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The onset of sedentism on the Tibetan Plateau is often presumed to be associated with the dispersal of agriculture or farmers from archaeological sites located in the low elevation margins of the plateau. Previous studies of the plateau assumed that all foragers were probably mobile, but few systematic excavations at forager sites have been conducted to inform us about their settlement patterns. Here we report the world's highest elevation sedentary way of living exhibited by the Mabu Co site at 4,446 metres above sea level, deep in the interior of the Tibetan Plateau 4,400–4,000 years ago. Our interdisciplinary study indicates that the site was occupied by Indigenous inhabitants of the plateau, representing the earliest known DNA evidence of foragers who predominantly harbour the southern plateau ancestry. The evidence shows that they had a sedentary lifestyle primarily supported by fishing at nearby lakes, supplemented by mammal and bird hunting, as well as small-scale exchanges of millet and rice crops.

The adoption of a sedentary lifestyle in the high-altitude regions of the Tibetan Plateau (>3,500 metres above sea level (MASL)) represents both a cultural and genetic adaptation to an environment characterized by low primary productivity, extreme weather conditions and hypoxia^{1–3}. Archaeological and linguistic models for the onset of and pathways to sedentism on the Tibetan Plateau see its origins as being intertwined with the dispersal of agriculture or farmers from elevations at less than 2,500 MASL^{4–8}. To date, very few systematic excavations have been carried out at sites occupied by foragers; thus, we know very little about the types of settlement and mobility patterns that foragers used. For the most part, sites that have been targeted by small-scale excavations

are consistent with small logistical campsites that are consistent with patterns of high mobility between high and low altitudes^{2,9–13}. Genomic analysis hypothesizes that early inhabitants, who can be traced back to Late Palaeolithic foragers, originally lived on the Tibetan Plateau¹⁴, contacted farmers at an altitude of about 3,000 MASL on the eastern margins of the Tibetan Plateau around 5,000 years ago¹⁵, and then shifted from patterns of high mobility to increased sedentism, represented by the Zongri (2,800 MASL) and Karuo (3,200 MASL) sites, with a diverse subsistence strategy, including millet cultivation and hunting^{5,16,17}. Agropastoral settlements emerged on the interior Tibetan Plateau by 3,500 calendar years before the present (cal BP), represented

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by the Qugong site (3,600 MASL) in Lhasa City, where millets followed by wheat, barley and buckwheat were grown and yak and sheep were herded^{18,19}.

Although the core of the Tibetan Plateau, with elevations well above 4,000 MASL, is considerably more environmentally challenging than these lower-altitude river valleys, at present the number of global permanent residents above this altitude is over 6.4 million people²⁰. Who the earliest permanent residents were and when and how processes of sedentism began in this area has been unclear because of the paucity of archaeological research. In this study, we report on findings from the Mabu Co site (Co is the Tibetan word for lake) at 4,446 MASL on the Tibetan Plateau. Our excavations and interdisciplinary research reveal that the early Indigenous inhabitants used ways of living that were much more sedentary than previously thought. Their lifestyle, 4,400–4,000 years ago, revolved around fishing, hunting and the exchange of crops cultivated in lower-altitude areas. Genetic analysis indicates that individuals at the site were ancestral to the current populations who live on the southern plateau.

Site description

The Mabu Co site (28.31° N, 89.43° E) is situated at the headwater region of the Nyang Qu River, one of the main tributaries in the middle reaches of the Yarlung Tsangpo River (Fig. 1a). Today, the landscape of this region is predominantly desert steppe with cold and dry climatic conditions. The mean annual temperature is 1 °C and the average annual precipitation is 277 mm, with rainfall concentrated in the summer²¹. Current livelihoods near the site focus primarily on herding yak, sheep, goat and horse, and planting cold-tolerant naked barley.

The site is situated on a 2-km-long sand ridge that lies between Mabu Co and Gala Co, stretching southward from the foot of a hill to the north (Fig. 1b,c). The site was discovered in 2019 and the entire area measures approximately 14 ha. During the excavations between 2020 and 2023, an area of 1,100 m² was uncovered (Extended Data Fig. 1). Burials, post mould structures, pits, stone features and living surfaces were distributed across the surface of the ridge (Extended Data Fig. 2). Refuse deposits were concentrated in the south end of the ridge, sandwiched between the topsoil and sandy gravel sediments of the lakeshore (Fig. 2a,b). Thousands of artefacts were uncovered, especially from the refuse deposits, including pottery sherds, crystal microliths, ground stone tools, bone tools and ornaments, among others (Extended Data Fig. 3).

Chronology

Abundant archaeobotanical and faunal remains were also recovered from the refuse deposits; 33 samples, including charred crop seeds and bone remains, were dated using accelerator mass spectrometry (AMS) (Methods and Supplementary Table 1). The ages of fish, bird and human bones were all anomalously older than the carbonized seeds and terrestrial mammal bones found from the same layer, indicating that they were probably affected by the radiocarbon reservoir effect of the lake²². They were thus excluded from consideration (Extended Data Fig. 4). Dates from the mammal bones and carbonized seeds place the occupation at 4,400–4,000 cal BP (Extended Data Fig. 4).

Indigenous Tibetan foragers

Nearly 100 burials were found at Mabu Co (Extended Data Fig. 1). We extracted DNA from seven human bones (from burials) and two teeth (from strata of refuse deposits) excavated during the 2020 and 2021 field seasons (Supplementary Table 2) according to a previously described protocol; the genomic data of these individuals were analysed alongside those of previously published individuals from ancient and present-day populations (Methods).

We found that the inhabitants of Mabu Co mainly possessed a southern plateau ancestry that spans the southern and south-western Tibetan Plateau along the Yarlung Tsangpo River valley.

Similarities were noted between the human remains at Mabu Co and 3,400–2,600-year-old individuals from the Shannan, Shigatse and Himalayan arc¹⁵. Their overall affinities to plateau populations are supported by the clustering of Mabu Co individuals with other ancient and present-day Tibetan individuals in principal component analysis (PCA), as well as the similar genetic profile shared by the Mabu Co individuals and both ancient and present-day Tibetans (Fig. 3a,b and Extended Data Figs. 5 and 6). Specifically, Mabu Co individuals are most closely related to ancient populations from Shannan and Nepal²³, as a more shared drift (f3 outgroup analysis (X, Y; Mbuti), where Mbuti (a present-day population from Central Africa) serves as an outgroup, X and Y are ancient Tibetan Plateau populations, listed symmetrically in the rows and columns) was observed between these groups (Fig. 3c, Extended Data Fig. 7, Supplementary Fig. 1 and Supplementary Data 1). The southern plateau ancestry of Mabu Co individuals is further supported by the f4 analysis, in which Mabu Co shows more connection with ancient southern plateau populations, including Shannan3k and Lubrak (Supplementary Table 3 and Supplementary Data 2). This affiliation with southern plateau lineage exhibits subtle differences within the Mabu Co E1 and Mabu Co E2 subgroups (Extended Data Figs. 8 and 9, Supplementary Text, Supplementary Figs. 2 and 3 and Supplementary Data 2); it was further confirmed by the fact that Mabu Co E2 can be used as a one-way source for Shannan3k and Lubrak in qpAdm (Fig. 3d and Supplementary Table 4). Mabu Co also showed features of a deep lineage gene flow that were similar with previous Shannan3k and Lubrak (Supplementary Data 3 and 4) and exhibit characteristic of genes adapted to the plateau. The homozygous *EPAS1* genotype, which confers adaptation to high altitude²⁴, is found in Mabu Co 1 individual, with two *EPAS1* heterozygotes, suggesting that this adaptive genetic trait may be undergoing selection in this population (Supplementary Tables 5 and 6).

Previous studies indicated that Tibetan Plateau ancestry is derived in large part from a single source related to a 9,500-year-old individual from the Yellow River region that diverges to three main lineages¹⁵. The northeastern lineage represented by the Zongri site can be traced back to 5,100 cal BP, but the more important southern lineage (which mainly contributes to present-day Tibetans) could only be traced back to 3,400 cal BP²³. Our study revealed that the inhabitants of Mabu Co and Zongri had genetically diverged by 4,400 cal BP (Fig. 3c and Extended Data Fig. 7). The genetic profile of Mabu Co individuals shows that southern plateau ancestry, one of the major genetic components for present-day Tibetans, occurred on the southern plateau by at least approximately 4,400 cal BP. This sheds light on the genetic profile of the oldest Indigenous foragers on the southern plateau, pushing back the emergence of the southern plateau ancestry by 1,000 years earlier than previous estimates.

Sedentary life based on fishing

We collected thousands of bones, both fragmented and complete, from excavation trenches in the refuse deposits. These were then identified by both osteomorphological and ancient DNA analyses (Methods). The identified animals include fish, birds and mammals, indicating diverse resources for meat consumption at the site. Fish are endemic Tibetan species, including *Gymnocypris* and *Schizopygopsis* spp. Birds include coot (*Fulica atra*), great cormorant (*Phalacrocorax carbo*), common merganser (*Mergus merganser*) and pochard (*Netta* and *Aythya* spp.). The remains of mammals included endemic species, such as the Himalayan marmot (*Marmota himalayana*), Przewalski gazelle (*Procapra przewalskii*), argali (*Ovis ammon*) and red deer (*Cervus elaphus*), as well as woolly hare (*Lepus oiostolus*), lynx (*Lynx lynx*) and wolf (*Canis lupus*) (Fig. 4a and Extended Data Fig. 10).

