	300	0	0.932	300	0
Soil silt content	0.082	300	0	0.977	300	0
Soil water	0.475	300	0	0.377	300	0

bio1 to bio11 temperature related environmental variables, *bio12 to bio18* precipitation variables, *WVP_01* water vapor pressure of the driest month (January is the driest month in Tigray, *WVP_07* water vapor pressure of the wettest month (July is the wettest month in Tigray) and land use variable (*Grass_C* grass land cover, *CMI* crop mask irrigation, *CL* cultivated land, *Fores_C* forest cover, *Crop_D* crop dominance.

Table S10. Spearman's correlation rank-order coefficients for the climatic and vegetation related environmental variables retrieved from the Tigray Region.

	bio1	bio2	bio3	bio4	bio5	bio6	bio7	bio8	bio9	bio10	bio11	bio12	bio13	bio14	bio15	bio16	bio17	bio18	bioelev	WVP_01	WVP_07
bio1	1.00	0.88	-0.21	0.58	0.98	0.99	0.82	0.98	0.99	1.00	0.99	0.58	0.34	-0.37	0.28	0.43	-0.36	-0.03	-0.99	0.83	0.98
bio2	0.88	1.00	-0.07	0.45	0.86	0.84	0.83	0.82	0.88	0.88	0.91	0.53	0.63	-0.58	0.58	0.68	-0.58	-0.21	-0.85	0.69	0.88
bio3	-0.21	-0.07	1.00	-0.77	-0.32	-0.28	-0.56	-0.32	-0.19	-0.24	-0.14	-0.12	0.26	0.16	0.18	0.00	0.16	-0.58	0.27	-0.16	-0.22
bio4	0.58	0.45	-0.77	1.00	0.65	0.63	0.80	0.66	0.56	0.60	0.51	0.27	-0.09	-0.20	-0.07	0.14	-0.20	0.40	-0.62	0.60	0.66
bio5	0.98	0.86	-0.32	0.65	1.00	0.99	0.88	0.99	0.98	0.99	0.97	0.60	0.31	-0.36	0.25	0.41	-0.36	0.05	-0.99	0.83	0.98
bio6	0.99	0.84	-0.28	0.63	0.99	1.00	0.83	0.99	0.98	0.99	0.97	0.59	0.27	-0.33	0.22	0.37	-0.32	0.05	-1.00	0.84	0.98
bio7	0.82	0.83	-0.56	0.80	0.88	0.83	1.00	0.83	0.81	0.84	0.80	0.50	0.36	-0.53	0.34	0.53	-0.52	0.11	-0.83	0.67	0.84
bio8	0.98	0.82	-0.32	0.66	0.99	0.99	0.83	1.00	0.97	0.98	0.96	0.54	0.21	-0.28	0.17	0.32	-0.28	0.09	-0.99	0.85	0.97
bio9	0.99	0.88	-0.19	0.56	0.98	0.98	0.81	0.97	1.00	0.99	0.99	0.61	0.35	-0.37	0.29	0.44	-0.37	-0.03	-0.99	0.83	0.98
bio10	1.00	0.88	-0.24	0.60	0.99	0.99	0.84	0.98	0.99	1.00	0.99	0.59	0.34	-0.36	0.28	0.42	-0.36	-0.01	-1.00	0.84	0.98
bio11	0.99	0.91	-0.14	0.51	0.97	0.97	0.80	0.96	0.99	0.99	1.00	0.58	0.42	-0.42	0.37	0.49	-0.42	-0.10	-0.98	0.80	0.98
bio12	0.58	0.53	-0.12	0.27	0.60	0.59	0.50	0.54	0.61	0.59	0.58	1.00	0.49	-0.23	0.28	0.49	-0.16	0.05	-0.59	0.57	0.55
bio13	0.34	0.63	0.26	-0.09	0.31	0.27	0.36	0.21	0.35	0.34	0.42	0.49	1.00	-0.68	0.92	0.92	-0.67	-0.62	-0.29	0.16	0.37
bio14	-0.37	-0.58	0.16	-0.20	-0.36	-0.33	-0.53	-0.28	-0.37	-0.36	-0.42	-0.23	-0.68	1.00	-0.82	-0.86	0.99	0.45	0.34	0.07	-0.38
bio15	0.28	0.58	0.18	-0.07	0.25	0.22	0.34	0.17	0.29	0.28	0.37	0.28	0.92	-0.82	1.00	0.92	-0.82	-0.68	-0.23	-0.01	0.31
bio16	0.43	0.68	0.00	0.14	0.41	0.37	0.53	0.32	0.44	0.42	0.49	0.49	0.92	-0.86	0.92	1.00	-0.85	-0.53	-0.38	0.11	0.44
bio17	-0.36	-0.58	0.16	-0.20	-0.36	-0.32	-0.52	-0.28	-0.37	-0.36	-0.42	-0.16	-0.67	0.99	-0.82	-0.85	1.00	0.46	0.33	0.08	-0.38
bio18	-0.03	-0.21	-0.58	0.40	0.05	0.05	0.11	0.09	-0.03	-0.01	-0.10	0.05	-0.62	0.45	-0.68	-0.53	0.46	1.00	-0.04	0.22	-0.05
bioelev	-0.99	-0.85	0.27	-0.62	-0.99	-1.00	-0.83	-0.99	-0.99	-1.00	-0.98	-0.59	-0.29	0.34	-0.23	-0.38	0.33	-0.04	1.00	-0.85	-0.98
WVP_01	0.83	0.69	-0.16	0.56	0.83	0.84	0.67	0.85	0.83	0.84	0.80	0.57	0.16	0.07	-0.01	0.11	0.08	0.22	-0.85	1.00	0.83
WVP_07	0.98	0.88	-0.22	0.60	0.98	0.98	0.84	0.97	0.98	0.98	0.98	0.55	0.37	-0.38	0.31	0.44	-0.38	-0.05	-0.98	0.83	1.00

Climatic variables (*bio1 – bio11* temperature related variables, *bio12 - 18* precipitation variables, *bioelev* elevation, *WVP_01* water vapor pressure of the driest month (January is the driest month in Tigray, *WVP_07* water vapor pressure of the wettest month (July is the wettest month in Tigray).

Table S11. Spearman's correlation rank-order coefficients for the soil related environmental variables retrieved from the Tigray Region.

	SBD	SCaE	SClC	SOC	SpH	SSaC	SSiC
SBD	1.00	0.15	-0.18	-0.48	0.30	0.17	-0.02
SCaE	0.15	1.00	0.71	0.11	0.10	-0.70	0.55
SClC	-0.18	0.71	1.00	0.27	-0.11	-0.94	0.62
SOC	-0.48	0.11	0.27	1.00	-0.30	-0.20	0.03
SpH	0.30	0.10	-0.11	-0.30	1.00	0.03	0.14
SSaC	0.17	-0.70	-0.94	-0.20	0.03	1.00	-0.81
SSiC	-0.02	0.55	0.62	0.03	0.14	-0.81	1.00

SSaC soil sand content, *SOC* Soil organic content, *SSiC* Soil silt content, *SBD* soil bulk density, *SClC* Soil clay content, *SCaE* Soil cation exchange capacity and *SpH* soil pH.

Table S12. Spearman's correlation rank-order coefficients for the vegetation and land use related environmental variables retrieved from the Tigray Region.

	Cult_L	Crop_D	Forest_C	Grass_C	CMI
Cult_L	1.00	-0.32	-0.02	-0.85	-0.18
Crop_D	-0.32	1.00	0.19	0.10	-0.09
Forest_C	-0.02	0.19	1.00	-0.33	-0.01
Grass_C	-0.85	0.10	-0.33	1.00	0.19
CMI	-0.18	-0.09	-0.01	0.19	1.00

Grass_C Grass land cover, *CMI* Crop mask irrigation, *CL* Cultivated land, *Fores_C* Forest cover, *Crop_D* Crop dominance.

Table S13. ENMeval results for all combinations of features and beta multipliers resulted from the environmental variables retrieved from the Tigray Region.

No[1]	Settings	FC	BM	Train. AUC	Avg-test. AUC	Var-test. AUC	Avg-dif. AUC	Var-dif AUC	Avg-test.	Var-test or MTP	Avg.test. or10pct	Var.test.	AICc	Delta-AICc	W.AIC	Parameters
1	L_0.1	L	0.1	0.7652	0.7497	0.0226	0.0319	0.0139	0.0125	0.0007	0.1156	0.0059	6754.3	221.2	8.27E-49	31
2	Q_0.1	Q	0.1	0.7786	0.7633	0.0223	0.0330	0.0124	0.0094	0.0009	0.1250	0.0037	6729.2	196.1	2.31E-43	33
3	P_0.1	P	0.1	0.8659	0.8413	0.0106	0.0314	0.0071	0.0063	0.0002	0.1344	0.0028	7323.7	790.6	1.86E-172	184
4	H_0.1	H	0.1	0.9373	0.8944	0.0112	0.0365	0.0091	0.0094	0.0002	0.1781	0.0102	7879.6	1346.5	3.56E-293	165
5	LQ_0.1	LQ	0.1	0.7960	0.7779	0.0223	0.0317	0.0142	0.0031	0.0001	0.1313	0.0063	6744.7	211.6	9.96E-47	53
6	HQC_0.1	HQC	0.1	0.9353	0.8980	0.0138	0.0348	0.0097	0.0063	0.0002	0.1625	0.0049	7752.0	1218.9	1.84E-265	148
7	LQP_0.1	LQP	0.1	0.8737	0.8497	0.0101	0.0267	0.0078	0.0094	0.0004	0.1313	0.0045	7627.8	1094.7	1.69E-238	208
8	HQP_0.1	HQP	0.1	0.9344	0.8437	0.1703	0.0234	0.0047	0.0125	0.0005	0.1469	0.0052	8194.7	1661.6	0	184
9	L_0.5	L	0.5	0.7639	0.7489	0.0220	0.0308	0.0126	0.0094	0.0004	0.1000	0.0045	6754.1	221.0	9.16E-49	27
10	Q_0.5	Q	0.5	0.7729	0.7593	0.0229	0.0323	0.0136	0.0094	0.0009	0.1156	0.0033	6729.0	195.9	2.50E-43	29
11	P_0.5	P	0.5	0.8600	0.8382	0.0132	0.0307	0.0107	0.0063	0.0002	0.1344	0.0039	7132.0	598.9	7.65E-131	166
12	H_0.5	H	0.5	0.9372	0.9132	0.0033	0.0272	0.0032	0.0063	0.0002	0.1469	0.0052	7498.1	965.0	2.49E-210	129
13	LQ_0.5	LQ	0.5	0.7876	0.7714	0.0216	0.0303	0.0126	0.0125	0.0009	0.1219	0.0027	6751.2	218.1	3.79E-48	49
14	HQC_0.5	HQC	0.5	0.9341	0.9099	0.0041	0.0287	0.0041	0.0094	0.0004	0.1656	0.0065	7553.0	1019.9	3.02E-222	141
15	LQP_0.5	LQP	0.5	0.8632	0.8422	0.0116	0.0304	0.0089	0.0094	0.0004	0.1313	0.0049	7198.4	665.3	3.00E-145	176
16	HQP_0.5	HQP	0.5	0.9483	0.9069	0.0073	0.0323	0.0052	0.0094	0.0002	0.1813	0.0052	7486.3	953.2	8.99E-208	141
17	L_1	L	1	0.7605	0.7446	0.0225	0.0313	0.0125	0.0094	0.0009	0.1031	0.0052	6744.2	211.1	1.29E-46	21
18	Q_1	Q	1	0.7685	0.7563	0.0221	0.0311	0.0127	0.0094	0.0009	0.1125	0.0029	6730.8	197.7	1.05E-43	26
19	P_1	P	1	0.8496	0.8274	0.0120	0.0326	0.0103	0.0094	0.0002	0.1469	0.0030	7018.7	485.6	3.15E-106	139

No[1]	Settings	FC	BM	Train. AUC	Avg-test. AUC	Var-test. AUC	Avg-dif. AUC	Var-dif AUC	Avg-test.	Var-test or MTP	Avg.test. or10pct	Var.test.	AICc	Delta-AICc	W.AIC	Parameters
20	H_1	H	1	0.9240	0.9004	0.0051	0.0277	0.0046	0.0094	0.0002	0.1594	0.0068	7663.7	1130.6	2.67E-246	129
21	LQ_1	LQ	1	0.7808	0.7646	0.0218	0.0302	0.0126	0.0094	0.0009	0.1063	0.0046	6738.3	205.2	2.40E-45	40
22	HQC_1	HQC	1	0.9347	0.9046	0.0048	0.0257	0.0042	0.0063	0.0002	0.1656	0.0065	7658.4	1125.3	3.84E-245	134
23	LQP_1	LQP	1	0.8602	0.8322	0.0152	0.0307	0.0112	0.0063	0.0002	0.1406	0.0035	6979.0	445.9	1.34E-97	146
24	HQP_1	HQP	1	0.9373	0.9118	0.0040	0.0269	0.0034	0.0125	0.0003	0.1719	0.0063	7718.5	1185.5	3.36E-258	154
25	L_1.5	L	1.5	0.7538	0.7408	0.0220	0.0313	0.0119	0.0094	0.0009	0.1031	0.0052	6754.0	220.9	9.60E-49	21
26	Q_1.5	Q	1.5	0.7656	0.7538	0.0220	0.0305	0.0123	0.0094	0.0009	0.1063	0.0024	6729.3	196.2	2.17E-43	22
27	P_1.5	P	1.5	0.8470	0.8185	0.0140	0.0324	0.0100	0.0031	0.0001	0.1313	0.0039	6872.8	339.7	1.51E-74	123
28	H_1.5	H	1.5	0.9160	0.8881	0.0087	0.0277	0.0070	0.0094	0.0002	0.1594	0.0051	6941.5	408.4	1.79E-89	125
29	LQ_1.5	LQ	1.5	0.7736	0.7618	0.0201	0.0292	0.0121	0.0094	0.0009	0.1031	0.0052	6734.8	201.7	1.37E-44	32
30	HQC_1.5	HQC	1.5	0.9115	0.8818	0.0103	0.0293	0.0081	0.0063	0.0002	0.1406	0.0070	6669.7	136.6	1.93E-30	123
31	LQP_1.5	LQP	1.5	0.8473	0.8186	0.0166	0.0346	0.0121	0.0031	0.0001	0.1375	0.0033	6922.8	389.7	2.05E-85	132
32	HQP_1.5	HQP	1.5	0.9280	0.9008	0.0064	0.0275	0.0052	0.0094	0.0002	0.1594	0.0057	7039.7	506.7	8.42E-111	155
33	L_2	L	2	0.7505	0.7360	0.0225	0.0321	0.0120	0.0094	0.0009	0.1031	0.0052	6760.1	227.0	4.36E-50	21
34	Q_2	Q	2	0.7631	0.7509	0.0217	0.0303	0.0121	0.0094	0.0009	0.1031	0.0026	6735.5	202.4	9.59E-45	22
35	P_2	P	2	0.8323	0.8096	0.0144	0.0329	0.0099	0.0063	0.0002	0.1156	0.0022	6813.6	280.5	1.08E-61	106
36	H_2	H	2	0.8943	0.8659	0.0112	0.0294	0.0082	0.0094	0.0002	0.1250	0.0054	6533.1	0.0	0.877266	93
37	LQ_2	LQ	2	0.7711	0.7561	0.0206	0.0303	0.0126	0.0094	0.0009	0.1031	0.0052	6743.1	210.0	2.24E-46	32
38	HQC_2	HQC	2	0.8851	0.8532	0.0161	0.0328	0.0120	0.0063	0.0002	0.1000	0.0047	6548.8	15.7	0.000348	95
39	LQP_2	LQP	2	0.8314	0.8124	0.0188	0.0333	0.0114	0.0063	0.0002	0.1219	0.0023	6890.2	357.1	2.48E-78	120
40	HQP_2	HQP	2	0.9139	0.8819	0.0076	0.0298	0.0067	0.0063	0.0002	0.1656	0.0054	6695.2	162.1	5.53E-36	137
41	L_2.5	L	2.5	0.7453	0.7317	0.0226	0.0323	0.0120	0.0063	0.0004	0.1063	0.0048	6771.0	237.9	1.90E-52	21
42	Q_2.5	Q	2.5	0.7594	0.7479	0.0215	0.0300	0.0118	0.0094	0.0009	0.1031	0.0024	6743.4	210.3	1.85E-46	22
43	P_2.5	P	2.5	0.8177	0.8039	0.0177	0.0335	0.0119	0.0063	0.0002	0.1219	0.0023	6830.8	297.7	1.94E-65	102

No[1]	Settings	FC	BM	Train. AUC	Avg-test. AUC	Var-test. AUC	Avg-dif. AUC	Var-dif AUC	Avg-test.	Var-test or MTP	Avg.test.or10pct	Var.test.	AICc	Delta-AICc	W.AIC	Parameters
44	H_2.5	H	2.5	0.8767	0.8475	0.0128	0.0305	0.0097	0.0094	0.0002	0.1156	0.0046	6574.1	41.0	1.12E-09	77
45	LQ_2.5	LQ	2.5	0.7677	0.7545	0.0211	0.0297	0.0123	0.0094	0.0009	0.1063	0.0053	6743.5	210.4	1.82E-46	29
46	HQC_2.5	HQC	2.5	0.8604	0.8336	0.0184	0.0334	0.0122	0.0063	0.0002	0.1031	0.0052	6537.0	3.9	0.122387	61
47	LQP_2.5	LQP	2.5	0.8296	0.7998	0.0221	0.0358	0.0143	0.0063	0.0002	0.1250	0.0026	6751.1	218.0	4.03E-48	89
48	HQP_2.5	HQP	2.5	0.8955	0.8605	0.0110	0.0316	0.0088	0.0031	0.0001	0.1406	0.0050	6619.0	85.9	1.93E-19	112
49	L_3	L	3	0.7412	0.7275	0.0232	0.0318	0.0119	0.0063	0.0004	0.1094	0.0044	6777.9	244.8	6.08E-54	20
50	Q_3	Q	3	0.7560	0.7440	0.0213	0.0297	0.0115	0.0094	0.0009	0.1000	0.0026	6748.8	215.7	1.26E-47	21
51	P_3	P	3	0.8203	0.7916	0.0170	0.0344	0.0121	0.0031	0.0001	0.1188	0.0015	6766.0	232.9	2.34E-51	88
52	H_3	H	3	0.8622	0.8343	0.0143	0.0308	0.0103	0.0094	0.0004	0.1219	0.0088	6611.5	78.4	8.13E-18	67
53	LQ_3	LQ	3	0.7631	0.7503	0.0211	0.0301	0.0123	0.0094	0.0009	0.1031	0.0044	6748.1	215.0	1.77E-47	27
54	HQC_3	HQC	3	0.8453	0.8216	0.0189	0.0332	0.0120	0.0125	0.0003	0.1156	0.0059	6574.7	41.6	7.93E-10	54
55	LQP_3	LQP	3	0.8168	0.7922	0.0185	0.0350	0.0122	0.0063	0.0002	0.1063	0.0022	6738.3	205.2	2.48E-45	77
56	HQP_3	HQP	3	0.8758	0.8450	0.0125	0.0327	0.0100	0.0063	0.0002	0.1281	0.0049	6655.6	122.5	2.22E-27	105
57	L_3.5	L	3.5	0.7352	0.7230	0.0238	0.0312	0.0119	0.0063	0.0004	0.1094	0.0035	6788.9	255.8	2.54E-56	19
58	Q_3.5	Q	3.5	0.7518	0.7395	0.0217	0.0298	0.0115	0.0063	0.0004	0.0969	0.0023	6758.0	224.9	1.26E-49	21
59	P_3.5	P	3.5	0.8045	0.7823	0.0171	0.0337	0.0122	0.0094	0.0002	0.1125	0.0020	6742.8	209.7	2.60E-46	70
60	H_3.5	H	3.5	0.8496	0.8251	0.0139	0.0297	0.0096	0.0094	0.0002	0.1219	0.0060	6627.6	94.5	2.67E-21	56
61	LQ_3.5	LQ	3.5	0.7596	0.7447	0.0218	0.0307	0.0124	0.0125	0.0016	0.1094	0.0040	6753.7	220.6	1.10E-48	26
62	HQC_3.5	HQC	3.5	0.8326	0.8099	0.0181	0.0324	0.0112	0.0125	0.0003	0.1188	0.0065	6599.8	66.7	2.82E-15	48
63	LQP_3.5	LQP	3.5	0.8023	0.7825	0.0194	0.0335	0.0131	0.0094	0.0002	0.1125	0.0024	6745.5	212.4	6.53E-47	71
64	HQP_3.5	HQP	3.5	0.8602	0.8343	0.0134	0.0320	0.0095	0.0063	0.0002	0.1250	0.0050	6638.6	105.5	1.08E-23	88
65	L_4	L	4	0.7319	0.7205	0.0239	0.0306	0.0115	0.0031	0.0001	0.1063	0.0031	6789.4	256.4	1.89E-56	16
66	Q_4	Q	4	0.7466	0.7339	0.0222	0.0300	0.0116	0.0063	0.0004	0.1031	0.0017	6769.0	235.9	5.32E-52	21
67	P_4	P	4	0.8003	0.7782	0.0176	0.0325	0.0116	0.0031	0.0001	0.1125	0.0018	6724.1	191.0	2.92E-42	60
68	H_4	H	4	0.8393	0.8133	0.0143	0.0302	0.0093	0.0094	0.0002	0.1188	0.0036	6663.9	130.8	3.50E-29	54

No[1]	Settings	FC	BM	Train. AUC	Avg-test. AUC	Var-test. AUC	Avg-dif. AUC	Var-dif AUC	Avg-test.	Var-test or MTP	Avg.test. or10pct	Var.test.	AICc	Delta-AICc	W.AIC	Parameters
69	LQ_4	LQ	4	0.7525	0.7392	0.0225	0.0310	0.0126	0.0063	0.0004	0.1000	0.0028	6773.1	240.0	6.57E-53	27
70	HQC_4	HQC	4	0.8202	0.7980	0.0179	0.0315	0.0105	0.0031	0.0001	0.1094	0.0037	6637.8	104.7	1.59E-23	47
71	LQP_4	LQP	4	0.7982	0.7790	0.0203	0.0330	0.0137	0.0063	0.0002	0.1063	0.0024	6718.0	184.9	6.18E-41	56
72	HQP_4	HQP	4	0.8526	0.8217	0.0132	0.0319	0.0100	0.0031	0.0001	0.1250	0.0041	6625.6	92.5	7.27E-21	75
73	L_4.5	L	4.5	0.7304	0.7195	0.0239	0.0302	0.0113	0.0031	0.0001	0.1094	0.0029	6797.4	264.3	3.50E-58	18
74	Q_4.5	Q	4.5	0.7410	0.7298	0.0225	0.0296	0.0112	0.0063	0.0004	0.1031	0.0020	6778.0	244.9	5.73E-54	20
75	P_4.5	P	4.5	0.7863	0.7664	0.0195	0.0344	0.0138	0.0063	0.0002	0.1156	0.0020	6749.9	216.8	7.33E-48	58
76	H_4.5	H	4.5	0.8270	0.7997	0.0157	0.0306	0.0094	0.0125	0.0005	0.1250	0.0037	6693.1	160.0	1.59E-35	48
77	LQ_4.5	LQ	4.5	0.7473	0.7335	0.0227	0.0309	0.0123	0.0063	0.0004	0.1031	0.0033	6777.0	243.9	9.78E-54	24
78	HQC_4.5	HQC	4.5	0.8084	0.7849	0.0181	0.0311	0.0103	0.0063	0.0004	0.1125	0.0042	6663.9	130.8	3.41E-29	42
79	LQP_4.5	LQP	4.5	0.7886	0.7719	0.0198	0.0325	0.0131	0.0063	0.0002	0.1094	0.0037	6731.7	198.6	6.44E-44	54
80	HQP_4.5	HQP	4.5	0.8367	0.8109	0.0147	0.0328	0.0107	0.0031	0.0001	0.1156	0.0037	6642.9	109.8	1.24E-24	66
81	L_5	L	5	0.7296	0.7185	0.0238	0.0299	0.0112	0.0031	0.0001	0.1094	0.0029	6797.1	264.0	4.12E-58	17
82	Q_5	Q	5	0.7386	0.7280	0.0224	0.0292	0.0110	0.0031	0.0001	0.1000	0.0023	6782.4	249.3	6.55E-55	19
83	P_5	P	5	0.7817	0.7628	0.0185	0.0331	0.0123	0.0063	0.0002	0.1125	0.0024	6733.2	200.1	3.05E-44	49
84	H_5	H	5	0.8126	0.7854	0.0176	0.0313	0.0097	0.0125	0.0009	0.1313	0.0039	6722.3	189.2	7.29E-42	41
85	LQ_5	LQ	5	0.7437	0.7302	0.0230	0.0307	0.0123	0.0063	0.0004	0.1094	0.0027	6778.0	244.9	5.88E-54	21
86	HQC_5	HQC	5	0.7947	0.7728	0.0186	0.0303	0.0100	0.0063	0.0004	0.1125	0.0031	6699.5	166.4	6.60E-37	40
87	LQP_5	LQP	5	0.7831	0.7665	0.0215	0.0324	0.0130	0.0063	0.0002	0.1125	0.0033	6722.4	189.3	7.01E-42	44
88	HQP_5	HQP	5	0.8274	0.8011	0.0147	0.0324	0.0102	0.0031	0.0001	0.1156	0.0024	6670.4	137.3	1.33E-30	61
89	L_5.5	L	5.5	0.7288	0.7178	0.0238	0.0298	0.0110	0.0031	0.0001	0.1094	0.0029	6797.0	263.9	4.44E-58	16
90	Q_5.5	Q	5.5	0.7363	0.7268	0.0226	0.0289	0.0107	0.0031	0.0001	0.1000	0.0023	6783.8	250.7	3.20E-55	17
91	P_5.5	P	5.5	0.7743	0.7562	0.0207	0.0331	0.0132	0.0063	0.0004	0.1125	0.0024	6745.1	212.0	8.16E-47	45
92	H_5.5	H	5.5	0.7974	0.7727	0.0204	0.0313	0.0103	0.0094	0.0004	0.1313	0.0052	6734.2	201.1	1.88E-44	30
93	LQ_5.5	LQ	5.5	0.7417	0.7288	0.0227	0.0302	0.0118	0.0031	0.0001	0.1000	0.0028	6780.9	247.8	1.34E-54	20

No[1]	Settings	FC	BM	Train. AUC	Avg-test. AUC	Var-test. AUC	Avg-dif. AUC	Var-dif AUC	Avg-test.	Var-test or MTP	Avg.test. or10pct	Var.test.	AICc	Delta-AICc	W.AIC	Parameters
94	HQC_5.5	HQC	5.5	0.7838	0.7644	0.0188	0.0294	0.0097	0.0063	0.0004	0.1063	0.0026	6711.2	178.1	1.87E-39	32
95	LQP_5.5	LQP	5.5	0.7796	0.7624	0.0214	0.0326	0.0137	0.0031	0.0001	0.1125	0.0029	6719.1	186.0	3.61E-41	39
96	HQP_5.5	HQP	5.5	0.8168	0.7937	0.0163	0.0325	0.0106	0.0031	0.0001	0.1188	0.0032	6684.2	151.1	1.38E-33	56
97	L_6	L	6	0.7278	0.7170	0.0236	0.0297	0.0107	0.0031	0.0001	0.1156	0.0024	6799.1	266.0	1.51E-58	16
98	Q_6	Q	6	0.7351	0.7258	0.0225	0.0284	0.0105	0.0031	0.0001	0.1000	0.0023	6782.4	249.3	6.34E-55	15
99	P_6	P	6	0.7623	0.7461	0.0209	0.0334	0.0132	0.0063	0.0004	0.1094	0.0029	6747.3	214.2	2.68E-47	37
100	H_6	H	6	0.7855	0.7625	0.0226	0.0299	0.0114	0.0094	0.0004	0.1313	0.0058	6766.1	233.0	2.17E-51	31
101	LQ_6	LQ	6	0.7393	0.7276	0.0230	0.0299	0.0118	0.0031	0.0001	0.1031	0.0022	6785.3	252.3	1.47E-55	19
102	HQC_6	HQC	6	0.7765	0.7588	0.0185	0.0284	0.0093	0.0063	0.0004	0.1094	0.0031	6722.0	189.0	8.18E-42	29
103	LQP_6	LQP	6	0.7705	0.7570	0.0235	0.0329	0.0141	0.0031	0.0001	0.1031	0.0033	6739.5	206.4	1.34E-45	39
104	HQP_6	HQP	6	0.8116	0.7833	0.0170	0.0328	0.0111	0.0063	0.0002	0.1094	0.0040	6673.1	140.0	3.44E-31	47
105	L_6.5	L	6.5	0.7268	0.7160	0.0236	0.0297	0.0105	0.0031	0.0001	0.1125	0.0024	6801.7	268.6	4.19E-59	16
106	Q_6.5	Q	6.5	0.7339	0.7250	0.0225	0.0281	0.0103	0.0031	0.0001	0.1031	0.0024	6787.3	254.2	5.47E-56	16
107	P_6.5	P	6.5	0.7612	0.7400	0.0220	0.0342	0.0132	0.0063	0.0004	0.1063	0.0029	6744.7	211.6	1.00E-46	36
108	H_6.5	H	6.5	0.7757	0.7528	0.0212	0.0288	0.0106	0.0063	0.0002	0.1344	0.0041	6779.4	246.3	2.88E-54	26
109	LQ_6.5	LQ	6.5	0.7380	0.7268	0.0227	0.0294	0.0114	0.0031	0.0001	0.1063	0.0022	6787.0	253.9	6.51E-56	18
110	HQC_6.5	HQC	6.5	0.7696	0.7533	0.0183	0.0277	0.0090	0.0063	0.0004	0.1031	0.0024	6736.7	203.6	5.32E-45	28
111	LQP_6.5	LQP	6.5	0.7659	0.7519	0.0234	0.0325	0.0141	0.0063	0.0004	0.1031	0.0030	6737.1	204.0	4.38E-45	32
112	HQP_6.5	HQP	6.5	0.8002	0.7742	0.0182	0.0332	0.0116	0.0031	0.0001	0.1188	0.0032	6699.7	166.6	5.75E-37	45
113	L_7	L	7	0.7258	0.7148	0.0234	0.0298	0.0103	0.0063	0.0004	0.1156	0.0024	6802.1	269.0	3.36E-59	15
114	Q_7	Q	7	0.7329	0.7243	0.0223	0.0278	0.0100	0.0031	0.0001	0.1063	0.0026	6788.0	254.9	3.98E-56	15
115	P_7	P	7	0.7514	0.7336	0.0237	0.0330	0.0129	0.0031	0.0001	0.0938	0.0026	6758.0	224.9	1.27E-49	31
116	H_7	H	7	0.7621	0.7478	0.0196	0.0274	0.0094	0.0063	0.0002	0.1344	0.0041	6798.8	265.7	1.81E-58	26
117	LQ_7	LQ	7	0.7367	0.7260	0.0224	0.0289	0.0110	0.0031	0.0001	0.1031	0.0022	6792.4	259.3	4.39E-57	19

No[1]	Settings	FC	BM	Train. AUC	Avg-test. AUC	Var-test. AUC	Avg-dif. AUC	Var-dif AUC	Avg-test.	Var-test or MTP	Avg.test. or10pct	Var.test.	AICc	Delta-AICc	W.AIC	Parameters
118	HQC_7	HQC	7	0.7656	0.7499	0.0179	0.0266	0.0084	0.0063	0.0004	0.1031	0.0024	6741.3	208.2	5.40E-46	24
119	LQP_7	LQP	7	0.7581	0.7472	0.0240	0.0324	0.0136	0.0063	0.0004	0.0969	0.0031	6749.8	216.7	7.90E-48	30
120	HQP_7	HQP	7	0.7890	0.7684	0.0180	0.0317	0.0116	0.0094	0.0004	0.1156	0.0033	6710.6	177.5	2.51E-39	39
121	L_7.5	L	7.5	0.7247	0.7138	0.0233	0.0299	0.0101	0.0063	0.0004	0.1125	0.0026	6805.2	272.1	7.23E-60	15
122	Q_7.5	Q	7.5	0.7317	0.7231	0.0223	0.0279	0.0098	0.0063	0.0004	0.1063	0.0029	6790.9	257.8	8.96E-57	15
123	P_7.5	P	7.5	0.7453	0.7282	0.0237	0.0335	0.0129	0.0031	0.0001	0.1031	0.0028	6762.7	229.6	1.22E-50	27
124	H_7.5	H	7.5	0.7586	0.7444	0.0200	0.0277	0.0096	0.0063	0.0002	0.1344	0.0041	6801.4	268.3	4.75E-59	21
125	LQ_7.5	LQ	7.5	0.7359	0.7250	0.0223	0.0286	0.0108	0.0031	0.0001	0.1000	0.0023	6792.7	259.6	3.73E-57	18
126	HQC_7.5	HQC	7.5	0.7610	0.7469	0.0180	0.0261	0.0082	0.0063	0.0004	0.1031	0.0020	6751.5	218.4	3.23E-48	23
127	LQP_7.5	LQP	7.5	0.7582	0.7426	0.0244	0.0319	0.0138	0.0063	0.0004	0.1031	0.0030	6745.7	212.6	6.06E-47	27
128	HQP_7.5	HQP	7.5	0.7848	0.7628	0.0183	0.0313	0.0113	0.0063	0.0004	0.1188	0.0032	6711.5	178.5	1.56E-39	34
129	L_8	L	8	0.7235	0.7126	0.0232	0.0299	0.0099	0.0063	0.0004	0.1125	0.0026	6808.4	275.3	1.47E-60	15
130	Q_8	Q	8	0.7306	0.7220	0.0223	0.0280	0.0096	0.0063	0.0004	0.1063	0.0029	6791.8	258.7	5.77E-57	14
131	P_8	P	8	0.7384	0.7229	0.0249	0.0335	0.0133	0.0031	0.0001	0.1063	0.0026	6774.3	241.2	3.66E-53	26
132	H_8	H	8	0.7563	0.7420	0.0204	0.0275	0.0097	0.0063	0.0002	0.1250	0.0046	6810.6	277.5	4.89E-61	19
133	LQ_8	LQ	8	0.7345	0.7236	0.0224	0.0287	0.0108	0.0031	0.0001	0.1000	0.0023	6793.6	260.5	2.40E-57	17
134	HQC_8	HQC	8	0.7578	0.7442	0.0182	0.0258	0.0082	0.0063	0.0004	0.1063	0.0018	6765.0	231.9	3.91E-51	25
135	LQP_8	LQP	8	0.7530	0.7393	0.0248	0.0319	0.0139	0.0063	0.0004	0.1031	0.0022	6754.5	221.4	7.48E-49	24
136	HQP_8	HQP	8	0.7774	0.7574	0.0196	0.0310	0.0115	0.0063	0.0004	0.1188	0.0030	6732.7	199.6	3.90E-44	35
137	L_8.5	L	8.5	0.7223	0.7113	0.0230	0.0299	0.0097	0.0063	0.0004	0.1125	0.0026	6809.4	276.3	8.79E-61	14
138	Q_8.5	Q	8.5	0.7293	0.7208	0.0222	0.0280	0.0095	0.0063	0.0004	0.1094	0.0024	6795.2	262.1	1.09E-57	14
139	P_8.5	P	8.5	0.7330	0.7174	0.0261	0.0347	0.0137	0.0031	0.0001	0.1125	0.0026	6783.0	249.9	4.86E-55	24
140	H_8.5	H	8.5	0.7533	0.7400	0.0205	0.0276	0.0099	0.0063	0.0002	0.1250	0.0046	6825.2	292.1	3.33E-64	19
141	LQ_8.5	LQ	8.5	0.7333	0.7225	0.0225	0.0288	0.0107	0.0031	0.0001	0.0969	0.0025	6798.8	265.7	1.77E-58	18

No[1]	Settings	FC	BM	Train. AUC	Avg-test. AUC	Var-test. AUC	Avg-dif. AUC	Var-dif AUC	Avg-test.	Var-test or MTP	Avg.test. or10pct	Var.test.	AICc	Delta-AICc	W.AIC	Parameters
142	HQC_8.5	HQC	8.5	0.7549	0.7417	0.0182	0.0255	0.0082	0.0063	0.0004	0.1063	0.0018	6765.7	232.6	2.71E-51	22
143	LQP_8.5	LQP	8.5	0.7487	0.7363	0.0254	0.0317	0.0144	0.0063	0.0004	0.1125	0.0020	6765.3	232.2	3.40E-51	25
144	HQP_8.5	HQP	8.5	0.7731	0.7520	0.0204	0.0315	0.0116	0.0063	0.0004	0.1219	0.0031	6732.3	199.2	4.81E-44	30
145	L_9	L	9	0.7209	0.7098	0.0229	0.0301	0.0096	0.0094	0.0009	0.1156	0.0026	6812.9	279.8	1.51E-61	14
146	Q_9	Q	9	0.7281	0.7196	0.0223	0.0280	0.0093	0.0063	0.0004	0.1125	0.0022	6798.6	265.5	1.97E-58	14
147	P_9	P	9	0.7276	0.7141	0.0260	0.0341	0.0131	0.0031	0.0001	0.1125	0.0033	6791.3	258.2	7.67E-57	23
148	H_9	H	9	0.7520	0.7372	0.0204	0.0277	0.0098	0.0063	0.0002	0.1250	0.0048	6833.1	300.0	6.15E-66	17
149	LQ_9	LQ	9	0.7323	0.7213	0.0224	0.0288	0.0106	0.0031	0.0001	0.0969	0.0025	6800.0	266.9	9.53E-59	17
150	HQC_9	HQC	9	0.7520	0.7392	0.0185	0.0257	0.0081	0.0063	0.0004	0.1094	0.0020	6768.5	235.4	6.77E-52	20
151	LQP_9	LQP	9	0.7464	0.7341	0.0247	0.0318	0.0141	0.0094	0.0009	0.1031	0.0017	6766.0	232.9	2.30E-51	22
152	HQP_9	HQP	9	0.7680	0.7475	0.0208	0.0314	0.0120	0.0063	0.0004	0.1156	0.0030	6735.6	202.5	9.14E-45	26
153	L_10	L	10	0.7181	0.7066	0.0226	0.0301	0.0094	0.0125	0.0016	0.1156	0.0028	6820.7	287.6	3.04E-63	14
154	Q_10	Q	10	0.7253	0.7170	0.0224	0.0281	0.0090	0.0125	0.0016	0.1063	0.0029	6803.7	270.6	1.56E-59	13
155	P_10	P	10	0.7227	0.7094	0.0264	0.0330	0.0129	0.0031	0.0001	0.1156	0.0033	6798.4	265.3	2.20E-58	21
156	H_10	H	10	0.7447	0.7321	0.0194	0.0281	0.0091	0.0063	0.0002	0.1219	0.0044	6858.4	325.3	2.02E-71	15
157	LQ_10	LQ	10	0.7290	0.7188	0.0223	0.0288	0.0102	0.0063	0.0004	0.1094	0.0024	6805.6	272.5	5.98E-60	16
158	HQC_10	HQC	10	0.7473	0.7333	0.0195	0.0266	0.0082	0.0125	0.0016	0.1125	0.0022	6774.4	241.3	3.51E-53	17
159	LQP_10	LQP	10	0.7434	0.7301	0.0253	0.0316	0.0142	0.0094	0.0009	0.1063	0.0020	6772.4	239.3	9.68E-53	21
160	HQP_10	HQP	10	0.7600	0.7412	0.0223	0.0318	0.0128	0.0063	0.0004	0.1156	0.0026	6754.9	221.8	6.12E-49	26
161	L_10.5	L	10.5	0.7166	0.7049	0.0225	0.0301	0.0093	0.0125	0.0016	0.1125	0.0031	6824.8	291.7	4.03E-64	14
162	Q_10.5	Q	10.5	0.7239	0.7156	0.0226	0.0282	0.0089	0.0125	0.0016	0.1125	0.0031	6807.0	273.9	2.96E-60	13
163	P_10.5	P	10.5	0.7206	0.7067	0.0266	0.0331	0.0128	0.0031	0.0001	0.1125	0.0029	6798.9	265.8	1.70E-58	19
164	H_10.5	H	10.5	0.7428	0.7299	0.0203	0.0281	0.0092	0.0063	0.0002	0.1188	0.0043	6867.2	334.1	2.46E-73	12
165	LQ_10.5	LQ	10.5	0.7276	0.7174	0.0225	0.0289	0.0102	0.0094	0.0009	0.1094	0.0024	6809.4	276.3	8.67E-61	16

No[1]	Settings	FC	BM	Train. AUC	Avg-test. AUC	Var-test. AUC	Avg-dif. AUC	Var-dif AUC	Avg-test.	Var-test or MTP	Avg.test. or10pct	Var.test.	AICc	Delta-AICc	W.AIC	Parameters
166	HQC_10.5	HQC	10.5	0.7444	0.7300	0.0200	0.0271	0.0082	0.0125	0.0016	0.1188	0.0026	6781.2	248.1	1.16E-54	17
167	LQP_10.5	LQP	10.5	0.7422	0.7291	0.0255	0.0317	0.0142	0.0063	0.0004	0.1031	0.0017	6774.1	241.0	4.02E-53	20
168	HQP_10.5	HQP	10.5	0.7580	0.7379	0.0226	0.0316	0.0126	0.0063	0.0004	0.1156	0.0026	6755.2	222.1	5.15E-49	23
169	L_11	L	11	0.7148	0.7033	0.0225	0.0301	0.0092	0.0125	0.0016	0.1094	0.0035	6829.4	296.3	4.03E-65	14
170	Q_11	Q	11	0.7224	0.7140	0.0227	0.0285	0.0089	0.0125	0.0016	0.1063	0.0031	6810.5	277.4	5.10E-61	13
171	P_11	P	11	0.7177	0.7039	0.0269	0.0332	0.0126	0.0031	0.0001	0.1125	0.0029	6806.9	273.8	3.02E-60	20
172	H_11	H	11	0.7409	0.7270	0.0204	0.0282	0.0093	0.0063	0.0002	0.1125	0.0033	6882.6	349.5	1.15E-76	12
173	LQ_11	LQ	11	0.7264	0.7159	0.0226	0.0290	0.0101	0.0125	0.0016	0.1125	0.0022	6810.6	277.5	4.74E-61	15
174	HQC_11	HQC	11	0.7419	0.7263	0.0206	0.0277	0.0083	0.0125	0.0016	0.1125	0.0026	6787.7	254.6	4.53E-56	17
175	LQP_11	LQP	11	0.7398	0.7272	0.0253	0.0318	0.0140	0.0094	0.0009	0.1000	0.0019	6779.5	246.4	2.73E-54	20
176	HQP_11	HQP	11	0.7551	0.7347	0.0231	0.0315	0.0126	0.0063	0.0004	0.1156	0.0022	6769.6	236.5	3.92E-52	26
177	L_11.5	L	11.5	0.7131	0.7016	0.0225	0.0301	0.0091	0.0094	0.0009	0.1094	0.0035	6833.8	300.7	4.51E-66	14
178	Q_11.5	Q	11.5	0.7206	0.7124	0.0230	0.0287	0.0089	0.0125	0.0016	0.1063	0.0031	6814.4	281.3	7.33E-62	13
179	P_11.5	P	11.5	0.7151	0.7013	0.0270	0.0336	0.0122	0.0031	0.0001	0.1188	0.0021	6812.8	279.7	1.62E-61	20
180	H_11.5	H	11.5	0.7393	0.7239	0.0198	0.0282	0.0090	0.0031	0.0001	0.1094	0.0024	6895.6	362.5	1.71E-79	11
181	LQ_11.5	LQ	11.5	0.7250	0.7145	0.0227	0.0291	0.0100	0.0125	0.0016	0.1063	0.0033	6816.4	283.3	2.65E-62	16
182	HQC_11.5	HQC	11.5	0.7388	0.7227	0.0213	0.0283	0.0084	0.0094	0.0009	0.1063	0.0022	6794.8	261.7	1.33E-57	17
183	LQP_11.5	LQP	11.5	0.7387	0.7248	0.0251	0.0315	0.0138	0.0094	0.0009	0.1000	0.0019	6783.5	250.4	3.68E-55	20
184	HQP_11.5	HQP	11.5	0.7523	0.7311	0.0242	0.0323	0.0133	0.0094	0.0009	0.1094	0.0029	6777.2	244.1	8.66E-54	26
185	L_12	L	12	0.7113	0.6998	0.0225	0.0301	0.0090	0.0094	0.0009	0.1094	0.0035	6835.7	302.6	1.73E-66	13
186	Q_12	Q	12	0.7191	0.7108	0.0231	0.0289	0.0089	0.0125	0.0016	0.1094	0.0024	6815.8	282.7	3.67E-62	12
187	P_12	P	12	0.7125	0.6988	0.0269	0.0337	0.0121	0.0031	0.0001	0.1156	0.0024	6814.1	281.0	8.45E-62	18
188	H_12	H	12	0.7366	0.7161	0.0200	0.0304	0.0098	0.0031	0.0001	0.1063	0.0029	6916.7	383.6	4.33E-84	13
189	LQ_12	LQ	12	0.7232	0.7129	0.0228	0.0293	0.0099	0.0125	0.0016	0.1063	0.0033	6817.9	284.8	1.23E-62	15

No[1]	Settings	FC	BM	Train. AUC	Avg-test. AUC	Var-test. AUC	Avg-dif. AUC	Var-dif AUC	Avg-test.	Var-test or MTP	Avg.test. or10pct	Var.test.	AICc	Delta-AICc	W.AIC	Parameters
190	HQC_12	HQC	12	0.7357	0.7191	0.0219	0.0288	0.0085	0.0094	0.0009	0.1063	0.0024	6799.6	266.5	1.21E-58	16
191	LQP_12	LQP	12	0.7367	0.7224	0.0257	0.0317	0.0142	0.0094	0.0009	0.1031	0.0020	6786.8	253.8	6.95E-56	19
192	HQP_12	HQP	12	0.7472	0.7279	0.0245	0.0322	0.0132	0.0094	0.0009	0.1125	0.0024	6778.1	245.0	5.65E-54	22

Table S14. Agro-ecological variables with major role for characterizing ecological niche for the indigenous cattle in Tigray (logistic model).

Populations	Major contributor parameters among the indigenous cattle in Tigray environmental niches (%)					
	bio4	bio12	bio16	bio18	CL	SBD
Abergelle	32.7	10.2	24.7	14.6	13.3	4.6
Arado	39	15.2	10.5	9.9	25.3	0.2
Begait	6.1	0.2	2.7	2.2	5.2	83.5
Erob	23.2	2.4	60.6	6.1	7.7	0
Raya	5.6	0.5	35.3	47	0.4	11.3

Table S15. Values for pairwise comparison of models for habitat suitability for the indigenous cattle in Tigray.

a) Correlation based ENMeVAL						b) Niche similarity based ENMeVAL				
Population	ABR	AR	BG	ER	RAY	ABR	AR	BG	ER	RAY
ABR		0.00	-0.15	-0.08	-0.09	1.00	0.55	0.36	0.32	0.28
AR			-0.16	0.29	-0.06		1.00	0.37	0.66	0.36
BG				-0.15	-0.09			1.00	0.17	0.31
ER					0.12				1.00	0.54
RAY										1.00

BG Begait, *RA* Raya, *AR* Arado, *AB* Abergelle, *ER* Erob

Table S16a. Numerical description of variants (SNPs and indels) statistics across individual genome of the indigenous cattle in Tigray.

Abergelle			Arado			Begait			Erob			Raya		
SID	SNPs	Indels	SID	SNPs	Indels	SID	SNPs	Indels	SID	SNPs	Indels	SID	SNPs	Indels
ABR02	13058773	1188687	AR01	13455910	1231918	BG01	13091236	1194836	ER01	13662412	1251926	RAY05	12787007	1158602
ABR07	12960882	1174721	AR05	12812530	1161847	BG02	12892820	1170639	ER04	13308307	1225010	RAY06	13542464	1245557
ABR10	12766726	1154975	AR06	13033024	1185364	BG05	13412787	1231333	ER06	12979295	1178184	RAY11	13088729	1204596
ABR11	13442658	1232531	AR10	12439525	1135780	BG07	12666214	1144657	ER07	13226134	1199475	RAY17	13330632	1218156
ABR12	12819542	1162114	AR11	12931734	1180923	BG13	12879773	1164489	ER10	13168691	1199070	RAY19	13089778	1191972
ABR13	13440482	1228474	AR13	13489412	1232186	BG15	12891752	1177252	ER11	13145366	1195947	RAY21	12913445	1173112
ABR14	13243509	1210777	AR23	13260526	1206400	BG17	13180771	1204943	ER13	13055806	1184993	RAY22	12519807	1139075
ABR15	13307556	1218162	AR24	13466640	1232561	BG19	13413410	1228804	ER15	13489909	1232265	RAY23	13576365	1246932
ABR16	12946145	1176254	AR30	13468688	1234899	BG20	12745009	1148088	ER17	13000399	1181237	RAY25	13495839	1235819
ABR21	13158414	1195051	AR31	12540490	1129855	BG21	12943679	1175761	ER18	13543563	1246164	RAY26	13152030	1211620
ABR29	12839547	1165276	AR32	12814441	1160965	BG31	13277275	1210669				RAY30	12763148	1152548

SID Sample ID, *ABR** Abergelle, *RA** Arado cattle, *BG** Begait, *ER** Erob and *RAY** Raya.

Table S16b. Numerical description of variants (SNPs and indels) statistics across the indigenous cattle in Tigray.

Variants	Populations					
	ABR (N = 11)	AR (N = 11)	BG (N = 11)	ER (N = 10)	RAY (N = 11)	ICT (N = 54)
SNPs						36003573
Shared	2113093 (7.15%)	2062642 (6.94%)	2182704 (7.54%)	2724442 (9.71%)	2161735 (7.35%)	674,019 (1.87%)
Indels						3703659
Shared	177353 (9.32%)	173842 (9.08%)	183302 (9.85)	228704 (12.59%)	181610 (9.58%)	1.43% (52,992)

ICT Indigenous cattle in Tigray (including all the five populations with 54 animals).

ABR Abergelle, *AR* Arado, *BG* Begait, *ER* Erob, *RAY* Raya.

Table S17. SNP density per kb in each chromosome (Mean ± SD) across the genome of the indigenous cattle in Tigray.

Chr	ABR (N = 11)	AR (N = 11)	BG (N = 11)	ER (N = 10)	RAY (N = 11)
1	11.956 ± 7.46	11.988 ± 7.46	11.522 ± 7.35	11.231 ± 7.25	11.863 ± 7.44
2	11.34 ± 7.02	11.333 ± 7.04	10.994 ± 6.94	10.735 ± 6.85	11.227 ± 7.03
3	11.07 ± 7.29	11.088 ± 7.28	10.884 ± 7.21	10.556 ± 7.15	10.971 ± 7.28
4	12.179 ± 8.62	12.166 ± 8.56	11.972 ± 8.54	11.545 ± 8.4	11.965 ± 8.57
5	11.47 ± 7.94	11.575 ± 7.94	11.22 ± 7.93	11.016 ± 7.86	11.341 ± 7.94
6	11.984 ± 7.14	11.965 ± 7.16	11.654 ± 7.09	11.203 ± 7.02	11.744 ± 7.13
7	11.328 ± 7.81	11.444 ± 7.92	11.034 ± 7.76	10.722 ± 7.63	11.237 ± 7.83
8	11.318 ± 7.06	11.456 ± 7.08	11.141 ± 6.99	10.604 ± 6.83	11.236 ± 7.05
9	11.636 ± 7.42	11.637 ± 7.42	11.45 ± 7.29	11.086 ± 7.22	11.472 ± 7.37
10	11.738 ± 8.53	11.763 ± 8.52	11.495 ± 8.42	11.165 ± 8.34	11.621 ± 8.5
11	11.18 ± 7.05	11.294 ± 7.08	11.196 ± 7.04	10.673 ± 6.9	11.221 ± 7.06
12	13.113 ± 9.43	13.099 ± 9.44	12.876 ± 9.18	12.361 ± 9.27	12.958 ± 9.2
13	11.128 ± 7.24	11.257 ± 7.24	10.976 ± 7.18	10.518 ± 7.01	11.073 ± 7.19
14	11.528 ± 7.13	11.655 ± 7.2	11.177 ± 7.01	10.913 ± 6.99	11.517 ± 7.16
15	13.089 ± 9.44	13.228 ± 9.47	12.868 ± 9.45	12.581 ± 9.18	13.231 ± 9.48
16	11.722 ± 7.52	11.709 ± 7.53	11.508 ± 7.42	11.042 ± 7.25	11.644 ± 7.52
17	12.202 ± 7.58	12.165 ± 7.55	11.888 ± 7.44	11.528 ± 7.41	11.958 ± 7.48
18	11.568 ± 8.41	11.684 ± 8.56	11.172 ± 8.34	11.027 ± 8.33	11.495 ± 8.49
19	10.921 ± 7.5	11.069 ± 7.54	10.986 ± 7.47	10.376 ± 7.25	11.168 ± 7.55
20	12.226 ± 7.45	12.303 ± 7.46	11.647 ± 7.29	11.505 ± 7.24	12.253 ± 7.49
21	11.79 ± 7.8	11.892 ± 7.76	11.45 ± 7.78	11.252 ± 7.62	11.919 ± 7.93
22	11.412 ± 7.18	11.33 ± 7.2	10.974 ± 7.06	10.705 ± 7.01	11.277 ± 7.14
23	14.116 ± 11.11	13.898 ± 11.13	13.721 ± 11.04	13.315 ± 10.85	14.156 ± 11.32
24	12.307 ± 7.22	12.377 ± 7.24	12.059 ± 7.18	11.621 ± 7.04	12.23 ± 7.2
25	11.781 ± 7.36	11.927 ± 7.4	11.601 ± 7.28	11.399 ± 7.24	11.799 ± 7.39
26	12.107 ± 7.73	12.225 ± 7.82	11.779 ± 7.7	11.551 ± 7.56	12.105 ± 7.71
27	13.644 ± 8.19	13.79 ± 8.28	13.747 ± 8.13	13.095 ± 8.06	13.373 ± 8.17
28	13.31 ± 8.04	13.625 ± 8.14	13.118 ± 7.94	12.88 ± 7.96	13.524 ± 8.13
29	13.247 ± 8.41	13.475 ± 8.47	13.178 ± 8.36	12.741 ± 8.34	13.387 ± 8.48
GWA	11.89 ± 7.86	11.94 ± 7.88	11.63 ± 7.8	11.27 ± 7.69	11.81 ± 7.86

ABR Abergelle, *AR* Arado, *BG* Begait, *ER* Erob, *RAY* Raya.

Table S18. Indel density per kb in each chromosome (mean ± SD) across the genome of the indigenous cattle in Tigray.

Chr	ABR (N = 11)	AR (N = 11)	BG (N = 11)	ER (N = 10)	RAY (N = 11)
1	1.181 ± 1.37	1.186 ± 1.38	1.139 ± 1.35	1.114 ± 1.34	1.182 ± 1.37
2	1.113 ± 1.32	1.111 ± 1.32	1.08 ± 1.3	1.059 ± 1.29	1.111 ± 1.32
3	1.067 ± 1.32	1.069 ± 1.32	1.051 ± 1.31	1.024 ± 1.29	1.068 ± 1.32
4	1.214 ± 1.45	1.216 ± 1.44	1.196 ± 1.44	1.157 ± 1.41	1.207 ± 1.44
5	1.114 ± 1.38	1.121 ± 1.38	1.087 ± 1.36	1.074 ± 1.36	1.111 ± 1.38
6	1.187 ± 1.36	1.189 ± 1.36	1.157 ± 1.35	1.115 ± 1.32	1.176 ± 1.36
7	1.13 ± 1.39	1.145 ± 1.41	1.103 ± 1.38	1.078 ± 1.36	1.132 ± 1.4
8	1.113 ± 1.32	1.128 ± 1.33	1.096 ± 1.31	1.051 ± 1.28	1.112 ± 1.32
9	1.152 ± 1.37	1.154 ± 1.37	1.136 ± 1.35	1.104 ± 1.34	1.144 ± 1.36
10	1.158 ± 1.43	1.159 ± 1.43	1.135 ± 1.41	1.107 ± 1.4	1.155 ± 1.43
11	1.061 ± 1.29	1.072 ± 1.3	1.062 ± 1.29	1.014 ± 1.27	1.076 ± 1.31
12	1.294 ± 1.56	1.297 ± 1.57	1.277 ± 1.55	1.233 ± 1.55	1.297 ± 1.58
13	1.069 ± 1.32	1.081 ± 1.33	1.055 ± 1.31	1.017 ± 1.28	1.075 ± 1.33
14	1.112 ± 1.32	1.123 ± 1.33	1.08 ± 1.3	1.057 ± 1.29	1.121 ± 1.33
15	1.295 ± 1.6	1.311 ± 1.61	1.277 ± 1.6	1.253 ± 1.57	1.321 ± 1.62
16	1.147 ± 1.38	1.145 ± 1.38	1.13 ± 1.37	1.088 ± 1.34	1.153 ± 1.39
17	1.208 ± 1.41	1.208 ± 1.41	1.177 ± 1.4	1.143 ± 1.37	1.194 ± 1.4
18	1.116 ± 1.43	1.129 ± 1.46	1.086 ± 1.43	1.073 ± 1.41	1.12 ± 1.44
19	1.038 ± 1.3	1.053 ± 1.31	1.045 ± 1.31	0.99 ± 1.26	1.069 ± 1.32
20	1.193 ± 1.39	1.199 ± 1.4	1.135 ± 1.36	1.129 ± 1.36	1.205 ± 1.4
21	1.16 ± 1.42	1.171 ± 1.41	1.125 ± 1.4	1.115 ± 1.39	1.185 ± 1.44
22	1.104 ± 1.35	1.102 ± 1.35	1.069 ± 1.32	1.045 ± 1.31	1.111 ± 1.35
23	1.335 ± 1.71	1.318 ± 1.71	1.306 ± 1.69	1.268 ± 1.67	1.356 ± 1.76
24	1.183 ± 1.36	1.193 ± 1.37	1.156 ± 1.35	1.121 ± 1.32	1.188 ± 1.36
25	1.062 ± 1.33	1.078 ± 1.33	1.046 ± 1.31	1.034 ± 1.3	1.077 ± 1.33
26	1.206 ± 1.44	1.22 ± 1.46	1.167 ± 1.42	1.16 ± 1.41	1.221 ± 1.45
27	1.338 ± 1.5	1.357 ± 1.51	1.35 ± 1.5	1.291 ± 1.47	1.331 ± 1.51
28	1.307 ± 1.51	1.344 ± 1.53	1.291 ± 1.5	1.276 ± 1.49	1.345 ± 1.53
29	1.28 ± 1.51	1.302 ± 1.54	1.276 ± 1.52	1.242 ± 1.5	1.31 ± 1.54
GWA	1.16 ± 1.4	1.17 ± 1.41	1.14 ± 1.39	1.08 ± 1.34	1.67 ± 1.41

ABR Abergelle, *AR* Arado, *BG* Begait, *ER* Erob, *GWA* Genome-wide average *RAY* Raya.

