

Supplementary Materials for

Genomic structure in Europeans dating back at least 36,200 years

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S1: Archaeological context and description of Kostenki 14

The Kostenki-Borshchevo localities

The village of Kostenki and its neighbouring archaeological sites (Kostenki and Borshchevo) are located on the west bank of the Middle Don River, Russia (51°24' N, 39°02' E), c. 40 km south of the city of Voronezh (Fig. 1A). The first archaeological site at Kostenki-Borshchevo (K1) was discovered in 1879, and the area has been the focus of archaeological research ever since. To date, twenty-one Upper Paleolithic open-air sites have been studied at Kostenki, and another five are known from Borshchevo (46). The sites are found stratified in fill of two main river terraces at 10-15 m and 15-20 m along the main river channel, as well as in the smaller ravines and gullies that drain the surrounding uplands (47, 48) (Fig. S1). The local Kostenki-Borshchevo stratigraphic sequence can be broadly described (following (48–53) as consisting of six main units (in stratigraphic sequence from bottom to top):

1. Chalky loam deposits (52), sometimes also described as upper alluvium interstratified with coarse slope deposits (54);
2. Lower Humic Complex/Bed (LHB): stratified loamy deposits with several humic ‘horizons’;
3. Whitish Loam (WL): homogenous whitish loam with some sub-horizontal lamination; it can include in its lower part, lenses of *in situ* or re-worked volcanic ash (Campanian Ignimbrite (CI) Y5 tephra); it forms a marker horizon that separates the Upper and Lower Humic Beds at all sites on the second terrace in the Kostenki-Borshchevo region (50);
4. Upper Humic Complex/Bed (UHB): consists of several humic ‘horizons’ separated by yellowish chalky loam;
5. Cover Loam (CL): a loess-like loam, including several humified horizons in some sites;
6. Modern chernozem: black, highly humic soil, with abundant bioturbation/burrows.

The Y5 CI tephra horizon (known as the “Paleolithic Pompeii”) is found underlying the UHB in the WL at several of the sixteen sites preserved on the second terrace (K1, 2, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18 and B5 (50, 55). This ash layer derives from the CI eruption at Campi Flegrei in Italy, independently dated to c. 39,300 calendar years ago (cal BP) (56–58), and represents a chronostratigraphic marker across parts of southern and eastern Europe as well as southwestern Asia. At Kostenki-Borshchevo, the sediments above the alluvium contain a long sequence of archeological layers of early to late Upper Paleolithic age, dating to > 42,000 to c. 14,000 cal BP (55, 59), stratified above and below the CI Y5 tephra. Most of the archeological layers represent primary buried horizons, and they include features, artifacts and fauna (49, 50, 60). The sites on the second terrace preserve early and mid-Upper Paleolithic assemblages above and below the CI Y5 tephra, in the Lower and Upper Humic Beds, including assemblages attributed to a local ‘Initial Upper Paleolithic’ tradition, the Aurignacian, the Gravettian,

and the local Gorodsovian (61). The Cover Loam (including the Gmelin Soil) is archaeologically extremely rich, including Eastern Gravettian artifacts and the famous large structure of Kostenki 1-Layer 1, dated to *c.* 29,000 cal BP (59), and the Epi-Gravettian features made of mammoth bones at Kostenki 11-Layer 1a, dating to between 19,000 and 14,000 cal BP (62, 63). Eight sites (K3, 4, 19, 21 and B1-4) are found in the soil and younger loess deposits of the first terrace (48) and preserve evidence of middle and late Upper Paleolithic occupations (64).

The Kostenki-Borshchevo sites were used recurrently for over 30,000 years, partly because of the presence of natural springs that attracted animals and people to the area. With their many features, they offer unique insights on the use of the landscape and the exploitation of the large mammals of the steppe-tundra from the earliest phases of the Upper Paleolithic onwards. In particular, the sites of K1, K12, K14 and K15 preserve concentrations of animal bones (horse in K14 and K15, reindeer in K12, mammoth in K1) that clearly indicate kill-butchery events (65). Together with the extensive, well-stratified chronological sequence covering all phases of the Upper Paleolithic, as well as the transition through the Last Glacial Maximum, the Kostenki-Borshchevo locality represents one of the key sources of information about the Upper Paleolithic of Eurasia and the Pleistocene modern human occupation of Eastern Europe.

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The site of Kostenki 14

The site of Kostenki 14 (K14), also called Markina Gora, is located on a promontory on the south flank of the Pokrosvskii Ravine (51, 63), where the sites K1, K12 and K16 are also found. K14 was discovered by P.P. Efimenko in 1928, who worked on the upper archaeological layers of the site; in 1953, Rogachev's excavations revealed the early Upper Paleolithic layers (51, 63). The site, which is extensive and covers hundreds of meters of sediments along the ravine, has been excavated since the 1950s through a set of trenches (Fig. S2). These can be separated into a western area (where most of the old excavations have taken place) and an eastern area of the post-1998 trench from the work of Sinitsyn and colleagues (51). Four cultural layers have been identified (Fig. S3), although because of the sloping deposition of sediments, these are not all equally visible at different parts of the site. Cultural Layer I (CL I), in the Cover Loam, dates to 27,600 – 26,500 cal BP (66), although this might be a minimum age (52); CL II and CL III are found in the Upper Humic Bed, above the CI Y5 tephra and are dated to 33,600-31,500

cal BP and 35,300-33,200 cal BP, respectively(52, 67); CL IV is in the Lower Humic Bed (LHB) below the CI Y5 ash deposit and dates to 32,800-31,800 cal BP (46). On the eastern slope within the LHB two horizons, named CL IVa and CL IVb, have been documented(51, 52, 67).

