Supplemental Information for:

Local adaptations of Mediterranean sheep and goats through an integrative approach

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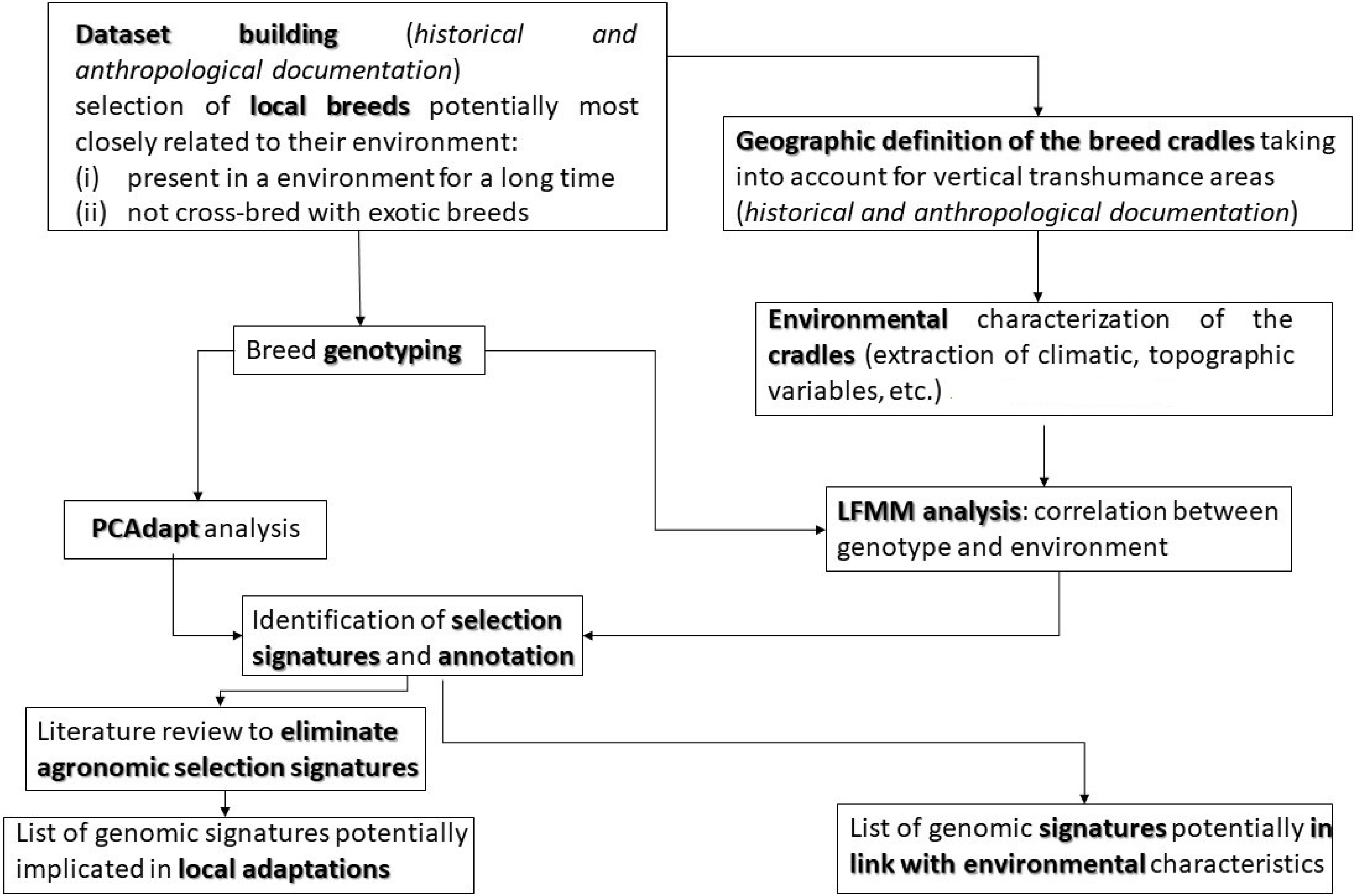
Goat breed	country
Alpine	France
Angora	France
Corse	France
Fosses	France
Poitevine	France
Provencale	France
Pyrenean	France
Saanen	France
Alpine	Italy
Argentata	Italy
Aspromontana	Italy
Bionda dell'Adamello	Italy
Ciociara Grigia	Italy
Di Teramo	Italy
Garganica	Italy
Girgentana	Italy
Jonica	Italy
Maltese sarda	Italy
Maltese	Italy
Nicastrese	Italy
Orobica	Italy
Rossa Mediterranea	Italy
Saanen	Italy
Sarda	Italy
Valdostana	Italy
Valpassiria	Italy
Bermeya	Spain
Mallorquina	Spain
Malaguena	Spain
Murciano-Granadina	Spain
Palmera (Canaria island breed)	Spain
Blanca de Rasquera	Spain

Sheep breed	country
Mourerous Alpes du Sud	France
Mérinos d'Arles	France
Lacaune (lait)	France
Blanche du Massif Central	France
Berrichon du Cher	France
Romane	France
Rouge de l'Ouest	France
Mérinos de Rambouillet	France
Tarasconnaise	France
Rava	France
Noire du Velay	France
Limousine	France
Lacaune (viande)	France
Préalpes du Sud	France
Manech tête rousse	France
Corse	France
Romanov	France
Suffolk	France
Vendéen	France
Charollais	France
Causses du Lot	France
Ouessant (Bretagne)	France
Charmoise	France
Roussin de la Hague	France
Île-de-France	France
Texel	France
Altamurana	Italy
Comisana	Italy
Leccese	Italy
Sarda	Italy
Appenninica	Italy
Sopravissana	Italy
Gentile Di Puglia	Italy
Delle Langhe	Italy
Pinzirita	Italy
Bergamasca	Italy
Bagnolese	Italy
Laticauda	Italy
Alpagota	Italy
Altamurana	Italy
Massese	Italy
Fabrianese	Italy
Ripollesa	Spain
Xisqueta	Spain
Roja Mallorquina	Spain
Canaria de pelo	Spain
Gallega	Spain
Segureña	Spain
Castellana	Spain
Churra	Spain
Ojalada	Spain

Supplementary Table 1



Dataset building (*historical and anthropological documentation*)
selection of **local breeds** potentially most closely related to their environment:
(i) present in a environment for a long time
(ii) not cross-bred with exotic breeds

Geographic definition of the breed cradles taking into account for vertical transhumance areas (*historical and anthropological documentation*)

Breed **genotyping**

Environmental characterization of the **cradles** (extraction of climatic, topographic variables, etc.)

PCAdapt analysis

LFMM analysis: correlation between genotype and environment

Identification of **selection signatures** and **annotation**

Literature review to **eliminate agronomic selection signatures**

List of genomic signatures potentially implicated in **local adaptations**

List of genomic **signatures** potentially **in link with environmental** characteristics

Supplementary Figure 1

Supplementary Table 2

Goat Breeds (code and number of individuals)	**country**	**Origin/History**	**Cradle of the breed/transhumant area if practiced in the past and/or today**	**Description/adaptation**	**Production/ use**	**Status** (according to FAO 2007 if not mentioned)
Bionda dell Adamello (BIO, n=24)	Italy	The breed seems to be ancient. A painting from around 1760 by the Milanese painter Francesco Londonio shows a goat of the Bionda dell'Adamello type (Bigi & Zanon, 2008).	The Val Camonica in the province of Brescia, in Lombardy in northern Italy. It takes its name from the massif of the Adamello, part of the Adamello-Presanella subsection of the Rhaetian Alps. Transhumance in Alpine pasture (Caballero et al., 2009).	Medium to large size long hair ranging from light brown to blonde two white streaks on the muzzle Adaptation to pasture in the mountains	Milk also meat Extensive management	Not at risk
Valdostana (also called Chamoisée Valdôtaine) (VAL, n=24)		Publications dating back to 1917 mention its existence, and suggest an older origin. It would have been the result of hybridation between wild and domesticated animals (http://www.agraria.com).	Aosta Valley in northwestern Italy, particularly in the lower Ayas and Lys valleys. Transhumance in Alpine pasture, (Caballero et al., 2009).	Medium-large-sized animals Short dark blond hair large horns (selection for the traditional "Batailles de Chèvres", Talenti et al., 2017) Adaptation to pasture in the mountains	Milk/meat Extensive management	Critical
Orobica (ORO, n=24)		Ancient breed: The Milanese painter (17th century) Lonati Verri represents goats of the Orobica type. A Milanese lithograph from the early 19th century depicts a goatherd with some of his animals near the Eastern Porta (now Porta Venezia). Official documents mention the existence of the breed as early as 1829 (Corti et al., 1997; Corti, 2006).	The Val Gerola in the province of Sondrio, in the Bergamo Alps of northern Italy. Transhumance in Alpine pasture (Caballero et al., 2009).	Medium size long horns with flat section in males and erect ears fine long hair, with a colour varying from uniform ash-grey to violet-beige Adaptation to pasture in the mountains	Milk Extensive management	Endangered

Val Passiria (also called Passiria/ Camosciata delle Alpi/Passeirer Gebirgsziege/Chèvre Chamoisée) (VSS, n=24)		Breed that seems to have originated from Switzerland (Porter, 2002).	Adapted to the valleys bordering Austria (Val Passiria, Upper Isarco, Sarntal and Val Senales) Transhumance in Alpine pasture (Caballero et al., 2009).	Medium size Medium to long hair dark coat (from black to grey) Adaptation to pasture in the mountains/ good adaptation to the most extreme areas	Meat Extensive management	Unkown
Di Teramo (DIT, n=24)		Indigenous breed of the province of Teramo, unknown origin but probable crossbreeds with Garganica goat (Porter, 2002; http://www.agraria.com).	Province of Teramo, Abruzzi Region. Transhumance in the mountain pastures of Abruzzo (Caballero et al., 2009).	Medium size horns in both sexes Long dark hair (black, brown, grey)	Milk	Critical
Ciociara Grigia (CCG, n=19)		Indigenous breed of Lazio in central Italy, unknown origin but probable crossbreeds with Garganica goat (Porter, 2002).	It is thought to have originated in the area of the Monti Aurunci and the Monti Ausoni. It takes its name from the Ciociaria, the area around Frosinone. Transhumance in the mountain pastures of Abruzzo and Campania plains (Caballero et al., 2009).	Medium sized, dark silvery grey and light coat	Milk/meat	Endangered
Garganica (GAR, n=20)		Indigenous to the Gargano, it derives from cross-breeding of local animals with goats imported from western Europe (Porter, 2002; http://www.agraria.com).	Gargano promontory in the Puglia region of southern Italy. Transhumance in Puglia.	Medium size black, with long hair Horns are quite big Hardy and gregarious animal, adapted to very difficult habitat (Bigi & Zanon, 2008)	Milk/meat	Endangered
Argentata Dell’Etna (ARG, n=25)		Indigenous breed of Mount Etna (Porter, 2002).	The area of Mount Etna in the province of Catania and the	Medium size silvery grey coat, medium-long hair	Raised primarily for milk	Not at risk

			Monti Peloritani in the province of Messina, in Sicily.	horns of the females are upright Adaptation to scarce pastures of Sicily (Rubino, 1993)	production, and also for meat	
Nicastrese (NIC, n=25)		Byzantine origin, photographic evidence suggests that it may be closely connected to the old "Araba" breed of the area (Bigi & Zannon, 2008).	The province of Catanzaro in southern Italy.	Small size Black coat (keshmir undercoat), long hair	Milk/meat	Critical
Girgentana (GGT, n=30)		Would have arrived in Sicily with the Greeks in the 8th century (http://www.agraria.com; Porter, 2002).	The Agrigento coast in Sicily.	Medium size Spiral horns, long and white hair Hardy breed	Milk High prolificity	Threatened by extinction, 400 heads recorded in 1950 (Bigi & Zannon, 2008)
Corse (CRS, n=29)	France	The presence on the island has been documented for several millennia (https://www.racesdefrance.fr).	Corsican massifs, in particular the valleys of Caccia and Niolo. Double transhumance between plains in winter and mountains in summer (Ravis-Giordani, 2001).	Small size curved parallel horns long hair, heterogeneous coat color Hardy breed/ adaptation to scarce and rugged pastures	Milk/meat Extensive management	Not at risk
Provençale (PVC, n=18)		Indigenous breed of Provence registered since the 19th century (https://www.racesdefrance.fr; Babo, 2000).	The cradle of the breed is located in the "Provence of hills" (Alpes de Haute Provence). This breed was not transhumant.	Large size large long hanging ears medium long hair, heterogeneous coat color Adaptation to scarce and dry pastures	Milk	Endangered This breed, which almost disappeared, was taken over in 1993 by a breeders' association (http://www.capgenes.com)
Pyrénéenne (PYR, n=25)		Very old origin in the Pyrenees (Fournier, 2006).	Pyrenees - Atlantic to Ariège.	Medium size Long hair, dark coat	Milk/meat	Endangered

			Transhumance in Pyrenean pastures (Fanica, 2008) some herds moved with the Pyrenean sheep across the Landes to Gironde and Dordogne.		Extensive management	It almost disappeared in the second half of the 20th century (https://www.chevredespyrenees.org)
Bermeya (BEY, n=24)	Spain	Indigenous breed of the North of Spain, probably descending from Capra aegagrus (https://www.mapa.gob.es).	The southern part of the Principality of Asturias, in northern Spain. Short transhumance (transtermitance).	Medium size Short hair, red coat suitable for mountainous areas and humidity	Mainly meat and also milk	Endangered
Blanqua De Rasquera (RAS, n=20)		Municipal Ordinances of Vila de Rasquera (Tarragona) refers to the goat population in 1573 (Sabaté et al., 2011).	Several regions in southern Catalonia (Baix Ebre, Ribera d'Ebre and Terra Alta), its name comes from the municipality of Rasquera, in the Ebro. Horizontal transhumance to the Pyrenean pastures (http://ipcite.cat).	Medium size short hair, white coat with sometimes wide black spots large, drooping ears Hardy breed	Meat and also milk Extensive management	Endangered
Malaguena (MLG, n=41)		Certainly very old origin of the breed; there are traces of its existence that date back to the 4th millennium BC (Garcia-Dory et al., 1990).	Malaga in the south of the Iberian Peninsula.	Medium size Short hair, sandy to red coat, horns sometimes twisted	Milk/meat	Not at risk
Mallorquina (MAL, n=20)		Ancient breed that was introduced to the island around 2500/1400 BC (Segui et al., 2005).	Majorca, mainly in the mountains: Sierra de tramuntana and Sierra de Llevant.	Medium size Short hair, red or red and black coat Adaptation to scarce, dry and rugged areas	Meat Extensive management	Endangered

Sheep Breeds (code)	**country**	**Origin/History**	**Cradle of the breed/transhumant area if practiced in the past and/or today**	**description**		**status**
Manech Tête Rousse (MTR, n=25)	France	Very ancient Basque origin (https://www.races-montagnes.com; Babo, 2000).	Basque hillsides (Basse Navarre, Basse Soule). Transhumance in Pyrenean pasture.	Medium size White wool, red head, long lopping ears Ability to breed out of season Hardy breed, good walker	Milk	Not at risk
Tarasconnaise (TAR, n=15)		Very old breed derived from an original population of the Pyrenees (https://www.races-montagnes.com).	Central Pyrenees and particularly in the Ariège, Hautes-Pyrénées and Haute-Garonne. Transhumance in Pyrenean pasture.	Medium size White wool, spiral horns in males Hardy breed, good walker, ability to breed out of season	Meat	Not at risk
Causse Du Lot (CDL, n=20)		It is believed to come from a very old sheep strain that lived on the northern slope of the Garonne. Its origin goes back at least to the Gallo-Roman period (https://www.races-montagnes.com; Clozier, 1932).	Limestone plateaus of the Lot (the Causses of Quercy) Horizontal transhumance linking the Lot to the Auvergne; winter transhumance was used during periods of extreme cold (Leveau, 2016; Clozier, 1932; Delhoume, 2005).	Medium to large size White coarse wool, black spots around the eyes and ears Hardy breed, it would be resistant to piroplasmosis; ability to breed out of season	Meat/milk Extensive management	Not at risk
Limousine (LIM, n=18)		The breed would have emerged at the end of the 19th century as a result of crossbreeding between different breeds of the Massif Central (https://www.races-montagnes.com).	Millevaches plateau, in the mid-mountain area.	Medium size White medium wool Adapted to a difficult territory with acid soil and harsh climate, ability to breed out of season	Meat	Not at risk

Rava (RAV, n=20)		Breed of the volcanic plateaus of Auvergne; it was first described in 1826 (https://www.races-montagnes.com).	The Chaîne des Puys in the Massif Central. Transhumance in the Massif Central.	Medium size White coarse wool, black spots on the head Adapted to a difficult territory with acid soil and harsh climate, ability to breed out of season	Meat	Not at risk
Blanche Du Massif (BMC, n=20)		Old breed that belongs to the Caussenard group (https://www.races-montagnes.com).	The Margeride in the South part of the Massif Central. Horizontal transhumance linking the Langedoc to the Auvergne (Leveau, 2016).	Medium size White wool Adapted to a difficult territory, ability to breed out of season	Meat	Not at risk
Noire Du Velay (NVE, n=19)		Very old breed of Auvergne; it seems to have arrived in France around 1500 BC when the Celtic peoples settled in the Massif Central; writings mention its existence as early as the 17th century (https://www.races-montagnes.com; Brunelin, 2012).	Velay volcanic plateau, in the Auvergne region. Horizontal transhumance linking the Languedoc to the Auvergne (Leveau, 2016).	Medium size black skin and wool of black-brownish colour Good walker, adapted to a difficult territory with acid soil and harsh climate, ability to breed out of season	Meat	Not at risk It almost disappeared at the beginning of the 20th century with the arrival of better conformed breeds
Préalpes Du Sud (PAS, n=17)		It would be the result of the old mixing of the Sahune, Quint and Savournon breeds (https://www.races-montagnes.com; Duclos & Mallen, 1998).	The Southern Alps at the border between the Dauphiné and Provence. Transhumance in Alpine pastures.	Medium size White wool Adaptation to dry mountain, ability to breed out of season	Meat	Not at risk
Mourerous, also called "La Rouge", "Péone" ou "Rouge de Guillaumes"		It could have been crossbred with breeds imported from North Africa (https://www.races-montagnes.com).	Péone in the department of Alpes Maritimes. Transhumance in Alpine pastures.	Medium size White wool, red head and legs Cold and drought resistance, ability to walk in the	Meat	Not at risk For a long time known as a "threatened" or "small breed"

(MOUR, n=16)				mountain, ability to breed out of season		
Corse (COR, n=16)		Ancestral breed of Corse; It would originate from a Pyrenean breed imported on the island several centuries ago (https://www.races-montagnes.com; Babo, 2000).	Mountainous areas of Corse. Double transhumance between plains in winter and mountains in summer (Ravis-Giordani, 2001).	Medium size Coarse wool, spiral horns in males Adaptation to mountain pastures, ability to breed out of season	Milk	Not at risk
Delle Langhe (DEL, n=24)	Italy	Indigenous breed of the Piedmont (Porter, 2002).	The mountainous area of the Alta Langa in Piedmont (province of Cuneo), in northwestern Italy. Transhumance in Alpine pasture (Caballero et al., 2009).	Medium to large size White coarse wool, polled, semi lop hears Adaptation to mountain pastures	Milk/meat	Endangered
Biellese (BIE, n=21)		Indigenous breed of the province of Biella in Piedmont (Porter, 2002).	The province of Biella, in Piedmont in north-western Italy. Transhumance in Alpine pasture, (Caballero et al., 2009, Battaglini 2014) still practice vertical trasterminance (3/4 of total) between the mountains and the plain areas of Lombardy or Emilia Romagna (Corti, 2007).	Medium to large size White coarse wool, polled, lop hears Adaptation to mountain pastures	Meat and also wool in the past	Not at risk
Bergamasca (BER, n=24)		Very ancient breed, we can trace its existence back to the 13th century (Astori, 1963).	The mountainous part of the province of Bergamo, in Lombardy in northern Italy.	Medium to large size White coarse wool, polled, lop hears	Meat	Not at risk

			Transhumance in Alpine pasture, (Caballero et al. 2009) still practice vertical trasterminance (3/4 of total) between the mountains and the plain areas of Lombardy or Emilia Romagna (Corti, 2007).	Adaptation to mountain pastures		
Alpagota (ALP, n=24)		Ancient breed, the sheep's emblem is found on the coat of arms of Chies d'Alpago (15th century) (Pastore, 2005).	The historic region of the Alpago in northern Italy Transhumance in Alpine pasture (Caballero et al., 2009).	Small to medium-size white with dark spots, polled small ears Adaptation to hills and mountains	Meat/milk	Not at risk
Massese (MAS, n=24)		Indigenous breed that belongs to the Apennine group, with an ancient origin: Machiavelli refers to the breed in his writings (early 16th century).	The Alpi Apuane mountains of the province of Massa Carrara, in Tuscany, central Italy. Transhumance in the mountain pastures of Appennins (Caballero et al., 2009).	Small to medium size lead-grey to black Adaptation to mountain pastures	Milk/meat	Not at risk
Appenninica (APP, n=24)		The origin of the breed can be traced back to the end of the 19th century, when sheep of the Bergamasque breed were imported into Tuscany, Umbria, Romagna, Marche and Abruzzo. These subjects were crossed with the pre-existing Apennine populations in order to intensify meat production (http://biodiversita.umbria.parco3a.org).	The central Apennine mountains of Italy. Transhumance in the mountain pastures of Appennins and Abruzzo (Caballero et al., 2009).	Medium size White, coarse wool, polled	Meat and also wool	Not at risk

Laticauda (LAT, n=24)		It should result from ancient hybridisation of local breeds with Barbary (or Barbarin) sheep of Maghrebi origin. The Bourbon king Charles VII of Naples could have brought it in the area (Bigi & Zannon 2008).	Campania and Calabria, in southern Italy, in particular the provinces of Avellino, Benevento and Caserta. This breed was not transhumant.	Medium to large size Generally white, fat tail, polled	Milk/meat	Unkonwn
Bagnolese (BAG, n=23)		A native campanian breed, that probably derives from the crossbreeding of the Barbaresca breed and the local breeds of the Appennines (http://www.agraria.com).	The area surrounding Bagnoli Irpino in the province of Avellino, in Campania in southern Italy. Transhumance to the mountain pastures in summer.	Medium size white fleece with dark spots, coarse wool, long hanging ears Well adapted to pasture in rough conditions	Milk/meat	Endangered-maintained
Valle Del Bellice (VAL, n=24)		It appears to result from the three-way hybridization of the Sicilian Pinzirita and Comisana breeds with Sarda stock brought from Sardinia (Porter, 2002).	The valley of the Belice river in south-western Sicily.	Medium size White coat (Sarda), black coat (Sardinian black), long coarse wool	Milk	Not at risk
Sardinian White (SAR, n=24)		Indigenous to the island of Sardinia with very ancient origin (http://www.agraria.com).	Mountains and plains of Sardinia. Transhumance to mountain pastures.	Medium size White coat long coarse wool	Milk	Not at risk
Latxa (LATX, n=24)	Spain	Basque breed called Manech in France, and one of the oldest breed in Spain. There are engravings dating back to 1872 that represent the breed (https://www.mapa.gob.es, Porter 2002; Garcia-Dory, 1990).	the north-west of Navarre and in the east and south of the province of Guipúzcoa, in the north of Spain Transhumance in Pyrenean pasture, (Caballero et al., 2009) still practice vertical trasterminance (3/4 of total) between the mountains and the plain areas.	Medium size White long wool, the colour of the head depends on the variety, twisted horns in males Adapted to rugged terrain and humidity	Milk and also meat	Not at risk

Gallega (GAL, n=27)		Very ancient Galician breed, originary from Ovis aries celtibericus, it would go back 6,000 years (Garcia-Dory, 1990).	South east of Gallicia.	Small to medium size White or black coat, spiral horns in males	Meat and also milk and wool	Unknown, according to FAO Undangered, according to gouvernemental Decret
Churra (CHU, n=30)		Primitive Iberian breed, it comes from *Ovis aries celticus* and gives its name to the Churro trunk. Traces of its existence date back to pre-Roman times (Garcia-Dory, 1990).	Zamora province in Castile and León.	Medium size White wool, head black spotted	Milk/meat	Not at risk
Ojalada (OJA, n=24)		Ancient breed that belongs to the Iberian Trunk, whose ancestral representative is the *Ovis aries Ibericus* (Garcia-Dory, 1990).	The province of Soria in central Spain.	Medium size White wool, black spots around the eyes, sometimes spiral horns in males	Milk/meat/wool	Not at risk according to FAO; Endangered according to the website of the Spanish Ministry of Agriculture
Roja Mallorquina (MAL, n=28)		Ancient breed, resulting from the crossing of two sheep trunks, one from the south of the European continent and the other from the North African countries (https://www.mapa.gob.es).	Island of Mallorca, especially the southern area.	Medium to large size Red coat, fat triangular tail Adapted to dryness	Meat/wool	Endangered