Table S19. Distribution of SNPs in each chromosome across the genome of the indigenous cattle in Tigray.

Chr	ABR (N = 11)	AR (N = 11)	BG (N =11)	ER (N = 10)	RAY (N = 11)
1	1895194	1,900,182	1,826,307	1,780,125	1,880,320
2	1544549	1,543,561	1,497,209	1,462,356	1,529,420
3	1339507	1,341,661	1,317,055	1,277,294	1,327,538
4	1460244	1,458,661	1,435,379	1,384,129	1,434,563
5	1377057	1,389,678	1,347,155	1,322,565	1,361,681
6	1411635	1,409,455	1,372,820	1,319,677	1,383,440
7	1253734	1,266,532	1,221,123	1,186,635	1,243,540
8	1281923	1,297,561	1,261,815	1,201,009	1,272,630
9	1217566	1,217,681	1,198,132	1,160,071	1,200,497
10	1212396	1,214,888	1,187,351	1,153,221	1,200,479
11	1195987	1,208,170	1,197,704	1,141,775	1,200,422
12	1143431	1,142,167	1,122,822	1,077,908	1,129,950
13	928830	939,587	916,171	877,905	924,207
14	949822	960,254	920,906	899,130	948,946
15	1112467	1,124,249	1,093,389	1,068,967	1,124,157
16	949498	948,485	932,183	894,414	943,196

17	892607	889,902	869,616	843,308	874,764
18	761353	769,041	735,312	725,745	756,596
19	692795	702,184	696,934	658,216	708,444
20	879832	885,408	838,218	827,931	881,798
21	823442	830,629	799,752	785,910	832,481
22	693462	688,530	666,849	650,517	685,255
23	741090	729,621	720,362	699,033	743,163
24	766788	771,143	751,405	724,076	762,019
25	498916	505,086	491,310	482,719	499,659
26	629323	635,505	612,407	600,460	629,255
27	622327	628,981	627,025	597,296	609,951
28	611423	625,899	602,596	591,700	621,247
29	676766	688,423	673,240	650,953	683,964
Total	29563964	29713124	28932547	28045045	29393582

ABR Abergelle, *AR* Arado, *BG* Begait, *ER* Erob, *RAY* Raya.

Table S20. Distribution of indels in each chromosome across the genome of the indigenous cattle in Tigray.

Chr	ABR (N = 11)	AR (N = 11)	BG (N = 11)	ER (N = 10)	RAY (N = 11)
1	187,247	188,006	180,517	176,599	187,280
2	151,585	151,320	146,978	144,195	151,243
3	129,160	129,320	127,148	123,890	129,175
4	145,565	145,732	143,373	138,675	144,690
5	133,749	134,632	130,501	129,001	133,333
6	139,792	140,092	136,332	131,397	138,491
7	125,024	126,720	122,112	119,288	125,328
8	126,026	127,780	124,145	118,993	125,998
9	120,568	120,770	118,829	115,544	119,682
10	119,605	119,727	117,175	114,320	119,239
11	113,471	114,679	113,578	108,512	115,122
12	112,838	113,054	111,382	107,520	113,055
13	89,186	90,229	88,045	84,855	89,717
14	91,617	92,560	88,962	87,046	92,378
15	110,041	111,382	108,471	106,412	112,243
16	92,867	92,750	91,490	88,087	93,376
17	88,394	88,354	86,132	83,632	87,312
18	73,419	74,316	71,456	70,648	73,692
19	65,853	66,752	66,281	62,797	67,812
20	85,829	86,273	81,684	81,258	86,709
21	81,012	81,755	78,609	77,879	82,783
22	67,102	66,937	64,924	63,518	67,500
23	70,105	69,180	68,548	66,555	71,189
24	73,715	74,306	72,033	69,805	74,003
25	44,992	45,663	44,302	43,803	45,618
26	62,691	63,408	60,686	60,322	63,471
27	61,026	61,888	61,597	58,882	60,726
28	60,056	61,739	59,322	58,627	61,767
29	65,370	66,533	65,187	63,436	66,912
Total	2,887,905	2,905,857	2,829,799	2,755,496	2,899,844

ABR Abergelle, *AR* Arado, *BG* Begait, *ER* Erob, *RAY* Raya.

Table S21. Proportion of alternate allele frequency (AAF) for SNPs and indels across genome of the indigenous cattle in Tigray.

Allelic frequency of detected variants	Population				
SNPs	Abergelle (N = 11)	Arado (N = 11)	Begait (N = 11)	Erob (N = 10)	Raya (N = 11)
No of SNPs with mean AAF < 0.5 (%)	23430191 (79.25)	23667911 (79.65)	22728344 (78.56)	21625611 (77.11)	23088375 (78.55)
No of SNPs with mean AAF > 0.5 (%)	6133773 (20.75)	6045213 (20.35)	6204203 (21.44)	6419434 (22.89)	6305207 (21.45)
No of SNPs with mean AAF > 0.9 (%)	1265652 (4.28)	1196058 (4.03)	1323911 (4.58)	1149665 (4.1)	1332822 (4.53)
µAAF	0.3	0.29	0.3	0.32	0.3
Indels					
No of SNPs with mean AAF < 0.5 (%)	2266334 (79.95)	2290912 (80.32)	2200959 (79.27)	2111465 (78.11)	2261134 (79.49)
No of SNPs with mean AAF > 0.5 (%)	568422 (20.05)	561197 (19.68)	575401 (20.73)	591902 (21.89)	583450 (20.51)
No of SNPs with mean AAF > 0.9 (%)	118404 (4.18)	112639 (3.95)	123254 (4.44)	109987 (4.07)	123839 (4.35)
µAAF	0.29	0.28	0.29	0.3	0.28

µAAF average alternate allele frequency.

Table S22. Description of genome-wide average nucleotide diversity, heterozygous-to-homozygous (Het/Hom) ratios for SNPs and indels and observed heterozygosity across the genome of the indigenous cattle in Tigray.

Population	Average nucleotide diversity π		Het/Hom[1]		H_O[2]	
	Mean	SD	SNPs	Indels	Mean	SD
Abergelle	0.00356	0.00176	1.64	1.61	0.287	0.010
Arado	0.00357	0.00176	1.68	1.65	0.302	0.010
Begait	0.00351	0.00175	1.59	1.57	0.283	0.012
Erob	0.00356	0.00177	1.60	1.58	0.284	0.008
Raya	0.00350	0.00177	1.52	1.52	0.278	0.016

[1] Population level average non-reference allele heterozygous to the homozygous ratio

[2] population level average observed heterozygosity

Table S23. ROH statistics in individual genome across the indigenous cattle in Tigray.

Sample[1]	Sex	Population	NROH[2]	Total ROH length in Kbp	Average ROH segment length Kbp	Minimum ROH length Kbp	Maxim ROH length Kbp	SNPs
ABR02	F	Abergelle	828	128342	155.002	100.037	511.969	1855813
ABR07	F	Abergelle	843	133654	158.545	100.076	743.581	1966156
ABR10	M	Abergelle	827	129313	156.364	100.004	792.798	1884691
ABR11	M	Abergelle	781	126326	161.748	100.035	896.19	1853192
ABR12	F	Abergelle	748	112939	150.988	100.058	547.677	1661218
ABR13	M	Abergelle	778	119221	153.24	100.002	569.855	1735227
ABR14	F	Abergelle	907	140996	155.453	100.007	526.116	2076081
ABR15	F	Abergelle	900	148830	165.366	100.049	787.31	2290024
ABR16	M	Abergelle	881	136537	154.98	100.131	649.346	1970678
ABR21	M	Abergelle	824	131304	159.35	100.072	582.281	1920166
ABR29	F	Abergelle	814	123965	152.292	100.01	608.765	1805870
AR01	F	Arado	782	127175	162.628	100.152	578.938	1655364
AR05	F	Arado	750	118918	158.557	100.003	619.765	1718422
AR06	F	Arado	835	131731	157.762	100.004	605.848	1948784
AR10	M	Arado	708	112441	158.815	100.003	535.183	1660465
AR11	M	Arado	861	135646	157.545	100.086	653.31	2011562
AR13	F	Arado	711	108019	151.925	100.004	572.658	1536829
AR23	F	Arado	778	120078	154.342	100.047	656.572	1731512
AR24	F	Arado	794	124269	156.511	100.06	686.549	1816894
AR30	F	Arado	838	132648	158.291	100.014	523.141	1941223
AR31	F	Arado	706	108766	154.06	100.028	696.998	1611131
AR32	M	Arado	793	122456	154.421	100.04	879.142	1789959
BG01	F	Begait	908	147052	161.951	100.14	660.291	2189614
BG02	F	Begait	882	140682	159.504	100.11	856.199	2066527
BG05	F	Begait	767	121138	157.938	100.03	863.883	1768534
BG07	F	Begait	849	131777	155.214	100.044	699.933	1944990
BG13	F	Begait	862	142015	164.75	100.069	772.951	2091634
BG15	M	Begait	1504	266709	177.333	100.04	1203.302	4057130
BG17	F	Begait	896	150278	167.721	100.07	825.919	2208658
BG19	F	Begait	940	156980	167	100.012	643.085	2341021
BG20	F	Begait	806	127691	158.426	100.197	595.476	1823180
BG21	F	Begait	782	123606	158.064	100.116	582.676	1819288
BG31	F	Begait	807	130173	161.305	100.091	707.055	1857526
ER01	M	Erob	830	131258	158.142	100.002	642.098	1965596

Sample[1]	Sex	Population	NROH[2]	Total ROH length in Kbp	Average ROH segment length Kbp	Minimum ROH length Kbp	Maxim ROH length Kbp	SNPs
ER04	F	Erob	1099	177459	161.474	100.163	666.114	2684630
ER06	M	Erob	789	125739	159.365	100.012	884.403	1860037
ER07	M	Erob	786	122677	156.077	100.041	520.163	1802205
ER10	F	Erob	857	138470	161.575	100.072	744.868	2067601
ER11	F	Erob	817	130545	159.786	100.374	827.319	1904007
ER13	F	Erob	810	126565	156.254	100.033	583.095	1825282
ER15	F	Erob	860	133288	154.986	100.068	693.829	1959606
ER17	M	Erob	796	122745	154.202	100.014	608.262	1796287
ER18	F	Erob	727	110403	151.861	100.134	505.474	1609470
RAY05	M	Raya	867	137997	159.166	100.132	917.33	2013202
RAY06	M	Raya	703	106297	151.205	100.011	590.014	1546638
RAY11	F	Raya	1662	297294	178.877	100.019	1180.322	4765199
RAY17	F	Raya	826	131153	158.781	100.005	974.976	1949028
RAY19	F	Raya	890	140242	157.575	100.048	572.079	2059272
RAY21	F	Raya	811	127877	157.678	100.067	724.247	1860730
RAY22	F	Raya	1467	253580	172.856	100.008	1040.337	3916061
RAY23	F	Raya	710	105866	149.108	100.004	604.694	1532947
RAY25	F	Raya	860	139991	162.781	100.031	595.453	2069018
RAY26	F	Raya	1347	220110	163.408	100.097	1002.7	3297432
RAY30	F	Raya	862	133322	154.666	100.045	581.401	1913403

[1] *ABR** Abergelle, *RA** Arado, *BG** Begait, *ER** Erob and *RAY** Raya

NROH[2] Number runs of homozygosity

Table S24. Chromosome wise number of ROH across the genome of the indigenous cattle in Tigray.

Chr	ABR		AR		BG		ER		RAY	
	Sum	AVG	Sum	AVG	Sum	AVG	Sum	AVG	Sum	AVG
1	600	55	549	50	527	48	635	64	633	58
2	543	49	569	52	608	55	467	47	623	57
3	445	40	408	37	464	42	426	43	492	45
4	423	38	391	36	348	32	346	35	674	61
5	482	44	452	41	645	59	399	40	467	42
6	441	40	374	34	471	43	512	51	627	57
7	471	43	493	45	508	46	449	45	532	48
8	422	38	368	33	433	39	473	47	536	49
9	390	35	404	37	434	39	296	30	575	52
10	352	32	340	31	433	39	356	36	480	44
11	438	40	387	35	426	39	416	42	445	40
12	282	26	253	23	271	25	218	22	412	37
13	282	26	261	24	371	34	289	29	423	38
14	276	25	259	24	445	40	294	29	364	33
15	267	24	275	25	270	25	140	14	354	32
16	321	29	308	28	406	37	289	29	435	40
17	235	21	250	23	266	24	280	28	449	41
18	242	22	226	21	297	27	213	21	227	21
19	292	27	281	26	265	24	228	23	259	24
20	242	22	237	22	297	27	234	23	266	24
21	260	24	222	20	379	34	204	20	236	21
22	285	26	235	21	279	25	245	25	242	22
23	144	13	135	12	163	15	119	12	151	14

Chr	ABR		AR		BG		ER		RAY	
	Sum	AVG	Sum	AVG	Sum	AVG	Sum	AVG	Sum	AVG
24	221	20	217	20	215	20	192	19	201	18
25	135	12	141	13	193	18	109	11	194	18
26	175	16	124	11	170	15	207	21	155	14
27	144	13	131	12	116	11	112	11	196	18
28	156	14	128	12	153	14	114	11	177	16
29	165	15	138	13	150	14	109	11	180	16

Chr Chromosome, *AVG* Average, *ABR* Abergelle, *AR* Arado, *BG* Begait, *ER* Erob, *RAY* Raya.

Table S25. Chromosome wise average size of ROH (in Mb) across the genome of the indigenous cattle in Tigray.

Chr	ABR		AR		BG		ER		RAY	
	Sum	AVG	Sum	AVG	Sum	AVG	Sum	AVG	Sum	AVG
1	93	8.45	86	7.82	85	7.73	100	10.00	104	9.45
2	90	8.18	92	8.36	100	9.09	76	7.60	104	9.45
3	72	6.55	63	5.73	73	6.64	67	6.70	77	7.00
4	64	5.82	59	5.36	59	5.36	51	5.10	110	10.00
5	74	6.73	71	6.45	112	10.18	61	6.10	73	6.64
6	68	6.18	58	5.27	73	6.64	84	8.40	100	9.09
7	73	6.64	75	6.82	81	7.36	73	7.30	84	7.64
8	69	6.27	59	5.36	68	6.18	78	7.80	86	7.82
9	62	5.64	65	5.91	73	6.64	48	4.80	99	9.00
10	55	5.00	52	4.73	71	6.45	56	5.60	83	7.55
11	70	6.36	67	6.09	70	6.36	64	6.40	70	6.36
12	43	3.91	38	3.45	43	3.91	32	3.20	68	6.18
13	44	4.00	40	3.64	63	5.73	46	4.60	69	6.27
14	43	3.91	40	3.64	73	6.64	45	4.50	60	5.45
15	39	3.55	43	3.91	41	3.73	21	2.10	56	5.09
16	50	4.55	47	4.27	69	6.27	46	4.60	71	6.45
17	38	3.45	38	3.45	41	3.73	45	4.50	84	7.64
18	39	3.55	37	3.36	52	4.73	34	3.40	38	3.45
19	45	4.09	45	4.09	43	3.91	36	3.60	42	3.82
20	37	3.36	38	3.45	48	4.36	36	3.60	42	3.82
21	40	3.64	36	3.27	68	6.18	32	3.20	37	3.36
22	45	4.09	37	3.36	46	4.18	39	3.90	38	3.45
23	22	2.00	19	1.73	24	2.18	18	1.80	22	2.00
24	34	3.09	35	3.18	34	3.09	29	2.90	32	2.91
25	19	1.73	21	1.91	33	3.00	16	1.60	30	2.73
26	28	2.55	20	1.82	27	2.45	33	3.30	24	2.18
27	22	2.00	21	1.91	18	1.64	17	1.70	34	3.09
28	26	2.36	19	1.73	22	2.00	17	1.70	29	2.64
29	25	2.27	21	1.91	24	2.18	17	1.70	27	2.45

Chr Chromosome, *AVG* Average, *ABR* Abergelle, *AR* Arado, *BG* Begait, *ER* Erob, *RAY* Raya.

Table S26. Chromosome wise incidence of SNPs on ROH across the genome of the indigenous cattle in Tigray.

Chr	ABR	AR	BG	ER	RAY
	Sum	Sum	Sum	Sum	Sum
1	127885	113383	116370	157209	143208
2	117423	118571	129131	109155	140474
3	92055	81256	94454	96197	101379

Chr	ABR	AR	BG	ER	RAY
	Sum	Sum	Sum	Sum	Sum
4	83466	77508	77727	72729	146011
5	93217	90461	144672	84575	93041
6	94542	82759	104415	131581	144961
7	85267	91627	99192	96636	104169
8	89971	77752	89882	112888	117202
9	82661	86825	97239	72362	134144
10	70247	66233	92406	77899	111736
11	94686	87331	93446	93163	92819
12	60274	51498	62334	50943	101137
13	52584	47817	81102	63335	87158
14	57570	53888	100450	67694	84051
15	56649	64325	60034	34088	82896
16	67522	62812	93698	69512	96626
17	52136	52862	56440	66974	117370
18	48353	46217	66764	47426	46813
19	57869	54964	53338	47677	51277
20	52695	53823	67977	55276	59750
21	54841	47417	88838	47286	49170
22	55774	46548	57371	53716	47106
23	32572	30685	35478	28654	33665
24	48517	48467	47604	46180	44590
25	27160	29512	45730	25492	43660
26	40574	27365	36599	51910	33127
27	33811	31288	28069	29191	52670
28	41402	31482	37730	29073	46658
29	39102	32456	38610	28652	40671
Sum	1910825	1787132	2197100	1947473	2447539

Chr Chromosome, *ABR* Abergelle, *AR* Arado, *BG* Begait, *ER* Erob, *RAY* Raya.

Table S27. Population level mean genomic inbreeding coefficients calculated from the excess of homozygosity (F_{HOM}) and from ROH (F_{ROH}) with a minimum length of 100 Kb (F_{ROH} >100) across the indigenous cattle in Tigray.

Populations	F_{HOM}		F_{ROH}	
	Mean	SD	Mean	SD
Abergelle	0.045	0.028	0.050	0.004
Arado	0.043	0.035	0.047	0.004
Begait	0.059	0.040	0.058	0.016
Erob	0.046	0.030	0.051	0.007
Raya	0.070	0.054	0.064	0.025

Table S28. F_{HOM} and F_{ROH} based inbreeding for the individual animal across the indigenous cattle in Tigray.

Sample[1]	Sex	Population	Inbreeding coefficient	
			F_{HOM}	F_{ROH}
ABR02	F	Abergelle	0.041	0.050
ABR07	F	Abergelle	0.060	0.053
ABR10	M	Abergelle	0.076	0.050
ABR11	M	Abergelle	0.004	0.049
ABR12	F	Abergelle	0.074	0.044
ABR13	M	Abergelle	0.011	0.046

Sample[1]	Sex	Population	Inbreeding coefficient	
			FHOM	FROH
ABR14	F	Abergelle	0.021	0.054
ABR15	F	Abergelle	0.016	0.057
ABR16	M	Abergelle	0.075	0.053
ABR21	M	Abergelle	0.054	0.051
ABR29	F	Abergelle	0.069	0.048
AR01	F	Arado	0.002	0.048
AR05	F	Arado	0.026	0.046
AR06	F	Arado	0.072	0.051
AR10	M	Arado	0.057	0.043
AR11	M	Arado	0.050	0.052
AR13	F	Arado	0.035	0.041
AR23	F	Arado	0.017	0.046
AR24	F	Arado	0.007	0.048
AR30	F	Arado	0.015	0.051
AR31	F	Arado	0.115	0.042
AR32	M	Arado	0.074	0.048
BG01	F	Begait	0.038	0.057
BG02	F	Begait	0.065	0.054
BG05	F	Begait	-0.016	0.047
BG07	F	Begait	0.091	0.051
BG13	F	Begait	0.069	0.055
BG15	M	Begait	0.107	0.103
BG17	F	Begait	0.017	0.058
BG19	F	Begait	0.006	0.060
BG20	F	Begait	0.072	0.050
BG21	F	Begait	0.046	0.048
BG31	F	Begait	-0.005	0.050
ER01	M	Erob	0.031	0.050
ER04	F	Erob	-0.001	0.070
ER06	M	Erob	0.091	0.048
ER07	M	Erob	0.085	0.048
ER10	F	Erob	0.069	0.054
ER11	F	Erob	0.079	0.051
ER13	F	Erob	0.074	0.049
ER15	F	Erob	0.057	0.051
ER17	M	Erob	0.026	0.049
ER18	F	Erob	0.081	0.043
RAY05	M	Raya	0.094	0.053
RAY06	M	Raya	0.026	0.042
RAY11	F	Raya	0.120	0.114
RAY17	F	Raya	0.016	0.051
RAY19	F	Raya	0.056	0.054
RAY21	F	Raya	0.066	0.050
RAY22	F	Raya	0.168	0.099
RAY23	F	Raya	0.013	0.053
RAY25	F	Raya	-0.001	0.053
RAY26	F	Raya	0.111	0.088
RAY30	F	Raya	0.106	0.042

[1] *ABR** Abergelle, *RA** Arado, *BG** Begait, *ER** Erob and *RAY** Raya.

Table S29. The low 1% *Hp* detected windows in Abergelle cattle.

Low 1% windows					Low 1% merged windows			
Chr	Start	End	nSNPs	*ZHp*	Chr	Start	End	Size (MB)
	2500001	2600000	810	-3.162277546	1	2500001	2600000	0.099999
1	30050001	30150000	706	-3.110182543	1	30050001	30150000	0.099999
1	54500001	54600000	729	-3.615645557	1	54500001	54650000	0.149999

Low 1% windows					Low 1% merged windows			
Chr	Start	End	nSNPs	*ZHp*	Chr	Start	End	Size (MB)
1	54550001	54650000	654	-3.419233044	1	79000001	79100000	0.099999
1	79000001	79100000	446	-3.030679434	1	87100001	87250000	0.149999
1	87100001	87200000	922	-3.342889495	1	91100001	91200000	0.099999
1	87150001	87250000	908	-3.86919927	1	105300001	105400000	0.099999
1	91100001	91200000	1230	-3.402177358	1	119700001	119800000	0.099999
1	105300001	105400000	1182	-2.965101445	1	129350001	129500000	0.149999
1	119700001	119800000	992	-2.993520111	2	20750001	20850000	0.099999
1	129350001	129450000	778	-6.093961739	2	25350001	25650000	0.299999
1	129400001	129500000	891	-5.777888669	2	40450001	40550000	0.099999
2	20750001	20850000	352	-3.128207214	2	42250001	42450000	0.199999
2	25350001	25450000	611	-3.479079817	2	51500001	51650000	0.149999
2	25400001	25500000	689	-4.889732788	2	53550001	53650000	0.099999
2	25450001	25550000	855	-4.169841786	2	61450001	61550000	0.099999
2	25500001	25600000	970	-3.148036986	2	61700001	61800000	0.099999
2	25550001	25650000	916	-3.170556496	2	70250001	70550000	0.299999
2	40450001	40550000	593	-3.425228501	2	70650001	70800000	0.149999
2	42250001	42350000	849	-3.378617937	2	90350001	90550000	0.199999
2	42300001	42400000	858	-3.26328965	2	90950001	91150000	0.199999
2	42350001	42450000	796	-3.185893948	2	133400001	133550000	0.149999
2	51500001	51600000	692	-3.06221464	3	9300001	9400000	0.099999
2	51550001	51650000	619	-3.049302678	3	22950001	23050000	0.099999
2	53550001	53650000	762	-3.228448938	3	29200001	29300000	0.099999
2	61450001	61550000	530	-3.122528835	3	42900001	43000000	0.099999
2	61700001	61800000	865	-3.075504919	3	58800001	58900000	0.099999
2	70250001	70350000	474	-7.040602615	3	58950001	59100000	0.149999
2	70300001	70400000	442	-7.385165755	3	59250001	59500000	0.249999
2	70350001	70450000	551	-5.341803916	3	59800001	59900000	0.099999
2	70400001	70500000	624	-3.487313549	3	65750001	65850000	0.099999
2	70450001	70550000	566	-3.028291489	3	68800001	69050000	0.249999
2	70650001	70750000	887	-3.671629101	3	85850001	85950000	0.099999
2	70700001	70800000	779	-3.890708831	3	92600001	92800000	0.199999
2	90350001	90450000	771	-3.322129637	3	109750001	109950000	0.199999
2	90400001	90500000	895	-3.72404418	4	40600001	40700000	0.099999
2	90450001	90550000	763	-3.591032394	4	65550001	65650000	0.099999
2	90950001	91050000	547	-3.839703444	4	74450001	74600000	0.149999
2	91000001	91100000	551	-4.423177597	4	88350001	88500000	0.149999
2	91050001	91150000	440	-3.809188902	4	112300001	112400000	0.099999
2	133400001	133500000	743	-3.40616657	5	100001	250000	0.149999
2	133450001	133550000	521	-3.241943997	5	18750001	18900000	0.149999
3	9300001	9400000	516	-3.468666204	5	34000001	34650000	0.649999
3	22950001	23050000	874	-3.003742029	5	47800001	47900000	0.099999
3	29200001	29300000	995	-4.267342218	5	48350001	48800000	0.449999
3	42900001	43000000	940	-2.959733807	5	58000001	58100000	0.099999
3	58800001	58900000	513	-3.132013576	5	76200001	76650000	0.449999
3	58950001	59050000	868	-3.565944723	5	78950001	79100000	0.149999
3	59000001	59100000	1009	-3.6123432	5	82600001	82700000	0.099999
3	59250001	59350000	848	-3.59840829	5	83500001	83650000	0.149999
3	59300001	59400000	798	-3.872368014	5	105800001	105900000	0.099999
3	59350001	59450000	513	-3.652964351	5	112300001	112650000	0.349999
3	59400001	59500000	473	-3.214984861	6	28850001	28950000	0.099999
3	59800001	59900000	340	-3.526120385	6	37350001	37600000	0.249999
3	65750001	65850000	1269	-3.187076057	6	51000001	51250000	0.249999
3	68800001	68900000	1133	-2.969704755	6	51300001	51700000	0.399999

Low 1% windows					Low 1% merged windows			
Chr	Start	End	nSNPs	*ZHp*	Chr	Start	End	Size (MB)
3	68900001	69000000	799	-3.39604297	6	52100001	52200000	0.099999
3	68950001	69050000	889	-3.121148428	6	52350001	52450000	0.099999
3	85850001	85950000	763	-4.518495879	6	60300001	60450000	0.149999
3	92600001	92700000	861	-3.197941471	6	77200001	77300000	0.099999
3	92650001	92750000	765	-4.235443947	6	77400001	77500000	0.099999
3	92700001	92800000	471	-4.084264598	6	78300001	78450000	0.149999
3	109750001	109850000	837	-3.520816969	6	79200001	79300000	0.099999
3	109800001	109900000	606	-3.508041507	6	79900001	80200000	0.299999
3	109850001	109950000	354	-3.158749667	6	82750001	82850000	0.099999
4	40600001	40700000	1006	-3.219963369	7	9900001	10000000	0.099999
4	65550001	65650000	1018	-3.257409994	7	21100001	21200000	0.099999
4	74450001	74550000	796	-4.069265584	7	34600001	34700000	0.099999
4	74500001	74600000	1032	-4.490922766	7	49700001	49800000	0.099999
4	88350001	88450000	746	-3.438912755	7	49850001	51150000	1.299999
4	88400001	88500000	943	-3.142355081	7	52100001	52350000	0.249999
4	112300001	112400000	699	-3.618859651	7	52700001	52800000	0.099999
5	100001	200000	804	-3.643871808	7	56500001	56650000	0.149999
5	150001	250000	683	-3.941510771	7	61250001	61450000	0.199999
5	18750001	18850000	416	-3.12506783	7	74150001	74300000	0.149999
5	18800001	18900000	805	-2.976925912	7	74350001	74450000	0.099999
5	34000001	34100000	878	-3.573963414	7	75850001	76050000	0.199999
5	34050001	34150000	864	-3.782237976	7	76100001	76200000	0.099999
5	34100001	34200000	803	-3.642854821	7	81200001	81350000	0.149999
5	34150001	34250000	649	-3.31548899	7	91350001	91450000	0.099999
5	34200001	34300000	422	-3.363843144	7	98300001	98500000	0.199999
5	34250001	34350000	421	-2.980067855	8	7200001	7400000	0.199999
5	34300001	34400000	388	-3.044682325	8	31950001	32050000	0.099999
5	34350001	34450000	337	-3.355540922	8	65700001	65800000	0.099999
5	34400001	34500000	306	-3.745497711	8	68500001	68600000	0.099999
5	34450001	34550000	343	-3.607881581	8	77700001	77850000	0.149999
5	34500001	34600000	505	-3.289724384	8	79150001	79250000	0.099999
5	34550001	34650000	475	-3.24920989	8	80050001	80150000	0.099999
5	47800001	47900000	508	-3.257829839	8	93500001	93600000	0.099999
5	48350001	48450000	246	-3.032384366	8	102800001	102900000	0.099999
5	48400001	48500000	245	-5.218689797	8	112100001	112200000	0.099999
5	48450001	48550000	382	-5.370003256	9	2100001	2200000	0.099999
5	48500001	48600000	544	-5.280306195	9	2900001	3000000	0.099999
5	48550001	48650000	514	-5.005484493	9	4100001	4250000	0.149999
5	48600001	48700000	564	-5.073457573	9	5150001	5250000	0.099999
5	48650001	48750000	542	-5.451002941	9	19250001	19350000	0.099999
5	48700001	48800000	360	-3.832979629	9	21900001	22050000	0.149999
5	58000001	58100000	861	-4.639342425	9	23650001	23750000	0.099999
5	76200001	76300000	604	-3.110840942	9	33050001	33150000	0.099999
5	76250001	76350000	484	-3.314550833	9	33350001	33500000	0.149999
5	76300001	76400000	557	-3.597524573	9	38850001	39250000	0.399999
5	76350001	76450000	611	-3.638817159	9	39400001	39550000	0.149999
5	76400001	76500000	457	-3.118719632	9	42500001	42600000	0.099999
5	76450001	76550000	342	-3.324043097	9	46500001	46650000	0.149999
5	76500001	76600000	494	-3.394721941	9	47750001	47850000	0.099999
5	76550001	76650000	680	-3.136835823	9	68000001	68100000	0.099999
5	78950001	79050000	1137	-3.382201075	9	71000001	71150000	0.149999
5	79000001	79100000	1052	-3.726873771	9	71750001	72000000	0.249999
5	82600001	82700000	1020	-3.362547647	9	78200001	78300000	0.099999

Low 1% windows					Low 1% merged windows			
Chr	Start	End	nSNPs	*ZHp*	Chr	Start	End	Size (MB)
5	83500001	83600000	652	-3.143467706	9	79250001	79350000	0.099999
5	83550001	83650000	612	-3.009490742	9	83500001	83600000	0.099999
5	105800001	105900000	455	-3.367312575	9	91400001	91500000	0.099999
5	112300001	112400000	509	-3.963564328	10	58600001	58750000	0.149999
5	112350001	112450000	615	-5.050070975	10	58850001	59150000	0.299999
5	112400001	112500000	639	-5.266144043	10	96200001	96350000	0.149999
5	112450001	112550000	514	-5.08448889	11	7700001	7800000	0.099999
5	112500001	112600000	318	-4.451153211	11	7850001	8000000	0.149999
5	112550001	112650000	583	-4.337994057	11	12900001	13050000	0.149999
6	28850001	28950000	1093	-3.240830042	11	13150001	13300000	0.149999
6	37350001	37450000	301	-3.01174768	11	13850001	13950000	0.099999
6	37400001	37500000	342	-3.406845249	11	14350001	14450000	0.099999
6	37450001	37550000	389	-3.872230436	11	14650001	14800000	0.149999
6	37500001	37600000	450	-3.796772999	11	15450001	15550000	0.099999
6	51000001	51100000	951	-3.327370538	11	16250001	16350000	0.099999
6	51050001	51150000	842	-3.930974003	11	16550001	16650000	0.099999
6	51100001	51200000	847	-4.035590993	11	22950001	23050000	0.099999
6	51150001	51250000	700	-3.759915705	11	38600001	38700000	0.099999
6	51300001	51400000	1037	-3.699952531	11	38800001	38900000	0.099999
6	51350001	51450000	832	-3.912471963	11	41150001	41300000	0.149999
6	51400001	51500000	867	-4.123691419	11	52700001	52800000	0.099999
6	51450001	51550000	1085	-4.001786676	11	69800001	69900000	0.099999
6	51500001	51600000	1299	-3.816477325	11	79750001	79900000	0.149999
6	51550001	51650000	1007	-4.072453467	11	96650001	96800000	0.149999
6	51600001	51700000	778	-3.109542715	11	101550001	101650000	0.099999
6	52100001	52200000	1049	-3.052712821	11	101750001	101850000	0.099999
6	52350001	52450000	1540	-3.254201664	11	101900001	102050000	0.149999
6	60300001	60400000	628	-4.275178773	11	102200001	102350000	0.149999
6	60350001	60450000	623	-4.084456868	12	20000001	20100000	0.099999
6	77200001	77300000	981	-2.978300262	12	29500001	29600000	0.099999
6	77400001	77500000	863	-3.345655918	12	52050001	52350000	0.299999
6	78300001	78400000	1366	-3.496362744	12	58450001	58550000	0.099999
6	78350001	78450000	1465	-4.239585928	12	70800001	70950000	0.149999
6	79200001	79300000	1046	-3.774828428	12	79450001	79550000	0.099999
6	79900001	80000000	1270	-4.262859916	13	26250001	26350000	0.099999
6	79950001	80050000	1150	-4.692572429	13	42650001	42750000	0.099999
6	80000001	80100000	776	-3.352300383	13	42800001	42900000	0.099999
6	80050001	80150000	971	-4.108787372	13	43400001	43500000	0.099999
6	80100001	80200000	1038	-4.112902944	13	48000001	48100000	0.099999
6	82750001	82850000	1337	-2.995031207	13	50200001	50350000	0.149999
7	9900001	10000000	114	-3.285114966	13	51150001	51300000	0.149999
7	21100001	21200000	623	-3.080043559	13	51400001	51500000	0.099999
7	34600001	34700000	610	-3.277385907	13	57450001	57550000	0.099999
7	49700001	49800000	222	-3.03327559	13	57900001	58050000	0.149999
7	49850001	49950000	291	-3.952587068	13	58250001	58350000	0.099999
7	49900001	50000000	422	-3.99121782	13	69650001	69800000	0.149999
7	49950001	50050000	449	-3.712289178	13	81850001	81950000	0.099999
7	50000001	50100000	380	-4.432749792	14	53600001	53900000	0.299999
7	50050001	50150000	357	-5.219122893	14	67900001	68100000	0.199999
7	50100001	50200000	343	-5.552583352	14	78850001	78950000	0.099999
7	50150001	50250000	352	-5.806043052	14	80750001	80850000	0.099999
7	50200001	50300000	498	-5.719239806	15	1500001	1600000	0.099999
7	50250001	50350000	695	-5.349337432	15	1700001	1800000	0.099999

Low 1% windows					Low 1% merged windows			
Chr	Start	End	nSNPs	*ZHp*	Chr	Start	End	Size (MB)
7	50300001	50400000	679	-4.820246275	15	14550001	14650000	0.099999
7	50350001	50450000	444	-4.501140981	15	21150001	21300000	0.149999
7	50400001	50500000	425	-3.250702197	15	51250001	51350000	0.099999
7	50500001	50600000	346	-3.887581192	15	63950001	64050000	0.099999
7	50550001	50650000	251	-4.754702828	15	64350001	64500000	0.149999
7	50600001	50700000	226	-4.781805779	15	72050001	72250000	0.199999
7	50650001	50750000	263	-5.222498323	16	17000001	17100000	0.099999
7	50700001	50800000	263	-5.054784182	16	19250001	19350000	0.099999
7	50750001	50850000	169	-4.896748319	16	19500001	19600000	0.099999
7	50800001	50900000	201	-5.29924119	16	20100001	20250000	0.149999
7	50850001	50950000	185	-5.284068308	16	35800001	35950000	0.149999
7	50900001	51000000	327	-5.201542588	16	36200001	36450000	0.249999
7	50950001	51050000	389	-5.080022861	16	41100001	41250000	0.149999
7	51000001	51100000	243	-4.851891142	16	54350001	54450000	0.099999
7	51050001	51150000	246	-4.749897586	16	69500001	69600000	0.099999
7	52100001	52200000	943	-4.030298487	17	650001	750000	0.099999
7	52150001	52250000	979	-5.113123582	17	22100001	22200000	0.099999
7	52200001	52300000	854	-4.42218412	17	29350001	29500000	0.149999
7	52250001	52350000	735	-4.391684925	17	68050001	68200000	0.149999
7	52700001	52800000	282	-3.059833887	18	13950001	14100000	0.149999
7	56500001	56600000	871	-3.931501116	18	15500001	15600000	0.099999
7	56550001	56650000	1119	-3.313011045	18	22200001	22350000	0.149999
7	61250001	61350000	573	-3.461336641	18	24100001	24200000	0.099999
7	61300001	61400000	504	-3.764822457	18	36900001	37100000	0.199999
7	61350001	61450000	721	-3.472481485	18	60700001	60800000	0.099999
7	74150001	74250000	1422	-3.060622532	19	13700001	13800000	0.099999
7	74200001	74300000	1385	-3.093314868	19	20150001	20300000	0.149999
7	74350001	74450000	1012	-3.261352603	19	26900001	27100000	0.199999
7	75850001	75950000	1185	-3.435257352	19	27200001	27350000	0.149999
7	75900001	76000000	872	-3.008372244	19	27400001	27650000	0.249999
7	75950001	76050000	706	-2.981674504	19	28150001	28250000	0.099999
7	76100001	76200000	943	-3.103765835	19	39250001	39400000	0.149999
7	81200001	81300000	892	-4.264993519	19	39450001	39550000	0.099999
7	81250001	81350000	768	-3.920582216	19	39650001	39950000	0.299999
7	91350001	91450000	487	-3.080073417	19	40100001	40550000	0.449999
7	98300001	98400000	764	-3.905457139	19	43900001	44150000	0.249999
7	98350001	98450000	865	-4.81048147	19	44200001	44350000	0.149999
7	98400001	98500000	939	-3.397239463	19	46050001	46200000	0.149999
8	7200001	7300000	339	-3.93278698	19	48700001	48800000	0.099999
8	7250001	7350000	208	-6.51739292	19	49700001	49800000	0.099999
8	7300001	7400000	249	-5.100934819	20	2900001	3000000	0.099999
8	31950001	32050000	595	-3.207402462	20	30700001	30850000	0.149999
8	65700001	65800000	1233	-3.226753666	20	39800001	39900000	0.099999
8	68500001	68600000	1142	-3.601486228	20	40200001	40400000	0.199999
8	77700001	77800000	917	-3.731903592	20	40450001	40550000	0.099999
8	77750001	77850000	960	-3.10956614	20	41200001	41350000	0.149999
8	79150001	79250000	412	-3.481631172	20	41400001	41500000	0.099999
8	80050001	80150000	782	-2.999975075	20	48800001	48950000	0.149999
8	93500001	93600000	1312	-3.003542702	20	49150001	49250000	0.099999
8	102800001	102900000	1012	-3.007653428	20	49900001	50000000	0.099999
8	112100001	112200000	993	-3.167628579	20	66650001	66750000	0.099999
9	2100001	2200000	1201	-2.973695147	21	10500001	10650000	0.149999
9	2900001	3000000	1398	-3.342643143	21	36800001	36900000	0.099999

Low 1% windows					Low 1% merged windows			
Chr	Start	End	nSNPs	*ZHp*	Chr	Start	End	Size (MB)
9	4100001	4200000	1579	-3.140739289	21	45450001	45550000	0.099999
9	4150001	4250000	1469	-4.048382658	21	50250001	50450000	0.199999
9	5150001	5250000	1324	-3.61701423	21	57800001	57950000	0.149999
9	19250001	19350000	1209	-2.985323544	21	58850001	58950000	0.099999
9	21900001	22000000	1275	-3.04132146	21	59300001	59450000	0.149999
9	21950001	22050000	676	-3.485044339	21	61450001	61550000	0.099999
9	23650001	23750000	1046	-3.125840347	22	1300001	1400000	0.099999
9	33050001	33150000	849	-3.078814017	22	10650001	10900000	0.249999
9	33350001	33450000	854	-3.05279058	22	10950001	11100000	0.149999
9	33400001	33500000	639	-3.124783021	22	11600001	11700000	0.099999
9	38850001	38950000	493	-3.541025796	22	14650001	14750000	0.099999
9	38900001	39000000	356	-3.608625006	22	26350001	26600000	0.249999
9	38950001	39050000	423	-3.934617156	22	32600001	32700000	0.099999
9	39000001	39100000	600	-4.490914282	23	1200001	1300000	0.099999
9	39050001	39150000	713	-3.558292389	23	8650001	8750000	0.099999
9	39100001	39200000	681	-3.303565348	23	9050001	9150000	0.099999
9	39150001	39250000	487	-3.721362072	23	47550001	47750000	0.199999
9	39400001	39500000	104	-4.104398664	24	34400001	34500000	0.099999
9	39450001	39550000	103	-3.672170839	25	1300001	1400000	0.099999
9	42500001	42600000	383	-3.040006233	25	9450001	9600000	0.149999
9	46500001	46600000	716	-3.095140769	25	26700001	26800000	0.099999
9	46550001	46650000	900	-3.115714785	25	30400001	30550000	0.149999
9	47750001	47850000	1210	-3.088727658	25	37650001	37750000	0.099999
9	68000001	68100000	1179	-2.997534464	26	18800001	18900000	0.099999
9	71000001	71100000	734	-3.297173747	26	30000001	30150000	0.149999
9	71050001	71150000	737	-3.500436987	26	31450001	31750000	0.299999
9	71750001	71850000	680	-4.187226495	26	38900001	39000000	0.099999
9	71800001	71900000	788	-4.986186787	27	10600001	10750000	0.149999
9	71850001	71950000	887	-4.275865599	27	21350001	21500000	0.149999
9	71900001	72000000	793	-3.616051183	27	21750001	21900000	0.149999
9	78200001	78300000	768	-3.037692533	27	34200001	34350000	0.149999
9	79250001	79350000	1096	-3.04163487	28	1300001	1400000	0.099999
9	83500001	83600000	1238	-2.991052865	28	1800001	1900000	0.099999
9	91400001	91500000	609	-3.227786695	28	15150001	15250000	0.099999
10	58600001	58700000	626	-3.729554032	28	32250001	32350000	0.099999
10	58650001	58750000	564	-4.432661601	29	1	350000	0.349999
10	58850001	58950000	721	-3.176331032	29	550001	650000	0.099999
10	58900001	59000000	698	-4.83142086	29	750001	900000	0.149999
10	58950001	59050000	673	-4.990174556	29	6050001	6200000	0.149999
10	59000001	59100000	398	-4.220702339	29	12650001	12800000	0.149999
10	59050001	59150000	223	-3.480882654	29	42850001	42950000	0.099999
10	96200001	96300000	1106	-3.553464724				
10	96250001	96350000	1126	-3.04655642				
11	7700001	7800000	859	-3.770528573				
11	7850001	7950000	702	-3.224991963				
11	7900001	8000000	1079	-3.026130118				
11	12900001	13000000	730	-3.758276639				
11	12950001	13050000	613	-4.146160093				
11	13150001	13250000	838	-4.129101159				
11	13200001	13300000	797	-3.639379238				
11	13850001	13950000	869	-3.045882883				
11	14350001	14450000	641	-3.150728568				
11	14650001	14750000	545	-3.908078511				

Low 1% windows					Low 1% merged windows			
Chr	Start	End	nSNPs	*ZHp*	Chr	Start	End	Size (MB)
11	14700001	14800000	779	-3.263668179				
11	15450001	15550000	456	-3.273856516				
11	16250001	16350000	958	-2.975654043				
11	16550001	16650000	1067	-3.581679085				
11	22950001	23050000	797	-3.510874976				
11	38600001	38700000	689	-3.001732025				
11	38800001	38900000	1061	-3.175341804				
11	41150001	41250000	578	-4.298843781				
11	41200001	41300000	515	-2.99160927				
11	52700001	52800000	1236	-2.975177568				
11	69800001	69900000	874	-3.313129653				
11	79750001	79850000	761	-3.124931325				
11	79800001	79900000	825	-3.47998508				
11	96650001	96750000	421	-3.531259729				
11	96700001	96800000	414	-3.099563262				
11	101550001	101650000	750	-3.921780652				
11	101750001	101850000	691	-3.13438187				
11	101900001	102000000	1468	-3.48731693				
11	101950001	102050000	1152	-3.883845508				
11	102200001	102300000	1162	-3.692768621				
11	102250001	102350000	957	-3.13375195				
12	20000001	20100000	564	-4.206993201				
12	29500001	29600000	386	-3.032213697				
12	52050001	52150000	537	-4.520119985				
12	52100001	52200000	500	-4.527681914				
12	52150001	52250000	544	-4.414795219				
12	52200001	52300000	621	-3.530438158				
12	52250001	52350000	753	-3.064391435				
12	58450001	58550000	910	-3.193226697				
12	70800001	70900000	973	-3.773305776				
12	70850001	70950000	715	-4.956874459				
12	79450001	79550000	943	-3.276775999				
13	26250001	26350000	1104	-3.042245069				
13	42650001	42750000	799	-3.832141815				
13	42800001	42900000	865	-4.615867131				
13	43400001	43500000	534	-3.429888459				
13	48000001	48100000	845	-2.999218669				
13	50200001	50300000	340	-3.452311865				
13	50250001	50350000	311	-4.090816365				
13	51150001	51250000	608	-3.070017291				
13	51200001	51300000	559	-4.402946716				
13	51400001	51500000	439	-3.67148268				
13	57450001	57550000	266	-3.42879011				
13	57900001	58000000	411	-3.275703447				
13	57950001	58050000	372	-3.722769859				
13	58250001	58350000	897	-2.990315374				
13	69650001	69750000	288	-3.024487902				
13	69700001	69800000	269	-3.815441917				
13	81850001	81950000	1093	-3.922125953				
14	53600001	53700000	727	-3.772570296				
14	53650001	53750000	826	-4.061186974				
14	53700001	53800000	726	-3.417391346				
14	53800001	53900000	819	-3.004987445				

Low 1% windows					Low 1% merged windows			
Chr	Start	End	nSNPs	*ZHp*	Chr	Start	End	Size (MB)
14	67900001	68000000	377	-3.634360279				
14	67950001	68050000	645	-3.482158106				
14	68000001	68100000	556	-2.985230645				
14	78850001	78950000	1458	-3.376596896				
14	80750001	80850000	1111	-3.084314678				
15	1500001	1600000	956	-3.141849423				
15	1700001	1800000	462	-3.631058665				
15	14550001	14650000	1019	-3.072719384				
15	21150001	21250000	1290	-3.679161594				
15	21200001	21300000	1082	-4.134024428				
15	51250001	51350000	659	-3.092733194				
15	63950001	64050000	912	-4.576917568				
15	64350001	64450000	957	-3.27350609				
15	64400001	64500000	1130	-3.220144166				
15	72050001	72150000	1187	-3.487757012				
15	72100001	72200000	1000	-3.845513167				
15	72150001	72250000	997	-4.016643156				
16	17000001	17100000	1465	-3.440847904				
16	19250001	19350000	662	-3.157457286				
16	19500001	19600000	757	-3.021760768				
16	20100001	20200000	919	-3.050597216				
16	20150001	20250000	1020	-3.066240497				
16	35800001	35900000	771	-3.397857579				
16	35850001	35950000	1095	-3.129387907				
16	36200001	36300000	738	-4.42915281				
16	36250001	36350000	681	-4.206949659				
16	36300001	36400000	724	-4.033500602				
16	36350001	36450000	754	-3.7732089				
16	41100001	41200000	728	-3.026380286				
16	41150001	41250000	765	-2.981522607				
16	54350001	54450000	866	-3.280731444				
16	69500001	69600000	526	-3.438170952				
17	650001	750000	988	-3.140209168				
17	22100001	22200000	958	-3.571038527				
17	29350001	29450000	273	-3.710591058				
17	29400001	29500000	320	-3.672845496				
17	68050001	68150000	662	-2.998762094				
17	68100001	68200000	899	-3.57853099				
18	13950001	14050000	607	-3.542367811				
18	14000001	14100000	647	-3.929842968				
18	15500001	15600000	685	-3.027572819				
18	22200001	22300000	565	-3.827773494				
18	22250001	22350000	579	-3.276588947				
18	24100001	24200000	367	-5.338678981				
18	36900001	37000000	504	-3.329309911				
18	36950001	37050000	586	-3.166676862				
18	37000001	37100000	692	-3.017433964				
18	60700001	60800000	1014	-2.999937159				
19	13700001	13800000	702	-3.2218078				
19	20150001	20250000	438	-3.38339597				
19	20200001	20300000	451	-3.803523482				
19	26900001	27000000	269	-4.092082597				
19	26950001	27050000	226	-3.639525024				

Low 1% windows					Low 1% merged windows			
Chr	Start	End	nSNPs	*ZHp*	Chr	Start	End	Size (MB)
19	27000001	27100000	187	-3.036534119				
19	27200001	27300000	653	-3.244697381				
19	27250001	27350000	385	-3.517213724				
19	27400001	27500000	254	-4.171822208				
19	27450001	27550000	258	-3.123311785				
19	27550001	27650000	341	-3.240934374				
19	28150001	28250000	586	-3.332063115				
19	39250001	39350000	425	-3.113854036				
19	39300001	39400000	283	-3.349398528				
19	39450001	39550000	546	-3.418834402				
19	39650001	39750000	536	-3.819860536				
19	39700001	39800000	372	-4.775844162				
19	39750001	39850000	237	-5.989293124				
19	39800001	39900000	199	-6.232950857				
19	39850001	39950000	303	-4.74753754				
19	40100001	40200000	259	-2.967135643				
19	40150001	40250000	343	-3.469986496				
19	40200001	40300000	575	-3.140900511				
19	40250001	40350000	743	-3.937550367				
19	40300001	40400000	538	-4.432044015				
19	40350001	40450000	346	-4.126244143				
19	40400001	40500000	421	-5.48143367				
19	40450001	40550000	481	-3.619100185				
19	43900001	44000000	515	-3.19020089				
19	43950001	44050000	439	-3.772547559				
19	44000001	44100000	634	-3.985529886				
19	44050001	44150000	690	-3.070069018				
19	44200001	44300000	277	-3.535751772				
19	44250001	44350000	392	-3.17964672				
19	46050001	46150000	858	-3.045123842				
19	46100001	46200000	847	-3.044360121				
19	48700001	48800000	402	-3.299681813				
19	49700001	49800000	1497	-2.960861204				
20	2900001	3000000	533	-3.043682739				
20	30700001	30800000	1231	-3.294814498				
20	30750001	30850000	1124	-3.069976358				
20	39800001	39900000	444	-3.246382326				
20	40200001	40300000	971	-3.368039791				
20	40250001	40350000	835	-4.44240124				
20	40300001	40400000	660	-4.090723828				
20	40450001	40550000	627	-3.377648741				
20	41200001	41300000	332	-3.155134497				
20	41250001	41350000	451	-2.986083036				
20	41400001	41500000	619	-3.067609987				
20	48800001	48900000	1107	-4.28048274				
20	48850001	48950000	910	-4.353327859				
20	49150001	49250000	1480	-3.598973115				
20	49900001	50000000	1395	-3.041586251				
20	66650001	66750000	1674	-3.027600931				
21	10500001	10600000	360	-3.6488084				
21	10550001	10650000	376	-4.104204444				
21	36800001	36900000	335	-3.807174336				
21	45450001	45550000	644	-3.186958164				

Low 1% windows					Low 1% merged windows			
Chr	Start	End	nSNPs	*ZHp*	Chr	Start	End	Size (MB)
21	50250001	50350000	1444	-3.145865999				
21	50300001	50400000	1332	-3.974628195				
21	50350001	50450000	1004	-3.381423295				
21	57800001	57900000	903	-3.246953837				
21	57850001	57950000	847	-3.393852624				
21	58850001	58950000	532	-3.087622428				
21	59300001	59400000	1427	-3.090867399				
21	59350001	59450000	1201	-3.240001189				
21	61450001	61550000	814	-3.037595762				
22	1300001	1400000	945	-3.312724053				
22	10650001	10750000	272	-3.337854261				
22	10700001	10800000	88	-3.042620654				
22	10800001	10900000	52	-3.049302678				
22	10950001	11050000	925	-3.826923365				
22	11000001	11100000	717	-3.572571027				
22	11600001	11700000	352	-3.020592917				
22	14650001	14750000	818	-3.106864576				
22	26350001	26450000	1005	-3.675295687				
22	26400001	26500000	819	-3.818403497				
22	26450001	26550000	768	-3.858541254				
22	26500001	26600000	858	-2.978017437				
22	32600001	32700000	1069	-3.363105524				
23	1200001	1300000	1037	-3.091295739				
23	8650001	8750000	538	-3.2628654				
23	9050001	9150000	915	-3.314756803				
23	47550001	47650000	714	-3.025994812				
23	47600001	47700000	680	-4.46744122				
23	47650001	47750000	754	-3.572535637				
24	34400001	34500000	518	-3.153233991				
25	1300001	1400000	644	-3.057617696				
25	9450001	9550000	955	-3.486452332				
25	9500001	9600000	845	-3.036636222				
25	26700001	26800000	467	-3.051856391				
25	30400001	30500000	500	-3.110218248				
25	30450001	30550000	537	-2.973023061				
25	37650001	37750000	761	-3.379160618				
26	18800001	18900000	656	-3.036587806				
26	30000001	30100000	941	-3.253627721				
26	30050001	30150000	806	-3.151057992				
26	31450001	31550000	331	-3.710408839				
26	31500001	31600000	361	-3.554428957				
26	31550001	31650000	539	-3.173613881				
26	31650001	31750000	800	-3.139584566				
26	38900001	39000000	558	-3.471856282				
27	10600001	10700000	758	-3.213119612				
27	10650001	10750000	695	-3.836479924				
27	21350001	21450000	735	-3.467571307				
27	21400001	21500000	774	-3.261341029				
27	21750001	21850000	1023	-3.795933047				
27	21800001	21900000	834	-3.377418651				
27	34200001	34300000	845	-3.286178535				
27	34250001	34350000	745	-3.034856373				
28	1300001	1400000	1124	-2.987053952				

Low 1% windows					Low 1% merged windows			
Chr	Start	End	nSNPs	*ZHp*	Chr	Start	End	Size (MB)
28	1800001	1900000	926	-3.628380952				
28	15150001	15250000	1087	-3.295622231				
28	32250001	32350000	692	-4.237016108				
29	1	100000	1191	-4.611864698				
29	50001	150000	1154	-5.168434062				
29	100001	200000	1234	-5.318255667				
29	150001	250000	1056	-5.426189892				
29	200001	300000	771	-4.96923191				
29	250001	350000	1259	-3.505576755				
29	550001	650000	663	-3.076318193				
29	750001	850000	785	-3.756136363				
29	800001	900000	957	-3.212804142				
29	6050001	6150000	1231	-3.236807644				
29	6100001	6200000	1499	-3.206524074				
29	12650001	12750000	1047	-3.234286663				
29	12700001	12800000	1277	-3.505418819				
29	42850001	42950000	702	-3.144728533				

Table S30. The low 1% *Hp* detected windows in Arado cattle.

