Whole-genome resequencing of wild and domestic sheep identifies genes associated with morphological and agronomic traits

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Understanding the genetic changes underlying phenotypic variation in sheep (Ovis aries) may facilitate our efforts towards further improvement. Here, we report the deep resequencing of 248 sheep including the wild ancestor (O. orientalis), landraces, and improved breeds. We explored the sheep variome and selection signatures. We detected genomic regions harboring genes associated with distinct morphological and agronomic traits, which may be past and potential future targets of domestication, breeding, and selection. Furthermore, we found non-synonymous mutations in a set of plausible candidate genes and significant differences in their allele frequency distributions across breeds. We identified PDGFD as a likely causal gene for fat deposition in the tails of sheep through transcriptome, RT-PCR, qPCR, and Western blot analyses. Our results provide insights into the demographic history of sheep and a valuable genomic resource for future genetic studies and improved genome-assisted breeding of sheep and other domestic animals.

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Sheep (*Ovis aries*) is an important livestock species, which has provided meat, wool, skin, and milk for humans since the Neolithic. Characterization of genome-wide sequence variation and identification of phenotype-associated functional variants are essential steps for guidance of genome-assisted breeding in the near future. The impact of domestication and subsequent selection on genomic variation has recently been investigated in sheep\(^1\),\(^2\), and a number of quantitative trait loci (QTLs) and functional genes have been associated with phenotypic traits\(^3\). However, most of these investigations focused on a few phenotypes and involved a limited number of molecular markers and breeds/populations. So far, whole-genome resequencing has allowed the identification of genomic variants involved in domestication and genetic improvement for several domestic plants (e.g., rice and soybean)\(^4\),\(^5\) and animals (e.g., cattle and sheep)\(^6\),\(^7\).

The completion of a sheep reference genome\(^7\) has allowed comparison of the genomes from a wide collection of phenotypically diverse authentic landraces and improved breeds of domestic sheep with their wild ancestors. In this study, we resequenced the genomes of 16 Asiatic mouflon, 172 sheep from 36 landraces and 60 sheep from six improved breeds to a depth of ~25.7x coverage. Tests for selective sweeps and genome-wide association studies (GWAS) identify a number of selected regions and genes potentially affected by domestication and associated with several important morphological and agronomic traits. Moreover, we conduct a survey of non-silent single-nucleotide polymorphisms (SNPs) and gene-containing copy number variations (CNVs), which are part of the selective signatures. These data provide a valuable genomic resource for facilitating future molecular-guided breeding and genetic improvement of domestic sheep, potentially valuable in the face of ongoing climate change and consequent impacts in agricultural practice. In addition, our findings contribute to further understanding of the demographic history of sheep and the molecular basis of distinct phenotypes in the species and other animals.

### Results

**Sequencing and variation calling.** Deep resequencing of the 248 samples of wild and domestic sheep (Fig. 1a and Supplementary Data 1) generated a total of 137.0 billion 150-bp paired-end reads (20.55 Tb), with an average depth of 25.7x per individual and an average genome coverage of 98.27%. The average sequence coverage was 27.71x (23.90–36.93x) for 16 Asiatic mouflon, 25.23x (17.15–31.35x) for 172 landraces and 26.51x (24.62–32.98x) for 60 improved sheep (Supplementary Fig. 1 and Supplementary Data 2). There was no significant difference in sequence coverage among individuals from the three groups (Kruskal-Wallis, \(P > 0.05\)). Of the Asiatic mouflon and domestic sheep sequencing reads, 99.04% were mapped to the *O. aries* reference genome for both datasets. We obtained a total of 67,314,959 and 91,772,948 SNPs after mapping with SAMtools and GATK, respectively, of which 50,520,459 were identified by both methods (Supplementary Data 3 and Supplementary Notes). After filtering, a final set of 28.36 million common SNPs was retained (6.69 million/individual in domestic sheep versus 8.40 million/individual in Asiatic mouflon; Mann-Whitney, \(P < 0.001\)) along with 4.80 million insertions and deletions (INDEls ≤100 bp; 1.16 million/individual for domestic sheep versus 1.38 million/individual for Asiatic mouflon; Mann-Whitney, \(P < 0.001\)) (Supplementary Fig. 1 and Supplementary Data 3) in the downstream analyses.

In addition, the high-depth whole-genome sequencing data enabled us to identify 13,551 autosomal CNVs (176 bp–224.6 kb; 311,804/individual; Supplementary Data 4) and 28,973 autosomal structural variations (SVs, 50 bp–984.0 kb; 4,515–6,657/individual; Supplementary Data 5) across all samples of wild and domestic sheep.

On average, 96.21% SNPs identified in the 232 domestic sheep and 81.26% SNPs identified in the 16 Asiatic mouflon were confirmed by the sheep dbSNP database v.151 (Supplementary Data 6). For the SNPs on the Ovine HD chip, an average of 98.98% genotypes identified in the sequenced samples were also validated by Ovine Infinium\(^8\) HD SNP BeadChip data available for 223 individuals (Supplementary Data 7). Using 10,007 homozygous reference loci on the Ovine HD BeadChip for 211 individuals, false-positive SNP calling rates of 6.38% and 5.37% were observed for GATK and SAMtools, respectively. After filtering, the false-positive rate for the SNP set identified by both methods was estimated to be 0.66%. Moreover, inspection of 68 randomly selected SNPs in candidate genes from 1,414 individuals of 21 breeds obtained by Sanger sequencing produced an overall validation rate of 95.69% (Supplementary Table 1 and Supplementary Methods). For PCR and qPCR validation of CNVs, we confirmed 78.79% concordant genotypes (36/48 deletions and 26/33 duplications; Supplementary Fig. 2, Supplementary Data 8 and Supplementary Methods). The high-quality genomic variants generated here added ~230,000 new SNPs to the public database of genetic variants for domestic sheep.

| Variations | Asiatic mouflon | Landraces | Improved breeds |
|------------|----------------|-----------|-----------------|
| SNPs       | 23,269,423     | 14,382,975| 14,008,509      |
| Indels     | 3,501,573      | 3,481,234 | 2,743,640       |
| Insertions | 1,351,550      | 1,343,664 | 1,099,340       |
| Deletions  | 2,150,021      | 2,137,570 | 1,644,300       |
| SVs        | 16,970         | 25,089    | 19,282          |
| CNVs       | 7,331          | 12,724    | 10,694          |

**Patterns of variation.** The 28.36 million SNPs were analyzed across the three groups of sheep (Asiatic mouflon, landraces, and improved breeds). A majority up to 23.27 million SNPs were observed in Asiatic mouflon at 7.77–9.16 million per individual (12.06 million to be unique for this group), followed by 14.38 million in landraces at 5.62–8.92 million per individual (1.06 million to be unique) and 14.01 million in improved breeds at 5.90–6.90 million per individual (1.08 million to be unique) (Fig. 2, Table 1, Supplementary Table 2, and Supplementary Data 3). Using the Asiatic mouflon reference genome (ftp://ftp. ebi.ac.uk/pub/databases/nextgen/ovis/assembly/mouflon.Oor1. PRJEB3141/) for SNP calling, we identified 28.75 million SNPs in Asiatic mouflon, which was higher than that based on the sheep reference genome Oar v.4.0 (23.27 million).