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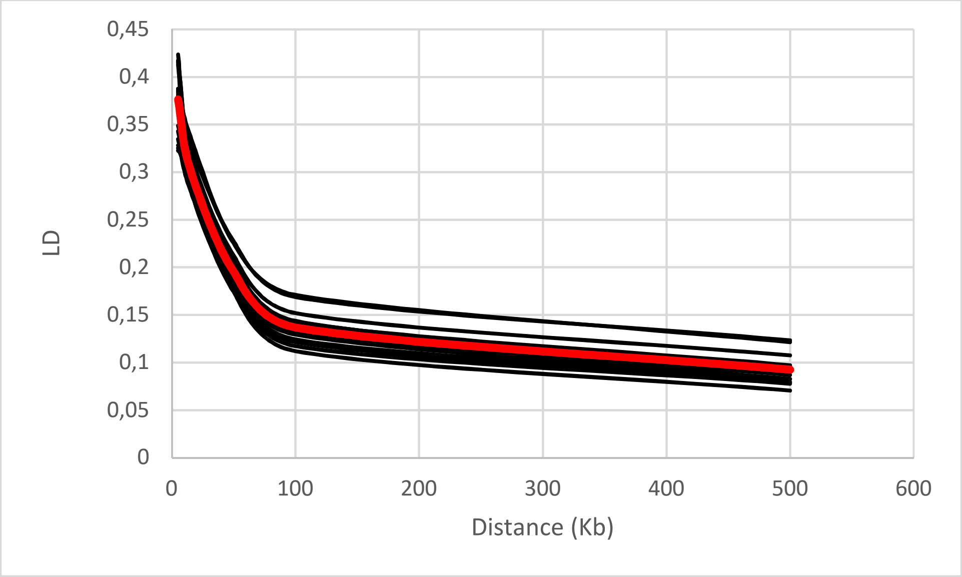
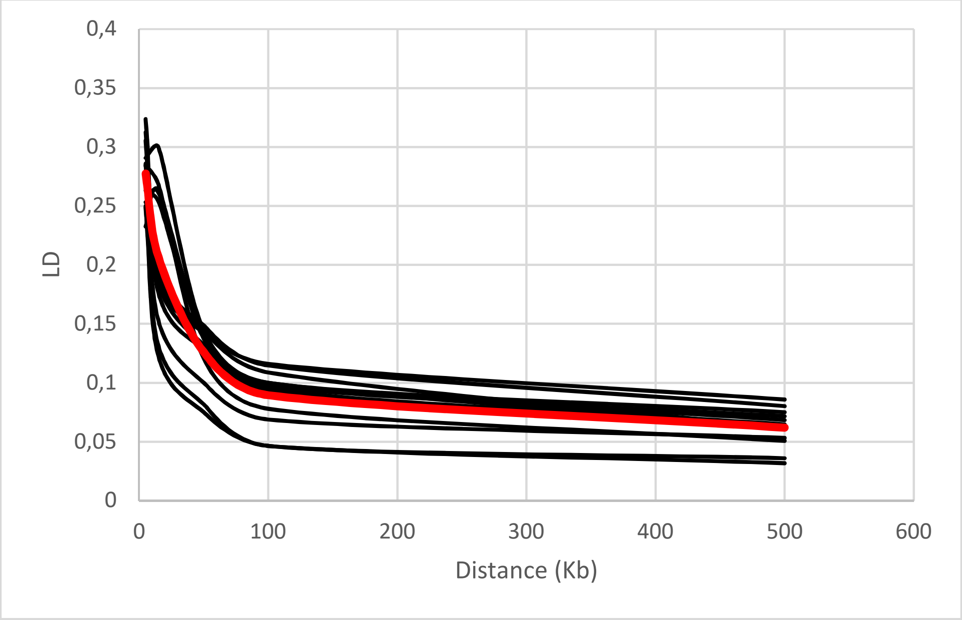
a)



Mean LD for sheep in red: 5Kb=0.37 ; 15Kb=0.30 ; 50Kb=0.19 ; 100Kb=0.13 ; 500Kb=0.09

b)



Mean LD for goat in red: 5Kb=0.28 ; 15Kb=0.21 ; 50Kb=0.13 ; 100Kb=0.09 ; 500Kb=0.06

Supplementary Figure 2

Supplementary Text 1

Genetic relationships between the Mediterranean goat breeds

For K=2 (Figure 1), the admixture analysis reveals a gradient that follows the geographical disposition of the goat breeds along the Mediterranean arc. Spanish breeds show a predominance of orange; the proportion of orange gradually decreases to give place to a dominant blue within the breeds of southern Italy. At K=3, the Italian DIT breed is individualized from GGT, then at K=4 it is the alpine ORO breed that stands out. At K=6, the proximity of the Spanish breeds is obvious, with a clear link between BEY and PYR, the breeds close to the Pyrenees, respectively Spanish and French. In the Italian group, the VAL and GAR breeds show their originality. At K=17, all breeds are individualized, with the exception of alpine breeds, BIO and VSS, which remain very close, as well as breeds from southern Italy, CCG, NIC and ARG.

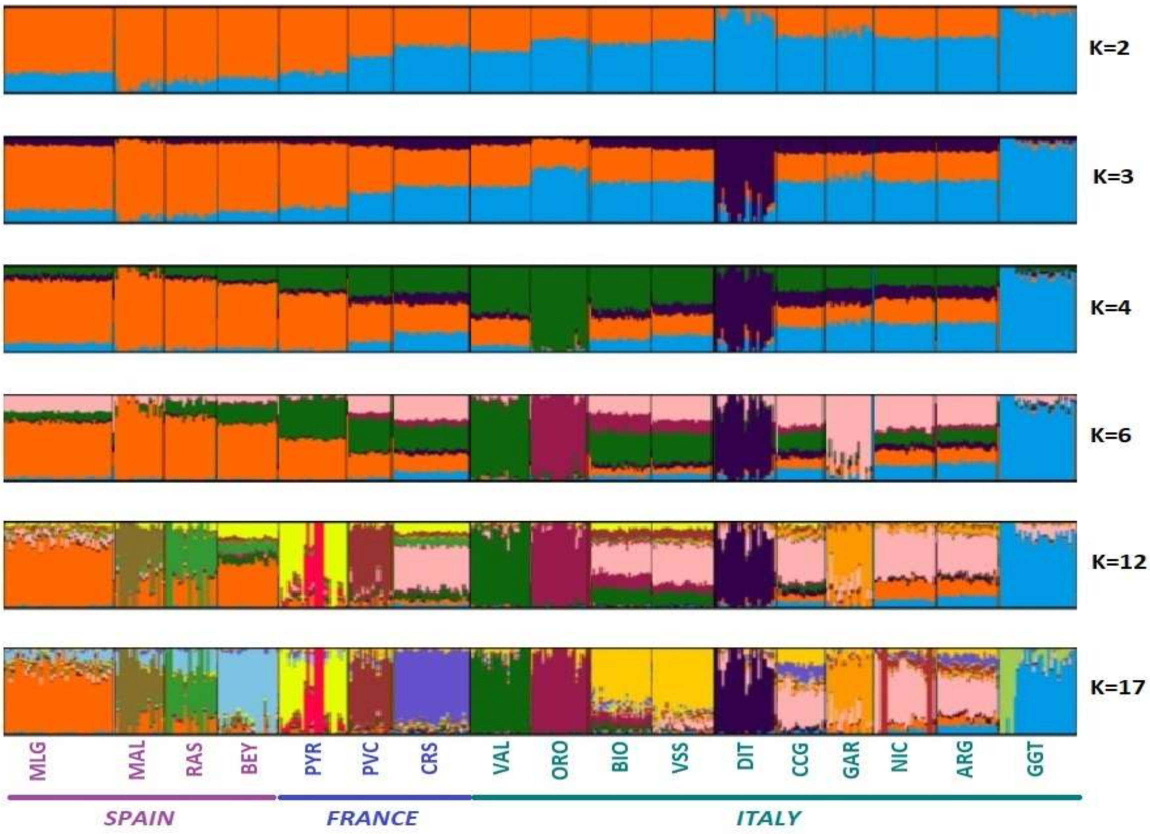


Figure 1. Bayesian clustering performed with ADMIXTURE software on Mediterranean goat breeds. K = number of clusters; see the correspondence between breed names and codes in Supplementary table 1.

Genetic relationships between the Mediterranean sheep breeds

For K=2 (Figure 2), the major contrast is established between the Italian Alpine breeds BIE, BER, ALP and the others. Within the Spanish group, the MAL breed is very clearly individualized from K=8. The Spanish Pyrenean breed LATX shows a strong proximity with the French MTR, also Pyrenean, and this even for K=25. As for the French breeds, the first to individualize are LIM, CDL and COR. At K=25, a clear link between PAS, MOUR and NVE is maintained. The Italian breeds, DEL, then SAR, VAL and MAS, are individualized between K=4 and K=8. At K=25, the analysis shows a very strong proximity between BIE and BER, as well as a persistent link between LAT and BAG.

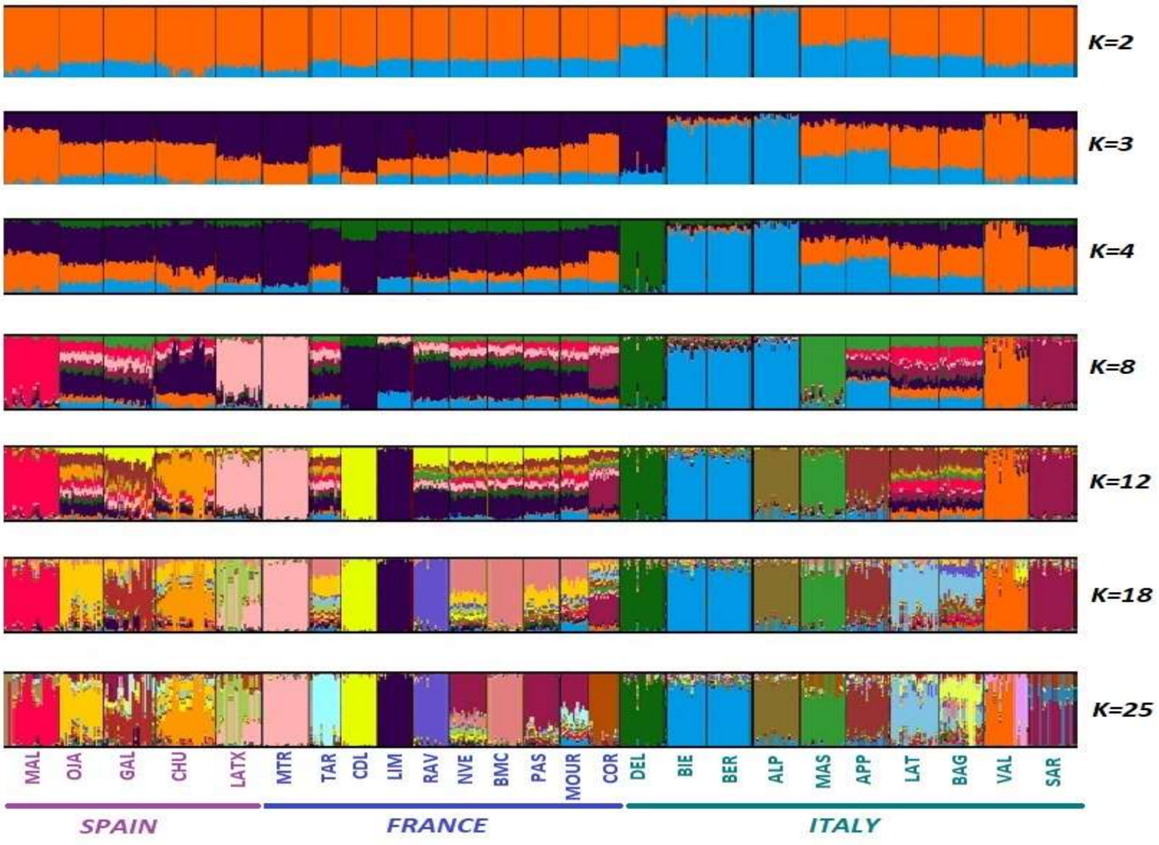


Figure 2. Bayesian clustering performed with ADMIXTURE software on Mediterranean sheep breeds. K = number of clusters; see the correspondence between breed names and codes in Supplementary table 1.

K choice

For both goats and sheep (Figure 3), the cross-entropy curve decreases as K increases, which is characteristic of a distance isolation pattern (François, 2016). A plateau reached at K=10 for goats and K=9 for sheep, indicating that fine structuring could be apparent from this threshold. In sheep, a dropout at K=3 could be the reflection of an under-structuring by country.

The Mantel tests showed correspondence between geographic and genetic distances (p-value = 0.049 for goats and 0.001 for sheep), supporting the Isolation By Distance (IBD) pattern.

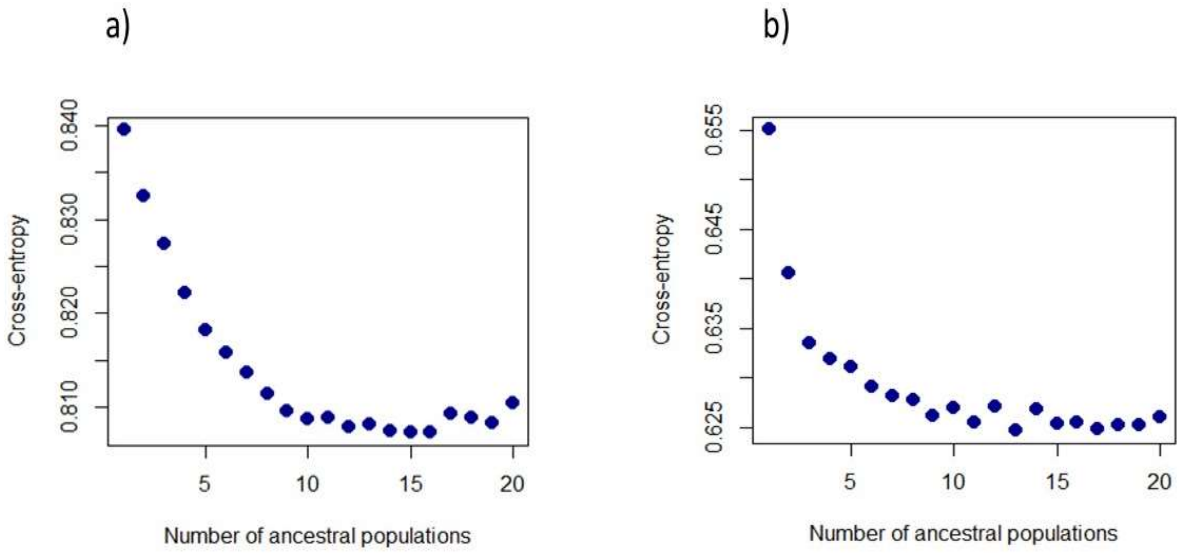


Figure 3. Cross-entropy plot for the number of cluster K = 1-20, considering: a) the goat dataset and b) the sheep dataset.

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Supplementary Text 2

Environmental characterization: comparison between GPS and cradle methods

For eight French sheep breeds (Rava, Limousine, Causse Du Lot, Tarasconnaise, Noire Du Velay, Préalpes Du Sud, Mourerous and Blanche Du Massif Central) we could compare Mean Annual Precipitation, Mean Annual Temperature and Altitude obtained via the GPS area method and the cradle method. Multiple comparisons with FDR adjusted p-values ($\alpha=0.05$) were realized with R, using the package rstatix. The analysis (Figure 1) generated 21 comparisons. All differences between the GPS area and the cradle were significant except for the variable, Mean Annual Precipitation, for the breeds Causse du Lot (CDL) and Préalpes du Sud (PAS). Overall, significantly higher mean Altitude values were provided by the cradle method, which resulted in higher Mean Annual Precipitation and lower Mean Annual Temperatures, compared to that obtained by the GPS area method. The differences were particularly strong for transhumant breeds such as Rava (RAV), Tarasconnaise (TAR) and Mourerous (MOUR), for which GPS sampling had mainly been carried out on the plains.

For goats, we compared the same three environmental parameters obtained by the GPS area and the cradle methods for all 17 breeds, (Figure 2), which resulted in 45 out of 51 significant differences. As found for sheep, significantly higher mean Altitude was always found for the cradle method, and resulted in lower Mean Annual Temperature. The rainfall pattern was less clear-cut, with 56% of the comparisons showing higher Mean Annual Precipitation when extracted at the level of cradle of origin.

These analyses showed that the environmental characterization depends on the definition of the distribution range based on the cradle or on the individual/breed GPS coordinates. The cradle method takes into account summer grazing areas, which implies the extraction of climatic data at higher altitudes than with the GPS method, generally resulting in lower temperatures and higher precipitations. In addition, for some breeds such as Garganica (GAR) and Mourerous (MOUR), individuals were sampled more than 100 km from their established cradle, which led to the consideration of different climatic environments depending on the method used. These breeds illustrate the move of the herds from their cradle of origin, caused by the intensification of agricultural practices.

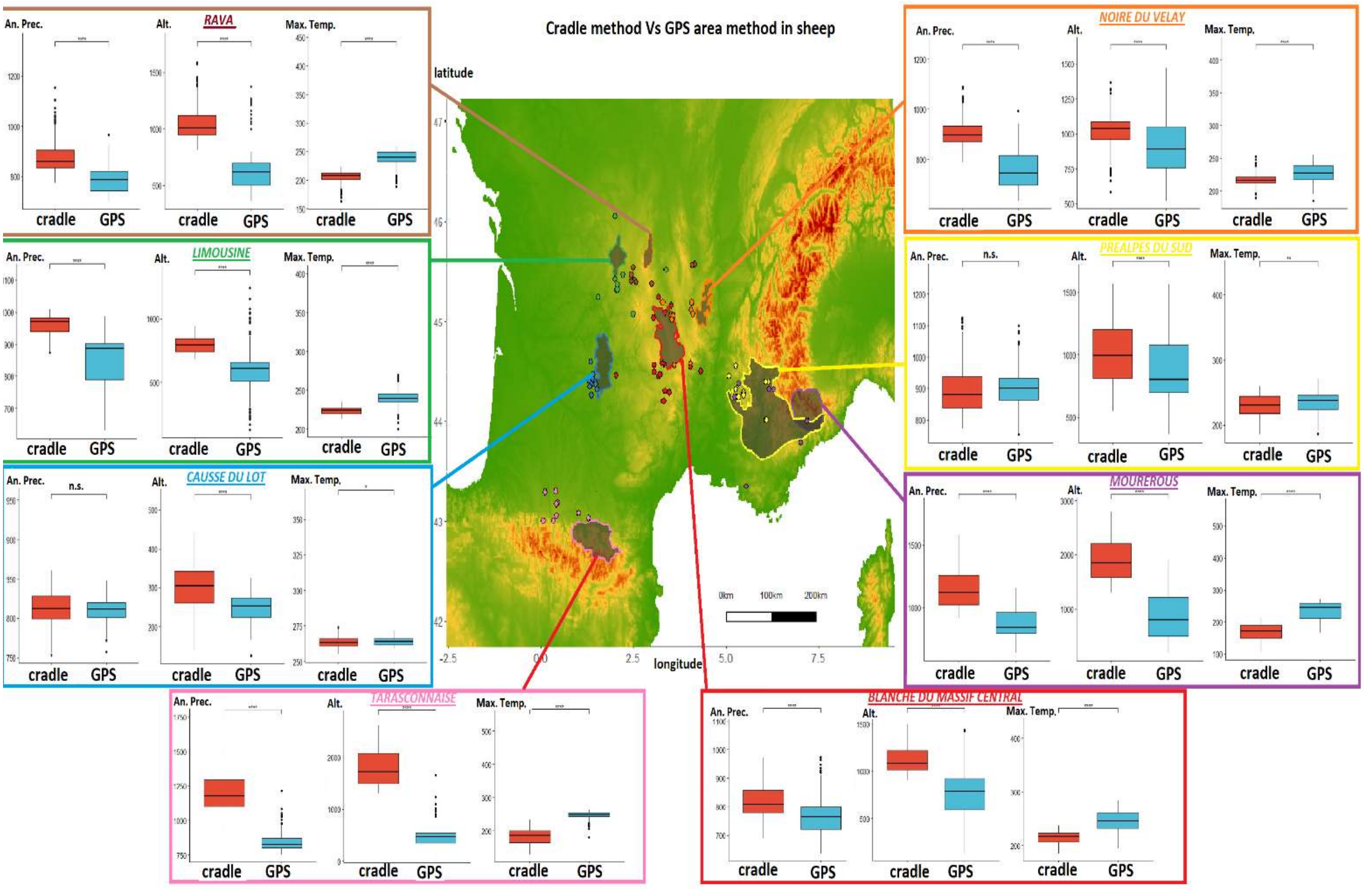


Figure 1. Mapping display for sheep of the geographical cradles and the GPS coordinates of the sampled points; statistical comparisons for the variables Annual Mean Temperature, Annual Mean Precipitation and Altitude between the distributions obtained by the cradle method and the GPS area method, display of the results via boxplots.