Low 1% windows					Low 1% merged windows			
Chr	Start	End	nSNPs	*ZHp*	Chr	Start	End	Size (MB)
1	3750001	3850000	390	-3.521109668	1	3750001	3850000	0.099999
1	16450001	16550000	1382	-4.329362592	1	16450001	16600000	0.149999
1	16500001	16600000	1323	-4.880472237	1	27400001	27550000	0.149999
1	27400001	27500000	1087	-3.260221901	1	28900001	29000000	0.099999
1	27450001	27550000	1074	-3.001545802	1	40600001	40700000	0.099999
1	28900001	29000000	1248	-3.384142695	1	44050001	44350000	0.299999
1	40600001	40700000	1080	-3.419771123	1	119700001	119800000	0.099999
1	44050001	44150000	504	-5.292826992	1	133250001	133350000	0.099999
1	44100001	44200000	368	-5.288950789	1	155750001	155850000	0.099999
1	44150001	44250000	372	-5.436760707	1	155950001	156050000	0.099999
1	44200001	44300000	323	-5.326659823	2	12850001	12950000	0.099999
1	44250001	44350000	258	-5.279291114	2	20750001	20850000	0.099999
1	119700001	119800000	1171	-2.956722926	2	40450001	40550000	0.099999
1	133250001	133350000	716	-3.104445847	2	61600001	61800000	0.199999
1	155750001	155850000	1049	-2.954393527	2	63400001	63500000	0.099999
1	155950001	156050000	1060	-3.259830162	2	70300001	70400000	0.099999
2	12850001	12950000	1236	-2.945063837	2	82100001	82200000	0.099999
2	20750001	20850000	391	-2.977680938	2	85950001	86050000	0.099999
2	40450001	40550000	537	-3.348312836	2	86250001	86450000	0.199999
2	61600001	61700000	757	-3.611860795	2	89500001	89600000	0.099999
2	61650001	61750000	744	-3.838775266	2	100250001	100350000	0.099999
2	61700001	61800000	837	-4.018112636	2	119800001	119900000	0.099999
2	63400001	63500000	1256	-3.481363745	2	126400001	126500000	0.099999
2	70300001	70400000	710	-3.03361595	3	8100001	8250000	0.149999
2	82100001	82200000	736	-3.281933861	3	17700001	17800000	0.099999
2	85950001	86050000	366	-3.253507754	3	44400001	44500000	0.099999
2	86250001	86350000	508	-3.035516023	3	47050001	47200000	0.149999
2	86300001	86400000	775	-3.798434598	3	50050001	50200000	0.149999
2	86350001	86450000	689	-3.813257109	3	51950001	52050000	0.099999
2	89500001	89600000	453	-3.332854589	3	53200001	53350000	0.149999

Low 1% windows					Low 1% merged windows			
Chr	Start	End	nSNPs	*ZHp*	Chr	Start	End	Size (MB)
2	100250001	100350000	1066	-3.238249344	3	57350001	57650000	0.299999
2	119800001	119900000	456	-3.522043001	3	59350001	59500000	0.149999
2	126400001	126500000	341	-3.069056009	3	59800001	59900000	0.099999
3	8100001	8200000	753	-4.203730194	3	60050001	60150000	0.099999
3	8150001	8250000	797	-3.730066272	3	66100001	66250000	0.149999
3	17700001	17800000	937	-3.27979643	3	98200001	98300000	0.099999
3	44400001	44500000	1157	-2.996507776	3	98350001	98450000	0.099999
3	47050001	47150000	866	-2.931228014	3	99000001	99100000	0.099999
3	47100001	47200000	1042	-3.431018423	4	5850001	5950000	0.099999
3	50050001	50150000	539	-3.063222279	4	14250001	14350000	0.099999
3	50100001	50200000	539	-2.975904973	4	31550001	31650000	0.099999
3	51950001	52050000	681	-3.180042651	4	41450001	41550000	0.099999
3	53200001	53300000	578	-2.98268913	4	41850001	42050000	0.199999
3	53250001	53350000	781	-3.449779048	4	44100001	44250000	0.149999
3	57350001	57450000	530	-3.422044455	4	48150001	48250000	0.099999
3	57400001	57500000	588	-3.148216234	4	66150001	66350000	0.199999
3	57450001	57550000	933	-3.459848633	4	95600001	95700000	0.099999
3	57500001	57600000	918	-3.644297687	4	112000001	112150000	0.149999
3	57550001	57650000	1007	-3.169752212	5	9150001	9250000	0.099999
3	59350001	59450000	582	-2.93331301	5	9750001	9850000	0.099999
3	59400001	59500000	497	-3.23753715	5	18250001	18400000	0.149999
3	59800001	59900000	331	-3.94537705	5	18700001	18850000	0.149999
3	60050001	60150000	1002	-3.005483706	5	28250001	28400000	0.149999
3	66100001	66200000	597	-3.607283559	5	34050001	34700000	0.649999
3	66150001	66250000	763	-2.905985126	5	36950001	37050000	0.099999
3	98200001	98300000	845	-3.180021201	5	65500001	65600000	0.099999
3	98350001	98450000	692	-3.370285756	5	66550001	66700000	0.149999
3	99000001	99100000	627	-2.932584122	5	80850001	80950000	0.099999
4	5850001	5950000	1490	-3.034848993	5	95650001	95750000	0.099999
4	14250001	14350000	432	-4.384392005	5	112300001	112450000	0.149999
4	31550001	31650000	339	-2.928645054	5	113700001	113800000	0.099999
4	41450001	41550000	853	-3.285268456	5	119200001	119850000	0.649999
4	41850001	41950000	746	-3.279689854	6	2850001	2950000	0.099999
4	41900001	42000000	916	-3.807118171	6	6200001	6300000	0.099999
4	41950001	42050000	796	-3.563589874	6	12250001	12350000	0.099999
4	44100001	44200000	938	-2.99235945	6	14250001	14350000	0.099999
4	44150001	44250000	1240	-3.233602502	6	41800001	41950000	0.149999
4	48150001	48250000	423	-2.985335062	6	42000001	42100000	0.099999
4	66150001	66250000	621	-2.998050025	6	42250001	42350000	0.099999
4	66200001	66300000	565	-3.797102753	6	44050001	44250000	0.199999
4	66250001	66350000	564	-3.133910311	6	44700001	44850000	0.149999
4	95600001	95700000	1362	-3.363872734	6	50950001	51500000	0.549999
4	112000001	112100000	544	-3.009571233	6	52350001	52450000	0.099999
4	112050001	112150000	562	-3.096669892	6	68450001	68550000	0.099999
5	9150001	9250000	739	-2.938238824	6	73650001	73750000	0.099999
5	9750001	9850000	1127	-3.469771506	6	79950001	80050000	0.099999
5	18250001	18350000	652	-3.517918285	6	86800001	86950000	0.149999
5	18300001	18400000	835	-3.220564853	6	101300001	101400000	0.099999
5	18700001	18800000	467	-4.833522631	6	101650001	101750000	0.099999
5	18750001	18850000	391	-3.004344423	7	9900001	10000000	0.099999
5	28250001	28350000	695	-4.198950657	7	21400001	21600000	0.199999
5	28300001	28400000	705	-3.053099936	7	21700001	21800000	0.099999
5	34050001	34150000	636	-2.998364463	7	21850001	21950000	0.099999

Low 1% windows					Low 1% merged windows			
Chr	Start	End	nSNPs	*ZHp*	Chr	Start	End	Size (MB)
5	34100001	34200000	705	-3.51136729	7	38350001	38500000	0.149999
5	34150001	34250000	674	-3.485710085	7	47000001	47150000	0.149999
5	34200001	34300000	385	-2.972078514	7	47300001	47400000	0.099999
5	34250001	34350000	431	-3.603016067	7	48500001	48600000	0.099999
5	34300001	34400000	435	-4.334098879	7	48900001	49050000	0.149999
5	34350001	34450000	329	-4.496195074	7	49850001	51150000	1.299999
5	34400001	34500000	272	-4.886163026	7	52100001	52350000	0.249999
5	34450001	34550000	315	-5.252622107	7	63500001	63600000	0.099999
5	34500001	34600000	410	-5.269663189	7	73450001	73550000	0.099999
5	34550001	34650000	328	-4.941780302	7	110300001	110400000	0.099999
5	34600001	34700000	244	-3.306534486	8	22550001	22650000	0.099999
5	36950001	37050000	977	-3.116691509	8	38700001	38800000	0.099999
5	65500001	65600000	865	-2.933261227	8	59550001	59700000	0.149999
5	66550001	66650000	789	-3.661269362	8	77400001	77550000	0.149999
5	66600001	66700000	956	-3.143305573	8	77650001	77850000	0.199999
5	80850001	80950000	771	-3.072757118	8	89000001	89100000	0.099999
5	95650001	95750000	1331	-2.944546383	9	850001	950000	0.099999
5	112300001	112400000	517	-3.243616178	9	1300001	1450000	0.149999
5	112350001	112450000	623	-3.18349326	9	3650001	3750000	0.099999
5	113700001	113800000	956	-3.637487984	9	4150001	4300000	0.149999
5	119200001	119300000	911	-4.597631696	9	5300001	5450000	0.149999
5	119250001	119350000	980	-3.291095999	9	19400001	19550000	0.149999
5	119350001	119450000	1154	-3.913170792	9	24150001	24250000	0.099999
5	119400001	119500000	875	-5.618997053	9	31050001	31150000	0.099999
5	119450001	119550000	360	-7.348919241	9	33000001	33100000	0.099999
5	119500001	119600000	435	-5.442334544	9	33350001	33700000	0.349999
5	119550001	119650000	592	-4.073377436	9	38800001	38950000	0.149999
5	119650001	119750000	923	-3.045650668	9	39000001	39250000	0.249999
5	119700001	119800000	872	-3.37129914	9	39300001	39550000	0.249999
5	119750001	119850000	638	-3.199724318	9	43900001	44000000	0.099999
6	2850001	2950000	978	-3.194425665	9	47750001	47850000	0.099999
6	6200001	6300000	1109	-3.12937619	9	62200001	62500000	0.299999
6	12250001	12350000	847	-3.024278	9	71700001	71950000	0.249999
6	14250001	14350000	1095	-3.55994352	9	72050001	72150000	0.099999
6	41800001	41900000	821	-3.765432533	9	72200001	72300000	0.099999
6	41850001	41950000	879	-2.946430364	9	73650001	73750000	0.099999
6	42000001	42100000	881	-3.33271355	9	75250001	75350000	0.099999
6	42250001	42350000	1156	-3.146520005	9	75600001	75700000	0.099999
6	44050001	44150000	796	-3.001649948	9	93700001	93850000	0.149999
6	44150001	44250000	876	-3.016428925	10	39150001	39250000	0.099999
6	44700001	44800000	590	-2.997639144	10	54200001	54350000	0.149999
6	44750001	44850000	449	-3.335876696	10	54450001	54550000	0.099999
6	50950001	51050000	988	-3.461725654	10	54700001	54800000	0.099999
6	51000001	51100000	850	-4.205935873	10	55050001	55250000	0.199999
6	51050001	51150000	582	-5.129835245	10	57400001	57500000	0.099999
6	51100001	51200000	535	-5.008102446	10	58650001	58750000	0.099999
6	51150001	51250000	439	-3.712693561	11	7150001	7250000	0.099999
6	51250001	51350000	975	-2.929384372	11	8300001	8500000	0.199999
6	51300001	51400000	1096	-3.579628607	11	12900001	13050000	0.149999
6	51350001	51450000	901	-3.515468781	11	13100001	13300000	0.199999
6	51400001	51500000	977	-3.625038843	11	13800001	13950000	0.149999
6	52350001	52450000	1485	-3.444281522	11	14650001	14800000	0.149999
6	68450001	68550000	774	-3.929945941	11	16200001	16350000	0.149999

Low 1% windows					Low 1% merged windows			
Chr	Start	End	nSNPs	*ZHp*	Chr	Start	End	Size (MB)
6	73650001	73750000	1156	-3.050529467	11	42500001	42600000	0.099999
6	79950001	80050000	1418	-3.450047993	11	46000001	46100000	0.099999
6	86800001	86900000	1003	-3.333026382	11	46200001	46400000	0.199999
6	86850001	86950000	1003	-2.989327941	11	73200001	73350000	0.149999
6	101300001	101400000	1262	-3.265594175	11	75200001	75350000	0.149999
6	101650001	101750000	632	-4.045732661	11	79800001	79950000	0.149999
7	9900001	10000000	136	-3.202940046	11	95250001	95350000	0.099999
7	21400001	21500000	373	-3.292813932	12	5550001	5750000	0.199999
7	21450001	21550000	469	-4.533152889	12	11950001	12050000	0.099999
7	21500001	21600000	587	-3.301901578	12	42150001	42250000	0.099999
7	21700001	21800000	608	-2.932915559	12	76700001	76900000	0.199999
7	21850001	21950000	725	-3.763580322	13	1050001	1150000	0.099999
7	38350001	38450000	279	-4.567635228	13	17550001	17650000	0.099999
7	38400001	38500000	279	-3.65782204	13	17700001	17950000	0.249999
7	47000001	47100000	653	-3.221430885	13	18050001	18200000	0.149999
7	47050001	47150000	857	-3.413863009	13	22450001	22600000	0.149999
7	47300001	47400000	749	-3.663184073	13	49600001	49700000	0.099999
7	48500001	48600000	903	-3.509967988	13	49800001	50000000	0.199999
7	48900001	49000000	691	-3.275480299	13	50150001	50300000	0.149999
7	48950001	49050000	575	-5.283052288	14	3350001	3450000	0.099999
7	49850001	49950000	335	-2.944106927	14	27800001	27900000	0.099999
7	49900001	50000000	474	-3.75152615	14	42300001	42400000	0.099999
7	49950001	50050000	460	-4.502067039	14	53650001	53800000	0.149999
7	50000001	50100000	374	-5.012099008	14	78300001	78450000	0.149999
7	50050001	50150000	350	-5.39212694	15	1300001	1400000	0.099999
7	50100001	50200000	337	-5.667079143	15	1450001	1650000	0.199999
7	50150001	50250000	348	-5.990638842	15	1700001	1900000	0.199999
7	50200001	50300000	494	-5.851709871	15	2850001	2950000	0.099999
7	50250001	50350000	700	-5.324161675	15	3200001	3300000	0.099999
7	50300001	50400000	679	-4.79190579	15	53150001	53300000	0.149999
7	50350001	50450000	436	-4.543792607	15	53450001	53550000	0.099999
7	50400001	50500000	422	-3.114195689	15	59900001	60000000	0.099999
7	50500001	50600000	378	-3.833446764	15	77050001	77150000	0.099999
7	50550001	50650000	319	-4.384068536	16	12100001	12250000	0.149999
7	50600001	50700000	312	-4.697331051	16	18500001	18600000	0.099999
7	50650001	50750000	352	-4.988736037	16	19250001	19500000	0.249999
7	50700001	50800000	312	-4.873933585	16	27350001	27550000	0.199999
7	50750001	50850000	210	-4.682229674	16	36300001	36450000	0.149999
7	50800001	50900000	239	-4.644463487	16	37550001	37700000	0.149999
7	50850001	50950000	220	-4.538911367	16	38950001	39050000	0.099999
7	50900001	51000000	373	-4.917254037	16	50500001	50650000	0.149999
7	50950001	51050000	433	-5.058424178	17	8650001	8750000	0.099999
7	51000001	51100000	321	-5.196098634	17	11450001	11600000	0.149999
7	51050001	51150000	360	-4.860311291	17	13200001	13300000	0.099999
7	52100001	52200000	835	-3.321614651	17	27200001	27300000	0.099999
7	52150001	52250000	773	-3.490614964	17	29350001	29500000	0.149999
7	52250001	52350000	609	-3.454643856	17	43600001	43700000	0.099999
7	63500001	63600000	1162	-3.175473898	18	7900001	8050000	0.149999
7	73450001	73550000	1048	-3.43332818	18	21550001	21750000	0.199999
7	110300001	110400000	1130	-2.956233947	18	30800001	30950000	0.149999
8	22550001	22650000	727	-3.16911152	18	35750001	35850000	0.099999
8	38700001	38800000	494	-3.00064964	18	36650001	36800000	0.149999
8	59550001	59650000	444	-3.659367387	18	36850001	37300000	0.449999

Low 1% windows					Low 1% merged windows			
Chr	Start	End	nSNPs	*ZHp*	Chr	Start	End	Size (MB)
8	59600001	59700000	453	-3.219862737	18	37400001	37550000	0.149999
8	77400001	77500000	788	-3.206632172	19	26350001	26500000	0.149999
8	77450001	77550000	770	-3.171984506	19	26700001	26800000	0.099999
8	77650001	77750000	731	-3.017246848	19	26850001	27000000	0.149999
8	77700001	77800000	917	-3.743429694	19	27500001	27650000	0.149999
8	77750001	77850000	915	-2.93058542	19	35650001	35800000	0.149999
8	89000001	89100000	1024	-3.11423488	19	39450001	39550000	0.099999
9	850001	950000	880	-2.949391899	19	39750001	40000000	0.249999
9	1300001	1400000	1506	-3.546420025	19	40350001	40650000	0.299999
9	1350001	1450000	1403	-3.672680847	19	41450001	41550000	0.099999
9	3650001	3750000	1262	-3.402718035	19	42550001	42650000	0.099999
9	4150001	4250000	1622	-3.654283467	19	52200001	52350000	0.149999
9	4200001	4300000	1939	-3.063209674	19	62250001	62350000	0.099999
9	5300001	5400000	1085	-3.393292267	20	21900001	22000000	0.099999
9	5350001	5450000	1249	-4.011783029	20	39750001	39850000	0.099999
9	19400001	19500000	1245	-3.011276918	20	39900001	40150000	0.249999
9	19450001	19550000	1236	-3.633054215	20	40200001	40400000	0.199999
9	24150001	24250000	442	-4.731797565	20	40450001	40650000	0.199999
9	31050001	31150000	1232	-3.048109215	20	40800001	41000000	0.199999
9	33000001	33100000	1059	-3.310140826	20	48650001	48950000	0.299999
9	33350001	33450000	1002	-3.166628327	20	49150001	49250000	0.099999
9	33400001	33500000	527	-3.711407028	20	49300001	49400000	0.099999
9	33450001	33550000	429	-4.210811401	20	54050001	54150000	0.099999
9	33500001	33600000	527	-4.049403651	20	54250001	54400000	0.149999
9	33550001	33650000	447	-3.719437971	20	66650001	66800000	0.149999
9	33600001	33700000	399	-3.339900036	21	51450001	51600000	0.149999
9	38800001	38900000	477	-4.441855797	21	55000001	55300000	0.299999
9	38850001	38950000	407	-4.06320599	21	57800001	57950000	0.149999
9	39000001	39100000	326	-2.939668162	21	58200001	58300000	0.099999
9	39100001	39200000	651	-3.176552148	21	59300001	59400000	0.099999
9	39150001	39250000	492	-3.23903736	21	61650001	61750000	0.099999
9	39300001	39400000	441	-3.744915148	22	10300001	10450000	0.149999
9	39350001	39450000	369	-4.18819326	22	10500001	10600000	0.099999
9	39400001	39500000	319	-3.645387963	22	10850001	11000000	0.149999
9	39450001	39550000	376	-3.104503723	22	11550001	11750000	0.199999
9	43900001	44000000	532	-3.27894632	22	13800001	13950000	0.149999
9	47750001	47850000	1024	-3.697744503	22	32600001	32700000	0.099999
9	62200001	62300000	481	-3.457233527	22	40600001	40800000	0.199999
9	62250001	62350000	610	-3.112026024	22	44650001	44850000	0.199999
9	62300001	62400000	455	-2.912474745	22	45050001	45150000	0.099999
9	62350001	62450000	241	-3.496782402	22	45300001	45400000	0.099999
9	62400001	62500000	380	-3.166697053	23	300001	500000	0.199999
9	71700001	71800000	580	-3.198980819	23	800001	950000	0.149999
9	71750001	71850000	769	-3.614777429	23	49100001	49200000	0.099999
9	71800001	71900000	875	-4.245323965	24	2350001	2450000	0.099999
9	71850001	71950000	968	-3.65264913	24	15050001	15200000	0.149999
9	72050001	72150000	673	-4.353390413	24	34400001	34500000	0.099999
9	72200001	72300000	706	-4.919537389	25	16150001	16250000	0.099999
9	73650001	73750000	847	-4.000293783	25	22650001	22800000	0.149999
9	75250001	75350000	1082	-2.905174118	25	30350001	30700000	0.349999
9	75600001	75700000	783	-3.173371524	26	38150001	38300000	0.149999
9	93700001	93800000	616	-2.920115755	26	38850001	38950000	0.099999
9	93750001	93850000	509	-3.128536866	27	12400001	12500000	0.099999

Low 1% windows					Low 1% merged windows			
Chr	Start	End	nSNPs	*ZHp*	Chr	Start	End	Size (MB)
10	39150001	39250000	1001	-2.933822127	27	15350001	15450000	0.099999
10	54200001	54300000	588	-3.236354041	27	21950001	22050000	0.099999
10	54250001	54350000	509	-3.234972973	27	23450001	23650000	0.199999
10	54450001	54550000	735	-3.276918995	27	23700001	23800000	0.099999
10	54700001	54800000	596	-3.196802294	27	23950001	24100000	0.149999
10	55050001	55150000	574	-3.117151219	27	34200001	34300000	0.099999
10	55100001	55200000	676	-3.447475271	27	34400001	34550000	0.149999
10	55150001	55250000	716	-3.181655467	28	1450001	1550000	0.099999
10	57400001	57500000	797	-2.995475678	28	21100001	21200000	0.099999
10	58650001	58750000	554	-3.890645724	28	32200001	32350000	0.149999
11	7150001	7250000	768	-4.1644254	28	39650001	39750000	0.099999
11	8300001	8400000	686	-3.666023634	29	50001	400000	0.349999
11	8350001	8450000	1023	-3.090796528	29	550001	650000	0.099999
11	8400001	8500000	927	-3.055557264	29	750001	900000	0.149999
11	12900001	13000000	768	-3.547679422	29	21200001	21300000	0.099999
11	12950001	13050000	622	-3.149573958	29	33100001	33200000	0.099999
11	13100001	13200000	753	-3.642391384				
11	13150001	13250000	646	-4.47079459				
11	13200001	13300000	520	-3.45936134				
11	13800001	13900000	878	-3.399333005				
11	13850001	13950000	712	-4.294899584				
11	14650001	14750000	585	-4.147609521				
11	14700001	14800000	724	-3.218549981				
11	16200001	16300000	735	-3.753061634				
11	16250001	16350000	1084	-3.320100958				
11	42500001	42600000	693	-3.112266741				
11	46000001	46100000	813	-3.270731057				
11	46200001	46300000	769	-3.707354036				
11	46250001	46350000	694	-4.421765837				
11	46300001	46400000	483	-4.195753645				
11	73200001	73300000	359	-3.263776138				
11	73250001	73350000	505	-3.113629038				
11	75200001	75300000	802	-3.650989104				
11	75250001	75350000	994	-4.47585245				
11	79800001	79900000	939	-3.060889652				
11	79850001	79950000	975	-3.019182344				
11	95250001	95350000	1040	-3.048464165				
12	5550001	5650000	1684	-2.940440564				
12	5600001	5700000	1815	-3.414333494				
12	5650001	5750000	1630	-3.353954581				
12	11950001	12050000	819	-2.95586618				
12	42150001	42250000	1371	-3.201243543				
12	76700001	76800000	418	-2.972511684				
12	76750001	76850000	569	-2.981163995				
12	76800001	76900000	615	-3.192303724				
13	1050001	1150000	1037	-3.061966883				
13	17550001	17650000	911	-2.967126217				
13	17700001	17800000	750	-3.62067337				
13	17750001	17850000	608	-4.297476959				
13	17800001	17900000	385	-4.71558704				
13	17850001	17950000	383	-3.579884766				
13	18050001	18150000	636	-3.373581076				
13	18100001	18200000	546	-4.083467136				

Low 1% windows					Low 1% merged windows			
Chr	Start	End	nSNPs	*ZHp*	Chr	Start	End	Size (MB)
13	22450001	22550000	760	-3.111656477				
13	22500001	22600000	752	-3.882906633				
13	49600001	49700000	875	-2.978620823				
13	49800001	49900000	694	-2.925726729				
13	49850001	49950000	762	-3.401589138				
13	49900001	50000000	576	-3.224828626				
13	50150001	50250000	472	-3.533430508				
13	50200001	50300000	391	-3.538108765				
14	3350001	3450000	1446	-3.193139232				
14	27800001	27900000	1433	-2.988210704				
14	42300001	42400000	790	-3.018452302				
14	53650001	53750000	1078	-3.351648457				
14	53700001	53800000	980	-3.076149906				
14	78300001	78400000	1191	-3.359517273				
14	78350001	78450000	1268	-3.050236417				
15	1300001	1400000	670	-3.200557314				
15	1450001	1550000	764	-3.022652609				
15	1500001	1600000	775	-3.316864393				
15	1550001	1650000	850	-3.000443405				
15	1700001	1800000	522	-3.625688184				
15	1750001	1850000	699	-3.457970242				
15	1800001	1900000	1029	-3.030221257				
15	2850001	2950000	1084	-3.085918838				
15	3200001	3300000	968	-3.0619538				
15	53150001	53250000	845	-3.499442109				
15	53200001	53300000	925	-3.606494669				
15	53450001	53550000	706	-3.377791533				
15	59900001	60000000	1023	-3.272524979				
15	77050001	77150000	413	-3.101799142				
16	12100001	12200000	519	-3.900624096				
16	12150001	12250000	664	-3.712508307				
16	18500001	18600000	1311	-2.960735622				
16	19250001	19350000	1074	-3.142585822				
16	19300001	19400000	1251	-2.96851178				
16	19350001	19450000	1260	-3.045591145				
16	19400001	19500000	1113	-3.458593211				
16	27350001	27450000	673	-3.330708782				
16	27400001	27500000	716	-3.791280151				
16	27450001	27550000	632	-2.950947188				
16	36300001	36400000	476	-3.01522199				
16	36350001	36450000	624	-3.301462215				
16	37550001	37650000	648	-3.443730089				
16	37600001	37700000	750	-3.193463464				
16	38950001	39050000	297	-3.122669193				
16	50500001	50600000	426	-3.156409386				
16	50550001	50650000	549	-2.933242478				
17	8650001	8750000	1048	-2.917921615				
17	11450001	11550000	680	-4.338435803				
17	11500001	11600000	794	-2.921179656				
17	13200001	13300000	501	-3.529645771				
17	27200001	27300000	779	-2.922861607				
17	29350001	29450000	474	-2.996515894				
17	29400001	29500000	545	-3.323227594				

Low 1% windows					Low 1% merged windows			
Chr	Start	End	nSNPs	*ZHp*	Chr	Start	End	Size (MB)
17	43600001	43700000	777	-2.927371259				
18	7900001	8000000	1090	-3.19950592				
18	7950001	8050000	925	-3.304063774				
18	21550001	21650000	552	-2.944692327				
18	21600001	21700000	488	-3.05712741				
18	21650001	21750000	571	-3.0523202				
18	30800001	30900000	747	-3.445369062				
18	30850001	30950000	405	-3.73366045				
18	35750001	35850000	674	-3.254667455				
18	36650001	36750000	566	-3.357930628				
18	36700001	36800000	528	-3.883162582				
18	36850001	36950000	592	-3.351407216				
18	36950001	37050000	644	-3.049278828				
18	37000001	37100000	668	-3.592472923				
18	37050001	37150000	704	-3.447709073				
18	37100001	37200000	642	-3.549209688				
18	37150001	37250000	557	-3.940447523				
18	37200001	37300000	575	-3.932729141				
18	37400001	37500000	659	-3.348174246				
18	37450001	37550000	756	-2.92604763				
19	26350001	26450000	408	-5.254327772				
19	26400001	26500000	274	-4.650787353				
19	26700001	26800000	580	-3.788860498				
19	26850001	26950000	320	-3.668954194				
19	26900001	27000000	257	-3.109309326				
19	27500001	27600000	190	-4.900761449				
19	27550001	27650000	344	-3.058690393				
19	35650001	35750000	692	-3.269269706				
19	35700001	35800000	521	-3.198680434				
19	39450001	39550000	529	-3.061760694				
19	39750001	39850000	265	-4.482539925				
19	39800001	39900000	204	-5.813782313				
19	39850001	39950000	275	-5.834777811				
19	39900001	40000000	418	-3.439413912				
19	40350001	40450000	354	-4.02432023				
19	40400001	40500000	410	-5.569222154				
19	40450001	40550000	509	-3.069617971				
19	40550001	40650000	619	-3.090861737				
19	41450001	41550000	880	-3.320917091				
19	42550001	42650000	448	-3.339327486				
19	52200001	52300000	588	-3.273908676				
19	52250001	52350000	663	-3.067954248				
19	62250001	62350000	1275	-2.937139639				
20	21900001	22000000	632	-3.606858214				
20	39750001	39850000	551	-2.930626307				
20	39900001	40000000	653	-3.587282095				
20	39950001	40050000	704	-3.929636777				
20	40050001	40150000	778	-3.38046439				
20	40200001	40300000	1132	-3.751313823				
20	40250001	40350000	1115	-4.136210797				
20	40300001	40400000	972	-3.643803353				
20	40450001	40550000	867	-3.181710908				
20	40500001	40600000	912	-3.362272946				

Low 1% windows					Low 1% merged windows			
Chr	Start	End	nSNPs	*ZHp*	Chr	Start	End	Size (MB)
20	40550001	40650000	956	-2.989999966				
20	40800001	40900000	896	-2.909696784				
20	40850001	40950000	900	-3.39460437				
20	40900001	41000000	795	-3.355795599				
20	48650001	48750000	1022	-3.747801696				
20	48700001	48800000	1036	-3.851957819				
20	48750001	48850000	1041	-3.601222446				
20	48800001	48900000	1158	-4.492725407				
20	48850001	48950000	919	-4.436374997				
20	49150001	49250000	1539	-3.677689141				
20	49300001	49400000	1400	-3.206966586				
20	54050001	54150000	960	-2.945705143				
20	54250001	54350000	1168	-3.708878767				
20	54300001	54400000	1090	-3.104507373				
20	66650001	66750000	1349	-3.800920674				
20	66700001	66800000	1251	-3.34232315				
21	51450001	51550000	993	-3.03584787				
21	51500001	51600000	1038	-3.061639585				
21	55000001	55100000	728	-3.414027393				
21	55050001	55150000	851	-3.153891552				
21	55100001	55200000	900	-3.129735797				
21	55150001	55250000	836	-3.324122605				
21	55200001	55300000	657	-3.207141175				
21	57800001	57900000	708	-2.943113729				
21	57850001	57950000	613	-3.220220608				
21	58200001	58300000	999	-3.465901837				
21	59300001	59400000	1062	-3.05789551				
21	61650001	61750000	817	-2.935280228				
22	10300001	10400000	605	-3.808140098				
22	10350001	10450000	511	-3.479088758				
22	10500001	10600000	683	-3.067305607				
22	10850001	10950000	285	-4.153187992				
22	10900001	11000000	814	-3.035468415				
22	11550001	11650000	557	-3.325286899				
22	11650001	11750000	492	-3.176772178				
22	13800001	13900000	801	-4.014879095				
22	13850001	13950000	1001	-3.580193756				
22	32600001	32700000	797	-3.179698491				
22	40600001	40700000	1080	-2.972296588				
22	40650001	40750000	1178	-3.689673419				
22	40700001	40800000	1149	-3.402340308				
22	44650001	44750000	680	-3.568810848				
22	44700001	44800000	449	-4.752823705				
22	44750001	44850000	468	-2.943343776				
22	45050001	45150000	396	-3.110565712				
22	45300001	45400000	420	-3.153155637				
23	300001	400000	749	-3.849443879				
23	350001	450000	688	-3.799613224				
23	400001	500000	784	-3.41226257				
23	800001	900000	1028	-3.003762031				
23	850001	950000	862	-3.451691837				
23	49100001	49200000	1566	-3.507542911				
24	2350001	2450000	691	-3.102046748				

Low 1% windows					Low 1% merged windows			
Chr	Start	End	nSNPs	*ZHp*	Chr	Start	End	Size (MB)
24	15050001	15150000	1059	-3.039895778				
24	15100001	15200000	1028	-2.947861076				
24	34400001	34500000	524	-3.852786555				
25	16150001	16250000	1064	-2.99240893				
25	22650001	22750000	1061	-3.535316709				
25	22700001	22800000	1332	-3.261491027				
25	30350001	30450000	635	-3.327437332				
25	30400001	30500000	657	-3.889395914				
25	30450001	30550000	676	-4.031073666				
25	30500001	30600000	721	-3.777486579				
25	30550001	30650000	723	-3.538419127				
25	30600001	30700000	673	-3.065439555				
26	38150001	38250000	650	-3.504934097				
26	38200001	38300000	751	-3.3591397				
26	38850001	38950000	911	-2.995052453				
27	12400001	12500000	847	-3.455340057				
27	15350001	15450000	717	-3.462720157				
27	21950001	22050000	1178	-2.915670092				
27	23450001	23550000	781	-3.164301853				
27	23500001	23600000	894	-3.527505826				
27	23550001	23650000	833	-3.488435911				
27	23700001	23800000	534	-2.94922434				
27	23950001	24050000	881	-3.03765474				
27	24000001	24100000	1207	-2.969518649				
27	34200001	34300000	916	-3.086133798				
27	34400001	34500000	648	-3.683040284				
27	34450001	34550000	751	-3.459262423				
28	1450001	1550000	1145	-3.260971804				
28	21100001	21200000	1711	-2.971665654				
28	32200001	32300000	614	-4.265599047				
28	32250001	32350000	368	-5.062578562				
28	39650001	39750000	1007	-3.555811299				
29	50001	150000	187	-3.743677528				
29	100001	200000	132	-3.555052123				
29	150001	250000	114	-3.550491305				
29	200001	300000	290	-3.461556908				
29	250001	350000	904	-3.193235801				
29	300001	400000	1892	-3.067667644				
29	550001	650000	500	-2.950148309				
29	750001	850000	645	-3.326654297				
29	800001	900000	775	-3.582441342				
29	21200001	21300000	1754	-3.183722352				
29	33100001	33200000	672	-3.021897022				

Table S31. The low 1% *Hp* detected windows in Begait cattle.

Low 1% windows					Low 1% merged windows			
Chr	Start	End	nSNPs	*ZHp*	Chr	Start	End	Size (MB)
1	31850001	31950000	1041	-3.118484386	1	31850001	31950000	0.099999
1	40600001	40700000	1122	-3.111310601	1	40600001	40700000	0.099999
1	44250001	44350000	301	-4.036837228	1	44250001	44350000	0.099999
1	50050001	50150000	615	-4.159851189	1	50050001	50200000	0.149999
1	50100001	50200000	683	-4.745948508	1	87150001	87250000	0.099999

Low 1% windows					Low 1% merged windows			
Chr	Start	End	nSNPs	*ZHp*	Chr	Start	End	Size (MB)
1	87150001	87250000	757	-3.016936069	1	133500001	133600000	0.099999
1	133500001	133600000	684	-3.113721506	1	155700001	155800000	0.099999
1	155700001	155800000	862	-3.099289422	2	350001	750000	0.399999
2	350001	450000	364	-3.918119856	2	12800001	12950000	0.149999
2	400001	500000	467	-5.457523497	2	14500001	14650000	0.149999
2	450001	550000	467	-5.006624209	2	30750001	30850000	0.099999
2	550001	650000	548	-3.821933884	2	32850001	32950000	0.099999
2	600001	700000	603	-5.306828412	2	53000001	53100000	0.099999
2	650001	750000	854	-3.359649083	2	60200001	60350000	0.149999
2	12800001	12900000	926	-4.018387309	2	69950001	70150000	0.199999
2	12850001	12950000	885	-3.681826905	2	70250001	70600000	0.349999
2	14500001	14600000	798	-3.84699304	2	70650001	70850000	0.199999
2	14550001	14650000	1017	-3.07237679	2	73100001	73250000	0.149999
2	30750001	30850000	629	-3.533226636	2	82050001	82200000	0.149999
2	32850001	32950000	737	-2.999334403	2	100250001	100350000	0.099999
2	53000001	53100000	607	-3.060655859	2	110550001	110750000	0.199999
2	60200001	60300000	1032	-3.510632336	2	132950001	133100000	0.149999
2	60250001	60350000	667	-3.64760484	3	57350001	57500000	0.149999
2	69950001	70050000	514	-3.186619919	3	57550001	57650000	0.099999
2	70000001	70100000	569	-3.38748827	3	58500001	58600000	0.099999
2	70050001	70150000	704	-2.969326349	3	58800001	58900000	0.099999
2	70250001	70350000	484	-5.048620021	3	59400001	59550000	0.149999
2	70300001	70400000	431	-7.313575733	3	59800001	59900000	0.099999
2	70350001	70450000	533	-5.735797413	3	59950001	60150000	0.199999
2	70400001	70500000	586	-4.44292147	3	60250001	60350000	0.099999
2	70450001	70550000	512	-3.942392897	3	65600001	65700000	0.099999
2	70500001	70600000	541	-3.31547052	3	82950001	83100000	0.149999
2	70650001	70750000	851	-4.70602109	3	95250001	95350000	0.099999
2	70700001	70800000	757	-5.677393418	3	100350001	100450000	0.099999
2	70750001	70850000	883	-2.982579279	3	100600001	100700000	0.099999
2	73100001	73200000	530	-3.440800417	4	14250001	14350000	0.099999
2	73150001	73250000	764	-4.19415113	4	92900001	93000000	0.099999
2	82050001	82150000	1126	-4.400292102	4	103000001	103100000	0.099999
2	82100001	82200000	715	-5.128180705	4	110500001	110600000	0.099999
2	100250001	100350000	1119	-2.971985773	4	112050001	112200000	0.149999
2	110550001	110650000	735	-3.621836925	5	700001	800000	0.099999
2	110600001	110700000	734	-4.05975605	5	8750001	8850000	0.099999
2	110650001	110750000	795	-3.142070494	5	11900001	12000000	0.099999
2	132950001	133050000	1507	-3.361302417	5	18700001	18850000	0.149999
2	133000001	133100000	880	-3.680105247	5	20000001	20100000	0.099999
3	57350001	57450000	622	-3.327059415	5	28050001	28400000	0.349999
3	57400001	57500000	592	-3.633470995	5	28700001	28800000	0.099999
3	57550001	57650000	1035	-2.983596699	5	30600001	30750000	0.149999
3	58500001	58600000	1140	-2.969380801	5	46650001	46750000	0.099999
3	58800001	58900000	744	-3.07450945	5	47450001	47900000	0.449999
3	59400001	59500000	506	-3.392340349	5	66600001	66750000	0.149999
3	59450001	59550000	336	-2.990184771	5	69700001	70000000	0.299999
3	59800001	59900000	444	-3.136304802	5	75800001	75900000	0.099999
3	59950001	60050000	629	-3.368342105	5	76550001	76650000	0.099999
3	60000001	60100000	1117	-3.065171666	5	84850001	84950000	0.099999
3	60050001	60150000	1418	-3.103477987	5	111400001	111600000	0.199999
3	60250001	60350000	1031	-3.291346727	5	112300001	112650000	0.349999
3	65600001	65700000	707	-3.038015323	5	113700001	113850000	0.149999

Low 1% windows					Low 1% merged windows			
Chr	Start	End	nSNPs	*ZHp*	Chr	Start	End	Size (MB)
3	82950001	83050000	653	-3.412234016	5	119200001	119300000	0.099999
3	83000001	83100000	739	-3.504699123	5	119350001	119550000	0.199999
3	95250001	95350000	412	-3.214612813	6	3350001	3450000	0.099999
3	100350001	100450000	1024	-3.291453346	6	7750001	7850000	0.099999
3	100600001	100700000	648	-4.045693606	6	12750001	12850000	0.099999
4	14250001	14350000	734	-3.0628931	6	15800001	15900000	0.099999
4	92900001	93000000	418	-3.304547104	6	20800001	20900000	0.099999
4	103000001	103100000	865	-2.972148668	6	25650001	25750000	0.099999
4	110500001	110600000	1663	-3.439094406	6	30650001	30750000	0.099999
4	112050001	112150000	605	-3.27841661	6	49150001	49300000	0.149999
4	112100001	112200000	968	-3.044216202	6	49500001	49650000	0.149999
5	700001	800000	905	-3.16969198	6	50650001	50900000	0.249999
5	8750001	8850000	1212	-3.404972911	6	50950001	51050000	0.099999
5	11900001	12000000	787	-3.370355413	6	51400001	51500000	0.099999
5	18700001	18800000	284	-4.588657121	6	60350001	60450000	0.099999
5	18750001	18850000	525	-3.277543717	6	73300001	73400000	0.099999
5	20000001	20100000	660	-3.005447194	6	75900001	76000000	0.099999
5	28050001	28150000	669	-3.216329868	6	78350001	78450000	0.099999
5	28100001	28200000	638	-3.710272488	6	79950001	80050000	0.099999
5	28150001	28250000	805	-3.161056135	6	113800001	113900000	0.099999
5	28200001	28300000	817	-3.088854592	7	9900001	10000000	0.099999
5	28250001	28350000	699	-3.958497999	7	38350001	38500000	0.149999
5	28300001	28400000	617	-3.741173739	7	40450001	40600000	0.149999
5	28700001	28800000	748	-3.93638135	7	41650001	41850000	0.199999
5	30600001	30700000	752	-3.244584321	7	44100001	44200000	0.099999
5	30650001	30750000	609	-3.077907853	7	49850001	50050000	0.199999
5	46650001	46750000	905	-3.745728634	7	50850001	51150000	0.299999
5	47450001	47550000	1177	-3.433244955	7	52100001	52400000	0.299999
5	47500001	47600000	930	-4.141147716	7	54000001	54450000	0.449999
5	47550001	47650000	657	-3.091497473	7	54550001	54700000	0.149999
5	47600001	47700000	551	-3.550002771	7	64150001	64250000	0.099999
5	47650001	47750000	438	-4.329246699	7	73400001	73600000	0.199999
5	47700001	47800000	466	-4.822098201	7	74400001	74500000	0.099999
5	47750001	47850000	489	-5.365487919	7	74950001	75100000	0.149999
5	47800001	47900000	520	-5.179844214	7	75250001	75350000	0.099999
5	66600001	66700000	992	-3.528727254	7	75450001	75600000	0.149999
5	66650001	66750000	813	-3.104108967	7	75700001	75800000	0.099999
5	69700001	69800000	383	-3.378837713	7	75850001	76000000	0.149999
5	69750001	69850000	363	-3.291721298	8	11900001	12000000	0.099999
5	69800001	69900000	439	-3.815085714	8	23050001	23200000	0.149999
5	69850001	69950000	567	-3.994157867	8	45650001	45750000	0.099999
5	69900001	70000000	552	-3.674687989	8	49450001	49700000	0.249999
5	75800001	75900000	404	-3.267363731	8	49750001	49900000	0.149999
5	76550001	76650000	456	-3.090343959	8	57950001	58100000	0.149999
5	84850001	84950000	812	-3.908881865	8	59350001	59700000	0.349999
5	111400001	111500000	562	-3.302949275	8	62050001	62200000	0.149999
5	111450001	111550000	434	-2.981338914	8	79000001	79250000	0.249999
5	111500001	111600000	380	-3.063293926	8	79350001	79950000	0.599999
5	112300001	112400000	451	-5.833872445	8	83900001	84000000	0.099999
5	112350001	112450000	613	-6.648931092	9	1900001	2000000	0.099999
5	112400001	112500000	612	-7.077231878	9	2100001	2400000	0.299999
5	112450001	112550000	502	-7.016838063	9	2500001	2600000	0.099999
5	112500001	112600000	342	-5.68831275	9	2900001	3000000	0.099999

Low 1% windows					Low 1% merged windows			
Chr	Start	End	nSNPs	*ZHp*	Chr	Start	End	Size (MB)
5	112550001	112650000	618	-3.241139136	9	3200001	3400000	0.199999
5	113700001	113800000	833	-5.299048091	9	15250001	15400000	0.149999
5	113750001	113850000	1344	-3.455310189	9	38950001	39250000	0.299999
5	119200001	119300000	1075	-2.968648644	9	39300001	39500000	0.199999
5	119350001	119450000	1204	-3.44406434	9	39950001	40050000	0.099999
5	119400001	119500000	988	-4.711469591	9	71800001	72050000	0.249999
5	119450001	119550000	562	-4.768926046	9	77350001	77450000	0.099999
6	3350001	3450000	941	-3.346030724	9	93450001	93750000	0.299999
6	7750001	7850000	1093	-3.1430254	10	58500001	58750000	0.249999
6	12750001	12850000	875	-3.195979114	10	58900001	59200000	0.299999
6	15800001	15900000	527	-3.107068929	10	76850001	77000000	0.149999
6	20800001	20900000	965	-3.37003194	10	102100001	102300000	0.199999
6	25650001	25750000	566	-3.26300747	10	102550001	102650000	0.099999
6	30650001	30750000	769	-3.946132739	11	7750001	7900000	0.149999
6	49150001	49250000	823	-3.167696898	11	12950001	13050000	0.099999
6	49200001	49300000	715	-3.444023123	11	13150001	13300000	0.149999
6	49500001	49600000	1272	-3.630828753	11	14650001	14850000	0.199999
6	49550001	49650000	974	-3.509044635	11	14950001	15200000	0.249999
6	50650001	50750000	897	-3.215693826	11	15400001	15550000	0.149999
6	50700001	50800000	885	-3.949153164	11	16550001	16650000	0.099999
6	50750001	50850000	912	-3.29601099	11	62100001	62250000	0.149999
6	50800001	50900000	758	-3.369998227	11	105250001	105350000	0.099999
6	50950001	51050000	545	-3.614698797	12	100001	250000	0.149999
6	51400001	51500000	750	-3.360652004	12	30550001	30650000	0.099999
6	60350001	60450000	189	-4.065862604	12	35050001	35150000	0.099999
6	73300001	73400000	996	-3.087115774	12	37600001	37700000	0.099999
6	75900001	76000000	1014	-3.327663077	12	37800001	37900000	0.099999
6	78350001	78450000	1699	-2.99148392	12	44700001	44800000	0.099999
6	79950001	80050000	1234	-3.651721164	12	45000001	45100000	0.099999
6	113800001	113900000	1562	-3.237511751	12	45500001	45600000	0.099999
7	9900001	10000000	129	-3.557832383	12	45850001	46050000	0.199999
7	38350001	38450000	264	-4.028526551	12	50050001	50150000	0.099999
7	38400001	38500000	266	-3.374057174	13	26600001	26700000	0.099999
7	40450001	40550000	1110	-3.00668436	13	49800001	50400000	0.599999
7	40500001	40600000	1021	-3.160124987	13	57400001	57500000	0.099999
7	41650001	41750000	892	-3.380583295	13	62200001	62300000	0.099999
7	41700001	41800000	852	-4.346895318	13	64100001	64250000	0.149999
7	41750001	41850000	1184	-3.231384362	13	69700001	69800000	0.099999
7	44100001	44200000	346	-3.1678652	14	47550001	47650000	0.099999
7	49850001	49950000	284	-3.443919688	14	60000001	60100000	0.099999
7	49900001	50000000	421	-4.003881683	14	66400001	66500000	0.099999
7	49950001	50050000	415	-3.322030723	14	81000001	81200000	0.199999
7	50850001	50950000	179	-3.154744355	15	16450001	16600000	0.149999
7	50900001	51000000	334	-3.035408334	15	20450001	20550000	0.099999
7	50950001	51050000	404	-3.072784258	15	56250001	56350000	0.099999
7	51000001	51100000	269	-3.403033234	15	59750001	59850000	0.099999
7	51050001	51150000	286	-3.455486974	15	59900001	60000000	0.099999
7	52100001	52200000	1042	-3.809628312	15	83750001	83850000	0.099999
7	52150001	52250000	994	-3.729349182	16	9050001	9200000	0.149999
7	52250001	52350000	797	-3.458920869	16	14800001	14950000	0.149999
7	52300001	52400000	595	-3.22869765	16	17200001	17300000	0.099999
7	54000001	54100000	249	-4.633041612	16	19600001	19700000	0.099999
7	54050001	54150000	314	-5.025946932	16	39700001	39800000	0.099999

Low 1% windows					Low 1% merged windows			
Chr	Start	End	nSNPs	*ZHp*	Chr	Start	End	Size (MB)
7	54100001	54200000	329	-4.718463324	16	50500001	50650000	0.149999
7	54150001	54250000	400	-4.269885716	16	69350001	69450000	0.099999
7	54200001	54300000	548	-4.117353469	17	750001	850000	0.099999
7	54250001	54350000	497	-4.113747388	17	13100001	13300000	0.199999
7	54300001	54400000	387	-4.036085774	17	42250001	42350000	0.099999
7	54350001	54450000	390	-4.063838419	17	56900001	57000000	0.099999
7	54550001	54650000	579	-3.7561867	17	58650001	58850000	0.199999
7	54600001	54700000	523	-3.07566371	17	63050001	63150000	0.099999
7	64150001	64250000	846	-3.372550097	17	72250001	72500000	0.249999
7	73400001	73500000	959	-3.086578508	18	3550001	3650000	0.099999
7	73450001	73550000	804	-3.826848388	18	6200001	6300000	0.099999
7	73500001	73600000	645	-3.144015186	18	24100001	24200000	0.099999
7	74400001	74500000	1205	-3.050801806	18	35200001	35350000	0.149999
7	74950001	75050000	683	-2.969278461	18	35600001	35800000	0.199999
7	75000001	75100000	633	-3.074987596	18	37050001	37300000	0.249999
7	75250001	75350000	601	-3.907682713	18	38650001	38800000	0.149999
7	75450001	75550000	978	-3.91591648	18	55800001	55950000	0.149999
7	75500001	75600000	886	-3.015209889	19	13300001	13450000	0.149999
7	75700001	75800000	864	-3.316079304	19	13700001	13800000	0.099999
7	75850001	75950000	816	-3.673804048	19	26600001	26750000	0.149999
7	75900001	76000000	565	-3.386189064	19	26800001	26950000	0.149999
8	11900001	12000000	1126	-3.145811858	19	38650001	38950000	0.299999
8	23050001	23150000	1241	-3.20605814	19	46050001	46200000	0.149999
8	23100001	23200000	812	-3.197098597	19	46550001	46700000	0.149999
8	45650001	45750000	750	-3.093412102	20	2850001	3000000	0.149999
8	49450001	49550000	892	-3.008055387	20	3050001	3150000	0.099999
8	49500001	49600000	1049	-3.984259915	20	11000001	11100000	0.099999
8	49550001	49650000	1215	-4.343167412	20	11900001	12000000	0.099999
8	49600001	49700000	911	-2.964767599	20	13900001	14000000	0.099999
8	49750001	49850000	729	-4.171676478	20	23650001	23850000	0.199999
8	49800001	49900000	747	-4.157316022	20	25100001	25300000	0.199999
8	57950001	58050000	601	-3.03792688	20	28650001	28750000	0.099999
8	58000001	58100000	735	-2.972152908	20	40200001	40400000	0.199999
8	59350001	59450000	396	-4.388832827	20	40450001	40550000	0.099999
8	59400001	59500000	567	-4.531947774	20	42400001	42500000	0.099999
8	59450001	59550000	620	-3.133243996	20	46800001	46950000	0.149999
8	59550001	59650000	370	-4.714477405	20	48800001	48950000	0.149999
8	59600001	59700000	362	-3.774978558	20	49150001	49250000	0.099999
8	62050001	62150000	890	-3.394393517	20	49300001	49400000	0.099999
8	62100001	62200000	939	-3.034953401	20	54250001	54400000	0.149999
8	79000001	79100000	607	-3.294629933	20	65650001	65800000	0.149999
8	79050001	79150000	529	-3.828164216	20	67300001	67400000	0.099999
8	79100001	79200000	410	-3.949464245	20	67600001	67750000	0.149999
8	79150001	79250000	292	-3.067216837	20	71250001	71650000	0.399999
8	79350001	79450000	868	-3.207770495	21	6850001	6950000	0.099999
8	79450001	79550000	325	-3.259823591	21	25500001	25600000	0.099999
8	79500001	79600000	396	-3.295233017	21	36800001	36900000	0.099999
8	79550001	79650000	531	-3.049557631	21	40700001	40800000	0.099999
8	79600001	79700000	636	-3.630899794	21	47200001	47350000	0.149999
8	79650001	79750000	877	-4.402085015	21	48850001	48950000	0.099999
8	79700001	79800000	1035	-3.121081665	21	49200001	49400000	0.199999
8	79800001	79900000	833	-3.516462344	21	57800001	57950000	0.149999
8	79850001	79950000	703	-3.607636587	21	58000001	58100000	0.099999

Low 1% windows					Low 1% merged windows			
Chr	Start	End	nSNPs	*ZHp*	Chr	Start	End	Size (MB)
8	83900001	84000000	921	-2.997140835	21	59300001	59450000	0.149999
9	1900001	2000000	1130	-3.511373573	22	10300001	10450000	0.149999
9	2100001	2200000	1164	-3.725115966	22	10700001	10800000	0.099999
9	2150001	2250000	1316	-3.841250625	22	10850001	10950000	0.099999
9	2200001	2300000	1534	-3.637807674	22	24900001	25000000	0.099999
9	2250001	2350000	1634	-3.485961255	22	25050001	25150000	0.099999
9	2300001	2400000	1266	-3.055670656	22	31600001	31800000	0.199999
9	2500001	2600000	1274	-3.047207628	22	32600001	32700000	0.099999
9	2900001	3000000	785	-4.052598876	22	32750001	32850000	0.099999
9	3200001	3300000	1049	-4.260153498	22	32900001	33050000	0.149999
9	3250001	3350000	702	-3.474928393	22	35650001	35750000	0.099999
9	3300001	3400000	962	-3.948881139	22	38200001	38400000	0.199999
9	15250001	15350000	1318	-3.863956835	22	48150001	48300000	0.149999
9	15300001	15400000	986	-3.065373271	22	50900001	51000000	0.099999
9	38950001	39050000	396	-3.16228218	22	51250001	51350000	0.099999
9	39000001	39100000	572	-3.734976065	24	46500001	46600000	0.099999
9	39050001	39150000	690	-2.99184548	25	2550001	2650000	0.099999
9	39150001	39250000	457	-3.498123741	25	29500001	29600000	0.099999
9	39300001	39400000	444	-3.082240676	25	30300001	30400000	0.099999
9	39350001	39450000	373	-3.979120134	25	30850001	30950000	0.099999
9	39400001	39500000	340	-2.98194717	26	16250001	16350000	0.099999
9	39950001	40050000	695	-2.986106932	26	22100001	22350000	0.249999
9	71800001	71900000	872	-2.968287791	26	31550001	31750000	0.199999
9	71850001	71950000	975	-3.298128046	26	39100001	39250000	0.149999
9	71900001	72000000	851	-3.550983984	26	50500001	50600000	0.099999
9	71950001	72050000	694	-3.39002874	27	12400001	12500000	0.099999
9	77350001	77450000	510	-3.010512836	27	18050001	18250000	0.199999
9	93450001	93550000	489	-3.225690321	27	21350001	21450000	0.099999
9	93500001	93600000	529	-3.500320644	27	21800001	21950000	0.149999
9	93550001	93650000	672	-3.574940479	27	34400001	34500000	0.099999
9	93600001	93700000	593	-3.749724438	28	1800001	1950000	0.149999
9	93650001	93750000	574	-3.816344078	28	5350001	5450000	0.099999
10	58500001	58600000	599	-3.191672648	28	6750001	6850000	0.099999
10	58550001	58650000	480	-3.115825035	28	15200001	15300000	0.099999
10	58650001	58750000	143	-3.48558074	28	32450001	32600000	0.149999
10	58900001	59000000	285	-3.686369157	28	33450001	33550000	0.099999
10	58950001	59050000	540	-4.310048131	28	37200001	37300000	0.099999
10	59000001	59100000	458	-4.468902036	29	1	350000	0.349999
10	59050001	59150000	270	-4.244833799	29	44250001	44400000	0.149999
10	59100001	59200000	476	-3.004766902	29	49450001	49600000	0.149999
10	76850001	76950000	687	-4.613980297				
10	76900001	77000000	964	-4.461023111				
10	102100001	102200000	945	-3.689151596				
10	102150001	102250000	999	-5.072534364				
10	102200001	102300000	1204	-4.384137668				
10	102550001	102650000	777	-3.007229973				
11	7750001	7850000	213	-3.113677241				
11	7800001	7900000	210	-4.208578387				
11	12950001	13050000	612	-3.045092947				
11	13150001	13250000	590	-5.25270828				
11	13200001	13300000	584	-3.969997427				
11	14650001	14750000	487	-4.234259511				
11	14700001	14800000	600	-4.595363344				

