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Cattle pastoralism plays a central role in human livelihood in Africa. However, the genetic history of its success remains unknown. Here, through whole-genome sequence analysis of 172 indigenous African cattle from 16 breeds representative of the main cattle groups, we identify a major taurine x indicine cattle admixture event dated to c. 750-1,050 years ago, which has shaped the genome of today's cattle in the Horn of Africa. We identify 16 loci linked to African environmental adaptations across crossbred animals showing an excess of taurine or indicine ancestry. These include immune, heat tolerance and reproduction-related genes. Moreover, we identify one highly divergent locus in African taurine cattle, which is putatively linked to trypanotolerance and present in crossbred cattle living in trypanosomosis infested areas. Our findings indicate that a combination of past taurine and recent indicine admixture-derived genetic resources is at the root of the present success of African pastoralism.

47 Cattle play an important role across African economies and societies as a primary source of
48 wealth[1,2]. They provide nutrition, manure, and draught power and are often used to pay as
49 bride wealth[1,2]. Today, at least 150 indigenous cattle breeds have been recognized across the
50 different agro-ecologies of the African continent[3], each with unique phenotypic and adaptive
51 characteristics[4,5].

52 Previous studies[5,6] have indicated that the dispersion and diversity of African cattle
53 followed the history and development of African pastoralism. It is understood that the
54 humpless *Bos taurus* and the humped *Bos indicus* originated from domestications of distinct
55 auroch *Bos primigenius* subspecies with an ancestral divergence time of ~ 200,000 to less
56 than 1 million years ago[7-10]. The oldest uncontroversial evidence of domestic cattle in Africa
57 dates back to c. 5,750-4,550 BC in Egypt's Western Desert at Nabta-Kiseiba and c. 7,000 BC
58 in Kerma, Sudan[11]. These *B. taurus* cattle were introduced through North Africa and reached
59 the Western and Eastern continent. They remained largely confined to the Saharan-Sahelian
60 belt[12,13], until c 4,000-3,000 years ago, when they reached the Tilemsi Valley tributary of the
61 Niger River in West Africa[14], the Lake Turkana basin of East Africa[15,16], and the Horn of
62 Africa[17]. The main arrival of *B. indicus* started around 700 AD along the Red Sea and the
63 Indian Ocean coastal areas, at the outset of the Swahili civilization[18,19] (**Fig. 1a**), which
64 subsequently led to crossbreeding between *B. indicus* and already established African taurine.

65 However, the timing of the taurine x indicine admixture event(s) and their impacts on
66 the development of African pastoralism remain unknown. Archaeological evidence indicates
67 that the development of sub-Saharan cattle pastoralism was a complex process that may not
68 have proceeded as smoothly as its modern prevalence suggests[20,21]. In particular,
69 environmental climatic and infectious disease challenges (e.g. bovine malignant catarrhal

fever, East Coast fever, foot-and-mouth disease, Rift Valley fever, and trypanosomosis) likely have led to patchy and delayed establishment of herding across East Africa[16,20,22].

Today, the majority of African cattle are *B. taurus* x *B. indicus* humped populations of diverse phenotypes. They are classified as African Sanga (crossbred between Taurine and Zebu cattle), African Zenga (crossbred between Sanga and Zebu), and African Zebu[3,23]. The African Sanga, an Abyssinian word meaning bull, likely originated in North-East Africa with subsequent dispersion in the Central Lake Region and Southern Africa[14]. A few taurine populations found within the tsetse-belt in West Africa are the only pure African taurine cattle left on the continent[6,24].

African humped cattle carry only taurine mtDNA haplotypes[25-27]. Y-chromosome microsatellite indicates the presence of both indicine and taurine Y-chromosomes on the continent[5,28]. Furthermore, autosomal genome-wide analyses show that African humped cattle contain taurine background with different levels of genetic contributions across populations, but with little variation within a population[29-31]. It suggests that selection played a role in shaping the *B. taurus* x *B. indicus* admixture proportion in African cattle, with admixture increasing diversity and providing new genetic resources for human and natural selection[32]. This may have facilitated dispersion and colonization of new habitats[33]. Several recent studies have addressed the effects of admixture and introgression among the *Bos* species. They have identified loci derived from donor species, which have contributed to the adaptation of recipient species[34-36]. However, admixture and introgression also have a cost as they may reduce the reproductive fitness due to genome incompatibility[37].

Here, we generated whole-genome sequences of 114 cattle that belong to 12 indigenous African cattle populations and two African buffalo. We combined these with the previously

93 sequenced genomes of 58 cattle from four additional African populations[31,38]. These
94 populations represent the main African cattle groups (**Supplementary Note**). Using this
95 unique set, we date a main taurine x indicine admixture event and assess the present genome
96 ancestry of African cattle, supporting that a combination of these two ancestries is at the root
97 of the success of African pastoralism.

98

RESULTS

Sequencing, mapping and identification of SNPs. Individual genomes of 114 indigenous African cattle and two African buffalo, *Syncerus caffer caffer* (AFB) were sequenced to an average of ~9.91× depth coverage and jointly genotyped with 217 publicly available genomes. A total of 45 cattle breeds or populations including 331 samples were classified according to their phenotypes as follows: African Taurine (AFT)[3], African Humped cattle (AFH) (including African Indicine (AFI)[3,31,39,40], African Sanga (AFS)[31,40], African Zenga (AFZ)[3], and Sheko), Eurasian Taurine (EAT) (including European Taurine (EUT) and Asian Taurine (AST)) and American-Australian-Asian Indicine (AAI) (including American-Australian Indicine (AMI) and Asian Indicine (ASI)) (**Fig. 1**, **Supplementary Note**, and **Supplementary Table 1**).

We generated ~35 billion reads or ~3.50 Tb of sequences. Sequence reads were aligned to the taurine reference genome (ARS-UCD 1.2) with an average alignment rate of 99.47% (min: 91.70%, max: 99.91%) and covering 94.93% (min: 83.05%, max: 96.20%) of the reference genome. Concordant with a previous analysis of a zebu cattle, Nelore[41], the average alignment rate for AFH (99.67%) was comparable to the one obtained for AFT (99.43%) (**Supplementary Table 2**). Average genotype concordance of 114 samples was 95.40%, which was subsequently improved to 97.35% after genotype refinement using BEAGLE[42] (**Supplementary Table 3** and **Extended Data Fig. 1**).

Population structure and genetic diversity of African cattle. *Population structure and relationships.* To characterize the structure of the African populations, we performed principal component analysis (PCA) of the 331 animals (**Fig. 2a**). All AFH position between

EAT and AAI, along eigenvector 1, which explains ~15% of the total variation. AFT Muturu and N'Dama are close to EAT along the eigenvector 1. Most of the AFH cattle cluster together regardless of their breed memberships, leaving only Ankole, Mursi and Sheko outside the main cluster toward the AFT Muturu and N'Dama. The PCA results also show that Muturu and N'Dama, our representative of AFT population, are separated from the other cattle groups (eigenvector 2, ~2.5% of total variation). Sheko positions close to the AFH, as similarly reported in other studies[5,43].