Fish bones dominate the faunal assemblage (Supplementary Table 7), consisting of 81.5% of the total number of recovered remains. Fishing tools like gorge hooks were recovered in large numbers (Fig. 2c). We identified the materials used to make the fish gorge hooks using

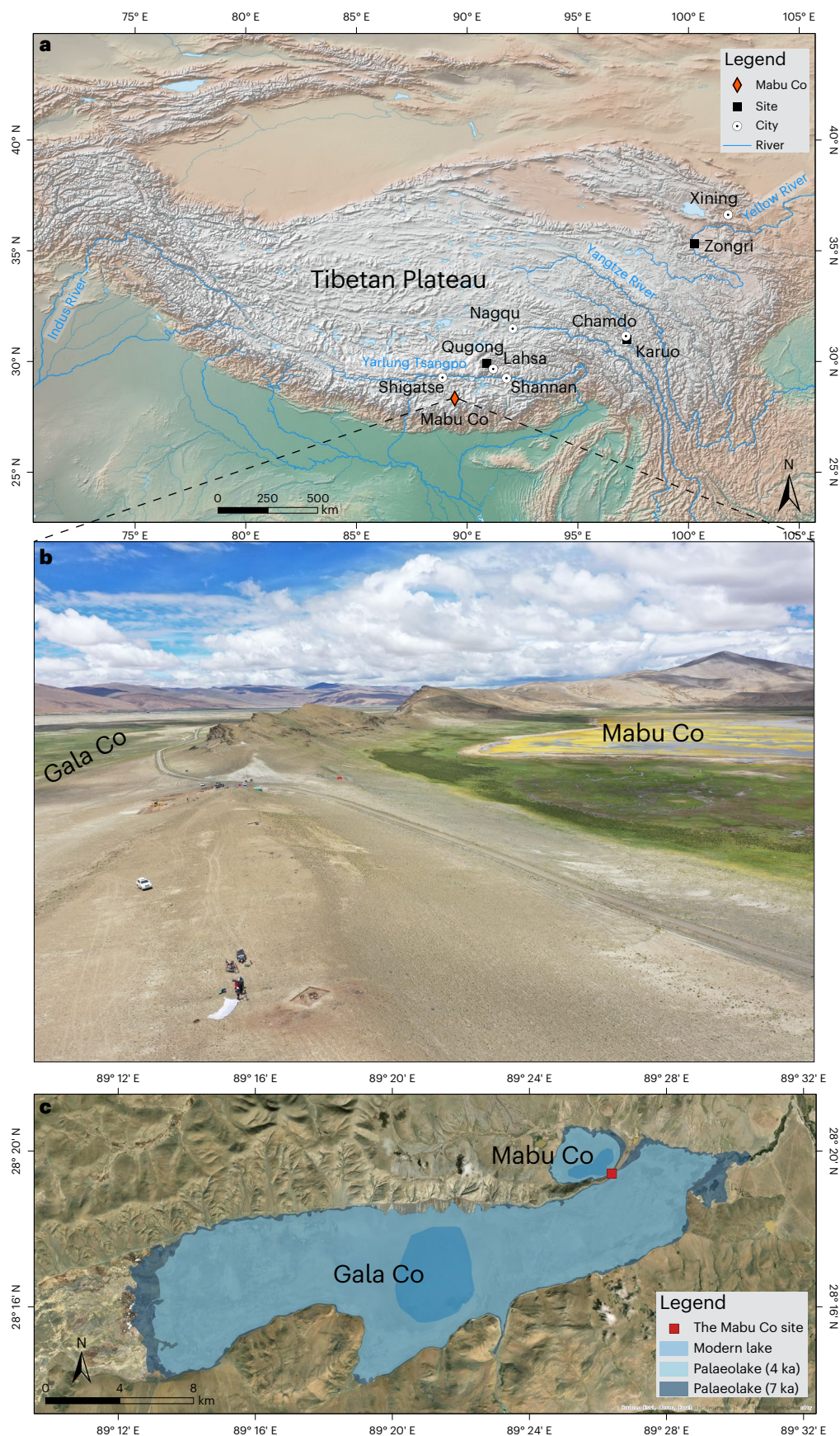


Fig. 1 | Geographical location and setting of the Mabu Co site. **a**, Location of the Mabu Co site and referenced sites on the Tibetan Plateau. The base map was obtained from the Natural Earth public domain map dataset (<https://www.naturalearthdata.com>). **b**, The Mabu Co site viewed from the northwest; team

members and burials are visible on the site. **c**, Evolution of the paleolake extents of Mabu Co and Gala Co before and during the period of human occupation of the site, based on data from ref. 27. The base map was prepared using ArcGIS 'World Imagery'.

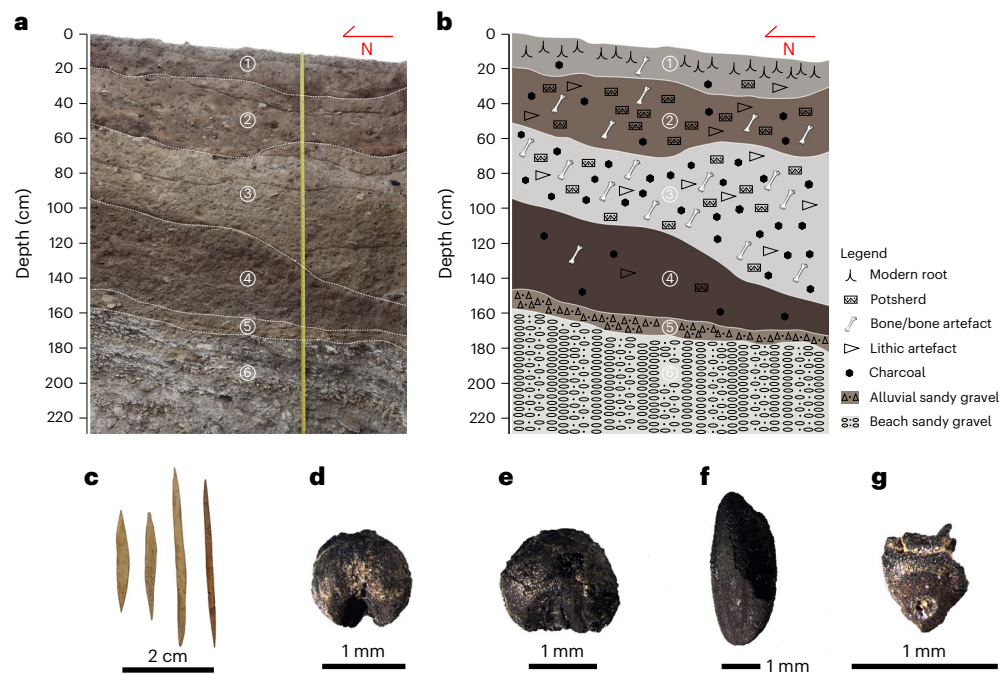


Fig. 2 | Typical profile of the Mabu Co site, fishing tools and charred crop plant remains. **a**, Photograph of the east wall of the trial excavation trench TNO6E03. **b**, Schematic drawing of the east wall of TNO6E03. Description of stratigraphic layers: (1) top sandy soil with abundant grass roots and few charcoal fragments, bones and artefacts; (2) yellowish brown silt with abundant charcoal fragments, animal bones, pottery sherds and a small number of human teeth, crystal artefacts, bone artefacts and ornaments; (3) light yellow silt with white

carbonate fragments and artefact assemblages similar to the upper layer; (4) dark brown sandy gravels with a few charcoal fragments, lithic artefacts and animal bones; (5) light yellow alluvial sandy gravels without artefacts; (6) natural deposits of lakeshore sandy gravels. **c**, Fish gorge hooks. **d**, Foxtail millet (*S. italica*). **e**, Broomcorn millet (*P. miliaceum*). **f**, Rice (*O. sativa* sp. *japonica*). **g**, Rice spikelet base. Scale bars, 2 cm (**c**) and 1 mm (**d–g**).

ancient DNA analysis (Methods); this type of tool was made using bird bones belonging to either cormorant or crane.

The stable carbon and nitrogen isotope analyses of charred millet grains and bone collagen from both human and animal remains provide evidence that the diet of humans was dominated by fish consumption (Fig. 5). We measured carbon and nitrogen stable isotopes from 41 samples, including 10 humans, 15 fish, 9 terrestrial animals, 6 birds and 1 crop plant (Methods). The human remains yielded the highest $\delta^{15}\text{N}$ values, which are approximately 5‰ higher than those of fish (Fig. 5 and Supplementary Table 8), which is consistent with the isotopic enrichment at each trophic level that is usually thought to range between 3‰ and 6‰ (refs. 25,26), indicating that fish was the dominant food for the site's inhabitants. The importance of fish in the diet is also reflected by the similar $\delta^{13}\text{C}$ values of the human remains and fish bones, which are markedly different from those of birds, terrestrial animals and crop plants (Fig. 5). This further bolsters our argument that the fish-dominated diet of humans resulted in a radiocarbon reservoir effect on the ages of the human bones (Extended Data Fig. 4). A recent study showed that Mabu Co and Gala Co spanned a total area of more than 100 km², much larger than their modern areas (8.8 km² in total), around 4,400–4,000 cal BP²⁷. It was this massive paleolake that provided a reliable source of fish for site residents (Fig. 1c).

The seasonal analysis of bone remains from hunted fish, mammals and birds showed that approximately two-thirds of fish were caught from May to October and about one-third from November to April (Fig. 4b); mammals and birds were hunted year-round (Fig. 4a,c and Supplementary Table 9). When fishing decreased from December to February during winter, supplementary resources were available because of wintering waterfowl, including great cormorants and pochards, which inhabited the study area in abundance²⁸ (Fig. 4a), and ungulates such as red deer (Fig. 4c), which provided meat to feed the

site inhabitants. In addition, ethnographic evidence suggested that fish were dried and stored for later consumption²⁹; fish from nearby lakes was dried and traded to Bhutan decades ago. Similar practices of drying and trading fish are documented at Qinghai and Yambrok lakes, where tens of thousands of tonnes of fish were harvested annually during the 1950s and 1960s^{29–31}.

We identified a very small proportion of cereals, including foxtail millet (*Setaria italica*), broomcorn millet (*Panicum miliaceum*) and rice (*Oryza sativa* sp. *japonica*) (Fig. 2d–g) from plant remains (Methods), indicating that residents also had a carbohydrate intake. However, neither millet nor rice can grow at Mabu Co at an altitude of 4,446 MASL because of the low temperatures around the site^{32,33}. Therefore, the cereal grains found at Mabu Co were most probably exchanged from lower-elevation areas where millet and rice could be cultivated. Although these domesticates make up less than 10% of the entire archaeobotanical assemblage (Supplementary Table 10), they were recovered from the bottom to the top of the refuse deposits, indicating an interaction network between the inhabitants of Mabu Co and farmers at lower elevations^{5,34}. In fact, to the east of the Tibetan Plateau, the mixed farming of millet and rice had been practised since 5,000 cal BP³⁴.