The oldest archaeological layer in the eastern part of the site, CL IVb, overlies the so-called 'Horizon of Hearths' (burnt reddish loam) and is buried on the sloping margins of a paleo-gully (67). CL IVb has been dated by 14C to 42,200 - 39,900 cal BP (52), although this might represent a minimum age for the assemblage. The underlying 'Horizon of Hearths' has been dated by 14C to 42,400 - 41,000 cal BP (52) and by OSL to 47,800 - 40,400 cal BP (48). A large number of lithic artifacts of typical Upper Paleolithic character (68) were recovered from CL IVb – based on the production of blades obtained unipolarly, including end scrapers, burins, splintered pieces, bifacial-oval tools, and a substantial bone and antler tool-kit (67, 69). The assemblage includes the head of a female figurine made on a mammoth tusk, and a pendant made on a shell of a *Columbellidae* gastropod, presently restricted to the Mediterranean, and suggesting long-distance contacts to the south. A human tooth, identified as modern (68) was also found in CL IVb.

Only a few lithic artifacts and faunal remains represent the Cultural Layer in the Fossil Soil (FS), dated by 14C to a minimum of 40,800 - 37,500 cal BP. The Cultural Layer IVa ("Horse Horizon"), also below the CI Y5 tephra and dated by 14C to 39,100 - 36,000 cal BP (52), preserves the remains of over fifty horses. These were found mostly broken, although some retained the original anatomical position, and given the extensive evidence of cut-marks, are suggestive of a preserved kill-butcher event (49, 65).

In the western part of the site, CL IV is a single layer located in the LHB, where early Upper Paleolithic artifacts (unipolar blades, end scrapers, burins, and retouched flakes and blades) and bone tools (an awl made from a horse phalange and fragments of rods with various cross-sections) were found (51).

Associated with the volcanic ash deposits, an Aurignacian layer (Cultural Layer in the Volcanic Ash – LVA) was documented in the eastern area of the K14 site. The finds include personal ornaments, abundant bladelets and tools like end scrapers (68).

CL III is a small assemblage including organic and lithic industries. The bone industry includes fragments of a rod with sub-rectangular cross-section and beads made on the long bones of birds. The lithic assemblage of CL III includes blades and broad end scrapers (51) and is undiagnostic in terms of specific affinities to known traditions.

The overlying CL II is a very rich assemblage with abundant organic tools as well as a huge lithic collection. The lithic technology is a flake-dominated one, and typical 'Upper Paleolithic' blades are missing. Various 'Middle Paleolithic' tool types (side scrapers, points, and knives) are present in the assemblage, which is currently assigned to the local 'Gorodsovian'. CL II is well-known for its bone tools, decorated bones and personal ornaments. Among them are 'shovels' made from mammoth long bones (51). The uppermost layer, CL I, consists of a large assemblage of mammoth bones and lithics attributed to the 'Kostenki-Avdeevo' culture (51).

The archeological remains include animal bones, features (such as hearths), ornaments, mobiliary art, as well as bone and stone artifacts, briefly described below. They also include one of the earliest modern human skeletons known from outside of Africa.

The Upper Paleolithic assemblages of Kostenki 14

The Kostenki sites preserve some of the most extensive Paleolithic records in Eastern Europe, but also show a considerable technological diversity. The different localities represent overlapping parts of a sequence extending from the very beginning of the Upper Paleolithic to its end in the region (>40,000 to 14,000 cal BP), but also indicate considerable pene-contemporary variation.

As mentioned in section S2 (*'The archaeological context of Upper Paleolithic ancient genomes'*), the early phases of the western Eurasian Upper Paleolithic (UP) are spatial and technologically complex. Three main groups of industries have been identified within the first Upper Paleolithic assemblages: the Initial Upper Paleolithic (IUP), the Aurignacian Complex (AC), and a number of industries known as 'transitional industries' or of very local character and/or undiagnostic features (e.g., (70, 71) and references therein). The latter ones are partly of unclear Neandertal or modern human association ((72) and references therein). Following Sinitsyn (46, 61), a local 'Initial Upper Palaeolithic' (IUP), an 'Early Upper Palaeolithic' (EUP) and a 'Mid-Upper Palaeolithic' (MUP) have been identified in the Kostenki-Borshchevo region. The 'IUP' is currently thought to fall into the chronological window > 40,000 cal BP and is found below the CI Y5 tephra deposits in the Lower Humic Bed (LHB). Archaeological assemblages belonging to this 'IUP' cluster are classified into two groups - those described as Spitsyanean, and the assemblage of K14-CL IVb. In the case of these two industries, which have only been described in the Kostenki-Borshchevo region and nowhere else, the label 'IUP' is largely a chronological attribution. It should be noted here that these Kostenki 'IUP' assemblages are quite different from the IUP techno-complex defined by (73) in terms of lithic technology, although further studies are needed to more precisely define these differences. The Kostenki IUP is a local description, whereas the formally defined IUP used more broadly is posited as representing a dispersal by modern humans into Europe (71, 74–78),

The EUP according to (61) is found within the chronological window between 40,000 and 34,000 cal BP and occurs below as well as above the CI Y5 tephra. Archeological assemblages within the EUP are attributed to the Aurignacian and the Streletskian traditions. While the Aurignacian is well known in most of western Eurasia, the Streletskian is a local industry, known from several sites in the Kostenki-Borshchevo locality and other regional localities. Within the schema of temporal phases of (61), the MUP dates to two separate time windows – first, between 34,000 and 30,000 cal BP, with assemblages attributed to the Gravettian and the Gorodsovian, and second, between 30,000 and 23,700 cal BP, with a range of localized traditions, including the evolved Gravettian.