Genetic clustering analysis using ADMIXTURE[44] corroborates the pattern found in PCA (**Fig. 2b** and **Extended Data Fig. 2**). Most of AFH show a similar proportion of taurine ancestry, around 25% on average. Only a few AFH breeds have elevated taurine ancestry: Ankole (53.37 ± 1.49%), Sheko (46.28 ± 2.03%) and Mursi (35.90 ± 2.16%). (**Fig. 2b**).

Genetic distance and diversity. Pairwise F_{st} were calculated to estimate the genetic distances between populations (n = 38) (**Extended Data Fig. 3**). Taurine (EUT, AST and AFT) show F_{st} values of 0.1568 and 0.3287 on average against AFH and AAI, respectively. Across AFH, pairwise F_{st} between breeds is close to zero, regardless of their phenotypic classification as African Zebu, Sanga or Zenga. Muturu and N'Dama show F_{st} value of 0.1769, 0.1847 and 0.3734 against AFH, EAT and AAI, respectively.

The genome-wide autosomal SNPs show reduced levels of heterozygosity in the taurine (0.0021 ± 0.0005/bp) compared to all other populations (0.0048 ± 0.0008/bp). Heterozygosity values of AFH are similarly higher across populations (0.0046 ± 0.0003/bp). AAI shows a higher level of heterozygosity compared to AFH (0.0052 ± 0.0014/bp) (**Extended Data Fig. 4**). The degree of inbreeding measured by runs of homozygosity (ROH) shows that taurine, including Muturu and N'Dama, have a higher level of inbreeding compared to the other

populations. AAI shows a similar pattern of ROH distribution to AFH (**Extended Data Fig. 5**).

Genome-wide admixture signatures in African cattle. *Evidence of intensive admixture across African cattle.* To further analyze and quantify admixture levels in African cattle, we examined patterns of allele sharing using f_3, D and f_4 ratio statistics[45]. In the group-based analyses, we used EAT and AAI as a single group considering their genetic similarity compared to the African populations. Only Muturu and N'Dama show no evidence of admixture in f_3 analysis assuming EAT and AAI as proxies for non-admixed taurine and indicine cattle, respectively. For the D statistics, which are more robust to the effect of population-specific drift, this is only the case for the Muturu (**Fig. 3a** and **Supplementary Tables 4** and **5**). The positive f_3 statistic in N'Dama is likely due to a recent population bottleneck and subsequent allele frequency changes by genetic drift[45], as suggested by its high ROH counts and lengths (**Extended Data Fig. 5**). As Muturu shows no evidence of admixture (**Supplementary Tables 4** and **5**), we re-calculated f_3 and D statistics using Muturu as a proxy for non-admixed taurine. These showed consistent results compared to those when EAT was the proxy (**Supplementary Tables 4** and **5**). The admixture proportions estimated by f_4 ratio statistics (**Fig. 3b** and **Supplementary Table 6**) range from 21.03% to 26.85% in the AFH (excluding Mursi, Ankole and Sheko).

Dating taurine x indicine admixture across African cattle. Having established the level of taurine x indicine admixture among African cattle, we then estimated the timing of its generation using admixture LD decay. We first employed a single-pulse admixture model using ALDER. Across all AFH populations, excluding the Kenya Boran, admixture times

range from 126.88 (Mursi) to 181.58 (Fogera) generations ago (mean 153.67) (**Fig. 3c** and **Supplementary Table 7**). Additionally, we analyzed our data using MALDER[46] to assess the possibility of multiple admixture events. After fitting a single-pulse model, MALDER analysis did not add a new admixture event with enough significance. Also, the lower significance (Z-score) and larger standard errors of the double-pulse model fitting compared to the single-pulse model fitting support the single-pulse admixture model for our data (**Fig. 3d**). When we combined AFH populations excluding Ankole, Kenya Boran, Mursi, and Sheko, we obtained a similar result (**Supplementary Table 8**).

Only the Kenya Boran has a different timing of admixture among the AFH populations, with a very recent admixture signal and similar significances for both the single- and double-pulse model fittings (**Fig. 3d**). It supports recent and ancient admixture signals in Kenya Boran (**Extended Data Fig. 6**). The Kenya Boran originates from the Ethiopian Boran[47,48]. After they migrated from Ethiopia to Kenya, they underwent selection and improvement with European taurine in the early 20th century[47,48]. These recent crossbreeding events most likely correspond to the admixture signal (12.77 ± 12.96 generations ago) of the Kenya Boran (**Extended Data Fig. 6**). We also detect an ancient admixture signal (132.28 ± 13.60 generations ago) in the Sheko.

In N'Dama, we detected only a recent admixture signal (21.36 ± 2.50 generations ago) (**Supplementary Table 7**). Previous studies have shown that the N'Dama is composed of several subpopulations with varying degree of indicine ancestry[5,24,49]. The N'Dama population here is from The Gambia, where an indicine ancestry has previously been documented[5,24,49]. Our results now provide a timescale for this recent admixture event.

We also performed GLOBETROTTER[50] analysis, based on haplotype-sharing, as an

alternative method to estimate admixture time. The 14 African cattle populations, excluding Muturu and N'Dama, show robust evidence of admixture (bootstrap $P < 0.01$) (**Supplementary Table 9**). In addition, admixture time estimates from the populations with best-guess model "one-date" range from 94.85 to 158.08 generations ago, in agreement with the results from ALDER (**Fig. 3e**). The exceptions are the Kenya Boran and Kenana, with best-guess model "multiple-dates" (**Supplementary Table 9**).

Selection signatures with an excess of taurine or indicine ancestry in African humped cattle. Our genome-wide analysis shows that all sampled African cattle breeds, except Muturu, have taurine and indicine ancestry, with little variation within a population. In such crossbreeds, a haplotype of either taurine or indicine ancestry may confer a relative adaptive advantage following selection pressures. Accordingly, such haplotype will be selected in the admixed African cattle population over time.

We employed two approaches to identify such loci and haplotypes. We first explored ongoing selective sweep using the integrated haplotype score (*iHS*). Taking the top 1% windows in terms of the proportion of SNPs with $|iHS| \geq 2$ ($\geq 60.00\%$), we obtained a total of 496 windows of 50 kb length as candidates under selection (**Extended Data Fig. 7a**). The 494 protein-coding genes overlapped with these windows show significant enrichment in "defense response to bacterium" (GO:0042742) and "keratinization" (R-BTA-6805567) (FDR-adjusted $P < 0.05$) (**Supplementary Table 10**). These 496 windows have a lower average taurine ancestry (26.14%) than other *iHS* percentiles as well as the whole genome (32.49%) (**Extended Data Figs. 8** and **9**). Also, the average taurine ancestry of the windows is outside the empirical distribution generated by resampling (**Extended Data Fig. 10**). This

indicates that the overall ancestry of these selected loci is more skewed toward indicine than the whole genome.