Low 1% windows					Low 1% merged windows			
Chr	Start	End	nSNPs	*ZHp*	Chr	Start	End	Size (MB)
11	14750001	14850000	499	-4.210001954				
11	14950001	15050000	635	-3.199141273				
11	15000001	15100000	550	-3.154376906				
11	15050001	15150000	577	-2.996867381				
11	15100001	15200000	552	-3.166592383				
11	15400001	15500000	894	-3.128140595				
11	15450001	15550000	773	-3.18697997				
11	16550001	16650000	1146	-3.337109724				
11	62100001	62200000	716	-3.599665126				
11	62150001	62250000	537	-3.472032793				
11	105250001	105350000	1596	-2.970849763				
12	100001	200000	448	-3.363410015				
12	150001	250000	379	-3.127702054				
12	30550001	30650000	915	-3.081884996				
12	35050001	35150000	645	-2.978768323				
12	37600001	37700000	1469	-3.113424449				
12	37800001	37900000	1270	-3.307742994				
12	44700001	44800000	1503	-2.953935711				
12	45000001	45100000	1493	-2.998057471				
12	45500001	45600000	970	-3.356632131				
12	45850001	45950000	1047	-3.485820504				
12	45900001	46000000	1251	-3.74233966				
12	45950001	46050000	1301	-3.504548896				
12	50050001	50150000	847	-3.334537082				
13	26600001	26700000	912	-3.483589875				
13	49800001	49900000	648	-3.19895835				
13	49850001	49950000	723	-3.84997379				
13	49900001	50000000	560	-4.018375206				
13	49950001	50050000	613	-4.234417844				
13	50000001	50100000	863	-4.465144337				
13	50050001	50150000	1119	-4.441788517				
13	50100001	50200000	848	-4.183421528				
13	50150001	50250000	452	-4.477029578				
13	50200001	50300000	373	-5.223696987				
13	50250001	50350000	418	-4.334703656				
13	50300001	50400000	448	-3.365506824				
13	57400001	57500000	557	-3.347600849				
13	62200001	62300000	572	-3.398803398				
13	64100001	64200000	264	-3.120250671				
13	64150001	64250000	352	-3.789610404				
13	69700001	69800000	402	-3.318969654				
14	47550001	47650000	623	-3.550116761				
14	60000001	60100000	886	-3.402108204				
14	66400001	66500000	1058	-3.807653579				
14	81000001	81100000	623	-3.202128121				
14	81050001	81150000	788	-3.41136679				
14	81100001	81200000	771	-3.183392761				
15	16450001	16550000	1259	-3.639109668				
15	16500001	16600000	1040	-3.518096045				
15	20450001	20550000	606	-3.719248359				
15	56250001	56350000	904	-3.532850981				
15	59750001	59850000	937	-3.292842345				
15	59900001	60000000	886	-3.320283455				

Low 1% windows					Low 1% merged windows			
Chr	Start	End	nSNPs	*ZHp*	Chr	Start	End	Size (MB)
15	83750001	83850000	1154	-3.100353249				
16	9050001	9150000	1182	-3.835603254				
16	9100001	9200000	1230	-3.359834926				
16	14800001	14900000	1444	-3.691656278				
16	14850001	14950000	1483	-3.499693201				
16	17200001	17300000	1103	-2.958337097				
16	19600001	19700000	1032	-3.023104726				
16	39700001	39800000	252	-3.770765459				
16	50500001	50600000	389	-4.881629626				
16	50550001	50650000	528	-4.867307929				
16	69350001	69450000	1056	-3.002114063				
17	750001	850000	1362	-3.207795082				
17	13100001	13200000	218	-3.864128139				
17	13150001	13250000	200	-4.424752424				
17	13200001	13300000	126	-4.897131285				
17	42250001	42350000	936	-3.820796317				
17	56900001	57000000	302	-3.279846795				
17	58650001	58750000	474	-3.000898552				
17	58700001	58800000	499	-3.170184995				
17	58750001	58850000	592	-2.951315416				
17	63050001	63150000	421	-3.442666213				
17	72250001	72350000	743	-3.442480371				
17	72300001	72400000	719	-5.709779511				
17	72350001	72450000	712	-6.82334258				
17	72400001	72500000	672	-3.35489527				
18	3550001	3650000	861	-3.038164115				
18	6200001	6300000	1194	-3.020168287				
18	24100001	24200000	517	-3.589620212				
18	35200001	35300000	380	-3.177180697				
18	35250001	35350000	362	-3.954155648				
18	35600001	35700000	222	-3.038819038				
18	35650001	35750000	330	-3.846331118				
18	35700001	35800000	547	-3.394590665				
18	37050001	37150000	700	-3.08155378				
18	37100001	37200000	602	-4.063311509				
18	37150001	37250000	541	-4.174229583				
18	37200001	37300000	472	-4.172946968				
18	38650001	38750000	357	-3.108410756				
18	38700001	38800000	474	-3.151756056				
18	55800001	55900000	706	-4.69161577				
18	55850001	55950000	552	-3.992572999				
19	13300001	13400000	1179	-3.025582653				
19	13350001	13450000	1354	-2.983455556				
19	13700001	13800000	823	-3.165168099				
19	26600001	26700000	385	-3.298723928				
19	26650001	26750000	641	-3.261028536				
19	26800001	26900000	454	-3.408847972				
19	26850001	26950000	401	-3.527487733				
19	38650001	38750000	495	-4.520853883				
19	38700001	38800000	352	-3.338887329				
19	38750001	38850000	345	-3.30792406				
19	38800001	38900000	450	-4.458222331				
19	38850001	38950000	548	-3.619160215				

Low 1% windows					Low 1% merged windows			
Chr	Start	End	nSNPs	*ZHp*	Chr	Start	End	Size (MB)
19	46050001	46150000	918	-3.330122942				
19	46100001	46200000	871	-3.125818587				
19	46550001	46650000	1485	-3.080474896				
19	46600001	46700000	1346	-3.212717923				
20	2850001	2950000	359	-3.075835954				
20	2900001	3000000	440	-4.687187151				
20	3050001	3150000	641	-3.177238882				
20	11000001	11100000	903	-3.233158645				
20	11900001	12000000	875	-3.053195512				
20	13900001	14000000	507	-4.304981114				
20	23650001	23750000	421	-3.268685808				
20	23700001	23800000	564	-4.08178143				
20	23750001	23850000	798	-3.017257004				
20	25100001	25200000	449	-3.441912674				
20	25150001	25250000	343	-4.371272172				
20	25200001	25300000	205	-3.642691595				
20	28650001	28750000	1260	-3.163576247				
20	40200001	40300000	1030	-3.077580819				
20	40250001	40350000	823	-3.212767336				
20	40300001	40400000	696	-3.262063463				
20	40450001	40550000	732	-3.627671872				
20	42400001	42500000	746	-3.110262066				
20	46800001	46900000	922	-3.132956952				
20	46850001	46950000	1174	-3.01961113				
20	48800001	48900000	1023	-5.230410172				
20	48850001	48950000	853	-4.933118914				
20	49150001	49250000	1419	-3.520408049				
20	49300001	49400000	1532	-3.109550851				
20	54250001	54350000	1328	-3.616656555				
20	54300001	54400000	1176	-3.014165986				
20	65650001	65750000	963	-3.181992832				
20	65700001	65800000	1000	-3.188325306				
20	67300001	67400000	1263	-3.059310614				
20	67600001	67700000	1227	-3.600832665				
20	67650001	67750000	874	-3.174863733				
20	71250001	71350000	897	-3.186983409				
20	71300001	71400000	957	-3.4735549				
20	71350001	71450000	1011	-3.421338924				
20	71400001	71500000	830	-3.420309049				
20	71450001	71550000	797	-4.54020732				
20	71500001	71600000	966	-4.330911949				
20	71550001	71650000	675	-3.395590992				
21	6850001	6950000	466	-3.385722203				
21	25500001	25600000	1045	-2.992410314				
21	36800001	36900000	297	-3.291671613				
21	40700001	40800000	680	-3.270392765				
21	47200001	47300000	565	-3.058345199				
21	47250001	47350000	600	-3.543331807				
21	48850001	48950000	1428	-3.369977277				
21	49200001	49300000	789	-3.565107556				
21	49250001	49350000	679	-3.686253712				
21	49300001	49400000	806	-3.479956735				
21	57800001	57900000	410	-4.004086097				

Low 1% windows					Low 1% merged windows			
Chr	Start	End	nSNPs	*ZHp*	Chr	Start	End	Size (MB)
21	57850001	57950000	352	-3.461323863				
21	58000001	58100000	565	-3.237593503				
21	59300001	59400000	1336	-2.998051423				
21	59350001	59450000	1081	-3.066868808				
22	10300001	10400000	469	-3.126699512				
22	10350001	10450000	490	-3.419965853				
22	10700001	10800000	81	-4.047993691				
22	10850001	10950000	220	-3.416536314				
22	24900001	25000000	616	-3.136496248				
22	25050001	25150000	818	-3.475415685				
22	31600001	31700000	458	-3.127374623				
22	31650001	31750000	411	-3.531380817				
22	31700001	31800000	332	-3.012579267				
22	32600001	32700000	1095	-3.120463358				
22	32750001	32850000	847	-3.079099638				
22	32900001	33000000	1004	-2.971965498				
22	32950001	33050000	891	-3.835610945				
22	35650001	35750000	1172	-3.081752621				
22	38200001	38300000	792	-3.114865052				
22	38250001	38350000	851	-3.347356192				
22	38300001	38400000	660	-3.031951914				
22	48150001	48250000	547	-3.073443178				
22	48200001	48300000	511	-3.080413026				
22	50900001	51000000	285	-5.083557072				
22	51250001	51350000	475	-5.218304127				
24	46500001	46600000	622	-3.242628553				
25	2550001	2650000	751	-3.034757317				
25	29500001	29600000	1282	-3.486591457				
25	30300001	30400000	360	-2.958558949				
25	30850001	30950000	490	-3.295314413				
26	16250001	16350000	622	-3.033565096				
26	22100001	22200000	548	-3.658120101				
26	22150001	22250000	523	-3.497910901				
26	22200001	22300000	521	-3.443923771				
26	22250001	22350000	562	-3.484142842				
26	31550001	31650000	470	-3.541261624				
26	31600001	31700000	770	-3.764214892				
26	31650001	31750000	618	-3.662740514				
26	39100001	39200000	1251	-3.064212821				
26	39150001	39250000	1032	-3.530421028				
26	50500001	50600000	1417	-3.211538257				
27	12400001	12500000	1007	-3.056786412				
27	18050001	18150000	1002	-3.148657973				
27	18100001	18200000	987	-4.192513629				
27	18150001	18250000	964	-3.071124668				
27	21350001	21450000	1011	-3.355015527				
27	21800001	21900000	808	-3.822249451				
27	21850001	21950000	901	-3.006834239				
27	34400001	34500000	774	-3.039714333				
28	1800001	1900000	1217	-3.420505793				
28	1850001	1950000	1284	-3.13711205				
28	5350001	5450000	1241	-3.158205054				
28	6750001	6850000	1346	-2.98976142				

Low 1% windows					Low 1% merged windows			
Chr	Start	End	nSNPs	*ZHp*	Chr	Start	End	Size (MB)
28	15200001	15300000	936	-3.246747009				
28	32450001	32550000	798	-3.327447219				
28	32500001	32600000	816	-5.076757317				
28	33450001	33550000	1136	-3.272961602				
28	37200001	37300000	897	-3.457968527				
29	1	100000	1347	-3.072861916				
29	50001	150000	1268	-3.412871876				
29	100001	200000	1400	-3.495909981				
29	150001	250000	1229	-3.602740534				
29	200001	300000	837	-3.535545781				
29	250001	350000	1240	-3.326672313				
29	44250001	44350000	771	-3.037520553				
29	44300001	44400000	580	-4.393471301				
29	49450001	49550000	556	-3.275489005				
29	49500001	49600000	496	-3.140471792				

Table S32. The low 1% *Hp* detected windows in Raya cattle.

Low 1% windows					Low 1% merged windows			
Chr	Start	End	nSNPs	*ZHp*	Chr	Start	End	Size (MB)
1	30000001	30100000	1131	-3.289067775	1	30000001	30200000	0.199999
1	30050001	30150000	1088	-3.808265626	1	33400001	33550000	0.149999
1	30100001	30200000	924	-3.909478712	1	44050001	44400000	0.349999
1	33400001	33500000	1132	-3.853938572	1	54500001	54650000	0.149999
1	33450001	33550000	1028	-4.040178552	1	65350001	65450000	0.099999
1	44050001	44150000	512	-5.137324475	1	83400001	83550000	0.149999
1	44100001	44200000	374	-5.087379353	1	118000001	118100000	0.099999
1	44150001	44250000	385	-5.275159741	1	133250001	133350000	0.099999
1	44200001	44300000	393	-5.136624866	1	155650001	156050000	0.399999
1	44250001	44350000	373	-4.943991988	2	17000001	17150000	0.149999
1	44300001	44400000	613	-3.197165543	2	20750001	20850000	0.099999
1	54500001	54600000	689	-5.640559202	2	41900001	42000000	0.099999
1	54550001	54650000	630	-5.367686599	2	53450001	53650000	0.199999
1	65350001	65450000	692	-3.004607391	2	53950001	54250000	0.299999
1	83400001	83500000	710	-3.651805625	2	61450001	61550000	0.099999
1	83450001	83550000	692	-3.060560018	2	61650001	61750000	0.099999
1	118000001	118100000	996	-3.078148322	2	70300001	70450000	0.149999
1	133250001	133350000	759	-3.256189664	2	78350001	78450000	0.099999
1	155650001	155750000	654	-3.052073122	2	82100001	82200000	0.099999
1	155700001	155800000	719	-5.038340258	2	91050001	91150000	0.099999
1	155750001	155850000	942	-4.361301041	2	91200001	91350000	0.149999
1	155800001	155900000	897	-3.765658239	2	105550001	105750000	0.199999
1	155850001	155950000	995	-3.2078182	2	126400001	126500000	0.099999
1	155900001	156000000	1162	-3.915115734	3	12400001	12500000	0.099999
1	155950001	156050000	1060	-4.18204777	3	12900001	13050000	0.149999
2	17000001	17100000	1036	-3.193378973	3	30050001	30200000	0.149999
2	17050001	17150000	730	-3.524029583	3	30550001	30700000	0.149999
2	20750001	20850000	326	-3.271849942	3	40900001	41000000	0.099999
2	41900001	42000000	1118	-3.009350178	3	49900001	50000000	0.099999
2	53450001	53550000	689	-3.156324196	3	59250001	59500000	0.249999
2	53500001	53600000	766	-3.549011281	3	59550001	59650000	0.099999
2	53550001	53650000	727	-3.959446571	3	59700001	60050000	0.349999

Low 1% windows					Low 1% merged windows			
Chr	Start	End	nSNPs	*ZHp*	Chr	Start	End	Size (MB)
2	53950001	54050000	823	-3.638283228	3	92600001	92800000	0.199999
2	54000001	54100000	969	-4.035326528	3	93750001	93850000	0.099999
2	54050001	54150000	1060	-3.307619145	4	12600001	12700000	0.099999
2	54100001	54200000	830	-3.183721622	4	52550001	52650000	0.099999
2	54150001	54250000	669	-3.451969511	4	74500001	74600000	0.099999
2	61450001	61550000	924	-3.209575094	4	78300001	78500000	0.199999
2	61650001	61750000	822	-3.107485445	5	23250001	23500000	0.249999
2	70300001	70400000	682	-4.045595385	5	66250001	66500000	0.249999
2	70350001	70450000	784	-3.076305592	5	76150001	76650000	0.499999
2	78350001	78450000	1298	-3.343052237	5	79000001	79100000	0.099999
2	82100001	82200000	1118	-3.875903367	5	84850001	84950000	0.099999
2	91050001	91150000	550	-3.495591189	5	86350001	86450000	0.099999
2	91200001	91300000	711	-3.230775279	5	91950001	92050000	0.099999
2	91250001	91350000	794	-3.083958409	5	95350001	95500000	0.149999
2	105550001	105650000	606	-3.721178128	5	112050001	112600000	0.549999
2	105600001	105700000	647	-3.722127699	5	119250001	119350000	0.099999
2	105650001	105750000	518	-3.353256023	5	119450001	119600000	0.149999
2	126400001	126500000	285	-3.77198209	6	2850001	2950000	0.099999
3	12400001	12500000	764	-3.440961541	6	6150001	6250000	0.099999
3	12900001	13000000	708	-3.853822911	6	13300001	13400000	0.099999
3	12950001	13050000	523	-4.216694758	6	32100001	32350000	0.249999
3	30050001	30150000	793	-4.04847969	6	39650001	39750000	0.099999
3	30100001	30200000	1029	-3.03971786	6	39800001	39900000	0.099999
3	30550001	30650000	469	-3.771392558	6	48350001	48550000	0.199999
3	30600001	30700000	379	-3.016728837	6	50650001	50900000	0.249999
3	40900001	41000000	1053	-4.265240965	6	51000001	51200000	0.199999
3	49900001	50000000	488	-2.981560461	6	51350001	51650000	0.299999
3	59250001	59350000	961	-3.003989701	6	75000001	75100000	0.099999
3	59300001	59400000	910	-3.632319441	6	79900001	80050000	0.149999
3	59350001	59450000	560	-4.344671924	6	86300001	86400000	0.099999
3	59400001	59500000	376	-3.12737181	6	98150001	98250000	0.099999
3	59550001	59650000	673	-3.646812133	7	21350001	21500000	0.149999
3	59700001	59800000	332	-5.137580525	7	31000001	31150000	0.149999
3	59750001	59850000	251	-5.138583105	7	31250001	31400000	0.149999
3	59800001	59900000	215	-4.312955617	7	31600001	31800000	0.199999
3	59850001	59950000	414	-3.366438137	7	52100001	52250000	0.149999
3	59900001	60000000	478	-3.384946103	7	57400001	57500000	0.099999
3	59950001	60050000	430	-3.773364695	7	60400001	60900000	0.499999
3	92600001	92700000	878	-3.073993416	7	75100001	75250000	0.149999
3	92650001	92750000	796	-2.991035931	7	75850001	76000000	0.149999
3	92700001	92800000	581	-3.147050692	7	80700001	80800000	0.099999
3	93750001	93850000	541	-3.150646606	7	96500001	96600000	0.099999
4	12600001	12700000	644	-3.571528986	7	98300001	98500000	0.199999
4	52550001	52650000	599	-3.401603712	8	12400001	12500000	0.099999
4	74500001	74600000	1350	-3.476235877	8	21600001	21700000	0.099999
4	78300001	78400000	511	-3.001529041	8	21800001	21900000	0.099999
4	78350001	78450000	897	-3.371076911	8	30500001	30650000	0.149999
4	78400001	78500000	943	-3.578822122	8	33000001	33100000	0.099999
5	23250001	23350000	903	-3.363763019	8	42450001	42600000	0.149999
5	23350001	23450000	748	-3.211732226	8	54750001	54900000	0.149999
5	23400001	23500000	632	-3.919055679	8	59200001	59900000	0.699999
5	66250001	66350000	419	-3.496579901	8	77650001	77750000	0.099999

Low 1% windows					Low 1% merged windows			
Chr	Start	End	nSNPs	*ZHp*	Chr	Start	End	Size (MB)
5	66300001	66400000	383	-3.705576296	8	79050001	79200000	0.149999
5	66400001	66500000	341	-3.927322149	8	79550001	79750000	0.199999
5	76150001	76250000	612	-4.065313185	8	79800001	79950000	0.149999
5	76200001	76300000	494	-4.655711642	8	94300001	94450000	0.149999
5	76250001	76350000	431	-4.074960176	8	103800001	104050000	0.249999
5	76300001	76400000	527	-4.340229797	8	104150001	104300000	0.149999
5	76350001	76450000	602	-4.498645761	9	3600001	3750000	0.149999
5	76400001	76500000	432	-4.161137394	9	3950001	4050000	0.099999
5	76450001	76550000	329	-3.891813699	9	5150001	5450000	0.299999
5	76500001	76600000	424	-4.030605905	9	11600001	11750000	0.149999
5	76550001	76650000	561	-4.342554113	9	11800001	11900000	0.099999
5	79000001	79100000	955	-3.444067134	9	19450001	19550000	0.099999
5	84850001	84950000	851	-3.116891182	9	28050001	28150000	0.099999
5	86350001	86450000	873	-3.474658751	9	33400001	33600000	0.199999
5	91950001	92050000	909	-3.979892383	9	38750001	38950000	0.199999
5	95350001	95450000	312	-3.676878567	9	62350001	62450000	0.099999
5	95400001	95500000	285	-3.588645137	9	68050001	68150000	0.099999
5	112050001	112150000	476	-3.046831783	9	71150001	71250000	0.099999
5	112100001	112200000	479	-3.551889671	9	71650001	72150000	0.499999
5	112150001	112250000	574	-4.231272763	9	93350001	93450000	0.099999
5	112200001	112300000	363	-3.573375795	10	17300001	17400000	0.099999
5	112300001	112400000	430	-4.778881796	10	58550001	58650000	0.099999
5	112350001	112450000	602	-5.52955165	10	59000001	59100000	0.099999
5	112400001	112500000	666	-5.950462121	10	76350001	76600000	0.249999
5	112450001	112550000	565	-5.797597124	11	12900001	13000000	0.099999
5	112500001	112600000	373	-3.739393871	11	13150001	13250000	0.099999
5	119250001	119350000	1016	-3.416064845	11	13800001	13900000	0.099999
5	119450001	119550000	609	-4.582025405	11	15450001	15550000	0.099999
5	119500001	119600000	559	-3.5746628	11	39700001	39800000	0.099999
6	2850001	2950000	898	-3.375395983	11	59250001	59350000	0.099999
6	6150001	6250000	988	-3.020392759	11	62100001	62250000	0.149999
6	13300001	13400000	597	-3.728117982	11	75100001	75350000	0.249999
6	32100001	32200000	858	-4.221292389	11	97300001	97400000	0.099999
6	32150001	32250000	883	-4.236050771	12	28800001	29500000	0.699999
6	32200001	32300000	787	-3.191885014	12	35250001	35400000	0.149999
6	32250001	32350000	882	-3.243013241	12	36600001	36700000	0.099999
6	39650001	39750000	1139	-3.362129836	12	44700001	44850000	0.149999
6	39800001	39900000	586	-3.117513635	12	48050001	48200000	0.149999
6	48350001	48450000	1166	-3.517214637	12	49300001	49450000	0.149999
6	48400001	48500000	1371	-3.577735804	12	52050001	52150000	0.099999
6	48450001	48550000	1373	-3.053520711	12	56750001	56900000	0.149999
6	50650001	50750000	900	-3.128968503	12	76150001	76250000	0.099999
6	50700001	50800000	818	-3.660938935	13	26250001	26350000	0.099999
6	50750001	50850000	935	-3.019172512	13	47150001	47550000	0.399999
6	50800001	50900000	1026	-3.122310708	13	47850001	48050000	0.199999
6	51000001	51100000	464	-3.500394472	13	57350001	57550000	0.199999
6	51050001	51150000	538	-4.356488017	13	63600001	63800000	0.199999
6	51100001	51200000	461	-3.87755284	13	63900001	64150000	0.249999
6	51350001	51450000	365	-3.223332484	13	69300001	69400000	0.099999
6	51400001	51500000	179	-4.827039483	13	69700001	69800000	0.099999
6	51450001	51550000	686	-5.082721552	13	76600001	76700000	0.099999
6	51500001	51600000	1239	-4.89344213	14	39150001	39400000	0.249999

Low 1% windows					Low 1% merged windows			
Chr	Start	End	nSNPs	*ZHp*	Chr	Start	End	Size (MB)
6	51550001	51650000	900	-4.254939709	14	60000001	60100000	0.099999
6	75000001	75100000	794	-3.137998838	14	64950001	65150000	0.199999
6	79900001	80000000	1286	-3.102974586	15	16500001	16600000	0.099999
6	79950001	80050000	1339	-4.050691532	15	35850001	35950000	0.099999
6	86300001	86400000	672	-2.988514215	15	37050001	37200000	0.149999
6	98150001	98250000	909	-3.241386833	15	76850001	77000000	0.149999
7	21350001	21450000	433	-3.204657805	15	84100001	84250000	0.149999
7	21400001	21500000	391	-3.018300813	16	8850001	9200000	0.349999
7	31000001	31100000	692	-3.641918745	16	10250001	10350000	0.099999
7	31050001	31150000	787	-3.284306277	16	14850001	14950000	0.099999
7	31250001	31350000	788	-4.323208146	16	17000001	17150000	0.149999
7	31300001	31400000	716	-4.379422728	16	17200001	17350000	0.149999
7	31600001	31700000	836	-3.290089272	16	19400001	19650000	0.249999
7	31650001	31750000	591	-3.623736135	16	27400001	27650000	0.249999
7	31700001	31800000	740	-3.428256663	16	37550001	37700000	0.149999
7	52100001	52200000	1018	-3.39512951	16	50450001	50700000	0.249999
7	52150001	52250000	1002	-3.132809426	16	51000001	51100000	0.099999
7	57400001	57500000	371	-3.807872282	16	51150001	51300000	0.149999
7	60400001	60500000	250	-3.663877933	16	54800001	54900000	0.099999
7	60500001	60600000	634	-3.350868278	16	55150001	55350000	0.199999
7	60550001	60650000	604	-5.263639497	17	8100001	8250000	0.149999
7	60600001	60700000	564	-5.251840528	17	11450001	11550000	0.099999
7	60650001	60750000	511	-5.405259988	17	13600001	13700000	0.099999
7	60700001	60800000	463	-4.56863978	17	29350001	29500000	0.149999
7	60750001	60850000	450	-4.096703819	17	60450001	60550000	0.099999
7	60800001	60900000	323	-4.432587156	17	68100001	68200000	0.099999
7	75100001	75200000	190	-3.835949813	18	12550001	13050000	0.499999
7	75150001	75250000	189	-3.265274044	18	24100001	24200000	0.099999
7	75850001	75950000	839	-4.057014104	18	35200001	35400000	0.199999
7	75900001	76000000	618	-3.351254	18	37450001	37550000	0.099999
7	80700001	80800000	1243	-3.94382098	19	13300001	13400000	0.099999
7	96500001	96600000	352	-3.14108956	19	13700001	13800000	0.099999
7	98300001	98400000	777	-5.878367713	19	26400001	26500000	0.099999
7	98350001	98450000	860	-7.81845315	19	39250001	39400000	0.149999
7	98400001	98500000	934	-5.255852309	19	39650001	39950000	0.299999
8	12400001	12500000	995	-3.488813875	19	40100001	40350000	0.249999
8	21600001	21700000	881	-3.144094691	19	40400001	40500000	0.099999
8	21800001	21900000	660	-3.300024332	19	46350001	46550000	0.199999
8	30500001	30600000	668	-3.050428535	19	46600001	46850000	0.249999
8	30550001	30650000	691	-3.295799674	19	49750001	49850000	0.099999
8	33000001	33100000	1185	-3.22896009	20	4500001	4600000	0.099999
8	42450001	42550000	750	-3.120820499	20	39950001	40150000	0.199999
8	42500001	42600000	769	-3.688527901	20	40300001	40550000	0.249999
8	54750001	54850000	804	-4.620073373	20	41150001	41250000	0.099999
8	54800001	54900000	818	-4.635008796	20	41550001	41650000	0.099999
8	59200001	59300000	351	-3.173982659	20	48800001	49000000	0.199999
8	59250001	59350000	400	-4.168178842	20	54250001	54350000	0.099999
8	59300001	59400000	380	-4.33395523	20	71450001	71600000	0.149999
8	59350001	59450000	376	-4.504460321	21	7850001	7950000	0.099999
8	59400001	59500000	547	-4.978557994	21	33200001	33350000	0.149999
8	59450001	59550000	608	-4.771929242	21	36750001	37000000	0.249999
8	59500001	59600000	451	-4.724732484	21	57800001	57950000	0.149999

Low 1% windows					Low 1% merged windows			
Chr	Start	End	nSNPs	*ZHp*	Chr	Start	End	Size (MB)
8	59550001	59650000	396	-5.897226152	21	59300001	59450000	0.149999
8	59600001	59700000	394	-5.700112558	22	10150001	10250000	0.099999
8	59650001	59750000	337	-4.215424935	22	10300001	10600000	0.299999
8	59700001	59800000	325	-4.016548255	22	10700001	10800000	0.099999
8	59750001	59850000	358	-3.957781948	22	10850001	10950000	0.099999
8	59800001	59900000	362	-3.992581856	22	26350001	26600000	0.249999
8	77650001	77750000	702	-3.086439223	22	30550001	30650000	0.099999
8	79050001	79150000	523	-3.677026346	22	51500001	51600000	0.099999
8	79100001	79200000	418	-3.789067779	23	29800001	29900000	0.099999
8	79550001	79650000	657	-3.063501694	23	30150001	30250000	0.099999
8	79600001	79700000	575	-3.214318218	24	4350001	4450000	0.099999
8	79650001	79750000	555	-2.998718522	24	42000001	42100000	0.099999
8	79800001	79900000	862	-3.896787156	24	52900001	53000000	0.099999
8	79850001	79950000	714	-3.763597106	24	54050001	54150000	0.099999
8	94300001	94400000	1593	-3.198675072	25	16150001	16250000	0.099999
8	94350001	94450000	1476	-3.240580436	25	22150001	22300000	0.149999
8	103800001	103900000	620	-3.263142657	25	24000001	24100000	0.099999
8	103850001	103950000	664	-4.033124151	25	26700001	26850000	0.149999
8	103900001	104000000	414	-3.684259411	25	29500001	29600000	0.099999
8	103950001	104050000	499	-3.074868858	25	30500001	30800000	0.299999
8	104150001	104250000	863	-3.425061408	26	14950001	15050000	0.099999
8	104200001	104300000	512	-3.852715219	26	38150001	38300000	0.149999
9	3600001	3700000	1563	-3.737479219	26	38900001	39000000	0.099999
9	3650001	3750000	1247	-3.1840109	26	42700001	42800000	0.099999
9	3950001	4050000	1148	-2.997758442	27	7000001	7100000	0.099999
9	5150001	5250000	704	-3.653517208	27	8000001	8100000	0.099999
9	5200001	5300000	955	-3.084854852	27	8250001	8400000	0.149999
9	5250001	5350000	1087	-3.288630955	27	13950001	14150000	0.199999
9	5300001	5400000	841	-3.875484924	27	21100001	21200000	0.099999
9	5350001	5450000	766	-3.745936837	27	21400001	21700000	0.299999
9	11600001	11700000	1321	-3.411614005	27	21750001	21900000	0.149999
9	11650001	11750000	1266	-3.559013796	28	19400001	19500000	0.099999
9	11800001	11900000	1005	-3.114411613	28	32500001	32600000	0.099999
9	19450001	19550000	1030	-3.268924374	28	41150001	41300000	0.149999
9	28050001	28150000	1011	-3.425606203	29	1	350000	0.349999
9	33400001	33500000	197	-4.780123184	29	750001	900000	0.149999
9	33500001	33600000	470	-3.687533774	29	1950001	2050000	0.099999
9	38750001	38850000	453	-3.43674772	29	18950001	19050000	0.099999
9	38800001	38900000	425	-3.94335714	29	21200001	21350000	0.149999
9	38850001	38950000	341	-2.987346193	29	22500001	22600000	0.099999
9	62350001	62450000	265	-3.703038627	29	39800001	39900000	0.099999
9	68050001	68150000	774	-3.150229611	29	48600001	48750000	0.149999
9	71150001	71250000	1135	-3.049729198				
9	71650001	71750000	614	-3.396333667				
9	71700001	71800000	529	-3.123397672				
9	71750001	71850000	704	-3.526847952				
9	71800001	71900000	736	-3.73857596				
9	71850001	71950000	844	-3.292572016				
9	71900001	72000000	880	-3.244454949				
9	71950001	72050000	815	-3.235219003				
9	72000001	72100000	791	-3.138354198				
9	72050001	72150000	675	-3.322917246				

Low 1% windows					Low 1% merged windows			
Chr	Start	End	nSNPs	*ZHp*	Chr	Start	End	Size (MB)
9	93350001	93450000	676	-3.153325797				
10	17300001	17400000	856	-3.05740519				
10	58550001	58650000	475	-3.185602173				
10	59000001	59100000	178	-5.125729152				
10	76350001	76450000	761	-3.045419874				
10	76400001	76500000	862	-4.743377821				
10	76450001	76550000	1006	-4.809907503				
10	76500001	76600000	893	-3.104094654				
11	12900001	13000000	867	-3.414981264				
11	13150001	13250000	598	-3.823544537				
11	13800001	13900000	893	-3.103163608				
11	15450001	15550000	684	-3.329617096				
11	39700001	39800000	850	-3.993811929				
11	59250001	59350000	1136	-3.825552339				
11	62100001	62200000	958	-3.577403693				
11	62150001	62250000	759	-3.190180259				
11	75100001	75200000	520	-3.662385392				
11	75200001	75300000	564	-4.894286358				
11	75250001	75350000	715	-5.119040703				
11	97300001	97400000	816	-3.352460111				
12	28800001	28900000	855	-3.963304637				
12	28850001	28950000	905	-4.54327301				
12	28950001	29050000	756	-3.680052599				
12	29000001	29100000	611	-4.805168591				
12	29050001	29150000	493	-4.398525544				
12	29100001	29200000	559	-6.149840806				
12	29150001	29250000	396	-7.602855015				
12	29200001	29300000	255	-7.855785767				
12	29250001	29350000	280	-7.490998229				
12	29300001	29400000	268	-7.237872472				
12	29350001	29450000	272	-6.424039266				
12	29400001	29500000	294	-4.322810643				
12	35250001	35350000	605	-4.685637853				
12	35300001	35400000	460	-3.654469028				
12	36600001	36700000	574	-3.219780216				
12	44700001	44800000	1323	-3.533907257				
12	44750001	44850000	1458	-3.79628836				
12	48050001	48150000	944	-2.982981793				
12	48100001	48200000	688	-3.517747648				
12	49300001	49400000	1316	-4.722402765				
12	49350001	49450000	1307	-3.585090955				
12	52050001	52150000	673	-3.038231625				
12	56750001	56850000	1012	-3.116795547				
12	56800001	56900000	974	-3.212789434				
12	76150001	76250000	646	-3.004430786				
13	26250001	26350000	852	-3.270175302				
13	47150001	47250000	484	-3.192448587				
13	47200001	47300000	466	-5.569701582				
13	47250001	47350000	371	-6.083265659				
13	47300001	47400000	255	-6.674806702				
13	47350001	47450000	326	-5.534865174				
13	47400001	47500000	434	-4.533647071				

Low 1% windows					Low 1% merged windows			
Chr	Start	End	nSNPs	*ZHp*	Chr	Start	End	Size (MB)
13	47450001	47550000	650	-3.12091442				
13	47850001	47950000	1092	-3.063718453				
13	47900001	48000000	1061	-3.02929767				
13	47950001	48050000	845	-3.899742395				
13	57350001	57450000	611	-4.799499389				
13	57400001	57500000	611	-5.596016797				
13	57450001	57550000	327	-4.382639918				
13	63600001	63700000	358	-3.673142486				
13	63650001	63750000	463	-4.270675293				
13	63700001	63800000	504	-3.757605568				
13	63900001	64000000	462	-3.186055727				
13	63950001	64050000	358	-3.649756411				
13	64000001	64100000	257	-3.483257538				
13	64050001	64150000	244	-3.058028231				
13	69300001	69400000	858	-3.870988141				
13	69700001	69800000	396	-3.266322054				
13	76600001	76700000	1237	-2.990503615				
14	39150001	39250000	853	-3.034278388				
14	39200001	39300000	1066	-3.582080805				
14	39250001	39350000	1086	-3.712819762				
14	39300001	39400000	1261	-3.93419716				
14	60000001	60100000	852	-3.38881146				
14	64950001	65050000	681	-3.097367019				
14	65000001	65100000	782	-3.070718137				
14	65050001	65150000	876	-3.038481046				
15	16500001	16600000	1003	-3.010465453				
15	35850001	35950000	782	-3.034020573				
15	37050001	37150000	751	-4.072778041				
15	37100001	37200000	911	-3.271160381				
15	76850001	76950000	377	-4.392793678				
15	76900001	77000000	442	-4.240502914				
15	84100001	84200000	1478	-3.507431475				
15	84150001	84250000	1797	-3.438414274				
16	8850001	8950000	890	-3.509173631				
16	8900001	9000000	835	-3.766455998				
16	8950001	9050000	1317	-3.907709607				
16	9000001	9100000	1514	-3.981986513				
16	9050001	9150000	1292	-3.991249178				
16	9100001	9200000	1583	-3.529906748				
16	10250001	10350000	998	-2.991069292				
16	14850001	14950000	1328	-3.027284044				
16	17000001	17100000	1560	-3.298549445				
16	17050001	17150000	1645	-3.212460917				
16	17200001	17300000	989	-3.934736222				
16	17250001	17350000	1006	-3.048397121				
16	19400001	19500000	1478	-3.505189888				
16	19450001	19550000	1129	-3.530061023				
16	19500001	19600000	883	-3.090922746				
16	19550001	19650000	649	-3.317802543				
16	27400001	27500000	960	-3.880332055				
16	27450001	27550000	687	-3.327986477				
16	27550001	27650000	484	-2.98245745				

Low 1% windows					Low 1% merged windows			
Chr	Start	End	nSNPs	*ZHp*	Chr	Start	End	Size (MB)
16	37550001	37650000	423	-4.29644516				
16	37600001	37700000	456	-4.005021506				
16	50450001	50550000	336	-4.238483116				
16	50500001	50600000	414	-5.171167702				
16	50550001	50650000	535	-5.095871312				
16	50600001	50700000	629	-2.990106745				
16	51000001	51100000	310	-3.210798877				
16	51150001	51250000	321	-3.490333798				
16	51200001	51300000	377	-3.835592906				
16	54800001	54900000	907	-3.314815532				
16	55150001	55250000	483	-4.661869594				
16	55200001	55300000	366	-4.249963099				
16	55250001	55350000	337	-3.002462431				
17	8100001	8200000	1102	-3.420113081				
17	8150001	8250000	1312	-3.371865649				
17	11450001	11550000	1301	-3.262355237				
17	13600001	13700000	831	-3.368966022				
17	29350001	29450000	430	-3.272662953				
17	29400001	29500000	494	-3.391238244				
17	60450001	60550000	658	-3.912468083				
17	68100001	68200000	947	-3.620796383				
18	12550001	12650000	1042	-3.569821042				
18	12600001	12700000	933	-3.227621834				
18	12650001	12750000	829	-3.411217232				
18	12700001	12800000	844	-3.239909309				
18	12800001	12900000	667	-3.994029217				
18	12850001	12950000	580	-4.959941781				
18	12900001	13000000	579	-4.560317382				
18	12950001	13050000	614	-4.242129623				
18	24100001	24200000	511	-4.914365469				
18	35200001	35300000	353	-3.301371839				
18	35250001	35350000	363	-4.150984406				
18	35300001	35400000	301	-3.29330465				
18	37450001	37550000	735	-2.989601085				
19	13300001	13400000	1055	-3.622598836				
19	13700001	13800000	774	-3.546212835				
19	26400001	26500000	408	-3.042752982				
19	39250001	39350000	399	-3.908066559				
19	39300001	39400000	310	-3.055848665				
19	39650001	39750000	491	-4.545066008				
19	39700001	39800000	369	-4.78311633				
19	39750001	39850000	285	-4.669435772				
19	39800001	39900000	263	-4.905202558				
19	39850001	39950000	362	-4.510360186				
19	40100001	40200000	276	-3.237251219				
19	40150001	40250000	354	-3.019800872				
19	40200001	40300000	564	-3.178753162				
19	40250001	40350000	753	-3.156390789				
19	40400001	40500000	489	-3.722491881				
19	46350001	46450000	1159	-3.272737774				
19	46400001	46500000	1206	-3.537578002				
19	46450001	46550000	943	-3.171566613				

Low 1% windows					Low 1% merged windows			
Chr	Start	End	nSNPs	*ZHp*	Chr	Start	End	Size (MB)
19	46600001	46700000	1280	-3.464993046				
19	46650001	46750000	931	-4.478876503				
19	46700001	46800000	977	-4.625077822				
19	46750001	46850000	962	-4.743775914				
19	49750001	49850000	1439	-3.329536965				
20	4500001	4600000	824	-3.059843926				
20	39950001	40050000	537	-3.117959032				
20	40000001	40100000	866	-3.210454576				
20	40050001	40150000	1268	-3.538836331				
20	40300001	40400000	668	-3.752668397				
20	40350001	40450000	668	-3.082047759				
20	40400001	40500000	703	-3.445979538				
20	40450001	40550000	751	-3.970365391				
20	41150001	41250000	768	-3.529039646				
20	41550001	41650000	793	-3.221326178				
20	48800001	48900000	1120	-4.571043581				
20	48850001	48950000	903	-4.998445167				
20	48900001	49000000	632	-3.078270684				
20	54250001	54350000	1041	-3.621903587				
20	71450001	71550000	938	-3.863385604				
20	71500001	71600000	1156	-3.60097107				
21	7850001	7950000	894	-2.994134905				
21	33200001	33300000	569	-3.077586933				
21	33250001	33350000	508	-3.268819043				
21	36750001	36850000	516	-3.482200426				
21	36800001	36900000	345	-4.539468978				
21	36850001	36950000	362	-3.345709296				
21	36900001	37000000	665	-3.380860519				
21	57800001	57900000	758	-3.045216935				
21	57850001	57950000	672	-3.236583625				
21	59300001	59400000	801	-3.628271921				
21	59350001	59450000	852	-3.078947633				
22	10150001	10250000	667	-3.171385108				
22	10300001	10400000	490	-2.998398393				
22	10350001	10450000	516	-3.461287569				
22	10450001	10550000	431	-3.269330412				
22	10500001	10600000	648	-3.646194953				
22	10700001	10800000	93	-3.069803557				
22	10850001	10950000	266	-3.187152708				
22	26350001	26450000	825	-3.744587928				
22	26400001	26500000	715	-3.28448041				
22	26450001	26550000	806	-3.347325369				
22	26500001	26600000	1082	-3.355504253				
22	30550001	30650000	464	-3.027366824				
22	51500001	51600000	791	-3.015266201				
23	29800001	29900000	1710	-2.996057603				
23	30150001	30250000	426	-3.044515409				
24	4350001	4450000	890	-3.26370247				
24	42000001	42100000	892	-3.132995285				
24	52900001	53000000	1045	-3.39285736				
24	54050001	54150000	1466	-3.097657554				
25	16150001	16250000	1240	-3.459872541				

Low 1% windows					Low 1% merged windows			
Chr	Start	End	nSNPs	*ZHp*	Chr	Start	End	Size (MB)
25	22150001	22250000	622	-3.150800738				
25	22200001	22300000	582	-3.356535253				
25	24000001	24100000	1316	-3.168727116				
25	26700001	26800000	384	-4.784552922				
25	26750001	26850000	273	-3.976997964				
25	29500001	29600000	923	-2.993893971				
25	30500001	30600000	588	-3.20466479				
25	30550001	30650000	708	-3.495976467				
25	30600001	30700000	688	-3.103173659				
25	30700001	30800000	854	-3.460615672				
26	14950001	15050000	573	-3.041418941				
26	38150001	38250000	736	-3.774840156				
26	38200001	38300000	857	-3.785131505				
26	38900001	39000000	550	-3.051700572				
26	42700001	42800000	621	-3.033092464				
27	7000001	7100000	2366	-3.015422202				
27	8000001	8100000	640	-3.079255854				
27	8250001	8350000	370	-3.814519151				
27	8300001	8400000	519	-3.901091475				
27	13950001	14050000	1013	-3.117644598				
27	14000001	14100000	877	-3.04718986				
27	14050001	14150000	932	-3.211388859				
27	21100001	21200000	813	-3.012616187				
27	21400001	21500000	190	-3.06608437				
27	21450001	21550000	600	-3.003264695				
27	21550001	21650000	1135	-3.034765323				
27	21600001	21700000	936	-3.063696306				
27	21750001	21850000	906	-3.933830543				
27	21800001	21900000	864	-3.302368817				
28	19400001	19500000	756	-3.000468639				
28	32500001	32600000	1018	-3.706511776				
28	41150001	41250000	472	-3.554255868				
28	41200001	41300000	724	-4.717212041				
29	1	100000	1213	-4.555981682				
29	50001	150000	1149	-5.087124651				
29	100001	200000	1208	-5.240916602				
29	150001	250000	1031	-5.331660723				
29	200001	300000	789	-4.808010659				
29	250001	350000	1325	-3.117181151				
29	750001	850000	938	-3.606144767				
29	800001	900000	1188	-3.810917009				
29	1950001	2050000	920	-2.98926482				
29	18950001	19050000	1788	-3.437724138				
29	21200001	21300000	1902	-3.786435214				
29	21250001	21350000	1783	-3.329695536				
29	22500001	22600000	866	-3.101678157				
29	39800001	39900000	470	-3.617424803				
29	48600001	48700000	819	-3.910383256				
29	48650001	48750000	797	-4.049668388				

Table S33. Overlapping selective sweep regions between high and low groups of the temperature seasonality (Begait and Abergelle) and annual precipitation (Raya and Arado).

Temperature seasonality (bio4)				Annual precipitation (bio12)			
Chr	Start	End	Size	Crh	Start	End	Size
1	87100001	87250000	0.10	1	44050001	44400000	0.35
2	70250001	70550000	0.30	1	133250001	133350000	0.10
2	70650001	70800000	0.15	1	155650001	156050000	0.40
3	58800001	58900000	0.10	2	20750001	20850000	0.10
3	59250001	59500000	0.10	2	61650001	61750000	0.10
3	59800001	59900000	0.10	2	70300001	70450000	0.15
5	18750001	18900000	0.10	2	82100001	82200000	0.10
5	47800001	47900000	0.10	2	126400001	126500000	0.10
5	76200001	76650000	0.10	3	59250001	59500000	0.25
5	112300001	112650000	0.35	3	59700001	60050000	0.35
6	51000001	51250000	0.05	5	112050001	112600000	0.55
6	51300001	51700000	0.10	5	119250001	119350000	0.10
6	60300001	60450000	0.10	5	119450001	119600000	0.15
6	78300001	78450000	0.10	6	2850001	2950000	0.10
6	79900001	80200000	0.10	6	6150001	6250000	0.10
7	9900001	10000000	0.10	6	51000001	51200000	0.20
7	49850001	51150000	0.20	6	51350001	51650000	0.30
7	49850001	51150000	0.30	6	79900001	80050000	0.15
7	52100001	52350000	0.25	7	21350001	21500000	0.15
7	74350001	74450000	0.05	7	52100001	52250000	0.15
7	75850001	76050000	0.15	8	59200001	59900000	0.70
8	79150001	79250000	0.10	8	77650001	77750000	0.10
9	2100001	2200000	0.10	9	71650001	72150000	0.50
9	2900001	3000000	0.10	9	3600001	3750000	0.15
9	38850001	39250000	0.30	9	5150001	5450000	0.30
9	39400001	39550000	0.10	9	19450001	19550000	0.10
9	71750001	72000000	0.20	9	33400001	33600000	0.20
10	58600001	58750000	0.15	9	38750001	38950000	0.20
10	58850001	59150000	0.25	9	62350001	62450000	0.10
11	7700001	7800000	0.05	11	12900001	13000000	0.10
11	7850001	8000000	0.05	11	13150001	13250000	0.10
11	12900001	13050000	0.10	11	13800001	13900000	0.10
11	13150001	13300000	0.15	11	75100001	75350000	0.25
11	14650001	14800000	0.15	16	19400001	19650000	0.25
11	15450001	15550000	0.10	16	27400001	27650000	0.25
11	16550001	16650000	0.10	16	37550001	37700000	0.15
13	50200001	50350000	0.15	16	50450001	50700000	0.25
13	57450001	57550000	0.05	17	11450001	11550000	0.10
13	69650001	69800000	0.10	17	29350001	29500000	0.15
18	24100001	24200000	0.10	18	37450001	37550000	0.10
18	36900001	37100000	0.05	19	26400001	26500000	0.10
19	13700001	13800000	0.10	19	39650001	39950000	0.30
19	26900001	27100000	0.05	19	40400001	40500000	0.10
19	46050001	46200000	0.15	20	40300001	40550000	0.25
20	2900001	3000000	0.10	20	39950001	40150000	0.20
20	40200001	40400000	0.20	20	48800001	49000000	0.20

Temperature seasonality (bio4)				Annual precipitation (bio12)			
Chr	Start	End	Size	Crh	Start	End	Size
20	40450001	40550000	0.10	20	54250001	54350000	0.10
20	48800001	48950000	0.15	21	57800001	57950000	0.15
20	49150001	49250000	0.10	21	59300001	59450000	0.15
21	36800001	36900000	0.10	22	10300001	10600000	0.30
21	57800001	57950000	0.15	22	10850001	10950000	0.10
21	59300001	59450000	0.15	25	16150001	16250000	0.10
22	10650001	10900000	0.10	25	30500001	30800000	0.30
22	10650001	10900000	0.05	26	38150001	38300000	0.15
22	32600001	32700000	0.10	26	38900001	39000000	0.10
26	31450001	31750000	0.20	29	1	350000	0.35
27	21350001	21500000	0.10	29	750001	900000	0.15
27	21750001	21900000	0.10	29	21200001	21350000	0.15
28	1800001	1900000	0.10				
28	15150001	15250000	0.05				
29	1	350000	0.35				

Table S34. Overlapping selective sweep regions between high and low groups of the precipitation of wettest (Begait and Raya) and warmest quarter precipitation ranges (Raya and Abergelle).

Precipitation of wettest quarter (bio16)				Precipitation of warmest quarter (bio18)			
Chr	Start	End	Size	Chr	Start	End	Size
1	44250001	44350000	0.10	1	30000001	30200000	0.20
1	155700001	155800000	0.10	1	54500001	54650000	0.15
2	70250001	70600000	0.35	2	20750001	20850000	0.10
2	82050001	82200000	0.15	2	53450001	53650000	0.20
3	59400001	59550000	0.15	2	61450001	61550000	0.10
3	59800001	59900000	0.10	2	61650001	61750000	0.10
3	59950001	60150000	0.20	2	70300001	70450000	0.15
5	76550001	76650000	0.10	2	91050001	91150000	0.10
5	84850001	84950000	0.10	3	59250001	59500000	0.25
5	112300001	112650000	0.35	3	59700001	60050000	0.35
5	119200001	119300000	0.10	3	92600001	92800000	0.20
5	119350001	119550000	0.20	4	74500001	74600000	0.10
6	50650001	50900000	0.25	5	76150001	76650000	0.50
6	50950001	51050000	0.10	5	79000001	79100000	0.10
6	51400001	51500000	0.10	5	112050001	112600000	0.55
6	79950001	80050000	0.10	6	51000001	51200000	0.20
7	52100001	52400000	0.30	6	51350001	51650000	0.30
7	75850001	76000000	0.15	6	79900001	80050000	0.15
8	59350001	59700000	0.35	7	52100001	52250000	0.15
8	79000001	79250000	0.25	7	75850001	76000000	0.15
8	79350001	79950000	0.60	7	98300001	98500000	0.20
9	71800001	72050000	0.25	8	77650001	77750000	0.10
10	58500001	58750000	0.25	8	79050001	79200000	0.15
10	58900001	59200000	0.30	9	5150001	5450000	0.30
11	12950001	13050000	0.10	9	33400001	33600000	0.20
11	13150001	13300000	0.15	9	38750001	38950000	0.20
11	15400001	15550000	0.15	9	68050001	68150000	0.10
11	62100001	62250000	0.15	9	71650001	72150000	0.50
12	44700001	44800000	0.10	10	58550001	58650000	0.10
13	57400001	57500000	0.10	10	59000001	59100000	0.10
13	64100001	64250000	0.15	11	12900001	13000000	0.10
13	69700001	69800000	0.10	11	13150001	13250000	0.10

Precipitation of wettest quarter (bio16)				Precipitation of warmest quarter (bio18)			
Chr	Start	End	Size	Chr	Start	End	Size
14	60000001	60100000	0.10	11	13800001	13900000	0.10
15	16450001	16600000	0.15	11	15450001	15550000	0.10
16	9050001	9200000	0.15	12	52050001	52150000	0.10
16	14800001	14950000	0.15	13	26250001	26350000	0.10
16	17200001	17300000	0.10	13	47850001	48050000	0.20
16	19600001	19700000	0.10	13	57350001	57550000	0.20
16	50500001	50650000	0.15	13	69700001	69800000	0.10
18	24100001	24200000	0.10	16	17000001	17150000	0.15
18	35200001	35350000	0.15	16	19400001	19650000	0.25
19	13300001	13450000	0.15	17	29350001	29500000	0.15
19	13700001	13800000	0.10	17	68100001	68200000	0.10
19	46550001	46700000	0.15	18	24100001	24200000	0.10
20	40200001	40400000	0.20	19	13700001	13800000	0.10
20	40450001	40550000	0.10	19	39250001	39400000	0.15
20	48800001	48950000	0.15	19	39650001	39950000	0.30
20	54250001	54400000	0.15	19	40100001	40350000	0.25
20	71250001	71650000	0.40	19	40400001	40500000	0.10
21	36800001	36900000	0.10	19	49750001	49850000	0.10
21	57800001	57950000	0.15	20	41150001	41250000	0.10
21	59300001	59450000	0.15	20	48800001	49000000	0.20
22	10300001	10450000	0.15	20	40300001	40550000	0.25
22	10700001	10800000	0.10	21	36750001	37000000	0.25
22	10850001	10950000	0.10	21	57800001	57950000	0.15
25	29500001	29600000	0.10	21	59300001	59450000	0.15
27	21350001	21450000	0.10	22	10700001	10800000	0.10
27	21800001	21950000	0.15	22	10850001	10950000	0.10
28	32450001	32600000	0.15	22	26350001	26600000	0.25
29	1	350000	0.35	25	26700001	26850000	0.15
				25	30500001	30800000	0.30
				26	38900001	39000000	0.10
				27	21400001	21700000	0.30
				27	21750001	21900000	0.15
				29	1	350000	0.35
				29	750001	900000	0.15

Table S35. Overlapping selective sweep regions between high and low groups of cultivated land (Arado and Begait) or soil bulk density in kg/m^3 (SBD) (Begait and Arado).

CL or SBD			
Chr	Start	End	Size
1	40600001	40700000	0.10
1	44050001	44350000	0.30
1	155750001	155850000	0.10
2	12850001	12950000	0.10
2	70300001	70400000	0.10
2	82100001	82200000	0.10
2	100250001	100350000	0.10
3	59350001	59500000	0.15
3	59800001	59900000	0.10
3	60050001	60150000	0.10
3	57350001	57650000	0.30
4	14250001	14350000	0.10

CL or SBD			
Chr	Start	End	Size
4	112000001	112150000	0.15
5	18700001	18850000	0.15
5	28250001	28400000	0.15
5	66550001	66700000	0.15
5	112300001	112450000	0.15
5	113700001	113800000	0.10
5	119200001	119850000	0.65
6	79950001	80050000	0.10
6	50950001	51500000	0.55
7	9900001	10000000	0.10
7	38350001	38500000	0.15
7	52100001	52350000	0.25
7	73450001	73550000	0.10
7	49850001	51150000	1.30
8	59550001	59700000	0.15
9	39000001	39250000	0.25
9	39300001	39550000	0.25
9	71700001	71950000	0.25
9	93700001	93850000	0.15
10	58650001	58750000	0.10
11	12900001	13050000	0.15
11	13100001	13300000	0.20
11	14650001	14800000	0.15
13	49800001	50000000	0.20
13	50150001	50300000	0.15
15	59900001	60000000	0.10
16	50500001	50650000	0.15
17	13200001	13300000	0.10
18	35750001	35850000	0.10
18	36850001	37300000	0.45
19	26700001	26800000	0.10
19	26850001	27000000	0.15
20	40200001	40400000	0.20
20	40450001	40650000	0.20
20	48650001	48950000	0.30
20	49150001	49250000	0.10
20	49300001	49400000	0.10
20	54250001	54400000	0.15
21	57800001	57950000	0.15
21	59300001	59400000	0.10
22	10300001	10450000	0.15
22	10850001	11000000	0.15
22	32600001	32700000	0.10
25	30350001	30700000	0.35
27	12400001	12500000	0.10
27	34400001	34550000	0.15
29	50001	400000	0.35

Table S36. F_{ST} selective sweep regions between high (Begait) and low (Abergelle) groups of the temperature seasonality (bio4).