Finally, the presence of many burials at Mabu Co (Extended Data Fig. 1) suggests that the site held notable ritual importance for its inhabitants. By choosing to bury their ancestors at this location, they symbolically and spiritually claimed the land around the site. Furthermore, the extensive scale of refuse deposits (Extended Data Fig. 1) indicates that people spent considerable periods of time at the site.

In summary, our datasets indicate that the inhabitants of the Mabu Co site fished year-round and fish were the primary food for providing sustainable, stable protein sources that supported daily dietary needs. Inhabitants also obtained carbohydrate-rich cereals by exchange.

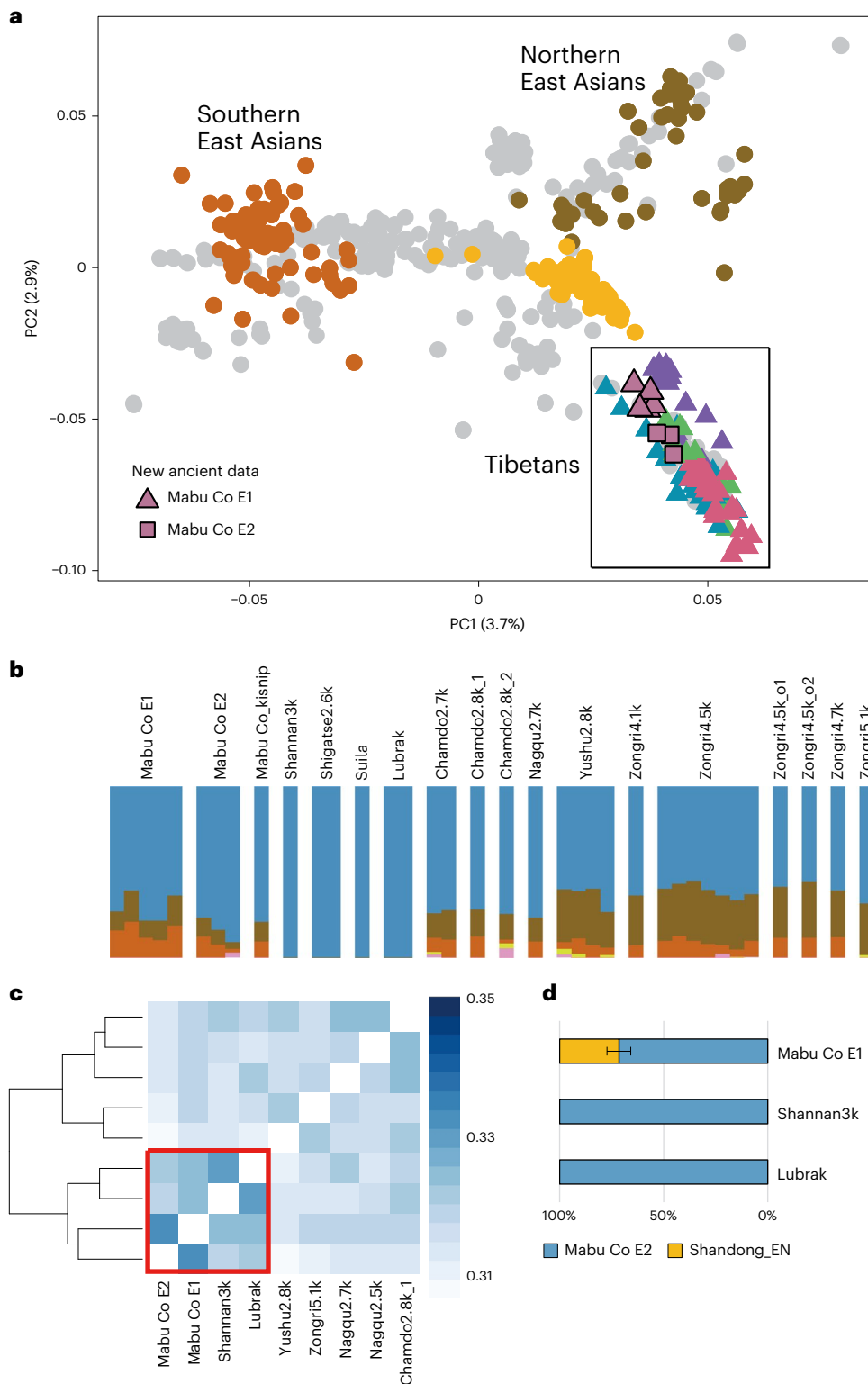


Fig. 3 | Genetic characterization of Mabu Co human bones. a, Ancient Mabu Co individuals (purple) were projected on principal components calculated from 315 present-day East Asian individuals, located in the enlarged Tibetan branch (black dotted box). The grey points represent the projected background of modern East Asian populations, forming three main branches and a Tibetan branch. The orange points represent ancient southern East Asian populations; the brown points represent ancient northern East Asian populations; the yellow points represent ancient Yellow River-related populations; and the purple, green, red and dark blue points represent ancient Tibetan Plateau individuals from the northeastern plateau, central plateau, southern plateau and Nepal, respectively.

The PCA details with coordinate axis and population categories can be found in Extended Data Fig. 5. **b**, ADMIXTURE plot for early ancient Tibetans ($k = 5$): blue, Tibetan ancestry; brown, Northern East Asian ancestry; orange, ancient southern East Asian ancestry. Details can be found in Extended Data Fig. 6. **c**, f_3 outgroup analysis for pattern F3(X, Y; Mbuti). The Mabu Co group cluster with ancient southern plateau populations; darker blue indicates higher genetic similarity. **d**, Genetic ancestry estimated with qpAdm. Mabu Co E2 could be a one-way source for later Shannan3k and Lubrak southern lineage populations, while Mabu Co E1 represents southern plateau ancestry (Mabu Co E2/Shannan3k) admixed with lowland Northern East Asia-related ancestry (Supplementary Table 4).

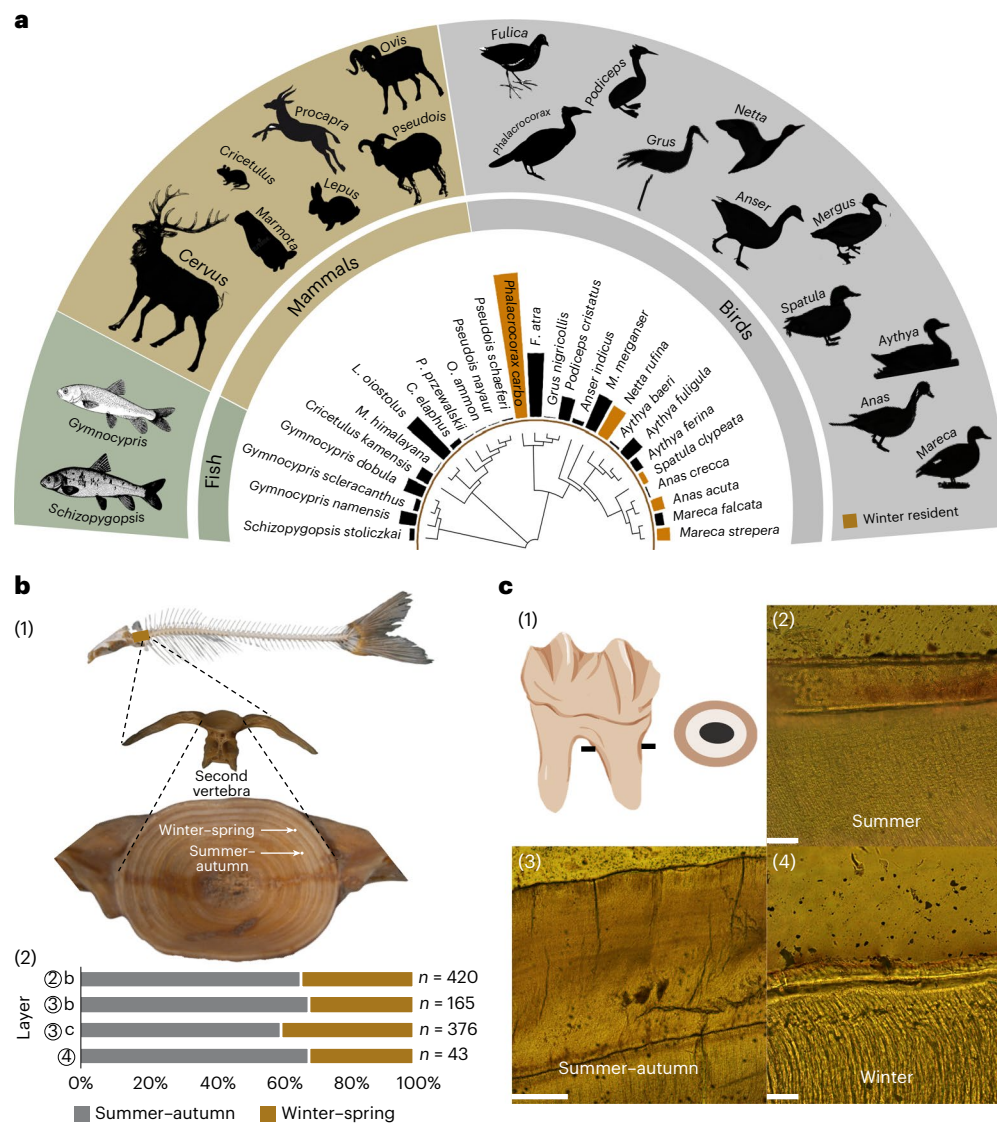


Fig. 4 | Evidence for year-round hunting. a, Hunted animals identified using ancient DNA. The silhouettes illustrate the identified genera. The bar heights represent the relative content of ancient DNA reads. The orange bars represent the winter resident birds. **b**, (1) Microscopic view of the second vertebra of schizothoracid fish (*Gymnocypris* and *Schizopygopsis* spp.) under reflected light, used to decide the death season; and (2) season at death distribution of fish recovered from the Mabu Co site indicating year-round fishing. The number

displayed on each bar indicates the quantity of fish second vertebrae used for identification. **c**, Thin sections of animal teeth at Mabu Co showing the death seasons: (1) thin section located at the tooth cervix; (2) gazelle (*Procapra* sp.) from TGI(3) c that died in the summer (clear dark-light-dark band); (3) red deer (*C. elaphus*) from TGI(2) b that died in the summer or autumn (a light band with a little darkness at the edge); (4) gazelle (*Procapra* sp.) from TGI(2) b that died in the winter (light-dark-light bands). Scale bars, 200 μ m.