We then inferred local ancestry across the genome using LOTER[51] and selected the top 0.5% windows with the highest taurine or indicine ancestry (**Extended Data Fig. 7b**). Of these 496 windows, 63 windows identified in the previous *iHS* analysis were further considered. After filtering out windows with pairwise F_{st} value between the reference populations (EAT and AAI) less than the genome-wide level (< 0.2296) and merging adjacent windows, 16 genomic regions were retained, of which three and 13 show an excess of taurine and indicine ancestry, respectively. Eleven of the regions with an excess of indicine ancestry have been identified as selection signal in previous African cattle studies (**Table 1**). None of the regions with an excess of taurine ancestry was previously reported under selection in African cattle. The taurine and indicine excess regions overlap with nine and 51 protein-coding genes, respectively.

The longest region, 600 kb in length, is observed at BTA7 (**Table 1**). It includes 12 significant windows with 92.05% average indicine ancestry, which is much higher than the 67.51% genome-wide average. Downstream of this region, we found three smaller regions of 150, 200 and 50 kb length with high average indicine ancestry of 91.28%, 91.28% and 92.62%, respectively (**Table 1**). This cluster of four candidate regions spans 1.40 Mb of BTA7 (49.75-51.15 Mb). It shows a reduced level of diversity within AFH and an increased level of genetic differentiation between AFH and EAT. Shared haplotypes are more commonly observed between AFH and AAI than AFH and EAT (**Fig. 4**). In this cluster, we identified 18 protein-coding genes, three related to the host immune (*MATR3*[52], *MZB1*[53] and *STING1*[54]) and one to the environmental thermal stresses (heat shock protein gene

237 *DNAJC18*[55]) responses. We also found one more heat shock protein gene (*HSPA9*[51]) with an
238 excess of indicine ancestry (BTA7: 49.85-49.95 Mb; 91.30% average indicine ancestry), but
239 here the *iHS* (36.98%) does not reach the significance threshold. Two protein-coding genes
240 linked to reproduction (*PAIP2*[56] and *SPATA24*[57]) are also found in this region, together with
241 *SEPTIN2*[58] on BTA3 (**Table 1**).

242 The region with the highest taurine ancestry (61.34%) is of 200 kb length (BTA11:
243 14.65-14.85 Mb) (**Table 1**). As for the BTA7 region, it shows reduced genetic diversity (**Fig.**
244 **5**). However, we observe an increased level of genetic differentiation between AFH and AAI
245 as well as extended haplotypes sharing between EAT and AFH (**Fig. 5**). This region overlaps
246 with seven protein-coding genes (**Table 1**), one of which linked to the inflammatory
247 response[59-61] and tick infestation[62] (*NLRC4*).

248

249 **African taurine-specific loci and their distribution in African humped cattle.** Taurine are
250 the most ancient African cattle population. They have adapted to the local environmental
251 challenges, as exemplified by the trypanotolerance traits of West African taurine[63].
252 Accordingly, their unique genetic components may confer a selective advantage in crossbreed
253 animals facing similar environmental challenges to the West African taurine.

254 To identify such loci, we performed PBS analysis[64], comparing AFT and EAT using AAI
255 as an outgroup. After filtering out windows with less than 10 SNPs, we remained with
256 1,239,021 autosomal windows (50 kb sliding windows with 2 kb overlapping step). PBS
257 values ranged from -0.1156 to 0.8341, with a mean of 0.0314. After removing windows with
258 F_{st} value (AFT *versus* EAT) less than 0.1 (**Supplementary Fig. 1**) from the highest 0.1%
259 PBS windows, we considered the remaining windows as candidate selection signal specific to

AFT (**Supplementary Table 11**).

The strongest PBS signal (0.6740) overlaps with *SDK1* on BTA25 (40,052,001-40,102,000), approximately 300 kb upstream of *CARD11* (**Fig. 6**). At this region, F_{st} values between AFT and EAT (F_{st} = 0.5173) or AAI (F_{st} = 0.5308) are much higher than the genome-wide level (F_{st} = 0.1106 and F_{st} = 0.1825, respectively) (**Fig. 6b**). We observe a unique AFT haplotype pattern compared to EAT and AAI, which is present in some AFH breeds (**Supplementary Figs. 2** and **3**).

DISCUSSION

In this study, we first highlighted the taurine x indicine admixture characteristics of 16 indigenous African cattle populations, 14 of them living in the Horn of Africa, the main entry point of Asian zebu on the African continent. Then, we identified and dated the main taurine x indicine admixture event, which has shaped today's genome of these crossbreeds, to around 150 generations ago. We also identified candidate selected regions in these admixed population, including immune response and heat tolerance-related genes in haplotypes of indicine origins and inflammatory responses in haplotypes of taurine origins. Last but not least, we identify a locus of African taurine origin putatively linked to trypanotolerance. Together, these results support our hypothesis that the present success and dispersion of African pastoralism followed the arrival of indicine cattle and their crossbreeding with local taurine.

Our estimation under a single-pulse admixture model dates back the admixture time of AFH to around 150 generations ago. Assuming a cattle generation time of 5-7 years[65,66], it corresponds to about 750–1050 years ago at the beginning of the 2nd millennium AD (950-1250 AD). According to historical records, Asian zebu arrival along the Horn of Africa started earlier, around 700 AD, following the Islamization of the East African coast and the onset of the Swahili civilization[19], in agreement with the earliest non-controversial archaeological evidence in the Horn of Africa for African humped cattle, dated around the mid-1st millennium AD[18]. Therefore, our results suggest that indicine cattle remained initially confined to the East African coastal areas for at least 2-3 centuries before crossing extensively with taurine. Then, during the 2nd millennium AD, the complex human history of the Horn of Africa, characterized by multiple human population movements and dispersion[67]

as well as climatic fluctuation[16,68], would have further contributed to the landscape of today's genome admixture in East African cattle. Interestingly, a previous study indicates an admixture event in two West African zebu populations at around 500 years ago[66]. This timing is in agreement with our earlier East African dating of taurine x indicine crossbreeding, which would have been followed by the movement of East African humped cattle along the Sahelian belt and crossbreeding with local taurine in West Africa. The same study identified a more recent admixture event in the West African Borgou around 20 generations ago[66]. This is at approximately the same time as the one identified in our study in the N'Dama from The Gambia. These more recent admixture events may have been linked to the rinderpest epidemics of the end of 19th century[69].

We cannot exclude the possibility that more ancient taurine x indicine admixture events have contributed to the genetic composition of the AFH population from the Horn of Africa. Indeed, the haplotype sharing-based and LD-based admixture dating have limited power to detect admixture signals older than about 200 generations ago[50,70]. However, if the case, their admixture signals would have been likely erased by the more recent ones identified here.