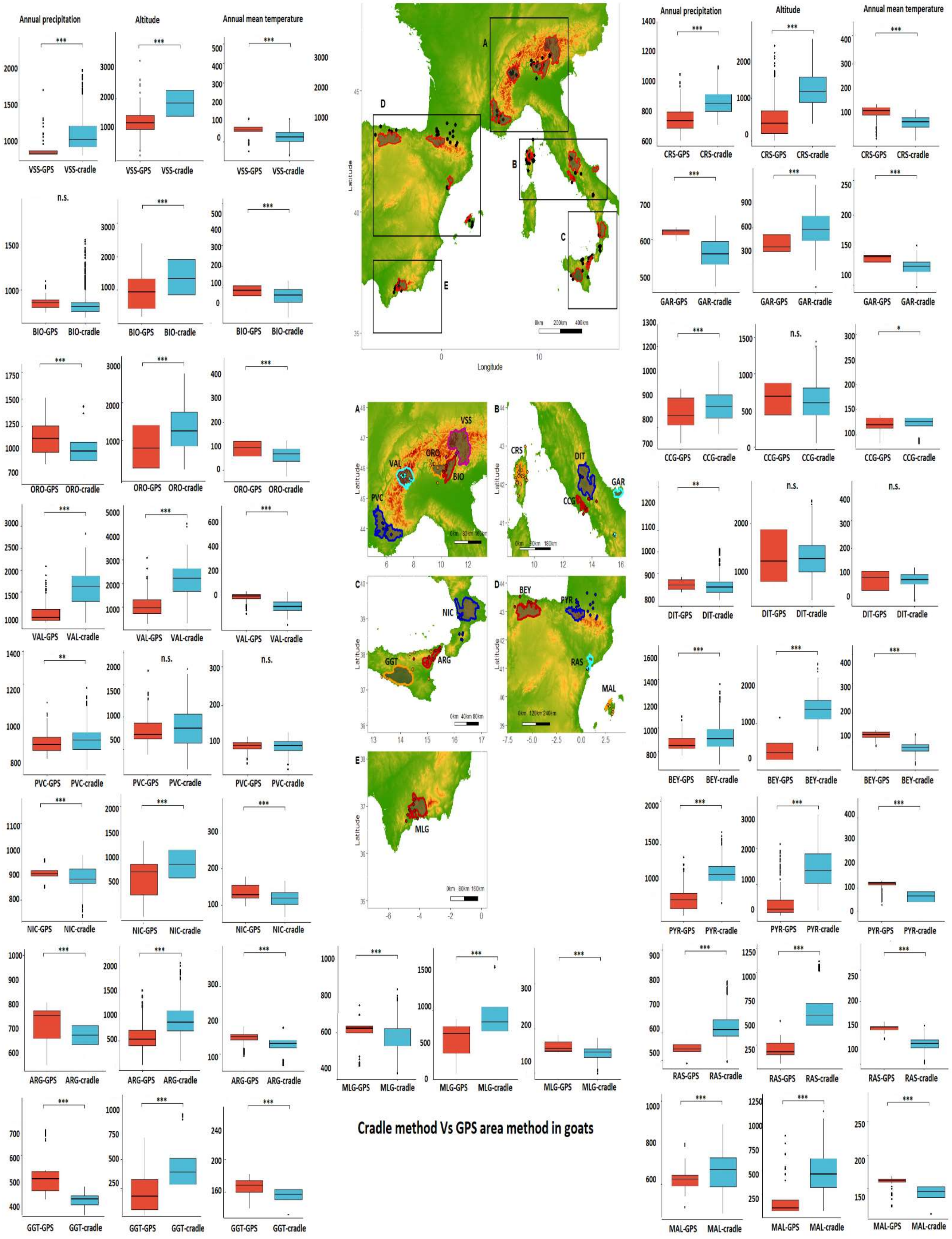
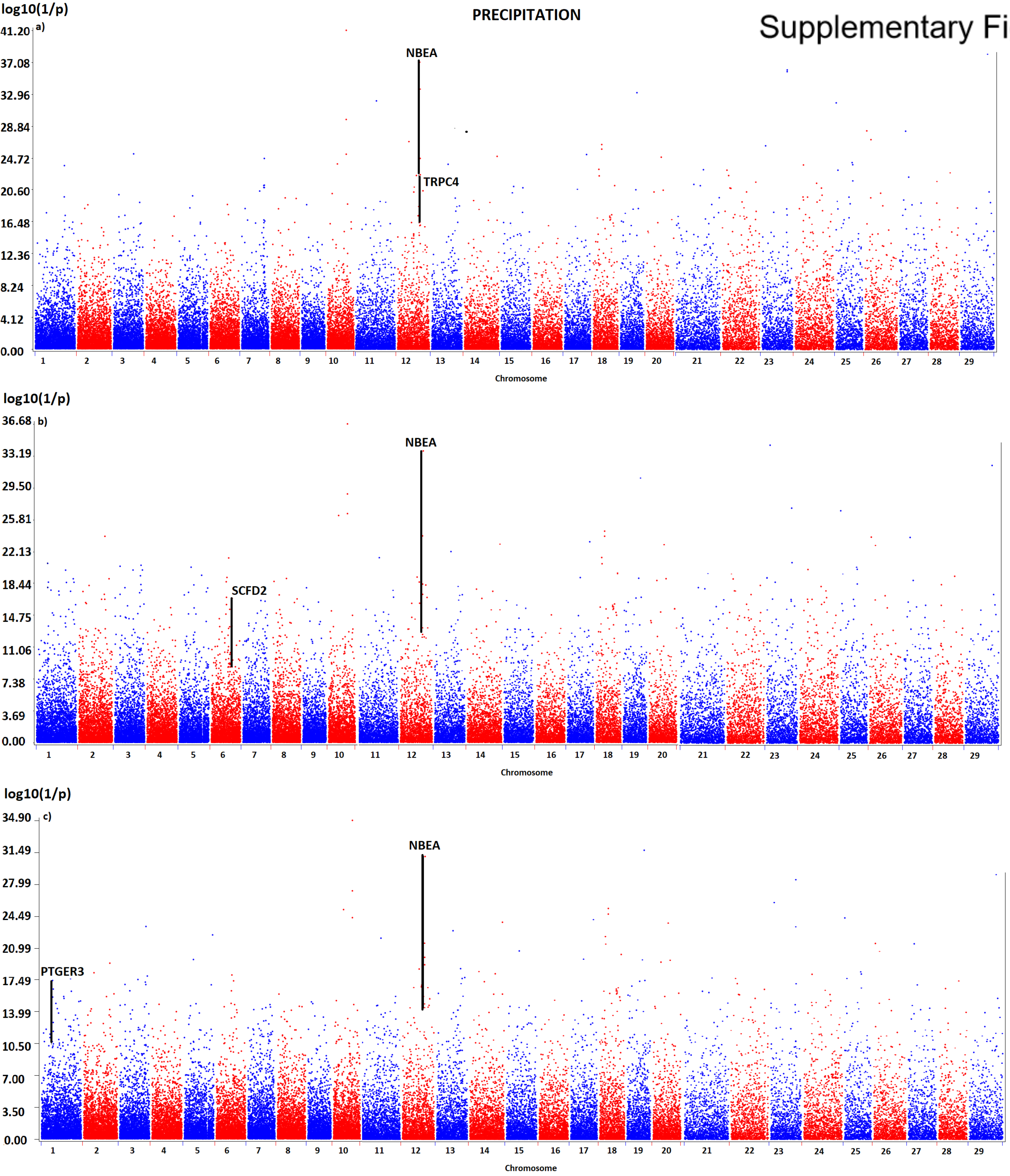


Figure 2. Mapping display for goat of the geographical cradles and the GPS coordinates of the sampled points; statistical comparisons for the variables Annual Mean Temperature, Annual Mean Precipitation and Altitude between the distributions obtained by the cradle method and the GPS area method, display of the results via boxplots.

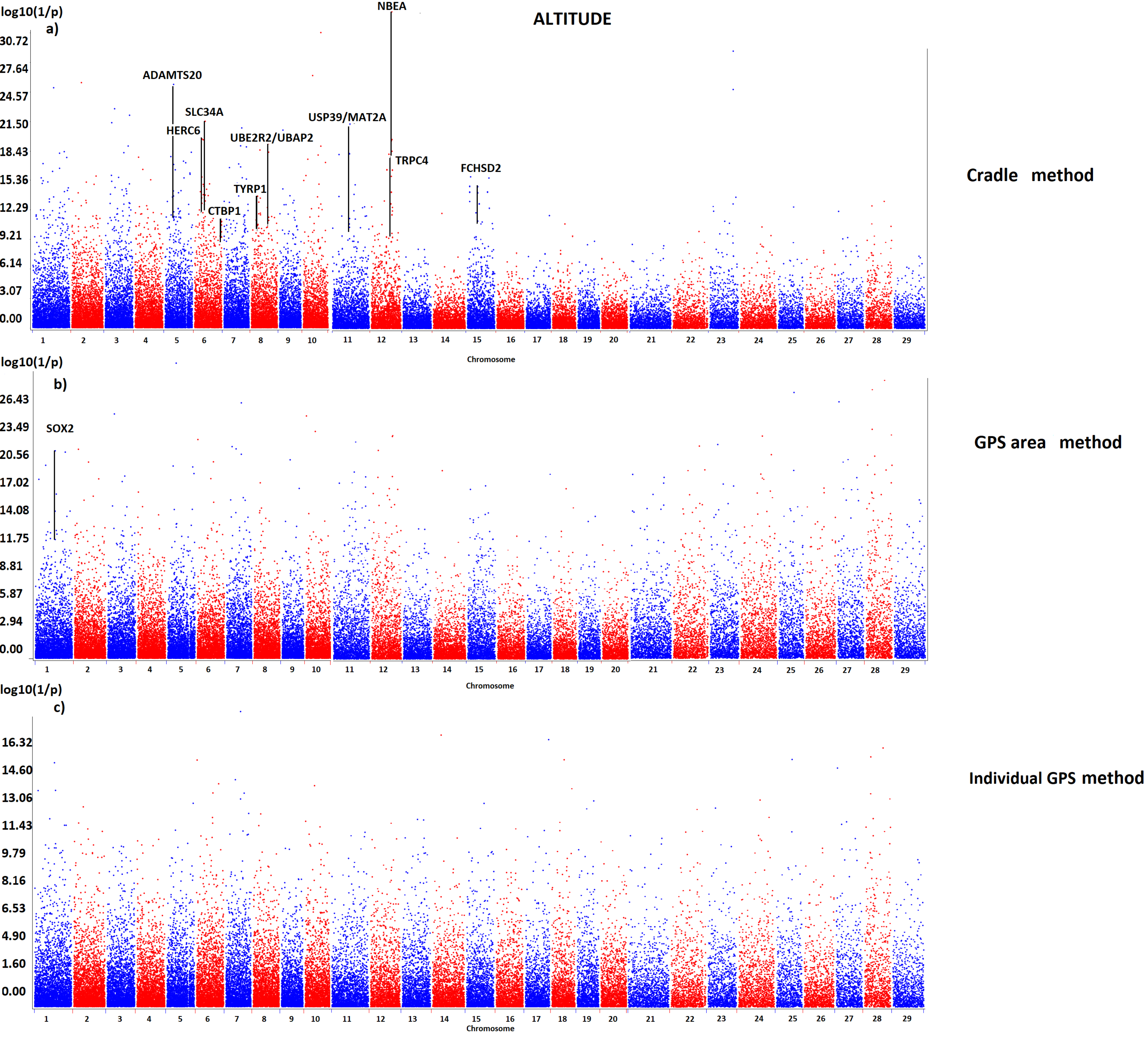
Supplementary Figure 3

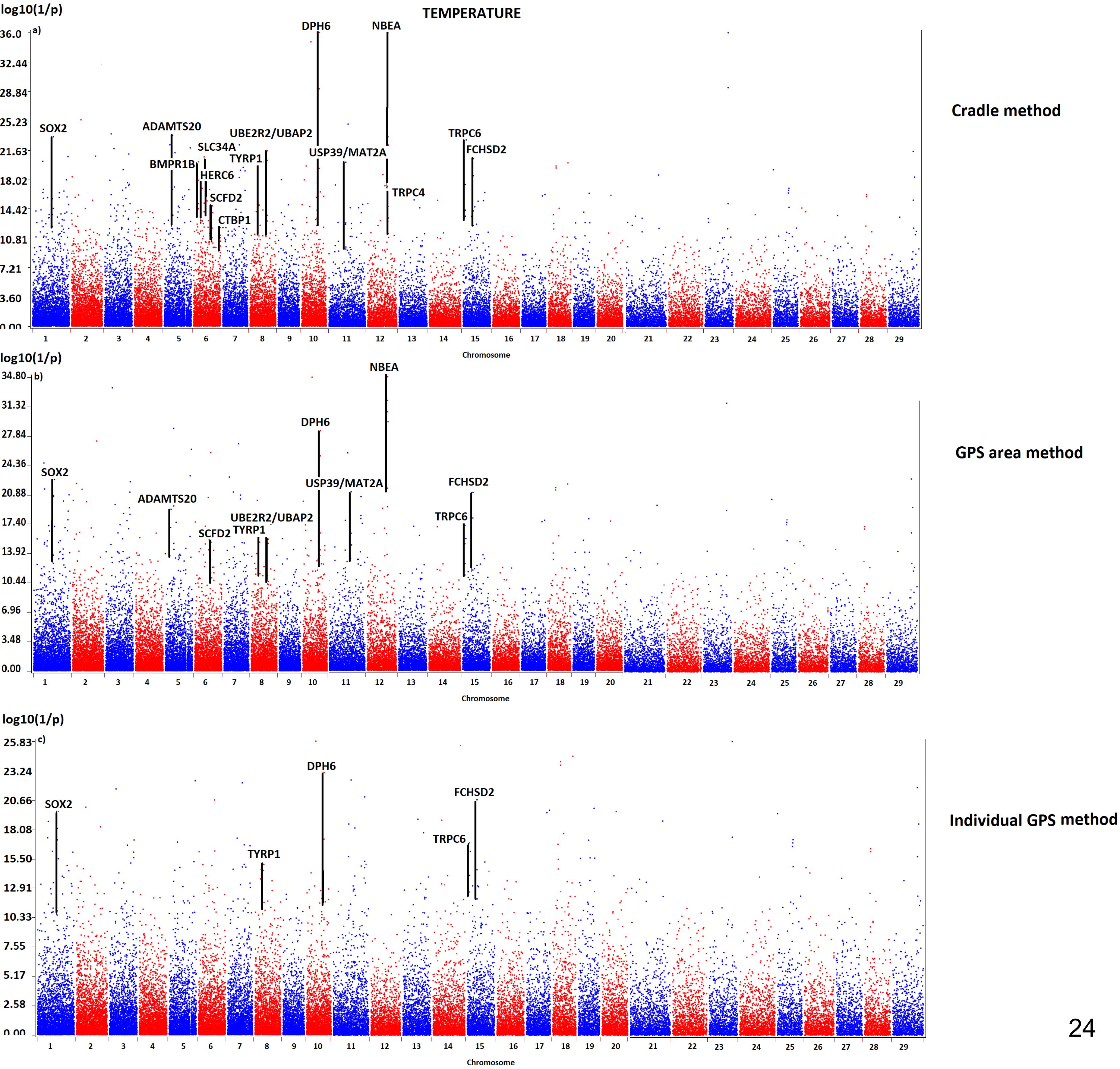


Cradle method

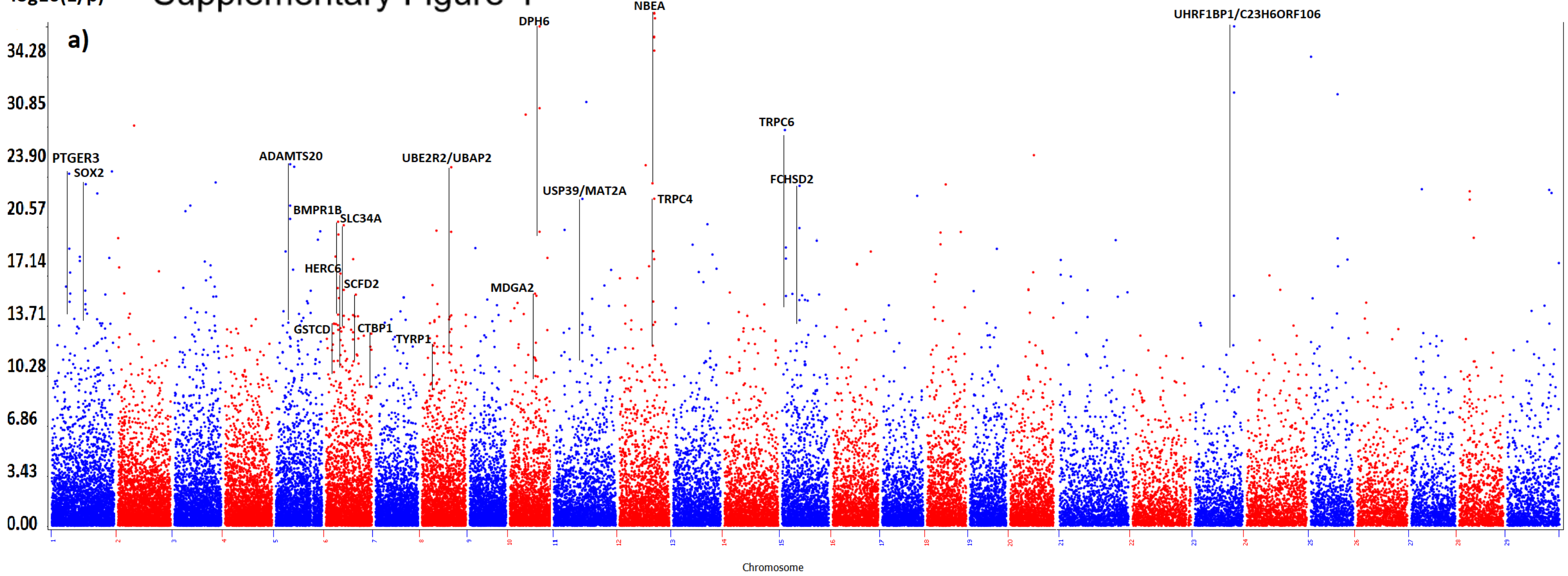
GPS area method

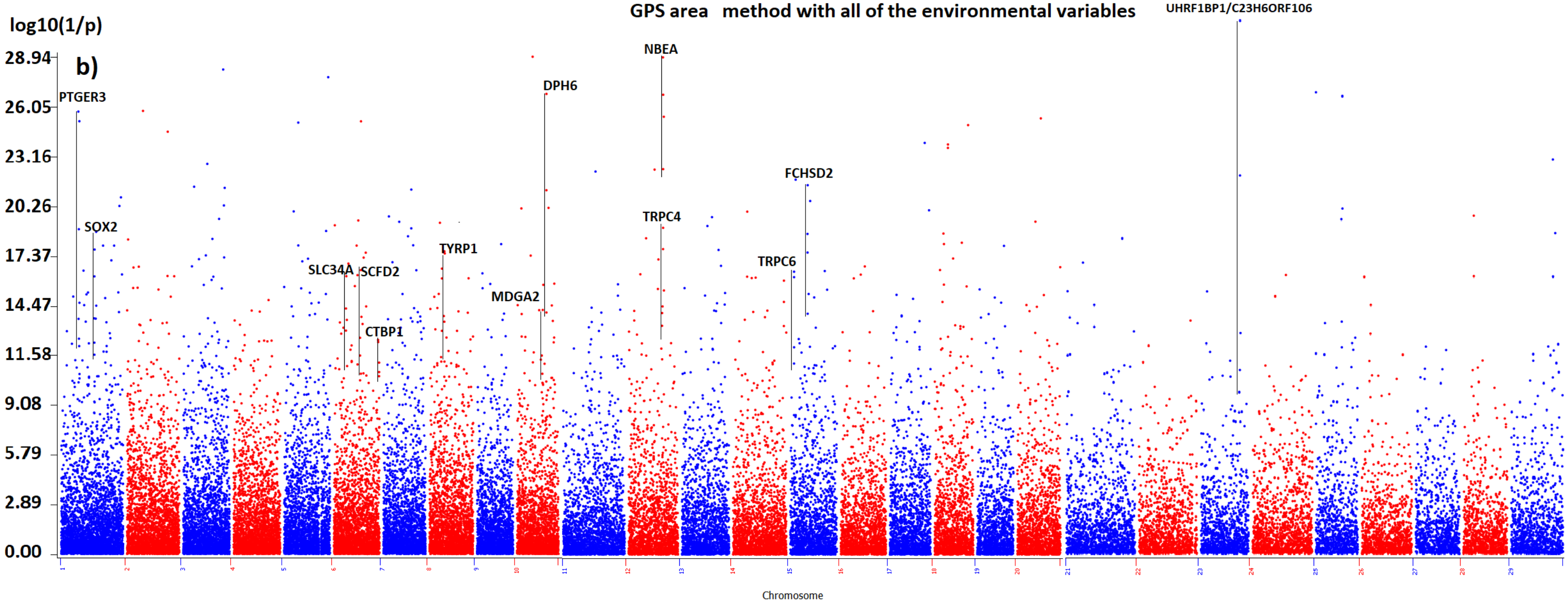
Individual GPS method


ALTITUDE
a)
log10(1/p)
30.72
27.64
24.57
21.50
18.43
15.36
12.29
9.21
6.14
3.07
0.00
NBEA
ADAMTS20
SLC34A
HERC6
USP39/MAT2A
UBE2R2/UBAP2
TRPC4
FCHSD2
TYRP1
CTBP1
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29
Chromosome
Cradle method
b)
log10(1/p)
26.43
23.49
20.56
17.02
14.08
11.75
8.81
5.87
2.94
0.00
SOX2
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29
Chromosome
GPS area method
c)
log10(1/p)
16.32
14.60
13.06
11.43
9.79
8.16
6.53
4.90
1.60
0.00
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29
Chromosome
Individual GPS method


TEMPERATURE
log10(1/p)
a)
36.0
32.44
28.84
25.23
21.63
18.02
14.42
10.81
7.21
3.60
0.00
SOX2
ADAMTS20
BMPR1B
SLC34A
HERC6
SCFD2
CTBP1
TYRP1
UBE2R2/UBAP2
DPH6
USP39/MAT2A
NBEA
TRPC4
TRPC6
FCHSD2
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29
Chromosome
Cradle method
log10(1/p)
b)
34.80
31.32
27.84
24.36
20.88
17.40
13.92
10.44
6.96
3.48
0.00
SOX2
ADAMTS20
SCFD2
TYRP1
UBE2R2/UBAP2
DPH6
USP39/MAT2A
NBEA
TRPC6
FCHSD2
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29
Chromosome
GPS area method
log10(1/p)
c)
25.83
23.24
20.66
18.08
15.50
12.91
10.33
7.55
5.17
2.58
0.00
SOX2
TYRP1
DPH6
TRPC6
FCHSD2
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29
Chromosome
Individual GPS method

Supplementary Figure 4


Cradle method with all of the environmental variables


GPS area method with all of the environmental variables

Supplementary Figure 5

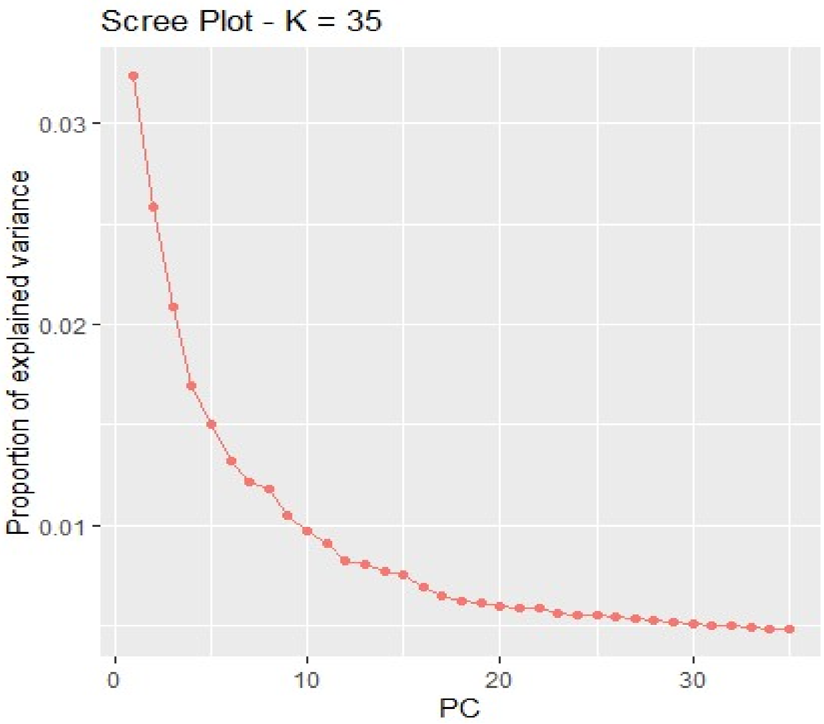
	C1	C2	C3	C4	C5
mean	156.9	133.1	128.5	107.6	81.9
s.d.	14.3	23.1	18.0	21.2	36.4

	C1	C2	C3	C4	C5
mean	632.0	692.1	884.2	873.6	949.8
s.d.	84.7	102.4	62.3	121.9	180.5

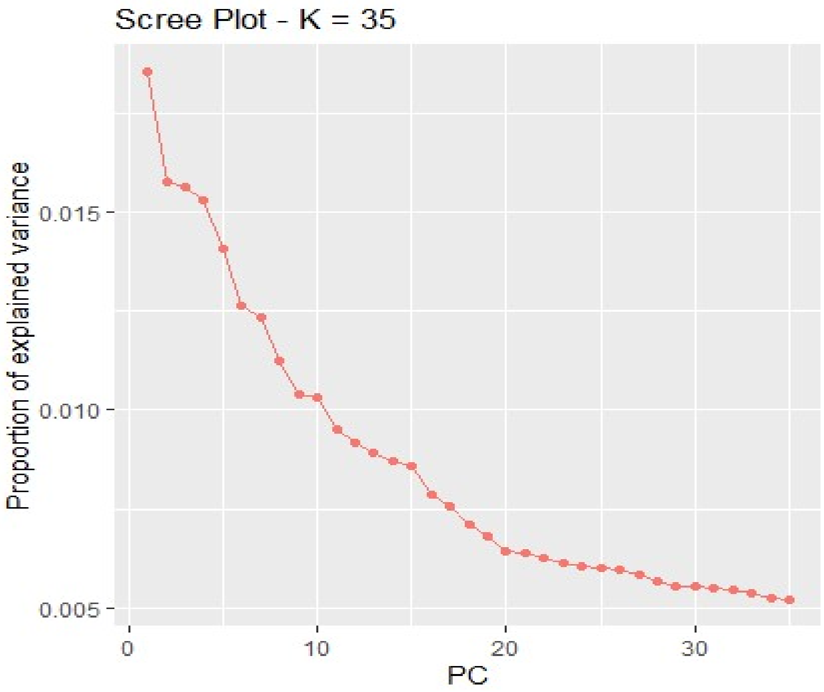
	C1	C2	C3	C4	C5
mean	444.3	485.3	614.6	578.0	1067.5
s.d.	287.1	426.7	326.6	448.1	631.8

Supplementary Figure 6

a)



b)