We observed 12.09 million SNPs shared between landraces and improved breeds, which exceeded that shared between the mouflon and landraces (10.38 million) or between the mouflon and improved breeds (9.98 million) (Fig. 2 and Table 1). Pairwise genome-wide \(F_{ST}\) values also indicated that genomic differentiation between landraces and improved breeds (\(F_{ST} = 0.032, \ P = 0.041\)) was less than that between Asiatic mouflon and landraces (\(F_{ST} = 0.125, \ P = 0.015\)) or between Asiatic mouflon and improved breeds (\(F_{ST} = 0.132, \ P = 0.016\)). The genomic diversities (\(\pi\)) in Asiatic mouflon, landraces, and improved breeds based on the SNPs with <10% missing data were 0.00127, 0.00113, and 0.00109, respectively. The distribution of SNPs at various regions near or within genes was similar in Asiatic mouflon, landraces, and improved breeds (Supplementary Table 6).
The abundance of SNPs identified in improved breeds (Supplementary Data 5). In contrast to the number of SVs per individual varied between 5,035 and 6,657 (mean = 6,166) for improved breeds (Supplementary Data 4). The number of SVs per individual varied between 5,035 and 6,657 (mean = 6,166) for improved breeds (Supplementary Data 4). The number of SVs per individual varied between 5,035 and 6,657 (mean = 6,166) for improved breeds (Supplementary Data 4). The number of SVs per individual varied between 5,035 and 6,657 (mean = 6,166) for improved breeds (Supplementary Data 4). The number of SVs per individual varied between 5,035 and 6,657 (mean = 6,166) for improved breeds (Supplementary Data 4). The number of SVs per individual varied between 5,035 and 6,657 (mean = 6,166) for improved breeds (Supplementary Data 4). The number of SVs per individual varied between 5,035 and 6,657 (mean = 6,166) for improved breeds (Supplementary Data 4). The number of SVs per individual varied between 5,035 and 6,657 (mean = 6,166) for improved breeds (Supplementary Data 4). The number of SVs per individual varied between 5,035 and 6,657 (mean = 6,166) for improved breeds (Supplementary Data 4). The number of SVs per individual varied between 5,035 and 6,657 (mean = 6,166) for improved breeds (Supplementary Data 4). The number of SVs per individual varied between 5,035 and 6,657 (mean = 6,166) for improved breeds (Supplementary Data 4). The number of SVs per individual varied between 5,035 and 6,657 (mean = 6,166) for improved breeds (Supplementary Data 4). The number of SVs per individual varied between 5,035 and 6,657 (mean = 6,166) for improved breeds (Supplementary Data 4). The number of SVs per individual varied between 5,035 and 6,657 (mean = 6,166) for improved breeds (Supplementary Data 4). The number of SVs per individual varied between 5,035 and 6,657 (mean = 6,166) for improved breeds (Supplementary Data 4). The number of SVs per individual varied between 5,035 and 6,657 (mean = 6,166) for improved breeds (Supplementary Data 4). The number of SVs per individual varied between 5,035 and 6,657 (mean = 6,166) for improved breeds (Supplementary Data 4). The number of SVs per individual varied between 5,035 and 6,657 (mean = 6,166) for improved breeds (Supplementary Data 4). The number of SVs per individual varied between 5,035 and 6,657 (mean = 6,166) for improved breeds (Supplementary Data 4). The number of SVs per individual varied between 5,035 and 6,657 (mean = 6,166) for improved breeds (Supplementary Data 4). The number of SVs per individual varied between 5,035 and 6,657 (mean = 6,166) for improved breeds (Supplementary Data 4). The number of SVs per individual varied between 5,035 and 6,657 (mean = 6,166) for improved breeds (Supplementary Data 4). The number of SVs per individual varied between 5,035 and 6,657 (mean = 6,166) for improved breeds (Supplementary Data 4). The number of SVs per individual varied between 5,035 and 6,657 (mean = 6,166) for improved breeds (Supplementary Data 4). The number of SVs per individual varied between 5,035 and 6,657 (mean = 6,166) for improved breeds (Supplementary Data 4). The number of SVs per individual varied between 5,035 and 6,657 (mean = 6,166) for improved breeds (Supplementary Data 4). The number of SVs per individual varied between 5,035 and 6,657 (mean = 6,166) for improved breeds (Supplementary Data 4). The number of SVs per individual varied between 5,035 and 6,657 (mean = 6,166) for improved breeds (Supplementary Data 4). The number of SVs per individual varied between 5,035 and 6,657 (mean = 6,166) for improved breeds (Supplementary Data 4). The number of SVs per individual varied between 5,035 and 6,657 (mean = 6,166) for improved breeds (Supplementary Data 4). The number of SVs per individual varied between 5,035 and 6,657 (mean = 6,166) for improved breeds (Supplementary Data 4). The number of SVs per individual varied between 5,035 and 6,657 (mean = 6,166) for improved breeds (Supplementary Data 4). The number of SVs per individual varied between 5,035 and 6,657 (mean = 6,166) for improved breeds (Supplementary Data 4). The number of SVs per individual varied between 5,035 and 6,657 (mean = 6,166) for improved breeds (Supplementary Data 4). The number of SVs per individual varied between 5,035 and 6,657 (mean = 6,166) for improved breeds (Supplementary Data 4). The number of SVs per individual varied between 5,035 and 6,657 (mean = 6,166) for improved breeds (Supplementary Data 4).

Table 2). The ratio of non-synonymous and synonymous substitutions in wild (0.55) and domestic sheep (0.53–0.54) was comparable.

To ascertain the effect of major evolutionary transitions (e.g., domestication and intensive artificial breeding) on CNVs and SVs, these variants were pooled for Asiatic mouflon, landraces, and improved breeds separately (Fig. 2 and Table 1). This yielded a high depth of coverage and information about the uniqueness and sharing of CNVs and SVs among the three groups (Fig. 2 and Table 1). The abundance of CNVs per individual ranged from 443 to 804 (average of 563) for Asiatic mouflon, from 311 to 777 (average of 589) for landraces, and from 514 to 686 (average of 616) for improved breeds (Supplementary Data 4). The number of SVs per individual varied between 5,035 and 6,657 (mean = 5,874) in Asiatic mouflon, between 4,515 and 6,323 (mean = 5,393) in landraces, and between 4,863 and 6,203 (mean = 5,366) in improved breeds (Supplementary Data 5). In contrast to the abundance of SNPs detected in the wild species, we detected significant differences in the numbers of CNVs (Kruskal-Wallis, $P = 0.047$) and SVs (Kruskal-Wallis, $P < 0.001$) per individual among the three groups (Supplementary Data 4 and 5).

From a total of 6,366 CNV regions (Table 2). The ratio of non-synonymous and synonymous substitutions in wild (0.55) and domestic sheep (0.53–0.54) was comparable.

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(Fig. 1b and Supplementary Fig. 3). This geographic subdivision was confirmed by principal component analysis (PCA; Fig. 1c) and clustering analysis based on maximum likelihood estimation (Supplementary Fig. 4). A neighbor-joining (NJ) tree constructed for the above four groups further revealed a close genetic affinity between East Asian and Middle Eastern populations, whereas the two African lineages showed larger genetic divergence from the other three subgroups (Fig. 1e). Nucleotide diversities (π) in European, Asian, African, and Middle Eastern populations based on the SNPs with <10% missing data were 0.00105, 0.00118, 0.00113, and 0.00114, respectively (Supplementary Fig. 5a). Asiatic mouflon were more genetically similar to Middle Eastern sheep than to other domestic populations as measured by pairwise FST (Supplementary Fig. 5b).