The ancestry of the selection signatures in AFH was found to be more skewed toward indicine than the genome-wide average. Domestic cattle are not native to the African continent; African taurine cattle originate from the Near East[3], while indicine cattle were introduced into Africa after their domestication on the Indian subcontinent[3]. On reaching the African tropical environments, the Near East taurine must have faced major environmental challenges. On the other hand, indicine cattle found across the tropical Indian subcontinent may have been better pre-adapted to African environments and in particular, to its climatic characteristics[71]. These pre-adaptations would have facilitated indicine introgression into

local inland taurine populations and the dispersion of crossbred animals. However, African livestock diseases (e.g. trypanosomosis, bovine malignant catarrhal fever, East Coast fever, and Rift Valley fever) would have represented major constraints to the dispersion of indicine x taurine crossbred cattle[22]. Here, the tolerance of African taurine cattle to trypanosomosis[4] as well as the resistance of indicine cattle to infestation with ticks and to heat stress have proven advantageous[72-74].

Heat tolerance, a characteristic of zebu cattle[73,74], is a candidate for indicine pre-adaptations to climatic challenges. We found two heat shock protein genes (*HSPA9* and *DNAJC18*) at BTA7, which were previously reported as candidate selective loci in African and Asian indicine cattle[30,75-77]. We also found a water reabsorption-related gene, *GNAS*, at BTA13. The protein encoded by *GNAS* mediates antidiuretic hormone arginine vasopressin (AVP) to aquaporin-2 (AQP2) water channels, contributing to the water conservation pathway of the kidney[78]. Considering the adaptation of Asian zebu cattle to the arid environments[79], we infer that the indicine haplotype of *GNAS* contributes to the local adaptation of AFH to the arid areas of the continent. Also, the immune-related genes at BTA7 (*MATR3, MZB1* and *STING1*) and BTA3 (*ATG4B*[80]) (**Table 1**) might be related to the resistance of indicine cattle to ticks and tick-borne diseases, such as East Coast fever. *STING1* is essential for DNA-mediated type I IFN production and host defense against DNA viral pathogens[81], and therefore might confer some tolerance to viral infections such as Rift Valley fever and food-and-mouth disease.

The identification of an autosomal taurine background in all African cattle leads us to expect a contribution of local taurine ancestry to environmental adaptation and thus its contribution to the success of African cattle pastoralism. One example is the candidate region

337 at BTA11, which overlaps with *NLRC4*[59] involved in the inflammatory response. It shows
338 extensive haplotype sharing between AFH and taurine (AFT and EAT). Considering the lack
339 of EAT ancestry in AFH cattle, this haplotype likely originates from AFT. Its presence in
340 AFH may have resulted from selection for a better control of the inflammatory response
341 following infectious with diseases such as East Coast Fever and Rift Valley Fever[82,83].

342 Similarly, across large areas of sub-Saharan Africa, cattle have been exposed to the
343 challenge of trypanosomosis, a severe obstacle to livestock productivity in Africa[84]. African
344 taurine show tolerance to *Trypanosoma sp* infection, controlling both the effect of infection
345 (e.g. anemia and weight loss) and the level of blood parasites[85]. Accordingly, we expect to
346 detect selection signals in some of the humped cattle exposed to trypanosomosis challenges.

347 In our PBS analysis, a selection signature in AFT was found upstream of *CARD11*,
348 which encodes a protein essential for the signaling of T- and B-cells in the innate and
349 adaptive immune systems[86-88]. Importantly, it was reported as a differentially expressed gene
350 between the trypanotolerant N'Dama and trypanosusceptible Kenya Boran[89]. We suggest that
351 this candidate region plays a role in regulating *CARD11* expression and contributes to the
352 adaptation of AFT and AFH populations to trypanosomosis challenge. Accordingly, this
353 taurine region is expected to be observed in crossbreeds (Sheko, Horro and Mursi), whose
354 natural habitats are infested with tsetse flies[90,91]. However, as a complex quantitative trait[92-94],
355 the potential regulatory element upstream of *CARD11* should be regarded as one of many
356 genetic factors contributing to trypanotolerance. Accordingly, it is worth mentioning that the
357 windows within the highest 0.1% PBS value include several genes (*FAAP24*[95], *WDR48*[96],
358 *LRRC8A*[97], and *IFNAR1*[98]) related to anemia and immune response (**Supplementary Table**
359 **11**).

In conclusion, despite the environmental complexity of the African continent, and cattle domestication outside its geographic area, we find today domestic cattle across all African agro-ecologies. The results presented here support that taurine x indicine admixture events followed by taurine and indicine ancestry selection across the genome is at the root of the success of African cattle pastoralism. These findings are far-reaching in today's context of improving livestock productivity to respond to the needs of the growing human populations, with further crossbreeding of indigenous African cattle with exotic cattle recommended as one of the pathways for the continent's food security. A complete characterization at the genome level of African cattle unique adaptations will open the door to sustainable crossbreeding programs combining local environmental adaptation and increased exotic productivity.

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AUTHOR CONTRIBUTIONS

K.K. and O.H. devised the main conceptual ideas. O.H. and H.K. managed the project. D.L., S.C., S.J.O., H.-K.L., O.A.M., T.D., S.K., O.H., and H.K. conceived of and designed all of the described experiments. O.A.M., T.D., B.S., G.M.T. and A.T. contributed to sample collection and laboratory work. K.K., T.K., D.Y., J. Jang, S.S., S.L., J. Jung, and H.J. analyzed the data. K.K., C.J., J.K., and O.H. drafted the manuscript. All authors read and approved the final manuscript.

COMPETING INTERESTS

The authors declare that they have no competing interests.

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FIGURE LEGENDS

Figure 1 | Historical and geographical origin of African cattle breeds in this study. a, Schematic diagram showing the relationships among the main cattle lineages. The divergence times are approximate estimates based on previous studies[3,10,19]. **b**, Geographical origin of the indigenous East African cattle breeds. The map in the background has been generated by R package 'ggmap'[99]. The different colors reflect the classification of the populations in different phenotypic groups, with the Sheko indicated in yellow. **c**, Photographs of each breed, photo credits: Muturu (Abdulfatai Tijjani), Butana and Kenana (Bashir Salim), Goffa (Chencha Chebo), Kenya Boran and Gambian N'Dama (Stephen Kemp), Fogera (ILRI – Eric Ouma), Horro (ILRI – Tadelle Dessie), Ankole and Sheko (ILRI – Steve Mann). The photographs of Arsi, Mursi, and Ogaden are from DAGRIS[36].