In general, the Kostenki-Borshchevo region shows substantial variability in lithic industries within each phase. The co-existence of several UP techno-complexes is unique to Kostenki; some of these techno-complexes are not known outside the Kostenki-Borshchevo region (e.g., the Gorodsovian), while others are recorded all over western Eurasia (e.g., the Aurignacian). In terms of human behavior, the variability in material

culture production is poorly understood, as the meaning of these taxonomic units is unclear. It has been suggested by some (e.g., (50, 70) that the Gorodsovian could represent a functional facies of the contemporary Gravettian.

The spatio-temporal diversity of the Kostenki-Borshchevo Upper Paleolithic sequence illustrates the complex demography and mobility of early modern human populations in Eurasia, as well as preserving unique evidence of the recurrent use of particularly rich localities in the landscape of the northern plains, which may have acted as regional foci of population ranges at the time.

The Markina Gora skeleton

The skeleton from Kostenki 14 was discovered in 1954 by A.N. Rogachev in a trench on the western portion of the site. The skeleton, of a relatively short man (1.60 m) aged 20-25 years old (79), has a robust skull, with strongly developed supraorbital tori, a deep infraglabellar notch, and short face (Fig. S4). The skeleton was found in a deeply flexed position on its left side with the face to the north and the hands by the face (Fig. S5). The burial pit was characterized by steep walls and an oval shape, about 99 x 39 cm (50). Its long axis was East-West oriented. The skeleton was found at its base and associated with dark red pigment (especially around the skull). The only finds with the skeleton are a few lithic flakes and animal bones. Their presence could be causally linked to the burial event or be the result of rodent activity. Based on this and the non-diagnostic nature of the flakes, no direct association with a particular Paleolithic archeological tradition at the site is possible.

The burial pit's mouth underlies and is sealed by Cultural Layer III; the pit cuts through the CI Y5 ash layer and its bottom cuts into the top of the Lower Humic Bed. Therefore, the human remains can be stratigraphically placed as younger than Cultural Layer IVa, younger than the CI Y5 volcanic ash horizon, and older than Cultural Layer III. The skeleton has been directly dated to $33,250 \pm 500$ radiocarbon years before present (14C BP) (25) which is 38,684 - 36,262 cal BP (Fig. S6), and is thus consistent with its stratigraphic position originating above the CI Y5 tephra dated to c. 39,300 cal BP (56). The close proximity in age of the skeleton and the tephra containing artifacts attributed to the Aurignacian in the eastern part of the site (68) has led to the association between the two. However, CL III, above the skeleton, contains a more blade-based industry generally assigned to the MUP, with possible affinities with the overlying Gorodsovian (CL II). Given the diversity and stratigraphic complexity of the lithic material preserved in the early horizons at Kostenki 14, a general 'Early Upper Paleolithic/EUP' archeological context for the Markina Gora skeleton is used here.

S2: The archaeological context of Upper Paleolithic ancient genomes

The context in which hominin ancient genomes should be assessed is that of human paleontology and Paleolithic archeology. The former is relatively scarce, making archeology the best indicator of past population parameters. However, as one of the main aims of current ancient genomics is to identify biological and geographical lineages, linkages to archeology are constrained by the fact that these data are not necessarily direct or simple indicators of prehistoric population distributions, contact, cultural affinities and isolation.

The relevant Eurasian Paleolithic entities – i.e. those likely to inform about Neandertals, Denisovans, other archaic populations and modern humans in Eurasia in the last 100,000 years are the Middle and Upper Paleolithic. Late Eurasian Middle Paleolithic (MP) sites are associated with Neandertals. Defined by an overall particular suite of behaviors, the MP ranges in age from over 200,000 to *c.* 40,000 cal BP (80–82), although the localised late survival of Neandertal groups until 30,000 cal BP has been reported (e.g., (83)). The Upper Paleolithic (UP) is known from *c.* 50,000 cal BP in southwest Asia and from *c.* 48,000 cal BP in Europe(71, 75, 76, 78, 84–87), although in some parts of Europe and Asia it does not become predominant until after 40,000 cal BP. The Upper Paleolithic is considered to record the modern human colonization of southwest Asia, Europe and northern Asia (although direct skeletal associations are few(72) and references therein). The transition between the two can be sharp (particularly in western Europe), but less straightforward in other places, and the presence/absence of Upper Paleolithic technologies is not necessarily a marker of modern or archaic hominins (42). It is, however, the units within each of these that provide the detailed context to which K14 and other ancient genomes discussed here genomes relate.