Chr	Numb. of signatures	Signature range	Identified by PCAdapt	Identified by LFMM	Gene(s) identified (genes around) In bold gene(s) with the highest probability of being under selection	Agronomic trait/function reported in the literature for domestic mammals	Literature on genes identified in relation to environmental adaptation in mammals and birds
1	2	46047752-46411087		🟩	**PTGER3** (ZRANB2)		
		84242981-84773966		🟩	Intergenic zone between ATP11B and **SOX2**		**SOX2**: implicated in circadian behavioral rhythms in murine (Cheng et al., 2019), cold adaptation in marmots (Bai et al., 2019)
5	1	36576428-37074733		🟩	**ADAMTS20**	**ADAMTS20:** Coat coloration (Oget, Servin, & Palhière 2019; Bertolini et al., 2018)	**ADAMTS20 :** associated with high altitude condition in Chinese sheep (Yang et al., 2016)
6	7	19677067-20300302		🟩	**GSTCD**/PPA2/**TET2** (ARHGEF38/INTS12/NPNT)		**GSTCD**: adaptation to hypoxia in yaks (Wang et al., 2019), adaptation to climate variables in South African goats (Mdladla, 2016)
		30139296-30874402		🟩	**BMPR1B/**PDLIM5/HPGDS/SMARCAD1 (UNC5C)	**BMPR1B**: Ovarian function/fecundity (Shokrollahi & Morammazi, 2018; Mulsant et al., 2001; Souza et al., 2001; Wilson et al., 2001), body size in sheep (Cao et al., 2015)	PDLIM5*: high altitude adaptation in Yaks (Qi et al., 2019)
		36835876-36949805	🟪	🟩	**HERC6**/PPM1K (HERC5/ABCG2)	**HERC6**/ABCG2**:** milk production (Yurchenko et al., 2019, Do et al., 2017)	**HERC6**: adaptation to climate variables in South African goats (Mdladla, 2016), associated with stress grazing tolerance in goats (Mwacharo et al., 2018); associated with arid adaptation in Chinese sheep (Yang et al., 2016)
		45415286-45625340		🟩	**SLC34A2** (ANAPC4/SEL1L3)	SEL1L3: milk production (Sanchez et al., 2007)	**SLC34A2:** adaptation to high altitude in cattle (Verma et al., 2018) SEL1L3*: high altitude adaptation in Ethiopian sheep (Edea, Dadi, Dessie, & Kim, 2019)
		69082499-69758377		🟩	**SCFD2**/LNX1 (FIP1L1/RASL11B)	**SCFD2:** milk constitution (Yodklaew et al., 2017), involved in lipid metabolism (Glastonbury et al., 2016)	
		85991683-86155374	🟪		**CSN1S1/CSN2**	**CSN1S1/CSN2:** structural genes of ruminant milk (see	

Supplementary Table 3

			🟪			Martin, Szymanowska, Zwierzchowski, & Leroux, 2002)	
		116501734-117144177		🟩	**CTBP1/**FAM193A/TNIP2/NOP14/GRK4/HTT (ADD1/SH3BP2/MFSD10)	**CTBP1**: lipid storage, fat cell regulation, fat tail deposition (Xu et al., 2017)	FAM193A: slope adaptation in Moroccan sheep (Benjelloun, 2015)
7	1	59624626-60848321	🟪		**SIL1/CTNNA1/**UBE2D2/CDC25C/LOC108636363 (TMEM173/ECSCR/DNAJC18/MATR3/SLC23A1/PAIP2/LRRTM2)	**CTNNA1/SIL1:** associated with fecundity (Lai et al., 2016), fat tail deposition in sheep (Ahbara et al., 2019) UBE2D2: fat tail deposition in sheep (Mastrangelo et al., 2019) **CTNNA1:** skeletal muscle (Sadkowski et al., 2008)	**SIL1:** associated with plateau condition in Chinese sheep (Yang et al., 2016) **CTNNA1*:** high altitude adaptation in Yaks (Qi et al., 2019) TMEM173: associated with desert condition in Chinese sheep (Yang et al., 2016)
8	2	74894754-75321840	🟪	🟩	**UBE2R2/UBAP2/**NOL6 (AQP7/AQP3/DCAF12)		**UBE2R2/UBAP2:** associated with hypoxia tolerance in humans (Udpa et al., 2014); associated with high altitude condition in Chinese sheep (Yang et al., 2016) AQP7: high altitude adaptation in Yaks (Qi et al., 2019) AQP7/AQP3*: implicated in thermal adaptation (Wollenberg Valero et al., 2014)
		31846675-32220312		🟩	Intergenic zone close to **TYRP1**	**TYRP1**: coat color (Gratten et al., 2007; Becker et al., 2015)	**TYRP1***: associated with desert condition in Chinese sheep (Yang et al., 2016)
10	3	49806948-50111884	🟪		**TCF12**	**TCF12:** associated with litter size (Tao et al., 2013), lactation (Ozdemir Ozgenturk et al., 2017), muscle lipid composition (Dunner et al., 2013)	**TCF12:** adaptation to climate variables in South African goats (Mdladla, 2016)
		61579137-63362001		🟩	**MDGA2** (RPL10L)		**MDGA2:** adaptation to climate variables in South African goats (Mdladla, 2016)
		71545588-71700461		🟩	Intergenic between **DPH6** and C10H15ORF41		**DPH6**: under selection in northern European cattle (Stronen et al., 2019); under selection in Yaks (Lan et al., 2018); associated with plateau condition in Chinese sheep (Yang et al., 2016)
11	3	37793580-38186897	🟪		**LOC106502619/**PNPT1/CFAP36		

			🟪		(SEC4R3B/EFEMP1)		
		48845878-49036557		🟩	**USP39/MAT2A**		
		61247655-61456836	🟪		**WDPCP** (EHBP1/OTX1)	**WDPCP**: regulates adipogenesis (Sazzini et al., 2016)	**WDPCP**: high altitude adaptation in Ethiopian sheep (Edea et al., 2019) and in Tibetan chicken (Wang et al., 2015) EHBP1: associated with desert condition in Chinese sheep (Yang et al., 2016)
12	4	43598089-44471339	🟪		Intergenic zone between **KLHL1** and **PCDH9**	**KLHL1**: associated with milk yield and lactation persistence (Yue et al., 2017), related to neuron motion and neuromuscular process (Shin et al., 2014) **KLHL1 and PCDH9:** associated with fat tail deposition (Mastrangelo et al., 2019)	**KLHL1**: associated with high altitude adaptation in Chinese sheep (Yang et al., 2016), under selection in human Tibetan (Wang et al., 2011) **PCDH9:** under selection in goat and sheep of arid environment (Kim et al., 2016)
		48839256-51252236	🟪		**RNF17/ZMYM2/PARP4/XPO4/** PSPC1/CRYL1/IFT88/CENPJ/EEF1AKMT1 (ZMYM5/GJB2/IL17D/MPHOSPH8/ATP12A)	**RNF17**: associated with fatty acid composition (Lemos et al., 2016) and growth traits (Edea et al., 2018, Puig-Oliveras et al., 2014) **PARP4**: influences carcass weight (Edea et al., 2018) MPHOSPH8/PARP4/CENPJ/RNF17: associated with growth rate (Mészáros et al., 2019) MPHOSPH8: up regulated in atretic follicles (Hatzirodos et al., 2014) IFT88: growth and feed intake (Yurchenko et al., 2019)	**RNF17:** adaptation to climate variables in South African goats (Mdladla, 2016) ATP12A: connected to APT mechanisms and high altitude, adaptation in goats (Wang et al. 2016); under selection in sheep of arid environment (Kim et al., 2016) **ZMYM2*/PARP4/**ZMYM5/PSPC1/CENPJ/GJB2: high altitude adaptation in Ethiopian sheep (Edea et al., 2019) GJB2: under selection in goat of arid environment (Kim et al., 2016), associated with high altitude adaptation in Tibetan sheep (Wei et al., 2016) and environmental adaptation via DNA repair mechanisms (Edea et al., 2014) **XPO4**/CRYL1/CENPJ/**RNF17**/MPHOSPH8/**PARP4**: associated with stress grazing tolerance in goats (Mwacharo et al., 2018) IFT88/XPO4: under selection in Moroccan goat (Benjelloun, 2015)
		60637258-60950668	🟪	🟩	**NBEA** (MAB21L1)	**NBEA**: wool trait (Wang et al., 2014)	**NBEA**: high altitude adaptation in Ethiopian sheep (Edea et al., 2019) and in cattle (Zeng, 2017); associated

			🟪	🟩			with body temperature regulation in cattle (Howard et al., 2013) under selection in Ugandan and Morocan goat (Onzima et al., 2018, Benjelloun, 2015); associated with desert adaptation and high altitude adaptation in Chinese sheep (Yang et al., 2016), high altitude adaptation in Yaks (Qi et al., 2019)
		62109741-62503627		🟩	**TRPC4** (POSTN/SUPT20H)		**TRPC4**: associated with resistance to *Haemonchus contortus* in goat (Corley et al. 2013), implicated in body temperature regulation in cattle (Howard et al., 2013)
13	1	46458560-46473488	🟪		**PRNP**		**PRNP***: associated with susceptibility to prion disease in sheep and goat (Greenlee, 2019 for a review)
14	1	16942897-17652266	🟪		**VPS13B**	**VPS13B**: milk-related trait (Liu et al., 2018); associated with leg morphology, related with fertility and milk production (Capitan et al., 2014)	**VPS13B**: under selection in Morocan goat (Benjelloun, 2015); associated with arid adaptation in Chinese sheep (Yang et al., 2016), high altitude adaptation in Yaks (Qi et al., 2019)
15	2	6473101-6606528		🟩	**TRPC6/** ANGPTL5 (CEP126)		**TRPC6*:** high altitude adaptation in Tibetan highlanders (Deng et al., 2019)
		30213116-30556088		🟩	**FCHSD2/**ARHGEF17 (P2RY6/P2RY2)		
18	2	36054355-37092141	🟪		**NFATC3**/NUFT2/SMPD3/PRMT7/SLC7A6/PSKH1/CENPT (SLC12A4)		
		39636636-39980690	🟪		**LOC108637979** (ZFHX3/PMFB1)		
19	1	32969117-33274858	🟪		**PIGL/**LOC102188626**/NCOR1**/CENPV (ADORA2B)		**PIGL**/CENPV: associated with high altitude in Chinese sheep (Yang et al., 2016) **NCOR1** belong to clock circadian gene network in cattle (Wang et al., 2015) ADORA2B*: implicated in thermal adaptation (Wollenberg Valero et al., 2014)
20	1	13992024-14204949	🟪		**ADAMTS6/**CENPK (PPWD1)	**ADAMTS6:** involved in growth traits in pig (Wu et al. 2019)	**ADAMTS6**/CENPK: associated with high altitude adaptation in Chinese sheep (Yang et al., 2016)
22	2	28867395-29079702	🟪		**SHQ1** (RYBP/PPP4R2/GXYLT2)	**SHQ1**/PPP4R2**:** associated with milk production	**SHQ1**: associated with plateau and desert condition in Chinese sheep (Yang et al., 2016)

			🟪			(Pasandideh et al., 2018; Stella et al., 2010)	
		33594470-34062919	🟪		**SUCLG2**	**SUCLG2 :** associated with milk production (Di Gerlando et al., 2019), associated with fat deposition in cattle (Silva-Vignato et al., 2019), associated with growth in pig (Yang et al., 2012)	**SUCLG2* :** under selection in sheep of arid environment (Kim et al. 2016); associated with desert condition in Chinese sheep (Yang et al., 2016), high altitude adaptation in Yaks (Qi et al., 2019)
23	2	36461204-36962562	🟪		**BTBD9**/ZFAND3		**BTBD9**: adaptation to climate variables in South African goats (Mdladla, 2016) ZFAND3: associated with high altitude condition in Chinese sheep (Yang et al., 2016)
		39855572-40059589		🟩	**UHRF1BP1/C23H6ORF106 (**SNRPC)		**UHRF1BP1** high altitude adaptation in Yaks (Qi et al., 2019)
25	1	30481819-30744262	🟪		**AUTS2**		
26	1	28596734-29498263	🟪		**FBXW4/BTRC/GBF1/**PSD/C26H10ORF76/DPCD (MFSD13A/ACTR1A/NFKB2/PITX3)	**BTRC:** associated with milk fatty acid composition (Palombo et al., 2018); associated with milk production (Paten, 2014); genes associated with fatty acid composition of pork (Viterbo et al., 2018)	**FBXW4/BTRC:** associated with desert in Chinese sheep (Yang et al., 2016) **BTRC:** adaptation to climate variables in goats (Mdladla, 2016), associated with high altitude condition in Chinese sheep (Yang et al., 2016)

*belong to the hypoxia regulated proteins database (http://www.hypoxiadb.com)

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Chr	Numb. of signatures	Signature range	Identified PCAdapt	Identified LFMM	Gene(s) identified In bold gene(s) with the highest probability of being under selection	Agronomic trait/function reported in the literature for domestic mammals	Literature on genes identified in relation to environmental adaptation in mammals and birds
1	3	117132460-117619369		🟩	CD247/MAEL/**POU2F1**/ LOC105612997/RCSD1	**POU2F1**: associated with lactase persistence (Lewinsky et al., 2005); involved in the expression of beta-casein in mammary gland (Zhao et al., 2002), involved in growth and fat deposition in pig (Pérez-Montarelo et al., 2014)	**POU2F1**: participate in the cellular response to hypoxia in human (Choi et al., 2005; Yan et al., 1999) RCSD1: association with endoparasite phenotypes in cattle (Twomey et al., 2019)
		170496673-170755505		🟩	**BBX**	**BBX:** would be associated with supernumerary nipple in sheep (Peng et al., 2017)	
		198199858-198342295		🟩	**MASP1**/RTP1 (LOC105602729)		
2	2	74396276-74749751		🟩	**KDM4C**	**KDM4C:** affect reproduction (Guan et al., 2016)	
		203734535-204610983		🟩	**NBEAL1/**ICA1L/ FAM117B (BMPR2)	**NBEA**: wool trait (Wang et al. 2014) ICA1L/FAM117: associated with the pygmy phenotype (Pemberton et al., 2017) BMPR2: involved in ovulation rate and litter size in sheep (Jansson, 2014)	**NBEA**: high altitude adaptation in Ethiopian sheep (Edea et al., 2019) and in cattle (Zeng, 2017); associated with body temperature regulation in cattle (Howard et al., 2013) under selection in Ugandan and Morocan goat (Onzima et al., 2018, Benjelloun, 2015); associated with desert adaptation and high altitude adaptation in Chinese sheep (Yang et al., 2016), high altitude adaptation in Yaks (Qi et al., 2019) BMPR2*: Associated with high Altitude Pulmonary Hypertension in Kyrgyz Highlanders (Iranmehr et al., 2019) and in cattle (Newman et al., 2011), associated with desert adaptation and plateau adaptation in Chinese sheep (Yang et al., 2016)

Supplementary Table 4

3	1	153576602-154585886	🟪	🟩	**MSRB3**/LOC105609946/WIF1	**MSRB3:** associated with hear phenotype (Wei et al., 2015, Chen et al., 2018, Webster et al., 2015), associated with fat deposition (Mastrangelo et al., 2019)	**MSRB3:** high altitude adaptation in Ethiopian sheep (Edea et al., 2019) and in dogs (Gou et al., 2014); identified as being under selection in Tibetan sheep (Wei et al. 2016), high altitude adaptation in Yaks (Qi et al., 2019)
4	3	24727308-25337674		🟩	**ISPD**/TSPAN13		
		43272227-43454930		🟩	**MAGI2**		**MAGI2*:** high altitude adaptation in Ethiopian sheep (Edea et al., 2019); associated with desert and arid adaptation in Chinese sheep (Yang et al., 2016), high altitude adaptation in Yaks (Qi et al., 2019)
		47614996-48783775		🟩	COG5/DUS4L/**BCAP29**/**SLC26A4**/CBLL1 (PIK3CG/HBP1/PRKAR2B/GPR22/SLC26A3)	SLC26A4: associated with hearing (Tsukamoto et al., 2003, Park et al., 2003)	**BCAP29/ SLC26A4**: associated with arid adaptation in sheep (Yang et al., 2016) PRKAR2B: associated with plateau adaptation in Chinese sheep (Yang et al., 2016)
5	1	51252017-51859391		🟩	**ARHGAP26**/NR3C1 (TAX1BP1)	**ARHGAP26/**NR3C1*:* affect growth and intra-muscular fatty acid in pig (Edea et al., 2017)	
6	1	36121839-37756801 (PCAdapt) 37536930-38567860 (LFMM)	🟪	🟩	**LCORL/**HERC3/HERC5/LOC105615454/NCAPG/DCAF16 (FAM184B/HERC6/SPP1/PKD2/LAP3/MED28/PPM1K/ABCG2/MEPE/IBSP)	**LCORL/** LAP3/ FAM184B: growth traits (Al-Mamun et al. 2015, Lindholm-Perry et al., 2001; Bongiorni et al., 2012; Eberlein et al., 2009) ABCG2/SPP1/LAP3/NCAPG/MEPE: milk production (see Ruiz-Larrañaga et al., 2018)	HERC6/SPP1*: associated with arid adaptation in Chinese sheep (Yang et al., 2016) HERC6: adaptation to climate variables in South African goats (Mdladla, 2016), associated with stress grazing tolerance in goats (Mwacharo et al., 2018); LAP3: under selection in goat of arid environment (Kim et al., 2016)
8	1	62665338-63271621		🟩	**ARFGEF3**/PERP (TNFAIP3)		**ARFGEF3:** associated with arid adaptation in Chinese sheep (Yang et al., 2016) TNFAIP3*: associated with parasite resistance in cattle (Tay et al., 2018)

9	1	34730111-35192293		🟩	LOC10114620/**ATP6V1H**/RGS20 (TCEA1/LYPLA1/SOX17)		**ATP6V1H**: under selection in goat of arid environment (Kim et al., 2016) **ATP6V1H**/SOX17/RGS20/LYPLA1*: associated with humidity condition in goat (Bertolini et al., 2018)
10	3	29413536-29776019 (PCAdapt) 29479711-29940445 (LFMM)	🟪	🟩	**RXFP2/** BLGALTL	**RXFP2:** involved in horn bud differentiation (Johnston et al., 2011; Allais-Bonnet et al., 2013)	**RXFP2**: associated with latitude, precipitation and temperature in free-ranging bighorn sheep (Roffler et al., 2016); identified as being under selection in Tibetan sheep (Wei et al., 2016).
		38196759-39403332 (PCAdapt) 37941892-39043416 (LFMM)	🟪	🟩	Intergenic zone before **PCDH9**	**KLHL1**: associated with milk yield and lactation persistence (Yue et al., 2017), related to neuron motion and neuromuscular process (Shin et al., 2014) **KLHL1 and PCDH9:** associated with fat tail deposition (Mastrangelo et al., 2019)	**KLHL1**: associated with high altitude adaptation in sheep (Yang et al., 2016); under selection in Tibetan (Wang et al., 2011) **PCDH9:** under selection in goat and sheep of arid environment (Kim et al., 2016)
		42194236-43935671	🟪		Intergenic zone between **PCDH9** and **KLHL1**		
12	1	38573067-39683281		🟩	**VPS13D**/TNFSF18 (TNFSF4/TNFRSF1B/DHRS3)		DHRS3*/TNFRSF1B: associated with arid adaptation in sheep (Yang et al., 2016)
13	3	48552093-49208171	🟪	🟩	Intergenic close to **BMP2**	**BMP2**: fat tail deposition (Zhu et al., 2019 ; Yuan et al., 2017 ; Mastrangelo et al., 2019)	**BMP2**: associated with arid condition in Chinese sheep (Yang et al., 2016); under selection in sheep of arid environment (Kim et al., 2016); identified as being under selection in Tibetan sheep (Wei et al., 2016); high altitude adaptation in Yaks (Qi et al., 2019)
		55025081-56301025		🟩	**CDH26**/FAM217B/PPP1R3D (SYCP2/CDH4/EDN3)	EDN3: associated with coat color (Gautier et al. 2015, Kaelin et al., 2012)	EDN3: associated with plateau adaptation in sheep (Yang et al., 2016), slope in Moroccan sheep (Benjelloun 2015); hypoxic adaptation in cetaceans (Tian et al., 2016)

				🟩		CDH26: associated with fecundity (Lai et al., 2016)	
		57302923-57809890		🟩	**RAB22A**/PMEPA1	**RAB22A:** implicated in fecundity (Lai et al., 2016)	**RAB22A:** implicated in hypoxia (Wang et al., 2014) (PMEPA1 belong to the hypoxia up-regulated proteins database)
15	1	59813250-60219075		🟩	**DCDC5** (DNAJC24/DCDC1)	**DCDC5**: associated with body conformation (Wu et al., 2013)	DNAJC24: associated with high altitude adaptation in sheep; Heat Shock protein (Yang et al., 2016); under selection in Uganda goat (Onzima et al., 2018)
17	1	55110665-55329873		🟩	**CIT**/TMEM233 (PRKAB1)		PRKAB1: under selection in goat of arid environment (Kim et al., 2015)
18	1	66257896-68025345		🟩	**TRAF3**/**CDC42BPB**/PPP1R13B (CKB/KLC1/TDRD9/AKT1/TMEM179/SIVA1/ADSSL1/INF2/C18H14orf180)		TMEM179B: associated with arid condition in sheep (Yang et al., 2016); implicated in hypoxia (Gao et al., 2017)
19	1	28133753-28962852		🟩	**PDZRN3/**GXYLT2 (PPP4R2/SHQ1)	PPP4R2/SHQ1: associated with growth rate (Pasandideh et al., 2018)	SHQ1 associated with plateau and desert condition in sheep (Yang et al., 2016)
21	1	17885334-18117515	🟪		**PAK1** (LOC101117288/AQP11)		PAK1 associated with plateau condition in sheep (Yang et al., 2016); under selection in sheep of arid environment (Kim et al., 2016)
25	1	19073058-19380300	🟪		**JMJD1C/**NRBF2 (REEP3)		REEP3 associated with plateau condition in sheep (Yang et al., 2016) **JMJD1C*/**NRBF2/REEP3:associated with high-altitude adaptation in pig (Dong et al., 2014)

*belong to the hypoxia regulated proteins database (http://www.hypoxiadb.com)

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Chr.	GOAT PCAdapt Signatures	GOAT LFMM Signatures	SHEEP LFMM Signatures	SHEEP PCAdapt Signatures
Chr 1		**46047752-46411087** **snp45739-scaffold627-5315341 46047752*** **snp45746-scaffold627-5616708 46348421** **snp45747-scaffold627-5650100 46381611** **snp12636-scaffold1480-1163799 46411087** **84242981-84773966** **snp32731-scaffold377-2079945 84242981** snp32730-scaffold377-2049881 84272916 **snp32729-scaffold377-2002407 84320917** **snp32728-scaffold377-1966001 84357680*** snp32723-scaffold377-1745669 84573836 snp32721-scaffold377-1639477 84680820 **snp32720-scaffold377-1606429 84713972** **snp32719-scaffold377-1576455 84743986** **snp32718-scaffold377-1546443 84773966**	**117132460-117619369** **s74762.1 117132460** **OAR1_127060133.1 117619369** **s71952.1 117697523** s49384.1 117771574 **OAR1_127291951.1 117853500*** **s73007.1 117916288*** **170496673-170755505** **OAR1_183962708.1 170496673** **OAR1_184162321.1 170690492** **s12579.1 170725424** **OAR1_184227318.1 170755505*** **198199858-198342295** **OAR1_214098599.1 198199858** **OAR1_214136810.1 198227861** **OAR1_214203546.1 198286740** **OAR1_214229899.1 198312258** **OAR1_214247090.1 198329788** **OAR1_214257185.1 198342295***	
Chr2			**74396276-74749751** **OAR2_79262293_X.1 74396276** **OAR2_79499240.1 74613800** **OAR2_79550682.1 74669837*** **OAR2_79594745.1 74714666***	