Lake-centred ways of living

While the transition to sedentism in some regions is closely intertwined with farming, the adoption of sedentary ways of living by groups who did not practise farming is an equally important global phenomenon³⁵. In other parts of the world, such as high-latitude environments with low terrestrial primary productivity, the concentrated stability and year-round availability of fish in lacustrine or maritime environments enabled increased degrees of sedentism. For instance, in Alaska and Northeast Asia, the high productivity of aquatic ecosystems allowed foragers to reduce mobility and invest in the production of pottery, which was used to process and cook these aquatic resources^{36–39}. Studies on 89 societies along the North American Pacific coast also suggest that freshwater and marine fish resources allowed communities to have higher population densities and greater sedentism compared to subsistence focused on hunting large terrestrial animals, which requires a higher degree of mobility⁴⁰. Scholars argued that we should expect

reduced mobility in foragers around environmental resources that are concentrated, highly productive and predictable⁴¹. Our study provides another model for pre-agricultural sedentism at very high altitudes (analogous to other high-latitude and high-altitude areas around the world), with ways of living reliant on stable food resources sourced from a massive paleolake system. Fish, waterfowl and large mammals that used the lakes as both water and food supply were reliable local resources, while crops were obtained via exchange with lower-altitude areas. This strategy contrasts with that on the lower-elevation eastern Tibetan Plateau where crops were cultivated locally by sedentary populations.

The Mabu Co inhabitants exhibited genetic consistency with other populations in the broader southern highlands during later periods. This new DNA evidence allowed us to gain new insights into the ancestral components of the southern highlands, which revealed a different genetic profile from the populations of the northeastern plateau. This

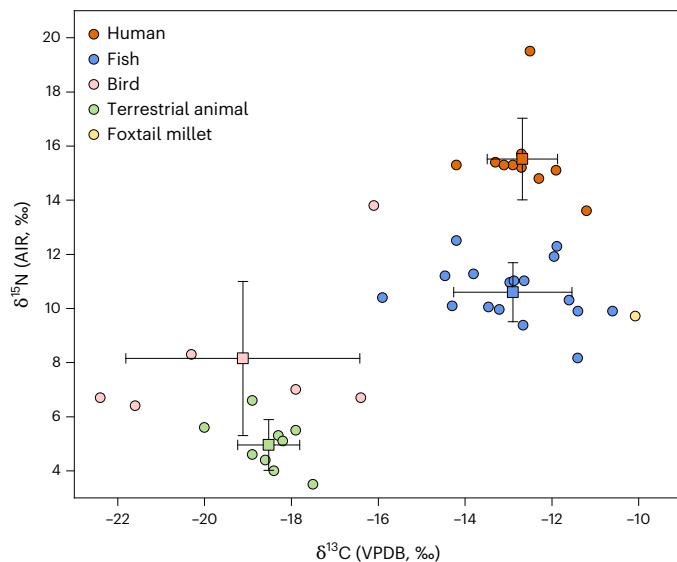


Fig. 5 $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ results for human, animal and crop remains from the Mabu Co site. Isotopic data are presented as scatter plots along with the means and s.d. The squares and bars represent the means and s.d., respectively. VPDB, Vienna Pee Dee Belemnite.

suggests that the southern plateau ancestry might have earlier origins than 4,400 years ago and a widespread presence in the foothills of the Himalayas, both north and south, and along the Yarlung Tsangpo River valley. Our research overturns previous assumptions about the origins and nature of sedentism on the plateau, which assumed that it was associated with the dispersal of agriculture or farmers^{4,6–8}, largely writing Indigenous foragers out of the history of the plateau. We demonstrated that Indigenous foraging populations who were genetically adapted to high altitudes practised sedentism by relying on year-round fishing at a highly productive lacustrine environment and hunting, and engaging in limited exchange for domestic crops. Overall, this study shows that foragers had an important role on the plateau throughout the Holocene and that they are genetic ancestors of present-day inhabitants of the plateau.

The Tibetan Plateau contains lakes covering a very large area of 50,000 km² (ref. 42), which are potential aquatic food resource providers. Future research may help us understand if this lake-centred lifestyle was a key component of the process of sedentism in other high-altitude areas with similar resource availability. A regional systematic survey at the high-altitude interior of the plateau should also be conducted to clarify the role that sites like Mabu Co had in regional settlement pattern systems, and to reveal the types of connections the foragers of the site held to those who grew crops at lower altitudes, in particular to clarify if they represented members of the same or different communities.

Methods

AMS ¹⁴C radiocarbon dating

Fourteen and 19 samples were AMS ¹⁴C-dated at Peking University and Beta Analytic, respectively (Supplementary Table 1). The IntCal20 curve and Libby half-life of 5,568 years were used in the tree-ring calculation of all dates⁴³. Calibration was carried out using the OxCal 4.4 program⁴⁴. All ages are reported as cal BP relative to 1,950 CE.

Ancient human DNA

Samples of human remains were collected during the 2020 and 2021 Mabu Co archaeological excavations using sterile protocols. Ancient DNA wet laboratory work and population genetics analysis were performed in the dedicated ancient DNA laboratory, using the data server

platform at the Institute of Vertebrate Paleontology and Paleoanthropology, Chinese Academy of Sciences, Beijing, China.

DNA extraction and in-solution capture. For all 12 samples, DNA was extracted from less than 100 mg of bone powder using an optimized silica-based extraction protocol⁴⁵. DNA libraries were prepared using either double-stranded (DS) or single-stranded (SS) protocols^{46,47}; all DS libraries were subjected to half uracil-DNA-glycosylase (UDG) treatment⁴⁸ (DS-half) (Supplementary Table 2). For the nine successful library samples, solution hybridization oligonucleotide probes were used to enrich endogenous DNA for a complete mitochondrial genome⁴⁹ and 1.2 million nuclear SNPs (1,240,000 SNPs)⁵⁰.

Sequencing and read alignment. For the enriched mitochondrial DNA libraries, Illumina HiSeq X Ten sequencing was used to generate 2 × 76 base pairs (bp) paired-end reads, while for the enriched nuclear DNA libraries, Illumina HiSeq 2500 sequencing was used to generate 2 × 150 bp paired-end reads. Adaptors were trimmed and sequences with a minimum overlap of 11 base pairs were merged into one sequence using leeHom (<https://github.com/greanud/leeHom>)⁵¹. Merged reads with a length of at least 30 bp from the mitochondrial DNA libraries and the nuclear DNA libraries were respectively aligned to the revised Cambridge Reference Sequence and the human nuclear reference (hg19) using the Burrows–Wheeler Aligner (v.0.7.17)⁵². For the mapped. bam file, duplicated reads with the same orientation, start and end positions were removed; fragments with a mapping quality score below 30 were removed.

Test for contamination and genotyping. To ensure the authenticity of ancient DNA, we first identified the terminal base C-T deamination ancient DNA damage signatures, then estimated the contemporary human contamination rates for each sample with a threshold of 3% contamination using ContamMix⁴⁹. All samples showed a low contamination level (0–1.6%). We then assessed pseudo-haploid genotypes by randomly sampling one fragment per position to determine the corresponding allele in that individual. The 2-bp ends of the sequencing reads for UDG-treated samples and 5-bp ends of the sequencing reads for the sample not treated with UDG were masked when determining the pseudo-haploid genotypes. We were able to obtain nine new ‘1,240,000’ capture genome datasets with ×0.53–×5.29 coverage.

Dataset for population analysis. Mabu Co populations were analysed using a worldwide reference genetic dataset containing 35 present-day populations, including populations from the Human Origin SNP panel⁵³, the Simons Genome Diversity Panel⁵⁴, the Human Genome Diversity Project⁵⁵ and the Tibetan, Sherpa and Han populations from previous Tibetan-related publications^{14,15,23}. All the ancient populations used for the analysis were based on already existing ancient plateau population datasets¹⁵ curated in the IVPP population genetics analysis platform.

Kinship. Genotyped data for the nine Mabu Co individuals were transformed from genotypic to .tped files using PLINK⁵⁶ (v.1.9) with the parameters --alleleACGT --recode transpose, after which the READ software⁵⁷ was used to calculate the average pairwise P0 used to infer kinship.

PCA. We used the smartpca program (v.16000) in EIGENSOFT (v.7.2.1) to perform the PCA, with the following parameters: numoutlierevec: 2; outliersigmathresh: 12; lsqproject: YES; and autoshrink: YES. Forty-three present-day East Asian populations on or near the Tibetan Plateau genotyped in the Human Origins dataset (597,573 SNPs) were used to construct the principal component space on which we projected all ancient individuals.