High 1% windows						High 1% merged windows			
Chr	Start	End	nSNPs	F_{ST}	ZF_{ST}	Chr	Start	End	Size (MB)
1	62950001	63050000	759	0.187782	3.568181	1	8650001	8800000	0.149999
1	8750001	8850000	589	0.18823	3.577086	1	66800001	66900000	0.099999
1	137000001	137100000	896	0.190904	3.630237	1	69700001	69850000	0.149999
1	69700001	69800000	345	0.193633	3.684481	1	69950001	70150000	0.199999
1	66800001	66900000	455	0.197793	3.767169	1	101200001	101300000	0.099999
1	101200001	101300000	1269	0.203387	3.87836	1	102150001	102400000	0.249999
1	8650001	8750000	839	0.204648	3.903424	1	115250001	115350000	0.099999
1	102250001	102350000	842	0.206406	3.938368	1	137000001	137100000	0.099999
1	69750001	69850000	228	0.208842	3.986788	2	350001	700000	0.349999
1	102300001	102400000	848	0.209741	4.004657	2	23700001	23800000	0.099999
1	115250001	115350000	808	0.21109	4.031471	2	51100001	51250000	0.149999
1	102150001	102250000	498	0.221616	4.240695	2	51350001	51500000	0.149999
1	102200001	102300000	701	0.22287	4.265621	2	66350001	66500000	0.149999
1	69950001	70050000	351	0.225486	4.317618	2	67850001	68050000	0.199999
1	70050001	70150000	876	0.228427	4.376076	2	73100001	73300000	0.199999
1	8700001	8800000	681	0.234238	4.491581	2	73300001	73550000	0.249999
1	70000001	70100000	562	0.253866	4.881724	2	80750001	80900000	0.149999
2	107100001	107200000	519	0.188645	3.585335	2	80950001	81150000	0.199999
2	67950001	68050000	779	0.191316	3.638426	2	89300001	89400000	0.099999
2	51350001	51450000	832	0.192554	3.663034	2	93900001	94100000	0.199999
2	66400001	66500000	940	0.196194	3.735385	2	106700001	107100000	0.399999
2	107000001	107100000	302	0.197379	3.75894	2	107150001	107300000	0.149999
2	107550001	107650000	894	0.197441	3.760172	2	107350001	107650000	0.299999
2	89300001	89400000	1196	0.197453	3.76041	2	121750001	121850000	0.099999
2	23700001	23800000	872	0.198235	3.775954	3	800001	1000000	0.199999
2	66350001	66450000	1053	0.200254	3.816086	3	3950001	4150000	0.199999
2	107200001	107300000	568	0.200792	3.826779	3	6950001	7100000	0.149999
2	93900001	94000000	951	0.202567	3.862061	3	10500001	10600000	0.099999
2	107150001	107250000	389	0.206345	3.937155	3	20150001	20350000	0.199999
2	73100001	73200000	486	0.206805	3.946299	3	23450001	23550000	0.099999
2	80950001	81050000	595	0.207072	3.951606	3	35650001	35750000	0.099999
2	106700001	106800000	520	0.208771	3.985377	3	85400001	85550000	0.149999
2	81000001	81100000	839	0.211537	4.040356	3	100550001	100750000	0.199999
2	73450001	73550000	1021	0.212247	4.054469	4	8950001	9050000	0.099999
2	107350001	107450000	453	0.212798	4.065421	4	17200001	17400000	0.199999
2	51400001	51500000	937	0.213393	4.077248	4	31600001	31700000	0.099999
2	550001	650000	656	0.215307	4.115292	4	43900001	44050000	0.149999
2	121750001	121850000	496	0.220809	4.224654	4	83950001	84150000	0.199999
2	51100001	51200000	648	0.222302	4.25433	4	92550001	92650000	0.099999
2	500001	600000	586	0.225091	4.309767	5	28700001	28850000	0.149999
2	107400001	107500000	464	0.227318	4.354033	5	31300001	31650000	0.349999
2	73300001	73400000	396	0.231701	4.441153	5	33300001	33450000	0.149999
2	94000001	94100000	751	0.233585	4.478601	5	35000001	35100000	0.099999
2	81050001	81150000	866	0.235052	4.50776	5	35150001	35500000	0.349999
2	106950001	107050000	581	0.236621	4.538947	5	35900001	36050000	0.149999
2	73200001	73300000	695	0.237115	4.548766	5	42950001	43050000	0.099999
2	80750001	80850000	826	0.238888	4.584008	5	47150001	47300000	0.149999
2	93950001	94050000	1071	0.24582	4.721794	5	47950001	48100000	0.149999
2	600001	700000	683	0.252853	4.861588	5	48250001	48800000	0.549999
2	73150001	73250000	721	0.254447	4.893272	5	57950001	58100000	0.149999
2	106850001	106950000	355	0.254465	4.89363	5	60950001	61100000	0.149999
2	106750001	106850000	628	0.255343	4.911082	5	79250001	79400000	0.149999
2	107450001	107550000	553	0.25614	4.926924	5	80300001	80450000	0.149999
2	106900001	107000000	568	0.256309	4.930283	5	85250001	85350000	0.099999
2	51150001	51250000	579	0.256311	4.930323	5	91700001	91900000	0.199999
2	106800001	106900000	441	0.257685	4.957633	5	104900001	105000000	0.099999

High 1% windows						High 1% merged windows			
Chr	Start	End	nSNPs	F_{ST}	ZF_{ST}	Chr	Start	End	Size (MB)
2	107500001	107600000	680	0.258104	4.965962	6	37200001	37350000	0.149999
2	80800001	80900000	887	0.261112	5.025751	6	37350001	37450000	0.099999
2	73400001	73500000	931	0.264865	5.100349	6	41350001	41550000	0.199999
2	67850001	67950000	982	0.267567	5.154056	6	53750001	53900000	0.149999
2	450001	550000	473	0.281201	5.425057	6	68700001	68900000	0.199999
2	400001	500000	593	0.287665	5.553541	6	68950001	69100000	0.149999
2	73350001	73450000	552	0.299687	5.792501	6	73300001	73400000	0.099999
2	350001	450000	521	0.319393	6.184194	6	75300001	75600000	0.299999
2	67900001	68000000	994	0.333328	6.461178	6	75600001	75750000	0.149999
3	4050001	4150000	1301	0.190044	3.613143	6	75800001	75950000	0.149999
3	3950001	4050000	1306	0.191983	3.651684	6	76700001	76900000	0.199999
3	10500001	10600000	1026	0.192875	3.669414	6	91600001	91700000	0.099999
3	800001	900000	940	0.197103	3.753454	6	94600001	94750000	0.149999
3	20150001	20250000	365	0.199228	3.795692	6	107950001	108150000	0.199999
3	23450001	23550000	977	0.203178	3.874205	7	1550001	1650000	0.099999
3	850001	950000	944	0.203416	3.878936	7	5350001	5600000	0.249999
3	900001	1000000	1252	0.204855	3.907539	7	43150001	43250000	0.099999
3	20200001	20300000	451	0.208479	3.979573	7	64150001	64250000	0.099999
3	100650001	100750000	564	0.208604	3.982057	7	104100001	104200000	0.099999
3	20250001	20350000	421	0.209399	3.997859	7	104450001	104550000	0.099999
3	4000001	4100000	1215	0.210822	4.026144	7	106300001	106450000	0.149999
3	35650001	35750000	1080	0.216593	4.140853	8	33400001	33500000	0.099999
3	85450001	85550000	645	0.232913	4.465244	8	49800001	49900000	0.099999
3	85400001	85500000	899	0.24716	4.748429	8	67350001	67550000	0.199999
3	7000001	7100000	886	0.284524	5.491108	8	72150001	72250000	0.099999
3	100550001	100650000	672	0.285447	5.509455	8	84500001	84650000	0.149999
3	6950001	7050000	592	0.29062	5.612278	8	97000001	97100000	0.099999
3	100600001	100700000	598	0.343183	6.657065	8	97600001	97700000	0.099999
4	93450001	93550000	581	0.187919	3.570904	8	101500001	101600000	0.099999
4	43900001	44000000	886	0.195004	3.711732	8	101600001	101750000	0.149999
4	17200001	17300000	1245	0.199495	3.800999	8	103350001	103450000	0.099999
4	31600001	31700000	582	0.202617	3.863055	9	67400001	67750000	0.349999
4	92550001	92650000	430	0.213364	4.076671	9	76300001	76450000	0.149999
4	84050001	84150000	887	0.218924	4.187186	9	76750001	76850000	0.099999
4	43950001	44050000	804	0.226098	4.329783	9	79500001	79650000	0.149999
4	17300001	17400000	1146	0.235542	4.5175	9	93900001	94000000	0.099999
4	83950001	84050000	751	0.238499	4.576276	9	103650001	104150000	0.499999
4	8950001	9050000	755	0.259948	5.002615	10	56150001	56250000	0.099999
4	17250001	17350000	1204	0.261679	5.037021	10	66650001	66750000	0.099999
4	84000001	84100000	1029	0.281537	5.431736	10	88550001	88700000	0.149999
5	36050001	36150000	1376	0.188775	3.587919	10	94600001	94700000	0.099999
5	104900001	105000000	1212	0.189472	3.601773	11	7750001	7900000	0.149999
5	33350001	33450000	913	0.190611	3.624413	11	41150001	41250000	0.099999
5	33300001	33400000	1170	0.193593	3.683686	11	43950001	44100000	0.149999
5	28750001	28850000	948	0.193808	3.687959	11	90700001	90800000	0.099999
5	48450001	48550000	376	0.195518	3.721949	11	90850001	91050000	0.199999
5	79250001	79350000	1406	0.195856	3.728667	11	98900001	99000000	0.099999
5	35000001	35100000	956	0.198602	3.783249	11	101450001	101800000	0.349999
5	48550001	48650000	505	0.198725	3.785694	12	29500001	29750000	0.249999
5	48500001	48600000	531	0.200594	3.822844	12	39800001	39900000	0.099999
5	42950001	43050000	923	0.201384	3.838546	12	54750001	55000000	0.249999
5	85250001	85350000	907	0.201823	3.847272	13	47300001	47400000	0.099999
5	91700001	91800000	1567	0.202462	3.859974	13	48350001	48450000	0.099999
5	35950001	36050000	861	0.203515	3.880904	13	50500001	50650000	0.149999
5	60950001	61050000	907	0.204889	3.908215	13	63350001	63550000	0.199999
5	48350001	48450000	244	0.206569	3.941608	13	77500001	77600000	0.099999

High 1% windows						High 1% merged windows			
Chr	Start	End	nSNPs	F_{ST}	ZF_{ST}	Chr	Start	End	Size (MB)
5	47950001	48050000	351	0.208412	3.978241	14	41400001	41600000	0.199999
5	48400001	48500000	237	0.208635	3.982673	14	43100001	43200000	0.099999
5	57950001	58050000	1481	0.211017	4.03002	14	43400001	43500000	0.099999
5	48600001	48700000	571	0.211587	4.04135	14	47000001	47100000	0.099999
5	47200001	47300000	1187	0.213936	4.088041	15	11250001	11350000	0.099999
5	35150001	35250000	1099	0.217584	4.160551	15	11450001	11750000	0.299999
5	35900001	36000000	1117	0.218885	4.186411	15	12100001	12250000	0.149999
5	80300001	80400000	461	0.219007	4.188836	15	12400001	12550000	0.149999
5	35400001	35500000	376	0.223195	4.272081	15	37800001	37950000	0.149999
5	47150001	47250000	1235	0.22998	4.406945	15	58050001	58400000	0.349999
5	79300001	79400000	1570	0.232523	4.457492	15	69250001	69450000	0.199999
5	31550001	31650000	945	0.233297	4.472877	15	71800001	71900000	0.099999
5	31350001	31450000	1179	0.236529	4.537119	16	12400001	12650000	0.249999
5	28700001	28800000	839	0.237355	4.553537	16	21800001	21950000	0.149999
5	48250001	48350000	598	0.252133	4.847277	16	25850001	26000000	0.149999
5	31400001	31500000	1317	0.26597	5.122313	16	27000001	27100000	0.099999
5	48700001	48800000	399	0.268307	5.168765	16	27150001	27250000	0.099999
5	61000001	61100000	868	0.269498	5.192439	16	28150001	28250000	0.099999
5	91800001	91900000	1044	0.271325	5.228754	16	28300001	28400000	0.099999
5	48300001	48400000	390	0.276094	5.323546	16	28450001	28700000	0.249999
5	48650001	48750000	545	0.278716	5.375663	16	32350001	32450000	0.099999
5	31300001	31400000	1245	0.281113	5.423308	16	65600001	65700000	0.099999
5	80350001	80450000	411	0.282137	5.443662	16	70350001	70450000	0.099999
5	35200001	35300000	802	0.283161	5.464016	16	70550001	70650000	0.099999
5	35350001	35450000	497	0.284091	5.482502	17	20650001	20750000	0.099999
5	35300001	35400000	505	0.291696	5.633665	17	21650001	21750000	0.099999
5	91750001	91850000	1548	0.292499	5.649626	17	38700001	38800000	0.099999
5	48000001	48100000	524	0.295608	5.711423	17	39650001	39750000	0.099999
5	35250001	35350000	577	0.303012	5.858592	17	62950001	63150000	0.199999
5	31450001	31550000	718	0.350182	6.796183	17	72350001	72500000	0.149999
5	31500001	31600000	516	0.353796	6.868018	17	73150001	73250000	0.099999
5	58000001	58100000	702	0.509618	9.96527	18	650001	800000	0.149999
6	75300001	75400000	1274	0.189728	3.606862	18	2550001	2650000	0.099999
6	37250001	37350000	975	0.195184	3.71531	18	14450001	14750000	0.299999
6	75800001	75900000	846	0.196463	3.740732	18	35500001	35650000	0.149999
6	37350001	37450000	319	0.197669	3.764704	18	35650001	35750000	0.099999
6	76700001	76800000	503	0.199619	3.803464	18	38400001	38750000	0.349999
6	91600001	91700000	813	0.200913	3.829184	18	59350001	59500000	0.149999
6	107950001	108050000	1196	0.203677	3.884124	18	59700001	59850000	0.149999
6	76800001	76900000	769	0.210194	4.013661	19	23350001	23500000	0.149999
6	41400001	41500000	567	0.213236	4.074127	19	26600001	26700000	0.099999
6	68700001	68800000	863	0.214105	4.0914	19	41000001	41200000	0.199999
6	75650001	75750000	951	0.214379	4.096846	19	46550001	46800000	0.249999
6	75850001	75950000	631	0.215203	4.113225	19	52300001	52400000	0.099999
6	68950001	69050000	647	0.223318	4.274525	19	52700001	52800000	0.099999
6	94600001	94700000	679	0.223825	4.284603	19	52900001	53050000	0.149999
6	73300001	73400000	913	0.224942	4.306805	20	6350001	6500000	0.149999
6	94650001	94750000	680	0.225201	4.311953	20	10850001	10950000	0.099999
6	69000001	69100000	768	0.230891	4.425053	20	13450001	13650000	0.199999
6	75500001	75600000	1183	0.232065	4.448388	20	25150001	25300000	0.149999
6	41350001	41450000	565	0.232868	4.464349	20	30650001	31200000	0.549999
6	75600001	75700000	900	0.237212	4.550694	20	31350001	31500000	0.149999
6	41450001	41550000	591	0.238104	4.568425	20	43150001	43300000	0.149999
6	37200001	37300000	959	0.244766	4.700844	20	47900001	48150000	0.249999
6	68800001	68900000	898	0.24588	4.722987	20	56050001	56200000	0.149999
6	75350001	75450000	1259	0.248006	4.765245	20	56250001	56500000	0.249999

High 1% windows						High 1% merged windows			
Chr	Start	End	nSNPs	F_{ST}	ZF_{ST}	Chr	Start	End	Size (MB)
6	53750001	53850000	880	0.266468	5.132212	20	67600001	67850000	0.249999
6	53800001	53900000	746	0.268482	5.172244	20	68900001	69000000	0.099999
6	68750001	68850000	995	0.271979	5.241753	21	10500001	10700000	0.199999
6	75400001	75500000	1015	0.300449	5.807647	21	31100001	31200000	0.099999
6	75450001	75550000	1025	0.301347	5.825497	21	37150001	37400000	0.249999
6	108050001	108150000	984	0.308096	5.959646	21	42650001	42750000	0.099999
6	108000001	108100000	1247	0.310594	6.009298	21	43500001	43700000	0.199999
6	76750001	76850000	508	0.321165	6.219416	21	47450001	47600000	0.149999
7	106250001	106350000	1008	0.188592	3.584282	21	63450001	63550000	0.099999
7	43150001	43250000	417	0.190503	3.622266	21	63800001	63900000	0.099999
7	1550001	1650000	935	0.190978	3.631708	21	64000001	64200000	0.199999
7	106350001	106450000	1083	0.194492	3.701555	21	67000001	67100000	0.099999
7	5500001	5600000	1165	0.196411	3.739699	21	67250001	67750000	0.499999
7	5350001	5450000	901	0.201611	3.843058	22	11750001	11900000	0.149999
7	104100001	104200000	1458	0.215066	4.110502	22	19800001	19950000	0.149999
7	104450001	104550000	792	0.220809	4.224654	22	34350001	34550000	0.199999
7	64150001	64250000	923	0.224181	4.291679	22	34550001	34700000	0.149999
7	106300001	106400000	1090	0.225366	4.315233	22	40200001	40400000	0.199999
7	5450001	5550000	1108	0.274229	5.286476	22	46750001	46850000	0.099999
7	5400001	5500000	1070	0.287215	5.544597	22	47050001	47150000	0.099999
8	101500001	101600000	805	0.189902	3.61032	22	51200001	51350000	0.149999
8	101600001	101700000	534	0.190961	3.63137	23	1050001	1250000	0.199999
8	72150001	72250000	988	0.191342	3.638943	23	1350001	1450000	0.099999
8	84500001	84600000	645	0.192934	3.670587	23	16800001	16900000	0.099999
8	49800001	49900000	736	0.197206	3.755501	23	26150001	26250000	0.099999
8	33400001	33500000	960	0.197703	3.76538	23	26300001	26450000	0.149999
8	97000001	97100000	1167	0.202597	3.862657	23	42200001	42300000	0.099999
8	84550001	84650000	831	0.209566	4.001179	23	45150001	45250000	0.099999
8	101650001	101750000	504	0.210338	4.016524	23	47600001	47750000	0.149999
8	103350001	103450000	446	0.211945	4.048466	23	47800001	47950000	0.149999
8	97600001	97700000	841	0.214559	4.100424	23	48050001	48150000	0.099999
8	67350001	67450000	570	0.225207	4.312073	23	51700001	51850000	0.149999
8	67450001	67550000	1044	0.255683	4.91784	23	52000001	52350000	0.349999
8	67400001	67500000	886	0.308605	5.969763	24	9000001	9100000	0.099999
9	79700001	79800000	845	0.188127	3.575039	24	13750001	13850000	0.099999
9	93900001	94000000	1163	0.189492	3.602171	24	19600001	19700000	0.099999
9	76300001	76400000	745	0.190578	3.623757	24	61150001	61300000	0.149999
9	103650001	103750000	1092	0.195332	3.718252	25	1100001	1450000	0.349999
9	79500001	79600000	941	0.196562	3.7427	25	26500001	26600000	0.099999
9	67650001	67750000	826	0.202103	3.852838	26	29050001	29150000	0.099999
9	103750001	103850000	766	0.20479	3.906247	27	1950001	2100000	0.149999
9	76350001	76450000	700	0.204841	3.907261	27	14500001	14650000	0.149999
9	103700001	103800000	862	0.210872	4.027138	28	7200001	7400000	0.199999
9	76750001	76850000	744	0.219517	4.198973	28	14050001	14250000	0.199999
9	79550001	79650000	916	0.231785	4.442823	28	25450001	25550000	0.099999
9	103800001	103900000	677	0.239015	4.586532	29	4950001	5100000	0.149999
9	67400001	67500000	699	0.241913	4.644136	29	20550001	20700000	0.149999
9	67450001	67550000	723	0.281658	5.434141	29	29250001	29350000	0.099999
9	103850001	103950000	574	0.283924	5.479182	29	34250001	34400000	0.149999
9	104000001	104100000	499	0.299007	5.778985				
9	103900001	104000000	581	0.303652	5.871313				
9	103950001	104050000	591	0.304355	5.885286				
9	104050001	104150000	342	0.313043	6.057976				
9	67500001	67600000	839	0.318902	6.174435				
9	67600001	67700000	923	0.36614	7.113378				
9	67550001	67650000	1048	0.377584	7.340849				

High 1% windows						High 1% merged windows			
Chr	Start	End	nSNPs	F_{ST}	ZF_{ST}	Chr	Start	End	Size (MB)
10	56200001	56300000	879	0.188493	3.582314				
10	56150001	56250000	823	0.192958	3.671064				
10	66650001	66750000	548	0.205578	3.92191				
10	94600001	94700000	946	0.214468	4.098615				
10	88550001	88650000	1102	0.239039	4.587009				
10	88600001	88700000	987	0.240227	4.610623				
11	7850001	7950000	419	0.189243	3.597221				
11	90850001	90950000	826	0.190757	3.627315				
11	98900001	99000000	909	0.192556	3.663073				
11	41150001	41250000	516	0.198943	3.790027				
11	43950001	44050000	1374	0.201756	3.845941				
11	7750001	7850000	313	0.202575	3.86222				
11	90700001	90800000	904	0.207561	3.961326				
11	44000001	44100000	1749	0.211141	4.032485				
11	101700001	101800000	653	0.219031	4.189313				
11	101450001	101550000	817	0.225323	4.314378				
11	90950001	91050000	901	0.245493	4.715295				
11	90900001	91000000	877	0.249583	4.796591				
11	101500001	101600000	584	0.263373	5.070693				
11	101650001	101750000	852	0.26767	5.156104				
11	101600001	101700000	865	0.343509	6.663545				
11	101550001	101650000	542	0.404625	7.878339				
11	7800001	7900000	164	0.413372	8.052202				
12	29650001	29750000	591	0.190705	3.626281				
12	39800001	39900000	907	0.201159	3.834074				
12	54750001	54850000	777	0.20741	3.958324				
12	29600001	29700000	690	0.212326	4.056039				
12	54800001	54900000	471	0.222842	4.265064				
12	29500001	29600000	407	0.223832	4.284742				
12	54850001	54950000	491	0.224779	4.303565				
12	54900001	55000000	573	0.226867	4.345068				
12	29550001	29650000	569	0.23224	4.451867				
13	48400001	48500000	556	0.188667	3.585772				
13	77500001	77600000	624	0.190641	3.625009				
13	47300001	47400000	250	0.195841	3.728369				
13	50500001	50600000	742	0.201403	3.838924				
13	48350001	48450000	777	0.204736	3.905174				
13	50550001	50650000	579	0.214798	4.105175				
13	63450001	63550000	491	0.219943	4.207441				
13	63350001	63450000	679	0.225343	4.314776				
13	63400001	63500000	574	0.235777	4.522171				
14	47000001	47100000	817	0.192714	3.666214				
14	43400001	43500000	625	0.201526	3.841369				
14	43100001	43200000	669	0.214539	4.100026				
14	41500001	41600000	951	0.30873	5.972247				
14	41400001	41500000	676	0.361546	7.022064				
14	41450001	41550000	796	0.436328	8.508495				
15	11400001	11500000	1341	0.188876	3.589927				
15	58050001	58150000	527	0.194646	3.704616				
15	58150001	58250000	493	0.197159	3.754567				
15	58100001	58200000	572	0.19786	3.7685				
15	11250001	11350000	1314	0.200834	3.827614				
15	12150001	12250000	1347	0.201866	3.848127				
15	11650001	11750000	1028	0.202304	3.856833				
15	12450001	12550000	1417	0.202388	3.858503				
15	37850001	37950000	611	0.215631	4.121732				

High 1% windows						High 1% merged windows			
Chr	Start	End	nSNPs	F_{ST}	ZF_{ST}	Chr	Start	End	Size (MB)
15	58300001	58400000	834	0.218925	4.187206				
15	69250001	69350000	1261	0.22004	4.209369				
15	11450001	11550000	1605	0.22535	4.314915				
15	37800001	37900000	582	0.229837	4.404103				
15	12400001	12500000	1403	0.230467	4.416625				
15	11500001	11600000	1532	0.236618	4.538888				
15	71800001	71900000	926	0.24619	4.729149				
15	58200001	58300000	672	0.259278	4.989297				
15	11550001	11650000	1481	0.262735	5.058011				
15	58250001	58350000	796	0.272697	5.256025				
15	11600001	11700000	1448	0.275236	5.306492				
15	12100001	12200000	992	0.284346	5.48757				
15	69350001	69450000	1084	0.311527	6.027843				
15	69300001	69400000	1455	0.322572	6.247383				
16	28350001	28450000	1299	0.188403	3.580525				
16	70550001	70650000	1067	0.190593	3.624055				
16	28150001	28250000	1030	0.195508	3.72175				
16	28600001	28700000	719	0.196298	3.737453				
16	27000001	27100000	1259	0.198752	3.78623				
16	28300001	28400000	1216	0.200659	3.824136				
16	65600001	65700000	605	0.201634	3.843516				
16	27150001	27250000	957	0.206868	3.947551				
16	25850001	25950000	1245	0.208155	3.973133				
16	21800001	21900000	619	0.212141	4.052362				
16	28450001	28550000	806	0.224205	4.292156				
16	32350001	32450000	708	0.226249	4.332784				
16	12400001	12500000	689	0.226358	4.334951				
16	28550001	28650000	785	0.226712	4.341987				
16	28500001	28600000	801	0.232145	4.449978				
16	12550001	12650000	670	0.238451	4.575322				
16	25900001	26000000	1190	0.238795	4.582159				
16	70350001	70450000	668	0.252821	4.860952				
16	12500001	12600000	646	0.268812	5.178803				
16	21850001	21950000	619	0.283919	5.479083				
16	12450001	12550000	639	0.340716	6.608029				
17	21650001	21750000	1859	0.189655	3.605411				
17	38700001	38800000	971	0.195466	3.720915				
17	20650001	20750000	1237	0.19939	3.798912				
17	72400001	72500000	602	0.207256	3.955263				
17	39650001	39750000	821	0.228798	4.383451				
17	62950001	63050000	734	0.230386	4.415015				
17	73150001	73250000	32	0.252564	4.855844				
17	63050001	63150000	391	0.265782	5.118576				
17	63000001	63100000	445	0.294519	5.689777				
17	72350001	72450000	591	0.302785	5.85408				
18	59750001	59850000	761	0.191288	3.63787				
18	35500001	35600000	221	0.191952	3.651068				
18	2550001	2650000	694	0.196239	3.73628				
18	700001	800000	1168	0.198499	3.781202				
18	59700001	59800000	631	0.201937	3.849538				
18	14450001	14550000	645	0.203651	3.883607				
18	35550001	35650000	210	0.206223	3.93473				
18	59400001	59500000	1074	0.208951	3.988955				
18	38650001	38750000	266	0.212649	4.062459				
18	38400001	38500000	410	0.218744	4.183609				
18	38450001	38550000	408	0.223036	4.26892				

High 1% windows						High 1% merged windows			
Chr	Start	End	nSNPs	F_{ST}	ZF_{ST}	Chr	Start	End	Size (MB)
18	14650001	14750000	500	0.225826	4.324377				
18	35650001	35750000	308	0.226414	4.336064				
18	38550001	38650000	249	0.228454	4.376613				
18	38500001	38600000	276	0.228731	4.382119				
18	650001	750000	1150	0.229836	4.404083				
18	59350001	59450000	1112	0.233721	4.481304				
18	14600001	14700000	497	0.243256	4.67083				
18	38600001	38700000	245	0.254198	4.888323				
18	14550001	14650000	321	0.278566	5.372682				
18	14500001	14600000	475	0.298609	5.771074				
19	52300001	52400000	885	0.192192	3.655838				
19	26600001	26700000	407	0.195176	3.715151				
19	23350001	23450000	562	0.195806	3.727673				
19	46700001	46800000	1125	0.200104	3.813104				
19	23400001	23500000	739	0.201133	3.833557				
19	52950001	53050000	1322	0.206753	3.945265				
19	46650001	46750000	853	0.21279	4.065262				
19	46550001	46650000	1156	0.214354	4.096349				
19	41100001	41200000	1112	0.21837	4.176175				
19	52700001	52800000	383	0.221429	4.236978				
19	52900001	53000000	1259	0.222585	4.259956				
19	46600001	46700000	992	0.228405	4.375639				
19	41000001	41100000	1008	0.247999	4.765106				
19	41050001	41150000	1014	0.264618	5.09544				
20	56250001	56350000	821	0.189971	3.611692				
20	56400001	56500000	778	0.191066	3.633457				
20	13550001	13650000	372	0.195086	3.713362				
20	47900001	48000000	1390	0.195557	3.722724				
20	67750001	67850000	1314	0.197741	3.766135				
20	6350001	6450000	700	0.198208	3.775417				
20	56300001	56400000	818	0.199166	3.79446				
20	56350001	56450000	744	0.204527	3.901019				
20	48050001	48150000	1084	0.207846	3.966991				
20	31100001	31200000	403	0.208436	3.978718				
20	67700001	67800000	1056	0.211014	4.029961				
20	56050001	56150000	1312	0.211144	4.032544				
20	31350001	31450000	625	0.212911	4.067667				
20	13500001	13600000	330	0.213197	4.073352				
20	25150001	25250000	450	0.215745	4.123998				
20	31400001	31500000	481	0.217715	4.163155				
20	67650001	67750000	850	0.221241	4.233241				
20	30700001	30800000	1054	0.225493	4.317758				
20	13450001	13550000	353	0.225811	4.324078				
20	30650001	30750000	969	0.226995	4.347613				
20	67600001	67700000	1221	0.23092	4.425629				
20	6400001	6500000	493	0.234529	4.497365				
20	56100001	56200000	1139	0.237372	4.553875				
20	25200001	25300000	384	0.239252	4.591243				
20	43150001	43250000	1119	0.243472	4.675124				
20	30750001	30850000	1017	0.244083	4.687268				
20	10850001	10950000	692	0.247969	4.76451				
20	47950001	48050000	1376	0.250095	4.806768				
20	48000001	48100000	979	0.25056	4.816011				
20	43200001	43300000	994	0.251382	4.832349				
20	68900001	69000000	1490	0.263659	5.076378				
20	30800001	30900000	522	0.292901	5.657617				

High 1% windows						High 1% merged windows			
Chr	Start	End	nSNPs	F_{ST}	ZF_{ST}	Chr	Start	End	Size (MB)
20	31050001	31150000	441	0.324489	6.285487				
20	30900001	31000000	625	0.425187	8.287047				
20	30850001	30950000	293	0.438571	8.553078				
20	31000001	31100000	493	0.439072	8.563037				
20	30950001	31050000	707	0.442797	8.637078				
21	12800001	12900000	1320	0.188227	3.577027				
21	31100001	31200000	756	0.189677	3.605848				
21	67000001	67100000	757	0.192946	3.670825				
21	67650001	67750000	950	0.198001	3.771303				
21	47450001	47550000	557	0.198511	3.78144				
21	37300001	37400000	883	0.201383	3.838526				
21	63450001	63550000	905	0.201688	3.844589				
21	43600001	43700000	642	0.202037	3.851526				
21	10600001	10700000	612	0.20356	3.881798				
21	67250001	67350000	738	0.207611	3.96232				
21	67300001	67400000	720	0.209197	3.993844				
21	64100001	64200000	910	0.210127	4.01233				
21	10500001	10600000	342	0.215971	4.12849				
21	63800001	63900000	964	0.217983	4.168482				
21	67350001	67450000	696	0.218137	4.171543				
21	42650001	42750000	812	0.223635	4.280826				
21	37150001	37250000	765	0.229992	4.407184				
21	47500001	47600000	742	0.23841	4.574507				
21	10550001	10650000	332	0.252528	4.855128				
21	67500001	67600000	647	0.268066	5.163975				
21	67550001	67650000	864	0.270361	5.209592				
21	43500001	43600000	1022	0.281689	5.434757				
21	67600001	67700000	960	0.284351	5.48767				
21	67400001	67500000	675	0.295597	5.711205				
21	64000001	64100000	1217	0.300968	5.817963				
21	67450001	67550000	588	0.321774	6.231521				
21	43550001	43650000	782	0.339434	6.582546				
21	64050001	64150000	1123	0.35854	6.962314				
21	37200001	37300000	992	0.377976	7.34864				
21	37250001	37350000	1032	0.37894	7.367802				
22	11750001	11850000	760	0.189992	3.612109				
22	46750001	46850000	901	0.193817	3.688138				
22	47050001	47150000	1185	0.196402	3.73952				
22	40200001	40300000	623	0.197782	3.76695				
22	51200001	51300000	443	0.198984	3.790842				
22	11800001	11900000	880	0.202215	3.855064				
22	40300001	40400000	601	0.211737	4.044331				
22	34350001	34450000	877	0.216122	4.131491				
22	19850001	19950000	1510	0.217143	4.151786				
22	34600001	34700000	435	0.222436	4.256994				
22	34450001	34550000	524	0.226052	4.328869				
22	34400001	34500000	821	0.240327	4.612611				
22	40250001	40350000	471	0.24125	4.630957				
22	34550001	34650000	326	0.244322	4.692019				
22	19800001	19900000	1549	0.248715	4.779338				
22	51250001	51350000	455	0.313076	6.058632				
23	1050001	1150000	1205	0.191364	3.63938				
23	52000001	52100000	456	0.193793	3.687661				
23	51700001	51800000	786	0.193819	3.688178				
23	26350001	26450000	3602	0.19588	3.729144				
23	45150001	45250000	1008	0.19604	3.732324				

High 1% windows						High 1% merged windows			
Chr	Start	End	nSNPs	F_{ST}	ZF_{ST}	Chr	Start	End	Size (MB)
23	48050001	48150000	519	0.198085	3.772973				
23	16800001	16900000	551	0.19832	3.777644				
23	47650001	47750000	882	0.199781	3.806684				
23	1350001	1450000	1173	0.200942	3.829761				
23	1100001	1200000	1194	0.202772	3.866135				
23	47800001	47900000	1185	0.20411	3.892731				
23	47600001	47700000	911	0.209257	3.995037				
23	42200001	42300000	1141	0.217974	4.168303				
23	51750001	51850000	999	0.218462	4.178003				
23	52250001	52350000	672	0.221771	4.243776				
23	1150001	1250000	1144	0.223488	4.277904				
23	47850001	47950000	1383	0.228976	4.386989				
23	52200001	52300000	611	0.234522	4.497226				
23	52150001	52250000	620	0.247373	4.752663				
23	26150001	26250000	2508	0.253921	4.882817				
23	52050001	52150000	332	0.262627	5.055865				
23	26300001	26400000	2797	0.276019	5.322056				
23	52100001	52200000	488	0.310282	6.003096				
24	19600001	19700000	941	0.19476	3.706882				
24	61150001	61250000	697	0.199302	3.797163				
24	9000001	9100000	1319	0.207499	3.960093				
24	61200001	61300000	792	0.214451	4.098277				
24	13750001	13850000	1059	0.221484	4.238071				
25	25650001	25750000	724	0.187778	3.568102				
25	1100001	1200000	859	0.203083	3.872317				
25	1150001	1250000	651	0.222802	4.264269				
25	1200001	1300000	586	0.259003	4.983831				
25	1350001	1450000	791	0.266868	5.140162				
25	26500001	26600000	322	0.270472	5.211799				
25	1250001	1350000	709	0.306599	5.92989				
25	1300001	1400000	747	0.313442	6.065907				
26	29050001	29150000	1628	0.205032	3.911057				
27	1950001	2050000	999	0.199483	3.80076				
27	2000001	2100000	1099	0.222213	4.252561				
27	14500001	14600000	667	0.233546	4.477826				
27	14550001	14650000	705	0.271401	5.230264				
28	7300001	7400000	709	0.189764	3.607577				
28	25450001	25550000	926	0.205885	3.928012				
28	7250001	7350000	953	0.211629	4.042185				
28	7200001	7300000	1123	0.227844	4.364488				
28	14150001	14250000	960	0.235254	4.511776				
28	14050001	14150000	913	0.28299	5.460617				
28	14100001	14200000	1038	0.308011	5.957956				
29	29250001	29350000	358	0.192142	3.654844				
29	34300001	34400000	958	0.194118	3.694121				
29	20550001	20650000	979	0.20794	3.968859				
29	34250001	34350000	1080	0.209058	3.991081				
29	5000001	5100000	1122	0.248106	4.767233				
29	4950001	5050000	1318	0.260711	5.017781				
29	20600001	20700000	1167	0.271728	5.236764				

Table S37. F_{ST} selective sweep regions between high (Raya) and low (Arado) groups of the annual precipitation (bio12).

High 1% windows						High 1% merged windows				
Chr	Start	End	nSNPs	F_{ST}	ZF_{ST}	Chr	Start	End	Size (MB)
1	83500001	83600000	525	0.147819	3.503265326	1	16500001	16600000	0.099999
1	119600001	119700000	816	0.149108	3.533212626	1	42150001	42250000	0.099999
1	42200001	42300000	1297	0.14933	3.538370346	1	90050001	90150000	0.099999
1	16150001	16250000	1151	0.15217	3.604351984	1	143350001	143550000	0.199999
1	52150001	52250000	426	0.153782	3.641803534	1	144800001	144900000	0.099999
1	144750001	144850000	1346	0.155649	3.685179492	1	148000001	148200000	0.199999
1	16450001	16550000	1471	0.157119	3.71933196	2	16850001	17100000	0.249999
1	90100001	90200000	555	0.159036	3.763869566	2	17100001	17250000	0.149999
1	52100001	52200000	342	0.160863	3.806316205	2	17250001	17350000	0.099999
1	142650001	142750000	825	0.161703	3.825831901	2	46050001	46150000	0.099999
1	52050001	52150000	675	0.162716	3.849366901	2	88950001	89050000	0.099999
1	90000001	90100000	605	0.162911	3.85389733	2	89150001	89650000	0.499999
1	33350001	33450000	1091	0.164607	3.89330045	2	129250001	129350000	0.099999
1	147150001	147250000	644	0.168678	3.987881877	3	28400001	28500000	0.099999
1	42150001	42250000	994	0.170601	4.032558881	3	29650001	29800000	0.149999
1	16500001	16600000	1426	0.1709	4.039505539	3	37000001	37150000	0.149999
1	143350001	143450000	1156	0.176074	4.159712933	3	43950001	44050000	0.099999
1	144800001	144900000	1440	0.181684	4.290049903	3	109950001	110050000	0.099999
1	148000001	148100000	969	0.188299	4.443736009	4	24200001	24350000	0.149999
1	90050001	90150000	598	0.18935	4.468153862	4	24400001	24500000	0.099999
1	148100001	148200000	825	0.19234	4.537620446	4	47800001	47950000	0.149999
1	143400001	143500000	1062	0.19819	4.673533329	4	48150001	48250000	0.099999
1	143450001	143550000	879	0.206155	4.858583946	4	48300001	48450000	0.149999
1	148050001	148150000	975	0.214307	5.047979129	4	53100001	53200000	0.099999
2	126850001	126950000	689	0.148082	3.509375597	4	53850001	53950000	0.099999
2	17400001	17500000	1089	0.149026	3.531307522	4	73450001	73600000	0.149999
2	88850001	88950000	828	0.149301	3.537696589	4	78950001	79100000	0.149999
2	129100001	129200000	879	0.149482	3.541901757	5	7550001	7650000	0.099999
2	88900001	89000000	962	0.152424	3.610253159	5	34300001	34600000	0.299999
2	113300001	113400000	1195	0.152881	3.620870627	5	35550001	35800000	0.249999
2	126800001	126900000	507	0.158785	3.75803809	5	38550001	38650000	0.099999
2	17300001	17400000	856	0.160833	3.805619216	5	89250001	89450000	0.199999
2	17350001	17450000	905	0.16162	3.823903564	5	93400001	93500000	0.099999
2	129200001	129300000	1109	0.163496	3.867488619	5	95250001	95550000	0.299999
2	17050001	17150000	717	0.166781	3.94380893	5	111850001	111950000	0.099999
2	89000001	89100000	924	0.167297	3.955797143	6	6250001	6450000	0.199999
2	17150001	17250000	804	0.169311	4.002588348	6	11750001	11900000	0.149999
2	16850001	16950000	1054	0.177031	4.181946887	6	61650001	61750000	0.099999
2	89150001	89250000	1394	0.177954	4.203390919	6	66350001	66600000	0.249999
2	88950001	89050000	870	0.17899	4.227460278	6	68400001	68600000	0.199999
2	89450001	89550000	568	0.181288	4.280849646	6	82150001	82550000	0.399999
2	17250001	17350000	944	0.185209	4.371946127	6	86750001	86900000	0.149999
2	46050001	46150000	839	0.188116	4.439484375	6	104000001	104100000	0.099999
2	89500001	89600000	441	0.19493	4.597793842	6	109650001	109850000	0.199999
2	89550001	89650000	330	0.206156	4.858607179	7	6450001	6650000	0.199999
2	89400001	89500000	740	0.207418	4.887927189	7	21300001	21450000	0.149999
2	16900001	17000000	1143	0.20821	4.906327703	7	22250001	22350000	0.099999
2	17100001	17200000	818	0.211232	4.976537742	7	35250001	35400000	0.149999
2	89300001	89400000	1013	0.223032	5.250686805	7	45050001	45150000	0.099999
2	129250001	129350000	847	0.229092	5.391478612	7	48500001	48650000	0.149999
2	89250001	89350000	1129	0.23289	5.479717437	7	93200001	93300000	0.099999
2	89350001	89450000	855	0.234742	5.5227449	7	109600001	109700000	0.099999
2	89200001	89300000	1304	0.238393	5.607568479	7	110350001	110450000	0.099999
2	17000001	17100000	970	0.240277	5.651339397	7	110500001	110600000	0.099999
2	16950001	17050000	1010	0.262376	6.164764833	8	21850001	22100000	0.249999
3	8900001	9000000	542	0.146877	3.481379867	8	22800001	23000000	0.199999
3	28150001	28250000	678	0.14886	3.527450849	8	23500001	23800000	0.299999
3	8750001	8850000	412	0.149655	3.545921061	8	30500001	30700000	0.199999
3	28250001	28350000	637	0.150493	3.565390291	8	33100001	33250000	0.149999

High 1% windows						High 1% merged windows			
Chr	Start	End	nSNPs	F_{ST}	ZF_{ST}	Chr	Start	End	Size (MB)
3	102350001	102450000	686	0.151758	3.59478	8	97350001	97450000	0.099999
3	350001	450000	916	0.152605	3.614458327	9	9400001	9650000	0.249999
3	37150001	37250000	1202	0.153426	3.633532597	9	11650001	11850000	0.199999
3	8700001	8800000	534	0.154669	3.66241118	9	27800001	27900000	0.099999
3	43900001	44000000	1107	0.15543	3.680091471	9	32100001	32200000	0.099999
3	71350001	71450000	809	0.1561	3.695657562	9	44900001	45000000	0.099999
3	28300001	28400000	606	0.158604	3.753832923	9	68100001	68200000	0.099999
3	30750001	30850000	389	0.160399	3.795536106	9	97400001	97550000	0.149999
3	28350001	28450000	751	0.164387	3.888189196	10	23200001	23300000	0.099999
3	37200001	37300000	1361	0.165273	3.908773609	10	55050001	55200000	0.149999
3	43950001	44050000	1127	0.171867	4.061971822	10	68400001	68500000	0.099999
3	109950001	110050000	793	0.171895	4.062622346	10	70500001	70650000	0.149999
3	29650001	29750000	950	0.17263	4.07969858	11	45950001	46400000	0.449999
3	28400001	28500000	759	0.175967	4.157227005	11	94950001	95150000	0.199999
3	37000001	37100000	1034	0.19076	4.500912351	11	95150001	95300000	0.149999
3	37050001	37150000	791	0.199131	4.695395555	11	103650001	103850000	0.199999
3	29700001	29800000	845	0.208917	4.922753414	12	20650001	20750000	0.099999
4	24450001	24550000	796	0.148157	3.51111807	12	20950001	21050000	0.099999
4	24300001	24400000	1143	0.151855	3.597033598	12	29100001	29300000	0.199999
4	4000001	4100000	1409	0.161131	3.812542641	12	43600001	43700000	0.099999
4	48100001	48200000	571	0.1618	3.828085499	12	44450001	44600000	0.149999
4	53050001	53150000	760	0.163367	3.864491565	13	1650001	1750000	0.099999
4	24400001	24500000	768	0.169335	4.003145939	13	1800001	1900000	0.099999
4	53100001	53200000	900	0.17112	4.044616793	13	38800001	38950000	0.149999
4	73450001	73550000	1326	0.173513	4.100213293	13	73650001	73750000	0.099999
4	79000001	79100000	1005	0.17625	4.163801936	14	42550001	42650000	0.099999
4	73500001	73600000	1305	0.189568	4.47321865	14	42700001	42800000	0.099999
4	48300001	48400000	485	0.190849	4.502980086	14	72700001	72850000	0.149999
4	48150001	48250000	341	0.194061	4.57760439	14	73700001	73950000	0.249999
4	53850001	53950000	556	0.194285	4.582808576	15	1500001	1700000	0.199999
4	48350001	48450000	504	0.194334	4.583946991	15	4600001	4800000	0.199999
4	47800001	47900000	980	0.195206	4.604206142	15	12400001	12500000	0.099999
4	24250001	24350000	1279	0.199346	4.700390644	15	29700001	29900000	0.199999
4	78950001	79050000	911	0.202994	4.785144524	15	32700001	32850000	0.149999
4	24200001	24300000	984	0.210893	4.968661765	15	35200001	35300000	0.099999
4	47850001	47950000	977	0.223599	5.2638599	15	47200001	47400000	0.199999
5	40550001	40650000	902	0.147739	3.501406688	15	51500001	51700000	0.199999
5	91950001	92050000	971	0.149404	3.540089585	16	19650001	19750000	0.099999
5	34250001	34350000	413	0.149813	3.549591871	16	36250001	36350000	0.099999
5	7450001	7550000	996	0.150872	3.574195587	17	9050001	9200000	0.149999
5	91900001	92000000	1092	0.151635	3.591922345	17	35050001	35200000	0.149999
5	17950001	18050000	590	0.153288	3.630326446	17	67200001	67400000	0.199999
5	95100001	95200000	986	0.154756	3.664432448	18	12950001	13050000	0.099999
5	95050001	95150000	844	0.157708	3.73301618	18	25450001	25600000	0.149999
5	93450001	93550000	1314	0.163649	3.871043263	18	29200001	29300000	0.099999
5	7500001	7600000	854	0.164197	3.883774932	18	36650001	36850000	0.199999
5	117150001	117250000	1822	0.16606	3.927057957	19	800001	950000	0.149999
5	117100001	117200000	1688	0.166227	3.930937864	19	19650001	19750000	0.099999
5	119900001	120000000	412	0.168683	3.987998041	19	46700001	46850000	0.149999
5	38550001	38650000	848	0.174625	4.126048358	20	39350001	39600000	0.249999
5	93400001	93500000	1011	0.17923	4.233036191	21	2250001	2350000	0.099999
5	89350001	89450000	1120	0.180404	4.260311699	21	4650001	4800000	0.149999
5	95250001	95350000	670	0.180541	4.263494617	21	5650001	5800000	0.149999
5	34500001	34600000	509	0.184146	4.347249479	21	7750001	8000000	0.249999
5	34300001	34400000	378	0.187384	4.42247784	21	36700001	36850000	0.149999
5	34350001	34450000	296	0.190388	4.492269686	21	36850001	37000000	0.149999
5	111850001	111950000	740	0.199256	4.698299677	21	43750001	43850000	0.099999
5	35550001	35650000	982	0.201391	4.747902071	21	55050001	55150000	0.099999
5	34400001	34500000	242	0.202194	4.766558147	22	3150001	3400000	0.249999

High 1% windows						High 1% merged windows				
Chr	Start	End	nSNPs	F_{ST}	ZF_{ST}	Chr	Start	End	Size (MB)
5	34450001	34550000	317	0.22	5.180244436	22	7000001	7150000	0.149999
5	89250001	89350000	853	0.22709	5.344966203	22	7150001	7300000	0.149999
5	95450001	95550000	496	0.228666	5.381581366	22	13750001	13850000	0.099999
5	7550001	7650000	767	0.230355	5.420821855	22	16800001	16950000	0.149999
5	35700001	35800000	913	0.240196	5.649457527	22	17250001	17400000	0.149999
5	95300001	95400000	494	0.243692	5.730679995	22	59100001	59250000	0.149999
5	89300001	89400000	985	0.25925	6.092138564	23	29850001	30000000	0.149999
5	35600001	35700000	1016	0.272744	6.40564428	23	43750001	43900000	0.149999
5	95400001	95500000	433	0.273791	6.429969201	24	55200001	55300000	0.099999
5	95350001	95450000	447	0.292595	6.866841996	26	5600001	5700000	0.099999
5	35650001	35750000	1033	0.324411	7.606022215	26	15350001	15450000	0.099999
6	55800001	55900000	1686	0.148144	3.510816041	27	5950001	6100000	0.149999
6	32450001	32550000	1315	0.149515	3.542668445	27	21350001	21450000	0.099999
6	36750001	36850000	863	0.152131	3.603445899	27	23450001	23700000	0.249999
6	86300001	86400000	656	0.153554	3.636506417	27	23900001	24050000	0.149999
6	105900001	106000000	1209	0.158923	3.76124424	27	24100001	24200000	0.099999
6	86850001	86950000	985	0.16193	3.831105785	28	19700001	19850000	0.149999
6	86700001	86800000	831	0.162644	3.847694127	29	13700001	13800000	0.099999
6	32500001	32600000	1438	0.168589	3.985814142	29	25650001	25750000	0.099999
6	6350001	6450000	907	0.171347	4.049890677	29	32950001	33050000	0.099999
6	109750001	109850000	1347	0.176896	4.178810436	29	50750001	50850000	0.099999
6	61650001	61750000	1055	0.179702	4.244002154				
6	86750001	86850000	704	0.179723	4.244490046				
6	82450001	82550000	1018	0.180795	4.269395791				
6	104000001	104100000	1113	0.180886	4.271509992				
6	68400001	68500000	1097	0.183081	4.322506364				
6	6250001	6350000	792	0.18361	4.334796606				
6	109650001	109750000	1096	0.184599	4.357774015				
6	6300001	6400000	860	0.186593	4.40410056				
6	82300001	82400000	1223	0.1872	4.418202973				
6	66400001	66500000	539	0.187385	4.422501073				
6	66350001	66450000	501	0.188584	4.450357406				
6	86800001	86900000	840	0.190021	4.483743186				
6	82150001	82250000	966	0.202056	4.763351997				
6	66500001	66600000	726	0.214871	5.061082525				
6	68500001	68600000	535	0.22455	5.285954456				
6	11750001	11850000	836	0.229451	5.399819249				
6	66450001	66550000	657	0.23257	5.472282887				
6	82350001	82450000	1174	0.235399	5.538008963				
6	82400001	82500000	980	0.247222	5.812692384				
6	11800001	11900000	926	0.261947	6.154797888				
6	68450001	68550000	751	0.264788	6.22080276				
6	82250001	82350000	1200	0.26694	6.270800114				
6	109700001	109800000	914	0.283752	6.66139283				
6	82200001	82300000	1015	0.322916	7.571288922				
7	90000001	90100000	1293	0.147539	3.496760094				
7	75900001	76000000	770	0.149469	3.541599729				
7	67850001	67950000	1139	0.151468	3.588042438				
7	21250001	21350000	500	0.152894	3.621172656				
7	110300001	110400000	1020	0.153208	3.628467809				
7	22300001	22400000	1054	0.154211	3.651770479				
7	97550001	97650000	1179	0.155557	3.683042059				
7	77350001	77450000	983	0.157599	3.730483786				
7	60850001	60950000	278	0.157674	3.732226259				
7	63550001	63650000	1054	0.159143	3.766355494				
7	77300001	77400000	851	0.159802	3.781666022				
7	109650001	109750000	899	0.162467	3.843581891				
7	67800001	67900000	894	0.166082	3.927569083				
7	110400001	110500000	1235	0.168945	3.99408508				

High 1% windows						High 1% merged windows			
Chr	Start	End	nSNPs	F_{ST}	ZF_{ST}	Chr	Start	End	Size (MB)
7	6400001	6500000	496	0.168992	3.99517703				
7	6500001	6600000	1085	0.173054	4.08954936				
7	35250001	35350000	1016	0.176749	4.175395189				
7	22250001	22350000	984	0.178778	4.222534888				
7	6550001	6650000	1451	0.179953	4.249833629				
7	110500001	110600000	815	0.183484	4.331869251				
7	6450001	6550000	614	0.18502	4.367555096				
7	21350001	21450000	404	0.188467	4.447639148				
7	93200001	93300000	554	0.195222	4.60457787				
7	109600001	109700000	1127	0.196555	4.635547421				
7	110350001	110450000	1095	0.196851	4.64242438				
7	48550001	48650000	906	0.197745	4.663194657				
7	21300001	21400000	450	0.217043	5.111544539				
7	35300001	35400000	893	0.222452	5.237211682				
7	48500001	48600000	1010	0.236097	5.554225577				
7	45050001	45150000	809	0.236414	5.561590429				
8	102700001	102800000	820	0.147982	3.5070523				
8	52100001	52200000	1047	0.15078	3.572058154				
8	30450001	30550000	746	0.151493	3.588623263				
8	21300001	21400000	876	0.155662	3.685481521				
8	8350001	8450000	960	0.160353	3.79446739				
8	59700001	59800000	282	0.163844	3.875573693				
8	59650001	59750000	294	0.168567	3.985303017				
8	8400001	8500000	983	0.169003	3.995432592				
8	97350001	97450000	768	0.169426	4.005260139				
8	33100001	33200000	1360	0.169973	4.017968575				
8	30600001	30700000	683	0.170002	4.018642331				
8	22800001	22900000	895	0.180244	4.256594424				
8	23700001	23800000	561	0.186964	4.412719992				
8	21950001	22050000	537	0.187296	4.420433338				
8	33150001	33250000	1340	0.187389	4.422594005				
8	22000001	22100000	451	0.191634	4.521217968				
8	23500001	23600000	1082	0.193175	4.557019977				
8	21850001	21950000	559	0.197289	4.652600422				
8	21900001	22000000	608	0.211338	4.979000437				
8	23600001	23700000	790	0.218616	5.148090003				
8	30500001	30600000	640	0.218916	5.155059895				
8	23650001	23750000	899	0.222495	5.238210699				
8	23550001	23650000	808	0.223126	5.252870704				
8	30550001	30650000	687	0.236242	5.557594358				
8	22900001	23000000	1099	0.271591	6.378856664				
8	22850001	22950000	846	0.318136	7.460235319				
9	9350001	9450000	1150	0.147421	3.494018603				
9	45000001	45100000	356	0.148411	3.517019245				
9	40200001	40300000	847	0.149544	3.543342201				
9	81050001	81150000	831	0.150412	3.563508421				
9	27750001	27850000	950	0.151957	3.599403361				
9	88400001	88500000	551	0.155264	3.676234798				
9	9600001	9700000	890	0.157482	3.727765529				
9	33700001	33800000	809	0.157921	3.737964803				
9	68050001	68150000	870	0.158408	3.74927926				
9	27650001	27750000	739	0.161119	3.812263846				
9	81000001	81100000	1021	0.161408	3.818978174				
9	27700001	27800000	1036	0.162824	3.851876062				
9	45950001	46050000	959	0.162844	3.852340721				
9	27600001	27700000	758	0.162903	3.853711467				
9	11000001	11100000	1060	0.164021	3.879685929				
9	103050001	103150000	875	0.164991	3.902221911				
9	46000001	46100000	1019	0.166071	3.92731352				

High 1% windows						High 1% merged windows			
Chr	Start	End	nSNPs	F_{ST}	ZF_{ST}	Chr	Start	End	Size (MB)
9	103100001	103200000	944	0.167048	3.950012133				
9	9400001	9500000	1311	0.169216	4.000381215				
9	97450001	97550000	1565	0.173402	4.097634434				
9	27800001	27900000	992	0.174212	4.11645314				
9	32100001	32200000	985	0.175146	4.138152736				
9	44900001	45000000	566	0.175176	4.138849725				
9	9550001	9650000	811	0.180335	4.258708624				
9	11650001	11750000	1187	0.181295	4.281012277				
9	68100001	68200000	564	0.193536	4.56540708				
9	9450001	9550000	1076	0.194003	4.576256878				
9	9500001	9600000	777	0.202662	4.777431177				
9	11750001	11850000	1223	0.207593	4.891992959				
9	97400001	97500000	1937	0.214246	5.046561918				
9	11700001	11800000	1376	0.21612	5.090100507				
10	55000001	55100000	596	0.160277	3.792701684				
10	70700001	70800000	1075	0.162443	3.8430243				
10	68400001	68500000	1046	0.17443	4.121517928				
10	23200001	23300000	2329	0.181651	4.289283215				
10	55100001	55200000	675	0.186369	4.398896374				
10	55050001	55150000	565	0.187096	4.415786744				
10	70500001	70600000	804	0.197789	4.664216908				
10	70550001	70650000	494	0.222238	5.232239826				
11	8900001	9000000	763	0.14828	3.513975726				
11	9650001	9750000	1031	0.149386	3.539671392				
11	16250001	16350000	841	0.149462	3.541437098				
11	95300001	95400000	880	0.15062	3.568340879				
11	45850001	45950000	884	0.152457	3.611019847				
11	36400001	36500000	479	0.156511	3.705206313				
11	45400001	45500000	1073	0.15782	3.735618273				
11	95350001	95450000	589	0.159611	3.777228525				
11	8850001	8950000	994	0.163252	3.861819774				
11	95100001	95200000	475	0.164512	3.891093318				
11	94950001	95050000	435	0.170591	4.032326551				
11	95050001	95150000	368	0.172339	4.072937785				
11	103650001	103750000	1301	0.176732	4.175000228				
11	103750001	103850000	931	0.177316	4.188568284				
11	95000001	95100000	469	0.177642	4.196142232				
11	95200001	95300000	971	0.185812	4.385955609				
11	45950001	46050000	535	0.192742	4.546960101				
11	103700001	103800000	1268	0.203613	4.799525733				
11	95150001	95250000	750	0.205127	4.834700452				
11	46250001	46350000	675	0.249617	5.86833535				
11	46050001	46150000	1493	0.278992	6.550803886				
11	46100001	46200000	1546	0.290624	6.821049809				
11	46200001	46300000	751	0.309373	7.25664479				
11	46300001	46400000	500	0.313859	7.3608679				
11	46000001	46100000	796	0.351202	8.228456752				
11	46150001	46250000	1057	0.382428	8.953929517				
12	74500001	74600000	1040	0.147095	3.486444654				
12	29350001	29450000	271	0.154328	3.654488737				
12	43700001	43800000	1097	0.156848	3.713035825				
12	20600001	20700000	1506	0.163504	3.867674482				
12	20450001	20550000	580	0.165362	3.910841343				
12	74650001	74750000	1088	0.168028	3.972780445				
12	74700001	74800000	1268	0.16884	3.991645618				
12	29200001	29300000	224	0.169681	4.011184547				
12	44500001	44600000	936	0.170381	4.027447627				
12	43600001	43700000	1302	0.172537	4.077537913				
12	20950001	21050000	876	0.177661	4.196583659				