Linkage disequilibrium (LD, measured as r²) decreased to half of its maximum value at 2.8 kb in Asiatic mouflon but at 12.1 kb and 17.1 kb in landraces and improved breeds, respectively (Fig. 1d, Supplementary Tables 3 and 4 and Supplementary Notes). LD comparison among domestic populations (Supplementary Fig. 6c and Supplementary Table 3) showed that European populations had a higher level of LD (25.1 kb) than that in Asian populations (9.8 kb). Pairwise sequentially Markovian coalescent (PSMC) analysis revealed concordant demographic trajectories for wild and domestic sheep, with two expansions and two contractions in Ne during the last one million years (Supplementary Fig. 7). The estimated Ne for Asiatic mouflon and domestic populations ~50 generations ago were 344.1 and 73.7–199.3, respectively, being inversely correlated with the extent of LD (Supplementary Fig. 5c) as expected. These observations suggested that artificial selection and genetic isolation, leading to the formation of breeds, had stronger effects on LD and Ne than on nucleotide diversity.

Genomic signatures related to domestication. To identify genomic regions influenced by domestication, we compared the genomes of 16 Asiatic mouflon and five old landrace populations representing different geographic and genetic origins: 5 Dutch Drentse Heathens10, 10 East-Asian Hu11, 10 Central-Asian Altay11, one African Djallonke12, and one Middle Eastern Karakul sheep13. Using the cross-population composite likelihood ratio (XP-CLR) test, we scanned for genomic regions with extreme allele frequency differentiation. The top 1% XP-CLR values identified 302 putative selective sweeps in the five old landraces after annotation and removing repeats (Fig. 3a and Supplementary Data 11). As genomic regions targeted by artificial selection may be expected to have decreased levels of genetic variation, we also measured and plotted nucleotide diversity (π) along their genomes. Selecting the windows with the top 1% diversity ratios, i.e., low diversity in the five old landraces but high in the Asiatic mouflon, we found 529 putative selective sweeps (Supplementary Data 12). Combination of the XP-CLR and π ratio analyses unveiled 144 putative selective regions covering or being near to 261 genes in the five old landraces (Supplementary Data 13). Additional analyses involving the integrated haplotype score (iHS) analysis (top 5% outliers) and the Hudson-Kreitman-Aguadé (HKA) test (χ² = 5.99, df = 2, P = 0.05) identified 899 and 1,503 putative selective sweeps, respectively (Supplementary Data 14 and 15). Sixty-five and 71 selected genes identified by both XP-CLR and π ratio analyses were also detected by the iHS and HKA analyses, respectively (Supplementary Data 16 and 17).

A comparison of the domestication-associated selective sweeps and known QTLs14 (permutation test, P < 0.001; Supplementary Table 5) revealed that the selected regions with high XP-CLR values but reduced diversity and significant values in the iHS or HKA analysis mostly spanned milk- and meat-related QTLs (Supplementary Data 18 and 19), reflecting human demands for milk and meat during sheep domestication.

Among the 261 candidate genes revealed by two (XP-CLR and π ratio) or three (XP-CLR, π ratio, and iHS or HKA) methods, 36
were also identified to be the targets of selection in the comparison of Asiatic mouflon with domestic sheep in two recent studies (Supplementary Table 6). In the same selection tests (XP-CLR and \( \pi \) ratio) between the Asiatic mouflon and the five old landraces, none of the 48 selected genes in the Asiatic mouflon (Supplementary Data 20) was found in the 261 selected genes in the five old landraces. Diverged selection has thus driven the domestic sheep away from the Asiatic mouflon, and the 36 consistently selected genes identified in domestic sheep were plausibly linked to domestication (Supplementary Table 6).

Inspection of the 261 selected genes in the five old landraces detected 14 (\( SLC11A1, HOXA11, CAMK4, LEFI, TET2, KDR, CTBP1, GAK, CPLX1, PGC3, FLT1, BC02, CHGA, \) and \( HTRA1) \) to be associated with known functions (e.g., female reproductive traits, resistance to infection, bone formation, fat deposition,
Fig. 3 Genome-wide annotations during sheep domestication and improvement. a Whole-genome screening for selected regions during domestication by comparing five old landrace populations (Drenthe Heathen (DRS) in Europe, Altay (ALS) in Central Asia, Hu sheep (HUS) in East Asia, Djallonké sheep (DJI) in Africa, and Karakul sheep (KAR) in the Middle East) with Asiatic mouflon (MOU) through the XP-CLR. The black horizontal dashed line corresponds to the genome-wide significance threshold (XP-CLR = 26.96). Candidate genes overlapping with regions which were significantly selected by XP-CLR & ln(π ratio)/ln(2), XP-CLR & ln(π ratio)/ln(2) & HKA, and XP-CLR & ln(x ratio)/ln(2) & HKA are marked by gray, orange, blue, and red colors, respectively. Below this plot genes near the peaks are indicated by green boxes. The pie charts represent the spectrum of allele frequencies at the non-synonymous loci of the focused genes PDE6B, BCO2, NXX2-1, ADAMTSL3, and LOC101108252 in Asiatic mouflon and the five old landraces. The type of variant allele is indicated in blue, whereas the reference allele in pink. b The patterns of genotypes of the LOC101108252 gene region among Asiatic mouflon and the five old landraces based on eight SNPs. c Genome-wide distribution of global $F_{ST}$, which is measured by the average value for each SNP across all 42 domestic breeds. The significance threshold ($F_{ST} = 0.27$) is denoted by black dashed line. Source data are provided as a Source Data file.

yellow fat, photoperiod, and recombination rate variation) in sheep in previous studies (Supplementary Data 21 and Supplementary Notes). Twenty-two other genes (e.g., IGF2BP2, RFX3, MRPL41, KITLG, HERSV, MAN2B1, FGFR1L, PDE6B, EDN3, RALY, GTF2I, GTF2IRD1) were previously found to be influenced by selection in other species including cattle, goat, horse, pig, dog, chicken, rabbit, and mice (Supplementary Data 21). These genes were associated with functions including immunity, pigmentation, coat color, photoreceptor, behavior, growth, and reproduction traits (Supplementary Data 21 and Supplementary Notes). We identified non-synonymous SNP mutations in the 59 most plausible domestication genes presented above (i.e., summing the unique genes in Supplementary Table 6 and Supplementary Data 21) and found that the variant allele frequencies of non-synonymous SNPs in five genes (PDE6B, BCO2, ADAMTSL3, NXX2-1, and an olfactory receptor 51A4-like gene LOC101108252) and the genotype pattern in LOC101108252 showed significant differences (Mann-Whitney, $P < 0.01$) between the Asiatic mouflon and the five old landraces (Fig. 3a, b and Supplementary Table 7).

In the functional enrichment analysis of the 261 genes putatively influenced by domestication, we identified the top 15 over-represented GO terms and 12 KEGG pathways (Supplementary Data 22). Specifically, four biological process GO terms and one KEGG pathway were associated with biosynthesis. Five biological process GO terms and four KEGG pathways were associated with metabolic processes. One KEGG pathway was associated with olfactory transduction.

In the selective sweep analysis of CNVs, we identified 137 candidate selected CNVs associated with domestication (Supplementary Data 23). Annotation of the CNVs indicated the CNVs to be located in genes (Supplementary Table 8) or coincident with regions with previously reported QTLs. Annotation of the CNVs indicated the CNVs to be associated with immune response, and immune system processes as well as 11 molecular function categories, such as cytokine activity and ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism associated with energy metabolism, and immune function (Supplementary Data 28). The most significantly enriched pathway was cytokine–cytokine receptor interaction (Supplementary Data 28).