Figure 2 | Population structure of indigenous African cattle. a, PCA results of 331 cattle samples (left), and percentage of eigenvalues (right). The Sheko is indicated in yellow. **b**, Results of admixture analysis for K 2 to 5. The forty-five cattle breeds are listed from left to right as follows: (1) Eastern Finn, (2) Western Finn, (3) Angus, (4) Hereford, (5) Jersey, (6) Holstein, (7) Simmental, (8) Limia, (9) Maronesa, (10) Pajuna, (11) Sayaguesa, (12) Boskarin, (13) Maremmana, (14) Podolica, (15) Hanwoo, (16) Muturu, (17) N'Dama, (18) Sheko (SH), (19) Ankole, (20) Afar, (21) Fogera, (22) Horro, (23) Mursi, (24) Kenya Boran, (25) Goffa, (26) Arsi, (27) Ethiopian Boran, (28) Ogaden, (29) Barka, (30) Kenana, (31) Butana, (32) Brahman, (33) Gir, (34) Nelore, (35) Hariana, (36) Achai, (37) Bhagnari, (38) Cholistani, (39) Dajal, (40) Dhanni, (41) Gabrali, (42) Lohani, (43) Red Sindhi, (44) Sahiwal, (45) Tharparkar.

Figure 3 | Admixture signatures in African cattle genomes. a, *D* statistics estimating indicine gene flow in African breed (X), using EAT/AAI as an ancestral taurine/indicine proxy and AFB as an outgroup; *D* (EAT, X; AAI, AFB). The dotted red line indicates the expected statistics at a neutral locus. Thick and thin horizontal bars represent ± 1 and ± 3 SEs, respectively. The Sheko is indicated in yellow. **b**, Admixture proportions measured by the f_4 ratio; f_4 (EATa, AFB; X, AAI)/f_4(EATa, AFB; EATb, AAI). EAT are randomly divided into two subgroups, EATa and EATb, and AFB is the outgroup. Blue and pink colors indicate taurine and indicine ancestries, respectively. **c**, Admixture times in generation estimated by ALDER[70] with two reference populations, EAT (n = 103) and AAI (n = 56). The number of biologically independent animals used in this analysis for each breed is as the following: Afar (9), Ankole (10), Arsi (10), Barka (9), Butana (20), Ethiopian Boran (10), Fogera (9), Goffa (10), Horro (11), Kenya Boran (10), Kenana (13), Mursi (10), N'Dama (13), Ogaden (9), and Sheko (9). The data points are presented as estimated admixture time in generation ± SE. Thick and thin horizontal bars represent ± 1 and 3 SEs, respectively. The Sheko is indicated

in yellow. **d**, Admixture times in generation estimated by both single- (left) and double-pulse (middle and right) model using MALDER[46] with two reference populations, EAT (n = 103) and AAI (n = 56). The number of biologically independent animals used in this analysis for each breed is identical as those of ALDER analysis in **c**. The data points are presented as estimated admixture time in generation ± 1 SE. y-axis indicates Z-score for each model fitting. **e**, The comparison between estimates from the GLOBETROTTER analysis (x-axis) and those from ALDER analysis (y-axis). The red line indicates $y = x$. The data points are presented as estimated admixture time in generation ± 1 SE (horizontal and vertical bars). SEs were estimated by leave-one-chromosome-out jackknifing (ALDER) or by bootstrapping (GLOBETROTTER). The number of biologically independent animals used in both of analyses for each breed is identical as those of ALDER analysis in **c**. The Sheko is indicated in yellow.

Figure 4 | Example of candidate selective loci on BTA7 with an excess of indicine ancestry. a, Proportion of SNPs with $|iHS| \geq 2$ in each non-overlapping 50 kb window around the candidate locus (BTA7: 49.75-51.15 Mb, the black square) including *MATR3*, *MZB1*, *STING1* (*TMEM173*), and *DNAJC18*. The dashed red line indicates the top 1% proportion of SNPs with $|iHS| \geq 2$ (60.00%). **b**, Nucleotide diversity calculated using VCFtools v0.1.17[100] for each 50 kb window with 20 kb step around the candidate locus. **c**, Average taurine ancestry (%) in each non-overlapping 50 kb window around the candidate locus. The lower and upper dashed red lines indicate the lowest and highest 0.5% of average taurine ancestry, respectively (10.31% and 57.67%). **d**, Pairwise F_{st} value calculated using VCFtools v0.1.17[100] for each 50 kb window with 20 kb step around the candidate locus. The blue line indicates the pairwise F_{st} value between AFH and EAT. The red line indicates the pairwise F_{st} value between AFH and AAI. **e**, Haplotype sharing at the candidate locus. The haplotypes were hierarchically clustered within each cattle group. The major allele in EAT (allele frequency ≥ 50%) is indicated in blue.

Figure 5 | Example of candidate selective loci on BTA11 with an excess of taurine ancestry. a, The proportion of SNPs with $|iHS| \geq 2$ in each non-overlapping 50 kb window around the candidate locus (BTA11: 14.65-14.85 Mb, the black square) including *NLRC4*. The dashed red line indicates the top 1% proportion of SNPs with $|iHS| \geq 2$ (60.00%). **b**, Nucleotide diversity calculated using VCFtools v0.1.17[100] for each 50 kb window with 20 kb step around the candidate locus. **c**, Average taurine ancestry (%) in each non-overlapping 50 kb window around the candidate locus. The lower and upper dashed red lines indicate the lowest and highest 0.5% of average taurine ancestry, respectively (10.31% and 57.67%). **d**, Pairwise F_{st} value calculated using VCFtools v0.1.17[100] for each 50 kb window with 20 kb step around the candidate locus. The blue line indicates the pairwise F_{st} values between AFH and EAT. The red line indicates the pairwise F_{st} value between AFH and AAI. **e**, Haplotype

724 sharing at the candidate locus. The haplotypes were hierarchically clustered within each cattle
725 group. The major allele in EAT (allele frequency ≥ 50%) is indicated in blue.

726

727 **Figure 6 | Unique selection signatures in African taurine following their separation from**
728 **the common ancestor with Eurasian taurine. a**, Genome-wide distribution of PBS values
729 with 50 kb window and 2 kb step. The windows with F_{st} value (AFT *versus* EAT) < 0.1 or
730 PBS < 0 are not plotted. The dashed line indicates top 0.1% PBS value. **b**, F_{st}-based
731 phylogeny among AFT, EAT and AAI. The branch lengths are proportional to F_{st} values.
732 Genome-wide F_{st} values ± standard deviations are as follows for each comparison; AFT
733 *versus* EAT: 0.1106 ± 0.0494, AFT *versus* AAI: 0.1825 ± 0.0490 and EAT *versus* AAI:
734 0.2296 ± 0.0493. **c**, PBS values around the peak with the highest PBS value. The PBS values
735 were calculated with 5 kb window and 2 kb step.

TABLES

Table 1 | Common African humped cattle (AFH) candidate regions identified in the *iHS* and local ancestry (taurine or indicine) inference (LOTER, top 0.5% windows) analysis. The proportion (%) of SNPs ($|iHS| \geq 2$) and ancestries are averaged values over windows. The F_{st} are pairwise values between reference populations (EAT and AAI) averaged over windows. Dashes (-) indicate that no genes have been annotated within the region or not overlapped with candidate selection signals in African cattle from previous studies.