High 1% windows						High 1% merged windows			
Chr	Start	End	nSNPs	F_{ST}	ZF_{ST}	Chr	Start	End	Size (MB)
12	20650001	20750000	1530	0.181227	4.279432435				
12	29150001	29250000	360	0.181547	4.286866986				
12	29100001	29200000	539	0.183738	4.337770426				
12	44450001	44550000	735	0.201545	4.751479948				
13	17900001	18000000	722	0.160667	3.801762543				
13	6100001	6200000	1621	0.167847	3.968575277				
13	73650001	73750000	458	0.169494	4.006839981				
13	38800001	38900000	1196	0.186636	4.405099577				
13	1800001	1900000	1330	0.189226	4.465272973				
13	1650001	1750000	1151	0.196926	4.644166853				
13	38850001	38950000	995	0.232535	5.471469733				
14	3150001	3250000	738	0.146861	3.481008139				
14	42600001	42700000	1230	0.146968	3.483494067				
14	55200001	55300000	1280	0.149102	3.533073228				
14	32750001	32850000	740	0.150302	3.560952794				
14	73250001	73350000	1452	0.154332	3.654581669				
14	18600001	18700000	899	0.156579	3.706786155				
14	1100001	1200000	653	0.157632	3.731250474				
14	11850001	11950000	1035	0.158293	3.746607468				
14	7600001	7700000	1048	0.159808	3.78180542				
14	40200001	40300000	899	0.160817	3.805247488				
14	7650001	7750000	998	0.163388	3.864979458				
14	40250001	40350000	1105	0.165127	3.905381595				
14	11900001	12000000	870	0.167299	3.955843609				
14	42750001	42850000	862	0.169148	3.998801373				
14	73700001	73800000	1383	0.176658	4.173280989				
14	73850001	73950000	480	0.194684	4.592078531				
14	73800001	73900000	689	0.196049	4.623791537				
14	42550001	42650000	1248	0.199549	4.705106937				
14	73750001	73850000	1051	0.208529	4.913739021				
14	72700001	72800000	1440	0.212462	5.005114297				
14	72750001	72850000	1362	0.216138	5.0905187				
14	42700001	42800000	948	0.222299	5.233657037				
15	50001	150000	974	0.148107	3.509956422				
15	35050001	35150000	908	0.149315	3.538021851				
15	32650001	32750000	931	0.152446	3.610764285				
15	35150001	35250000	1517	0.154724	3.663688993				
15	32800001	32900000	791	0.154731	3.663851624				
15	44300001	44400000	1095	0.154854	3.66670928				
15	29850001	29950000	515	0.156471	3.704276994				
15	82450001	82550000	737	0.159598	3.776926496				
15	32900001	33000000	635	0.16117	3.813448727				
15	35350001	35450000	866	0.163431	3.865978476				
15	100001	200000	938	0.164257	3.88516891				
15	44250001	44350000	935	0.164844	3.898806664				
15	800001	900000	1230	0.167522	3.961024562				
15	1600001	1700000	555	0.173319	4.095706097				
15	35200001	35300000	1404	0.175941	4.156622948				
15	47300001	47400000	1619	0.177006	4.181366063				
15	1500001	1600000	663	0.183195	4.325154923				
15	51500001	51600000	1462	0.184573	4.357169957				
15	32700001	32800000	763	0.190047	4.484347243				
15	29700001	29800000	705	0.192606	4.543800417				
15	12400001	12500000	1186	0.194153	4.579741824				
15	1550001	1650000	653	0.197715	4.662497668				
15	51600001	51700000	953	0.205465	4.842553196				
15	47200001	47300000	956	0.217949	5.132593611				
15	32750001	32850000	737	0.220722	5.197018641				
15	47250001	47350000	1287	0.231547	5.448515557				

High 1% windows						High 1% merged windows			
Chr	Start	End	nSNPs	F_{ST}	ZF_{ST}	Chr	Start	End	Size (MB)
15	4700001	4800000	1540	0.241995	5.691253642				
15	4600001	4700000	1497	0.257684	6.055755731				
15	29800001	29900000	760	0.260238	6.11509274				
15	51550001	51650000	1117	0.275663	6.473461324				
15	29750001	29850000	853	0.279748	6.568368012				
15	4650001	4750000	1518	0.320305	7.510627634				
16	10300001	10400000	1096	0.152083	3.602330716				
16	19600001	19700000	747	0.15242	3.610160227				
16	10250001	10350000	951	0.165193	3.906914971				
16	19650001	19750000	892	0.169386	4.00433082				
16	36250001	36350000	650	0.175901	4.155693629				
17	29000001	29100000	972	0.15038	3.562764966				
17	40700001	40800000	1245	0.152456	3.610996614				
17	35050001	35150000	664	0.173697	4.10448816				
17	9050001	9150000	833	0.179333	4.235429187				
17	67300001	67400000	951	0.183664	4.336051186				
17	9100001	9200000	922	0.187648	4.428611344				
17	67200001	67300000	779	0.207969	4.900728557				
17	67250001	67350000	788	0.212718	5.011061938				
17	35100001	35200000	519	0.221236	5.208960388				
18	7250001	7350000	466	0.151213	3.582118031				
18	12900001	13000000	546	0.156728	3.710247868				
18	12850001	12950000	523	0.156833	3.71268733				
18	36800001	36900000	546	0.157619	3.730948446				
18	36600001	36700000	661	0.162429	3.842699038				
18	29200001	29300000	1157	0.172518	4.077096487				
18	12950001	13050000	619	0.174303	4.118567341				
18	25450001	25550000	993	0.187766	4.431352835				
18	25500001	25600000	876	0.205995	4.854866671				
18	36750001	36850000	565	0.225462	5.307142926				
18	36650001	36750000	517	0.309884	7.268516839				
18	36700001	36800000	440	0.324724	7.613294135				
19	46700001	46800000	1074	0.173282	4.094846477				
19	19650001	19750000	474	0.179273	4.234035209				
19	850001	950000	984	0.190329	4.490898941				
19	46750001	46850000	964	0.200186	4.71990634				
19	800001	900000	1047	0.204359	4.81685753				
20	69450001	69550000	1612	0.148479	3.518599087				
20	49250001	49350000	1179	0.151327	3.584766589				
20	40900001	41000000	769	0.154771	3.664780943				
20	30000001	30100000	591	0.155052	3.671309408				
20	39350001	39450000	676	0.172351	4.073216581				
20	39500001	39600000	641	0.199367	4.700878536				
20	39450001	39550000	696	0.223731	5.266926652				
20	39400001	39500000	609	0.259278	6.092789087				
21	46850001	46950000	778	0.150343	3.561905346				
21	20950001	21050000	1154	0.152334	3.608162192				
21	7950001	8050000	536	0.154394	3.656022113				
21	55000001	55100000	756	0.155398	3.679348016				
21	46750001	46850000	625	0.155864	3.690174581				
21	50450001	50550000	1368	0.156427	3.703254744				
21	46800001	46900000	683	0.164402	3.888537691				
21	36900001	37000000	498	0.169498	4.006932913				
21	5650001	5750000	759	0.169981	4.018154438				
21	55050001	55150000	757	0.17077	4.036485253				
21	43750001	43850000	1019	0.172613	4.079303619				
21	4700001	4800000	1798	0.173064	4.089781689				
21	36850001	36950000	342	0.173451	4.098772849				
21	4650001	4750000	1564	0.178247	4.21019818				

High 1% windows						High 1% merged windows			
Chr	Start	End	nSNPs	F_{ST}	ZF_{ST}	Chr	Start	End	Size (MB)
21	7750001	7850000	530	0.198056	4.670420111				
21	36750001	36850000	516	0.198815	4.688053936				
21	5700001	5800000	1116	0.21226	5.000421237				
21	2250001	2350000	466	0.223434	5.26002646				
21	7900001	8000000	688	0.227926	5.364388967				
21	36700001	36800000	549	0.22872	5.382835947				
21	7800001	7900000	682	0.250145	5.880602359				
21	7850001	7950000	834	0.257592	6.053618297				
22	28800001	28900000	759	0.146953	3.483145573				
22	28850001	28950000	515	0.150169	3.557862809				
22	24250001	24350000	1060	0.152247	3.606140923				
22	58850001	58950000	1054	0.162896	3.853548836				
22	6950001	7050000	1552	0.164957	3.90143199				
22	58900001	59000000	1262	0.166105	3.928103441				
22	59100001	59200000	739	0.170419	4.02833048				
22	3150001	3250000	1251	0.180764	4.268675569				
22	59150001	59250000	833	0.18411	4.346413092				
22	3200001	3300000	1274	0.185474	4.378102865				
22	13750001	13850000	542	0.195278	4.605878916				
22	3300001	3400000	1193	0.199233	4.697765318				
22	7050001	7150000	1326	0.208243	4.907094391				
22	7200001	7300000	1014	0.219645	5.171996731				
22	16800001	16900000	671	0.221221	5.208611894				
22	3250001	3350000	1312	0.223323	5.2574476				
22	16850001	16950000	543	0.227789	5.36120605				
22	7150001	7250000	910	0.239882	5.642162374				
22	7000001	7100000	1424	0.245062	5.762509165				
22	17300001	17400000	652	0.249178	5.858136076				
22	17250001	17350000	423	0.274167	6.438704799				
23	29850001	29950000	1896	0.173521	4.100399157				
23	43800001	43900000	1332	0.178071	4.206109177				
23	43750001	43850000	1159	0.185246	4.372805747				
23	29900001	30000000	1699	0.234441	5.515751776				
24	52900001	53000000	1056	0.149869	3.550892917				
24	54000001	54100000	1276	0.153297	3.630535543				
24	54050001	54150000	1325	0.158043	3.740799226				
24	52300001	52400000	1437	0.164444	3.889513476				
24	55200001	55300000	822	0.217684	5.126436874				
25	18150001	18250000	1028	0.148923	3.528914526				
25	18200001	18300000	986	0.150134	3.557049655				
25	8500001	8600000	799	0.150157	3.557584013				
25	19550001	19650000	1647	0.150563	3.567016599				
25	2750001	2850000	1086	0.154845	3.666500183				
25	19500001	19600000	1691	0.169145	3.998731674				
26	5550001	5650000	1769	0.158004	3.73989314				
26	5500001	5600000	1595	0.158879	3.76022199				
26	15400001	15500000	778	0.163367	3.864491565				
26	5600001	5700000	1811	0.185743	4.384352534				
26	15350001	15450000	855	0.192657	4.544985298				
27	21300001	21400000	842	0.147887	3.504845168				
27	22050001	22150000	831	0.150207	3.558745662				
27	6100001	6200000	1554	0.150846	3.57359153				
27	7850001	7950000	864	0.152345	3.608417754				
27	7800001	7900000	845	0.152901	3.621335287				
27	24000001	24100000	1263	0.157783	3.734758653				
27	6150001	6250000	1215	0.159792	3.781433693				
27	6050001	6150000	1265	0.163681	3.871786718				
27	21400001	21500000	627	0.166744	3.94294931				
27	7400001	7500000	1061	0.168049	3.973268338				

High 1% windows						High 1% merged windows			
Chr	Start	End	nSNPs	F_{ST}	ZF_{ST}	Chr	Start	End	Size (MB)
27	24050001	24150000	1408	0.169056	3.99666394				
27	24100001	24200000	1355	0.16997	4.017898876				
27	23900001	24000000	680	0.175903	4.155740095				
27	5950001	6050000	1903	0.183675	4.336306749				
27	23950001	24050000	1038	0.194874	4.596492796				
27	6000001	6100000	1637	0.196249	4.628438132				
27	23600001	23700000	611	0.199537	4.704828142				
27	23450001	23550000	714	0.204582	4.822038482				
27	21350001	21450000	678	0.209291	4.931442545				
27	23550001	23650000	827	0.234318	5.512894121				
27	23500001	23600000	859	0.243374	5.72329191				
28	19750001	19850000	982	0.184117	4.346575722				
28	19700001	19800000	788	0.220326	5.187818384				
29	49200001	49300000	855	0.14846	3.51815766				
29	27200001	27300000	2247	0.150145	3.557305217				
29	25600001	25700000	1007	0.158636	3.754576378				
29	50700001	50800000	707	0.159272	3.769352547				
29	39800001	39900000	475	0.164005	3.879314201				
29	33000001	33100000	959	0.164608	3.893323683				
29	25700001	25800000	770	0.16499	3.902198678				
29	9350001	9450000	883	0.167261	3.954960756				
29	50750001	50850000	710	0.189603	4.474031804				
29	13700001	13800000	1265	0.196011	4.622908684				
29	32950001	33050000	1053	0.206037	4.855842456				
29	25650001	25750000	676	0.21673	5.104272619				

Table S38. F_{ST} selective sweep regions between high (Begait) and low (Raya) groups of the wettest quarter precipitation (bio16).

High 1% windows						High 1% merged windows			
Chr	Start	End	nSNPs	F_{ST}	ZF_{ST}	Chr	Start	End	Size (MB)
1	70450001	70550000	806	0.198506	3.562938342	1	1050001	1200000	0.149999
1	70400001	70500000	734	0.201702	3.623398759	1	23750001	23850000	0.099999
1	76900001	77000000	1280	0.212498	3.827632383	1	38000001	38100000	0.099999
1	89700001	89800000	907	0.213178	3.840496302	1	48100001	48200000	0.099999
1	89000001	89100000	830	0.214348	3.862629809	1	50050001	50200000	0.149999
1	52550001	52650000	1046	0.216219	3.898024502	1	52500001	52600000	0.099999
1	77000001	77100000	931	0.216556	3.904399709	1	76600001	76700000	0.099999
1	89500001	89600000	1042	0.220477	3.978575334	1	76950001	77050000	0.099999
1	89550001	89650000	753	0.222327	4.013572759	1	89400001	89550000	0.149999
1	76600001	76700000	905	0.222701	4.020647914	1	89550001	89750000	0.199999
1	93050001	93150000	935	0.222918	4.024753018	1	89750001	89850000	0.099999
1	89400001	89500000	863	0.224067	4.046489257	1	93050001	93150000	0.099999
1	112400001	112500000	1245	0.224417	4.053110391	1	110000001	110150000	0.149999
1	89750001	89850000	881	0.224418	4.053129309	1	112400001	112500000	0.099999
1	48100001	48200000	1535	0.225815	4.079557094	1	146950001	147100000	0.149999
1	147000001	147100000	988	0.231398	4.185173649	1	157450001	157550000	0.099999
1	146950001	147050000	883	0.234219	4.238539994	2	350001	550000	0.199999
1	76950001	77050000	1151	0.235308	4.259141181	2	550001	700000	0.149999
1	23750001	23850000	1097	0.235793	4.268316181	2	66350001	66500000	0.149999
1	52500001	52600000	1002	0.239105	4.330971032	2	66550001	66650000	0.099999
1	89650001	89750000	754	0.244218	4.427696349	2	81000001	81200000	0.199999
1	157450001	157550000	761	0.245579	4.453443104	2	85950001	86500000	0.549999
1	38000001	38100000	942	0.248794	4.514262954	2	110250001	110800000	0.549999
1	89450001	89550000	1054	0.258627	4.700279	2	119200001	119300000	0.099999
1	110050001	110150000	474	0.26663	4.85167597	2	126400001	126500000	0.099999
1	89600001	89700000	597	0.27333	4.978423403	2	128050001	128200000	0.149999
1	1100001	1200000	1170	0.28093	5.122196611	3	600001	700000	0.099999

High 1% windows						High 1% merged windows			
Chr	Start	End	nSNPs	F_{ST}	ZF_{ST}	Chr	Start	End	Size (MB)
1	110000001	110100000	399	0.292836	5.347428691	3	6950001	7100000	0.149999
1	1050001	1150000	1169	0.319208	5.84632172	3	49000001	49100000	0.099999
1	50050001	50150000	498	0.347434	6.380287845	3	85350001	85500000	0.149999
1	50100001	50200000	522	0.363553	6.685219468	3	100600001	100700000	0.099999
2	109900001	110000000	970	0.200328	3.597406076	4	12550001	12700000	0.149999
2	126450001	126550000	373	0.203782	3.662747215	4	13100001	13200000	0.099999
2	46850001	46950000	1553	0.205124	3.688134537	4	25800001	25900000	0.099999
2	650001	750000	1014	0.206394	3.712159797	4	41000001	41450000	0.449999
2	72550001	72650000	748	0.207748	3.737774129	4	73500001	73600000	0.099999
2	80950001	81050000	622	0.209623	3.773244492	4	114500001	114700000	0.199999
2	119150001	119250000	716	0.210824	3.795964443	5	2250001	2450000	0.199999
2	105600001	105700000	689	0.213167	3.840288209	5	17600001	17700000	0.099999
2	105650001	105750000	480	0.214875	3.872599346	5	17850001	18150000	0.299999
2	46900001	47000000	1330	0.215316	3.880941975	5	31300001	31400000	0.099999
2	110200001	110300000	598	0.21612	3.896151667	5	31400001	31500000	0.099999
2	128000001	128100000	828	0.218836	3.947531671	5	31500001	31600000	0.099999
2	125100001	125200000	794	0.21983	3.966335693	5	32900001	33000000	0.099999
2	86400001	86500000	531	0.221806	4.003716727	5	33000001	33150000	0.149999
2	66550001	66650000	795	0.223649	4.03858173	5	35150001	35400000	0.249999
2	450001	550000	548	0.225798	4.079235496	5	42950001	43050000	0.099999
2	128100001	128200000	432	0.226519	4.092875033	5	46600001	46750000	0.149999
2	66400001	66500000	893	0.227458	4.110638592	5	47500001	47650000	0.149999
2	119200001	119300000	878	0.229448	4.148284471	5	47700001	47950000	0.249999
2	128050001	128150000	672	0.231494	4.186989732	5	51000001	51100000	0.099999
2	81000001	81100000	865	0.23763	4.303067679	5	58000001	58100000	0.099999
2	550001	650000	700	0.240246	4.352555931	5	80300001	80450000	0.149999
2	86050001	86150000	341	0.243601	4.416024235	5	91600001	91700000	0.099999
2	86100001	86200000	328	0.244106	4.425577586	5	91750001	91900000	0.149999
2	81100001	81200000	1116	0.244712	4.437041607	5	91950001	92050000	0.099999
2	66350001	66450000	1086	0.248181	4.50266651	5	92300001	92500000	0.199999
2	85950001	86050000	288	0.26431	4.807787307	5	92550001	92750000	0.199999
2	126400001	126500000	256	0.269899	4.913517367	5	95300001	95550000	0.249999
2	600001	700000	789	0.283077	5.162812542	5	111850001	112000000	0.149999
2	86000001	86100000	276	0.285189	5.202766359	6	11750001	11900000	0.149999
2	400001	500000	643	0.292102	5.333543226	6	39750001	39850000	0.099999
2	86150001	86250000	233	0.292466	5.340429205	6	66050001	66300000	0.249999
2	350001	450000	548	0.293812	5.365892197	6	66350001	66500000	0.149999
2	81050001	81150000	872	0.314926	5.765316868	6	73300001	73400000	0.099999
2	86200001	86300000	253	0.316344	5.792141922	6	76750001	76850000	0.099999
2	110700001	110800000	722	0.321561	5.890834662	6	82350001	82450000	0.099999
2	86350001	86450000	572	0.357476	6.570257654	6	104000001	104100000	0.099999
2	110250001	110350000	603	0.362583	6.666869466	6	117050001	117150000	0.099999
2	86250001	86350000	461	0.364524	6.703588387	6	117700001	117850000	0.149999
2	110600001	110700000	453	0.372424	6.853036852	7	44350001	44450000	0.099999
2	110450001	110550000	577	0.384296	7.077625736	7	54550001	54650000	0.099999
2	86300001	86400000	724	0.386233	7.114268987	7	60550001	60650000	0.099999
2	110300001	110400000	689	0.393267	7.247334874	7	60700001	60800000	0.099999
2	110400001	110500000	544	0.400123	7.377033441	7	73700001	73800000	0.099999
2	110550001	110650000	152	0.40331	7.4373236	7	96450001	96550000	0.099999
2	110500001	110600000	434	0.404656	7.462786592	8	54800001	54900000	0.099999
2	110350001	110450000	647	0.410855	7.580056344	8	55000001	55150000	0.149999
2	110650001	110750000	802	0.416799	7.692502126	8	55150001	55250000	0.099999
3	49100001	49200000	963	0.199866	3.588666179	8	76200001	76350000	0.149999
3	10500001	10600000	1052	0.202679	3.641881183	9	11600001	11700000	0.099999
3	87100001	87200000	976	0.210482	3.789494648	9	11750001	11900000	0.149999
3	48950001	49050000	688	0.212271	3.823338105	9	39950001	40050000	0.099999
3	41400001	41500000	794	0.212438	3.826497332	9	61700001	61800000	0.099999
3	49050001	49150000	665	0.215377	3.882095944	10	59450001	59600000	0.149999
3	650001	750000	830	0.218864	3.948061362	10	70500001	70650000	0.149999

High 1% windows						High 1% merged windows				
Chr	Start	End	nSNPs	F_{ST}	ZF_{ST}	Chr	Start	End	Size (MB)
3	100600001	100700000	629	0.226364	4.089942817	10	94400001	94500000	0.099999
3	85350001	85450000	1031	0.230154	4.161640245	11	50450001	50600000	0.149999
3	49000001	49100000	557	0.241526	4.376770365	11	53700001	53800000	0.099999
3	600001	700000	698	0.247426	4.488383776	12	27400001	27500000	0.099999
3	85400001	85500000	930	0.281992	5.142287025	12	27700001	27850000	0.149999
3	7000001	7100000	857	0.293344	5.357038794	12	28800001	28950000	0.149999
3	6950001	7050000	530	0.297731	5.440029987	12	29000001	29500000	0.499999
4	12500001	12600000	906	0.1998	3.587417622	12	29550001	29700000	0.149999
4	66000001	66100000	717	0.202494	3.63838144	12	84400001	84550000	0.149999
4	63450001	63550000	696	0.210962	3.798575061	13	47200001	47500000	0.299999
4	12400001	12500000	683	0.213753	3.85137388	13	47950001	48050000	0.099999
4	66100001	66200000	734	0.215158	3.877953006	13	63600001	63700000	0.099999
4	12200001	12300000	518	0.21682	3.909393936	13	77100001	77350000	0.249999
4	87700001	87800000	1042	0.217559	3.923373989	14	3150001	3300000	0.149999
4	66050001	66150000	827	0.217719	3.926400793	14	23250001	23350000	0.099999
4	87650001	87750000	963	0.21867	3.944391362	14	28100001	28200000	0.099999
4	41350001	41450000	797	0.234643	4.246561025	14	73200001	73350000	0.149999
4	12600001	12700000	806	0.237793	4.306151236	15	29750001	29850000	0.099999
4	41100001	41200000	819	0.240537	4.358060931	15	38000001	38150000	0.149999
4	25800001	25900000	664	0.241954	4.384867067	15	38200001	38300000	0.099999
4	114600001	114700000	521	0.242841	4.401646914	15	59750001	59850000	0.099999
4	41150001	41250000	1344	0.243502	4.414151399	15	78100001	78250000	0.149999
4	41050001	41150000	671	0.243667	4.417272791	16	44000001	44150000	0.149999
4	73500001	73600000	1276	0.244943	4.441411556	16	65600001	65700000	0.099999
4	41000001	41100000	873	0.253462	4.602569971	16	66450001	66550000	0.099999
4	12550001	12650000	737	0.258961	4.706597454	17	41950001	42100000	0.149999
4	13100001	13200000	984	0.261748	4.759320602	17	42250001	42350000	0.099999
4	41300001	41400000	1300	0.262733	4.777954367	17	60450001	60600000	0.149999
4	41200001	41300000	1522	0.269062	4.897683397	18	950001	1100000	0.149999
4	41250001	41350000	1383	0.271347	4.940909947	18	3550001	3700000	0.149999
4	114500001	114600000	974	0.283355	5.168071614	18	14550001	14750000	0.199999
4	114550001	114650000	593	0.327688	6.006742352	18	22450001	22550000	0.099999
5	95500001	95600000	676	0.200148	3.594000921	18	43250001	43400000	0.149999
5	92450001	92550000	479	0.200449	3.599695097	18	61000001	61100000	0.099999
5	47600001	47700000	520	0.206693	3.717816137	18	61400001	61550000	0.149999
5	32950001	33050000	958	0.207478	3.732666396	19	41000001	41200000	0.199999
5	2200001	2300000	836	0.209412	3.769252894	19	46500001	46900000	0.399999
5	92900001	93000000	525	0.209538	3.771636503	20	2600001	2700000	0.099999
5	35700001	35800000	967	0.210721	3.794015937	20	4500001	4600000	0.099999
5	47350001	47450000	950	0.211154	3.802207227	20	10350001	10450000	0.099999
5	50950001	51050000	560	0.212545	3.828521507	20	11850001	12050000	0.199999
5	17650001	17750000	795	0.214176	3.859375994	20	12250001	12350000	0.099999
5	95250001	95350000	656	0.214484	3.865202593	20	30900001	31100000	0.199999
5	35100001	35200000	960	0.215232	3.879352903	20	39450001	39600000	0.149999
5	47400001	47500000	1074	0.215521	3.884820068	20	50850001	51000000	0.149999
5	35350001	35450000	620	0.216121	3.896170585	21	2250001	2350000	0.099999
5	31350001	31450000	1365	0.216135	3.89643543	21	14150001	14250000	0.099999
5	91900001	92000000	851	0.216627	3.905742853	21	39350001	39550000	0.199999
5	17800001	17900000	569	0.218003	3.931773371	21	43750001	43850000	0.099999
5	47450001	47550000	921	0.218148	3.934516413	21	57900001	58100000	0.199999
5	42900001	43000000	456	0.218764	3.946169609	21	62600001	62750000	0.149999
5	31450001	31550000	1003	0.21966	3.963119714	21	64050001	64150000	0.099999
5	51000001	51100000	707	0.222589	4.018529151	21	67550001	67700000	0.149999
5	31400001	31500000	1576	0.223468	4.035157658	22	24250001	24350000	0.099999
5	17600001	17700000	555	0.22538	4.07132797	22	46750001	46850000	0.099999
5	92650001	92750000	766	0.226793	4.098058436	23	45100001	45250000	0.149999
5	33000001	33100000	846	0.227561	4.112587097	24	36550001	36650000	0.099999
5	91750001	91850000	1517	0.227596	4.11324921	24	36700001	36800000	0.099999
5	47500001	47600000	650	0.228046	4.121762098	24	37000001	37100000	0.099999

High 1% windows						High 1% merged windows				
Chr	Start	End	nSNPs	F_{ST}	ZF_{ST}	Chr	Start	End	Size (MB)
5	17900001	18000000	782	0.229409	4.147546687	24	41400001	41650000	0.249999
5	91800001	91900000	1027	0.230513	4.168431637	24	47550001	47750000	0.199999
5	35300001	35400000	542	0.231415	4.185495247	25	8150001	8350000	0.199999
5	31500001	31600000	676	0.233054	4.216501074	25	26650001	26750000	0.099999
5	2250001	2350000	895	0.234935	4.252084943	26	11000001	11100000	0.099999
5	92300001	92400000	1238	0.23564	4.2654218	27	8000001	8300000	0.299999
5	35200001	35300000	859	0.235832	4.269053965	27	21450001	21600000	0.149999
5	31300001	31400000	1351	0.237151	4.294006184	28	150001	300000	0.149999
5	47550001	47650000	602	0.23779	4.306094483	29	18850001	19000000	0.149999
5	35150001	35250000	1073	0.238116	4.312261597	29	39800001	39950000	0.149999
5	91950001	92050000	1030	0.238979	4.328587423	29	48650001	48750000	0.099999
5	32900001	33000000	974	0.242544	4.396028408				
5	17950001	18050000	593	0.247011	4.480533003				
5	17850001	17950000	658	0.247192	4.483957075				
5	33050001	33150000	723	0.249189	4.521735377				
5	46650001	46750000	881	0.249234	4.522586666				
5	80300001	80400000	477	0.249859	4.53441012				
5	46600001	46700000	1093	0.252179	4.578298784				
5	35250001	35350000	608	0.25526	4.636583685				
5	111900001	112000000	833	0.255291	4.637170129				
5	2300001	2400000	1033	0.272418	4.961170618				
5	92550001	92650000	755	0.274257	4.995959951				
5	92400001	92500000	624	0.279376	5.092798773				
5	91600001	91700000	949	0.28057	5.115386301				
5	42950001	43050000	691	0.280694	5.117732074				
5	2350001	2450000	1181	0.281176	5.126850322				
5	47850001	47950000	496	0.281591	5.134701096				
5	92600001	92700000	772	0.283426	5.169414759				
5	80350001	80450000	400	0.291492	5.322003534				
5	58000001	58100000	768	0.300594	5.494190867				
5	111850001	111950000	733	0.329007	6.03169457				
5	92350001	92450000	954	0.343859	6.312657685				
5	18050001	18150000	992	0.354452	6.513051052				
5	47700001	47800000	400	0.355587	6.534522445				
5	95450001	95550000	452	0.372979	6.86353608				
5	95300001	95400000	462	0.386562	7.120492853				
5	18000001	18100000	706	0.390286	7.190941725				
5	47800001	47900000	486	0.405198	7.473039892				
5	95400001	95500000	395	0.416957	7.695491095				
5	47750001	47850000	448	0.437097	8.076490095				
5	95350001	95450000	424	0.446737	8.258855058				
6	65800001	65900000	942	0.19847	3.562257311				
6	65750001	65850000	927	0.198546	3.563695043				
6	66300001	66400000	297	0.202196	3.632744017				
6	15850001	15950000	535	0.202572	3.639857007				
6	66250001	66350000	393	0.204359	3.673662629				
6	65650001	65750000	759	0.207596	3.734898665				
6	39700001	39800000	895	0.209062	3.76263176				
6	3850001	3950000	942	0.210943	3.798215628				
6	82400001	82500000	988	0.211408	3.807012279				
6	76800001	76900000	795	0.212939	3.835975013				
6	3700001	3800000	901	0.214192	3.859678675				
6	76700001	76800000	512	0.216726	3.907615689				
6	117050001	117150000	551	0.226935	4.100744725				
6	11750001	11850000	749	0.233051	4.216444322				
6	66400001	66500000	533	0.233897	4.23244855				
6	117750001	117850000	413	0.239541	4.339219074				
6	73300001	73400000	913	0.242114	4.387893871				
6	82350001	82450000	1098	0.242186	4.389255933				

High 1% windows						High 1% merged windows			
Chr	Start	End	nSNPs	F_{ST}	ZF_{ST}	Chr	Start	End	Size (MB)
6	117700001	117800000	781	0.242473	4.394685264				
6	66050001	66150000	722	0.242745	4.399830831				
6	66200001	66300000	658	0.257543	4.6797724				
6	104000001	104100000	1038	0.26313	4.785464625				
6	11800001	11900000	904	0.268023	4.878028086				
6	66350001	66450000	484	0.274558	5.001654127				
6	66100001	66200000	801	0.275402	5.01762052				
6	66150001	66250000	768	0.277373	5.054906966				
6	39750001	39850000	499	0.277945	5.065727792				
6	76750001	76850000	538	0.319128	5.844808318				
7	108400001	108500000	914	0.199115	3.574459116				
7	57450001	57550000	317	0.202585	3.640102935				
7	96500001	96600000	354	0.205314	3.691728867				
7	57400001	57500000	298	0.2054	3.693355775				
7	73750001	73850000	944	0.207831	3.739344283				
7	60750001	60850000	383	0.208136	3.745114129				
7	60650001	60750000	466	0.216616	3.905534761				
7	96450001	96550000	475	0.226147	4.085837713				
7	54550001	54650000	582	0.233577	4.226394941				
7	44350001	44450000	913	0.235431	4.261468037				
7	60550001	60650000	573	0.245757	4.456810423				
7	73700001	73800000	828	0.250621	4.548825276				
7	60700001	60800000	406	0.286829	5.233791104				
8	33100001	33200000	1354	0.19983	3.587985148				
8	76300001	76400000	938	0.200613	3.602797572				
8	83950001	84050000	811	0.201328	3.616323604				
8	100800001	100900000	834	0.203452	3.656504431				
8	33250001	33350000	1324	0.204373	3.673927474				
8	54750001	54850000	877	0.205958	3.703911755				
8	59650001	59750000	227	0.21478	3.870802181				
8	55200001	55300000	771	0.215624	3.886768574				
8	76250001	76350000	1141	0.228185	4.124391634				
8	55150001	55250000	703	0.229228	4.144122615				
8	76200001	76300000	941	0.2304	4.166293957				
8	55050001	55150000	1137	0.230983	4.177322875				
8	54800001	54900000	903	0.260195	4.729941682				
8	55000001	55100000	1037	0.262207	4.768003747				
9	11550001	11650000	1494	0.201315	3.616077676				
9	90500001	90600000	1221	0.202421	3.637000461				
9	101600001	101700000	1422	0.207656	3.736033716				
9	102900001	103000000	1207	0.211377	3.806425835				
9	61650001	61750000	739	0.212298	3.823848878				
9	11450001	11550000	985	0.213192	3.840761147				
9	39900001	40000000	747	0.214835	3.871842645				
9	101650001	101750000	1452	0.217204	3.916658267				
9	11750001	11850000	1264	0.235671	4.266008243				
9	11800001	11900000	1007	0.23677	4.286798606				
9	39950001	40050000	564	0.249163	4.521243521				
9	11600001	11700000	1326	0.276237	5.033416655				
9	61700001	61800000	808	0.276303	5.034665212				
10	94350001	94450000	1115	0.198439	3.561670867				
10	101950001	102050000	779	0.201616	3.621771851				
10	69300001	69400000	772	0.202062	3.630209069				
10	59400001	59500000	323	0.205651	3.698104074				
10	21300001	21400000	1074	0.210267	3.78542738				
10	94450001	94550000	1162	0.211224	3.803531454				
10	54000001	54100000	763	0.212115	3.82038697				
10	57400001	57500000	815	0.212718	3.831794239				
10	70700001	70800000	1111	0.214029	3.856595118				

High 1% windows						High 1% merged windows			
Chr	Start	End	nSNPs	F_{ST}	ZF_{ST}	Chr	Start	End	Size (MB)
10	101900001	102000000	1125	0.215558	3.885520017				
10	59500001	59600000	258	0.224291	4.050726783				
10	59450001	59550000	316	0.233662	4.228002931				
10	70500001	70600000	945	0.250284	4.542450069				
10	94400001	94500000	1105	0.262667	4.77670581				
10	70550001	70650000	588	0.286524	5.228021258				
11	42200001	42300000	594	0.203921	3.665376752				
11	53650001	53750000	1633	0.204742	3.680908042				
11	50450001	50550000	1238	0.226775	4.09771792				
11	53700001	53800000	1530	0.234997	4.25325783				
11	50500001	50600000	1179	0.246535	4.47152826				
12	27500001	27600000	534	0.201774	3.624760821				
12	29500001	29600000	316	0.202344	3.635543811				
12	5150001	5250000	1164	0.207	3.723623818				
12	86950001	87050000	604	0.209557	3.771995936				
12	27350001	27450000	523	0.210117	3.782589751				
12	48000001	48100000	1311	0.210694	3.793505164				
12	28950001	29050000	712	0.218647	3.943956259				
12	28900001	29000000	784	0.221286	3.993879613				
12	5200001	5300000	1307	0.221299	3.994125541				
12	28800001	28900000	603	0.22821	4.124864572				
12	27700001	27800000	426	0.228642	4.133036944				
12	27750001	27850000	478	0.232619	4.20827195				
12	29000001	29100000	552	0.235834	4.2690918				
12	29600001	29700000	721	0.237416	4.299019328				
12	29550001	29650000	521	0.241709	4.380232273				
12	27400001	27500000	532	0.256602	4.661971007				
12	28850001	28950000	633	0.257695	4.682647864				
12	29050001	29150000	462	0.26891	4.894807933				
12	84400001	84500000	1215	0.271952	4.952355051				
12	29150001	29250000	358	0.272357	4.960016649				
12	29400001	29500000	278	0.272757	4.96758366				
12	29100001	29200000	544	0.286154	5.221021773				
12	84450001	84550000	1346	0.289739	5.288841109				
12	29200001	29300000	219	0.295075	5.389785034				
12	29250001	29350000	238	0.317472	5.813480893				
12	29350001	29450000	221	0.322641	5.911265591				
12	29300001	29400000	194	0.335329	6.151291178				
13	47600001	47700000	1580	0.202581	3.640027265				
13	77500001	77600000	653	0.203209	3.651907472				
13	77450001	77550000	647	0.205242	3.690366805				
13	77300001	77400000	443	0.216281	3.899197389				
13	47900001	48000000	894	0.21714	3.915447545				
13	47950001	48050000	692	0.227277	4.107214519				
13	63600001	63700000	345	0.23705	4.292095513				
13	77200001	77300000	579	0.246411	4.469182486				
13	77150001	77250000	620	0.25013	4.53953677				
13	47400001	47500000	542	0.263912	4.800258131				
13	77250001	77350000	484	0.278209	5.070722019				
13	77100001	77200000	734	0.2854	5.206757958				
13	47200001	47300000	434	0.308414	5.642125931				
13	47350001	47450000	286	0.318695	5.836617029				
13	47250001	47350000	344	0.37837	6.96552047				
13	47300001	47400000	212	0.434233	8.022310297				
14	32550001	32650000	859	0.199397	3.579793858				
14	32500001	32600000	1143	0.199735	3.586187983				
14	78200001	78300000	1225	0.201203	3.613958913				
14	11400001	11500000	1099	0.203387	3.655274792				
14	73500001	73600000	775	0.20359	3.65911505				

High 1% windows						High 1% merged windows			
Chr	Start	End	nSNPs	F_{ST}	ZF_{ST}	Chr	Start	End	Size (MB)
14	23300001	23400000	395	0.2049	3.683897011				
14	41450001	41550000	787	0.208928	3.760096811				
14	54850001	54950000	851	0.210356	3.78711104				
14	65550001	65650000	659	0.212224	3.822448981				
14	65600001	65700000	702	0.218437	3.939983578				
14	3150001	3250000	707	0.22722	4.10613622				
14	23250001	23350000	512	0.236778	4.286949946				
14	3200001	3300000	1084	0.239645	4.341186497				
14	73200001	73300000	1508	0.271793	4.949347164				
14	73250001	73350000	1413	0.285648	5.211449504				
14	28100001	28200000	325	0.297139	5.42883081				
15	4600001	4700000	1602	0.199497	3.581685611				
15	49600001	49700000	1958	0.199599	3.583615199				
15	54600001	54700000	835	0.200117	3.593414478				
15	35950001	36050000	567	0.202756	3.643337832				
15	35200001	35300000	1402	0.212811	3.833553569				
15	37800001	37900000	584	0.21478	3.870802181				
15	34650001	34750000	877	0.216039	3.894619347				
15	58400001	58500000	429	0.21772	3.926419711				
15	29800001	29900000	722	0.22065	3.981848066				
15	59750001	59850000	953	0.222229	4.011718841				
15	29750001	29850000	832	0.226602	4.094445188				
15	38200001	38300000	902	0.226863	4.099382663				
15	78150001	78250000	1914	0.23095	4.176698597				
15	38050001	38150000	719	0.235044	4.254146954				
15	78100001	78200000	1734	0.258737	4.702359928				
15	38000001	38100000	499	0.265632	4.832796278				
16	66500001	66600000	781	0.20581	3.701111961				
16	37600001	37700000	422	0.212046	3.819081661				
16	37550001	37650000	365	0.220415	3.977402447				
16	66450001	66550000	976	0.222361	4.014215955				
16	65600001	65700000	603	0.249836	4.533975017				
16	44000001	44100000	570	0.298516	5.454880246				
16	44050001	44150000	804	0.31448	5.756879651				
17	56350001	56450000	689	0.19921	3.576256281				
17	61950001	62050000	402	0.201019	3.610478088				
17	56650001	56750000	1160	0.203774	3.662595875				
17	21650001	21750000	1556	0.20503	3.68635629				
17	42250001	42350000	966	0.239156	4.331935826				
17	42000001	42100000	1312	0.242255	4.390561243				
17	60500001	60600000	632	0.242366	4.392661088				
17	41950001	42050000	1571	0.266278	4.845017001				
17	60450001	60550000	639	0.286958	5.236231465				
18	14850001	14950000	854	0.199837	3.58811757				
18	23500001	23600000	850	0.200995	3.610024067				
18	6300001	6400000	1220	0.204451	3.675403041				
18	14750001	14850000	581	0.205382	3.693015259				
18	14500001	14600000	591	0.210653	3.792729545				
18	60950001	61050000	1494	0.213006	3.837242487				
18	14700001	14800000	387	0.217715	3.926325123				
18	1050001	1150000	1624	0.22076	3.983928994				
18	14800001	14900000	758	0.221141	3.991136572				
18	950001	1050000	1825	0.225988	4.082829826				
18	14550001	14650000	448	0.227289	4.107441529				
18	3600001	3700000	946	0.230121	4.161015967				
18	22450001	22550000	1093	0.230538	4.168904576				
18	61000001	61100000	1068	0.238321	4.31613969				
18	61450001	61550000	2602	0.239202	4.332806032				
18	43250001	43350000	1418	0.239582	4.339994692				

High 1% windows						High 1% merged windows			
Chr	Start	End	nSNPs	F_{ST}	ZF_{ST}	Chr	Start	End	Size (MB)
18	43300001	43400000	1489	0.241319	4.372854437				
18	14600001	14700000	561	0.26624	4.844298135				
18	61400001	61500000	3182	0.266711	4.85320829				
18	1000001	1100000	1581	0.275733	5.023882221				
18	14650001	14750000	540	0.279111	5.087785629				
18	3550001	3650000	803	0.291649	5.324973586				
19	19100001	19200000	890	0.200905	3.608321489				
19	29650001	29750000	791	0.203463	3.656712524				
19	46400001	46500000	976	0.211074	3.800693824				
19	41150001	41250000	916	0.215402	3.882568883				
19	41000001	41100000	990	0.243155	4.407587017				
19	41050001	41150000	956	0.259312	4.713237506				
19	41100001	41200000	1064	0.279993	5.104470888				
19	46500001	46600000	841	0.286337	5.224483681				
19	46800001	46900000	661	0.322335	5.905476828				
19	46550001	46650000	1246	0.376332	6.926966549				
19	46600001	46700000	1103	0.407005	7.507223864				
19	46650001	46750000	843	0.482402	8.933548668				
19	46750001	46850000	972	0.506278	9.38522355				
19	46700001	46800000	1034	0.516231	9.573509699				
20	2650001	2750000	1085	0.200212	3.595211643				
20	18650001	18750000	606	0.20032	3.597254736				
20	56100001	56200000	1066	0.202445	3.637454481				
20	10400001	10500000	1452	0.203052	3.648937421				
20	51100001	51200000	802	0.203153	3.650848091				
20	11600001	11700000	875	0.205477	3.694812424				
20	11750001	11850000	973	0.207221	3.727804592				
20	39400001	39500000	575	0.212072	3.819573517				
20	30850001	30950000	271	0.2157	3.888206306				
20	10300001	10400000	1075	0.221262	3.993425592				
20	11800001	11900000	999	0.221464	3.997246933				
20	2600001	2700000	1425	0.223184	4.02978508				
20	31000001	31100000	445	0.231123	4.179971329				
20	10350001	10450000	1282	0.231636	4.189676021				
20	30900001	31000000	517	0.236528	4.282220564				
20	50850001	50950000	861	0.23707	4.292473864				
20	11950001	12050000	923	0.237454	4.299738194				
20	50900001	51000000	1030	0.240497	4.35730423				
20	12250001	12350000	756	0.24891	4.516457387				
20	11850001	11950000	885	0.249271	4.523286614				
20	30950001	31050000	577	0.249802	4.533331821				
20	4500001	4600000	776	0.268294	4.883154736				
20	11900001	12000000	869	0.291364	5.31958209				
20	39450001	39550000	701	0.35004	6.429586922				
20	39500001	39600000	643	0.371249	6.830808758				
21	67100001	67200000	752	0.199949	3.590236333				
21	19450001	19550000	814	0.201643	3.622282625				
21	39300001	39400000	800	0.204825	3.682478196				
21	36450001	36550000	1071	0.20712	3.725893922				
21	67650001	67750000	912	0.217097	3.914634091				
21	62650001	62750000	1118	0.226444	4.091456219				
21	14150001	14250000	611	0.228131	4.123370087				
21	43750001	43850000	746	0.231864	4.193989217				
21	64050001	64150000	1165	0.235571	4.26411649				
21	62600001	62700000	936	0.237359	4.297941029				
21	39350001	39450000	672	0.23947	4.337875929				
21	2250001	2350000	466	0.25219	4.578506876				
21	67550001	67650000	880	0.258188	4.691974205				
21	39450001	39550000	723	0.277608	5.059352585				

High 1% windows						High 1% merged windows			
Chr	Start	End	nSNPs	F_{ST}	ZF_{ST}	Chr	Start	End	Size (MB)
21	57900001	58000000	390	0.27833	5.07301104				
21	39400001	39500000	620	0.281086	5.125147745				
21	67600001	67700000	958	0.284711	5.193723781				
21	57950001	58050000	567	0.319601	5.853756308				
21	58000001	58100000	724	0.344477	6.324348717				
22	24300001	24400000	1159	0.20435	3.673492371				
22	3700001	3800000	1237	0.206061	3.70586026				
22	19750001	19850000	1436	0.215394	3.882417542				
22	19800001	19900000	1514	0.218971	3.950085537				
22	46750001	46850000	935	0.227259	4.106874004				
22	24250001	24350000	1032	0.262131	4.766566015				
23	14050001	14150000	1654	0.198191	3.55697932				
23	37400001	37500000	804	0.204081	3.668403556				
23	17200001	17300000	649	0.215571	3.885765945				
23	45100001	45200000	891	0.31531	5.772581199				
23	45150001	45250000	991	0.345447	6.342698719				
24	36900001	37000000	478	0.201607	3.621601594				
24	36500001	36600000	937	0.202245	3.633670976				
24	47500001	47600000	384	0.210635	3.79238903				
24	10050001	10150000	1269	0.213265	3.842142127				
24	36950001	37050000	554	0.221261	3.993406675				
24	41400001	41500000	341	0.221671	4.001162861				
24	36550001	36650000	942	0.222298	4.013024151				
24	36700001	36800000	645	0.223527	4.036273792				
24	41550001	41650000	449	0.227651	4.114289674				
24	37000001	37100000	709	0.230584	4.169774782				
24	47550001	47650000	664	0.231096	4.179460556				
24	41500001	41600000	380	0.235886	4.270075512				
24	41450001	41550000	336	0.24646	4.470109445				
24	47650001	47750000	752	0.249637	4.530210429				
24	47600001	47700000	839	0.269054	4.897532057				
25	26650001	26750000	608	0.227206	4.105871375				
25	8250001	8350000	1063	0.263672	4.795717925				
25	8150001	8250000	1115	0.294551	5.37987225				
25	8200001	8300000	1106	0.359111	6.601187812				
26	43350001	43450000	1441	0.214574	3.86690517				
26	11000001	11100000	845	0.274724	5.004794436				
27	21550001	21650000	1130	0.198481	3.562465403				
27	22050001	22150000	749	0.216806	3.909129091				
27	8100001	8200000	462	0.231762	4.192059629				
27	8150001	8250000	515	0.260077	4.727709414				
27	8200001	8300000	471	0.271937	4.952071288				
27	8000001	8100000	644	0.286429	5.226224093				
27	8050001	8150000	636	0.298507	5.454709988				
27	21500001	21600000	1139	0.31567	5.779391509				
27	21450001	21550000	849	0.32339	5.925434819				
28	41200001	41300000	566	0.213888	3.853927746				
28	1	100000	984	0.218997	3.950577393				
28	150001	250000	1271	0.228842	4.136820449				
28	200001	300000	997	0.230667	4.171344937				
29	18800001	18900000	1544	0.208957	3.760645419				
29	19350001	19450000	980	0.209454	3.77004743				
29	48650001	48750000	791	0.232165	4.199683392				
29	39800001	39900000	449	0.241434	4.375029953				
29	39850001	39950000	420	0.255419	4.639591572				
29	18900001	19000000	1834	0.310093	5.673888459				
29	18850001	18950000	1378	0.390444	7.193930694				

Table S39. F_{ST} selective sweep regions between high (Raya) and low (Abergelle) groups of the warmest quarter precipitation (bio18).

High 1% windows						High 1% merged windows			
Chr	Start	End	nSNPs	F_{ST}	ZF_{ST}	Chr	Start	End	Size (MB)
1	52650001	52750000	764	0.156577	3.53997	1	16950001	17050000	0.099999
1	52700001	52800000	724	0.156695	3.542622	1	32900001	33000000	0.099999
1	39750001	39850000	1171	0.156759	3.54406	1	53100001	53300000	0.199999
1	119400001	119500000	798	0.15712	3.552173	1	92550001	92700000	0.149999
1	129850001	129950000	637	0.159478	3.605164	1	112900001	113000000	0.099999
1	92500001	92600000	949	0.162334	3.669347	1	114050001	114200000	0.149999
1	32250001	32350000	1778	0.164359	3.714855	1	119450001	119550000	0.099999
1	16900001	17000000	1130	0.164569	3.719574	1	129350001	129500000	0.149999
1	1900001	2000000	355	0.166038	3.752587	1	129800001	129900000	0.099999
1	119500001	119600000	922	0.167894	3.794297	2	36500001	36750000	0.249999
1	87250001	87350000	843	0.169915	3.839715	2	74250001	74400000	0.149999
1	93050001	93150000	899	0.170613	3.855402	2	106700001	106850000	0.149999
1	1950001	2050000	380	0.170823	3.860121	2	109650001	109750000	0.099999
1	32200001	32300000	1502	0.172042	3.887516	2	109800001	109900000	0.099999
1	32900001	33000000	997	0.180541	4.078514	2	109950001	110050000	0.099999
1	129350001	129450000	1240	0.195874	4.423093	2	110050001	110200000	0.149999
1	119450001	119550000	964	0.196541	4.438083	2	110250001	110700000	0.449999
1	129400001	129500000	1250	0.198793	4.488692	2	121750001	121850000	0.099999
1	114100001	114200000	1535	0.200954	4.537256	2	133500001	133600000	0.099999
1	16950001	17050000	1208	0.201528	4.550156	3	550001	1050000	0.499999
1	112900001	113000000	993	0.201744	4.55501	3	18950001	19050000	0.099999
1	53100001	53200000	686	0.202453	4.570943	3	22350001	22450000	0.099999
1	114050001	114150000	1220	0.207264	4.679061	3	51350001	51550000	0.199999
1	92600001	92700000	1240	0.244446	5.514654	3	61800001	61950000	0.149999
1	129800001	129900000	455	0.261593	5.9	3	65700001	65900000	0.199999
1	53200001	53300000	630	0.267711	6.03749	3	67900001	68150000	0.249999
1	92550001	92650000	874	0.281706	6.352	3	71850001	71950000	0.099999
1	53150001	53250000	736	0.341856	7.703754	3	84550001	84650000	0.099999
2	110000001	110100000	905	0.156026	3.527587	4	24050001	24200000	0.149999
2	105800001	105900000	810	0.157453	3.559656	4	40550001	40700000	0.149999
2	130550001	130650000	1468	0.157515	3.561049	4	46850001	47050000	0.199999
2	126400001	126500000	295	0.157572	3.56233	4	87600001	87750000	0.149999
2	106950001	107050000	500	0.157758	3.56651	4	89900001	90050000	0.149999
2	105750001	105850000	703	0.15787	3.569027	4	118800001	119000000	0.199999
2	67900001	68000000	884	0.163527	3.696157	4	119300001	119550000	0.249999
2	109700001	109800000	1094	0.165784	3.746879	5	47700001	47950000	0.249999
2	63650001	63750000	857	0.166945	3.77297	5	48400001	48800000	0.399999
2	133450001	133550000	755	0.167017	3.774588	5	50650001	50800000	0.149999
2	109900001	110000000	1024	0.170095	3.84376	5	82050001	82200000	0.149999
2	106900001	107000000	538	0.171543	3.876301	5	95300001	95500000	0.199999
2	108050001	108150000	730	0.17324	3.914438	5	111850001	111950000	0.099999
2	109850001	109950000	816	0.174523	3.943271	6	11800001	11900000	0.099999
2	110050001	110150000	913	0.181326	4.096155	6	32100001	32250000	0.149999
2	106700001	106800000	517	0.184293	4.162833	6	37350001	37650000	0.299999
2	36500001	36600000	546	0.18482	4.174676	6	39700001	39850000	0.149999
2	109950001	110050000	1126	0.185291	4.185261	6	53750001	53900000	0.149999
2	74300001	74400000	987	0.185646	4.193239	6	69750001	69900000	0.149999
2	106750001	106850000	611	0.188866	4.265602	6	83600001	83700000	0.099999
2	109800001	109900000	890	0.191307	4.320459	6	95350001	95500000	0.149999
2	110100001	110200000	957	0.195647	4.417992	6	104000001	104100000	0.099999
2	133500001	133600000	901	0.21006	4.741896	6	104450001	104600000	0.149999
2	74250001	74350000	1267	0.210607	4.754189	6	108050001	108150000	0.099999
2	110600001	110700000	807	0.228699	5.160771	6	108200001	108350000	0.149999

High 1% windows						High 1% merged windows			
Chr	Start	End	nSNPs	F_{ST}	ZF_{ST}	Chr	Start	End	Size (MB)
2	110400001	110500000	508	0.230688	5.20547	7	31050001	31250000	0.199999
2	109650001	109750000	533	0.230877	5.209717	7	54950001	55100000	0.149999
2	110250001	110350000	608	0.231073	5.214122	7	61200001	61400000	0.199999
2	36650001	36750000	400	0.232756	5.251944	7	71050001	71150000	0.099999
2	110350001	110450000	602	0.233286	5.263855	7	96450001	96600000	0.149999
2	36600001	36700000	477	0.233786	5.275092	7	109600001	109700000	0.099999
2	110300001	110400000	685	0.237523	5.359073	8	7250001	7350000	0.099999
2	36550001	36650000	581	0.239623	5.406267	8	17800001	17900000	0.099999
2	110450001	110550000	580	0.247556	5.584546	8	20750001	20850000	0.099999
2	110500001	110600000	478	0.273056	6.157608	8	30500001	30600000	0.099999
2	121750001	121850000	483	0.291637	6.57518	8	40600001	40700000	0.099999
2	110550001	110650000	350	0.321329	7.24245	8	59500001	59600000	0.099999
3	59700001	59800000	289	0.160615	3.630716	8	66100001	66250000	0.149999
3	51500001	51600000	756	0.162207	3.666493	8	67100001	67200000	0.099999
3	61900001	62000000	1024	0.165142	3.732451	8	97350001	97450000	0.099999
3	85850001	85950000	735	0.165185	3.733418	8	101300001	101400000	0.099999
3	37200001	37300000	1369	0.167843	3.793151	8	101400001	101600000	0.199999
3	29200001	29300000	976	0.173399	3.918011	8	104850001	104950000	0.099999
3	61800001	61900000	853	0.177532	4.010893	9	44350001	44600000	0.249999
3	22350001	22450000	906	0.179571	4.056715	9	44600001	44700000	0.099999
3	18950001	19050000	664	0.179875	4.063547	9	92250001	92350000	0.099999
3	51450001	51550000	759	0.181861	4.108178	9	94050001	94200000	0.149999
3	71850001	71950000	687	0.186969	4.222971	10	22500001	22650000	0.149999
3	67900001	68000000	942	0.19174	4.33019	10	23200001	23300000	0.099999
3	84550001	84650000	496	0.193702	4.374282	10	59400001	59550000	0.149999
3	51400001	51500000	783	0.200693	4.531391	10	86450001	86550000	0.099999
3	51350001	51450000	675	0.201148	4.541616	10	100850001	100950000	0.099999
3	550001	650000	1008	0.203057	4.584517	11	8850001	8950000	0.099999
3	61850001	61950000	971	0.209457	4.728345	11	16400001	16500000	0.099999
3	650001	750000	946	0.209786	4.735738	11	18750001	18850000	0.099999
3	950001	1050000	1204	0.213157	4.811495	11	53650001	53800000	0.149999
3	700001	800000	946	0.222344	5.017955	11	96450001	96800000	0.349999
3	600001	700000	821	0.223917	5.053305	11	101950001	102100000	0.149999
3	65700001	65800000	1051	0.245782	5.544678	12	35650001	35950000	0.299999
3	65800001	65900000	1074	0.259811	5.859953	12	36000001	36200000	0.199999
3	900001	1000000	1180	0.274079	6.180598	12	36400001	36550000	0.149999
3	68050001	68150000	808	0.277977	6.268198	12	36600001	36700000	0.099999
3	68000001	68100000	898	0.308536	6.954952	12	39200001	39350000	0.149999
3	850001	950000	924	0.309689	6.980864	12	42350001	42450000	0.099999
3	67950001	68050000	794	0.318569	7.180424	12	44700001	44800000	0.099999
3	65750001	65850000	1153	0.351192	7.913563	12	49300001	49400000	0.099999
3	750001	850000	906	0.356739	8.038221	12	55200001	55300000	0.099999
3	800001	900000	905	0.384123	8.653623	12	60300001	60400000	0.099999
4	88100001	88200000	941	0.157117	3.552105	12	84400001	84550000	0.149999
4	88050001	88150000	745	0.161878	3.659099	13	6100001	6200000	0.099999
4	114550001	114650000	658	0.162497	3.67301	14	17150001	17250000	0.099999
4	40650001	40750000	1080	0.162902	3.682112	14	23250001	23350000	0.099999
4	88300001	88400000	744	0.165494	3.740362	14	49600001	49700000	0.099999
4	59550001	59650000	1043	0.167615	3.788027	15	800001	900000	0.099999
4	119500001	119600000	984	0.169621	3.833108	15	11550001	11750000	0.199999
4	114600001	114700000	480	0.17233	3.893988	15	12100001	12200000	0.099999
4	118750001	118850000	1049	0.174453	3.941698	15	12400001	12500000	0.099999
4	118850001	118950000	1440	0.177467	4.009432	15	31900001	32050000	0.149999
4	119300001	119400000	903	0.181603	4.10238	15	35150001	35300000	0.149999
4	119350001	119450000	930	0.185314	4.185778	15	35300001	35600000	0.299999
4	46950001	47050000	774	0.185562	4.191351	15	35800001	35900000	0.099999