Supplementary Table 5

			s62643.1 74749751* 203734535-204610983 s34105.1 203717963 OAR2_215477291.1 203734535 OAR2_215596955.1 203761367 OAR2_215636399.1 203797311* OAR2_215711808.1 203869407 OAR2_216615372.1 204610983	
Chr 3			153576602-154585886 OAR3_164422954.1 153576602 s26177.1 153826281* s69653.1 153976304* s69686.1 153996225 OAR3_165009241.1 154033734 OAR3_165050963.1 154072493 OAR3_165200988.1* 154223123 s75917.1 154318689* s61003.1 154585886	153889169-154318689 OAR3_164788310.1 153889169 s16949.1 153927239 s69653.1 153976304 s69686.1 153996225 OAR3_165009241.1 154033734 OAR3_165050963.1 154072493* s75917.1 154318689
Chr 4			24727308-25337674 OAR4_26039959.1 24727308* OAR4_26021918.1 24745112* OAR4_26202538_X.1 24891467* OAR4_26645098.1 25337674 43272227-43454930 OAR4_45683707.1 43272227 OAR4_45746457.1 43333090*	

			s36928.1 43433914 **OAR4_45871691.1 43454930*** **47614996-48783775** **OAR4_50346558.1 47614996** s34975.1 47852019 OAR4_50737323.1 47928357 **s24500.1 47960510** **s39886.1 48085823** **s32219.1 48284042** **OAR4_51241289.1 48402666** **OAR4_51315739.1 48480244** **OAR4_51346813.1 48510936** **OAR4_51441757.1 48607563** **OAR4_51489408.1 48649775*** **s46022.1 48737779*** **OAR4_51625352.1 48783775**	
Chr 5		**36576428-37074733** **snp9058-scaffold1329-759519 36576428** **snp9059-scaffold1329-790608 36606034** **snp9062-scaffold1329-936768 36750654** **snp9063-scaffold1329-976103 36790914*** snp9066-scaffold1329-1128684 36939084 **snp12728-scaffold149-35530 37074733**	**51252017-51859391** **s44340.1 51252017*** **OAR5_55651844.1 51284980** **OAR5_55827200.1 51367486** **OAR5_55949772.1 51459909*** OAR5_56305688.1 51818687 **OAR5_56351796.1 51859391***	
Chr 6	**36835876-36949805** **snp26737-scaffold281-187160 36835876** **snp26738-scaffold281-221127 36870090**	**19677067-20300302** snp49755-scaffold710-1594826 19677067 **snp49753-scaffold710-1514064 19757830**	**37536930-38567860** **OAR6_41850329.1 37536930** OAR6_42094768.1 37756801	**36121839-37756801** OAR6_40409402.1 36121839 **OAR6_40496376.1 36210335**

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Chr 21				**17885334-18117515** **OAR21_20255140_X.1 17885334** **s23216.1 17896095*** **OAR21_20293826.1 17924936** **OAR21_20301210.1 17931634*** **OAR21_20371526.1 18002035** **OAR21_20401829.1 18030662** **s62605.1 18117515**
Chr 22	**28867395-29079702** **snp3022-scaffold1091-866051 28867395** **snp3023-scaffold1091-919725 28921320*** **snp3024-scaffold1091-953204 28955150*** **snp3025-scaffold1091-1001799 29004527*** **snp3026-scaffold1091-1047549 29050298** **snp3027-scaffold1091-1076915 29079702** **33594470-34062919** **snp13803-scaffold154-526016 33594470** snp13800-scaffold154-407557 33709623 **snp13799-scaffold154-347555 33769647** **snp13798-scaffold154-300085 33818637** **snp13797-scaffold154-243475 33876201** **snp13796-scaffold154-213942 33905179** **snp13795-scaffold154-182886 33936550** snp13794-scaffold154-139936 33979489			

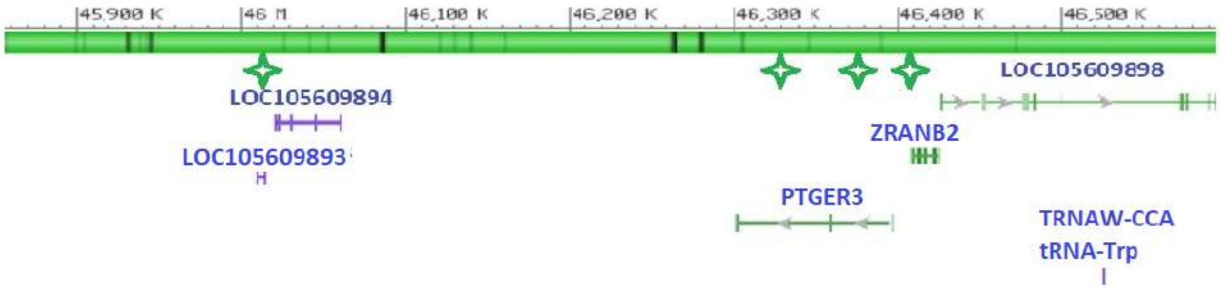
	snp13793-scaffold154-98284 34020913* **snp13792-scaffold154-56173 34062919**			
Chr 23	**36461204-36962562** **snp59312-scaffold975-869095 36461204** **snp59311-scaffold975-838707 36491546*** **snp59310-scaffold975-794737 36534387** snp59309-scaffold975-765057 36564031 **snp59308-scaffold975-735328 36594106** snp59307-scaffold975-682257 36642064 snp59299-scaffold975-362386 36962562	**39855572-40059589** **snp23559-scaffold2376-180998 39855572** **snp23560-scaffold2376-217634 39892708** snp23561-scaffold2376-253763 39928817 **snp23562-scaffold2376-312530 39987612*** **snp23563-scaffold2376-384575 40059589***		
Chr 25	**30481819-30744262** **snp9550-scaffold1343-2237381 30481819** **snp9551-scaffold1343-2270352 30514941*** snp9553-scaffold1343-2330570 30576113 **snp9554-scaffold1343-2381252 30626531** **snp9556-scaffold1343-2459116 30704234** snp9557-scaffold1343-2499155 30744262			**19073058-19380300** **OAR25_19823535.1 19073058** **OAR25_19926183.1 19174899** **OAR25_19941944.1 19190707** **OAR25_20026839.1 19273755*** **OAR25_20041897.1 19290987*** **OAR25_20106030.1 19342453*** OAR25_20142347.1 19380300
Chr 26	**28596734-29498263** snp41096-scaffold532-288303 28596734 **snp41097-scaffold532-332094 28640088** **snp41098-scaffold532-368969 28677110** **snp41099-scaffold532-409992 28717972** snp41100-scaffold532-448160 28756401 snp41101-scaffold532-481203 28788742 snp41104-scaffold532-649324 28957011 snp41105-scaffold532-692721 29001092 snp41109-scaffold532-897192 29205431 **snp41110-scaffold532-933054 29241421*** **snp41111-scaffold532-965874 29274605***			

	snp41112-scaffold532-1001039 29309963 snp41113-scaffold532-1051457 29360578 **snp41114-scaffold532-1082302 29391742** **snp41117-scaffold532-118800329498263**			

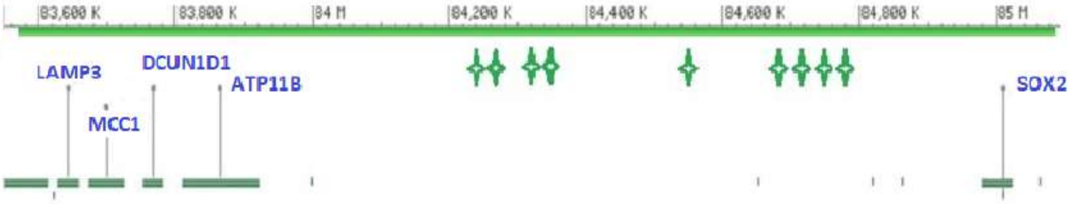
The beginning and end of each signature is indicated in base pairs and underlined; SNPs showing p-value$<10^{-6}$ are indicated for each signature; in bold SNPs showing p-value$<1.10^{-9}$; *SNPs showing highest p-values of the signatures.

Supplementary Table 6

GOAT

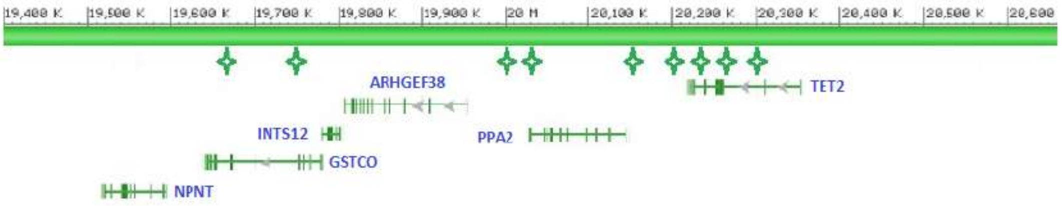


Chr. 1



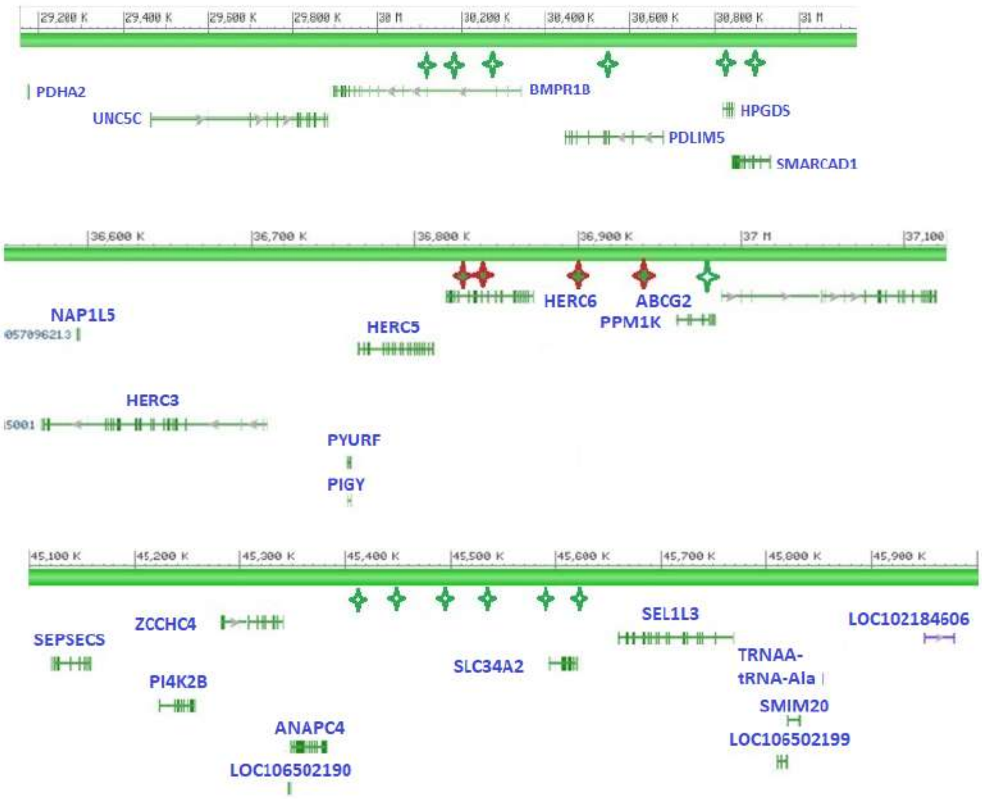
GOAT

Chr. 5

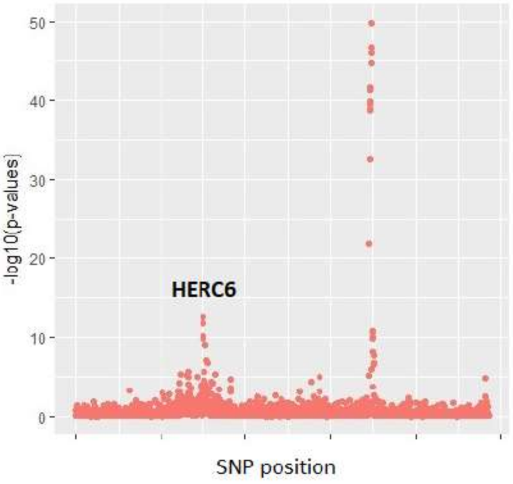


Chr. 6

GOAT

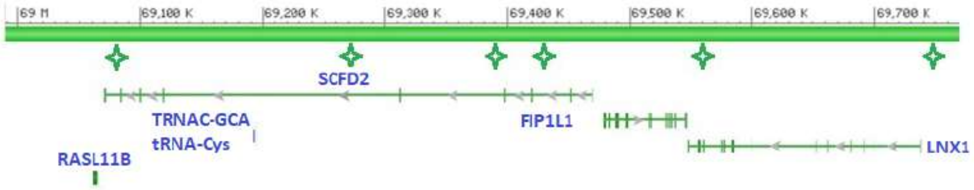


Chr. 6

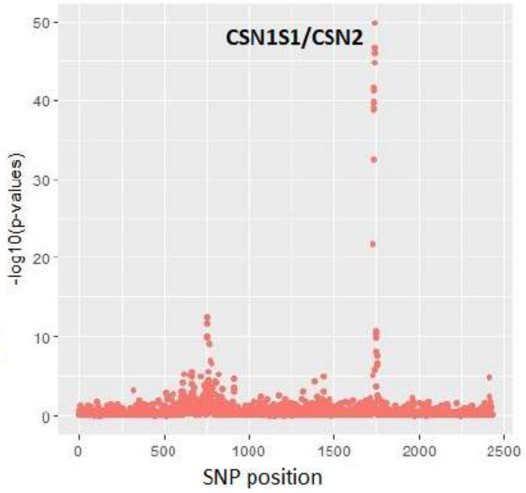


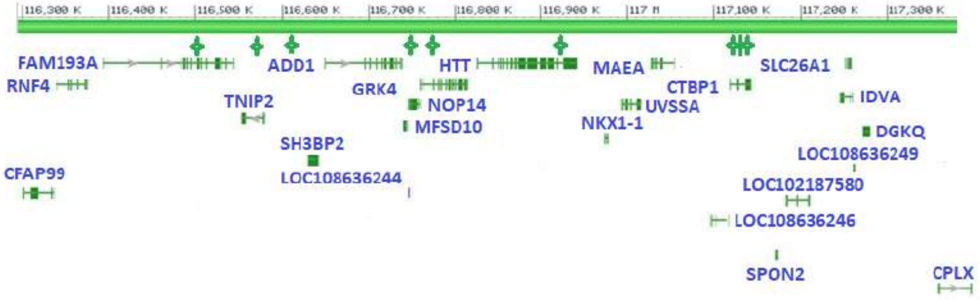
Chr. 6

GOAT

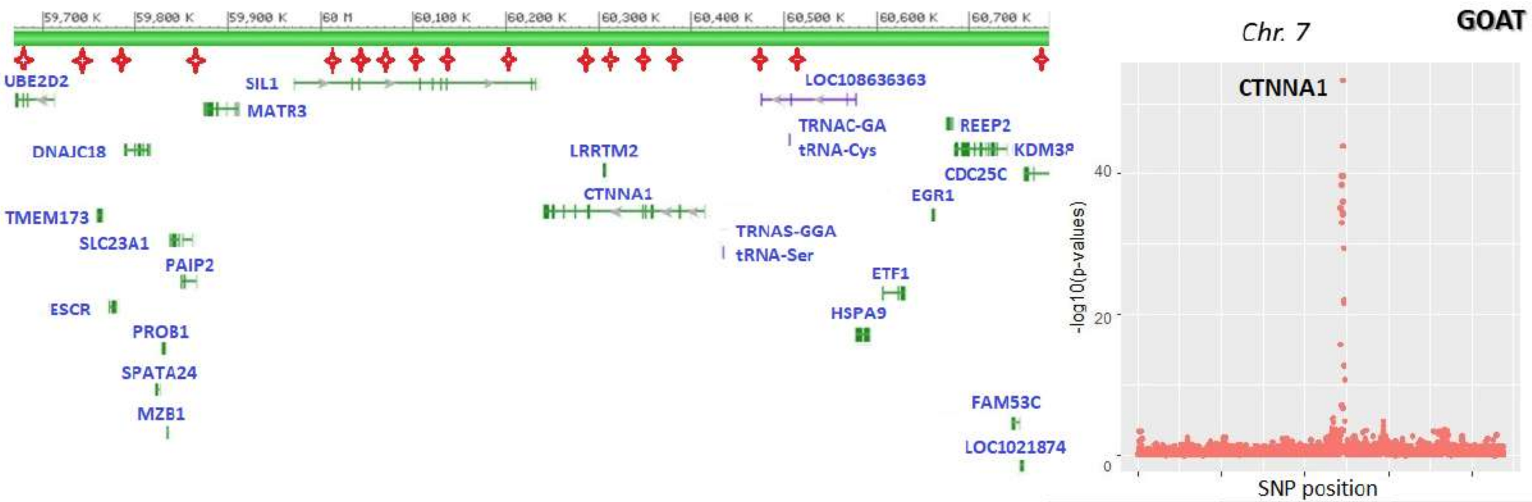


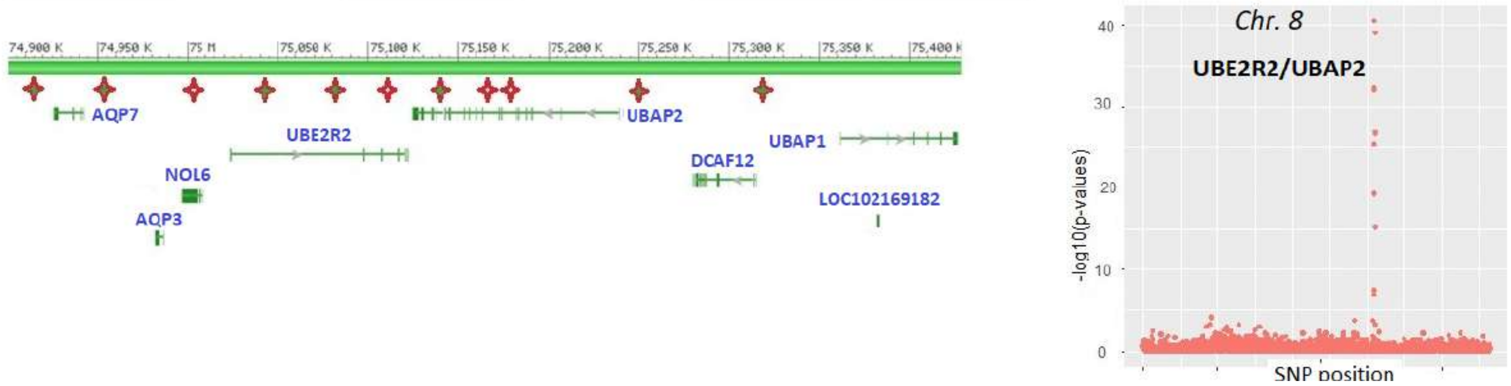
Chr. 6



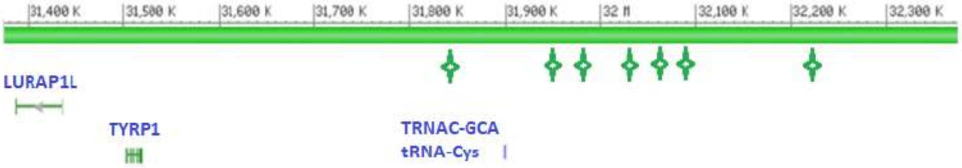


Chr. 6

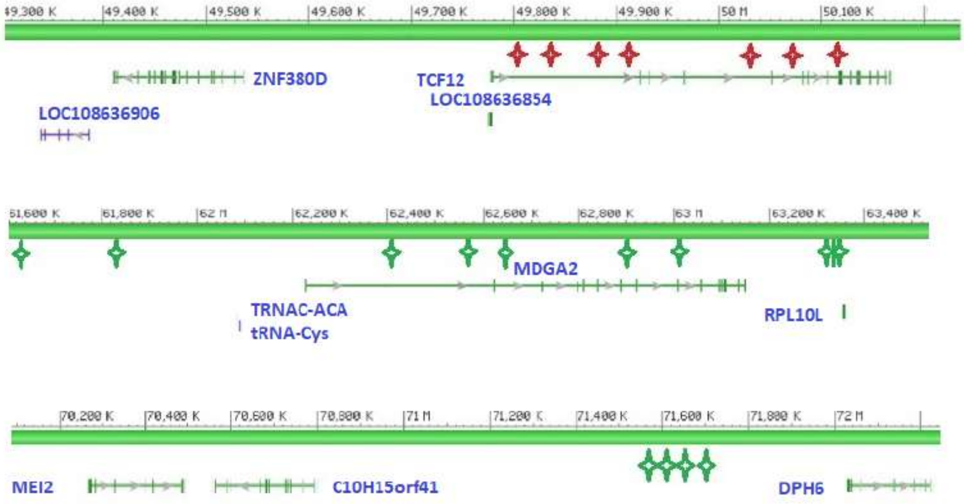

GOAT
Chr. 7
CTNNA1
59,700 K
59,800 K
59,900 K
60 M
60,100 K
60,200 K
60,300 K
60,400 K
60,500 K
60,600 K
60,700 K
UBE2D2
SIL1
MATR3
LOC108636363
TRNAC-GA
tRNA-Cys
REEP2
KDM3B
CDC25C
DNAJC18
LRRTM2
CTNNA1
EGR1
TMEM173
SLC23A1
PAIP2
TRNAS-GGA
tRNA-Ser
ETF1
HSPA9
ESCR
PROB1
SPATA24
MZB1
FAM53C
LOC1021874
-log10(p-values)
0
20
40
SNP position

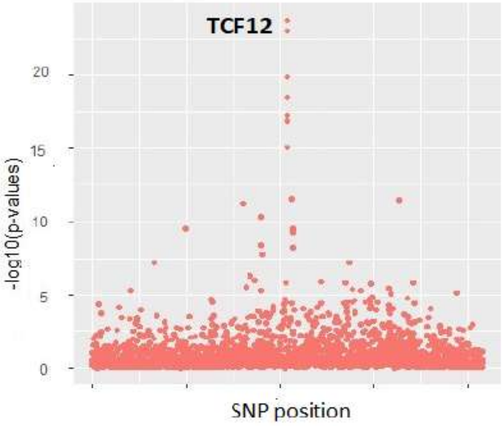

Chr. 8
UBE2R2/UBAP2
74,900 K
74,950 K
75 M
75,050 K
75,100 K
75,150 K
75,200 K
75,250 K
75,300 K
75,350 K
75,400 K
AQP7
UBE2R2
UBAP2
UBAP1
NOL6
DCAF12
LOC102169182
AQP3
-log10(p-values)
0
10
20
30
40
SNP position