For tracking the dispersals of modern humans in Eurasia, the characteristics of the Upper Paleolithic are the main source of information. Terminology for the chronologically overlapping but technologically distinct parts of the first lithic assemblages identified as UP is not universal. For the purposes of the brief summary here we divide the Upper Paleolithic into three informal units that are essentially chronological – early, middle and late.

The Early Upper Paleolithic (EUP) covers the period from *c.* 50,000 cal BP to around 30,000 cal BP and encompasses a set of industries that are technologically variable. We describe here the archeological entities involved, largely defined on the basis of lithic technology, and which are relevant to the associations of the K14 skeleton. In addition to these are what have been referred to as ‘Transitional Industries’ (e.g., Châtelperronian, Szeletian, Uluzzian) (72). The position of these industries in relation to the Middle and Upper Paleolithic transition has been extensively debated, and their association with Neandertal remains in some cases (e.g. Châtelperronian) and possibly modern humans in others (e.g. Uluzzian, Lincombian) complicate interpretations even more. As these are not found at Kostenki-Borshchevo, they will not be discussed further.

What is probably the earliest of the Western Eurasian EUP is referred to as the 'Initial Upper Paleolithic' (IUP), defined technologically as a combination of Levallois production with prismatic blade elements (73). Regional variants exist, for example the Emiran in southwest Asia (88), the Bohunician in Central Europe (84), and a Siberian version known from the Altai Mountains and Baikal region (from the sites of Kara-Bom, Makarovo-4 and Varvarina Gora, for example; (89, 90). The earliest dates for the 'IUP' may be older than 50,000 cal BP in southwest Asia (Boker Tatchit, (88)), 49,000-48,000 cal BP or 47,500 cal BP in Europe [depending on whether they pre-date (71) or coincide (78, 85) with the Greenland Interstadial 12 at Bohunice], and as early as 45,000 cal BP in Siberia (89, 91). Despite these very early occurrences, most of the dates center on the period 45,000 - 40,000 cal BP (92); there is no evidence for its persistence beyond 35,000 cal BP. The industry from Kostenki 14 CL IVb (underlying the skeleton and dated to 42,200 - 39,900 cal BP, (52)) has been referred to as IUP (61) but using a different and broader definition than that of Kuhn and colleagues (73).

The key elements of the Western Eurasian 'IUP' are its very extensive geographical distribution (southwest Asia, southeastern and eastern Europe, and Central Asia), mixed technological status (i.e., persistence of Middle Paleolithic aspects in the technology), its early age and – at some sites - prolonged existence (>10,000 years). This prolonged existence might also be an artefact of dating inaccuracies. The 'IUP' has been proposed as the signal of the earliest modern human expansion into Europe and northern Asia (71, 74–78, 93). Nevertheless, the archeological record for the transition between the Middle and Upper Paleolithic is not clear-cut, revealing both geographical and spatial variation in the extent to which Upper Paleolithic elements become incorporated in lithic assemblages associated with late Neandertals (as seen for example in the Châtelperronian), or to which Middle Paleolithic aspects of the technology persist at early modern human sites (as seen for example in the 'IUP' sites).

A second element of the Western Eurasian EUP is what has been referred to as the 'Aurignacian Complex' *sensu lato*. However, the linkage between the Aurignacian *sensu stricto* and the other industries implied by the shared name is not accepted by all or fully demonstrated. The Ahmarian-Proto-Aurignacian variant (APA) is characterised by a greater dependence upon large bladelet technology than found in the 'IUP' (but lacking the specific markers of the Early Aurignacian), and includes industries like the Ahmarian from the Levant and Anatolia (94), the Kozarnikan from southeastern Europe (95), and the Archaic or Proto-Aurignacian from southern Europe (96). The APA ranges in date from c. 47,000 to 35,000 cal BP (72, 86, 94, 97, 98). These technological entities are strongly Mediterranean in Europe, with little evidence of an existence north of the Alps, but this partly depends on whether the term is broadened to include a greater range of industries. APA assemblages have also been identified as far east as the Zagros, with affinities to the Kozarnikan (99, 100).

The Aurignacian is the major, widespread EUP techno-complex of Western Eurasia. It is homogenous and unified technologically and culturally, and has been proposed as an ethnically-based entity (101). It is characterized by split-based bone points, carinated end scrapers, and retouched bladelets, and has an associated complex of mobile art and

personal ornaments. The earliest Aurignacian is found at Willendorf II dated to 43,500 cal BP (87) the youngest *c.* 32,000 cal BP (102–106). The Aurignacian is a western Eurasian phenomenon, occurring in western, central and eastern Europe, as well as southwest Asia, and it is found in both the warmer and colder parts of the continent. Kostenki is probably one of the most easterly occurrences of the Aurignacian, and the K14 skeleton occurs in a pit cut through an ephemeral, ashy layer in which Aurignacian lithics were identified in the eastern part of the site (61).