Notably, the selective region with the highest $F_{ST}$ value ($F_{ST} = 0.56$) was located near the gene PAPPA2, which has been reported to be associated with fat deposition in humans and has been identified as a candidate gene for milk, reproduction, and body size traits in cattle. Comparison of allele frequencies at non-synonymous SNPs in candidate selected genes revealed four (e.g., SPAG8, FAM184B, PDE6B, and PDGFD) with significantly differentiated allele frequencies among domestic sheep breeds (Supplementary Data 29).

Of these 391 selected genes, nine were also among the previously identified 59 most plausible domestication genes (Supplementary Table 6 and Supplementary Data 21) and they (RASGRF2, FBXO39, XAF1, GMSD, HOXA11, PDE6B, FLT1, EDN3, and RALY) were linked to both domestication and breed-level genetic differentiation. In addition, 22 selected genes were confirmed to be under selection in our analyses for specific phenotypic traits such as reproduction, presence of horns, fat tail, wool fineness, nipple number, and ear size (see below; Supplementary Table 11). Moreover, 52 selected genes (e.g., SOCS2, EDAR, PDE6B, PDGFD, HOXA10, etc.) have been shown to be under selection in sheep, humans, and other domestic animals in previous investigations (Supplementary Data 27). Additionally, a comparison of the selected genomic regions with previously reported QTLs revealed 131 regions...
with high $F_{ST}$ values spanning the QTLs. These regions covered 19.97 Mb of the sheep genome and were found to be associated with morphological and production traits, such as reproductive seasonality, milk related traits, body weight, meat-related traits, teat number, tail fat deposition, and presence of horns (Supplementary Data 30).

Genetic mechanisms of the tail configuration trait. We implemented genome-wide selection tests between domestic breeds representing contrasting phenotypes for several traits that are relevant for sheep husbandry (Supplementary Table 12), such as morphological traits. Focusing on an iconic trait, tail configuration (Fig. 4a), we performed separate pairwise-population
selection tests through comparisons of fat-rumped (Altaf (ALS) and Bashibai (BSB)), long fat-tailed (Large-tailed Han sheep (HDW)) and long wool-tailed (Drenthe Heathens sheep (DRS)) breeds with short fat-tailed (Tan sheep (TAN)) and short thin-tailed (Shetland sheep (SHE)) breeds. We selected regions with differences in allele frequencies by XP-CLR in Supplementary Table 31 and Supplementary Fig. 9) and reduced π values (Supplementary Data 32) in the pairs of breeds of ALS versus SHE, BSB versus SHE, HDW versus SHE, HDW versus TAN, and DRS versus SHE, and detected 105, 81, 88, 101, and 122 common selective sweeps that overlapped with annotated genes, respectively (Supplementary Data 33). Among these sweeps, we identified 21, 22, 18, 25, and 17 (Supplementary Data 34) and 16, 4, 5, 15, and 74 (Supplementary Data 35) sweeps overlapping with the selective signals detected by the iHS analysis (Supplementary Data 36) and the HKA test (Supplementary Data 37), respectively. Of these sweeps identified, we focused on genes involved in fat deposition and hair growth, and annotated functional genes with high credibility (Supplementary Data 38), including some previously reported (e.g., PDGFD, NRIP1, KRT5, and KRT71) and novel (e.g., XYL8B, TSHR, SGCZ, CNOT3, CFLAR, GLIS3, MSRA, MAP2K3, and FG7) genes.

We dissected the genomic architecture of the selected genes by calculating the frequency of the variant allele at non-synonymous SNPs. The frequencies of one variant allele each at genes PDGFD, XYL8B, TSHR, and SGCZ as well as the genotype pattern located in the promoter region of PDGFD were different (Mann-Whitney, P < 0.001) between the fat-tailed (e.g., HDW, ALS, BSB, and TAN) and thin-tailed (e.g., SHE, Gotland sheep (GOT) and Finnsheep (FIN)) breeds (Fig. 4d, e, Supplementary Fig. 10 and Supplementary Data 39).

Remarkably, PDGFD was consistently selected by multiple comparisons (Supplementary Data 38). Transcriptome analysis among populations with different tail configurations (Supplementary Table 13) also identified PDGFD as significantly differentially expressed gene (log2(fold change) = 3.08; Padj = 0.045) between the fat-tailed/fat-rumped and the thin-tailed sheep (Supplementary Data 40). Furthermore, we detected four transcripts (i.e., transcripts I, II, III, and IV) of the PDGFD gene with the transcript I to be the most differentially expressed isoform between the thin-tailed and the fat-tailed/fat-rumped sheep (Fig. 4f), indicating its primary role in regulating fat deposition in tail. Furthermore, RT-PCR, qPCR, and western blot analyses demonstrated that gene expression level and protein level of PDGFD were consistently correlated negatively with fat deposition in sheep tail, with the highest level observed in the thin-tailed Merino sheep (MFW), followed sequentially by the small-tailed Han sheep (SXW), the large-tailed Han sheep (HDW), and fat-rumped Altaf sheep (ALS) (Fig. 4g-j and Supplementary Fig. 11).

Selective and association signatures for other traits. Apart from tail configuration, we found many selected regions, novel functional genes, and non-synonymous SNPs related to the potentially selected genes, which may be responsible for traits such as reproduction, milk yield, wool fineness, meat production, and growth rate as well as for morphological traits including numbers of horns and nipples, pigmentation, and ear size (Fig. 5, Supplementary Figs. 10 and 12-20, Supplementary Data 38 and 39 and Supplementary Notes). Also, we presented a selective sweep analysis of CNVs for nine phenotypic traits (34 pairwise comparisons between domestic breeds; Supplementary Table 12) and Supplementary Notes). For both SNPs and CNVs, we observed quite a number of the selective sweeps overlapped with known QTLs associated with several production traits (Supplementary Data 43-45 and Supplementary Notes). On top of the detection of previously known QTLs, our results also revealed several novel selective sweeps, CNVs, and genes to be potentially responsible for the trait of ear size (Supplementary Fig. 20 and Supplementary Data 39).

To fine-map regions identified using selective sweep methodologies and search for direct evidence of genotype-phenotype associations, we performed GWAS for three quantitative traits (i.e., litter size and numbers of horns and nipples) with informative phenotypic records (Supplementary Fig. 21). Using a panel of samples from multiple breeds and high-quality SNPs as well as the mixed linear model (MLM), we identified 600, 989, and 1969 significant GWAS signals for litter size (109 samples from 11 breeds; 14,574,050 SNPs), number of horns (146 samples from 15 breeds; 14,556,831 SNPs), and number of nipples (123 samples from 13 breeds; 14,415,949 SNPs) with the thresholds of −log10(P value) = 6, 6, 4, respectively (Fig. 5c, Supplementary Fig. 22 and Supplementary Data 46). Furthermore, we detected 20, 56, and one of these respective GWAS signals to be overlapped with selective sweeps detected for the three traits (Supplementary Data 47). Suggesting the significance of these genomic regions in shaping the traits.