High 1% windows						High 1% merged windows			
Chr	Start	End	nSNPs	F_{ST}	ZF_{ST}	Chr	Start	End	Size (MB)
4	87650001	87750000	1049	0.187584	4.236792	15	77900001	78050000	0.149999
4	119400001	119500000	702	0.189763	4.28576	15	78050001	78200000	0.149999
4	118800001	118900000	1392	0.189855	4.287828	16	28150001	28250000	0.099999
4	40550001	40650000	1166	0.191763	4.330707	16	28300001	28700000	0.399999
4	87600001	87700000	1012	0.192059	4.337359	16	53700001	53800000	0.099999
4	118900001	119000000	1267	0.192086	4.337965	16	53950001	54050000	0.099999
4	119450001	119550000	680	0.192889	4.356011	16	80550001	80700000	0.149999
4	46850001	46950000	727	0.193685	4.3739	17	6300001	6400000	0.099999
4	89950001	90050000	1299	0.221726	5.004067	17	60450001	60550000	0.099999
4	40600001	40700000	1166	0.229345	5.175289	17	71700001	71800000	0.099999
4	24100001	24200000	855	0.230925	5.210796	18	35600001	35750000	0.149999
4	46900001	47000000	715	0.249233	5.622233	18	38600001	38700000	0.099999
4	24050001	24150000	725	0.264045	5.955104	20	7450001	7550000	0.099999
4	89900001	90000000	1064	0.292724	6.599608	21	37150001	37350000	0.199999
5	65950001	66050000	452	0.161932	3.660313	21	39350001	39550000	0.199999
5	95450001	95550000	426	0.173174	3.912955	21	44400001	44550000	0.149999
5	82050001	82150000	889	0.182801	4.129303	21	50350001	50450000	0.099999
5	95300001	95400000	445	0.186973	4.223061	21	50450001	50550000	0.099999
5	82100001	82200000	1319	0.192367	4.34428	22	2100001	2250000	0.149999
5	48700001	48800000	461	0.192774	4.353427	22	3150001	3300000	0.149999
5	50650001	50750000	1170	0.197192	4.452713	23	14500001	14650000	0.149999
5	95400001	95500000	355	0.207195	4.677511	23	26300001	26450000	0.149999
5	48400001	48500000	239	0.208659	4.710411	23	44100001	44200000	0.099999
5	50700001	50800000	1021	0.217729	4.914242	23	47600001	47700000	0.099999
5	48450001	48550000	374	0.220148	4.968604	23	48050001	48200000	0.149999
5	48550001	48650000	518	0.225566	5.090363	24	45550001	45650000	0.099999
5	48500001	48600000	538	0.225861	5.096993	24	62250001	62400000	0.149999
5	47700001	47800000	445	0.227651	5.137219	25	8450001	8600000	0.149999
5	95350001	95450000	376	0.22955	5.179896	25	9450001	9750000	0.299999
5	48600001	48700000	636	0.230819	5.208414	25	29500001	29650000	0.149999
5	48650001	48750000	636	0.240982	5.436808	26	4550001	4650000	0.099999
5	47850001	47950000	539	0.241395	5.446089	26	30050001	30150000	0.099999
5	111850001	111950000	710	0.24881	5.612727	26	33600001	33750000	0.149999
5	47750001	47850000	533	0.32653	7.359332	26	42650001	42850000	0.199999
5	47800001	47900000	560	0.32986	7.434168	27	1950001	2100000	0.149999
6	65650001	65750000	741	0.156219	3.531924	28	17250001	17450000	0.199999
6	62250001	62350000	1087	0.156629	3.541138	28	17500001	17600000	0.099999
6	63950001	64050000	1025	0.157277	3.555701	28	19450001	19550000	0.099999
6	104200001	104300000	728	0.157534	3.561476	28	19700001	19850000	0.149999
6	78750001	78850000	1327	0.160401	3.625907	28	41150001	41350000	0.199999
6	108100001	108200000	741	0.160991	3.639166	28	41400001	41550000	0.149999
6	37250001	37350000	1114	0.161679	3.654627	29	13650001	13800000	0.149999
6	79350001	79450000	1937	0.163149	3.687663	29	45050001	45450000	0.399999
6	108150001	108250000	768	0.164384	3.715417	29	48600001	48800000	0.199999
6	104350001	104450000	807	0.170493	3.852705				
6	37300001	37400000	656	0.171079	3.865874				
6	108000001	108100000	1217	0.171317	3.871223				
6	78700001	78800000	1049	0.171855	3.883313				
6	83650001	83750000	894	0.172907	3.906955				
6	37200001	37300000	1084	0.173983	3.931136				
6	115550001	115650000	1008	0.175228	3.959115				
6	115600001	115700000	827	0.175562	3.966621				
6	39650001	39750000	1172	0.175693	3.969565				
6	32150001	32250000	812	0.177137	4.002016				
6	108050001	108150000	970	0.182287	4.117752				
6	32100001	32200000	774	0.182307	4.118201				

High 1% windows						High 1% merged windows			
Chr	Start	End	nSNPs	F_{ST}	ZF_{ST}	Chr	Start	End	Size (MB)
6	53800001	53900000	766	0.183921	4.154473				
6	69750001	69850000	830	0.184995	4.178609				
6	69800001	69900000	813	0.187068	4.225196				
6	95400001	95500000	1178	0.190173	4.294974				
6	11800001	11900000	896	0.191783	4.331156				
6	104500001	104600000	1035	0.192331	4.343471				
6	53750001	53850000	918	0.193315	4.365585				
6	104450001	104550000	1198	0.193621	4.372461				
6	83600001	83700000	747	0.193876	4.378192				
6	108250001	108350000	959	0.197756	4.465388				
6	104000001	104100000	946	0.199827	4.511929				
6	108200001	108300000	868	0.208893	4.71567				
6	37350001	37450000	382	0.22387	5.052249				
6	95350001	95450000	1185	0.224698	5.070857				
6	39700001	39800000	977	0.225022	5.078138				
6	39750001	39850000	539	0.227463	5.132994				
6	37500001	37600000	457	0.227655	5.137309				
6	37550001	37650000	576	0.228828	5.16367				
6	37400001	37500000	385	0.229831	5.186211				
6	37450001	37550000	422	0.252128	5.687292				
7	31250001	31350000	997	0.161012	3.639638				
7	61350001	61450000	721	0.163912	3.70481				
7	55050001	55150000	339	0.165681	3.744564				
7	31050001	31150000	808	0.179177	4.047861				
7	109600001	109700000	1103	0.18195	4.110179				
7	54950001	55050000	658	0.186966	4.222903				
7	71050001	71150000	670	0.1952	4.407946				
7	31150001	31250000	1134	0.198822	4.489344				
7	61300001	61400000	526	0.200661	4.530672				
7	31100001	31200000	877	0.207595	4.6865				
7	96450001	96550000	486	0.207959	4.69468				
7	61200001	61300000	790	0.211006	4.763155				
7	61250001	61350000	585	0.252412	5.693675				
7	96500001	96600000	306	0.285598	6.439465				
7	55000001	55100000	472	0.324001	7.302498				
8	59250001	59350000	435	0.155242	3.509968				
8	67150001	67250000	1192	0.15583	3.523182				
8	59450001	59550000	657	0.159875	3.614086				
8	26750001	26850000	1039	0.161963	3.66101				
8	67350001	67450000	556	0.16411	3.709259				
8	21850001	21950000	529	0.164216	3.711641				
8	83100001	83200000	610	0.16534	3.736901				
8	101250001	101350000	618	0.165928	3.750115				
8	67050001	67150000	1607	0.166414	3.761037				
8	21900001	22000000	585	0.166499	3.762947				
8	72200001	72300000	925	0.166816	3.770071				
8	45950001	46050000	764	0.168427	3.806275				
8	45000001	45100000	905	0.168672	3.811781				
8	30550001	30650000	675	0.169107	3.821557				
8	59300001	59400000	470	0.172576	3.899516				
8	101350001	101450000	1033	0.174965	3.953204				
8	66100001	66200000	830	0.177333	4.00642				
8	17800001	17900000	995	0.178321	4.028624				
8	101300001	101400000	904	0.179563	4.056535				
8	66150001	66250000	1211	0.183132	4.136742				
8	40600001	40700000	500	0.183156	4.137281				

High 1% windows						High 1% merged windows			
Chr	Start	End	nSNPs	F_{ST}	ZF_{ST}	Chr	Start	End	Size (MB)
8	20750001	20850000	907	0.184681	4.171552				
8	104850001	104950000	916	0.184881	4.176047				
8	101400001	101500000	1126	0.185695	4.19434				
8	30500001	30600000	634	0.186557	4.213712				
8	101500001	101600000	1054	0.192381	4.344595				
8	67100001	67200000	1438	0.200225	4.520874				
8	101450001	101550000	1292	0.20363	4.597394				
8	59500001	59600000	351	0.209055	4.719311				
8	97350001	97450000	700	0.2099	4.7383				
8	7250001	7350000	215	0.220743	4.981976				
9	92300001	92400000	1155	0.157566	3.562196				
9	44550001	44650000	474	0.160456	3.627143				
9	94000001	94100000	1097	0.160508	3.628311				
9	28150001	28250000	902	0.163462	3.694697				
9	92200001	92300000	1119	0.164561	3.719395				
9	27900001	28000000	738	0.167504	3.785533				
9	88400001	88500000	515	0.169379	3.82767				
9	46500001	46600000	578	0.171122	3.86684				
9	88450001	88550000	567	0.17532	3.961182				
9	44650001	44750000	586	0.176518	3.988105				
9	44500001	44600000	446	0.194356	4.388979				
9	44600001	44700000	604	0.19613	4.428846				
9	44350001	44450000	843	0.198639	4.485231				
9	92250001	92350000	1055	0.201503	4.549594				
9	94100001	94200000	1041	0.204128	4.608586				
9	44450001	44550000	578	0.251799	5.679899				
9	94050001	94150000	1079	0.256638	5.788646				
9	44400001	44500000	732	0.258977	5.84121				
10	86400001	86500000	648	0.157779	3.566982				
10	3100001	3200000	811	0.158817	3.590309				
10	66650001	66750000	450	0.159135	3.597456				
10	66700001	66800000	343	0.164558	3.719327				
10	86100001	86200000	800	0.167892	3.794252				
10	100900001	101000000	1473	0.170503	3.852929				
10	59450001	59550000	316	0.180393	4.075188				
10	86450001	86550000	745	0.181297	4.095504				
10	23200001	23300000	2317	0.185152	4.182137				
10	59400001	59500000	325	0.189292	4.275176				
10	22500001	22600000	1648	0.194319	4.388148				
10	100850001	100950000	1667	0.21081	4.758751				
10	22550001	22650000	2127	0.240691	5.430268				
11	53550001	53650000	1259	0.157558	3.562016				
11	41150001	41250000	482	0.157826	3.568039				
11	90950001	91050000	954	0.165517	3.740879				
11	58250001	58350000	1140	0.170885	3.861514				
11	58300001	58400000	980	0.174551	3.9439				
11	18750001	18850000	712	0.177904	4.019253				
11	8850001	8950000	1108	0.178585	4.034557				
11	16400001	16500000	952	0.183174	4.137686				
11	53650001	53750000	1588	0.188403	4.255197				
11	102000001	102100000	842	0.190988	4.31329				
11	101950001	102050000	1114	0.194277	4.387204				
11	96700001	96800000	415	0.196258	4.431723				
11	96450001	96550000	493	0.221513	4.99928				
11	53700001	53800000	1497	0.235985	5.32451				
11	96650001	96750000	364	0.250299	5.646189				

High 1% windows						High 1% merged windows			
Chr	Start	End	nSNPs	F_{ST}	ZF_{ST}	Chr	Start	End	Size (MB)
11	96600001	96700000	372	0.284711	6.419532				
11	96500001	96600000	501	0.306057	6.899241				
11	96550001	96650000	454	0.315077	7.101948				
12	29350001	29450000	266	0.160221	3.621862				
12	60450001	60550000	1286	0.163485	3.695214				
12	55150001	55250000	782	0.167419	3.783623				
12	84500001	84600000	1247	0.167436	3.784005				
12	36500001	36600000	406	0.175301	3.960755				
12	36550001	36650000	476	0.176391	3.985251				
12	49300001	49400000	1307	0.178824	4.039928				
12	36000001	36100000	706	0.179381	4.052445				
12	55200001	55300000	956	0.179505	4.055232				
12	60300001	60400000	877	0.18347	4.144338				
12	42350001	42450000	1106	0.186404	4.210273				
12	36600001	36700000	421	0.186848	4.220252				
12	44700001	44800000	1472	0.1888	4.264119				
12	35850001	35950000	431	0.189223	4.273625				
12	36400001	36500000	520	0.197978	4.470377				
12	36450001	36550000	554	0.206626	4.664724				
12	84400001	84500000	1181	0.207733	4.689601				
12	36100001	36200000	354	0.217828	4.916467				
12	39250001	39350000	1245	0.229081	5.169356				
12	35650001	35750000	335	0.231741	5.229134				
12	35750001	35850000	367	0.232934	5.255945				
12	35800001	35900000	340	0.236349	5.33269				
12	35700001	35800000	310	0.238838	5.388625				
12	84450001	84550000	1347	0.239158	5.395817				
12	39200001	39300000	830	0.245896	5.54724				
12	36050001	36150000	444	0.246562	5.562207				
13	63350001	63450000	776	0.159067	3.595928				
13	6050001	6150000	1347	0.163104	3.686651				
13	63400001	63500000	646	0.165784	3.746879				
13	6150001	6250000	1885	0.170441	3.851536				
13	6100001	6200000	1575	0.202453	4.570943				
14	44450001	44550000	1037	0.161925	3.660156				
14	72150001	72250000	1453	0.162546	3.674111				
14	39150001	39250000	819	0.163099	3.686539				
14	70350001	70450000	1337	0.167588	3.787421				
14	23250001	23350000	515	0.177371	4.007274				
14	49600001	49700000	545	0.180571	4.079188				
14	17150001	17250000	799	0.18145	4.098942				
15	23700001	23800000	829	0.159649	3.609007				
15	77850001	77950000	1297	0.161441	3.649279				
15	35100001	35200000	1058	0.162365	3.670044				
15	32800001	32900000	678	0.162739	3.678449				
15	32000001	32100000	1070	0.163774	3.701708				
15	850001	950000	1566	0.163956	3.705798				
15	22250001	22350000	877	0.16494	3.727912				
15	77750001	77850000	1248	0.165294	3.735867				
15	10300001	10400000	1014	0.165822	3.747733				
15	400001	500000	999	0.167018	3.774611				
15	77700001	77800000	1064	0.169412	3.828411				
15	35750001	35850000	689	0.170141	3.844794				
15	78000001	78100000	1621	0.172425	3.896123				
15	12350001	12450000	916	0.173287	3.915494				
15	31850001	31950000	1218	0.17528	3.960283				

High 1% windows						High 1% merged windows			
Chr	Start	End	nSNPs	F_{ST}	ZF_{ST}	Chr	Start	End	Size (MB)
15	35300001	35400000	822	0.179753	4.060805				
15	31900001	32000000	1215	0.183037	4.134607				
15	35450001	35550000	773	0.184683	4.171597				
15	35800001	35900000	670	0.187219	4.228589				
15	12100001	12200000	969	0.187739	4.240275				
15	35500001	35600000	581	0.187759	4.240724				
15	77950001	78050000	1354	0.199524	4.50512				
15	78100001	78200000	1704	0.200683	4.531166				
15	31950001	32050000	1159	0.201372	4.54665				
15	11650001	11750000	1132	0.204875	4.625373				
15	35400001	35500000	1133	0.20851	4.707063				
15	12400001	12500000	1214	0.214183	4.834552				
15	35350001	35450000	1074	0.231403	5.221538				
15	35150001	35250000	1492	0.232381	5.243517				
15	800001	900000	1000	0.235904	5.32269				
15	78050001	78150000	1506	0.236365	5.33305				
15	77900001	78000000	1416	0.248603	5.608075				
15	11550001	11650000	1658	0.259738	5.858312				
15	35200001	35300000	1428	0.261054	5.887887				
15	11600001	11700000	1582	0.297708	6.711614				
16	25800001	25900000	1240	0.156975	3.548914				
16	70350001	70450000	674	0.1614	3.648357				
16	54000001	54100000	971	0.163851	3.703439				
16	12600001	12700000	982	0.168811	3.814905				
16	40700001	40800000	581	0.169676	3.834344				
16	12550001	12650000	680	0.175159	3.957564				
16	28600001	28700000	728	0.178237	4.026736				
16	53950001	54050000	1020	0.189079	4.270389				
16	28400001	28500000	1039	0.200395	4.524694				
16	28550001	28650000	800	0.206913	4.671173				
16	53700001	53800000	1077	0.209013	4.718367				
16	80550001	80650000	738	0.216776	4.892825				
16	28500001	28600000	829	0.225911	5.098116				
16	28150001	28250000	950	0.226327	5.107465				
16	80600001	80700000	732	0.22759	5.135849				
16	28350001	28450000	1283	0.233501	5.268687				
16	28450001	28550000	843	0.242529	5.471573				
16	28300001	28400000	1208	0.260915	5.884763				
17	35700001	35800000	830	0.155619	3.518441				
17	40700001	40800000	1215	0.158304	3.578781				
17	71700001	71800000	1121	0.179413	4.053164				
17	6300001	6400000	1475	0.181283	4.095189				
17	60450001	60550000	852	0.206073	4.652296				
18	35150001	35250000	267	0.155527	3.516373				
18	35100001	35200000	237	0.156373	3.535385				
18	34650001	34750000	385	0.157162	3.553117				
18	17100001	17200000	961	0.158692	3.5875				
18	35400001	35500000	218	0.163957	3.705821				
18	35350001	35450000	219	0.166136	3.75479				
18	35550001	35650000	202	0.166875	3.771397				
18	35500001	35600000	212	0.167136	3.777263				
18	3450001	3550000	1326	0.169953	3.840569				
18	3500001	3600000	1090	0.17474	3.948148				
18	38600001	38700000	242	0.187344	4.231398				
18	35600001	35700000	197	0.192616	4.349876				
18	35650001	35750000	275	0.310944	7.009067				

High 1% windows						High 1% merged windows			
Chr	Start	End	nSNPs	F_{ST}	ZF_{ST}	Chr	Start	End	Size (MB)
19	54650001	54750000	889	0.163419	3.69373				
19	54700001	54800000	901	0.167508	3.785623				
19	19150001	19250000	980	0.168552	3.809085				
19	45750001	45850000	996	0.170005	3.841738				
20	47200001	47300000	1094	0.166739	3.768341				
20	4500001	4600000	763	0.17226	3.892415				
20	39500001	39600000	493	0.174344	3.939248				
20	39450001	39550000	558	0.175679	3.96925				
20	7450001	7550000	923	0.181114	4.091391				
21	10350001	10450000	1212	0.158463	3.582354				
21	25600001	25700000	1011	0.158567	3.584691				
21	50400001	50500000	1058	0.163621	3.69827				
21	50300001	50400000	1709	0.169963	3.840794				
21	10400001	10500000	1170	0.170436	3.851424				
21	44450001	44550000	891	0.177573	4.011814				
21	37150001	37250000	1047	0.180156	4.069862				
21	50350001	50450000	1324	0.18887	4.265692				
21	50450001	50550000	1287	0.18966	4.283446				
21	39450001	39550000	827	0.205527	4.640026				
21	37250001	37350000	1080	0.206786	4.668319				
21	39350001	39450000	724	0.209576	4.731019				
21	44400001	44500000	1117	0.212985	4.80763				
21	37200001	37300000	1093	0.244904	5.524947				
21	39400001	39500000	699	0.253545	5.719137				
22	30650001	30750000	582	0.161192	3.643683				
22	32450001	32550000	447	0.16291	3.682292				
22	24000001	24100000	1027	0.16494	3.727912				
22	3250001	3350000	1282	0.165508	3.740677				
22	2200001	2300000	1169	0.171585	3.877245				
22	40100001	40200000	1147	0.175714	3.970037				
22	3200001	3300000	1166	0.206563	4.663308				
22	3150001	3250000	1088	0.211411	4.772257				
22	2150001	2250000	1035	0.245995	5.549465				
22	2100001	2200000	943	0.261476	5.89737				
23	47800001	47900000	1223	0.157555	3.561948				
23	47600001	47700000	786	0.178537	4.033478				
23	14500001	14600000	1403	0.179624	4.057906				
23	44100001	44200000	810	0.189075	4.270299				
23	26350001	26450000	4172	0.194141	4.384147				
23	48100001	48200000	507	0.204977	4.627665				
23	14550001	14650000	1379	0.225743	5.094341				
23	26300001	26400000	3291	0.231264	5.218415				
23	48050001	48150000	385	0.304737	6.869577				
24	45600001	45700000	1071	0.161327	3.646717				
24	11650001	11750000	1377	0.170389	3.850368				
24	62200001	62300000	1179	0.174021	3.93199				
24	62250001	62350000	626	0.180261	4.072222				
24	62300001	62400000	19	0.181238	4.094178				
24	45550001	45650000	1480	0.183349	4.141618				
25	29650001	29750000	1636	0.156336	3.534554				
25	36350001	36450000	875	0.166597	3.76515				
25	29600001	29700000	1387	0.174855	3.950732				
25	9450001	9550000	968	0.183526	4.145596				
25	29500001	29600000	1059	0.193433	4.368237				
25	8450001	8550000	826	0.193752	4.375405				
25	29550001	29650000	1232	0.195177	4.40743				

High 1% windows						High 1% merged windows			
Chr	Start	End	nSNPs	F_{ST}	ZF_{ST}	Chr	Start	End	Size (MB)
25	9500001	9600000	823	0.203903	4.603529				
25	9550001	9650000	670	0.209704	4.733896				
25	9650001	9750000	471	0.21839	4.929096				
25	9600001	9700000	599	0.222959	5.031776				
25	8500001	8600000	735	0.242675	5.474855				
26	37800001	37900000	617	0.156202	3.531542				
26	33550001	33650000	502	0.158477	3.582669				
26	46850001	46950000	1207	0.16271	3.677797				
26	37850001	37950000	722	0.171785	3.88174				
26	29800001	29900000	855	0.174199	3.93599				
26	33650001	33750000	690	0.182288	4.117774				
26	42650001	42750000	1000	0.187788	4.241376				
26	42750001	42850000	697	0.18969	4.28412				
26	4550001	4650000	1428	0.192182	4.340123				
26	33600001	33700000	589	0.199397	4.502266				
26	30050001	30150000	768	0.218172	4.924197				
26	42700001	42800000	540	0.271543	6.123607				
27	14950001	15050000	970	0.155528	3.516396				
27	6100001	6200000	1387	0.158903	3.592242				
27	6050001	6150000	1225	0.167115	3.776791				
27	1950001	2050000	997	0.218725	4.936625				
27	2000001	2100000	1084	0.244555	5.517104				
28	19500001	19600000	900	0.159069	3.595973				
28	25450001	25550000	1060	0.160212	3.621659				
28	45800001	45900000	1257	0.163418	3.693708				
28	41350001	41450000	840	0.172692	3.902123				
28	17500001	17600000	890	0.177997	4.021343				
28	17250001	17350000	1121	0.179852	4.06303				
28	19450001	19550000	630	0.190821	4.309537				
28	41450001	41550000	1085	0.192951	4.357405				
28	41400001	41500000	1042	0.209785	4.735716				
28	41150001	41250000	458	0.211084	4.764908				
28	17350001	17450000	1114	0.23379	5.275181				
28	19750001	19850000	879	0.243005	5.482271				
28	41250001	41350000	742	0.258065	5.820715				
28	17300001	17400000	1146	0.274215	6.183655				
28	41200001	41300000	563	0.331483	7.470641				
28	19700001	19800000	705	0.33195	7.481136				
29	10150001	10250000	831	0.158869	3.591478				
29	10100001	10200000	767	0.161114	3.64193				
29	13650001	13750000	1626	0.180617	4.080222				
29	45050001	45150000	524	0.185451	4.188857				
29	45200001	45300000	345	0.187954	4.245107				
29	48700001	48800000	700	0.192718	4.352168				
29	45150001	45250000	436	0.204939	4.626811				
29	13700001	13800000	1244	0.220832	4.983976				
29	45100001	45200000	481	0.224825	5.073711				
29	45250001	45350000	493	0.241265	5.443168				
29	48600001	48700000	741	0.24618	5.553623				
29	45350001	45450000	997	0.251337	5.669516				
29	48650001	48750000	805	0.289711	6.531897				
29	45300001	45400000	816	0.322908	7.277935				

Table S40. F_{ST} selective sweep regions between high and low groups of cultivated land (CL) or soil bulk density (SBD) (Begait and Arado).

High 1% windows						High 1% merged windows			
Chr	Start	End	nSNPs	F_{ST}	ZF_{ST}	Chr	Start	End	Size (MB)
1	8900001	9000000	435	0.189285	3.591040693	1	8850001	8950000	0.099999
1	21150001	21250000	771	0.190349	3.612114906	1	46100001	46200000	0.099999
1	66700001	66800000	718	0.190398	3.613085429	1	65000001	65200000	0.199999
1	66950001	67050000	577	0.190674	3.618552048	1	66750001	66950000	0.199999
1	127550001	127650000	935	0.193209	3.668761756	1	70000001	70200000	0.199999
1	88600001	88700000	574	0.196831	3.740501229	1	70400001	70650000	0.249999
1	8800001	8900000	668	0.197095	3.745730169	1	143350001	143500000	0.149999
1	133800001	133900000	1283	0.197232	3.748443672	2	400001	550000	0.149999
1	143350001	143450000	1167	0.210746	4.016109944	2	600001	700000	0.099999
1	65100001	65200000	419	0.212471	4.050276314	2	51200001	51300000	0.099999
1	143400001	143500000	1140	0.213026	4.061268972	2	57350001	57450000	0.099999
1	70550001	70650000	1014	0.21491	4.098584589	2	69500001	69600000	0.099999
1	66850001	66950000	407	0.217098	4.141921411	2	69650001	69800000	0.149999
1	46100001	46200000	517	0.223319	4.265138214	2	71550001	71650000	0.099999
1	65000001	65100000	714	0.228314	4.364072136	2	72950001	73100000	0.149999
1	8850001	8950000	597	0.230188	4.401189688	2	73100001	73250000	0.149999
1	65050001	65150000	648	0.233007	4.457024468	2	81050001	81150000	0.099999
1	70500001	70600000	1198	0.237358	4.543202946	2	85900001	86550000	0.649999
1	66800001	66900000	455	0.241378	4.622825442	2	89250001	89450000	0.199999
1	70100001	70200000	673	0.257875	4.949574775	2	102150001	102400000	0.249999
1	66750001	66850000	608	0.285816	5.502990736	2	110350001	110450000	0.099999
1	70400001	70500000	792	0.317398	6.128522496	2	110650001	110750000	0.099999
1	70050001	70150000	774	0.338402	6.544540135	2	114150001	114300000	0.149999
1	70450001	70550000	811	0.346217	6.699328644	2	127900001	128000000	0.099999
1	70000001	70100000	471	0.347882	6.732306619	2	129250001	129350000	0.099999
2	51250001	51350000	1196	0.187963	3.564856379	3	8950001	9100000	0.149999
2	500001	600000	673	0.18808	3.567173751	3	9200001	9350000	0.149999
2	85000001	85100000	1418	0.188439	3.574284317	3	10500001	10600000	0.099999
2	110250001	110350000	799	0.190985	3.624711898	3	48700001	48950000	0.249999
2	71650001	71750000	267	0.192586	3.65642225	3	48950001	49250000	0.299999
2	550001	650000	759	0.193112	3.666840517	3	49800001	49900000	0.099999
2	66350001	66450000	1086	0.194005	3.684527803	3	100550001	100700000	0.149999
2	16900001	17000000	1140	0.194552	3.695362008	4	16000001	16100000	0.099999
2	1150001	1250000	1009	0.195235	3.70888991	4	20500001	20600000	0.099999
2	24150001	24250000	715	0.195539	3.714911113	4	24650001	24750000	0.099999
2	71600001	71700000	307	0.196202	3.728042883	4	31600001	31700000	0.099999
2	129400001	129500000	795	0.196394	3.731845749	4	41300001	41450000	0.149999
2	51150001	51250000	649	0.19868	3.777123616	4	41500001	41600000	0.099999
2	68350001	68450000	765	0.199403	3.791443781	4	41650001	41800000	0.149999
2	71500001	71600000	391	0.201957	3.842029815	4	41800001	42050000	0.249999
2	73350001	73450000	484	0.202142	3.845694034	4	66200001	66350000	0.149999
2	126400001	126500000	271	0.202407	3.850942781	4	92550001	92650000	0.099999
2	66400001	66500000	886	0.203946	3.881425125	4	107900001	108000000	0.099999
2	16950001	17050000	1010	0.205609	3.914363486	4	118800001	118900000	0.099999
2	110400001	110500000	722	0.207074	3.943380142	5	9100001	9250000	0.149999
2	110300001	110400000	893	0.209302	3.987509226	5	9500001	9650000	0.149999
2	73100001	73200000	485	0.21031	4.00747427	5	31500001	31600000	0.099999
2	69500001	69600000	1266	0.216919	4.138376031	5	34650001	34750000	0.099999
2	89250001	89350000	1156	0.21874	4.174443833	5	42950001	43050000	0.099999
2	71550001	71650000	298	0.218849	4.176602752	5	46600001	46750000	0.149999
2	110350001	110450000	849	0.219623	4.191933053	5	47750001	47850000	0.099999
2	57350001	57450000	918	0.219815	4.195735919	5	87500001	87700000	0.199999
2	600001	700000	854	0.220386	4.207045482	5	88900001	89050000	0.149999
2	110650001	110750000	656	0.220551	4.21031357	5	89200001	89450000	0.249999

High 1% windows						High 1% merged windows			
Chr	Start	End	nSNPs	F_{ST}	ZF_{ST}	Chr	Start	End	Size (MB)
2	73000001	73100000	803	0.220733	4.213918369	6	41850001	41950000	0.099999
2	127900001	128000000	763	0.221801	4.235071808	6	63850001	63950000	0.099999
2	114200001	114300000	839	0.222544	4.249788106	6	68450001	68550000	0.099999
2	102150001	102250000	1333	0.226027	4.318774462	7	27500001	27650000	0.149999
2	102300001	102400000	1113	0.226926	4.336580588	7	42650001	42900000	0.249999
2	129250001	129350000	642	0.228324	4.364270202	7	43100001	43500000	0.399999
2	102250001	102350000	1147	0.228743	4.372569164	7	47650001	48000000	0.349999
2	73150001	73250000	727	0.230104	4.399525934	7	48500001	48650000	0.149999
2	69650001	69750000	541	0.231352	4.42424456	7	72650001	72750000	0.099999
2	69700001	69800000	623	0.237284	4.541737258	7	89950001	90050000	0.099999
2	81050001	81150000	874	0.238786	4.571486758	8	23050001	23200000	0.149999
2	114150001	114250000	809	0.241054	4.616408106	8	38300001	38450000	0.149999
2	102200001	102300000	1339	0.242229	4.639680851	8	38800001	38900000	0.099999
2	72950001	73050000	776	0.242423	4.64352333	8	100800001	100900000	0.099999
2	89350001	89450000	842	0.248438	4.762659975	9	9300001	9400000	0.099999
2	51200001	51300000	846	0.251449	4.822297621	9	22750001	22900000	0.149999
2	450001	550000	556	0.26145	5.020383338	9	33700001	33800000	0.099999
2	400001	500000	658	0.262867	5.048449278	9	97400001	97500000	0.099999
2	86450001	86550000	526	0.264444	5.079684272	9	101450001	101600000	0.149999
2	89300001	89400000	1025	0.283664	5.460366952	9	102850001	103250000	0.399999
2	86100001	86200000	374	0.287109	5.528600659	9	103600001	103750000	0.149999
2	86050001	86150000	384	0.2884	5.554170968	9	103750001	103900000	0.149999
2	86400001	86500000	552	0.296019	5.705077385	9	103950001	104150000	0.199999
2	86150001	86250000	254	0.345538	6.685879969	10	55050001	55200000	0.149999
2	85900001	86000000	377	0.356234	6.897731267	10	57350001	57550000	0.199999
2	86200001	86300000	269	0.365438	7.080031132	11	7700001	7850000	0.149999
2	86000001	86100000	292	0.406927	7.901786789	11	46000001	46100000	0.099999
2	86350001	86450000	599	0.40965	7.955720136	11	46150001	46250000	0.099999
2	86250001	86350000	487	0.428663	8.332302853	11	83100001	83300000	0.199999
2	86300001	86400000	761	0.448519	8.725582525	11	83350001	83500000	0.149999
2	85950001	86050000	290	0.490611	9.559281557	11	84050001	84150000	0.099999
3	49750001	49850000	1116	0.188889	3.583197283	12	42950001	43050000	0.099999
3	10550001	10650000	964	0.188931	3.58402916	12	43950001	44050000	0.099999
3	81800001	81900000	823	0.189348	3.592288508	12	44450001	44550000	0.099999
3	20350001	20450000	514	0.195041	3.705047431	13	6600001	6700000	0.099999
3	9050001	9150000	520	0.196855	3.740976587	13	81850001	81950000	0.099999
3	48900001	49000000	710	0.199608	3.795504133	14	27800001	27900000	0.099999
3	56950001	57050000	1144	0.205198	3.906222977	14	36900001	37000000	0.099999
3	49850001	49950000	582	0.2092	3.985488954	14	59800001	59900000	0.099999
3	48950001	49050000	709	0.215708	4.114390249	14	73400001	73500000	0.099999
3	8950001	9050000	632	0.217013	4.14023785	15	17900001	18000000	0.099999
3	49050001	49150000	681	0.218751	4.174661706	15	32100001	32200000	0.099999
3	9250001	9350000	367	0.21935	4.186525854	15	53350001	53450000	0.099999
3	9200001	9300000	606	0.221814	4.235329294	15	69800001	70150000	0.349999
3	10500001	10600000	1038	0.223314	4.265039181	16	12450001	12550000	0.099999
3	49100001	49200000	1007	0.230873	4.414757203	16	19650001	19800000	0.149999
3	49150001	49250000	841	0.232291	4.442842949	16	20300001	20400000	0.099999
3	49000001	49100000	569	0.235427	4.504956418	16	32350001	32450000	0.099999
3	48700001	48800000	809	0.249935	4.792310442	16	44000001	44100000	0.099999
3	48850001	48950000	808	0.250511	4.803719038	17	21650001	21750000	0.099999
3	49800001	49900000	992	0.255575	4.904019616	17	43600001	43700000	0.099999
3	9000001	9100000	586	0.266578	5.121951537	17	52350001	52450000	0.099999
3	100550001	100650000	681	0.270537	5.200365831	17	72200001	72500000	0.299999
3	48800001	48900000	922	0.273138	5.251882775	17	72600001	72800000	0.199999
3	48750001	48850000	941	0.278547	5.359016626	18	3550001	3650000	0.099999
3	100600001	100700000	626	0.316617	6.113053548	18	14600001	14750000	0.149999
4	105150001	105250000	2316	0.191959	3.644003517	18	14800001	14900000	0.099999
4	66150001	66250000	480	0.192126	3.647311218	18	33050001	33150000	0.099999
4	107850001	107950000	898	0.19484	3.701066306	19	15850001	15950000	0.099999

High 1% windows						High 1% merged windows			
Chr	Start	End	nSNPs	F_{ST}	ZF_{ST}	Chr	Start	End	Size (MB)
4	78050001	78150000	920	0.195323	3.71063289	19	29600001	29750000	0.149999
4	105100001	105200000	2253	0.19796	3.76286287	19	41050001	41200000	0.149999
4	41450001	41550000	797	0.201895	3.840801806	19	46550001	46750000	0.199999
4	118750001	118850000	1176	0.203817	3.878870074	19	52700001	52800000	0.099999
4	31550001	31650000	337	0.206137	3.924821366	19	60950001	61050000	0.099999
4	41250001	41350000	1582	0.208348	3.968613739	20	2650001	2750000	0.099999
4	41950001	42050000	719	0.213548	4.071608012	20	7400001	7550000	0.149999
4	41700001	41800000	552	0.215237	4.105061345	20	11700001	12050000	0.349999
4	118800001	118900000	1580	0.216389	4.127878537	20	25200001	25600000	0.399999
4	66200001	66300000	438	0.219358	4.186684306	20	30850001	31150000	0.299999
4	92550001	92650000	428	0.22028	4.204945983	20	49200001	49350000	0.149999
4	66250001	66350000	470	0.222811	4.255076465	20	54050001	54150000	0.099999
4	41500001	41600000	564	0.226453	4.32721207	20	55100001	55300000	0.199999
4	31600001	31700000	552	0.228153	4.360883275	20	67600001	67750000	0.149999
4	41800001	41900000	523	0.228226	4.362329156	20	68900001	69000000	0.099999
4	41350001	41450000	841	0.228466	4.367082738	20	69500001	69600000	0.099999
4	41900001	42000000	821	0.231123	4.41970885	21	4600001	4900000	0.299999
4	41650001	41750000	849	0.233708	4.470908888	21	47300001	47450000	0.149999
4	20500001	20600000	750	0.233817	4.473067807	21	51350001	51500000	0.149999
4	24650001	24750000	1187	0.235062	4.497727013	21	64000001	64200000	0.199999
4	107900001	108000000	1097	0.235877	4.513869384	22	13750001	13900000	0.149999
4	41300001	41400000	1447	0.238684	4.569466486	22	16850001	16950000	0.099999
4	16000001	16100000	707	0.247938	4.752756679	23	900001	1300000	0.399999
4	41850001	41950000	655	0.252841	4.849868396	23	32000001	32100000	0.099999
5	42900001	43000000	629	0.188276	3.571055842	23	51600001	51950000	0.349999
5	87650001	87750000	717	0.194113	3.686666915	23	52100001	52200000	0.099999
5	29150001	29250000	598	0.194548	3.695282782	24	13750001	13950000	0.199999
5	29100001	29200000	686	0.196178	3.727567525	24	13950001	14150000	0.199999
5	32900001	33000000	980	0.197319	3.750166846	25	1250001	1350000	0.099999
5	9450001	9550000	545	0.197673	3.757178379	25	25650001	25850000	0.199999
5	91750001	91850000	1436	0.199312	3.789641382	26	22150001	22350000	0.199999
5	47100001	47200000	965	0.202481	3.852408469	26	39300001	39450000	0.149999
5	57000001	57100000	231	0.203298	3.868590454	26	39450001	39550000	0.099999
5	88850001	88950000	955	0.206049	3.923078386	26	43350001	43500000	0.149999
5	9200001	9300000	490	0.207446	3.950748193	27	8000001	8200000	0.199999
5	46550001	46650000	1244	0.208541	3.972436411	28	13950001	14150000	0.199999
5	31500001	31600000	677	0.210107	4.003453532	28	21100001	21250000	0.149999
5	87600001	87700000	787	0.212632	4.053465175	28	39650001	39800000	0.149999
5	87500001	87600000	978	0.21487	4.097792326	29	18850001	18950000	0.099999
5	88900001	89000000	671	0.217545	4.150774957				
5	47750001	47850000	458	0.217766	4.155152213				
5	9550001	9650000	1188	0.21844	4.168501856				
5	34650001	34750000	261	0.219273	4.185000746				
5	88950001	89050000	719	0.219276	4.185060166				
5	46650001	46750000	1230	0.239802	4.591610254				
5	42950001	43050000	851	0.246862	4.731444787				
5	46600001	46700000	1296	0.252499	4.843094541				
5	9500001	9600000	969	0.254403	4.880806291				
5	87550001	87650000	843	0.269591	5.181628796				
5	89200001	89300000	669	0.314231	6.065795022				
5	9100001	9200000	894	0.340427	6.584648482				
5	89350001	89450000	1095	0.347987	6.734386311				
5	9150001	9250000	733	0.385233	7.472102602				
5	89250001	89350000	839	0.403841	7.840663649				
5	89300001	89400000	963	0.446469	8.684979013				
6	110550001	110650000	1461	0.190945	3.623919634				
6	41800001	41900000	996	0.202194	3.846723977				
6	44900001	45000000	853	0.202956	3.861816599				
6	92950001	93050000	1368	0.207784	3.957442821				

High 1% windows						High 1% merged windows			
Chr	Start	End	nSNPs	F_{ST}	ZF_{ST}	Chr	Start	End	Size (MB)
6	25400001	25500000	959	0.208088	3.963464025				
6	63850001	63950000	1396	0.219876	4.196944121				
6	41850001	41950000	1109	0.254808	4.88882796				
6	68450001	68550000	745	0.261543	5.022225351				
7	48850001	48950000	663	0.189964	3.604489368				
7	27450001	27550000	1355	0.190245	3.61005502				
7	90000001	90100000	1223	0.190579	3.616670422				
7	48900001	49000000	629	0.191884	3.642518023				
7	54550001	54650000	616	0.193651	3.677516269				
7	72700001	72800000	1229	0.204847	3.899270863				
7	82750001	82850000	657	0.207052	3.942944397				
7	42650001	42750000	669	0.212117	4.04326478				
7	43400001	43500000	206	0.214212	4.084759589				
7	43250001	43350000	255	0.216144	4.123025923				
7	47650001	47750000	1205	0.22015	4.202371127				
7	27550001	27650000	1284	0.220501	4.20932324				
7	43100001	43200000	788	0.227244	4.342879084				
7	42800001	42900000	945	0.234421	4.485030988				
7	43300001	43400000	218	0.235454	4.505491196				
7	43200001	43300000	261	0.24516	4.697733969				
7	47800001	47900000	1200	0.246848	4.731167495				
7	89950001	90050000	1007	0.248956	4.772919789				
7	47700001	47800000	1234	0.257698	4.946069008				
7	27500001	27600000	1202	0.258099	4.954011451				
7	43350001	43450000	174	0.260873	5.008954935				
7	48550001	48650000	910	0.264629	5.083348491				
7	47850001	47950000	1072	0.269634	5.18248048				
7	42750001	42850000	980	0.282458	5.436480204				
7	43150001	43250000	392	0.285429	5.495325586				
7	72650001	72750000	1203	0.286027	5.507169927				
7	42700001	42800000	915	0.286245	5.511487764				
7	48500001	48600000	1004	0.29803	5.74490844				
7	47900001	48000000	1052	0.303531	5.853864497				
7	47750001	47850000	1128	0.305901	5.900806118				
8	100850001	100950000	804	0.205159	3.90545052				
8	38850001	38950000	629	0.205519	3.912580892				
8	38800001	38900000	867	0.213635	4.073331186				
8	38300001	38400000	528	0.232553	4.448032276				
8	38350001	38450000	387	0.237718	4.550333319				
8	100800001	100900000	825	0.265989	5.110285455				
8	23050001	23150000	1150	0.29509	5.686677062				
8	23100001	23200000	761	0.360939	6.990921278				
9	62400001	62500000	370	0.189535	3.595992341				
9	101550001	101650000	1352	0.191659	3.63806154				
9	33650001	33750000	657	0.1917	3.63887361				
9	103350001	103450000	1019	0.192488	3.654481204				
9	103200001	103300000	1007	0.192924	3.663116878				
9	9250001	9350000	1391	0.19436	3.691559143				
9	103400001	103500000	828	0.194702	3.698332997				
9	103550001	103650000	843	0.195645	3.717010612				
9	2400001	2500000	968	0.197035	3.744541774				
9	2250001	2350000	1598	0.19743	3.752365377				
9	102450001	102550000	1044	0.197492	3.753593386				
9	102400001	102500000	1323	0.197725	3.758208322				
9	2450001	2550000	1494	0.200724	3.817608288				
9	9500001	9600000	782	0.203874	3.87999905				
9	103900001	104000000	589	0.204509	3.892576235				
9	103850001	103950000	586	0.204569	3.893764631				
9	2350001	2450000	781	0.205474	3.911689596				

High 1% windows						High 1% merged windows			
Chr	Start	End	nSNPs	F_{ST}	ZF_{ST}	Chr	Start	End	Size (MB)
9	2300001	2400000	1198	0.206863	3.939200951				
9	103700001	103800000	874	0.209449	3.990420795				
9	103950001	104050000	581	0.210708	4.015357294				
9	103800001	103900000	663	0.21448	4.090067755				
9	104000001	104100000	467	0.215763	4.115479611				
9	103750001	103850000	717	0.218439	4.168482049				
9	104050001	104150000	317	0.221022	4.219642474				
9	33700001	33800000	837	0.221417	4.227466077				
9	102850001	102950000	1018	0.231637	4.429889438				
9	103150001	103250000	888	0.232881	4.454528838				
9	22800001	22900000	703	0.236042	4.517137472				
9	103600001	103700000	1119	0.236884	4.533814622				
9	22750001	22850000	815	0.237248	4.541024221				
9	103650001	103750000	1182	0.237657	4.549125117				
9	97400001	97500000	1861	0.23974	4.590382246				
9	9300001	9400000	1411	0.253877	4.870388024				
9	101450001	101550000	1206	0.26243	5.039793797				
9	101500001	101600000	966	0.2649	5.088716077				
9	102900001	103000000	1142	0.293515	5.655481681				
9	103100001	103200000	925	0.305373	5.890348238				
9	102950001	103050000	1004	0.311004	6.001879153				
9	103000001	103100000	634	0.316619	6.113093162				
9	103050001	103150000	732	0.332877	6.435108719				
10	54000001	54100000	752	0.188253	3.570600291				
10	86050001	86150000	678	0.189818	3.601597606				
10	94900001	95000000	1199	0.190679	3.618651081				
10	101950001	102050000	782	0.191043	3.62586068				
10	57500001	57600000	757	0.195952	3.723091236				
10	86000001	86100000	539	0.200649	3.816122794				
10	51800001	51900000	839	0.205452	3.911253851				
10	55150001	55250000	610	0.207269	3.947242427				
10	55050001	55150000	471	0.25565	4.90550511				
10	55100001	55200000	552	0.255864	4.90974372				
10	57350001	57450000	813	0.286588	5.518281425				
10	57450001	57550000	791	0.300243	5.788740426				
10	57400001	57500000	773	0.366864	7.10827533				
11	69750001	69850000	1085	0.188874	3.582900184				
11	83250001	83350000	1326	0.191796	3.640775043				
11	7650001	7750000	866	0.207685	3.955481969				
11	83300001	83400000	1083	0.208863	3.978814133				
11	46150001	46250000	1053	0.210307	4.007414851				
11	46000001	46100000	844	0.213158	4.063883442				
11	84050001	84150000	1189	0.221586	4.230813391				
11	83100001	83200000	1480	0.240622	4.607851659				
11	83400001	83500000	957	0.269727	5.184322493				
11	83200001	83300000	1448	0.272724	5.243682846				
11	7750001	7850000	385	0.306697	5.916572165				
11	83350001	83450000	814	0.314784	6.076748067				
11	83150001	83250000	1491	0.326205	6.302959144				
11	7700001	7800000	761	0.329141	6.361111295				
12	28900001	29000000	837	0.188054	3.566658779				
12	44000001	44100000	1643	0.196049	3.725012475				
12	44500001	44600000	918	0.200152	3.806278918				
12	23850001	23950000	973	0.200173	3.806694856				
12	43000001	43100000	770	0.206069	3.923474518				
12	43950001	44050000	1490	0.230781	4.412934996				
12	42950001	43050000	1320	0.233403	4.464867878				
12	44450001	44550000	760	0.249564	4.784962197				
13	45450001	45550000	1326	0.190093	3.607044418				

High 1% windows						High 1% merged windows			
Chr	Start	End	nSNPs	F_{ST}	ZF_{ST}	Chr	Start	End	Size (MB)
13	77450001	77550000	691	0.196511	3.73416312				
13	77500001	77600000	766	0.198259	3.768785041				
13	81800001	81900000	1019	0.208068	3.963067893				
13	6600001	6700000	933	0.216658	4.13320651				
13	81850001	81950000	1127	0.255755	4.907584802				
14	36850001	36950000	836	0.194914	3.702531994				
14	27750001	27850000	1156	0.205568	3.913551415				
14	73400001	73500000	963	0.211707	4.035144078				
14	59800001	59900000	742	0.216069	4.121540428				
14	36900001	37000000	734	0.240092	4.597354166				
14	27800001	27900000	1030	0.257023	4.932699559				
15	59050001	59150000	534	0.192288	3.650519886				
15	53400001	53500000	626	0.193294	3.670445316				
15	1500001	1600000	609	0.198673	3.77698497				
15	69300001	69400000	1408	0.199826	3.799821969				
15	17950001	18050000	1061	0.202017	3.84321821				
15	12400001	12500000	1354	0.208702	3.975625272				
15	70050001	70150000	1057	0.212922	4.059209086				
15	53350001	53450000	805	0.21349	4.07045923				
15	32100001	32200000	1226	0.224217	4.282924532				
15	69800001	69900000	961	0.234585	4.488279269				
15	69900001	70000000	1167	0.2695	5.179826396				
15	69950001	70050000	951	0.271411	5.217676792				
15	70000001	70100000	1020	0.27358	5.260637288				
15	17900001	18000000	884	0.289758	5.581068319				
15	69850001	69950000	1069	0.304828	5.879553646				
16	43950001	44050000	433	0.189117	3.587713185				
16	19750001	19850000	919	0.201559	3.834146792				
16	19600001	19700000	639	0.206204	3.926148407				
16	12400001	12500000	728	0.20813	3.964295902				
16	12450001	12550000	740	0.21024	4.006087809				
16	44000001	44100000	562	0.211853	4.03803584				
16	32350001	32450000	778	0.220936	4.217939107				
16	20300001	20400000	1190	0.23555	4.507392629				
16	19700001	19800000	782	0.259944	4.990554612				
16	19650001	19750000	802	0.308659	5.955432697				
17	43650001	43750000	913	0.199941	3.802099727				
17	72450001	72550000	663	0.201103	3.825114986				
17	41950001	42050000	1476	0.206166	3.925395757				
17	42250001	42350000	696	0.207113	3.944152599				
17	72150001	72250000	841	0.208879	3.979131038				
17	52350001	52450000	475	0.212294	4.046770547				
17	72600001	72700000	761	0.2179	4.157806297				
17	21650001	21750000	1781	0.224109	4.280785421				
17	72700001	72800000	822	0.230779	4.412895383				
17	72200001	72300000	871	0.242146	4.638036904				
17	43600001	43700000	738	0.250391	4.801342247				
17	72650001	72750000	807	0.299768	5.779332295				
17	72250001	72350000	601	0.319127	6.162768092				
17	72400001	72500000	581	0.32002	6.180455378				
17	72300001	72400000	579	0.452095	8.796410895				
17	72350001	72450000	605	0.463169	9.015749085				
18	33000001	33100000	1064	0.188664	3.5787408				
18	14150001	14250000	659	0.19093	3.623622535				
18	14850001	14950000	824	0.198393	3.771439124				
18	14600001	14700000	497	0.215751	4.115241932				
18	33050001	33150000	999	0.230522	4.407805089				
18	3550001	3650000	726	0.235687	4.510106132				
18	14650001	14750000	492	0.242197	4.63904704				

High 1% windows						High 1% merged windows			
Chr	Start	End	nSNPs	F_{ST}	ZF_{ST}	Chr	Start	End	Size (MB)
18	14800001	14900000	766	0.248179	4.757530068				
19	21250001	21350000	554	0.207115	3.944192212				
19	29600001	29700000	1103	0.210622	4.013653927				
19	46550001	46650000	1189	0.210747	4.016129751				
19	29650001	29750000	791	0.212603	4.052890784				
19	41050001	41150000	974	0.215365	4.107596588				
19	15850001	15950000	959	0.216376	4.127621052				
19	46600001	46700000	1078	0.218816	4.175949134				
19	46650001	46750000	949	0.223636	4.271416903				
19	52700001	52800000	383	0.223983	4.27828979				
19	41100001	41200000	1065	0.226567	4.329470021				
19	60950001	61050000	776	0.237122	4.53852859				
20	55250001	55350000	1474	0.189223	3.589812684				
20	25150001	25250000	485	0.191072	3.626435071				
20	69450001	69550000	1442	0.191674	3.638358639				
20	6850001	6950000	1368	0.192986	3.664344886				
20	3150001	3250000	802	0.197187	3.747552376				
20	3100001	3200000	822	0.198971	3.782887334				
20	2600001	2700000	1406	0.200428	3.811745537				
20	30800001	30900000	500	0.201671	3.83636513				
20	55300001	55400000	1158	0.201953	3.841950589				
20	11600001	11700000	829	0.20834	3.968455286				
20	69500001	69600000	1232	0.22159	4.230892618				
20	7450001	7550000	1056	0.225693	4.312159061				
20	31050001	31150000	494	0.227471	4.34737518				
20	68900001	69000000	1504	0.227676	4.351435531				
20	7400001	7500000	927	0.228923	4.37613435				
20	55200001	55300000	1271	0.229025	4.378154622				
20	25350001	25450000	804	0.229236	4.382333813				
20	2650001	2750000	1046	0.233574	4.468254805				
20	11700001	11800000	886	0.234445	4.485506346				
20	25300001	25400000	1012	0.239505	4.585727697				
20	11950001	12050000	894	0.240719	4.609772898				
20	54050001	54150000	596	0.245325	4.701002057				
20	55150001	55250000	1177	0.252628	4.845649592				
20	25400001	25500000	568	0.252671	4.846501275				
20	55100001	55200000	1486	0.253308	4.859118074				
20	67650001	67750000	872	0.257037	4.932976852				
20	25250001	25350000	743	0.263199	5.055025066				
20	11850001	11950000	795	0.269409	5.178023997				
20	25500001	25600000	570	0.270974	5.209021312				
20	67600001	67700000	1239	0.277016	5.328692735				
20	11800001	11900000	911	0.293779	5.660710621				
20	30850001	30950000	300	0.29915	5.767091822				
20	25200001	25300000	403	0.305345	5.889793654				
20	11900001	12000000	795	0.309277	5.96767317				
20	49200001	49300000	1184	0.310429	5.990490363				
20	30900001	31000000	631	0.323716	6.253660538				
20	25450001	25550000	564	0.324444	6.268079737				
20	11750001	11850000	912	0.326702	6.312803019				
20	49250001	49350000	1078	0.331238	6.402645717				
20	31000001	31100000	505	0.333087	6.439268103				
20	30950001	31050000	707	0.349071	6.755856655				
21	51450001	51550000	1119	0.192099	3.64677644				
21	36000001	36100000	925	0.193822	3.680903197				
21	14100001	14200000	731	0.199999	3.80324851				
21	14150001	14250000	590	0.200433	3.81184457				
21	47400001	47500000	817	0.202362	3.850051484				
21	51350001	51450000	1045	0.217512	4.150121339				

High 1% windows						High 1% merged windows			
Chr	Start	End	nSNPs	F_{ST}	ZF_{ST}	Chr	Start	End	Size (MB)
21	4800001	4900000	1604	0.225745	4.313189004				
21	64000001	64100000	1136	0.227451	4.346979048				
21	51400001	51500000	1035	0.228182	4.361457666				
21	4600001	4700000	1434	0.244936	4.693297293				
21	64100001	64200000	813	0.256324	4.918854752				
21	47350001	47450000	883	0.273327	5.25562622				
21	47300001	47400000	606	0.291341	5.612422152				
21	4750001	4850000	1305	0.292797	5.641260549				
21	64050001	64150000	970	0.30016	5.787096479				
21	4700001	4800000	1678	0.356988	6.912665437				
21	4650001	4750000	1486	0.363144	7.034594812				
22	34400001	34500000	861	0.188109	3.567748142				
22	9850001	9950000	798	0.189364	3.592605413				
22	11900001	12000000	1043	0.193922	3.682883856				
22	34450001	34550000	575	0.202199	3.84682301				
22	33450001	33550000	764	0.202832	3.859360582				
22	33500001	33600000	961	0.207634	3.954471833				
22	13700001	13800000	778	0.209623	3.993867142				
22	13800001	13900000	794	0.210243	4.006147229				
22	16850001	16950000	547	0.217633	4.152517937				
22	13750001	13850000	541	0.287293	5.532245071				
23	1600001	1700000	1273	0.188868	3.582781344				
23	1350001	1450000	1115	0.192792	3.660502408				
23	45150001	45250000	1033	0.19289	3.662443454				
23	52150001	52250000	570	0.194479	3.693916127				
23	51250001	51350000	536	0.198513	3.773815915				
23	45100001	45200000	939	0.201336	3.829729922				
23	31950001	32050000	416	0.201912	3.841138518				
23	12350001	12450000	388	0.207184	3.945558867				
23	32000001	32100000	444	0.217106	4.142079863				
23	52100001	52200000	504	0.219801	4.195458626				
23	1200001	1300000	923	0.231064	4.418540262				
23	51600001	51700000	956	0.242332	4.64172093				
23	900001	1000000	775	0.258531	4.962567899				
23	51850001	51950000	1124	0.262779	5.046706298				
23	51650001	51750000	984	0.265574	5.10206572				
23	1100001	1200000	1191	0.278354	5.355193954				
23	1050001	1150000	1218	0.281395	5.415425797				
23	1150001	1250000	1076	0.285002	5.486868171				
23	51700001	51800000	731	0.30353	5.853844691				
23	1000001	1100000	1161	0.313218	6.045730945				
23	950001	1050000	965	0.313331	6.04796909				
23	51800001	51900000	1128	0.358493	6.942474356				
23	51750001	51850000	937	0.380206	7.372534869				
24	47450001	47550000	482	0.196393	3.731825942				
24	13700001	13800000	1335	0.203677	3.876097152				
24	14050001	14150000	1432	0.216932	4.138633516				
24	13950001	14050000	947	0.22192	4.237428793				
24	14000001	14100000	1362	0.257745	4.946999918				
24	13850001	13950000	963	0.274172	5.27236279				
24	13800001	13900000	1297	0.335865	6.494290813				
24	13750001	13850000	1064	0.356391	6.900840902				
25	1300001	1400000	694	0.194621	3.696728663				
25	1200001	1300000	656	0.198583	3.775202377				
25	1250001	1350000	693	0.214477	4.090008335				
25	25650001	25750000	716	0.223325	4.265257053				
25	25700001	25800000	777	0.23666	4.529377945				
25	25750001	25850000	696	0.242454	4.644137334				
26	50450001	50550000	705	0.188293	3.571392554				

High 1% windows						High 1% merged windows			
Chr	Start	End	nSNPs	F_{ST}	ZF_{ST}	Chr	Start	End	Size (MB)
26	39250001	39350000	610	0.189421	3.593734389				
26	15350001	15450000	853	0.191169	3.62835631				
26	50500001	50600000	915	0.196051	3.725052088				
26	39400001	39500000	575	0.196604	3.736005133				
26	22300001	22400000	389	0.204798	3.89830034				
26	22100001	22200000	548	0.205621	3.914601165				
26	43300001	43400000	1426	0.207148	3.944845829				
26	39450001	39550000	465	0.212509	4.051028964				
26	39350001	39450000	708	0.23634	4.523039836				
26	22150001	22250000	503	0.243315	4.661190809				
26	22250001	22350000	553	0.245812	4.710647867				
26	22200001	22300000	485	0.252054	4.834280608				
26	43400001	43500000	1192	0.258127	4.954566036				
26	43350001	43450000	1323	0.268262	5.155305837				
26	39300001	39400000	770	0.269692	5.183629262				
27	8100001	8200000	469	0.215422	4.108725564				
27	8000001	8100000	677	0.259074	4.973322878				
27	8050001	8150000	687	0.278044	5.349053911				
28	200001	300000	1020	0.190957	3.624157313				
28	23000001	23100000	1499	0.19314	3.667395101				
28	13900001	14000000	839	0.209556	3.992540101				
28	21150001	21250000	1468	0.211607	4.033163419				
28	39650001	39750000	688	0.214102	4.082580864				
28	14050001	14150000	903	0.226526	4.328657951				
28	21100001	21200000	1442	0.237013	4.536369672				
28	39700001	39800000	773	0.247971	4.753410297				
28	14000001	14100000	953	0.260042	4.992495658				
28	13950001	14050000	937	0.28106	5.408790589				
29	18900001	19000000	1821	0.193057	3.665751154				
29	18850001	18950000	1385	0.277446	5.337209569				

Table S41. Overlap of *Hp* and F_{ST} detected regions and corresponding protein codding genes in the groups SBD (high group, Begait and Low group, Arado) for Soil bulk density (SB).