In Northern and Eastern Asia the emergence of the Upper Paleolithic is not so well-known; however, what we do know suggests a connection with parts of the Western Eurasian EUP – the IUP and the APA techno-complexes from southwest Asia and Kostenki (93, 107); but see (92)). Earliest regional cases of the northern and eastern Asian EUP include Kara-Bom in the Altai (49,000 - 45,000 cal BP), Makarovo-4 in the Cis-Baikal (>43,000 cal BP), Varvarina Gora and Kamenka in the Trans-Baikal (>40,000 cal BP), Tolbor 4 in north-central Mongolia (possibly >44,000 cal BP), and Shuidonggou in north China (43,000 - 40,000 cal BP) (89, 91, 108–112). Lithic industries from these sites center on production of blades from parallel, “flat-faced” blade cores, a Levallois-like technology albeit on simply prepared cores with smooth platforms (90, 92, 113–115). Like the EUP in western Eurasia, the lithic tool-kit is composed of distinctive endscrapers, burins, pointed blades with invasive ventral retouch, and occasional bifaces, as well as side scrapers, notches and denticulates (113). Many of these sites also contain bone, antler and ivory tools, ornaments including ostrich-eggshell pendants, ochre concentrations, occasional zoomorphic statuettes, and possibly a musical flute (116–118). These features are obviously distinctive from the region’s earlier Middle Paleolithic, and together they indicate the presence of a well-established EUP tradition across the vast steppes of inner Asia 45,000 - 35,000 cal BP. Whether modern or archaic humans created this record cannot be discerned at present, because no diagnostic human remains have been reported from any inner Asian EUP site, and the two earliest cases of supposed modern humans from Siberia (the Baigara talus, >47,000 cal BP (119) and the Ust’-Ishim femur, 45,000 cal BP (120)) were in re-deposited contexts devoid of artifacts. Nonetheless, the Kostenki genomic analysis reported here implies the existence of a widespread western Eurasian modern human population that extended eastward to Lake Baikal during MIS 3, and the inner Asian EUP may represent the archeological manifestation of that population.

The key elements of the period from about 50,000 to 32,000 cal BP (EUP) are that there is evidence for different Upper Paleolithic traditions, with quite distinctive distributions but overlapping in time. There is also evidence to suggest a considerable difference between Eastern and Western Eurasia, and a degree of convergence in technological innovations (e.g., (121)). Views differ considerably as to whether the patterns of similarities and differences among various industries that can be observed in the early phases of the Upper Paleolithic represent population dynamics, or local *in situ* and variable, convergent, adaptive change among modern human groups at the time. The homogeneity of the Aurignacian may be the one case indicative of cultural contact across a large area.

By 32,000 cal BP, there is a new form of technology, and a new widespread tradition, the Gravettian, part of the middle Upper Paleolithic (MUP). This is, like the Aurignacian, highly uniform, characterized by blades and bladelets, steeply backed, and often associated with a distinctive set of figurines. The Gravettian is widespread, from western Europe to Russia, with some indications of extending into Siberia (Mal'ta), and suggestions that it can be divided into an Eastern and Western form. The ancient genome extracted from the Ma'lta boy indicates ancestry to both Europeans and Native Americans, the latter not shared by later European Mesolithic groups.

The period of the Gravettian coincides with a major deterioration in climate that leads to the Last Glacial Maximum (LGM, 25,000 – 15,000 cal BP, with a peak at 20,000 - 18,000 cal BP). Archaeologically, the LGM *sensu lato* is associated with depopulation of northern latitudes and demographic fragmentation (Lahr & Foley 2003), with sites becoming scarce, and local traditions developing (e.g. the West European Solutrean)(122).

In Siberia, MUP techno-complexes replace those of the EUP around 34,000 cal BP, but there is much variation in lithic industries from then until the LGM. Considering only well-dated sites in the Yenisei and Baikal regions (e.g., (117, 123, 124)), bladelet technologies become much more common, with full-blown microblade inset technologies appearing just before or after the LGM. This period of climatic deterioration paradoxically is often referred to as the “Golden Age” of the Upper Paleolithic in the area, because many of Siberia’s MUP sites contain incredibly rich inventories of hearths and dwelling features, bone tools, items of personal adornment, and even small female statuettes, or “Venuses”, harkening again a connection across the mammoth-steppe to western Eurasia. The Mal'ta site represents the “type site” for this phase of the Upper Paleolithic, and for decades archeologists and biological anthropologists have hypothesized a link to the Gravettian World far to the west (125–127). Whether the Kostenki-Mal'ta connection is rooted in an eastward expansion of Gravettian-like cultures, or earlier EUP cultures (as argued above), cannot be determined without genomic data from a northern and northeastern Asian EUP individual.

From 15,000 cal BP, climatic conditions improve substantially, although not consistently, as there is a short period of low temperatures between 12,800 - 11,500 cal BP known as the Younger Dryas. The post-LGM archeological record (the Late Upper Palaeolithic (LUP)) demonstrates the re-population of Europe (128, 129) presumably from southern refugia, such as those proposed in Spain, Italy, southeast Europe and western Asia. The western Eurasian postglacial archeological record is normally divided into the late Upper Paleolithic or Epi-Paleolithic, which sees a large number of local traditions develop (Ahrensburgian, Hamburgian, Epi-Gravettian, Magdalenian, etc.), and the Mesolithic (after 10,000 cal BP), the latter being early Holocene cultural entities (e.g., Azilian, Maglemosian, Tardenoisian). These have generally been considered to represent population expansions within Europe, in contrast to the subsequent expansion of farmers from southwest Asia (Neolithic). The ancient genomes from La Braña (Spain), Loschbour (Luxembourg), and Ajvide and Motala (Sweden) are those of Mesolithic hunter-gatherers.