Except for previously reported major candidate genes (e.g., BMP1R1B, INHBB, and ESRI), annotation of the significant GWAS signals revealed that those for litter size were mapped to a number of novel genes, such as NOX4, IRF2, PDE11A, ZFAT, ZFP91, TENM1, BICCI, LRRTM3, CTNN3, SMYD3, KCNN3, and
Fig. 5 Selective and association signatures for sheep horn number. 

a Different phenotypes of horn types between Sishui Fur sheep (SSS), Small-tailed Han sheep (SXW), and Hu sheep (HUS); picture credit: Meng-Hua Li. 

b, c Manhattan plot and quantile-quantile plot of association signals for the number of horns based on whole-genome CNV data b and SNPs c. The horizontal dashed lines correspond to the genome-wide significance thresholds (−log10(0.05/Total CNVs) = 5.29 for CNVs and −log10(P value) = 6 for SNPs). 

d, e Manhattan plot of selective sweeps for polycerate trait (SSS versus SXW) on chromosome 2. Allele frequency distribution of one non-synonymous SNP at the downstream of HOXD1 gene in one polycerate breed (SSS), two two-horned breeds (SXW and TAN) and one polled breed (HUS). The horizontal dashed line corresponds to the genome-wide significance threshold (XP-CLR = 5.17). 

e Manhattan plot of selective sweeps for polled trait (HUS versus SXW) on chromosome 10. Allele frequency distribution of one non-synonymous SNP at the downstream of RXFP2 gene in one polycerate breed (SSS), two two-horned breeds (SXW and TAN) and one polled breed (HUS). The horizontal dashed line corresponds to the genome-wide significance threshold (XP-CLR = 4.49). In all pie chart figures, the variant allele is indicated in blue, whereas the reference allele is indicated in pink. 

f Genotype patterns of the genes HOXD3 and HOXD8 among one polycerate breed and three two-horned breeds. 

g Genotype patterns of the gene RXFP2 among four horned breeds and seven polled breeds. Source data are provided as a Source Data file.
CD96 (Supplementary Fig. 22a), which play roles in various reproductive functions, including embryogenesis, uterine remodeling, follicular development and ovulation\(^{27,28}\). Focusing on 600 significant SNPs, we found 323 SNPs in intergenic regions, one in the downstream and 276 SNPs in the coding regions (only one SNP in the exon but 275 in the introns). For the number of horns, several GWAS peaks were situated in HOXD1, HOXD3, and RXFP2 (Fig. 5c) as well-characterized functional genes for the polycerate and polled phenotypes in sheep\(^{29}\). For the number of horns, most of the significant GWAS signals were located in genes associated with breast cancer, including five genes (LRP1B, GRM3, MACROD2, SETBP1, and GPC3) reported previously\(^{30}\).

In particular, we detected seven novel genes (PHGDH, KDM3A, GLIS3, FSHR, CSN2, CSN1S1, and ROBO2; Supplementary Fig. 22b), which were reported to be associated with mammary and nipple development in mice\(^{31,32}\).

To investigate the genetic architecture of litter size, numbers of horns and nipples, we calculated the proportion of phenotypic variation explained by the genetic variants identified in GWAS. Focusing on 189 signals located within 20 kb of 25 genes (i.e., NOX4, IRF2, PDE11A, ZFAT, ZFPP1, TENM1, BICC1, LRRTM3, CTNN3, MYD3, KCN3, and CD96 for litter size; RXFP2 for number of horns; LRP1B, GRM3, MACROD2, SETBP1, GPC3, PHGDH, KDM3A, GLIS3, FSHR, CSN2, CSN1S1, and ROBO2 for number of nipples) identified in this study, we detected 80 SNPs to explain 1.2–16.8% phenotypic variation in litter size, 106 SNPs to explain 7.0–16.1% variation in number of nipples, and three SNPs to explain 14.1–17.0% variation in number of horns (Fig. 6 and Supplementary Data 48).

Finally, we examined a total of 3,558 significant association signals with previously reported QTLs for reproduction, numbers of horns and nipples, and mapped 121 signals in five QTLs responsible for reproductive seasonality and total lambs born (permutation test, \(P < 0.001\)), 87 signals in one QTL associated with horns (permutation test, \(P < 0.001\)), and 31 signals in four QTLs related to teat placement, udder depth, udder shape and udder attachment (Supplementary Table 5 and Supplementary Data 49). We also implemented GWAS analyses using the CNV data for litter size, numbers of horns and nipples (Fig. 5b, Supplementary Fig. 23 and Supplementary Tables 14 and 15). We detected a total of 11 significant association signals and associated functional genes for the three traits (litter size: SMARCA1 and APP; number of horns: RXFP2; and number of nipples: GPC5) (Supplementary Notes). Several significant CNVs found by GWAS were in common with CNVs identified by selective sweep analysis. Two of these common CNVs were associated with reproductive traits while three CNVs with horn related traits (Supplementary Table 16).

**Discussion**

In this study, we re-sequenced the whole genomes of 248 wild, landrace, and improved sheep with an emphasis on local breeds with distinct phenotypes that have not been studied previously at the genomic level. Our exploration of the sheep variome and selective sweeps focused specifically on domestication and selective breed formation.

Deciphering the genetic basis of animal domestication is an active research area. The availability of whole-genome sequences provides an opportunity to study this at the gene mutation level. Such genomic studies have been implemented in other domestic animals\(^{33,34}\) and recently also in sheep\(^{1,2}\). These studies were based on genome sequences of low-to-medium coverages (8.4–17.2× in ref. 2, 12–14× in ref. 3). We have complemented this work using a hierarchically structured breed panel and high-depth whole-genome sequencing (mean depth of 25.7×).

We observed a lower level of genomic diversity in domestic breeds than their wild ancestors. This suggested that a substantial proportion of the genomic variation has been lost during and after domestication, whereas the genomic diversity in landraces has been largely retained in improved breeds. It should be noted that the nearly identical nucleotide diversity between landraces and improved breeds was also consistent with the observation that very strong positive selective pressure on modern breeds has only been in practice over the last ~200 generations\(^{9}\). Similar patterns of changes in genomic diversity through domestication have been observed in yak\(^{35}\) and soybean\(^{3}\). The estimates of the ratio of non-synonymous and synonymous substitutions in wild (0.55) and domestic sheep (0.53–0.54) were lower than those in a previous study with a lower sequencing coverage (domestic sheep 0.66, European mouflon 0.69)\(^{22}\). The low values in both wild and domestic sheep suggested a strong impact of purifying selection.