GOAT



Chr. 8

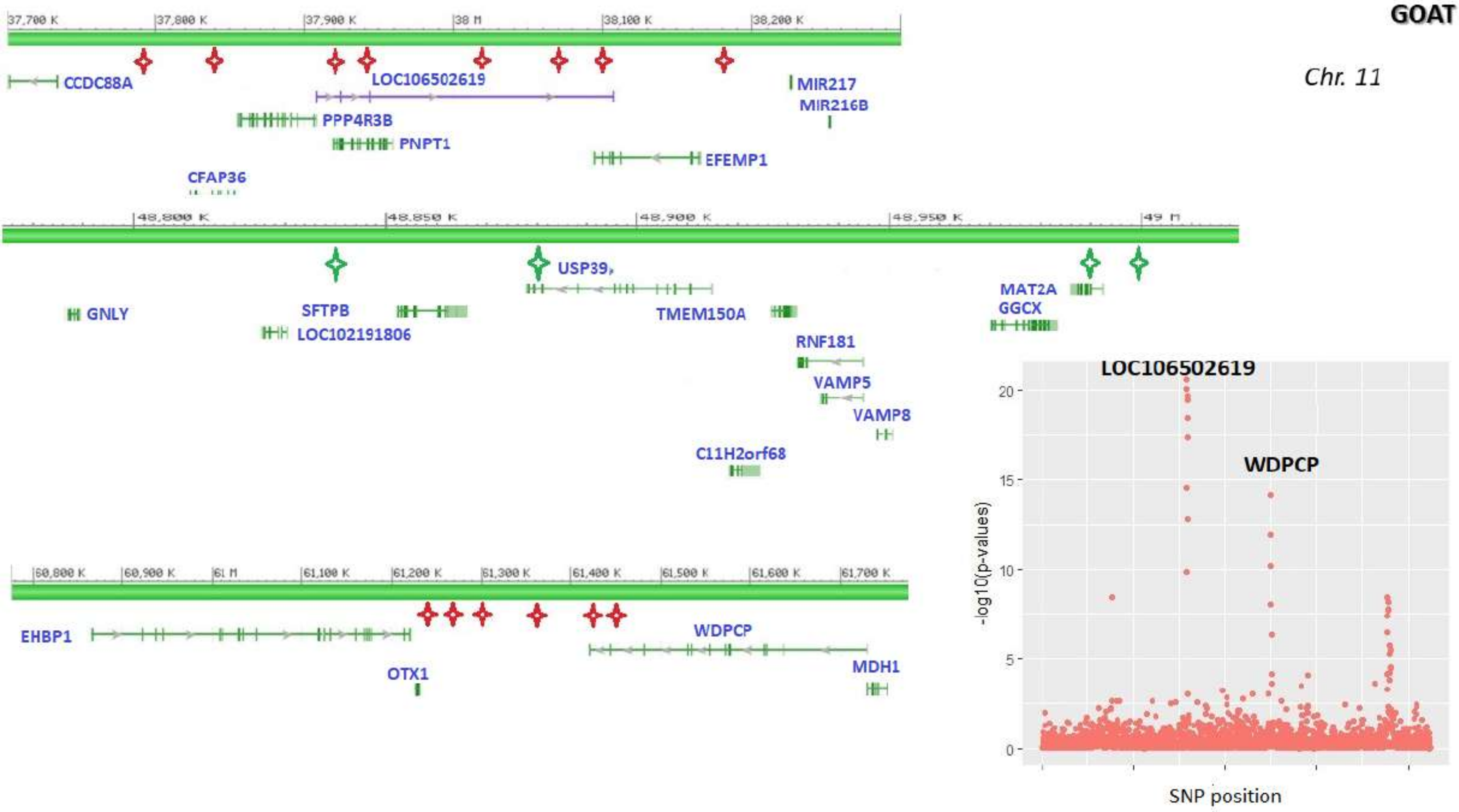




Chr. 10

GOAT

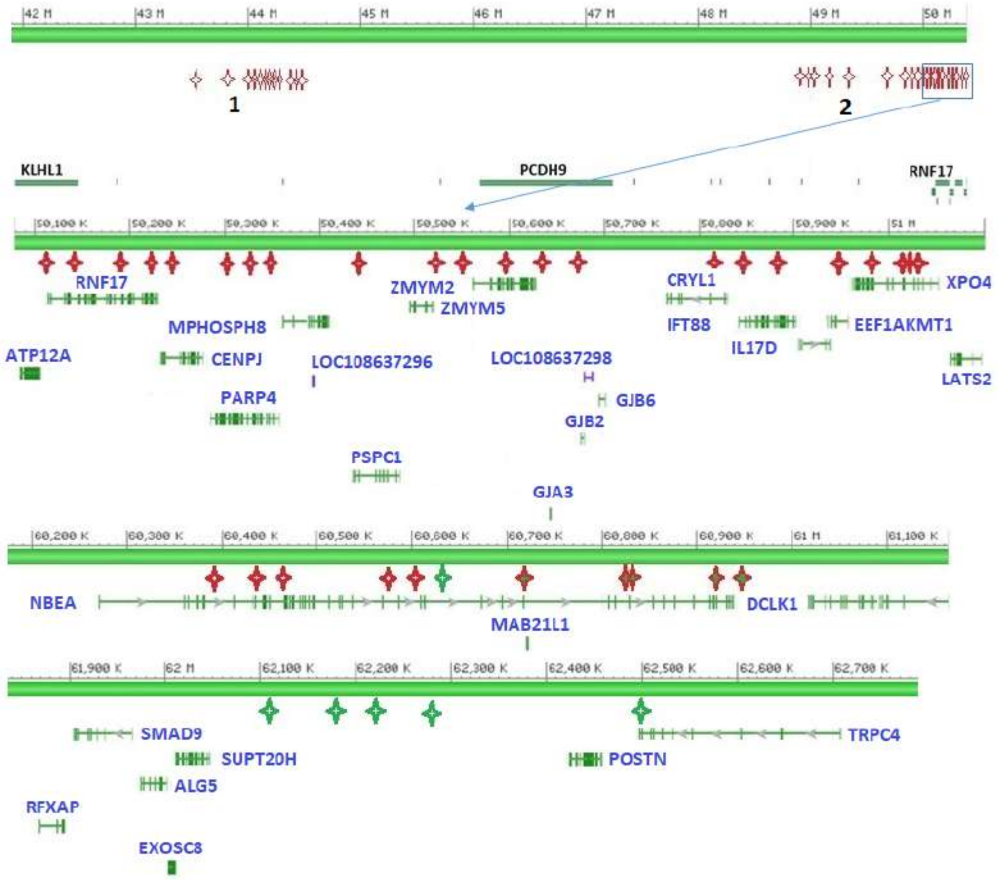
Chr. 11



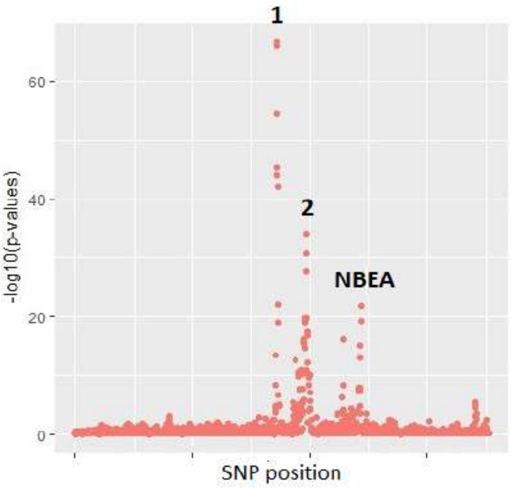
37,700 K
37,800 K
37,900 K
38 M
38,100 K
38,200 K
CCDC88A
LOC106502619
MIR217
MIR216B
PPP4R3B
PNPT1
EFEMP1
CFAP36
48,800 K
48,850 K
48,900 K
48,950 K
49 M
USP39
SFTPB
GNLY
LOC102191806
TMEM150A
MAT2A
GGCX
RNF181
VAMP5
VAMP8
C11H2orf68
60,800 K
60,900 K
61 M
61,100 K
61,200 K
61,300 K
61,400 K
61,500 K
61,600 K
61,700 K
EHBP1
WDPCP
OTX1
MDH1
LOC106502619
WDPCP
20
15
10
5
0
-log10(p-values)
SNP position

Chr. 12

GOAT

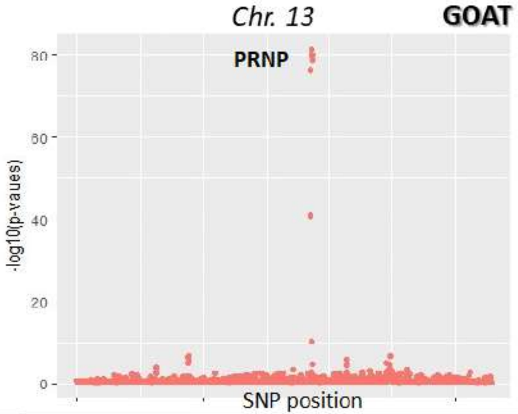


42 M
43 M
44 M
45 M
46 M
47 M
48 M
49 M
50 M
1
2
KLHL1
PCDH9
RNF17
50,100 K
50,200 K
50,300 K
50,400 K
50,500 K
50,600 K
50,700 K
50,800 K
50,900 K
51 M
RNF17
ZMYM2
ZMYM5
CRYL1
XPO4
MPHOSPH8
IFT88
IL17D
EEF1AKMT1
ATP12A
CENPJ
LOC108637296
LOC108637298
LATS2
PARP4
GJB6
GJB2
PSPC1
GJA3
60,200 K
60,300 K
60,400 K
60,500 K
60,600 K
60,700 K
60,800 K
60,900 K
61 M
61,100 K
NBEA
MAB21L1
DCLK1
61,900 K
62 M
62,100 K
62,200 K
62,300 K
62,400 K
62,500 K
62,600 K
62,700 K
SMAD9
TRPC4
SUPT20H
POSTN
ALG5
RFXAP
EXOSC8

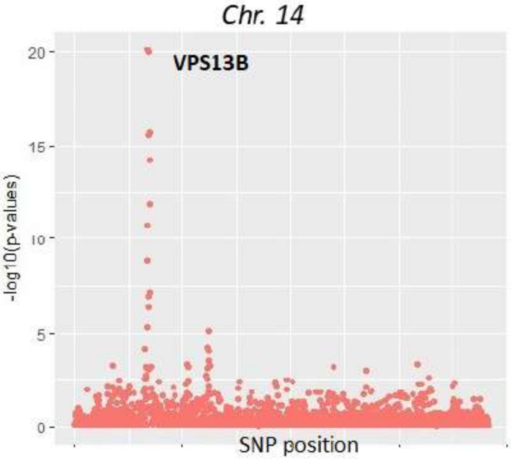


1
2
NBEA
60
40
20
0
-log10(p-values)
SNP position

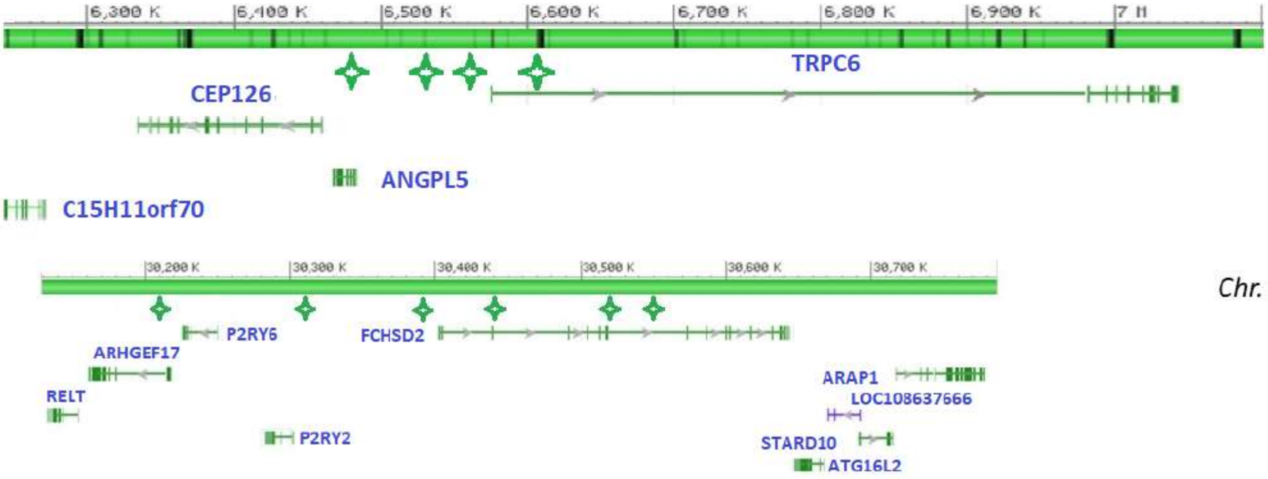

46,420 K
46,440 K
46,460 K
46,480 K
46,500 K
46,520 K
PRNP
LOC108637395
PRND


Chr. 13
GOAT
PRNP
-log10(p-vaues)
80
60
40
20
0
SNP position

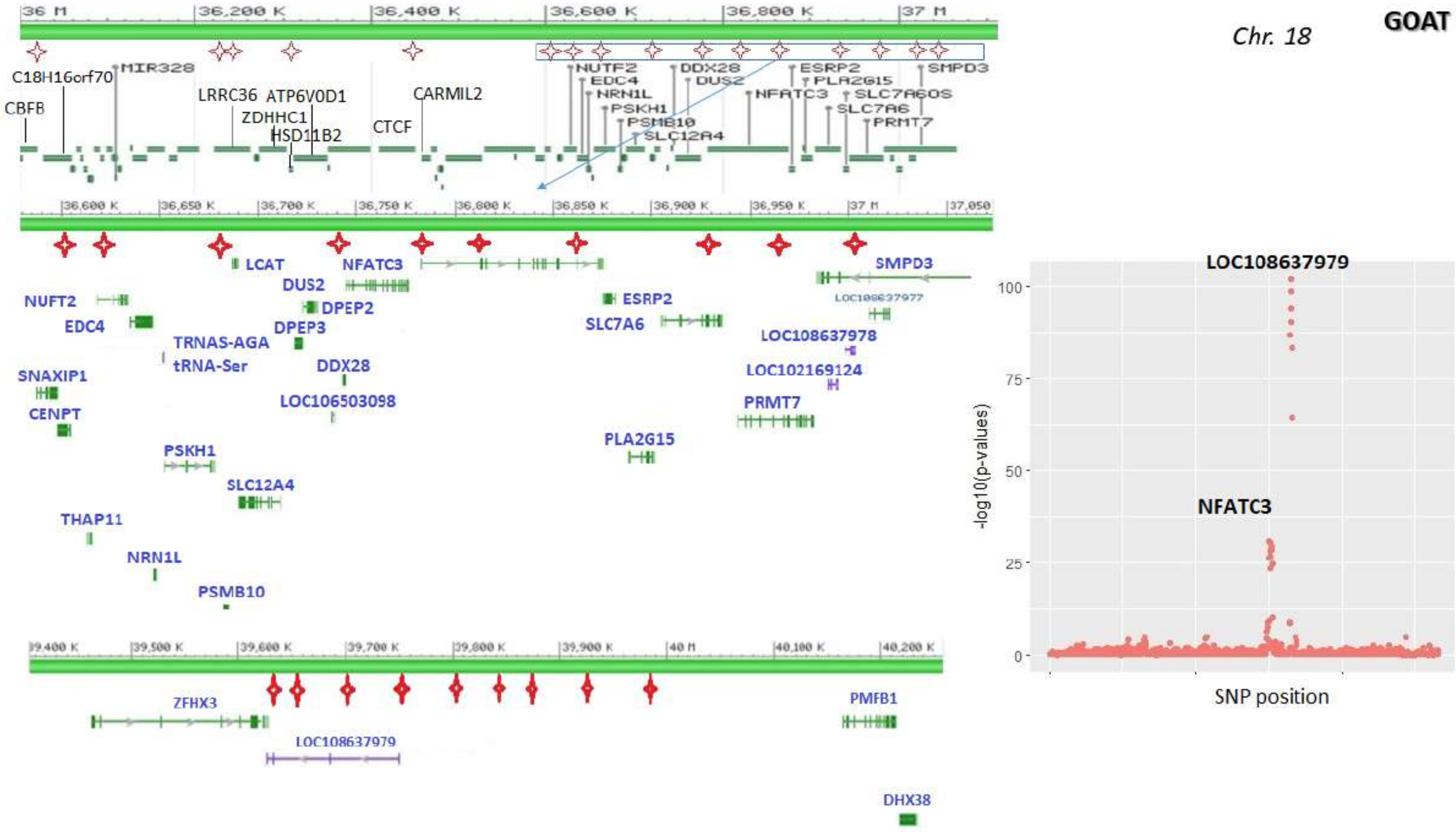

16,900 K
17 M
17,100 K
17,200 K
17,300 K
17,400 K
17,500 K
17,600 K
17,700 K
VPS13B
LOC108637516
TRNAS-GGA
tRNA-Ser
TRNAC-GCA
tRNA-Cys
LOC108637473


Chr. 14
VPS13B
-log10(p-values)
20
15
10
5
0
SNP position

GOAT

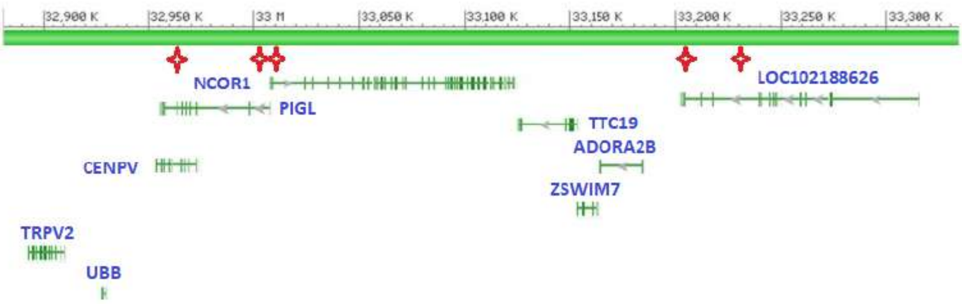

6,300 K
6,400 K
6,500 K
6,600 K
6,700 K
6,800 K
6,900 K
7 M
TRPC6
CEP126
ANGPL5
C15H11orf70
30,200 K
30,300 K
30,400 K
30,500 K
30,600 K
30,700 K
P2RY6
FCHSD2
ARHGEF17
RELT
P2RY2
ARAP1
LOC108637666
STARD10
ATG16L2

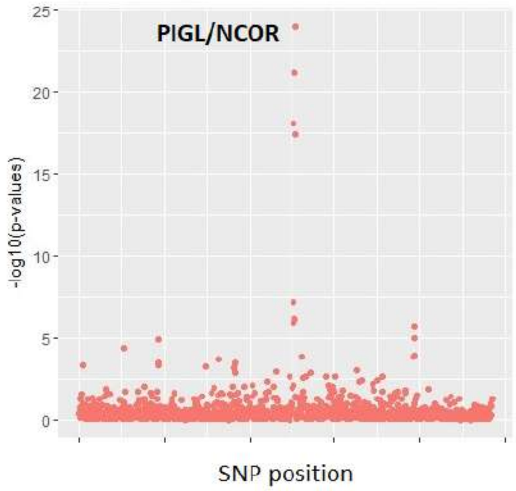
Chr. 15


Chr. 18
GOAT
36 M
36,200 K
36,400 K
36,600 K
36,800 K
37 M
C18H16orf70
MIR328
CBFB
LRRC36
ATP6V0D1
ZDHHC1
HSD11B2
CTCF
CARMIL2
NUTF2
EDC4
NRN1L
PSKH1
PSMB10
SLC12A4
DDX28
DUS2
NFATC3
ESRP2
PLA2G15
SLC7A6OS
SLC7A6
PRMT7
SMPD3
36,600 K
36,650 K
36,700 K
36,750 K
36,800 K
36,850 K
36,900 K
36,950 K
37 M
37,050
LCAT
NFATC3
SMPD3
DUS2
DPEP2
ESRP2
LOC108637977
NUFT2
EDC4
DPEP3
SLC7A6
LOC108637978
TRNAS-AGA
tRNA-Ser
SNAXIP1
DDX28
LOC102169124
CENPT
LOC106503098
PRMT7
PSKH1
PLA2G15
SLC12A4
THAP11
NRN1L
PSMB10
39,400 K
39,500 K
39,600 K
39,700 K
39,800 K
39,900 K
40 M
40,100 K
40,200 K
ZFHX3
LOC108637979
PMFB1
DHX38
LOC108637979
NFATC3
100
75
50
25
0
-log10(p-values)
SNP position

GOAT

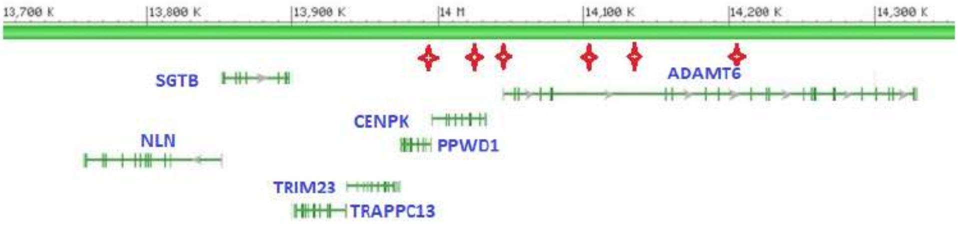
Chr. 19

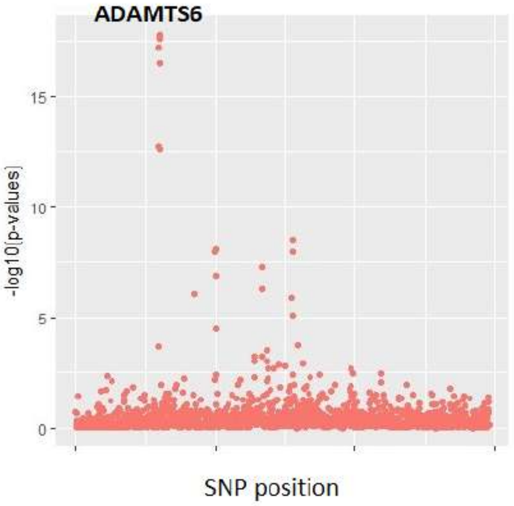

32,900 K
32,950 K
33 M
33,050 K
33,100 K
33,150 K
33,200 K
33,250 K
33,300 K
NCOR1
LOC102188626
PIGL
TTC19
ADORA2B
CENPV
ZSWIM7
TRPV2
UBB


PIGL/NCOR
25
20
15
10
5
0
-log10(p-values)
SNP position

GOAT

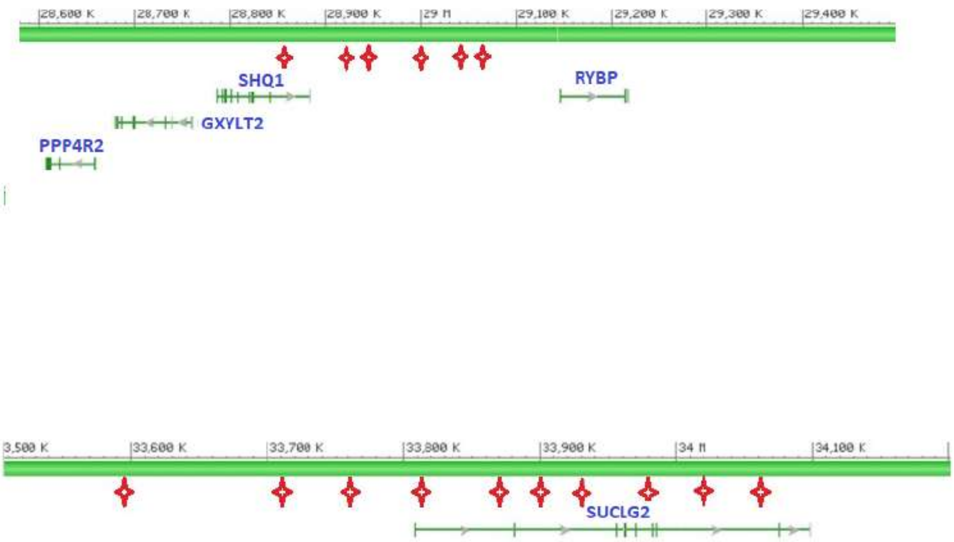
Chr. 20

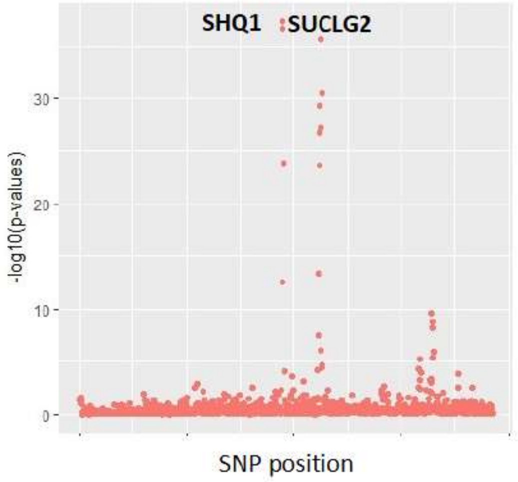

13,700 K
13,800 K
13,900 K
14 M
14,100 K
14,200 K
14,300 K
SGTB
ADAMT6
CENPK
NLN
PPWD1
TRIM23
TRAPPC13


ADAMTS6
15
10
5
0
-log10(p-values)
SNP position

GOAT

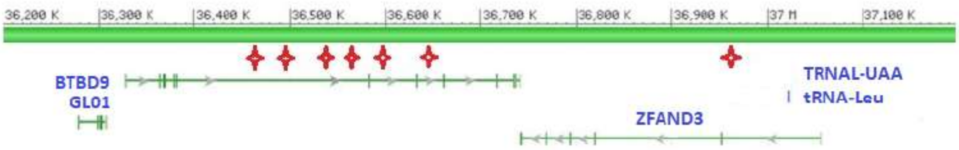
Chr. 22

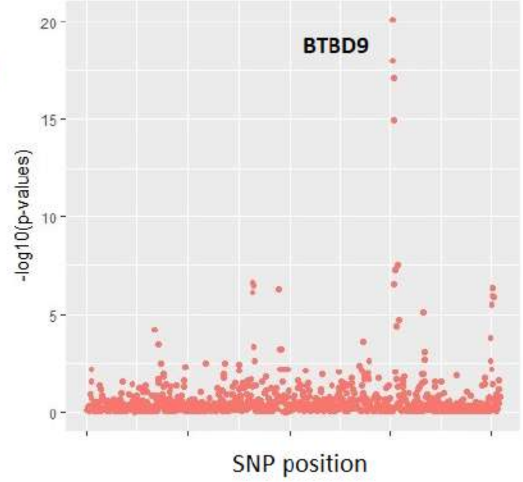

28,600 K
28,700 K
28,800 K
28,900 K
29 M
29,100 K
29,200 K
29,300 K
29,400 K
SHQ1
RYBP
GXYLT2
PPP4R2
3,500 K
33,600 K
33,700 K
33,800 K
33,900 K
34 M
34,100 K
SUCLG2