The main aspects of the end of the Pleistocene and the Holocene are the impact of the LGM, and the re-growth and expansion of populations as the climate warmed after 15,000 cal BP, producing an entirely new configuration of populations prior to the arrival of farmers in Europe from the Middle East and their subsequent expansion eastwards. Post-glacial hunter-gatherer populations of Europe expand from glacial refugia, and their distribution, demography and density across Eurasia would have varied considerably, producing very different interactions and genetic outcomes in different areas (*130*). In comparative terms, it is likely that the level of depopulation was higher in Western Europe than in Asia, and continuity was greater in Asia, but it should be noted that the latter is vast by comparison, and less well researched.

S3: Samples and laboratory methodologies applied

Samples

The K14 sample used in this study was obtained from the **left tibia (dorsal side of the shaft)**. Note that the tibia was washed before sampling. As described in S1, the skeleton has been directly dated to 38,684 - 36,262 cal BP. According to the complete mitochondrial sequence of the tibia that has been characterized in previous ancient DNA analyses, the K14 individual belonged to mitochondrial haplogroup U2 (*131*). Two other samples, K1 and K15, were also analyzed but endogenous DNA contents and levels of contamination by modern humans were found incompatible with the characterization of the whole genome sequence by shotgun sequencing.

DNA extraction

All pre-PCR steps were conducted at the Centre for GeoGenetics, University of Copenhagen, Denmark, in state-of-the-art ancient DNA facilities dedicated to the analysis of ancient hominin remains, and separated from any building where fresh DNA or post-PCR DNA is processed. Each extraction session included a mock extraction blank where no bone powder is added to the extraction reagents.

We extracted 89 to 260 mg of bone powder per extraction session, using either a microdismembrator or low speed drill (Table S1). We first followed the extraction procedure described in (*132*), which is based on DNA binding to silica pellets in solution. We also performed extraction following the procedure described by Dabney and colleagues (*133*), which is tailored to ultra-short DNA fragments and performs DNA purification on MinElute (Qiagen) silica-columns (*133*).

When using silica pellets, we performed a pre-digestion of the sample by incubating in 5 ml digestion buffer (0.45 M EDTA, 0.25mg/ml proteinase K, 0.5% N-laurylsarcosyl) at 37°C for 30 min or 4h. After spinning 2 min at 2,000 rpm, the supernatant, representing the first fraction, was transferred into a new falcon tube. The remaining pellet was further digested for 24h at 37°C in 5 ml fresh digestion buffer. After spinning 2 min at 2,000 rpm we kept the supernatant, which represented the second fraction. Both first and second fractions were incubated with 50 µl freshly prepared silica pellets and 20 ml of binding buffer (5M Guanidinium thiocyanate, 50 mM Tris, 25 mM NaCl, 15 mM EDTA, 0.8 % TritonX-100, pH 4.0-5.0) for 3h at room temperature. The supernatant was discarded and pellets were washed twice with 1 ml of fresh 80% ethanol before eluting the DNA in 120-130 µl EB incubated 30 min at 37°C.

For the silica column-based approach (*30*), we pre-digested the sample in 1mL extraction buffer (0.45M EDTA, 0.25mg/mL proteinase K) for 1h at 37°C. After centrifugation for 2 min at 16,000g, we discarded the supernatant and incubated the pellet for 36 h at 37°C in 1mL of fresh extraction buffer. After centrifugation for 2 min at

13,000 rpm, we transferred the supernatant mixed with 13 mL of binding buffer (5M guanidine hydrochloride, 40% isopropanol, 0.05% Tween 20, 90 mM sodium acetate) on a Zymo-Spin V reservoir (Zymo Research) fitted on a MinElute column (Qiagen). The reservoir-MinElute device was centrifuged at 3,000 rpm for a total of up to 8 min. The MinElute column was then placed on a collection tube and centrifuged at 6,000 g for 1 min. The column was washed twice with 750 µl PE and dry-spin at 13,000 rpm. The DNA was eluted twice in 28 or 35 µl EB after 10 min incubation at 37°C.

All extracts were stored at -20°C in siliconized tubes. Each of the following steps (methylated DNA enrichment, USER treatment, library building and library PCR enrichment) was accompanied by a negative control where the sample is replaced by EB buffer, until the library-building step. Interestingly, DNA libraries constructed on USER-treated extracts generated following in-solution DNA purification showed higher variance in endogenous DNA content (average = 0.820%, range = 0.117-8.029%) than those constructed on USER-treated extracts obtained following purification on silica-columns (average = 0.308%, range = 0.296-0.485%).