Chr	Start	End	Direction	nSNPs	Min. F_{ST}	Min. ZF_{ST}	Max. *F*ST	Max. ZF_{ST}	Overlapping protein codding genes
2	400001	550000	high	658	0.263	5.048	0.263	5.048	*ENSBTAG00000040536,*
2	85900001	86550000	low	377-526	0.264	5.080	0.356	6.898	*ENSBTAG00000012171, SF3B1, COQ10B, HSPD1, HSPE1, MOB4, RFTN2, MARS2, BOLL*
2	126400001	126500000	low	271	0.202	3.851	0.202	3.851	*ARID1A*
3	100550001	100700000	high	626-681	0.271	5.200	0.317	6.113	*PRDX1, MMACHC, ENSBTAG00000017029*
4	31550001	31700000	low	337-552	0.206	3.925	0.228	4.361	*ENSBTAG00000033806*
4	66150001	66350000	low	470-480	0.192	3.647	0.223	4.255	*MTURN, PLEKHA8, FKBP14*
5	9100001	9300000	low	490-894	0.207	3.951	0.340	6.585	*PAWR, ENSBTAG00000048833*
6	68450001	68550000	low	745	0.262	5.022	0.262	5.022	*RASL11B*
8	23050001	23200000	high	761-1150	0.295	5.687	0.361	6.991	*ENSBTAG00000051881 (LOC783912) interferon alpha-H, ENSBTAG00000053037 (LOC523509) interferon omega-1, ENSBTAG00000053413, IFNB3 (LOC100848709) (ENSBTAG00000055306), IFNB3 (LOC112447877) (ENSBTAG00000049948) interferon beta-3, IFNB3 (LOC112447878) (ENSBTAG00000055103) interferon beta-3*
9	33650001	33800000	low	657-837	0.192	3.639	0.221	4.227	*RFX6*
10	55050001	55250000	low	471-610	0.207	3.947	0.256	4.906	*RSL24D1*
11	46150001	46250000	low	1053	0.210	4.007	0.210	4.007	*TTL*
15	1500001	1600000	low	609	0.199	3.777	0.199	3.777	*ANKRD49, AASDHPPT*
15	53350001	53500000	low	626-805	0.193	3.670	0.213	4.070	*DNAJB13, UCP2, UCP3*
17	43600001	43750000	low	738-913	0.200	3.802	0.250	4.801	*GUCY1A1*
17	72150001	72550000	high	841	0.209	3.979	0.209	3.979	*ENSBTAG00000047538, HIC2, ENSBTAG00000030927, PI4KA, SERPIND1, SNAP29, CRKL, AIFM3, LZTR1, THAP7, TUBA3E, LRRC74B, P2RX6, SLC7A4, TUBA3C, MZT2B, SMPD4, ENSBTAG00000031018, MED15, KLHL22*
20	3100001	3250000	high	802-822	0.197	3.748	0.199	3.783	*NPM1*
20	11700001	12050000	high	886-894	0.234	4.486	0.241	4.610	*ENSBTAG00000034170*
20	25150001	25600000	high	485-570	0.191	3.626	0.271	5.209	*NDUFS4*
20	67600001	67750000	high	872-1239	0.257	4.933	0.277	5.329	*ICE1*
21	47300001	47500000	high	606-817	0.202	3.850	0.291	5.612	*MIPOL1*
22	13700001	13900000	low	778-794	0.210	3.994	0.210	4.006	*CTNNB1*
26	22100001	22400000	high	389-548	0.205	3.898	0.206	3.915	*BTRC, POLL, DPCD, ENSBTAG00000053939*
26	50500001	50600000	high	915	0.196	3.725	0.196	3.725	ENSBTAG00000049317

Table S42. Bio4-overlapping selective sweep regions to F_{ST} and both (high and low), low (Abergelle) or high groups (Begait) with their F_{ST} and ZF_{ST} values and the corresponding overlapping genes.

Chr	Start	End	Direction	nSNPs	Min. F_{ST}	Min. ZF_{ST}	Max. F_{ST}	Max. ZF_{ST}	Overlapping protein codding genes
2	350001	700000	high	521-683	0.253	4.862	0.319	6.184	*ENSBTAG00000040536*
2	73100001	73300000	high	486-695	0.207	3.946	0.237	4.549	no
3	100550001	100750000	high	564-672	0.209	3.982	0.285	5.509	*PRDX1, MMACHC, ENSBTAG00000017029, TESK2*
5	28700001	28850000	high	948	0.194	3.688	0.194	3.688	*SLC11A2, ENSBTAG00000049198*
5	48250001	48800000	low	399-598	0.252	4.847	0.268	5.169	*MSRB3, LEMD3, WIF1*
5	57950001	58100000	low	702-1481	0.211	4.03	0.51	9.965	*OR6C202*
6	37350001	37450000	low	319	0.198	3.765	0.198	3.765	no
6	73300001	73400000	high	913	0.225	4.307	0.225	4.307	no
6	75800001	75950000	high	631	0.215	4.113	0.215	4.113	no
7	64150001	64250000	high	923	0.224	4.292	0.224	4.292	no
8	49800001	49900000	high	736	0.197	3.756	0.197	3.756	no
11	7750001	7900000	both	164-313	0.203	3.862	0.413	8.052	no
11	41150001	41250000	low	516	0.199	3.79	0.199	3.79	no
11	101450001	101800000	high	653-817	0.219	4.189	0.225	4.314	*FAM78A, PLPP7, PRRC2B, POMT1, UCK1, PRRT1B*
12	29500001	29750000	low	407-591	0.191	3.626	0.224	4.285	*ENSBTAG00000053332*
17	62950001	63150000	high	391-734	0.23	4.415	0.266	5.119	*UNC119B, ACADS, SPPL3*
17	72350001	72500000	high	591-602	0.207	3.955	0.303	5.854	*LRRC74B, P2RX6, SLC7A4, TUBA3C, MZT2B, SMPD4, ENSBTAG00000031018, MED15*
18	35500001	35650000	high	210-221	0.192	3.651	0.206	3.935	*NFATC3, PLA2G15, SLC7A6 (overlapped in two regions)*
18	35650001	35750000	high	308	0.226	4.336	0.226	4.336	*SLC7A6OS, PRMT7, SLC7A6 (overlapped in two regions*
18	38400001	38750000	high	266-410	0.213	4.062	0.219	4.184	no
19	26600001	26700000	high	407	0.195	3.715	0.195	3.715	*ZMYND15, CXCL16, MED11, PELP1, ARRB2*
19	46550001	46800000	high	1125-1156	0.2	3.813	0.214	4.096	no
20	25150001	25300000	high	384-450	0.216	4.124	0.239	4.591	no
20	30650001	31200000	low	403-969	0.208	3.979	0.227	4.348	*ENSBTAG00000033187*
20	67600001	67850000	high	1221-1314	0.198	3.766	0.231	4.426	*ICE1, ADAMTS16*
21	10500001	10700000	Low	342-612	0.204	3.882	0.216	4.128	*NR2F2,*
22	51200001	51350000	high	443-455	0.199	3.791	0.313	6.059	*NCKIPSD, CELSR3, SLC26A6, TMEM89, UQCRC1, UCN2*
23	1050001	1250000	low	1144-1205	0.191	3.639	0.223	4.278	no
23	47600001	47750000	low	911-882	0.2	3.807	0.209	3.995	*ENSBTAG00000054759*
25	1100001	1450000	low	791-859	0.203	3.872	0.267	5.14	*UNKL, C25H16orf91, CCDC154, CLCN7, PTX4, TELO2, IFT140, TMEM204, CRAMP1, JPT2, MAPK8IP3, ENSBTAG00000052060, NME3, MRPS34, EME2, SPSB3, NUBP2, IGFALS, HAGH, FAHD1, MEIOB*

Table S43. Bio12-overlapping selective sweep regions to F_{ST} and both, low (Arado) or high (Raya) groups with their F_{ST} and ZF_{ST} values.

Chr	Start	End	Direction	nSNPs	Min. F_{ST}	Min. ZF_{ST}	Max. F_{ST}	Max. ZF_{ST}	Overlapping protein codding genes
1	16450001	16600000	low	1426-1471	0.157	3.719	0.171	4.04	no
1	33350001	33450000	high	1091	0.165	3.893	0.165	3.893	no
1	83500001	83600000	high	525	0.148	3.503	0.148	3.503	*KLHL6*
2	16850001	17250000	high	804-1054	0.169	4.003	0.177	4.182	no
2	89150001	89650000	low	330-1394	0.178	4.203	0.206	4.859	no
4	48100001	48250000	low	341-571	0.162	3.828	0.194	4.578	no
5	34250001	34600000	low	413-509	0.15	3.55	0.184	4.347	*ARID2*
5	91900001	92050000	high	971-1092	0.149	3.54	0.152	3.592	*RERGL*
5	95250001	95550000	high	496-670	0.181	4.263	0.229	5.382	*PLBD1, ENSBTAG00000054625, ATF7IP*
6	6250001	6450000	low	792-907	0.171	4.05	0.184	4.335	no
6	68400001	68600000	low	535-1097	0.183	4.323	0.225	5.286	*RASL11B*
6	86300001	86400000	high	656	0.154	3.637	0.154	3.637	*DCK*
6	86700001	86950000	low	831-985	0.162	3.831	0.163	3.848	no
7	21250001	21450000	both	404-500	0.153	3.621	0.188	4.448	*LINGO3, PEAK3, OAZ1, DOT1L, PLEKHJ1, SF3A2, AMH, JSRP1, AP3D1*
7	48500001	48650000	low	906-1010	0.198	4.663	0.236	5.554	no
7	60850001	60950000	high	278	0.158	3.732	0.158	3.732	*CSNK1A1*
7	63550001	63650000	low	1054	0.159	3.766	0.159	3.766	no
7	75900001	76000000	high	770	0.149	3.542	0.149	3.542	no
7	110300001	110500000	low	1020-1235	0.153	3.628	0.169	3.994	no
8	21850001	22100000	high	451-559	0.192	4.521	0.197	4.653	*CDKN2B*
8	30450001	30700000	high	683-746	0.151	3.589	0.17	4.019	no
8	59650001	59800000	both	282-294	0.164	3.876	0.169	3.985	*RUSC2, FAM166B*
9	11650001	11850000	high	1187-1223	0.181	4.281	0.208	4.892	no
9	68050001	68200000	high	564-870	0.158	3.749	0.194	4.565	no
10	55000001	55200000	low	596-675	0.16	3.793	0.186	4.399	*RAB27A, RSL24D1*
11	16250001	16350000	low	841	0.149	3.541	0.149	3.541	no
11	45950001	46400000	low	500-535	0.193	4.547	0.314	7.361	*TTL, POLR1B, CHCHD5, SLC20A1*
11	94950001	95300000	low	435-971	0.171	4.032	0.186	4.386	*LHX2*
11	95300001	95450000	low	589-880	0.151	3.568	0.16	3.777	*NEK6*
12	29100001	29300000	high	224-539	0.17	4.011	0.184	4.338	*RXFP2*
12	29350001	29450000	high	271	0.154	3.654	0.154	3.654	no
13	17900001	18000000	low	722	0.161	3.802	0.161	3.802	*PDSS1, ENSBTAG00000048553*
15	1500001	1700000	low	555-663	0.173	4.096	0.183	4.325	*ANKRD49, AASDHPPT, KBTBD3*
16	10250001	10400000	high	951-1096	0.152	3.602	0.165	3.907	no
16	19600001	19750000	high	747-892	0.152	3.61	0.169	4.004	no

Chr	Start	End	Direction	nSNPs	Min. F_{ST}	Min. ZF_{ST}	Max. F_{ST}	Max. ZF_{ST}	Overlapping protein codding genes
16	36250001	36350000	low	650	0.176	4.156	0.176	4.156	*DPT*
18	12850001	13050000	high	523-619	0.157	3.713	0.174	4.119	*FBXO31, MAP1LC3B, ZCCHC14*
18	36600001	36900000	low	661-546	0.158	3.731	0.162	3.843	*ENSBTAG00000052086, NFAT5, NQO1, NOB1*
19	46700001	46850000	high	964-1074	0.173	4.095	0.2	4.72	no
20	40900001	41000000	low	769	0.155	3.665	0.155	3.665	NPR3
20	49250001	49350000	low	1179	0.151	3.585	0.151	3.585	no
21	7750001	8050000	high	530-536	0.154	3.656	0.198	4.67	no
21	36700001	36850000	high	516-549	0.199	4.688	0.229	5.383	no
21	36850001	37000000	high	342-498	0.169	4.007	0.173	4.099	no
21	55000001	55150000	low	756-757	0.155	3.679	0.171	4.036	*TGM7, LCMT2, ADAL, ZSCAN29*
22	13750001	13850000	low	542	0.195	4.606	0.195	4.606	*CTNNB1*
23	29850001	30000000	high	1896-1699	0.174	4.1	0.234	5.516	*OR2J1, OR2W1D, OR2W1, OR2AD1, OR2AD1B*
24	52900001	53000000	high	1056	0.15	3.551	0.15	3.551	no
24	54000001	54150000	high	1276-1325	0.153	3.631	0.158	3.741	no
27	21300001	21500000	high	627-842	0.148	3.505	0.167	3.943	no
27	23450001	23700000	low	611-714	0.2	4.705	0.205	4.822	no
27	23900001	24200000	low	680-1355	0.17	4.018	0.176	4.156	*TRMT9B*
29	39800001	39900000	high	475	0.164	3.879	0.164	3.879	*DDB1, TKFC, CYB561A3, TMEM138, ENSBTAG00000053752, TMEM216*

Table S44. Bio16-overlapping selective sweep regions to F_{ST} and both, low (Raya) or high (Begait) groups with their F_{ST} and ZF_{ST} values.

Chr	Start	End	Direction	nSNPs	Min. F_{ST}	Min ZF_{ST}	Max. F_{ST}	Max. ZF_{ST}	Overlapping protein codding genes
1	50050001	50200000	High	498-522	0.347	6.380	0.364	6.685	no
2	350001	550000	High	548	0.226	4.079	0.294	5.366	*ENSBTAG00000040536*
2	550001	750000	High	700-1014	0.206	3.712	0.240	4.353	no
2	105600001	105750000	Low	480-689	0.213	3.840	0.215	3.873	no
2	110200001	110800000	High	598-722	0.216	3.896	0.322	5.891	*ENSBTAG00000051776, PAX3, ENSBTAG00000053079, ENSBTAG00000051776, SGPP2*
2	126400001	126550000	Low	373	0.204	3.663	0.204	3.663	*ARID1A*
3	100600001	100700000	High	629	0.226	4.090	0.226	4.090	no
4	12550001	12700000	Low	806-906	0.200	3.587	0.238	4.306	PON3
5	46600001	46750000	High	881-1093	0.252	4.578	0.249	4.523	no
5	47350001	47700000	High	520-950	0.207	3.718	0.211	3.802	*HELB, ENSBTAG00000053419, IRAK3, ENSBTAG00000052954, TMBIM4, LLPH*

Chr	Start	End	Direction	nSNPs	Min. F_{ST}	Min ZF_{ST}	Max. F_{ST}	Max. ZF_{ST}	Overlapping protein codding genes
5	47700001	47950000	High	400-496	0.281	5.135	0.356	6.535	*HMGA2*
5	91900001	92050000	Low	851-1030	0.217	3.906	0.239	4.329	*RERGL*
5	95250001	95550000	Low	452-656	0.214	3.865	0.373	6.864	*PLBD1, ENSBTAG00000054625, ATF7IP*
6	15850001	15950000	High	535	0.203	3.640	0.203	3.640	*ENSBTAG00000049691*
6	39700001	39850000	Low	499-895	0.209	3.763	0.278	5.066	no
6	73300001	73400000	High	913	0.242	4.388	0.242	4.388	no
7	54550001	54650000	High	582	0.234	4.226	0.234	4.226	no
7	57400001	57550000	Low	298-317	0.203	3.640	0.205	3.693	*RBM27, POU4F3*
7	60550001	60650000	Low	573	0.246	4.457	0.246	4.457	*ENSBTAG00000048563*
7	60650001	60850000	Low	383-466	0.208	3.745	0.217	3.906	*AFAP1L1, ENSBTAG00000052766, GRPEL2, PCYOX1L, IL17B*
7	96450001	96600000	Low	354-475	0.205	3.692	0.226	4.086	*ENSBTAG00000003118, LIX1*
8	54750001	54900000	Low	877-903	0.206	3.704	0.260	4.730	no
8	59650001	59750000	both	227	0.215	3.871	0.215	3.871	*ENSBTAG00000011402*
8	83950001	84050000	High	811	0.201	3.616	0.201	3.616	*OGN, OMD*
9	11550001	11700000	Low	1326-1494	0.201	3.616	0.276	5.033	no
9	11750001	11900000	Low	1007-1264	0.236	4.266	0.237	4.287	no
9	39900001	40050000	High	564-747	0.215	3.872	0.249	4.521	*CDC40*
12	28800001	29500000	Low	278-603	0.228	4.125	0.273	4.968	*RXFP2*
12	48000001	48100000	Low	1311	0.211	3.794	0.211	3.794	no
13	47200001	47500000	Low	434-542	0.264	4.800	0.308	5.642	*SLC23A2, TMEM230, PCNA, CDS2*
13	47900001	48050000	Low	692-894	0.217	3.915	0.227	4.107	*SHLD1*
13	63600001	63700000	Low	345	0.237	4.292	0.237	4.292	*ASIP*
15	59750001	59850000	High	953	0.222	4.012	0.222	4.012	no
16	37550001	37700000	Low	365-422	0.212	3.819	0.220	3.977	*KIFAP3*
17	42250001	42350000	High	966	0.239	4.332	0.239	4.332	no
17	60450001	60600000	Low	639-632	0.242	4.393	0.287	5.236	no
18	3550001	3700000	high	803-946	0.230	4.161	0.292	5.325	no
19	46400001	46500000	low	976	0.211	3.801	0.211	3.801	*ENSBTAG00000051312*
19	46500001	46900000	both	661-841	0.286	5.224	0.322	5.905	*EFCAB3, METTL2A*
20	4500001	4600000	low	776	0.268	4.883	0.268	4.883	*DUSP1*
20	11750001	12050000	high	923-973	0.207	3.728	0.237	4.300	*ENSBTAG00000034170*
21	57900001	58100000	both	390-724	0.278	5.073	0.344	6.324	*ENSBTAG00000053789*
25	26650001	26750000	low	608	0.227	4.106	0.227	4.106	*ITGAL, ENSBTAG00000048731, ENSBTAG00000052789, ENSBTAG00000043974, ENSBTAG00000051451, ZNF688*
27	8000001	8300000	low	471-644	0.272	4.952	0.286	5.226	no
27	21450001	21600000	low	849-1139	0.316	5.779	0.323	5.925	no
28	41200001	41300000	low	566	0.214	3.854	0.214	3.854	no

Chr	Start	End	Direction	nSNPs	Min. F_{ST}	Min ZF_{ST}	Max. F_{ST}	Max. ZF_{ST}	Overlapping protein codding genes
29	18800001	19000000	low	1544	0.209	3.761	0.209	3.761	no
29	39800001	39950000	low	420-449	0.241	4.375	0.255	4.640	*DDB1, TKFC, CYB561A3, TMEM138, ENSBTAG00000053752, TMEM216, CPSF7, SDHAF2*
29	48650001	48750000	low	791	0.232	4.200	0.232	4.200	*PHLDA2, SLC22A18, CDKN1C*

Table S45. Bio18-overlapping selective sweep regions to F_{ST} and both, low (Abergelle) or high (Raya) groups with their F_{ST} and ZF_{ST} values.

Chr	Start	End	Direction	nSNPs	Min. F_{ST}	Min. ZF_{ST}	Max. F_{ST}	Max. ZF_{ST}	Overlapping protein codding regions
1	129350001	129500000	Low	1240-1250	0.196	4.423	0.199	4.489	no
2	126400001	126500000	High	295	0.158	3.562	0.158	3.562	ARID1A
2	133450001	133600000	Low	755-901	0.167	3.775	0.210	4.742	*UBR4*
3	29200001	29300000	Low	976	0.173	3.918	0.173	3.918	*SYT6*
3	59700001	59800000	High	289	0.161	3.631	0.161	3.631	*ENSBTAG00000053100, SAMD13*
3	65700001	65900000	Low	1051-1074	0.246	5.545	0.260	5.860	*ADGRL4*
3	85850001	85950000	Low	735	0.165	3.733	0.165	3.733	no
4	40550001	40750000	Low	1080-1166	0.163	3.682	0.192	4.331	*GNAT3*
4	88300001	88400000	Low	744	0.165	3.740	0.165	3.740	*ENSBTAG00000031958*
5	47700001	47950000	Low	445-539	0.228	5.137	0.241	5.446	no
5	48400001	48800000	Low	239-461	0.193	4.353	0.209	4.710	*LEMD3, WIF1*
5	95300001	95550000	High	445-426	0.173	3.913	0.187	4.223	*ENSBTAG00000054625, ATF7IP*
6	32100001	32250000	High	774-812	0.177	4.002	0.182	4.118	no
6	37200001	37650000	Low	576-1084	0.174	3.931	0.229	5.164	*NCAPG, DCAF16, LCORL*
6	39650001	39850000	High	539-1172	0.176	3.970	0.227	5.133	no
7	31050001	31250000	High	808-1134	0.179	4.048	0.199	4.489	no
7	31250001	31350000	High	997	0.161	3.640	0.161	3.640	no
7	61200001	61450000	Low	721-790	0.164	3.705	0.211	4.763	*SLC26A2, HMGXB3, CSF1R*
7	96450001	96600000	High	306-486	0.208	4.695	0.286	6.439	*ENSBTAG00000003118, LIX1*
8	7250001	7350000	Low	215	0.221	4.982	0.221	4.982	*ENSBTAG00000025954, ENSBTAG00000035768, ENSBTAG00000008678, ENSBTAG00000039873*
8	21850001	22000000	High	529-585	0.164	3.712	0.166	3.763	no
8	30500001	30650000	High	675	0.169	3.822	0.169	3.822	no
8	59250001	59400000	High	435-470	0.155	3.510	0.173	3.900	*PHF24, DNAJB5, C8H9orf131, VCP, FANCG, PIGO, STOML2, FAM214B*
8	59450001	59600000	High	351-657	0.160	3.614	0.209	4.719	*UNC13B*

Chr	Start	End	Direction	nSNPs	Min. F_{ST}	Min. ZF_{ST}	Max. F_{ST}	Max. ZF_{ST}	Overlapping protein codding regions
9	46500001	46600000	Low	578	0.171	3.867	0.171	3.867	no
11	41150001	41250000	Low	482	0.158	3.568	0.158	3.568	no
11	96450001	96800000	Low	415-493	0.196	4.432	0.222	4.999	PBX3
11	101950001	102100000	Low	842-1114	0.191	4.313	0.194	4.387	no
12	29350001	29450000	High	266	0.160	3.622	0.160	3.622	no
12	36400001	36700000	High	421-520	0.187	4.220	0.198	4.470	*CENPJ, RNF17, ATP12A*
12	44700001	44850000	High	1472	0.189	4.264	0.189	4.264	no
12	49300001	49400000	High	1307	0.179	4.040	0.179	4.040	no
14	39150001	39250000	High	819	0.163	3.687	0.163	3.687	no
15	35750001	35900000	High	670-689	0.170	3.845	0.187	4.229	no
17	60450001	60550000	High	852	0.206	4.652	0.206	4.652	no
18	35100001	35250000	High	237-267	0.156	3.516	0.156	3.535	*RIPOR1, CTCF, CARMIL2, ACD, PARD6A, ENKD1, C18H16orf86*
18	35350001	35500000	High	218-219	0.164	3.706	0.166	3.755	*NUTF2, EDC4, NRN1L, PSKH1, PSMB10, LCAT, SLC12A4, DPEP3, DPEP2, DDX28*
20	4500001	4600000	High	763	0.172	3.892	0.172	3.892	*DUSP1*
21	50300001	50550000	Low	1287-1709	0.170	3.841	0.190	4.283	no
23	47600001	47700000	Low	786	0.179	4.033	0.179	4.033	*ENSBTAG00000054759*
25	9450001	9750000	Low	471-968	0.184	4.146	0.218	4.929	*TVP23A, CIITA, DEXI*
25	29500001	29750000	high	1059-1636	0.156	3.535	0.193	4.368	no
26	30050001	30150000	low	768	0.218	4.924	0.218	4.924	no
26	42650001	42850000	high	697-1000	0.188	4.241	0.190	4.284	*ENSBTAG00000055162, ENSBTAG00000051599, ENSBTAG00000023846, ENSBTAG00000023845, PSTK, IKZF5, ENSBTAG00000048256*
28	19450001	19600000	high	630-900	0.159	3.596	0.191	4.310	no
28	41150001	41350000	high	458-742	0.211	4.765	0.258	5.821	*WAPL, OPN4*
29	48600001	48800000	high	700-741	0.193	4.352	0.246	5.554	*ENSBTAG00000048649, NAP1L4, PHLDA2, SLC22A18, CDKN1C*

Table S46. CL-overlapping selective sweep regions to F_{ST} and both, low (Begait) or high (Arado) groups with their F_{ST} and ZF_{ST} values.

Chr	Start	End	Direction	nSNPs	Min. F_{ST}	Min. ZF_{ST}	Max. F_{ST}	Max. ZF_{ST}	Overlapping protein codding genes
2	400001	550000	low	658	0.263	5.048	0.263	5.048	*ENSBTAG00000040536*
2	550001	700000	low	759-854	0.193	3.667	0.220	4.207	no
2	73100001	73250000	low	485-727	0.210	4.007	0.230	4.400	no
2	85900001	86550000	high	377-526	0.264	5.080	0.356	6.898	*ENSBTAG00000012171, SF3B1, COQ10B, HSPD1, HSPE1, MOB4, RFTN2, MARS2, BOLL*

Chr	Start	End	Direction	nSNPs	Min. F_{ST}	Min. ZF_{ST}	Max. F_{ST}	Max. ZF_{ST}	Overlapping protein codding genes
2	110650001	110750000	low	656	0.221	4.210	0.221	4.210	no
2	126400001	126500000	high	271	0.202	3.851	0.202	3.851	*ARID1A*
3	100550001	100700000	low	626-681	0.271	5.200	0.317	6.113	*PRDX1, MMACHC, ENSBTAG00000017029*
4	31550001	31700000	high	337-552	0.206	3.925	0.228	4.361	*ENSBTAG00000033806*
4	41450001	41600000	high	564-797	0.202	3.841	0.226	4.327	no
4	41800001	42050000	high	523-719	0.214	4.072	0.228	4.362	no
4	66150001	66350000	high	470-480	0.192	3.647	0.223	4.255	*MTURN, PLEKHA8, FKBP14*
5	9100001	9300000	high	490-894	0.207	3.951	0.340	6.585	*PAWR, ENSBTAG00000048833*
5	34650001	34750000	high	261	0.219	4.185	0.219	4.185	no
5	46550001	46750000	low	1230-1244	0.209	3.972	0.240	4.592	no
5	47750001	47850000	low	458	0.218	4.155	0.218	4.155	no
6	41800001	41950000	high	996-1109	0.202	3.847	0.255	4.889	no
6	68450001	68550000	high	745	0.262	5.022	0.262	5.022	*RASL11B*
7	48500001	48650000	high	910-1004	0.265	5.083	0.298	5.745	no
7	48850001	49000000	high	629-663	0.190	3.604	0.192	3.643	no
7	54550001	54650000	low	616	0.194	3.678	0.194	3.678	no
8	23050001	23200000	low	761-1150	0.295	5.687	0.361	6.991	*ENSBTAG00000051881, ENSBTAG00000053037, ENSBTAG00000053413, IFNB3, IFNB3*
9	2250001	2550000	low	1494-1598	0.197	3.752	0.201	3.818	no
9	33650001	33800000	high	657-837	0.192	3.639	0.221	4.227	*RFX6*
10	55050001	55250000	high	471-610	0.207	3.947	0.256	4.906	*RSL24D1*
10	57350001	57600000	high	757-813	0.196	3.723	0.287	5.518	no
11	7650001	7850000	low	385-866	0.208	3.955	0.307	5.917	no
11	46000001	46100000	high	844	0.213	4.064	0.213	4.064	no
11	46150001	46250000	high	1053	0.210	4.007	0.210	4.007	TTL
14	27750001	27900000	high	1030-1156	0.206	3.914	0.257	4.933	no
15	1500001	1600000	high	609	0.199	3.777	0.199	3.777	*ANKRD49, AASDHPPT*
15	53350001	53500000	high	626-805	0.193	3.670	0.213	4.070	*DNAJB13, UCP2, UCP3*
16	19600001	19850000	low	639-919	0.202	3.834	0.206	3.926	no
17	42250001	42350000	low	696	0.207	3.944	0.207	3.944	no
17	43600001	43750000	high	738-913	0.200	3.802	0.250	4.801	*GUCY1A1*
17	72150001	72550000	low	841	0.209	3.979	0.209	3.979	*ENSBTAG00000047538, HIC2, ENSBTAG00000030927, PI4KA, SERPIND1, SNAP29, CRKL, AIFM3, LZTR1, THAP7, TUBA3E, LRRC74B, P2RX6, SLC7A4, TUBA3C, MZT2B, SMPD4, ENSBTAG00000031018, MED15, KLHL22*
18	3550001	3650000	low	726	0.236	4.510	0.236	4.510	no

Chr	Start	End	Direction	nSNPs	Min. F_{ST}	Min. ZF_{ST}	Max. F_{ST}	Max. ZF_{ST}	Overlapping protein codding genes
19	46550001	46750000	low	949-1189	0.211	4.016	0.224	4.271	no
20	3100001	3250000	low	802-822	0.197	3.748	0.199	3.783	*NPM1*
20	11700001	12050000	low	886-894	0.234	4.486	0.241	4.610	*ENSBTAG00000034170*
20	25150001	25600000	low	485-570	0.191	3.626	0.271	5.209	*NDUFS4*
20	49200001	49350000	both	1078-1184	0.310	5.990	0.331	6.403	no
20	54050001	54150000	high	596	0.245	4.701	0.245	4.701	no
20	67600001	67750000	low	872-1239	0.257	4.933	0.277	5.329	*ICE1*
21	47300001	47500000	low	606-817	0.202	3.850	0.291	5.612	*MIPOL1*
21	51350001	51550000	high	1045-1119	0.192	3.647	0.218	4.150	no
22	13700001	13900000	high	778-794	0.210	3.994	0.210	4.006	*CTNNB1*
23	900001	1300000	high	775-923	0.231	4.419	0.259	4.963	no
26	22100001	22400000	low	389-548	0.205	3.898	0.206	3.915	*BTRC, POLL, DPCD, ENSBTAG00000053939*
26	50500001	50600000	low	915	0.196	3.725	0.196	3.725	*ENSBTAG00000049317*
28	21100001	21250000	high	1442-1468	0.212	4.033	0.237	4.536	no
28	39650001	39800000	high	688-773	0.214	4.083	0.248	4.753	no

Table S47. SBD-overlapping selective sweep regions to F_{ST} and both, low (Arado) or high (Begait) groups with their F_{ST} and ZF_{ST} values.

Chr	Start	End	Direction	nSNPs	Min. F_{ST}	Min. ZF_{ST}	Max. F_{ST}	Max. ZF_{ST}	Overlapping protein codding genes
2	400001	550000	high	658	0.263	5.048	0.263	5.048	*ENSBTAG00000040536*
2	550001	700000	high	759-854	0.193	3.667	0.220	4.207	no
2	73100001	73250000	high	485-727	0.210	4.007	0.230	4.400	no
2	85900001	86550000	low	377-526	0.264	5.080	0.356	6.898	*ENSBTAG00000012171, SF3B1, COQ10B, HSPD1, HSPE1, MOB4, RFTN2, MARS2, BOLL*
2	110650001	110750000	high	656	0.221	4.210	0.221	4.210	no
2	126400001	126500000	high	271	0.202	3.851	0.202	3.851	*ARID1A*
3	100550001	100700000	high	626-681	0.271	5.200	0.317	6.113	*PRDX1, MMACHC, ENSBTAG00000017029*
4	31550001	31700000	low	337-552	0.206	3.925	0.228	4.361	*ENSBTAG00000033806*
4	41450001	41600000	low	564-797	0.202	3.841	0.226	4.327	no
4	41800001	42050000	low	523-719	0.214	4.072	0.228	4.362	no
4	66150001	66350000	low	470-480	0.192	3.647	0.223	4.255	*MTURN, PLEKHA8, FKBP14*
5	9100001	9300000	low	490-894	0.207	3.951	0.340	6.585	*PAWR, ENSBTAG00000048833*

Chr	Start	End	Direction	nSNPs	Min. F_{ST}	Min. ZF_{ST}	Max. F_{ST}	Max. ZF_{ST}	Overlapping protein codding genes
5	34650001	34750000	low	261	0.219	4.185	0.219	4.185	no
5	46550001	46750000	high	1230-1244	0.209	3.972	0.240	4.592	no
5	47750001	47850000	high	458	0.218	4.155	0.218	4.155	no
6	41800001	41950000	low	996-1109	0.202	3.847	0.255	4.889	no
6	68450001	68550000	low	745	0.262	5.022	0.262	5.022	*RASL11B*
7	48500001	48650000	low	910-1004	0.265	5.083	0.298	5.745	no
7	48850001	49000000	low	629-663	0.190	3.604	0.192	3.643	no
7	54550001	54650000	high	616	0.194	3.678	0.194	3.678	no
8	23050001	23200000	high	761-1150	0.295	5.687	0.361	6.991	*ENSBTAG00000051881, ENSBTAG00000053037, ENSBTAG00000053413, IFNB3, IFNB3*
9	2250001	2550000	high	1494-1598	0.197	3.752	0.201	3.818	no
9	33650001	33800000	low	657-837	0.192	3.639	0.221	4.227	*RFX6*
10	55050001	55250000	low	471-610	0.207	3.947	0.256	4.906	*RSL24D1*
10	57350001	57600000	low	757-813	0.196	3.723	0.287	5.518	no
11	7650001	7850000	high	385-866	0.208	3.955	0.307	5.917	no
11	46000001	46100000	low	844	0.213	4.064	0.213	4.064	no
11	46150001	46250000	low	1053	0.210	4.007	0.210	4.007	*TTL*
14	27750001	27900000	low	1030-1156	0.206	3.914	0.257	4.933	no
15	1500001	1600000	low	609	0.199	3.777	0.199	3.777	*ANKRD49, AASDHPPT*
15	53350001	53500000	low	626-805	0.193	3.670	0.213	4.070	*DNAJB13, UCP2, UCP3*
16	19600001	19850000	high	639-919	0.202	3.834	0.206	3.926	no
17	42250001	42350000	high	696	0.207	3.944	0.207	3.944	no
17	43600001	43750000	low	738-913	0.200	3.802	0.250	4.801	*GUCY1A1*
17	72150001	72550000	high	841	0.209	3.979	0.209	3.979	*ENSBTAG00000047538, HIC2, ENSBTAG00000030927, PI4KA, SERPIND1, SNAP29, CRKL, AIFM3, LZTR1, THAP7, TUBA3E, LRRC74B, P2RX6, SLC7A4, TUBA3C, MZT2B, SMPD4, ENSBTAG00000031018, MED15, KLHL22*
18	3550001	3650000	high	726	0.236	4.510	0.236	4.510	no
19	46550001	46750000	high	949-1189	0.211	4.016	0.224	4.271	no
20	3100001	3250000	high	802-822	0.197	3.748	0.199	3.783	*NPM1*
20	11700001	12050000	high	886-894	0.234	4.486	0.241	4.610	*ENSBTAG00000034170*
20	25150001	25600000	high	485-570	0.191	3.626	0.271	5.209	*NDUFS4*
20	49200001	49350000	both	1078-1184	0.310	5.990	0.331	6.403	no
20	54050001	54150000	low	596	0.245	4.701	0.245	4.701	no

Chr	Start	End	Direction	nSNPs	Min. F_{ST}	Min. ZF_{ST}	Max. F_{ST}	Max. ZF_{ST}	Overlapping protein codding genes
20	67600001	67750000	high	872-1239	0.257	4.933	0.277	5.329	*ICE1*
21	47300001	47500000	high	606-817	0.202	3.850	0.291	5.612	*MIPOL1*
21	51350001	51550000	low	1045-1119	0.192	3.647	0.218	4.150	no
22	13700001	13900000	low	778-794	0.210	3.994	0.210	4.006	*CTNNB1*
23	900001	1300000	low	775-923	0.231	4.419	0.259	4.963	no
26	22100001	22400000	high	389-548	0.205	3.898	0.206	3.915	*BTRC, POLL, DPCD, ENSBTAG00000053939*
26	50500001	50600000	high	915	0.196	3.725	0.196	3.725	*ENSBTAG00000049317*
28	21100001	21250000	low	1442-1468	0.212	4.033	0.237	4.536	no
28	39650001	39800000	low	688-773	0.214	4.083	0.248	4.753	no

Table S48. Functional annotation of genes in the groups under temperature seasonality (Abergelle or Begait).

Category	ID	Term	Enriched genes	*P v*alue
GOTERM_BP	GO:0030321	transepithelial chloride transport	*CLCN7, LOC100295712*	0.017974
GOTERM_BP	GO:0006241	CTP biosynthetic process	*UCK1, NME3*	0.038543
GOTERM_BP	GO:0009209	pyrimidine ribonucleoside triphosphate biosynthetic process	*UCK1, NME3*	0.041447
GOTERM_BP	GO:0046036	CTP metabolic process	*UCK1, NME3*	0.044342
GOTERM_BP	GO:0000712	resolution of meiotic recombination intermediates	*EME2, HAGH*	0.044342
GOTERM_BP	GO:0009208	pyrimidine ribonucleoside triphosphate metabolic process	*UCK1, NME3*	0.047229
GOTERM_BP	GO:0061061	muscle structure development	*A0A3Q1M0M7_BOVIN, NFATC3, A0A3Q1MV06_BOVIN, TMEM204, UQCC4*	0.047676
GOTERM_CC	GO:0031229	intrinsic component of nuclear inner membrane	*P2RX6, SLC26A6*	0.042320
GOTERM_CC	GO:0005639	integral component of nuclear inner membrane	*P2RX6, SLC26A6*	0.042320
GOTERM_CC	GO:0044453	nuclear membrane part	*P2RX6, SLC26A6*	0.045275
GOTERM_MF	GO:0060090	binding, bridging	*UCN2, ADAMTS16, MAPK8IP3, UQCC4*	0.025609

Table S49. Functional annotation of genes in the groups under the annual precipitation (Arado and Raya).

Category	ID	Term	Enriched genes	*P v*alue
GOTERM_BP	GO:2000677	regulation of transcription regulatory region DNA binding	*CTNNB1, DOT1L, LHX2*	0.006020
GOTERM_BP	GO:1901659	glycosyl compound biosynthetic process	*LCMT2, ADAL, DCK*	0.007215

GOTERM_BP	GO:0010564	regulation of cell cycle process	*FBXO31 (ENSBTAG00000002226), CDKN2B, TTL, NEK6, CTNNB1, DDB1*	0.012044
GOTERM_BP	GO:0007346	regulation of mitotic cell cycle	*FBXO31, TTL, NEK6, CTNNB1, DDB1*	0.026829
GOTERM_BP	GO:0051726	regulation of cell cycle	*FBXO31, CDKN2B, TTL, NEK6, CTNNB1, DDB1, DOT1L*	0.029115
GOTERM_BP	GO:0051101	regulation of DNA binding	*CTNNB1, DOT1L, LHX2*	0.029182
GOTERM_BP	GO:0043414	macromolecule methylation	*LCMT2, CTNNB1, ATF7IP, TRMT9B*	0.030503
GOTERM_BP	GO:0051983	regulation of chromosome segregation	*TTL, NEK6, CTNNB1*	0.033903
GOTERM_BP	GO:0045814	negative regulation of gene expression, epigenetic	*DOT1L, ATF7IP, LHX2*	0.033903
GOTERM_BP	GO:0051098	regulation of binding	*CSNK1A1, CTNNB1, DOT1L, LHX2*	0.040649
GOTERM_BP	GO:0032259	methylation	*LCMT2, CTNNB1, ATF7IP, TRMT9B*	0.046088
GOTERM_BP	GO:1901657	glycosyl compound metabolic process	*LCMT2, ADAL, DCK*	0.046886
GOTERM_BP	GO:0046661	male sex differentiation	*AMH, CTNNB1, RXFP2*	0.047577
GOTERM_BP	GO:0045786	negative regulation of cell cycle	*FBXO31, CDKN2B, CTNNB1, DOT1L*	0.047705
GOTERM_BP	GO:0000278	mitotic cell cycle	*FBXO31, CDKN2B, TTL, NEK6, CTNNB1, DDB1*	0.049458
GOTERM_CC	GO:0030877	beta-catenin destruction complex	*CSNK1A1, CTNNB1*	0.021859
GOTERM_CC	GO:0005667	transcription factor complex	*NFAT5, NFE2L1 (A0A3Q1MA42_BOVIN), CTNNB1, ATF7IP*	0.046148
GOTERM_MF	GO:0005160	transforming growth factor beta receptor binding	*AMH, RASL11B*	0.049218
KEGG_PATHWAY	bta05225	Hepatocellular carcinoma	*CSNK1A1, CTNNB1, NQO1, ARID2*	0.009357

Table S50. Functional annotation of genes in the groups under the precipitation of the wettest month (Begait and Raya).

Category	ID	Term	Enriched genes	*P v*alue
GOTERM_BP	GO:2000780	negative regulation of double-strand break repair	*HELB, HMGA2, SHLD1*	0.004016
GOTERM_BP	GO:0045738	negative regulation of DNA repair	*HELB, HMGA2, SHLD1*	0.004267
GOTERM_BP	GO:0006282	regulation of DNA repair	*HELB, PCNA, HMGA2, SHLD1*	0.005608
GOTERM_BP	GO:2001021	negative regulation of response to DNA damage stimulus	*HELB, HMGA2, SHLD1*	0.016295
GOTERM_BP	GO:2001020	regulation of response to DNA damage stimulus	*HELB, PCNA, HMGA2, SHLD1*	0.020982
GOTERM_BP	GO:2000779	regulation of double-strand break repair	*HELB, HMGA2, SHLD1*	0.024486
GOTERM_BP	GO:0051052	regulation of DNA metabolic process	*HELB, PCNA, HMGA2, SHLD1, ATF7IP*	0.025235
GOTERM_BP	GO:0071901	negative regulation of protein serine/threonine kinase activity	*DUSP1, CDKN1C, IRAK3*	0.027327
GOTERM_BP	GO:2001022	positive regulation of response to DNA damage stimulus	*HELB, HMGA2, SHLD1*	0.037908
GOTERM_BP	GO:0080134	regulation of response to stress	*HELB, DUSP1, PCNA, IRAK3, IL17B, TKFC, A0A3Q1MGV2_BOVIN, SHLD1*	0.038713
GOTERM_BP	GO:0006281	DNA repair	*HELB, PCNA, DDB1, HMGA2, SHLD1*	0.040408

Category	ID	Term	Enriched genes	*P v*alue
GOTERM_BP	GO:0031328	positive regulation of cellular biosynthetic process	*CDKN1C, ASIP, PCNA, RXFP2, DDB1, HMGA2, ARID1A, ATF7IP, PAX3*	0.042997
GOTERM_BP	GO:0009891	positive regulation of biosynthetic process	*CDKN1C, ASIP, PCNA, RXFP2, DDB1, HMGA2, ARID1A, ATF7IP, PAX3*	0.046589
GOTERM_CC	GO:0035861	site of double-strand break	*HELB, DDB1, SHLD1*	0.01627
GOTERM_CC	GO:0000228	nuclear chromosome	*HELB, PCNA, KIFAP3, HMGA2*	0.020589
GOTERM_CC	GO:0090734	site of DNA damage	*HELB, DDB1, SHLD1*	0.026932
GOTERM_CC	GO:0005694	chromosome	*HELB, LLPH, PCNA, KIFAP3, DDB1, HMGA2, SHLD1, G3MXG7_BOVIN*	0.03001

Table S51. Functional annotation of genes in the groups under the precipitation of the warmest month (Abergelle and Raya).

Category	ID	Term	Enriched genes	*P v*alue
GOTERM_BP	GO:0008406	gonad development	*LOC782699, G3X800_BOVIN, G5E622_BOVIN, G5E6C5_BOVIN, FANCG*	0.002767
GOTERM_BP	GO:0045137	development of primary sexual characteristics	*LOC782699, G3X800_BOVIN, G5E622_BOVIN, G5E6C5_BOVIN, FANCG*	0.00295
GOTERM_BP	GO:0008584	male gonad development	*LOC782699, G3X800_BOVIN, G5E622_BOVIN, G5E6C5_BOVIN*	0.003166
GOTERM_BP	GO:0046546	development of primary male sexual characteristics	*LOC782699, G3X800_BOVIN, G5E622_BOVIN, G5E6C5_BOVIN*	0.005428
GOTERM_BP	GO:0048608	reproductive structure development	*PHLDA2, LOC782699, G3X800_BOVIN, G5E622_BOVIN, G5E6C5_BOVIN, FANCG*	0.005773
GOTERM_BP	GO:0061458	reproductive system development	*PHLDA2, LOC782699, G3X800_BOVIN, G5E622_BOVIN, G5E6C5_BOVIN, FANCG*	0.005928
GOTERM_BP	GO:0007548	sex differentiation	*LOC782699, G3X800_BOVIN, G5E622_BOVIN, G5E6C5_BOVIN, FANCG*	0.006029
GOTERM_BP	GO:0046661	male sex differentiation	*LOC782699, G3X800_BOVIN, G5E622_BOVIN, G5E6C5_BOVIN*	0.006181
GOTERM_BP	GO:1905634	regulation of protein localization to chromatin	*WAPL, VCP*	0.006252
GOTERM_BP	GO:0045838	positive regulation of membrane potential	*STOML2, VCP*	0.006342
GOTERM_BP	GO:0010918	positive regulation of mitochondrial membrane potential	*STOML2, VCP*	0.009155
GOTERM_BP	GO:0034502	protein localization to chromosome	*WAPL, CTCF, ACD*	0.020318
GOTERM_BP	GO:0003006	developmental process involved in reproduction	*PHLDA2, LOC782699, G3X800_BOVIN, G5E622_BOVIN, G5E6C5_BOVIN, FANCG*	0.027671
GOTERM_CC	GO:0098590	plasma membrane region	*LOC782699, SLC22A18, G3X800_BOVIN, PARD6A, OPN4, G5E622_BOVIN, G5E6C5_BOVIN, ATP12A, UNC13B*	0.027671
GOTERM_CC	GO:0031225	anchored component of membrane	*DPEP2, NRN1L, DPEP3*	0.027671
GOTERM_MF	GO:0004175	endopeptidase activity	*PSMB10, A0A3Q1LWX0_BOVIN, LOC782699, G3X800_BOVIN, G5E6C5_BOVIN, A0A3Q1MIK6_BOVIN (ENSBTAG00000051599)*	0.031971

Category	ID	Term	Enriched genes	*P v*alue
GOTERM_MF	GO:0004222	metalloendopeptidase activity	*LOC782699, G3X800_BOVIN, G5E622_BOVIN, G5E6C5_BOVIN*	0.034582
GOTERM_MF	GO:0070573	metallodipeptidase activity	*DPEP2, DPEP3*	0.040485
GOTERM_MF	GO:0016805	dipeptidase activity	*DPEP2, DPEP3*	0.041337
GOTERM_MF	GO:0019899	enzyme binding	*DUSP1, STOML2, SLC22A18, ACD, VCP, NUTF2, PARD6A, SLC12A4, CSF1R, CENPJ*	0.044341

Table S52. Functional annotation of genes in the groups under the CL or SBD (Begait and Arado).

Category	ID	Term	Enriched genes	*P* value
GOTERM_BP	GO:0019221	cytokine-mediated signaling pathway	*LOC112447878, LOC112447877, LOC783912, LOC100848709, LOC523509*	0.001194
GOTERM_BP	GO:0009409	response to cold	*HSPD1, UCP2, UCP3*	0.002298
GOTERM_BP	GO:0051607	defense response to virus	*LOC112447878, LOC112447877, LOC783912, LOC100848709, LOC523509*	0.003687
GOTERM_BP	GO:0045893	positive regulation of transcription, DNA-templated	*NPM1, ANKRD49, CTNNB1, ARID1A, BTRC*	0.018122
GOTERM_BP	GO:1990845	adaptive thermogenesis	*UCP2, UCP3*	0.025713
GOTERM_BP	GO:1990542	mitochondrial transmembrane transport	*UCP2, UCP3*	0.028881
GOTERM_BP	GO:1904888	cranial skeletal system development	*CTNNB1, CRKL*	0.032039
GOTERM_BP	GO:0045333	cellular respiration	*COQ10B, NDUFS4*	0.032039
GOTERM_BP	GO:0007283	spermatogenesis	*COQ10B, ANKRD49, BOLL, CRKL*	0.035484
GOTERM_BP	GO:0006839	mitochondrial transport	*UCP2, UCP3*	0.044571
GOTERM_BP	GO:0045945	positive regulation of transcription from RNA polymerase III promoter	*SF3B1, ICE1*	0.047679
GOTERM_CC	GO:0005743	mitochondrial inner membrane	*HSPD1, UCP2, AIFM3, NDUFS4, UCP3*	0.012881
GOTERM_CC	GO:0005737	cytoplasm	*NPM1, RFX6, MZT2B, PAWR, LOC101902172, BTRC, TUBA3E, LOC613401, KLHL22, MTURN, BOLL, FST, CTNNB1, MOB4, AIFM3, P2RX6, PI4KA, LOC100295712, MMACHC*	0.020905
GOTERM_CC	GO:0005813	centrosome	*NPM1, MZT2B, KLHL22, CTNNB1, SNAP29*	0.037751
GOTERM_MF	GO:0005125	cytokine activity	*LOC112447878, LOC112447877, LOC783912, LOC100848709, LOC523509*	0.002463
GOTERM_MF	GO:0017077	oxidative phosphorylation uncoupler activity	*UCP2, UCP3*	0.014089
GOTERM_MF	GO:0051087	chaperone binding	*HSPD1, HSPE1, DNAJB13,*	0.020616
GOTERM_MF	GO:0016651	oxidoreductase activity, acting on NAD(P)H	*AIFM3, NDUFS4*	0.022449
KEGG_PATHWAY	bta05163	Human cytomegalovirus infection	*CTNNB1, LOC112447878, LOC112447877, LOC783912, CRKL, LOC100848709*	0.001092

Category	ID	Term	Enriched genes	*P* value
KEGG_PATHWAY	bta04936	Alcoholic liver disease	*CTNNB1*, *LOC112447878*, *LOC112447877*, *LOC783912*, *LOC100848709*	0.001382
KEGG_PATHWAY	bta04623	Cytosolic DNA-sensing pathway	*LOC112447878*, *LOC112447877*, *LOC783912*, *LOC100848709*	0.001589
KEGG_PATHWAY	bta05160	Hepatitis C	*CTNNB1*, *LOC112447878*, *LOC112447877*, *LOC783912*, *LOC100848709*	0.002074
KEGG_PATHWAY	bta04217	Necroptosis	*LOC613401*, *LOC112447878*, *LOC112447877*, *LOC783912*, *LOC100848709*	0.002448
KEGG_PATHWAY	bta05152	Tuberculosis	*HSPD1*, *LOC112447878*, *LOC112447877*, *LOC783912*, *LOC100848709*	0.003913
KEGG_PATHWAY	bta04630	JAK-STAT signaling pathway	*LOC112447878*, *LOC112447877*, *LOC783912*, *LOC100848709*, *LOC523509*	0.004411
KEGG_PATHWAY	bta05167	Kaposi sarcoma-associated herpesvirus infection	*CTNNB1*, *LOC112447878*, *LOC112447877*, *LOC783912*, *LOC100848709*	0.005031
KEGG_PATHWAY	bta04620	Toll-like receptor signaling pathway	*LOC112447878*, *LOC112447877*, *LOC783912*, *LOC100848709*	0.005903
KEGG_PATHWAY	bta05417	Lipid and atherosclerosis	*HSPD1*, *LOC112447878*, *LOC112447877*, *LOC783912*, *LOC100848709*	0.006734
KEGG_PATHWAY	bta05171	Coronavirus disease - COVID-19	*LOC112447878*, *LOC112447877*, *LOC783912*, *RSL24D1*, *LOC100848709*	0.011915
KEGG_PATHWAY	bta05135	Yersinia infection	*LOC112447878*, *LOC112447877*, *CRKL*, *LOC100848709*	0.013497
KEGG_PATHWAY	bta04650	Natural killer cell mediated cytotoxicity	*LOC112447878*, *LOC112447877*, *LOC783912*, *LOC100848709*	0.013497
KEGG_PATHWAY	bta05162	Measles	*LOC112447878*, *LOC112447877*, *LOC783912*, *LOC100848709*	0.014199
KEGG_PATHWAY	bta05161	Hepatitis B	*LOC112447878*, *LOC112447877*, *LOC783912*, *LOC100848709*	0.018571
KEGG_PATHWAY	bta04060	Cytokine-cytokine receptor interaction	*LOC112447878*, *LOC112447877*, *LOC783912*, *LOC100848709*, *LOC523509*	0.020767
KEGG_PATHWAY	bta05164	Influenza A	*LOC112447878*, *LOC112447877*, *LOC783912*, *LOC100848709*	0.021758
KEGG_PATHWAY	bta04621	NOD-like receptor signaling pathway	*LOC112447878*, *LOC112447877*, *LOC783912*, *LOC100848709*	0.023616
KEGG_PATHWAY	bta05165	Human papillomavirus infection	*CTNNB1*, *LOC112447878*, *LOC112447877*, *LOC783912*, *LOC100848709*	0.024888
KEGG_PATHWAY	bta04540	Gap junction	*TUBA3E*, *GUCY1A1*, *LOC100295712*	0.034827
KEGG_PATHWAY	bta05169	Epstein-Barr virus infection	*LOC112447878*, *LOC112447877*, *LOC783912*, *LOC100848709*	0.038572