SHQ1
SUCLG2
30
20
10
0
-log10(p-values)
SNP position

GOAT

Chr. 23

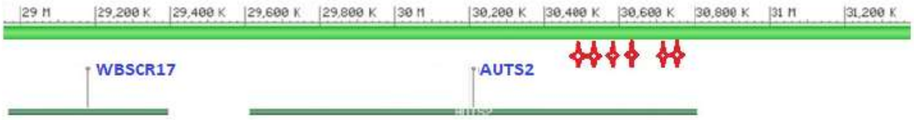

36,200 K
36,300 K
36,400 K
36,500 K
36,600 K
36,700 K
36,800 K
36,900 K
37 M
37,100 K
BTBD9
GLO1
TRNAL-UAA
tRNA-Leu
ZFAND3


BTBD9
20
15
10
5
0
-log10(p-values)
SNP position

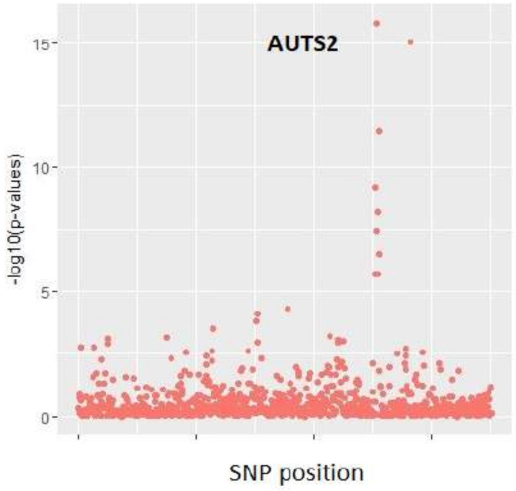

39,800 K
39,850 K
39,900 K
39,950 K
40 M
40,050 K
ANKS1A
C23H6orf106
UHRF1BP1
TAF11
SNRPC

GOAT

Chr. 25

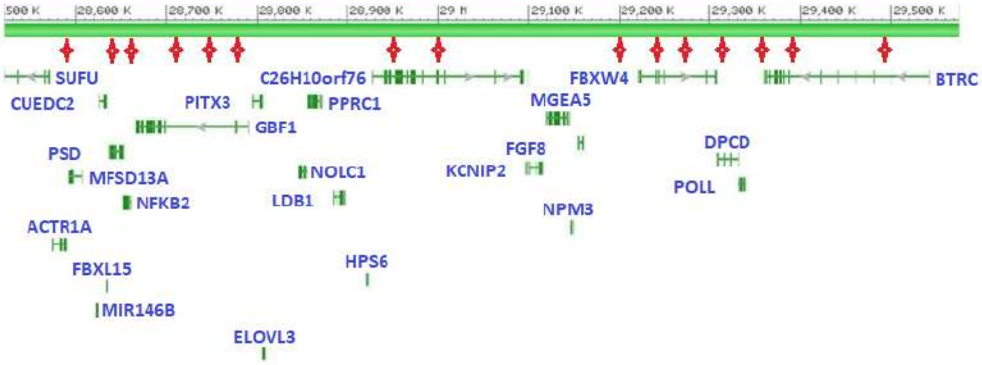


29 M
29,200 K
29,400 K
29,600 K
29,800 K
30 M
30,200 K
30,400 K
30,600 K
30,800 K
31 M
31,200 K
WBSCR17
AUTS2



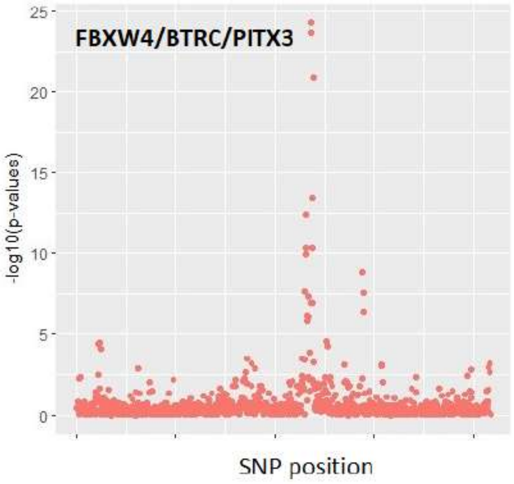
AUTS2
-log10(p-values)
15
10
5
0
SNP position

GOAT



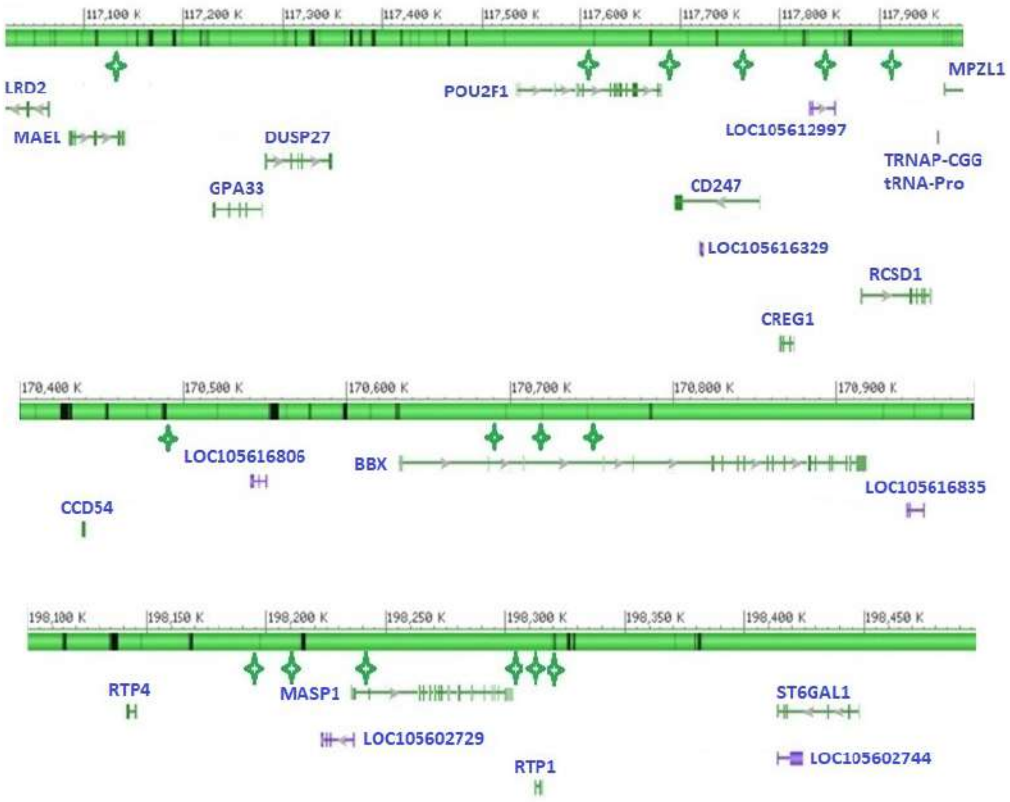
500 K
28,600 K
28,700 K
28,800 K
28,900 K
29 M
29,100 K
29,200 K
29,300 K
29,400 K
29,500 K
SUFU
C26H10orf76
FBXW4
BTRC
CUEDC2
PITX3
PPRC1
MGEA5
GBF1
DPCD
PSD
FGF8
MFSD13A
NOLC1
KCNIP2
POLL
NFKB2
LDB1
NPM3
ACTR1A
FBXL15
HPS6
MIR146B
ELOVL3

Chr. 26



FBXW4/BTRC/PITX3
25
20
15
10
5
0
-log10(p-values)
SNP position

Supplementary Table 7

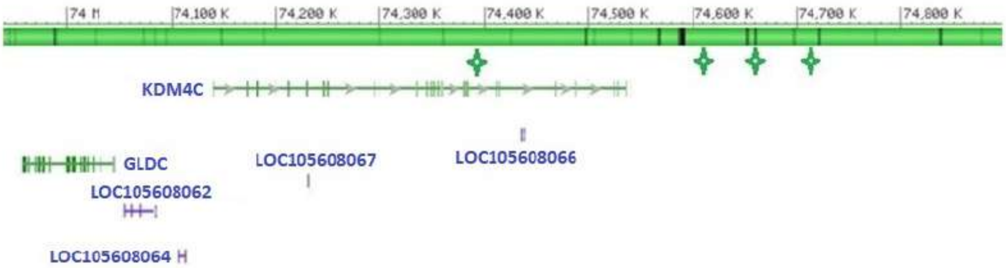


SHEEP

Chr. 1

SHEEP

Chr. 2


74 M
74,100 K
74,200 K
74,300 K
74,400 K
74,500 K
74,600 K
74,700 K
74,800 K
KDM4C
LOC105608066
GLDC
LOC105608067
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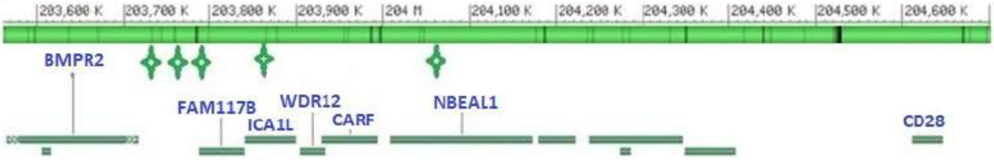
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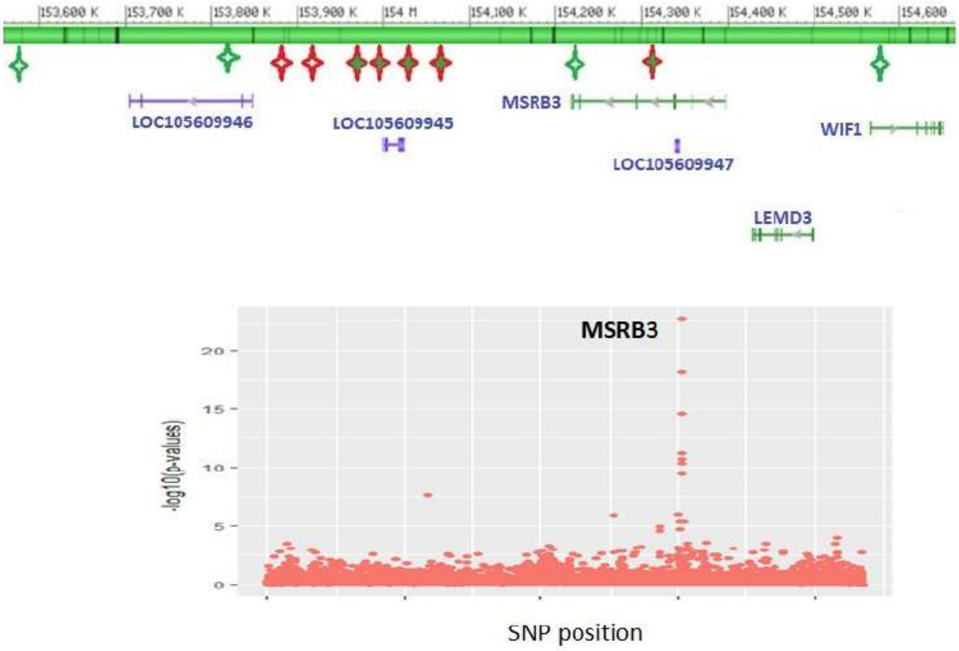
Chr. 3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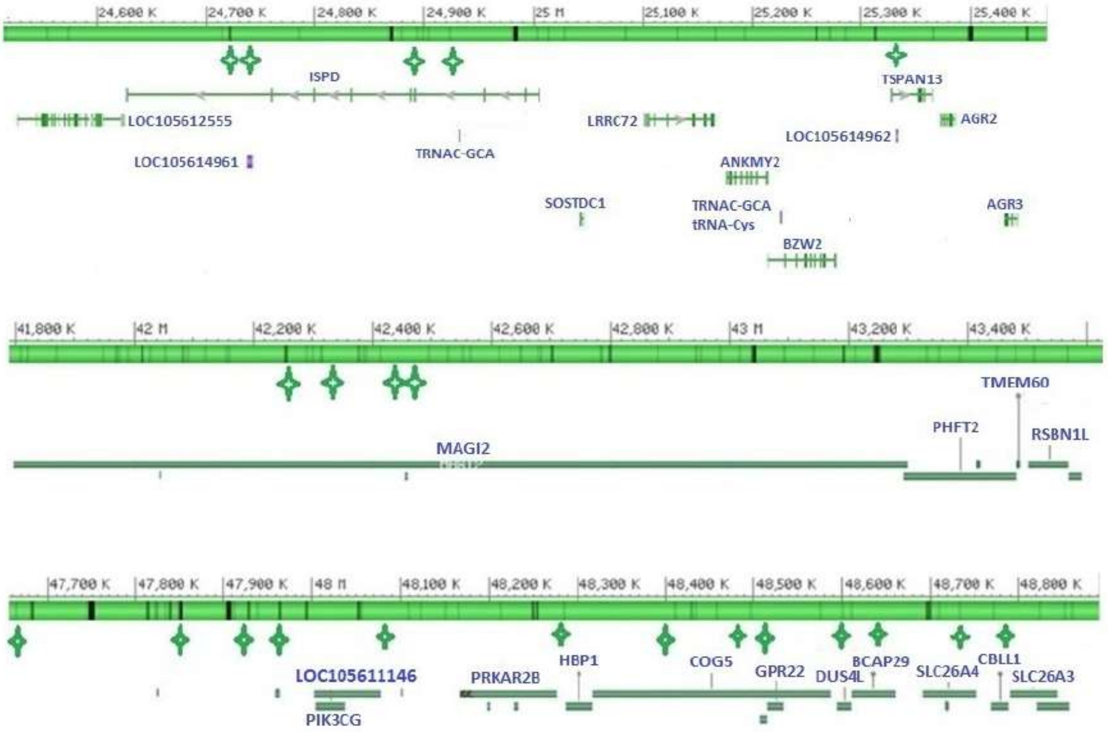

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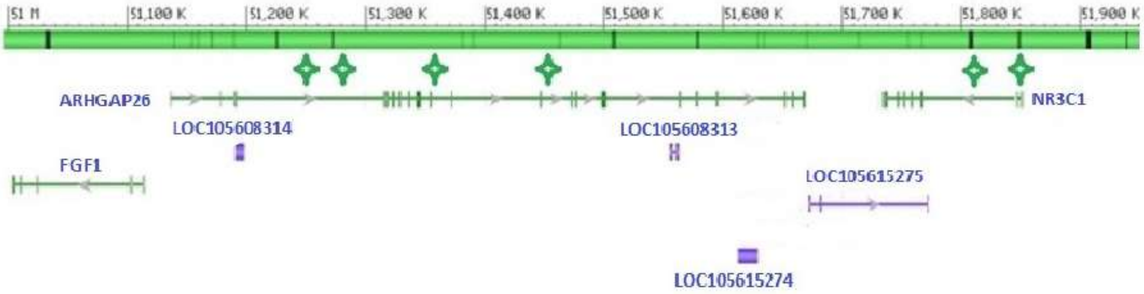
SHEEP

Chr. 4

SHEEP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Chr. 5

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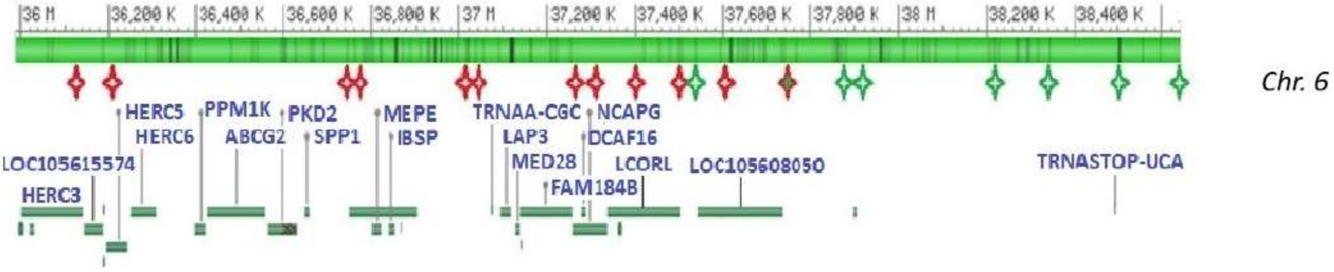
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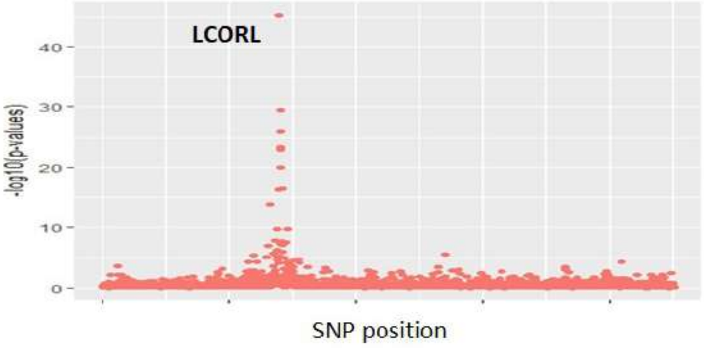
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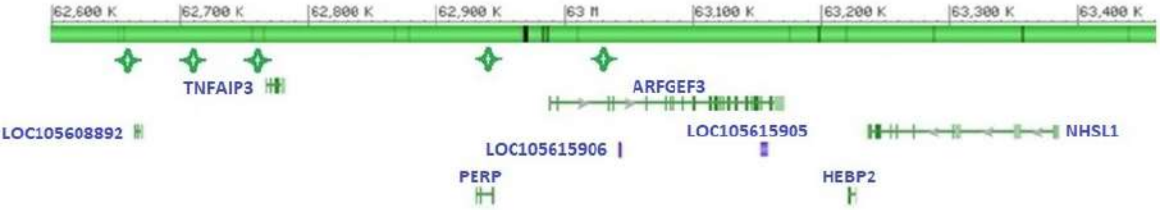
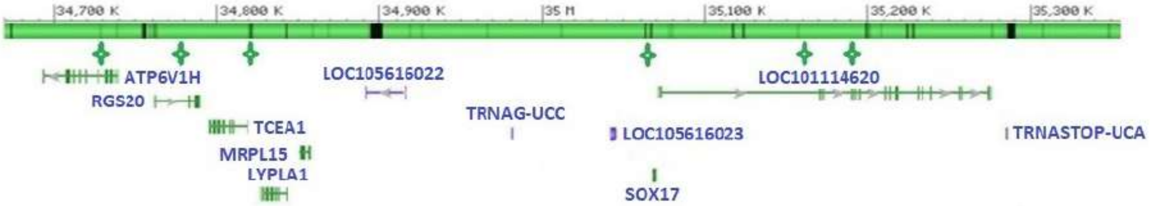


Chr. 8



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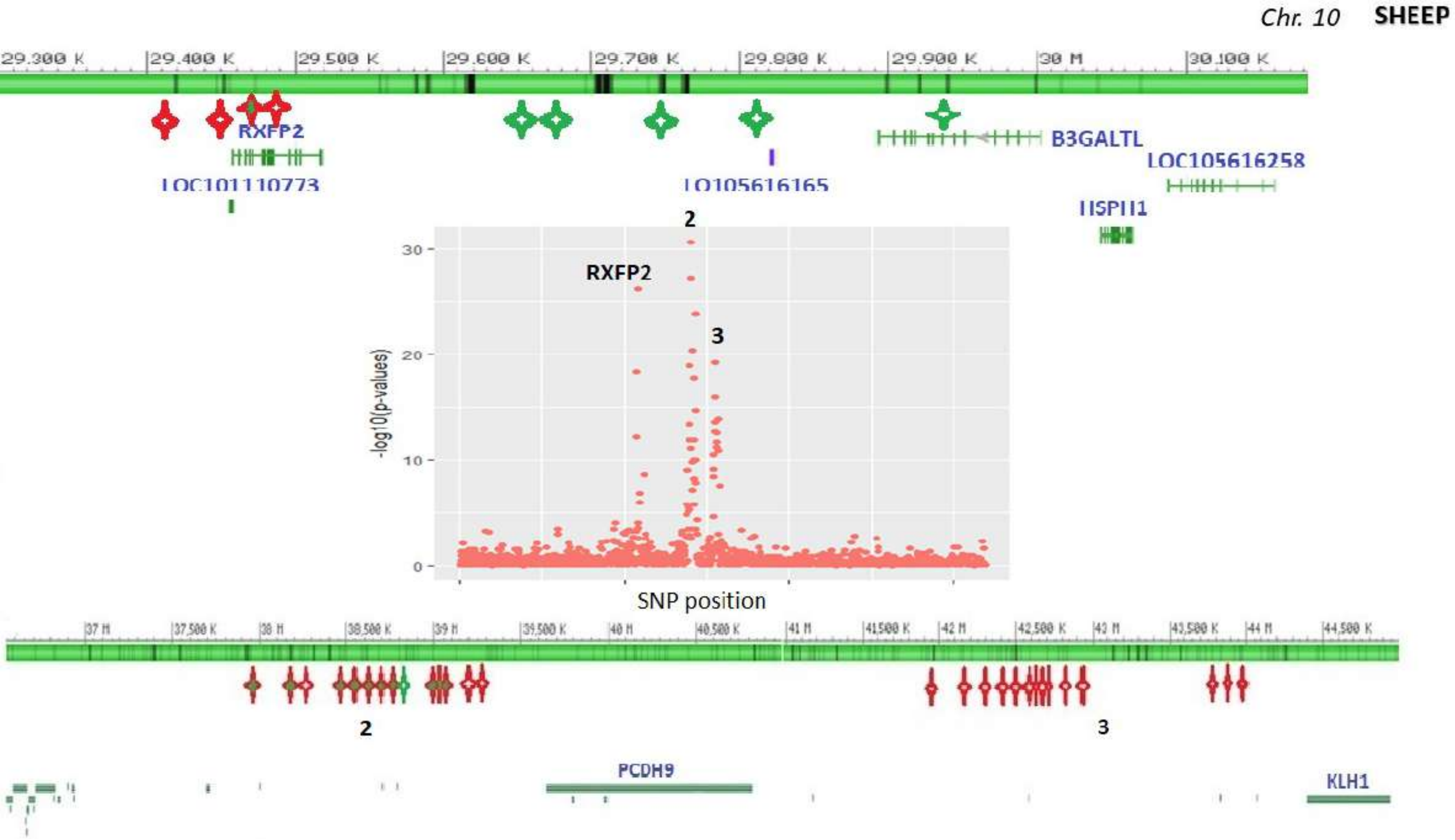