Methylated DNA enrichment

It has been recently shown that methylated cytosines can survive after death and be characterized either directly (134, 135) or indirectly by exploiting patterns of post-mortem DNA degradation (136, 137). Methylated cytosines can be used as targets for enriching DNA extracts in DNA fragments of vertebrate origin, and therefore preferentially get access DNA material of human origin. Microbial DNA indeed often dominates ancient DNA extracts, but generally do not show high-densities of 5methyl-cytosines (^{5m}C) at CpG sites in contrast to human DNA. Therefore, we attempted to enrich a fraction of our DNA extracts for ^{5m}CpG sites using the EpiMark Methylated DNA Enrichment kit (NEB, reference E2600) following the manufacturer's instructions, except for the slight modifications described below. A total of 50 µl of DNA extract was incubated for 20 min at room temperature with 10 µl of pre-bound MBD2-Fc to Protein A Magnetic Beads, in a total volume of 100 µl 1X Bind/Wash Buffer. Beads were concentrated using a magnetic rack and the supernatant, containing the un-methylated DNA fraction, was discarded. Beads were washed twice with 950 µl of a 0.4M KCl solution and methylated DNA was eluted in 150 µl of 1M KCl, after 5 min incubation at room temperature on a rotor. Samples were purified on a MinElute column and eluted in 32.5 µl EB after 15 min incubation at 37°C, and further processed for USER treatment.

USER treatment

We removed the most frequent *post-mortem* DNA damage from 11 out of the 13 DNA extracts (previously enriched or not for methylated DNA), namely cytosines that have been deaminated into uracils, following incubation with Uracil DNA glycosylase and DNA glycosylase-Lyase Endonuclease VIII, as proposed in (137). More specifically, a volume of 32.5 µl of the ancient DNA extract was incubated with 10 µl of USER enzyme mix (1U/ µl, NEB reference M5505) for 3h at 37°C. If not processed

immediately for sequencing library building, the repaired DNA solution was stored at +4°C for no more than 16h.

Library building and sequencing

Illumina sequencing libraries were built following a protocol described in (138) and based on an end-repair step of 21.25 µl of the DNA solution, a ligation step with 12.5 pmol blunt-ended adapters (139) and an adapter fill-in step. We used the NEBNext DNA Library Prep Master Mix Set for 454 (NEB reference E6070) without the ssDNA isolation module. Libraries were enriched and indexed by performing 8 to 14 PCR cycles in 50 µl reactions using 5U of the AmpliTaq Gold DNA polymerase (Life Technologies) as described in (140). After purification on MinElute columns and elution in 20 µl EB following 15 min incubation at 37°C, library concentration and size were checked on a Bioanalyzer 2100 High-Sensitivity Assay (Agilent). Whenever concentrations were not directly compatible with Illumina sequencing, the purified PCR product was re-amplified in four parallel 50 µl reactions for 6 or 8 additional cycles, before being pooled, purified and checked on the Bioanalyzer again.

Final libraries were pooled with non-human indexed samples and sequenced 100SR or Rapid 75PE at the Danish National High-Throughput DNA Sequencing Centre, University of Copenhagen, Denmark, on a HiSeq 2500 (Illumina).

S4: Read processing and mapping

Illumina reads were processed and aligned to the human reference genome hg19 available from the UCSC genome browser (<http://hgdownload.cse.ucsc.edu/goldenPath/hg19/chromosomes/>) using the PALEOMIX pipeline (*141*) with default parameters, except for the minimal mapping quality threshold, which was set to 30, and seeding, which was disabled. PALEOMIX implements in an automatic manner all the analyses described in (*132, 142*), which enabled previous characterizations of ancient and modern genomes. Briefly, Illumina sequencing reads were trimmed for adapter sequences using AdapterRemoval (*143*). When overlapping for at least 11 nucleotides and with a maximal edit distance of 1, paired-end reads were collapsed and base quality-scores at overlapping positions were recalculated using the quality scores of both reads at each overlapping position (*132*). Collapsed reads were further treated as single-end reads. Trimmed reads and collapsed reads were aligned against hg19 using bwa version 0.5.9-r26-dev (*144*), filtered for duplicates and re-aligned around indels using GATK (*145*). Uncollapsed read pairs were filtered from the final BAM alignment file, as this fraction corresponds to relatively long templates and is therefore likely to be enriched in contaminating templates of modern origin. We repeated the full procedure to generate read alignments against the revised Cambridge reference mitochondrial sequence (rCRS, Accession Nb. = NC_012920). Summary statistics, including the total number of Single End (SE) and Paired-End (PE) reads generated, endogenous DNA content per library (the fraction of high-quality hits mapping uniquely against the reference genomes considered), and the contribution of each library to the final coverage estimate, were directly obtained from PALEOMIX (Table S2).

The existence of nucleotide mis-incorporation and DNA fragmentation patterns, which represent the signature of post-mortem degradation reactions (*33*) was investigated using alignment BAM files and mapDamage2 (*146*) DNA libraries that were not USER-treated showed a progressive decline of C→T substitution rates from read starts, mirrored by a progressive increase of G→A substitution rates towards read ends (Fig. S7). Additionally, genomic positions preceding read start coordinates were found to be enriched in purines, particularly in Guanine residues. Genomic positions following read end coordinates were found to be enriched in pyrimidines, particularly in Cytosine residues. This is in agreement with previous reports, suggesting depurination as the main driver for post-mortem DNA degradation. Read alignments from USER-treated DNA libraries showed C→T and G→A mis-incorporations restricted mostly to read-starts and read-ends (Fig. S8), in line with previous observations suggesting low base excision performance for bases located at the very ends of ancient DNA molecules (*139*). The base composition of the genomic coordinate preceding read-starts was enriched in cytosine residues, as expected from the enzymatic fragmentation performed, which takes place 3' of uracil residues. Overall, this indicates that USER treatment significantly reduced the level of nucleotide-misincorporations resulting from post-mortem DNA decay.