Admixture. Admixture is a method for fast model-based estimation of ancestry in unrelated individuals⁵⁸. We first pruned the dataset to account for linkage disequilibrium using PLINK (v.1.90) with the parameters ‘--indep-pairwise 200 25 0.4’. We then used ADMIXTURE (v.1.30) to estimate individual ancestries and determine the population structure parameter ‘-j10’, running the software ten times using different seeds to estimate the lowest cross-validation error for the ‘best’ *k*. The results were plotted using the AdmixturePlotter-master R script.

f3 analysis. The *f*3 statistic, which was introduced in ref. 53, quantified the population genetic drift on different population trees and tested the occurrence of admixture. The *f*3 outgroup, *f*3(outgroup; X, Y), is the average of $(P_{out} - P_X)(P_{out} - P_Y)$ across sites, where P_X and P_Y are the frequencies of a diallelic SNP in X and Y. qp3Pop (v.412) from the ADMIXTOOLS package was used to calculate the *f*3 statistics. We used the Indigenous Mbuti population as the *f*3 outgroup (X, Y; Mbuti). Higher *f*3 values can be interpreted as having high genetic similarity with each other; the heatmap based on the *f*3 value matrix of pairs of people related to each other was used to cluster the related populations.

f4 analysis. qpDstat (v.712) was used to calculate the *f*4 statistics by turning on the ‘f4mode: YES’ option. Autosomal SNPs from the 1,240,000 dataset were used unless mentioned otherwise. The general form of the *f*4 statistic we used is *f*4(Mbuti, P2; P3, P4), where the Mbuti are again used as an outgroup to the individuals or populations represented by P2, P3 and P4. An $f_4 > 0$ ($Z > 3$) indicates that P2 shares more alleles with P4 than P3, an $f_4 < 0$ ($Z < -3$) indicates that P2 shares more alleles with P3 than P4, and $f_4 = 0$ ($Z < 3$) indicates that P2 shares a similar number of alleles with both P3 and P4.

MDS. Multidimensional scaling demonstrates the differences (or similarities) between objects by graph. Based on the genetic relation *f*3 outgroup value, we used multidimensional scaling to convert the *f*3 outgroup matrix into two-dimensional coordinate vectors using the cmdscale function in R (v.4.2.0).

qpAdm. qpAdm is a method based on the *f*4 statistic that models the mixture of ancestry for a target population. We used qpAdm (v.634) in the ADMIXTOOLS package with the parameters ‘details: YES’ and ‘allsnps: YES’ to model ancient Mabu Co populations using genetic libraries from both ancient Tibetans and ancient lowland East Asian populations.

EPAS1 haplotype. The 30 most differential SNPs were selected to determine the *EPAS1* haplotype²⁴. We used SAMtools⁵⁹ (v.1.5) mpileup to summarize the *EPAS1* SNPs from the BAM files. The generated results were then co-analysed with previously published ancient genomic data. Changes in the *EPAS1* frequency of southern plateau populations was plotted using a bar chart.

Animal species identification

Animal remains were identified according to morphology and using bulk bone shotgun metagenomics (BBSM). The results from both methods agreed with each other. BBSM was used to compile the animal species while morphological analysis was performed to identify every fragment of the animal remains and calculate the relative proportions of the species.

Morphology and osteostructure. The animal remains from the trial excavation trench TG2 were analysed by layers. The assemblage from each layer was categorized into mammal, bird, fish and mollusc according to morphology and micromorphological structure. Each category was further sorted, identified and recorded. Identification procedures were undertaken with the aid of the reference collection in the Institute of Tibetan Plateau Research and zooarchaeological atlases^{60–63}. An ivory

bangle was identified by observing the Schreger pattern with both the naked eye and a Dino-Lite Digital Microscope⁶⁴.

BBSM. Three samples of mammals, fish and birds, respectively, were collected from each layer. Fifteen samples collected from five layers of the trial excavation trench TG6 included 1,890 bone fragments (Supplementary Table 11). These cultural layers are consistent with those in the excavation trench TG2 in terms of relative chronology and artefact styles. In addition, 12 fragmented fish gorge hooks, originally constructed from skeletal remains in TG2, were collected and combined into a single sample for material identification. The sampler conducted the sampling wearing a face mask, full-body suit, nitrile gloves and using sterile metal forceps. DNA extraction and library preparation were performed in a dedicated ancient DNA laboratory at the China University of Geosciences at Wuhan. Total genomic DNA was extracted using a modified protocol⁶⁵. A doubled quantity of bone powder, EDTA and proteinase K was used. A volume of 20 μ l DNA extract was used for dsDNA library construction according to the standard protocol⁴⁶. DNA sequencing was conducted on an Illumina HiSeq 2500 platform. Sequencing reads were trimmed using the ‘Holi’ pipeline to remove low-complexity reads, duplicates and reads below 30 bp in size. These reads were thereafter aligned against the NCBI database of full mitochondrial genomes within Metazoa (downloaded November 2021). The alignments were eventually parsed through ngsLCA (<https://github.com/miwipe/ngsLCA>); reads with 100% similarity to the reference were retained for taxonomic assignment⁶⁶. The identified taxa for each sample were profiled at the species and genus level by merging all reads below the taxon. In addition, reads were only considered as genuine if the corresponding taxa could be found in the study area (Tibetan Plateau) (Supplementary Table 12).

Seasonal animal death determination

Annulus increment analysis. The second vertebra of cyprinids has a distinctive shape that helped us identify the specimen to the species, and were thus selected for the annulus increment analysis. Only fish remains recovered from cultural layers were sampled for reconstruction of fishing seasonality. Vertebrae were cleaned using ultrasonication to reveal the annuli on the anterior and posterior articular surfaces. Both articular surfaces of each vertebra were examined and photographed using an M165 FC microscope (Leica Microsystems) with a DFC450C digital camera (Leica Microsystems). Unlike modern specimens on which the summer and winter growth rings can be discerned by their opaqueness and transparency, the summer and winter growth rings on the archaeological specimens were distinguished by the regular change of hues: the darker rings were winter growth rings, while the lighter rings were summer growth rings (Fig. 4b). The outermost ring type indicated the death season of the fish.

Cementum increment analysis. Seventeen specimens, including two isolated teeth and 15 teeth removed from jaws, each representing one individual, were selected for the cementum increment analysis (Supplementary Table 9). Although research suggested that molars are better samples for such analysis than premolars, canines and incisors, because of the limited number of teeth, premolars and incisors were also examined in our study. The samples were cleaned using ultrasonication and embedded in polyester resin. The embedded specimens were cross-sectioned at the tooth cervix and polished to obtain microscopic thin sections in thicknesses between 40 and 100 μ m. The thin sections were observed with a transmitted light polarized light microscope (DM3000, Leica Microsystems). The warm and cold season growth rings on the archaeological specimens were also distinguished by the regular change of hues: the light rings were winter growth rings and the dark rings were summer growth rings under transmitted light. Eight samples displayed clear cementum increment layers (Fig. 4c).

Stable isotope analysis

Bone collagen. The stable isotope values of bone and teeth reflected the isotopic composition of dietary components with known fraction offsets and were used to investigate the paleodiet of ancient people^{67,68}. Stable nitrogen isotope values show a 3‰ to 6‰ stepwise enrichment in each trophic level from plants to herbivores to carnivores in aquatic and terrestrial ecosystems^{25,26}. Hence, nitrogen isotope values could potentially tell us about the intake of animal versus plant proteins and aquatic versus terrestrial proteins in the past⁶⁹. There is a small stepwise increase in $\delta^{13}\text{C}$ values of about 1‰ between trophic levels in both aquatic and terrestrial ecosystems, thus the $\delta^{13}\text{C}$ values of humans are close to those of their animal-based food^{70,71}. Relying on bone and teeth collagen $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values, we reconstructed the paleodiet of the Mabu Co site.

Stable carbon and nitrogen isotope data were recovered from 40 bone collagen samples of the Mabu Co site (Supplementary Table 8). Sixteen samples were measured by Beta Analytic (Supplementary Data 5), after direct radiocarbon dating; four samples were measured at the Joint International Research Laboratory of Environmental and Social Archaeology, Shandong University (Supplementary Data 6) while the other 20 samples were measured at the Environmental Stable Isotope Laboratory (ESIL), Institute of Environment and Sustainable Development of Agriculture, Chinese Academy of Agricultural Sciences (Supplementary Data 7). At Beta Analytic, after removing surface contamination, bone collagen was extracted using their protocol⁷². A subsample of each sample was routinely analysed with isotope ratio mass spectrometry (IRMS), using the DELTA V Advantage (50–40,000 mV, Thermo Fisher Scientific), wrapped in a standard IRMS tin boat and placed into an auto-dispenser on a Costech 4010 Elemental Analyzer. The %N, %C and C:N ratio were determined using the ECS Clarity software. Measurement errors were less than $\pm 0.3\%$ for $\delta^{13}\text{C}$ and $\pm 0.5\%$ for the $\delta^{15}\text{N}$ values.

At ESIL, after collagen was extracted at ITPCAS, samples were measured using an IsoPrime 100 IRMS (Elementar) coupled with an Elementar Vario (Elementar), and calibrated with USGS 40 ($\delta^{13}\text{C} = -26.39 \pm 0.04\%$, $\delta^{15}\text{N} = -4.52 \pm 0.06\%$) and USGS 41a ($\delta^{13}\text{C} = +36.55 \pm 0.08\%$, $\delta^{15}\text{N} = +47.55 \pm 0.15\%$) as reference materials. For every 12 samples, a laboratory reference—gelatine from bovine skin ($\delta^{13}\text{C} = -14.7 \pm 0.2\%$; $\delta^{15}\text{N} = +7.1 \pm 0.2\%$)—was inserted for calibration and to monitor stability. Measurement errors were less than $\pm 0.2\%$ for both $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values. The %N and %C of ten of the fish samples were previously measured on a Vario EL III Elemental Analyzer (Elementar) at the Analysis and Testing Center, College of Chemistry and Chemical Engineering, Lanzhou University.

At the Joint International Research Laboratory of Environmental and Social Archaeology, both collagen extraction and isotopic measurement of those four samples were done in the laboratory. Samples were extracted according to the protocol published in ref. 69 and then measured using an DELTA V Advantage IRMS (Thermo Fisher Scientific) coupled with a Flash 2000 HT Elemental Analyzer (Thermo Fisher Scientific), and calibrated with USGS 40 ($\delta^{13}\text{C} = -26.39 \pm 0.04\%$; $\delta^{15}\text{N} = -4.52 \pm 0.10\%$), USGS 62 ($\delta^{13}\text{C} = -14.79 \pm 0.04\%$; $\delta^{15}\text{N} = +20.17 \pm 0.06\%$) and USGS 41a ($\delta^{13}\text{C} = +36.55 \pm 0.08\%$; $\delta^{15}\text{N} = +47.55 \pm 0.15\%$), with the internal standard alanine peptide ($\delta^{13}\text{C} = -17.94 \pm 0.12\%$; $\delta^{15}\text{N} = -0.98 \pm 0.21\%$) as reference materials. For every ten samples, a laboratory reference—EMA B2155 (casein) ($\delta^{13}\text{C} = -27.21 \pm 0.08\%$; $\delta^{15}\text{N} = +6.00 \pm 0.10\%$)—was inserted; for every 20 samples, the internal standard alanine peptide was inserted for calibration and to monitor stability. Measurement errors were less than $\pm 0.1\%$ for $\delta^{13}\text{C}$ and $\pm 0.2\%$ for $\delta^{15}\text{N}$.