BTA[a]	Region (Mb)	#Windows	Proportion of SNPs with $\|iHS\| \geq 2$ (%)	Ancestry (%)	F_{st}	Genes identified	Previous studies
Regions with an excess of indicine ancestry							
3	120.30-120.40	2	67.74%	93.02%	0.3390	*PASK, PPP1R7, SNED1, MTERF4*	Kim et al.[31]
3	120.45-120.55	2	63.33%	92.86%	0.2913	*SEPTIN2, FARP2, HDLBP*	Makina et al.[101]
3	120.60-120.65	1	79.35%	92.62%	0.2875	*FARP2, STK25, BOK*	Makina et al.[101]
3	120.70-120.80	2	83.36%	92.62%	0.2553	*ING5, D2HGDH, THAP4, ATG4B, DTYMK*	Kim et al.[31] Makina et al.[101]
3	120.85-120.90	1	79.25%	92.62%	0.3182	*RTP5*	Makina et al.[101]
7	49.75-49.80	1	65.74%	92.62%	0.3817	*KDM3B*	Gautier et al.[102]
7	50.05-50.25	4	67.90%	91.28%	0.4179	*CTNNA1, LRRTM2, ENSBTAG00000004415*	Kim et al.[31] Gautier et al.[102]

7	50.30-50.45	3	75.17%	91.28%	0.6321	*SIL1*	Kim et al.[31] Gautier et al.[102]
7	50.55-51.15	12	86.06%	92.05%	0.4861	*PSD2, NRG2, DNAJC18, ECSCR, SMIM33, STING1, CXXC5, UBE2D2, MATR3, PAIP2, SLC23A1, MZB1, PROB1, SPATA24*	Bahbahani et al.[30] Kim et al.[31] Bahbahani et al.[76] Gautier et al.[102]
13	56.95-57.00	1	82.80%	93.58%	0.3090	-	-
13	57.05-57.10	1	73.94%	93.76%	0.2685	*EDN3*	-
13	57.15-57.65	10	81.95%	92.69%	0.3114	*PRELID3B, ATP5F1E, TUBB1, CTSZ, NELFCD, ZNF831, GNAS*	Kim et al.[31] Bahbahani et al.[76]
19	39.65-39.85	4	67.07%	92.44%	0.2982	*STAC2, FBXL20, MED1, PLXDC1, CACNB1, RPL19, ENSBTAG00000008368, ENSBTAG00000050597*	Bahbahani et al.[30] Gautier et al.[102]
Regions with an excess of taurine ancestry							
10	92.15-92.25	2	72.23%	59.98%	0.3211	*CEP128, ENSBTAG00000047322*	-
11	14.40-14.45	1	67.08%	61.19%	0.4337	-	-
11	14.65-14.85	4	78.31%	61.34%	0.2870	*MEMO1, DPY30, SPAST, SLC30A6, NLRC4, ENSBTAG00000048521, ENSBTAG00000049576*	-

[a]*Bos taurus* autosomes.

METHODS

Ethics statement. Blood samples were collected during routine veterinary treatments with the logistical support and agreement of relevant agricultural institutions in each country: International Trypanotolerance Center, The Gambia and International Livestock Research Institute (ILRI – Kenya) (N'Dama, Kenya Boran); Ministry of Animal Resources, Sudan (Kenana, and Butana); Ol Pejeta Conservancy, Kenya (Ankole, African Buffalo); Ethiopian Ministry of Agriculture, Ethiopia (Afar, Arsi, Barka, Ethiopian Boran, Fogera, Goffa, Horro, Mursi, Ogaden, and Sheko). No further ethics permissions were required for this study. For European and Asian taurine, all animal works were approved by the Institutional Animal Care and Use Committee of the National Institute of Animal Science in Korea under approval numbers 2012-C-005 (Holstein and Hanwoo) and NIAS-2014-093 (Angus and Jersey). All animals were handled in strict accordance with good animal practice.

Sequencing and variant calling. All sequenced samples (n = 116) were prepared according to the Illumina protocols (TruSeq DNA Sample Prep Kit v2 Support (FC121-2001)). Briefly, 1 μg of genomic DNA was fragmented using a Covaris Focused-Ultrasonicator, and repaired. An 'A' was ligated to the 3' end of the fragments, followed by Illumina adapter ligation. The product was further size-selected for 400-500 bp, PCR-amplified and validated using the Agilent Bioanalyzer. Finally, the DNA was sequenced using the HiSeq2000 platform (Illumina, Inc.) by Macrogen (Seoul, Korea).

Our previously published data of 53 commercial taurine[31,103,104] and 48 African[31] cattle, as well as publicly available data of 10 African taurine, 50 European taurine, 34 American-

764 Australian zebu and 22 Asian zebu[105,106], were used in this study in addition to the newly
765 generated sequence data. We generated genotype data following the 1000 bull genomes
766 project Run 8 guideline (17/10/2019) (http://www.1000bullgenomes.com/). We first
767 examined a per-base sequence quality for the raw sequence reads using the fastQC software
768 v0.11.8[107], and removed low-quality bases and artefact sequences using Trimommatic
769 v0.39[108]. The high-quality sequence reads were mapped against the bovine reference genome
770 (ARS-UCD1.2) using bwa mem v0.7.17[109] with default parameters. We then used Samtools
771 v1.9[110] to sort bam files and create index files. For the mapped reads, potential PCR
772 duplicates were identified using the "MarkDuplicates" of Picard v2.20.2
773 (http://broadinstitute.github.io/picard). The "BaseRecalibrator" and "PrintReads" of GATK
774 Genome analysis toolkit v3.8 (GATK)[111] was used to perform base quality score recalibration
775 (BQSR). The known variants file (ARS1.2PlusY_BQSR_v3.vcf.gz) provided by the 1000
776 bull genomes project was used for masking known sites for all individuals except the two
777 African Buffalos (AFB). The before/after BQSR reports were checked by running
778 "AnalyzeCovariates" to ensure that base quality scores are corrected as expected. For the two
779 AFB samples, we performed an initial round of variant calling on unrecalibrated data. We
780 then performed BQSR by feeding the variants obtained from the initial variant calling, as
781 known sites to BaseRecalibrator and finally checked the convergence of base quality
782 improvement.