By contrasting Asiatic mouflon to the most primitive sheep landraces in our panel, we focused on the early stage of
domestication. Results of functional enrichment analysis of the 261 candidate genes were in agreement with previous evidence that metabolic process and olfactory transduction were involved as primary functional categories in sheep domestication. Furthermore, functions of the domestication-related genes and significant differences in non-synonymous SNP allele frequencies between Asiatic mouflon and domestic sheep provided additional evidence for signatures of selection on these genes and associated traits (e.g., reproduction, immunity, fat, photoreceptor, and olfaction) brought about by domestication. Nevertheless, by annotation of the 260 fixed SNPs (derived allele frequency ≥0.95) in the 209 putative selective sweeps, we detected 206 SNPs located in the non-coding regions but only two SNPs in the exon regions including a single non-synonymous mutation. This finding suggested domestication as a quantitative trait (e.g., litter size) to be affected mostly by mutations in non-coding regions, whereas very few mutations were non-synonymous. In addition to the functional non-synonymous SNPs, we observed differentiated frequencies in SVs between Asiatic mouflon and domestic sheep (Supplementary Tables S). Thus, SVs in functional genes could also account for the changes in phenotypic traits during domestication. In particular, our results indicated that not only SNPs but also CNVs associated with adipogenesis (BC0219) and protostasis (LOC101122355) have been under selection during domestication. Interestingly, as SVs in GTF2I have been found to be linked to Williams-Beuren syndrome in humans and hypersocial behavior (i.e., a feature of the domestication syndrome) in domestic dogs, the specific SV present in GTF2I may account for some behavioral differences between Asiatic mouflon and domestic sheep gained or lost during domestication. This work may inform ongoing and further analysis of ancient DNA in order to pinpoint more accurately the origin and time of sheep domestication and associated impact at the genomic level. We noted that Asiatic mouflon have several subspecies (e.g., Ovis orientalis gmelini, O. o. ophion, and O. o. laristanica) and are distributed in various geographic areas such as Iran, Turkey, Azerbaijan, and Cyprus, therefore a comprehensive sampling of all of them would be necessary in future investigations. It would also be interesting to compare genetic mechanisms responsible for specific domestication traits, and identify general patterns across different species of domestic animals.

In addition, we detected a few selective signatures associated with phenotypic and production traits during breeding and improvement. Functions of the candidate genes implied potential roles of human-induced changes in growth rate (SPAG8), reproduction (FAM184B), photoreceptor development (PDE6B), and tail configuration (PDGFD) during the development of specific breeds (Supplementary Notes). In particular, a strong selective signature located near the PAPPA2 gene implied intense artificial selections for body fat or types of tail (e.g., fat and thin tails) and production traits in sheep towards unique breeds. It is worth noting that the most significantly enriched pathway for the 391 selected genes identified from FCg analysis (Supplementary Data 26) was cytokine–cytokine receptor interaction (ACVR2B, TNFSF4, CCL25, etc.) (Supplementary Data 28). Previous studies have revealed that, instead of artificial selection, this important pathway for immune function can also be impacted by long-term natural selection.

We investigated various phenotypic traits using an integrated analysis of whole-genome selection scans and GWAS. Although some of the candidate genes have been functionally associated with various traits in previous investigations, we used high-coverage sequencing data to identify a number of novel candidate genes. In particular, we mapped novel candidate genes associated with popular traits that were studied previously (e.g., litter size, ear size, and coat color) or unique traits that were rarely studied in sheep and other livestock (tail configuration and numbers of horns and nipples). Moreover, our findings will help to narrow down the functional sub-regions within the QTLs and pinpoint the causal genes associated with these breeding-related traits. In particular, we identified several previously reported and a few novel genes to be associated with the tail configuration in sheep (Supplementary Data 38). Previous studies revealed that amino-acid changes in PDGFD (cysteine/tyrosine) have an important role in fat metabolism and adipogenesis in humans. We envisage that non-synonymous variants with deviating allele frequencies between wild and domestic sheep and large effects on specific phenotypes in domestic sheep might be useful, for instance, as targets in CRISPR/Cas experiments. Transcriptome analysis showed significant differential expressions of PDGFD transcripts among populations with different tail configurations (Supplementary Data 40). This may be ascribed to the distinct genotypic pattern in the promoter region of PDGFD (Fig. 4e). PDGFD functions by causing dimerization and further activating PDGF receptor PDGFRB. Early studies showed that PDGFRB signaling has an essential role in inhibiting differentiation of white adipocytes by regulating the expression of C/EBPα and C/EBPβ, which were identified as the key transcriptional regulators of adipogenesis (Fig. 4k). Therefore, our results provide in-depth insights into the genomic architecture and molecular mechanism for tail configuration in sheep at the genotype, variant allele, transcript, and protein levels.

All our efforts have resulted in a unique data resource in terms of the sheep varioime and selective sweeps with different categories of genetic markers, allele distributions in different breeds, and associations with phenotypes with different degrees of experimental validation. This will underpin more-accurate identification of causative gene variants in the near future and facilitate novel breeding strategies, like marker-assisted or genomic selection and genome editing targeting favorable traits towards a cost-effective and environmentally friendly sheep industry.

**Methods**

**Sample collection, DNA extraction, and sequencing.** Blood samples were collected from a total of 248 individuals comprising 232 domestic sheep (O. aries) and 16 wild sheep (Asiatic mouflon O. a. orientalis). The domestic sheep represent 36 landraces (172 individuals) and six improved breeds (60 individuals) with different geographic origins from Asia, Europe, Africa, and the Middle East (Fig. 1a). More specifically, the domestic samples represent various geographic origins, morphological characteristics, and production traits (Supplementary Data 1). Breed origins of the domestic sheep samples included populations from geographic areas underrepresented in earlier work (China, Afghanistan, Iran, Iraq, Azerbaijan, South Africa, Ethiopia, Burkina Faso, Niger, Nigeria, Chad, and Cameroon) as well as Germany, Spain, England, Finland, France, Scotland, Sweden, and the Netherlands (Fig. 1a and Supplementary Data 1). All the domestic sheep were typical of the breeds and unrelated according to pedigree records or herdsmen’s information (Fig. 1a and Supplementary Data 1). The Asiatic mouflon were collected from captivity in Iran, which is within the putative geographic center of sheep domestication. To minimize potential bias as a result of overrepresentation of local effects (e.g., inbreeding), individuals from different locations were sampled. Preparation of the samples is detailed in Supplemental Methods. DNA was extracted following the standard phenol-chloroform extraction procedure. For genome sequencing, at least 0.5 μg of genomic DNA from each sample was used to construct a library with an insert size of ~350 bp. Paired-end sequencing libraries were constructed according to the manufacturer’s instructions (Illumina Inc., San Diego, CA, USA) and sequenced on the Illumina HiSeq X Ten Sequencer (Illumina Inc.).

**Sequence read mapping.** We obtained ~82.86 Gb of raw sequences for each sample, giving an average depth of 25.7× coverage for clean reads (17.2–37.0×) (Supplementary Data 2). The 150-bp paired-end reads were mapped onto the sheep genome reference Oar.v4.9 (https://www.ncbi.nlm.nih.gov/assembly/ GCF_000298735.2) with the Burrows-Wheeler Aligner v.0.7.8 (ref. 47) using the default parameters. Mapping results were then converted into the BAM format and sorted with SAMtools v.1.3.1 (ref. 48). Duplicate reads were removed using SAMTools. If multiple read pairs had identical external coordinates, only the pair with the highest mapping quality was retained.

**Supplementary Information**

The accompanying Supplementary Information contains further details of the methods and data analysis.
SNP calling, validation, and annotation. After mapping, we performed SNP calling separately for the two sets of samples (see below) using the Bayesian approach implemented in SAMtools and the PHYLIP v.3.7 (ref. 49), with all individuals in each set simultaneously. One set included the 228 wild/domestic sheep with at least five samples per breed/population, which was used in all analyses, whereas the other set consisted of the 20 domestic sheep from the Middle East and Africa with one individual per breed, which was used to explore population structure and demographic changes. We chose this strategy to understand the Old World and to identify significant signatures associated with domestication and improvement (e.g., global FST analysis). Only SNPs detected by both methods were kept for further analyses. The detailed processes were as follows: (i) For the GATK, the variant genotype parameters were used to annotate SNPs and then SVs using the SelectVariant package, and SNPs with missing rates ≤0.1 and minor allele frequencies (MAF) <0.05 from the three groups (Asian moulin, landraces, and improved breeds) were filtered out from further analysis. For Asiatic moulin and each breed of domestic sheep, we estimated the site frequency spectrum (Supplementary Fig. 24) based on individual genotypes like-likelihoods assuming Hardy–Weinberg equilibrium using the ANGSD v.0.915 (ref. 90) with the parameters: −dosaf 1 −fold 1 −maxIter 100.