Collagen quality was assessed after considering several preservation criteria: collagen yield greater than 1%, %C = 30–44%, %N = 11–16% and C:N ratio = 2.9–3.6 (refs. 69,73–75). According to the %C, %N and C:N ratio, all samples were well-preserved and yielded good-quality collagen for carbon and nitrogen extraction,

indicating that $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ could be used to reconstruct the paleodiet in these samples.

Charred millet grains. One charred millet sample (totalling 21 individual grains) floated from deposits of TG3 during the 2020 excavation of the Mabu Co site were analysed. First, millet grains were soaked with 0.5 M HCl at 80 °C for 60 min. Second, we rinsed the millet grains with ultra-pure water six times. Third, we freeze-dried the grains and crushed them into a homogeneous powder. Finally, a 3.1-mg sample was weighed into tin containers for isotopic measurement. The $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values of the powder samples were measured using an IsoPrime 100 IRMS (Elementar) at ESIL, Institute of Environment and Sustainable Development of Agriculture, Chinese Academy of Agricultural Sciences. For every 12 samples, a laboratory reference gelatine from bovine skin ($\delta^{13}\text{C} = -14.7 \pm 0.2\%$; $\delta^{15}\text{N} = +7.1 \pm 0.2\%$) was inserted for calibration and to monitor stability. Measurement errors were less than $\pm 0.2\%$ for both $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$.

Flotation and identification of macroscopic plant remains

For the analysis of macroscopic plant remains, blanket flotation samples were collected during excavation along with opportunistic sampling targeting daily refuse deposits from the cultural layers. The sediment samples were processed using the bucket flotation method in the field⁷⁶. Macroscopic plant remains were collected in 0.45 mm mesh bags and then air-dried in the shade. These remains were sorted and identified under a $\times 6.8$ – $\times 47$ binocular stereomicroscope in the ITPCAS laboratory, using our collections and the atlas of modern seeds in China for identification^{77–80}; 126 litres of sediments from six cultural layers of trench TG2 were examined (Supplementary Table 10). All the specimens were sorted and photographed using an M165FC microscope (Leica Microsystems) with a DFC450C digital camera (Leica Microsystems).

Ethics and inclusion statement

Our excavation and research work on the Mabu Co site were approved and supported by relevant government departments at the national, provincial and county levels: National Cultural Heritage Administration; Tibetan Cultural Heritage Administration; and Cultural Heritage Administration of Kangmar County, Tibet Autonomous Region. Before the start of the excavation, three major participating institutes, Lanzhou University, the Institute of Tibetan Plateau Research of the Chinese Academy of Sciences and the Tibetan Institute of the Preservation of Cultural Relics, signed mutually beneficial cooperation agreements. The main terms of the agreements include that the Tibetan Institute of the Preservation of Cultural Relics leads the excavation work and has the ownership of archaeological samples for the purposes of preservation and study. Lanzhou University and the Institute of Tibetan Plateau Research of the Chinese Academy of Sciences provide financial support for the excavations, participate in the excavations, carry out multidisciplinary scientific analysis of archaeological samples and provide training opportunities for the personnel of the Tibetan Institute of the Preservation of Cultural Relics. This research article is the result of collaboration among these three institutions. The researchers, including S.W. (Tibetan ancestry), Y.T. and Y. Li, from the local research institute, have appeared as co-authors. Among them, S.W. is one of the corresponding authors. S.W. worked with the Gala Town community at Mabu Co, which consented to and participated in the excavations. The involvement of the local community was ensured through community meetings, consultations and ongoing engagement. Local community members who participated in the excavations are listed in the Acknowledgements.

Reporting summary

Further information on research design is available in the Nature Portfolio Reporting Summary linked to this article.

Data availability

Key data used in this study are available in the main text, Extended Data Figs. 1–10 and the accompanying Supplementary Information. Other datasets generated in this study are available from the corresponding authors upon reasonable request. The raw sequencing reads, aligned BAM files and the mitochondria FASTA files are available through the Genome Sequence Archive and the Genbase datasets (<https://bigd.big.ac.cn/gsa-human> and <https://ngdc.cncb.ac.cn/genbase>; accession no. PRJCA024667; <https://ngdc.cncb.ac.cn/gsa-human/s/LZ2Q-zlVY>; <https://ngdc.cncb.ac.cn/genbase/review/4969bfb8c3f4>). The pseudo-diploid genotype calls are available through the OMIX database, China National Center for Bioinformatics/Beijing Institute of Genomics, Chinese Academy of Sciences (accession no. OMIX006078; <https://ngdc.cncb.ac.cn/omix/preview/g7zYGtIX>; <https://share.cncb.ac.cn/9eac48fa9254>). Ancient human and archaeological samples have been stored at the Tibetan Institute of the Preservation of Cultural Relics.

Code availability

The software used for the population genetics analysis (smartpca, f3, f4, qpAdm) was based on the ADMIXTOOLS (<https://github.com/DReichLab/AdmixTools>) and EIG (<https://github.com/DReichLab/EIG>) tools developed by the David Reich lab. All PAR files containing the parameters used in the analysis and the scripts used for plotting and table creation are available at <https://github.com/RickRan/MabuCo>.

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Author contributions

F.C., X.Y. and S.W. designed the project. S.W., X.Y., Y.G. and Songtao Chen directed the excavation. Y. Tong., N.J., Q.W., Y. Li, J.Y., Ying Zhang, Q.Y., Y.W., Y.H., S.H., Y. Tian, J.G.J. X.L., T.Y., J.R., Z.D., L.Q. and Y. Zhuang participated in the excavation. Q.F., J.R., T.W. and Y.L. performed the human ancient DNA research. Ying Zhang and Q.W. performed the zooarchaeological research. Y.G. identified the archaeobotanical remains. Songtao Chen, Y.H. and J.Y. carried out the stable isotope analysis. Yunan Zhang, Y.G. and X.W. processed the dating samples. Z.G., Shungang Chen and Q.W. performed the animal ancient DNA analysis. X.Y., F.C., S.W., Y.G., J.Y., Q.F., J.R., T.W., Y. Liu, Songtao Chen, Ying Zhang and Q.W. analysed the data. J.Y., J.R. and Q.W. performed the data visualization. X.Y., Y.G., J.R., J.Y., Songtao Chen, L.P., J.D.G., Ying Zhang, Q.W., Y. Liu, Q.F. and F.C. wrote the paper with contributions from all authors.

Competing interests

The authors declare no competing interests.

Additional information

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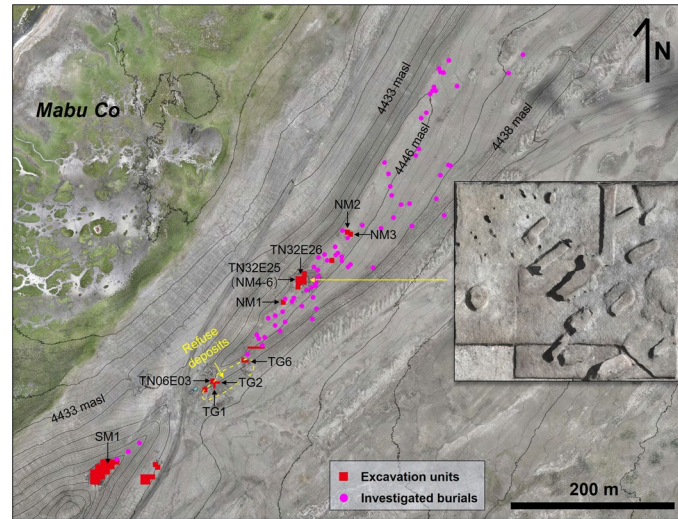
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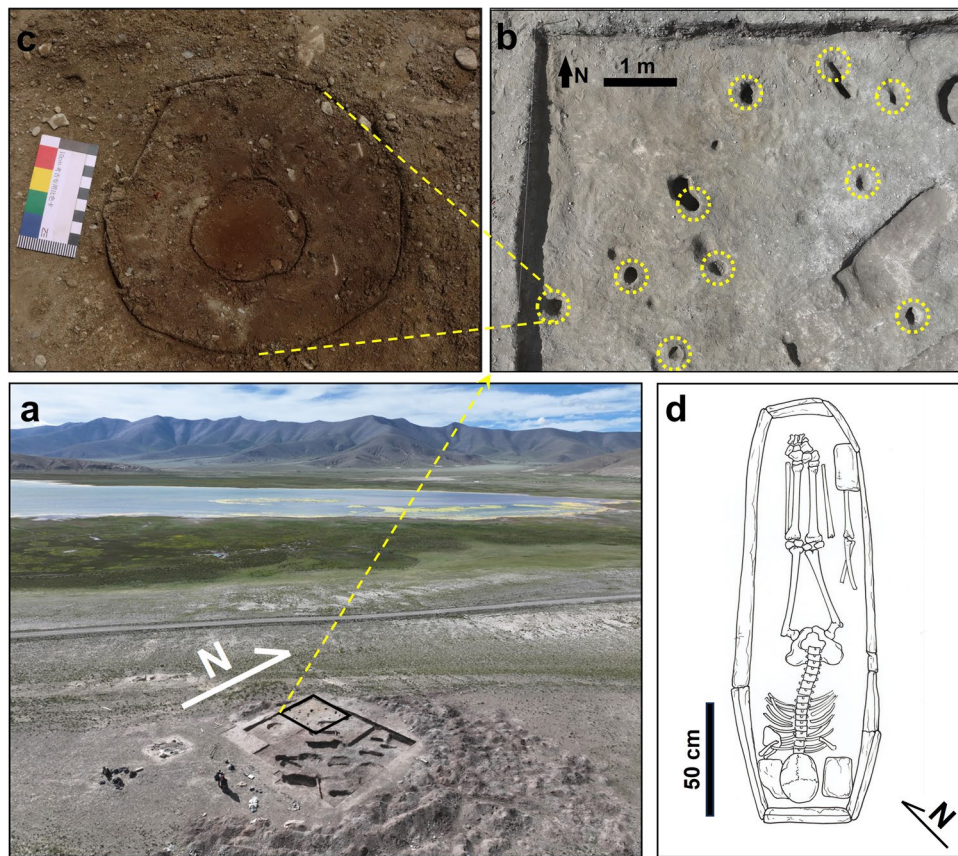
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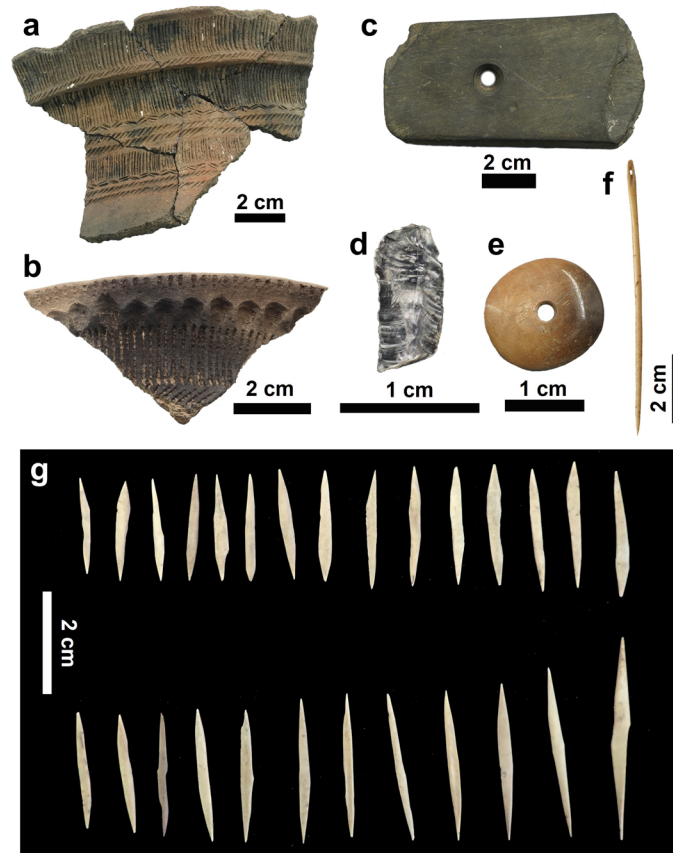