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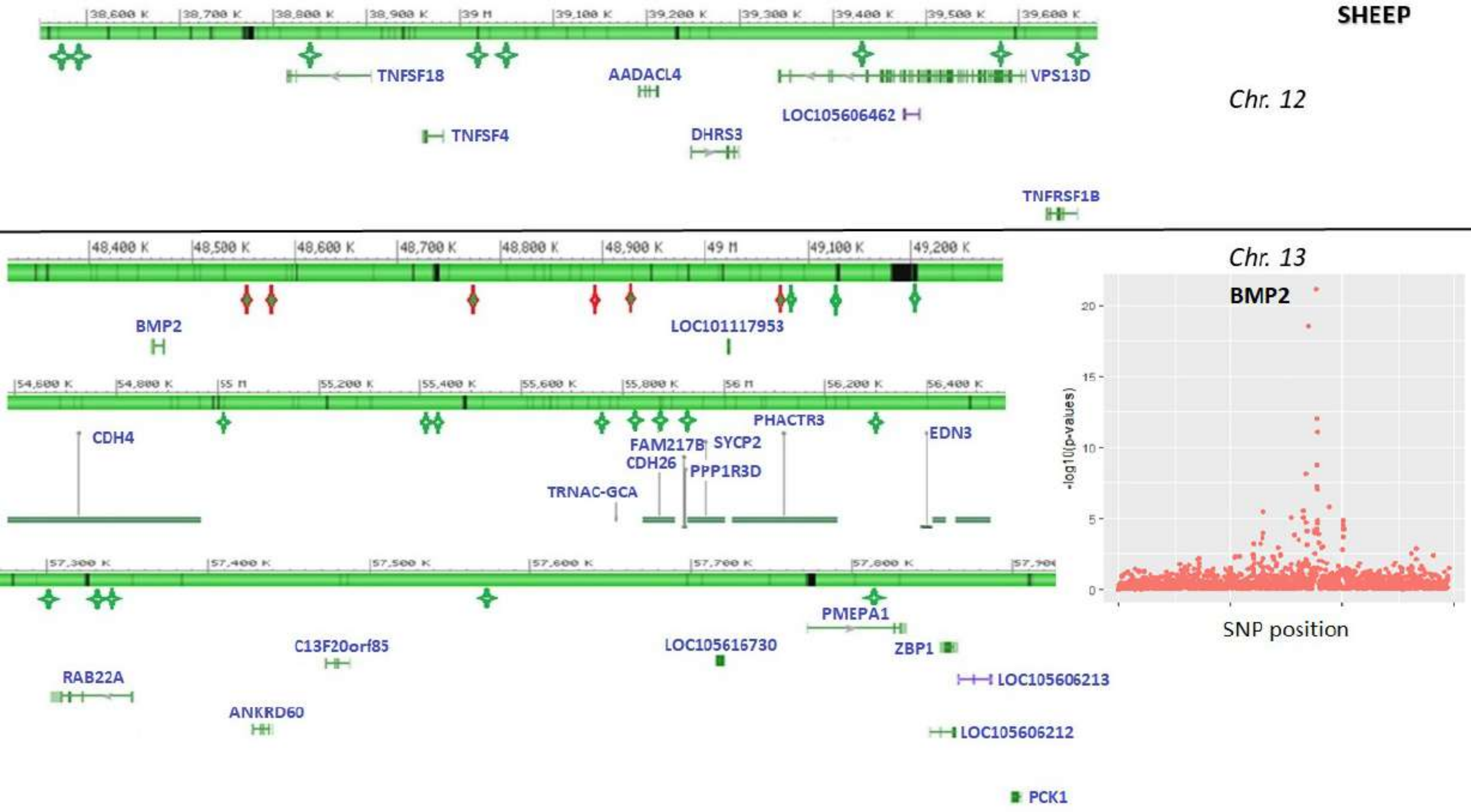
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SNP position

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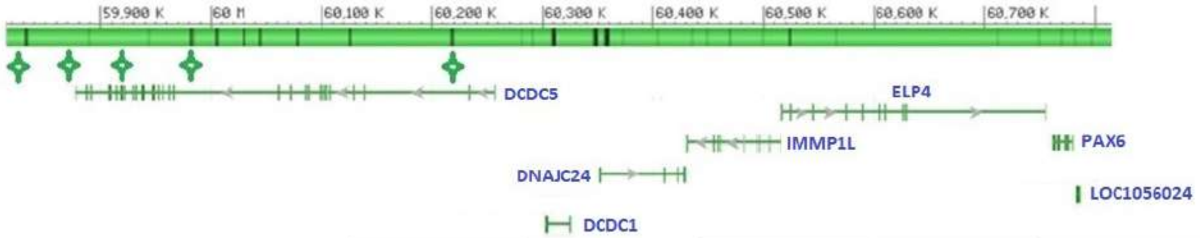

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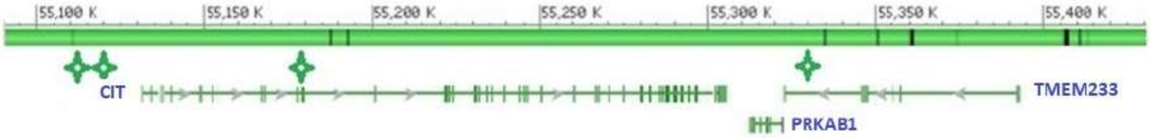

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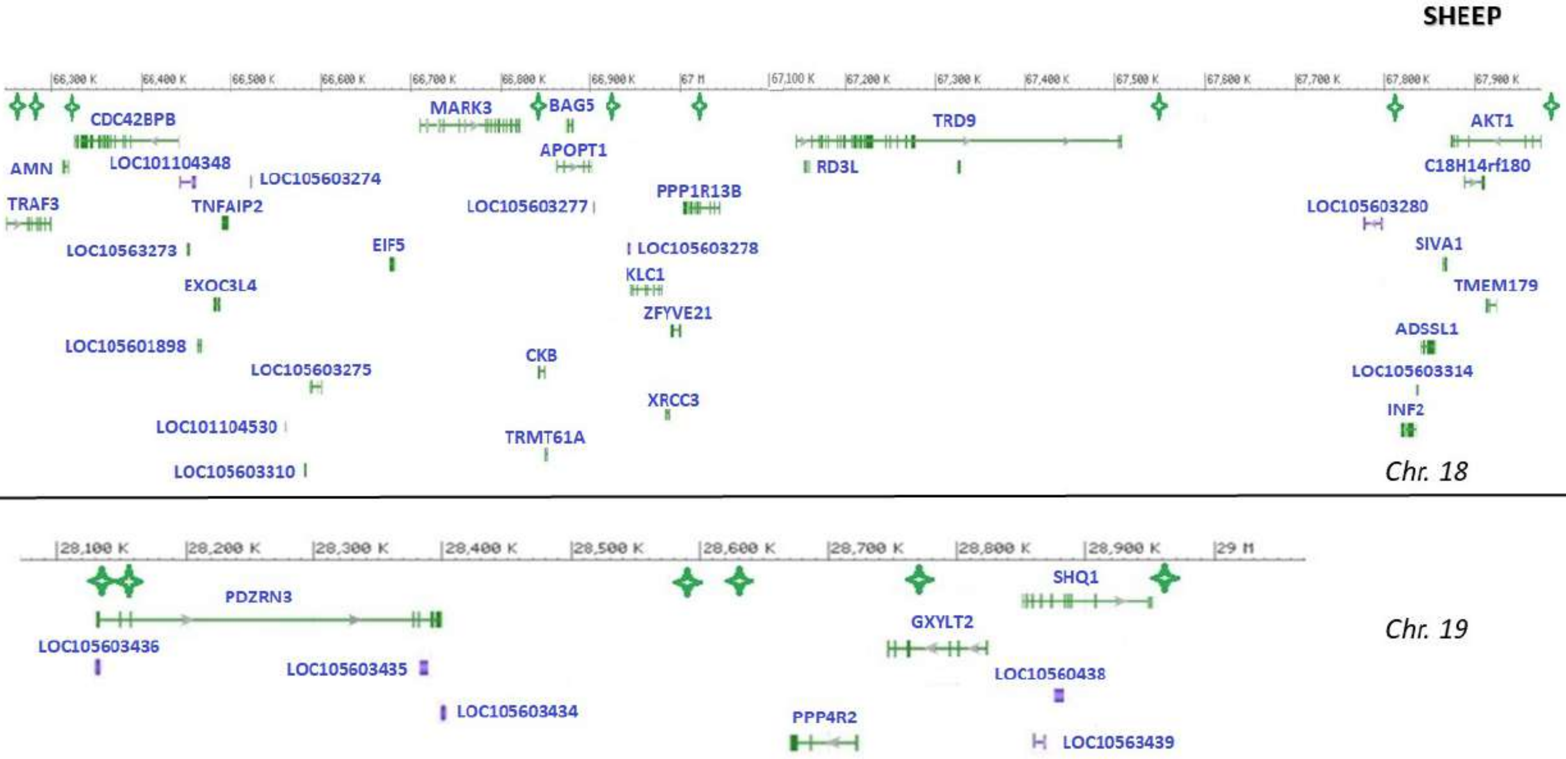
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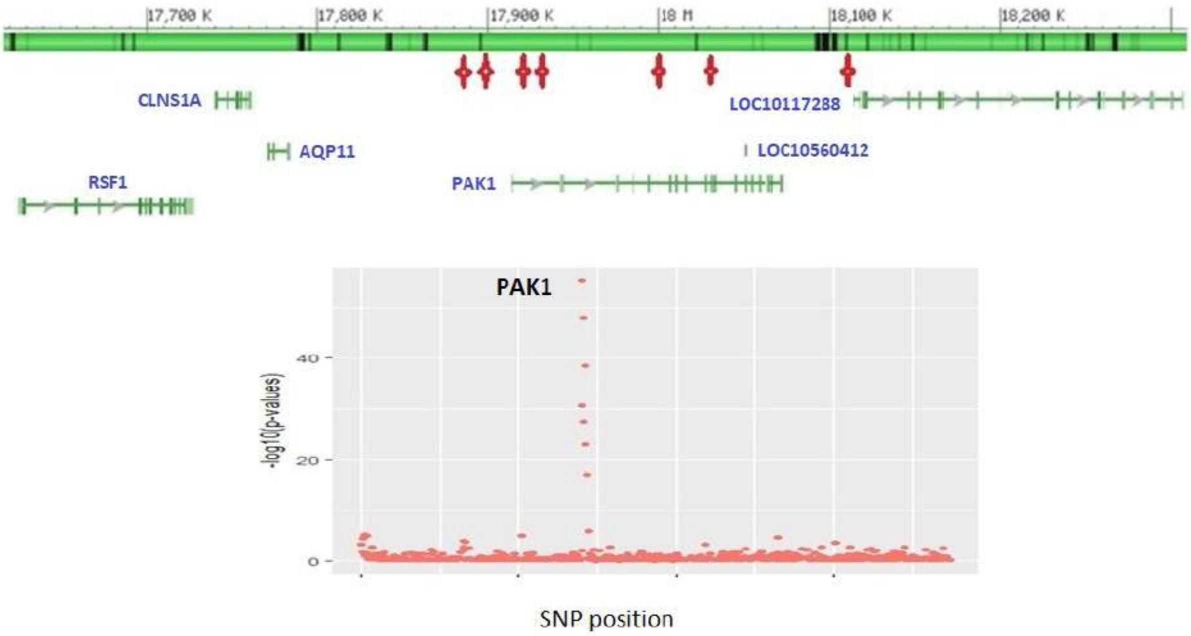
Chr. 19

SHEEP

Chr. 21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SNP position

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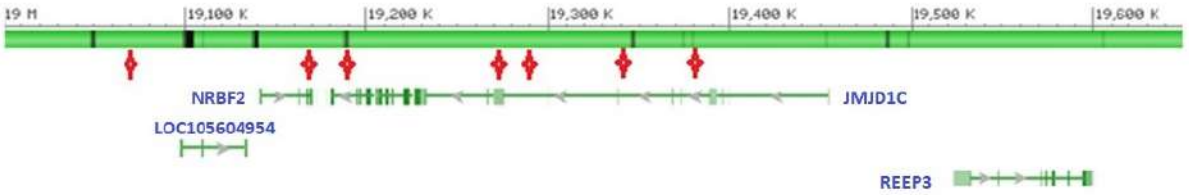
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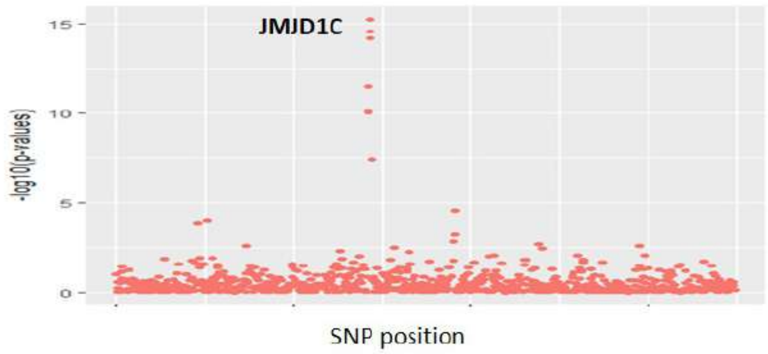
Chr. 25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Literature and classification of the genes identified

The highlighted selection signatures can be clustered according to different major adaptation mechanisms. Classifying genes according to the major functions in which they can be involved should be regarded with due caution. Indeed, a large number of genes are pleiotropic, like ADAMTS6 (see Wu et al., 2019). For the classification we tried to identify in the literature the major mechanisms associated with the genes under consideration. For example, the proposed classifications did not take into account the fact that MAGI2, KDM4C and JMJD1C are also related to spermatogenesis (Sujit et al., 2018); nor the fact that VPS13 family may play a role in the maintenance of neuronal processes in mammals; or that PCDH9 and KLHL1, were found associated with fat tail deposition by the study of Mastrangelo et al. (2019). Finally, a correlation between genetic variation and a trait does not imply a causal relationship.

- Selection signatures involved in lipid storage

A large number of the genes identified seems to be involved in lipid metabolism. Most of them are also involved in the production/composition of milk. (i) For goats we can mention: PTGER3 (Strong et al., 1992), CTBP1 (Xu et al., 2017), TCF12 (Ozdemir Ozgenturk et al., 2017; Dunner et al., 2013), SCFD2 (Yodklaew et al., 2017; Glastonbury et al., 2016), UHRF1BP1 (Justice et al., 2018), BTRC (Ishimoto et al., 2017), CTNNA1/SIL1(fat tail deposition in sheep: Ahbara et al., 2019), VPS13B (Liu et al., 2018; Capitan et al., 2014), WDPCP (Sazzini et al., 2016) and SUCLG2 (Silva-Vignato et al. 2019; Di Gerlando et al., 2019).

WDPCP has also been identified as being under selection in Ethiopian sheep of high altitude (Edea et al., 2019) as well as in Tibetan chicken (Wang et al., 2015), suggesting a probable mechanism common to these taxa of homeoterms. WDPCP is related to the BBSome, a protein complex in primary cilia with important role in leptin receptor (LepR) trafficking; in humans it is linked to obesity (Foucan et al., 2018).

(ii) The identified genes in sheep implied in lipid metabolism and milk production are the followings: ARHGAP26/NR3C1 (Edea et al., 2017), ABCD4/VSX2/LIN52 (fat tail deposition: Zhu et al., 2019), POU2F1 (Lewinsky et al., 2005; Zhao et al., 2002; Pérez-Montarelo et al., 2014), VPS13D, MSRB3 and BMP2 (these last two genes are discussed in the article).

We identified VPS13B in goats and VPS13D in sheep. The gene VPS13B was found under selection in Moroccan goats (Benjelloun, 2015), was associated to adaptation to dry areas in Chinese sheep (Yang et al., 2016), and with high altitude conditions in Yaks (Qi et al., 2019). Mammalian VPS13 proteins are involved in lipid transfer (Gao et al., 2018). VPS13D is involved in lactase persistence and lipid pathway in the Maasai (Wagh et al., 2012). The VPS13B protein could play an important role in the development of nerve cells (neurons) and in the growth and development of adipocytes as reported by Seifert et al. (2011).

- Selection signatures involved in seasonal patterns and circadian behaviors

The analysis detected a strong link between the environmental gradient and the BMPR1B gene in goats. This gene is involved in ovarian function and fertility (Shokrollahi & Morammazi, 2018; Mulsant et al., 2001; Souza et al., 2001; Wilson et al., 2001). The influence of the photoperiod on ovarian function is well known in mammals, where melatonin provides the hormonal signal transducing day length (Walton et al., 2011). This could explain the correlation between BMPR1B and the latitudinal gradient, i.e. a proxy for seasonality, found in our study. Moreover, seasonal patterns are frequently expressed at many levels (foraging, adipocity, growth, immune function *etc.*, see the review by Prendergast, Nelson, & Zucker, 2009). These elements could explain the link established by Cao et al. (2015) between BMPR1B and growth in sheep. The role of this gene in thermogenesis, has been demonstrated in murine adipose tissue (Whittle et al., 2015).

Similarly, SOX2, implicated in behavioral rhythms linked to environmental light cycles (Cheng et al., 2019) and DPH6, a circadian rhythm-related GO categories, were also identified by the LFMM approach as correlated with the environmental gradient in goats (see detailed discussion in the article).

- Selection signatures involved in hypoxia and/or heat stress response

Hypoxia is a major stimulus for physiological processes such as adaptation to life at high altitude, but it is also an important factor of many human pathologies, such as cancer (Kenneth & Rocha, 2008). We identified MAT2A in goats and JMJD1C and KDM4C (a JmjC domain-containing protein) in sheep. It is shown that hypoxia induces genomic DNA demethylation through the activation of HIF-1α and transcriptional upregulation of MAT2A (Liu et al., 2011). Moreover, the Jumonji C (JmjC) domain contains demethylases, allowing genes such as JMJD1C and KDM4C to trigger mechanisms to respond to hypoxia (Xia et al., 2009; Melvin & Rocha, 2012). In sheep, EDN3, RAB22A and DNAJC24 were identified by us. The gene EDN3, was previously associated with hypoxia tolerance in cetaceans as vasoconstrictor-related gene (Tian et al., 2016). RAB22A was found involved in hypoxia process in humans (Wang et al., 2014). DNAJC24 was associated with high altitude adaptation in sheep (Yang et al., 2016) and appeared under selection in Ugandan goats (Onzima et al., 2018). DNAJC24 belongs to the heat shock protein 70 family, that are produced in response to exposure to stressful conditions, as cold, UV light, *etc*.

The signature centered on PIGL/LOC102188626 in goats, and bordered by NCOR1/ADORA2B deserves special attention. PIGL was previously identified in Chineese sheep at high altitudes (Yang et al., 2016). NCOR1 belong to clock circadian gene network in cattle (Wang et al., 2015), whereas ADORA2B (an adenosine receptor, belonging to the hypoxia database) appears implicated in thermal adaptation (Wollenberg Valero et al., 2014).

Finally, in goats, both PCAdapt and LFMM highlighted the signature near UBE2R2/UBAP2 and bordered by AQP7/AQP3. UBE2R2/UBAP2, have been found to be associated with hypoxia tolerance in humans (Udpa et al., 2014) and with highlands in Chinese sheep (Yang et al., 2016). AQP7 was linked to high altitudes in yaks (Qi et al., 2019). The aquaporins AQP7 and AQP3, which belong to the hypoxia-related genes, have been identified in thermal adaptation through the regulation of evapotranspiration and cryoprotectant transport (Wollenberg Valero et al., 2014).

- Selection signatures implicated in coat color or horns

First, considering morphological adaptations, two genes known to affect coat colour, ADAMTS20 (Oget, Servin, & Palhière 2019; Bertolini et al., 2018) and TYRP1 (Gratten et al., 2007; Becker et al., 2015), were identified in goats. The pigmentation (fiber and skin), by influencing the ability to absorb solar radiation, corresponds to a primordial adaptive mechanism that is highly submitted to natural selection in mammals (Caro, 2005). In Western Europe, sheep have been subjected to strong artificial selection, over the past 200 years, on the quality of the wool but also on its colour; the white colour being particularly prized (Lauvergne, 1969; Mellah, 2015). This could explain why we did not found any selection signatures in sheep for this type of gene in connection with the environment.

With regard to horns, the RXFP2 gene is known to be strongly involved in this process (Johnston et al., 2011; Allais-Bonnet et al., 2013; Kijas et al., 2012; Fariello et al., 2014) and appeared to be selected in sheep. Indeed, the production of polled animals has been a major objective of artificial breeding for decades. Also, we were not surprised to observe a majority of sheep breeds of the dataset without horn. RXFP2 was identified by both PCAdapt and LFMM approaches (see details in Supplementary Text 2). It is the receptor of the peptide hormone INSL3 and plays a regulatory role in testis and ovaries of various mammalian species (Hanna et al., 2010). In the seasonally breeding roe deer, with a periodic variation in the volume of the testicles, the seasonal expression of INSL3/RXFP2 was correlated with the differentiation of Leydig cells in the testis (Hombach-Klonisch et al., 2004). Interestingly, RXFP2 was associated with latitude, precipitation and temperature in free-ranging bighorn sheep (Roffler et al., 2016); and identified as being under selection in Tibetan sheep (Wei et al., 2016). Moreover, RXFP2, as MSRB3 and SLC26A4 (also identified by our study) showed signs of rapid evolution in semi-feral breeds' sheep (Pan et al., 2018). This suggests an adaptive role in the wild or, potentially, in traditional livestock farming with limited human intervention. In goats, the gene involved in the presence or absence of horn is pleiotropic, so that selecting individuals without horn induces undesirable secondary phenotypes, often in association with reduced fertility (Liron, 2011).

- Selection signatures implicated in immunity

In sheep, MASP-1, a serine protease, was identified. It functions as a component of the lectin pathway of complement activation, and as such, plays an essential role in the innate and adaptive immune response (Ammitzbøll et al., 2013). In goat, the genes PRNP, NFATC3/LRRC36 appeared selected. A large literature links PRNP to susceptibility to prion disease, in small ruminants (see Greenlee, 2019 for a review). The NFAT (nuclear factor of activated T cells) family of transcription factors is well documented for its role in T lymphocytes (Minematsu et al., 2011). LRR-containing proteins are also well known for their role in innate immunity (Ng et al., 2011). Finally, JAZF1, identified in sheep, plays a role in adipose tissue inflammation by limiting macrophage populations and restricting their antigen presentation function. Thus, this gene seems to act at the interface between immune system and adipose metabolism (Meng et al., 2018).

- Signatures involved in lung function

The GSTCD gene, highlighted in goat, plays a role in cellular homeostasis associated with lung function (Artigas et al. 2015; Obeidat et al., 2013; Henry et al., 2019). The SLC34A2 gene, identified in the goat dataset as selected and very close to SEL1L3, was previously associated with high altitude conditions in cattle (Verma et al., 2018). Moreover, Edea et al. (2019) linked SEL1L3, with high altitude adaptation in sheep. In humans, SLC34A2 is mainly located in the lungs, and produces and recycle surfactant, that makes breathing easy (Ma et al., 2018). Finally, SEL1L3 belong to the hypoxia regulated proteins database (http://www.hypoxiadb.com).

- Signature selection involved in neuronal function

MAGI2, detected in sheep, may play a central role in adaptation as it was also identified by Edea et al. (2019) in high altitude Ethiopian sheep, by Qi et al. (2019) in high altitude yaks and by Yang et al. (2016) associated with desert and arid conditions in Chinese sheep. The MAGI2 gene that belongs to the hypoxia regulated proteins database, plays the critical role of maintaining synaptic strength (Danielson et al., 2012).

BTBD9, highlighted in goat, is mainly expressed in brain structure (Stefansson et al., 2007). It plays a role in the regulation of ion channels' tetramerization and gating, and hence is potentially involved in neuronal signal transduction (Stogios et al., 2005).

AUTS2, also detected in goat, is a critical neuronal gene implicated in many neurological disorders as autism. Interestingly, several predicted protein–protein interaction domains (SH2 and SH3) were observed for this protein (Oksenberg, Stevison, Wall, & Ahituv, 2013), whereas SH3 gene was found under selection in the sheep dataset. SH3 domains are eukaryotic protein domains that are involved in a plethora of cellular processes including signal transduction.

The MDGA2 gene, was identified in goats. Mutations in MDGA2 were associated with autism potentially through its ability to modulate excitatory/inhibitory transmission. Indeed, MDGA2 is able to block neuroligin-1 interaction with neurexins and then to suppresses excitatory synapse development (Connor et al., 2016).

The genes TRPC4, TRPC6 and NBEA are discussed in detailed in the manuscript.

- "Complex" selection signatures

The following selection signatures appear more difficult to analyze and are processed on a case-by-case basis, due to the difficulty of categorizing them. In goats, HERC6 was identified as being under selection at the level of a rather small signature that was framed by HERC5 on one side and ABCG2 on the other. In sheep, HERC6 was found in a particularly large signature (it should be noted that PCAdapt predicts a zone lagged with respect to LFMM). A total of 16 genes were involved in this signature, which also included HERC5 and ABCG2. The HERC family emerged more than 595 million years ago. HERC5 and HERC6 contain a domain implicated in antiviral activity, which gives them great importance in terms of intrinsic immunity (Paparisto et al., 2018). In terms of adaptation, HERC6 was found to be linked to arid environments adaptation (Yang et al., 2016; Mdladla, 2016) and also to stress grazing adaptation (Mwacharo et al., 2018). With regard to the other genes found in the sheep signature: a very large literature links ABCG2/SPP1/LAP3/NCAPG/MEPE to milk production, particularly ABCG2 (see Ruiz-Larrañaga et al., 2018); the remaining genes LCORL/LAP3/FAM184B may be related to growth traits (Al-Mamun et al., 2015; Lindholm-Perry et al., 2001; Bongiorni et al., 2012; Eberlein et al., 2009). Only more in-depth research will make it possible to understand the mechanisms underlying the adaptations in relation to these genome areas.

In goat, the large selection signature located on chromosome 12 and including amongst others genes RNF17, ZMYM2, PARP4 and XPO4, seems to play an important role in adaptation processes. Here again the situation is particularly complex and fine studies focused on this area are needed, while this area appears linked with lipid metabolic processes, growth, DNA repair, and also associated with adaptation to high altitude, stress grazing and arid environments (see Supplementary Table 3).

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