To validate the SNPs detected, we first compared the identified set with the O. aries dbSNP v.151 at the National Center for Biotechnology Information (NCBI; http://www.ncbi.nlm.nih.gov/SNP). Next, we compared the genotypes of the called SNPs with those on the Ovine Infinium HD BeadChip array (~600 k SNPs) (Iluminia, San Diego, CA) for 223 samples with available chip data (Supplementary Methods). In addition, to assess the performances of the GATK and SAMtools variant calling methods, we employed a false-positive measure by determining the rate of the monomorphic reference loci on the Ovine Infinium HD BeadChip array that were called as variant loci (GATK) or as variant calling methods. We calculated the false-positive rates as the number of false heterozygous SNPs divided by the total number of homozygous reference loci.

SNPs were annotated using the ANNOVAR v.2016-06-21 (ref. 52) based on the ovine reference genome Oar v.4.0 and then categorized as variations in exonic regions, intronic regions, upstream and downstream regions, and intergenic regions. Those in exons were further classified into synonymous or non-synonymous SNPs.

Identification of Indels, CNVs, and SVs. Similar to SNP calling, the calling of INDELS was conducted using SAMtools with minimum depth 24 and QQ >20, and only INDELS <100 bp were retained. CNVs were detected using both CNVnator v.0.3.2 (ref. 53) and DELLY v.0.7.9 (ref. 54). For CNVnator, the analyses were performed on the BAM files with a bin size of 100 bp and with the length >200 bp (Supplementary Methods). For DELLY, the analyses were conducted with default parameters, and deletions and duplications were considered to be CNVs (Supplementary Methods). Only the CNVs calling with >50% of their lengths being overlapping between the two approaches were kept in the final set of CNVs. The CNVs that overlapped with gaps or genomic repeats were removed, and the remaining CNVs were segregated into short CNV bins (≥100 bp) across the genomes among the 248 individuals for subsequent analyses.

SVs were identified through the Manta v.1.6.0 (ref. 54) and DELLY v.0.7.9 (ref. 54). For CNVnator, the analyses were performed on the BAM files with a bin size of 100 bp and with the length >200 bp (Supplementary Methods). The SURVIVOR v.1.0.6 (ref. 56) was employed to detect the overlapping SVs identified by the two approaches with the command line: .SURVIVOR merge sample_files 1000 2 1 1 50 sample_merge.vcf.

Population genetics analysis. After filtering, we generated a set of SNPs for the following analyses. First, an individual-based neighbor-joining (NJ) tree was constructed for all the samples based on the nucleotide p-distance matrix using the TreeBIST v.1.9.2 (ref. 57). The NJ tree was rooted with the outgroup of 16 Asiatic moulin and visualized using the FigTree v.1.4.3 (http://tree.bio.ed.ac.uk/software/figtree/). PCA of whole-genome SNPs for 248 individuals was performed with the MANT Rust et al. (23). Furthermore, population structure was assessed using the default setting in the ADMIXTURE v.1.23 (ref. 59). The number of assumed genetic clusters K ranged from 2 to 7. To construct a NJ tree for the four subgroups of domestic sheep (i.e., African, East Asian, Middle Eastern, and European groups; see “Results”), 1–2 individuals from each landrace and two individuals from each sampling site of Asiatic moulin were selected, totaling 50 individuals (i.e., 10 for each group; Supplementary Table 17). SNPs for the 50 individuals were extracted from the dataset of landraces and Asiatic moulin. To mitigate the possible effect of LD, we implemented LD pruning using the parameter --inde-pairwise (30 0.4) in PLINK v.1.07 (ref. 60). To eliminate the potential influence of selective SNPs, we only retained the SNPs located within 150 kb away from genes and with default parameters --max-extents and without minor allele frequency extremes. Eventually, a final set of 59,943 SNPs for the 50 individuals were kept for the construction of NJ tree. Reynolds genetic distances (ref. 61) among the five groups were calculated using Arlequin v.3.5.2.2 (ref. 62) (Supplementary Table 18). A NJ tree was then constructed based on the Reynolds genetic distances with 1000 bootstrap replications (ref. 63) within the PHYLIP v.3.7 (ref. 64), with all individuals in each set simultaneously. One set included the 228 wild/domestic sheep with at least five samples per breed/population, which was used in all analyses, whereas the other set consisted of the 20 domestic sheep from the Middle East and Africa with one individual per breed, which was used to explore population structure and demographic changes. The LD decay plot was depicted against the length of distance using the R script (http://www.r-project.org). Nucleotide diversity (θ) and global FST were calculated using the vcftools v.0.1.14 (ref. 65). The FST values between populations were estimated using the ARLSUMSTAT implemented in the Arlequin v.3.5.2.2 (ref. 62), with a sliding window size of 50 kb. The FST values for each population were converted into the Arlequin format (apf) using the VCF2Arlequin python script. Statistical significance (P values) of the FST values were tested through 100,000 Markov chains following 10,000 burn-in steps. The average FST and associated P values over all sliding windows were regarded as the values at the whole-genome level.

Estimates of effective population size. We used the PMSC method to estimate changes in effective population size (Ne) over the last one million years. The PMSC method compared the identifications of SNPs with the Selscan v.1.2.0 (ref. 70) using a panel of 114,260 SNPs obtained through the Illumina HD BeadChip array (http://www.ncbi.nlm.nih.gov/SNP, NIH, Maryland, USA). PMSC was performed using the MLM in the GEMMA v.0.96 (ref. 73) based on a panel of 109,260 SNPs, 1,000 wild sheep, 200 domestic sheep, 500 landraces, and 500 improved breeds. For SNPs, we performed tests for selective sweeps during domestication and breeding using two approaches based on the SNPs with less than 10% missing data: the XP-CLR approach implemented in the XP-CLR v.1.0 (ref. 65), and by the comparison of θ ratios calculated using the vcftools v.0.1.14 (ref. 65). To detect genomic regions under selection during domestication, we calculated the ln(rO/oriental−rLandrace)/ln(2). Also, we estimated the ln(rControl/πtotal))/ln(2) between populations of domestic sheep with contrasting phenotypes for a specific target trait. The specific populations involved in comparisons between wild and domestic sheep and pairwise comparisons between domestic sheep populations for detecting the signals associated with partial traits are shown in Supplementary Table 12. Values of Ne were calculated with a 50 kb sliding window and a 25 kb stepping step. For the XP-CLR approach, a 0.5 cm sliding window with a spacing of 2 kb across the whole genomes were used for scanning, and 200 SNPs were assessed in each window with the parameters: −s 0.005 −p 200 −r 0.95. To assess the empirical distribution of the proportion scores obtained with these windows, in each comparison, the genomic regions in the top 1% XP-CLR values and ln(πControl/πTotal) values across the whole-genome were considered to be the selective sweeps.