Extended Data Fig. 1 | Aerial view of the Mabu Co site. Plan view map of excavation units and burials referred in this study at the Mabu Co site.



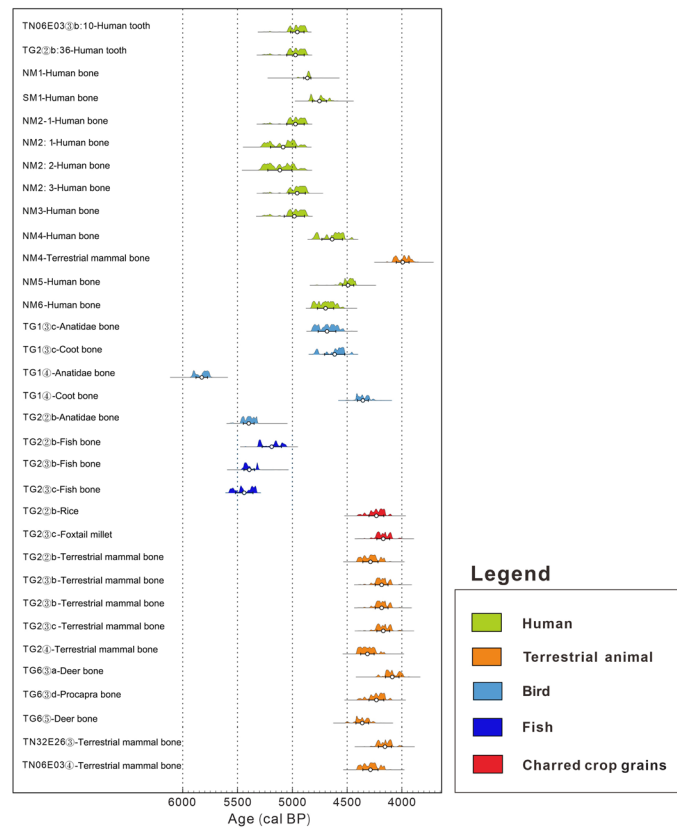
Extended Data Fig. 2 | Post molds and typical burial from the Mabu Co site. a, Overhead view of the trench (TN32E25) where the post molds are located. **b,** Post molds. Yellow dotted circles outline the locations of post molds. Postholes were found in an irregular alignment which may correspond to a living structure. While the upper portion of this living structure was not found, it is possible that this structure was finished using organic material such as animal hide that was reused and moved from place to place as is common in other areas of the world.

c, Close-up view of post molds. **d,** Illustration image of the burial NM3. Grave of women about 25-year-old, southwest-northeast orientation. A unique, local mortuary practice. The typical stone coffin burial, characterized by stone walls surrounding the occupants who were placed in an extended prone position. The positioning of the heads and feet of the human remains on a flat stone with the head facing front.

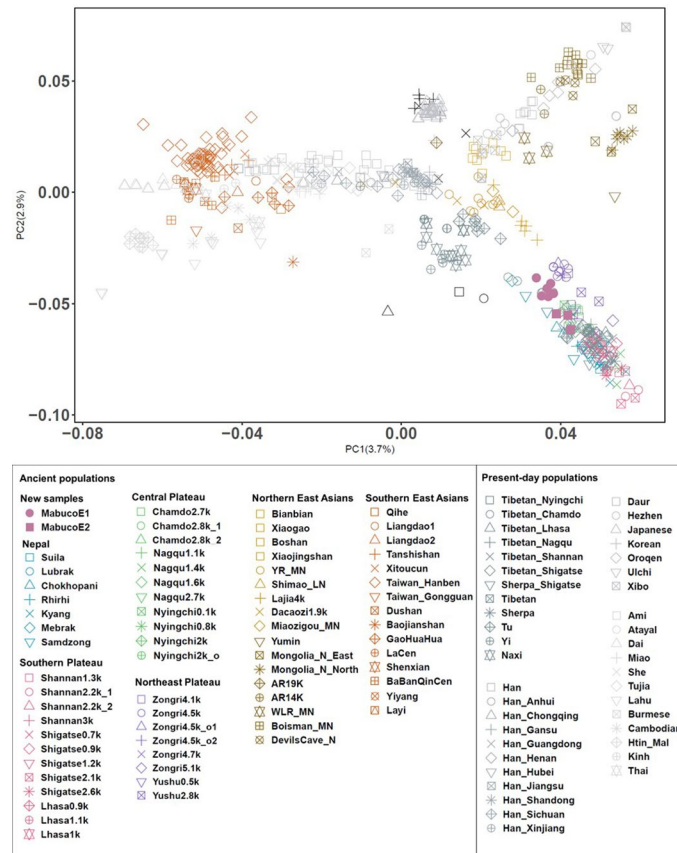


Extended Data Fig. 3 | Selected artifacts from the Mabu Co site. a and b, Pottery sherds. The pottery styles point to a connection to the East. The shapes of the pottery objects and their characteristic decorative patterns with engraving, stamping, embossing, and stacking techniques are similar to contemporaneous

pottery assemblages from the southeastern margin of the Tibetan Plateau more than 1000 km from Mabu Co^{81,82}. **c,** Stone axe. **d,** Crystal microliths. **e,** Bone bead. **f,** Bone needle. **g,** Fish gorge hooks.



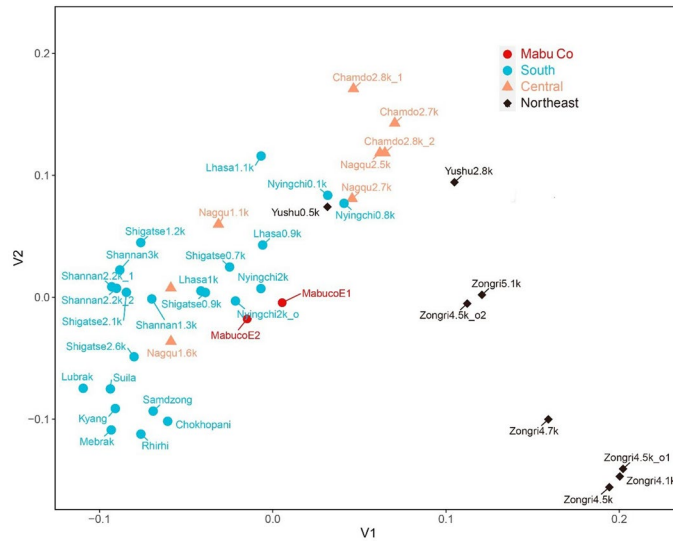
Extended Data Fig. 4 | Age of the Mabu Co site. The calibrated dates have been produced using OxCal v.4.4. The colored shadows represent the 95.4% probability density distribution of the calibrated ages. The white circles and bar ranges indicate the modeled mean ages and age ranges, with 68.2% probability intervals.



Extended Data Fig. 5 | Principal component analysis of East Asia populations. PCA of ancient East Asian populations projected on present-day East Asia populations (including Tibetans).