783 For the calling of the candidate SNPs from the bam files, we created GVCF file using
784 "HaplotypeCaller" in GATK with "-ERC GVCF" option. Individual GVCF files were merged
785 by breeds using "CombineGVCFs" in GATK. We called and selected candidate SNPs from
786 these combined GVCF files using "GenotypeGVCFs" and "SelectVariants", respectively. To
787 avoid possible false-positive calls, we used "VariantFiltration" of GATK as recommended by

GATK best practice: (1) SNP clusters were filtered with "--clusterSize 3" and "--clusterWindowSize 10" options; (2) SNPs with mean DP (for all individuals) < 1/3 × and > 3 × (×: overall mean sequencing depth across all SNP sites); (3) QD (Quality by Depth) < 2; (4) phred-scaled variant quality score (QUAL) < 30; (5) SOR (Strand Odds Ratio) > 3; (6) FS (Fisher Strand) > 60; (7) MQ (Mapping Quality) < 40; (8) MQRankSum (Mapping Quality Rank Sum test) < -12.5, and; (9) ReadPosRankSum (Read Pos Rank Sum test) < -8 were filtered. We then filtered out non-biallelic SNPs or SNPs with missing genotype rates > 0.01. For the remaining SNPs, genotype refinement, imputation and phasing were simultaneously performed using BEAGLE 4.0 (r1399)[42], while excluding AFB individuals. After filtering out SNPs with MAF < 0.01, the remaining high-quality SNPs were annotated according to their positions using SnpEff v4.3[112] and were used in the downstream analysis (**Supplementary Tables 12** and **13**).

To check the confidence of variant calls from the resequencing analysis, we additionally genotyped 69 cattle samples using the BovineSNP50 Genotyping BeadChip (Illumina, Inc.). After filtering out SNPs based on GeneCall score < 0.7, common loci of SNP chip and DNA resequencing data were extracted and examined to assess concordance between genotypes from the two different platforms. We also incorporated the genotype data of 45 samples from our previously published study[21] into this assessment to check the reliability of our current pipeline.

Population differentiation and structure. For principal component analysis (PCA), we used the Genome-wide Complex Trait Analysis (GCTA)[113] tool v1.93.0 to estimate the eigenvalue and eigenvectors, incorporating genotype data from 331 individuals, excluding two African

Buffalos. For admixture analysis, we performed LD-based pruning for the genotype data using PLINK v1.9[114] with "--indep-pairwise 50 10 0.1" option as recommended by the developer. Admixture v1.3.0[44] was run increasing K from 1 to 10, where K is the assumed number of ancestral populations. The Delta K method was used to choose the optimal K[115]. Genetic distances between cattle breeds were estimated with the F_{st} estimator as described in Weir and Cockerham[116] using PLINK v1.9[114].

Phylogenetic reconstruction and genetic diversity. For the most significant candidate region in PBS analysis (BTA 25: 40,052,001~40,102,000), we split the phased VCF and generated reference-based consensus sequences for the 50 kb window using bcftools v1.8 (http://samtools.github.io/bcftools/bcftools.html). A maximum-likelihood tree for the generated 666 haplotypes was reconstructed using IQ-TREE v1.6.12[117] with the following options: Modelfinder Plus[118] --mset phyml, -cmin 4, -cmin 6, and -mset phyml. The best-fit model was determined to TVM+F+I+G4 under Bayesian Information Criterion. The reconstructed trees were visualized using FigTree v1.4.4 (http://tree.bio.ed.ac.uk/software/figtree/).

Individual heterozygosity (theta) based on Felsenstein's model of substitutions[119] was estimated using the ATLAS v0.9[120] program, which takes into account depth coverage and sequencing error of each locus. Runs of homozygosity (ROH) were analyzed using VCFtools v0.1.17[100], filtering out ROH segments < 50 kb.

Test for admixture and estimation of admixture proportion. We used the *f* and *D* statistics

to test and quantify admixture in African cattle. We used our variant calls (~17.7 million SNPs) and the linearly interpolated recombination map derived from a large USDA dairy cattle pedigree[121]. All statistics were computed using ADMIXTOOLS v5.1[45] with standard errors obtained from a block jackknife with 5 cM block size. Z score was calculated on the standard errors. Three types of statistics were used in these analyses with the following notations. Note that *EAT* was replaced with *Muturu*, when we used Muturu as the surrogate population close to the source population in the three statistics.

$$f_3(X; EAT, AAI)$$

f_3 statistic was used to test for evidence that African cattle populations are derived from the admixture of two populations (EAT and AAI). *X* is the target African population of interest and *EAT* and *AAI* are populations close to the source populations. Significant negative f_3 statistics is considered as an evidence of historical admixture in the *X* population. In contrast, a positive value does not always mean there is no admixture, as high degree of drift specific to the *X* population can mask the negative signal[45].

$$D(EAT, X; AAI, AFB)$$

The *D* statistic was used to evaluate gene flow between different cattle populations. *X* is the target African population. If we ascertain *AFB* as an outgroup, a significant positive value indicates gene flow between *EAT* and *AAI*, while a significant negative value indicates gene flow between *X* and *AAI*.

$$\text{alpha} = f_4(EATa, AFB; X, AAI) / f_4(EATa, AFB; EATb, AAI)$$

f_4 ratio (alpha) quantifies the mixing proportion of an admixture event using the ratio of two f_4 statistics. We specified *X* as the target African population and *AFB* as an outgroup. *EAT*

855 is randomly divided into two subgroups, *EATa* and *EATb* to provide a pair of populations that
856 is completely admixed. Under this specification, the alpha value is interpreted as the mixing
857 proportion of *EAT* ancestry in the target African population X.

858

859 **Estimation of admixture time.** The time of admixture was first estimated with ALDER
860 v1.03[70], which provides an LD-based admixture time, using the default parameters with a
861 minimum genetic distance (mindis) of 0.5 cM. For this, we used our variant calls (~17.7
862 million SNPs) and the linearly interpolated recombination map derived from a large USDA
863 dairy cattle pedigree[121]. If a population is derived from an admixture between two source
864 populations close to the reference populations, the pairwise LD in this population, weighted
865 by the allele frequencies in the reference populations, shows an exponential decay as a
866 function of the genetic distance. ALDER fits this decay and then infers the admixture time
867 from the decay rate of the fitted curve.

868 We additionally used the modified version of ALDER (MALDER v1.0[46]), which allows
869 multiple admixture events, to compare the agreements of single and double-pulse admixture
870 models with our data. For estimating admixture time using ALDER and MALDER, we
871 performed two analyses for each African cattle population using two sets of reference
872 populations (EAT and AAI, Muturu and AAI). The fitted curve of both the single and double-
873 pulses admixture models for Kenya Boran was visually checked using the 'nls' function
874 implemented in R. For all the admixture time estimations, standard errors were estimated
875 from a leave-one-chromosome-out jackknifing.

876 In addition, we used GLOBETROTTER[50] on 14 African cattle populations (AFH) to
877 estimate haplotype sharing-based admixture time. The GLOBETROTTER method uses a

878 coancestry curve, in which a measure of how often pairs of haplotypes separated by a genetic
879 distance X come from each respective source populations is plotted as a function of the
880 genetic distance X[50]. Given a single admixture event, haplotypes inherited from each source
881 populations theoretically have an exponential size distribution, which leads to an exponential
882 decay of the coancestry curve[50]. GLOBETROTTER fits this curve, allowing us to estimate
883 the rate of the exponential decay, which is an estimate of the admixture time[50].