Moreover, we estimated the iHS across the genomes of Asiatic moulin and different groups of domestic sheep populations using the Selscan v.1.2.0 (ref. 65) after filtering all missing data, with 50 kb sliding windows and 25 kb stepwise, a recombinant rate of 1 cM Mb. To test genomic regions under selective during domestication, we calculated the ln(rO/oriental−rLandrace)/ln(2). Also, we estimated the ln(rControl/πtotal))/ln(2) between populations of domestic sheep with contrasting phenotypes for a specific target trait. The specific populations involved in comparisons between wild and domestic sheep and pairwise comparisons between domestic sheep populations for detecting the signals associated with partial traits are shown in Supplementary Table 12. Values of Ne were calculated with a 50 kb sliding window and a 25 kb stepping step. For the XP-CLR approach, a 0.5 cm sliding window with a spacing of 2 kb across the whole genomes were used for scanning, and 200 SNPs were assessed in each window with the parameters: −s 0.005 −p 200 −r 0.95. To assess the empirical distribution of the proportion scores obtained with these windows, in each comparison, the genomic regions in the top 1% XP-CLR values and ln(πControl/πTotal) values across the whole-genome were considered to be the selective sweeps.

GWAS. Association analyses of litter size, numbers of horns and nipples were performed using the MLM in the GEMMA v.0.96 (ref. 72) based on a panel of 109
the SNPs, and the proportion of variance explained by the markers was calculated using TASSEL v.5.0 (ref. 74). To avoid potential false positives in multiple comparisons, the whole-genome significance threshold was adjusted via the Bonferroni test 75. For SNPs, we set the thresholds as $-\log_{10}(P \text{ value}) = 6, 6, and 4 for litter size, numbers of horns and nipples, respectively. For CNVs, we set the thresholds as $-\log_{10}(0.05/\text{total CNVs}) = 5.28, 5.29$ for litter size and number of horns, respectively, but $-\log_{10}(P \text{ value}) = 4 for number of nipples using GEMMA v.0.96 based on the genotypes of CNVs selected by the DELLY and CNVnator. In addition, the quantile–quantile (Q-Q) plots of the MLM for individual traits were implemented in R Bioconductor.

**Permutation test for QTL overlaps.** We performed permutation test to check if the overlaps between selective sweeps/GWAS hits and QTL regions were significantly different from those expected at random. To this end, we used BEDTools v.2.26.0 shuffle to generate simulated data sets by randomly selecting genomic regions of equal number and size to the observed selective sweeps/GWAS hits in the sheep genome, and we replicated this process 10,000 times 76. We compared the number of overlaps between the observed selective sweeps/GWAS hits and the QTL regions with the distribution of overlap statistics between the simulated selective sweeps/GWAS hits data sets and the QTL regions, and calculated the statistical significance of P values (i.e., the probability that a higher number of overlaps would be observed by chance).

**RNA-Seq analysis.** We collected tail adipose tissues from thin-tailed, short fat-tailed, long fat-tailed, and fat-rumped sheep for RNA-Seq analysis (Supplementary Table 1). Each group included three independent samples from different individuals as biological replicates. We used the Trizol RNA Reagent (Takara, Dalian, China) to extract total RNA from the tissues and measured the concentration and integrity of the RNA with the Agilent 2100 RNA Nanoplot Kit (Agilent Technologies, Waldbronn, Germany). Subsequently, the libraries of mRNA were constructed using the NEBNext Ultra™ II DNA Library Prep Kit (New England Biolabs, Ipswich, MA, USA) and sequenced using the Illumina HiSeq X Ten System to generate 150-bp paired-end reads. We used the HISAT v.2.1.0, StringTie v.2.0, and Ballgown package in R version 3.5.3 (ref. 77) to map the paired-end reads to the sheep reference genome, assemble the reads, and estimate the gene expression. The number of reads matched to an expressed gene was standardized as fragments per kilobase of exon per million mapped fragments (FPKM) values. We employed the stattest function in the Ballgown package 77 to search for transcripts that were differentially expressed between the thin-tailed breed (Chinese Merino sheep) and fat-tailed/fat-rumped breeds (Small-tailed Han sheep, Large-tailed Han sheep, and Altay sheep), allowing correction for any differences in expression owing to population variables. This allowed us to get the confidence-adjusted fold changes between the two tested groups. The genes that exhibited $|\log_{10}(\text{fold change})| > 2$ and adjusted P < 0.05 in the comparisons between fat-tailed/fat-rumaped and thin-tailed individuals were considered as differentially expressed genes.

**Gene expression and western blot analysis of PDGFD gene.** We examined the gene expression level of PDGFD in the adipose tissues from the thin-tailed, short fat-tailed, long fat-tailed, and fat-rumped sheep through reverse transcription PCR (RT-PCR) and qPCR. The three biological replicates of adipose samples from different individuals for each trait type were used. The total RNA was extracted using the Trizol RNA Reagent (Takara, Dalian, China) and were treated with RNase-free DNase I to remove DNA using the RapidOut DNA Removal Kit (Thermo Fisher Scientific, Waltham, MA, USA). The first-strand cDNA was synthesized using the RevertAid First Strand cDNA Synthesis Kit (Thermo Fisher Scientific, Waltham, MA, USA). Following the manufacturer’s instruction, 500 ng of RNA was reverse transcribed as the template for RT-PCR in 40 μl volume (including 20 μl RNA, 2 μl Random Hexamer Primer (100 μM), 8 μl 5× Reaction Buffer (including 250 mM Tris-HCl (pH 8.3), 250 mM KCl, 20 mM MgCl₂, 50 mM DTT), 2 μl Ribolock RNase Inhibitor (20 U μl⁻¹), 4 μl 10 mM dNTP Mix, 2 μl RevertAid RT (200 μl μl⁻¹) and 2 μl nuclease-free water) and a thermocycling condition at 25 °C for 5 min, 42 °C for 60 min, and 70 °C for 5 min. Subsequently, the qPCR reaction was performed on the SYBR Green (Promega, Madison, WI, USA) using the QuantStudio™ 6 Flex Real-Time PCR System (Life Technologies, Carlsbad, CA, USA) using the following parameters: 1) 5 min at 95 °C 2) 40 cycles of 95 °C for 15 s, 60 °C for 30 s, and 72 °C for 30 s, followed by a melting curve analysis. The expression of β-actin served as the internal control. The qPCR reactions and conditions were set as described above. Each qPCR was run three times for each sample as technical replicates. Based on the qPCR results, the expression level was calculated using the 2 $^{-\Delta\Delta C_{T}}$ method 78 and normalized according to the internal control β-actin gene. The primers for β-actin were β-actin F (5′-CCAGGCTGAGAAGATGGC-3′) and β-actin R (CCCGAGGCTTAAGGGAGAC-3′).

**Phenotyping.** Individual phenotype for traits, such as coat color, fibers of fiber fineness, ear size, number of nipples and horns, and tail configurations were recorded for all the breeds whenever possible during sampling. Five different coat colors or color patterns, including white, white body with black head, black, brown, and gray were recorded for the animals sampled. The number of nipples ranged from 2 (normal) to 5 (selected). The horn phenotypes varied from polled to horned animals with 2–5 horns. The wool was graded into three classes (coarse, fine, and superior quality) according to the British Wool Grading System ( Supplementary Fig. 1). 4.19

**Data availability.** Raw sequencing data that support the findings of this study have been deposited to the NCBI BioProject database under accession PRJNA624020. The source data underlying Figs. 1, 3, 4, and 5 and Supplementary Figs. 1–7, 9, 11–21, and 24 are provided as a Source Data file.

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Competing interests
The authors declare no competing interests.

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