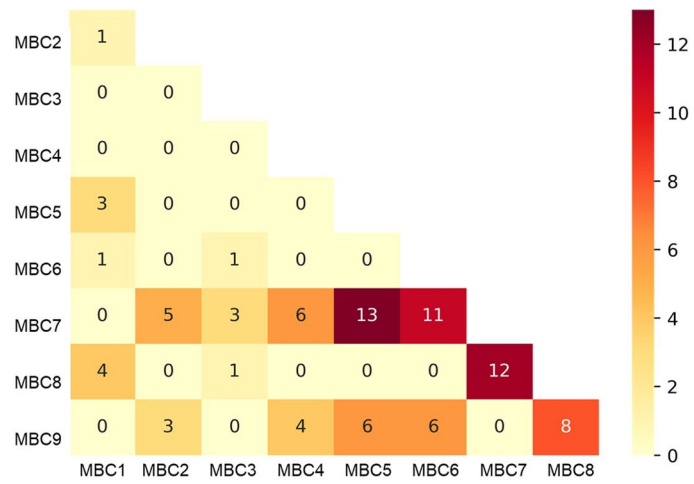


Extended Data Fig. 6 | ADMIXTURE displaying ancestry components. ADMIXTURE results for selected surrounding populations for K=2 to K=12.

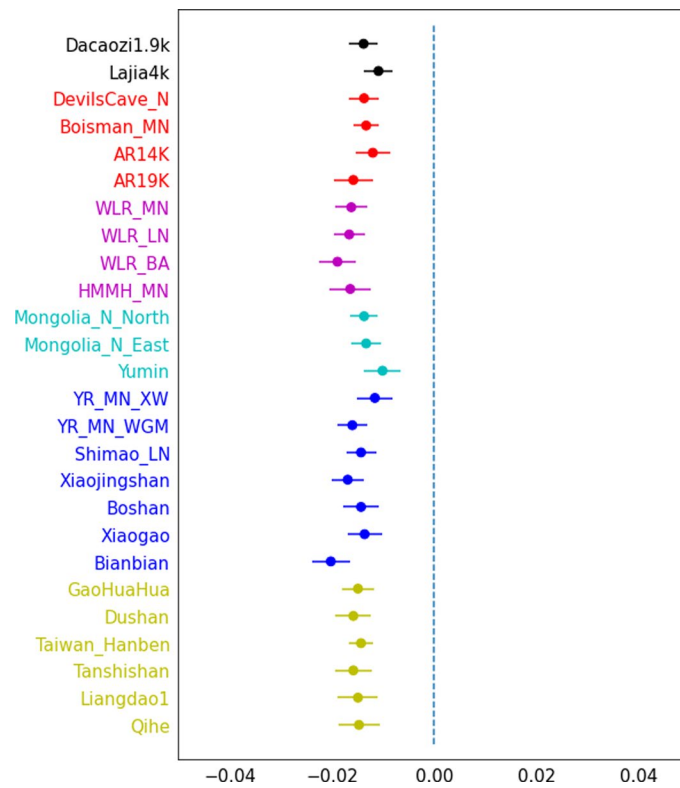


Extended Data Fig. 7 | Multidimensional scaling (MDS) of ancient Tibetans populations based on the genetic relation f_3 -outgroup value. Here, the south, central, and northeast subgroups of the plateau are primarily distinguished by

blue, orange, and black. The Mabu Co population clustered with the ancient South-southwest population lineage, represented by the color blue, mainly including ancient Shannan, Nepal populations.

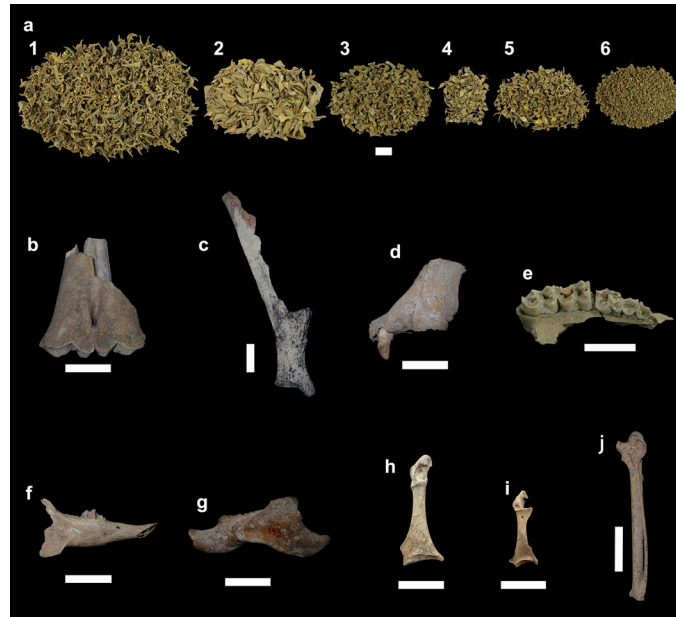


Extended Data Fig. 8 | Pair-wise individuals f4 (Mbuti, X; Mabuco_ind, Mabuco_ind) for grouping Mabu Co ancient samples. We used world-wide 30 outgroup (X) to test the differences between each pair individuals, and the sum of the number of outgroups with significant differences ($|Z| > 3$) was shown in heatmap.



Extended Data Fig. 9 | Genetic differences inside Mabuco groups by $f_4(\text{Mbuti}, X; \text{MabucoE1}, \text{MabucoE2})$. Certain degree of variation between MabucoE1 and MabucoE2 two groups is further verified, based on the degree of their connections with lowland East Asians (for example Qihe, Bianbian,

DevilsCave_N), $f_4(\text{Mbuti}, X; \text{MabucoE1}, \text{MabucoE2}) < 0$, where solid dots represent the $|Z| > 3$, Z-scores are calculated with 5 cM jackknifing standard error (SE), and the horizontal lines mark ± 3 SEs ranges.



Extended Data Fig. 10 | Selected animal fossils from the Mabu Co site.

a, Schizothoracids (*Gymnocypris* sp.). (1) Pharyngeal; (2) Cleithrum; (3) Basioccipital; (4) Vertebra I; (5) Vertebra II; (6) Other vertebrae. **b**, Red deer (*Cervus elaphus*) left metatarsal. **c**, Argali (*Ovis ammon*) right scapula. **d**, Lynx (*Lynx lynx*) left premaxilla and maxilla. **e**, Gazelle (*Procapra przewalskii*) right

maxilla. **f**, Woolly hare (*Lepus oiostolus*) right mandible. **g**, Himalayan marmot (*Marmota himalayana*) left mandible. **h**, Pochard (*Netta* spp. & *Aythya* spp.) left coracoid. **i**, Coot (*Fulica atra*) left coracoid. **j**, Great cormorant (*Phalacrocorax carbo*) right carpometacarpal. Scale bars, 2 cm.

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the Genome Sequence Archive (<https://bigd.big.ac.cn/gsa-human>; accession number: PRJCA024667), and OMIX database, China National Center for Bioinformatics/Beijing Institute of Genomics, Chinese Academy of Sciences (<https://ngdc.cncb.ac.cn/omix>, accession number: OMIX006078).

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Reporting on sex and gender	The sex of all 9 ancient human individuals was genetically determined by comparing the amount of sequence data that map to the Y chromosome to the amount of sequence data that map to the autosomes or the X chromosome.
Reporting on race, ethnicity, or other socially relevant groupings	Ancient human bone samples only. No modern human participants.
Population characteristics	None
Recruitment	None
Ethics oversight	Permission to sampled human ancient DNA from the associated human specimens was granted by the provincial archaeological institutes that manage and care for the specimens.

Note that full information on the approval of the study protocol must also be provided in the manuscript.

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Study description	Archaeological and paleogenomic study that aims to reveal what populations were and how they lived in lake basins in the ultra-high altitude areas of the Tibetan Plateau about 4000 years ago. This study includes paleogenomic analysis of ancient human bones, bulk bone metagenomics analysis of ancient animal bones, morphological analysis of plant and animal remains, stable isotope analysis of human, animal and plant remains.
Research sample	Research samples includes human, animal and plant remains from an archaeological site.
Sampling strategy	Archaeological sample size was not pre-determined as we sampled the maximum number of human, animal and plants remains have definite provenience informations.
Data collection	The radiocarbon dating of archaeological remains are carried out in Peking University and Beta Analytic, respectively. Ancient DNA wet lab work and population genetics analysis were performed in the dedicated ancient DNA laboratory and data server platform at the Institute of Vertebrate Paleontology and Paleoanthropology (IVPP), Chinese Academy of Sciences. The isotope data are measured in Beta Analytic and the Environmental Stable Isotope Laboratory (ESIL), Institute of Environment and Sustainable Development of Agriculture, Chinese Academy of Agricultural Sciences. The morphological analysis of plant and animal remains was in the State Key Laboratory of Tibetan Plateau Earth System, Resources and Environment (TPESRE), Institute of Tibetan Plateau Research, Chinese Academy of Sciences, and Key Scientific Research Base of Bioarchaeology in Cold and Arid Regions (National Cultural Heritage Administration), Lanzhou University.
Timing and spatial scale	Archaeological samples were obtained during the survey and excavation of the archaeological site of Mabu Co from 2019-2021. All samples were collected at and around the Mabu Co site.
Data exclusions	No data were excluded from the analyses.
Reproducibility	Almost all of the samples involved in our study were left over for reproducible testing.
Randomization	No randomization was performed.
Blinding	No blinding was performed.
Did the study involve field work?	<input checked="" type="checkbox"/> Yes <input type="checkbox"/> No

Field work, collection and transport

Field conditions	<input type="text" value="The mean annual temperature is 1°C, and the average annual precipitation is 277 mm."/>
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Palaeontology and Archaeology

Specimen provenance	<input type="text" value="We collected the archaeological samples with permission from relevant authorities, such as National Cultural Heritage Administration, Tibetan Cultural Heritage Administration, and Cultural Heritage Administration of Kangmar County."/>
Specimen deposition	<input type="text" value="Archaeological samples are curated in Tibetan Institute of the Preservation of Cultural Relics and Lanzhou University."/>
Dating methods	<input type="text" value="14C dates were obtained from Peking University and Beta Analytic. The IntCal20 curve and the Libby half-life of 5568 yr were used in the tree-ring calculation of all dates, with the calibration performed using the OxCal 4.4 program. OSL dates were measured in Lanzhou University."/>
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Ethics oversight	<input type="text" value="Our archaeological and environmental samples were collected with the permission of local institutes."/>

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