884 We specified the 14 African humped cattle populations and the other non-African cattle
885 populations as target and donor populations, respectively. This specification indicates that
886 target haplotypes are allowed to be copied from the donor haplotypes, not from the other
887 target haplotypes. This is recommended when a similar admixture history is shared across the
888 target populations[50].

889 To reduce the computational load, we performed LD-based pruning for the phased data
890 using PLINK v1.9[114] with "--indep-pairwise 50 10 0.1" option. The known genetic map[121]
891 was interpolated against this reduced data, not allowing interpolation for gaps larger than 50
892 kb. Using the loci of the LD-pruned data, for which the recombination rates are available on
893 the interpolated genetic map (~0.72 million SNPs), we performed GLOBETROTTER
894 analysis as the following: (1) first, we ran 10 rounds of the expectation–maximization (EM)
895 iterations for BTA 1, 2, 7 and 12 using ChromoPainter v2[122] with '-in' and '-iM' switches,
896 which result in estimates of the switch rate and global mutation rate parameters; (2) we then
897 averaged the estimated parameters from (1) over all individuals and chromosomes, and used
898 it as fixed estimated values (-n 514.030 -M 0.005127882) for the second running of
899 ChromoPainter v2[122] on all individuals; (3) we summed the "chunk length" output from (2)
900 across chromosomes using ChromoCombine, and obtained a single "chunk length" output;

(4) we also obtained ten painting samples for each target individuals by running ChromoPainter v2[122] with the fixed parameters averaged over all target individuals (-n 632.949 -M 0.006501492); (5) using the summed chunk length from (3) and ten painting samples from (4), we ran GLOBETROTTER with the 'prop.ind: 1' and 'null.ind: 1' options; (6) to check the significance of admixture evidence, bootstrapping was performed with 100 replicates using 'prop.ind: 0' and 'bootstrap.date.ind: 1' options. In the bootstrap replicates, the proportion of inferred generations(s) that are between 1 and 400 was considered as an evidence of detectable admixture[50].

Detection of selection signatures in African humped cattle. To detect ongoing selection signatures in AFH genomes (n = 149), we employed the integrated haplotype score (*iHS*)[123] implemented in HAPBIN v1.3.0[124] using the default settings except "-f 0.01" option. For each SNP, the ancestral allele was defined as the allele fixed in the AFB outgroup. After computing *iHS* value for each SNP, they were grouped into 2% frequency bins and standardized. A proportion of SNPs with $|iHS| \geq 2$ was then calculated in each non-overlapping windows of 50 kb. In this step, windows with less than 10 SNPs were removed. We considered windows within the highest 1% of the empirical distribution for the proportion of SNPs with $|iHS| \geq 2$ as candidate regions with selection signal.

Local ancestry inference in African humped cattle. Using the genotype data phased in the *iHS* analysis, we performed local ancestry inference implemented in the LOTER package[51] to infer taurine-indicine ancestry along the AFH genomes. We specified 103 individuals of EAT and 56 individuals of AAI as reference populations, assuming that a haplotype of an admixed

AFH consists of a mosaic of existing haplotypes from the two reference populations. Using LOTER, we first assigned each allele to taurine or indicine ancestry and calculated the frequency of assigned taurine or indicine ancestry within AFH. The resulting frequencies were then averaged over each non-overlapping window of 50 kb. For the windows with the highest or lowest 0.5% of the empirical distribution for averaged taurine ancestry, we additionally filtered out windows with pairwise F_{st} values between reference populations less than genome-wide level (< 0.2296) to reduce false positives from the admixture in each reference population. The remaining windows were considered as candidate regions with excess or deficiency of taurine ancestry. In light of the history of indicine cattle on the Indian subcontinent and the Americas, it is possible that they contain some taurine background, although at low frequencies[125-127]. However, this will not result in false positives. Rather, it could lead to few false negatives since there are similar haplotypes to select in the LOTER algorithm, which may mask an excess of a particular ancestry.

Detection of selection signatures in African taurine cattle. To detect selection signatures in AFT after divergence from EAT, we employed the Population Branch Statistics (PBS) developed by Yi *et al.*[64]. For each window with 50 kb size and 2 kb step, we calculated the PBS statistic as follows:

$$\mathrm{T} = -\log(1 - F_{st})$$

$$\mathrm{PBS} = \frac{T^{AE} + T^{AO} - T^{EO}}{2}$$

where T^{ij} represents estimated branch length between *i* and *j* populations based on pairwise Weir and Cockerham[116] F_{st} estimated by VCFtools v0.1.17[100]. *A* represents the target

944 population (AFT), while *E* and *O* represents the control population (EAT) and the outgroup
945 (AAI), respectively. A population PBS value conceptually represents the amount of allele
946 frequency change at a given locus since its divergence from the other two populations. From
947 this statistic, we intended to discover selection signatures in AFT following their ancestral
948 migration into the African continent.

949

950 **Annotation and functional enrichment analysis.** The annotation of the candidate regions
951 was based on the ARS-UCD1.2 Gene Transfer Format file (.gtf) from Ensembl release 99[128].
952 For functional enrichment analysis of a candidate gene set, statistical overrepresentation test
953 in PANTHER v15.0[129] was used based on GO-Slim Biological Process terms and
954 REACTOME pathway[130] with default settings. An FDR-adjusted *P*-value of 0.05 was used as
955 the threshold for statistical significance.

956

DATA AVAILABILITY

The newly generated sequences for 114 African cattle and 2 African buffalo samples are available from Sequence Read Archive (SRA) with the Bioproject accession number PRJNA574857. The publicly available sequences were downloaded from SRA and China National GeneBank (CNGB) with following project accession numbers; CNP0000189 (Achai, Bhagnari, Cholistani, Dajal, Dhanni, Gabrali, Hariana, Lohani, Red Sindhi, Sahiwal, and Tharparkar), PRJNA318087 (Angus, Ankole, Jersey, Kenya Boran, Kenana, N'Dama, and Ogaden), PRJNA514237 (Boskarin, Limia, Maremmana, Maronesa, Pajuna, Podolica, and Sayaguesa), PRJNA324822 (Brahman), PRJNA343262 (Brahman, Gir, Hereford, Nelore, and Simmental), PRJNA432125 (Brahman), PRJEB28185 (Eastern Finn, and Western Finn), PRJNA210523 (Hanwoo), PRJNA379859 (Hariana, Sahiwal, and Thaparkar), PRJNA210521 (Holstein), PRJNA386202 (Muturu), and PRJNA507259 (Nelore). The known variants file (ARS1.2PlusY_BQSR_v3.vcf.gz) for base quality score recalibration is provided by the 1000 bull genomes project (http://www.1000bullgenomes.com/). The annotation of the candidate regions was based on the ARS-UCD1.2 Gene Transfer Format file (.gtf) from Ensembl release 99 (http://www.ensembl.org/). PANTHER database (http://pantherdb.org/) was used for functional enrichment analysis of a candidate gene set.

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