S5: Mitochondrial DNA analyses

We used high-quality hits against the rCRS mitochondrial genome to reconstruct the mitochondrial sequence of the K14 individual. Briefly, we generated a VCF file to identify sequence variants using samtools and bcftools (*147*), and called a final mitochondrial consensus sequence based on a majority rule and requiring a minimal depth-of-coverage of 3. The mitochondrial sequence was identical to the one previously reported by Krause and colleagues (*33*), thus providing independent replication of our results and supporting the authenticity of the data generated. We then mapped all sequence reads against the K14 mitochondrial sequence using PALEOMIX and the methods described above. This provided one of the two input files for contamMix (version 1.0-10). This software was kindly provided by Dr. Philip Johnson and implements the procedure described by Fu and colleagues (*148*) to estimate the level of DNA contamination based on mitochondrial read alignments, assuming that the data consists of a mixture of endogenous sequence reads and contaminants. The second input file used by contamMix consists of an alignment of 311 whole mitochondrial genomes described in (*33*) appended with the K14 sequence. Contamination levels were estimated using 4 MCMC chains of 50,000 iterations each. Contamination levels estimated on libraries showing less than 100 mitochondrial hits should be disregarded, as not enough information was available to achieve proper estimates. The contamination level of the 8 libraries that were chosen for downstream analysis are shown in (Table S3).

S6: Error and X-based contamination estimation

The error rate was estimated by using a method similar to (149). This method is based on the assumption that the number of derived alleles is the same for all individuals. By comparing the sample of interest and a ‘high quality’ sequenced individual to an outgroup (the chimpanzee), the number of derived alleles can be assessed. The excess of derived alleles in the sample of interest can then roughly be interpreted as relative error rates. For a high quality sample we used an individual from the 1000 genomes project (NA12778.mapped.ILLUMINA.bwa.CEU.low_coverage.20130415.bam). After removing reads with a mapping quality below 35 and base quality below 35, a single base was sampled for each position of the high quality genome. We estimated both the type specific error rates and the overall error rates (Fig. S9) for all USER libraries. For this analysis we discarded reads with a mapping quality below 30 and bases with a quality score below 20 (0.1% and 1% error rate respectively). The method is described in details in the supplementary of (132), and is implemented in the software ANGSD.

From Fig. S8 we observe that the USER treatment still has increased error rates for the first base pairs in each end. We therefore applied our error estimation by discarding the first 1 to 5 base pairs from each end (Fig. S10). Which shows decreasingly lower error rates and we therefore used the five base pair trimmed version of the data in all subsequent analysis. We also estimated the type specific error rates for all ancient samples (Fig. S11) and the overall error rates (Fig. S12). The analysis was performed using the software ANGSD.

X chromosome-based DNA contamination estimation

We estimated contamination of the Kostenki sample using the method described in (150). This method works for chromosomes that exist in one copy for which we would expect to observe a single base for all sites. Hence for male human samples, like the Kostenki sample, it can be applied to the X chromosome. If multiple different base types are observed at a site, it is interpreted as either the result of sequencing errors or contamination. However, note that human contamination can only cause base discordance at polymorphic sites, whereas it can be assumed that sequencing errors lead to the same discordance rate in polymorphic sites as in their neighboring non-polymorphic sites. For this reason, presence of human contamination will cause an excess base discordance in polymorphic sites compared to their neighboring non-polymorphic sites. The estimation method we used for our analyses takes advantage of this logic: it estimates the extent of contamination based on a comparison of base discordance in a set of known polymorphic sites on the X chromosome to the base discordance rates in the 8 nearest sites to each of polymorphic sites; 4 sites to each side. For more details about the method see the supplementary of (150).

The set of known polymorphic sites used in our analyses was identified using 60 unrelated CEPH individuals from the HapMap phase II release 27 data (151). The set was pruned such that no polymorphic sites were less than 10 bases apart. Allele frequencies were also estimated in these individuals.

Before performing the analyses the following filtering was applied to the Kostenki sample:

- The X chromosome was trimmed to remove the regions that are homologous with the Y chromosome (first and last 5Mb).
- The sites were then filtered based on mappability (100mer), so that no region will map to another region of the genome with an identity above 98%
- Reads with a mapping quality score of less than 30 and bases with a base quality score less than 20 were removed.
- Sites with a read depth of less than 2 or above 40 were removed

The analyses were performed using ANGSD and gave contamination estimates of 2.0% when using all reads (Method 1) and when sampling a single read for each site (Method 2), respectively (Table S4).

Contamination was also estimated for the samples Loschbour, Motala2, Motala 3, Motala6, Motala9 and Motala12 (Table S5) using the same approach. It was not possible to do so for the samples LBK, Motala1 and Motala4, because they are females. Based on (1) the endogenous content (Table S2), (2) the error rates per library (Fig. S9), the contamination estimates from both the X-based and the mitochondrial analysis we choose eight libraries for downstream analyses.

S7: Y chromosome analysis

We used three publically available datasets (152–154), to infer the chromosome Y haplogroup for K14 (Fig. S13, Table S6). Each dataset consists of a table of SNPs that are phylogenetically informative for a particular haplogroup (hg). For each SNP in the datasets, we then determined whether K14 carries the derived allele by selecting the most frequently occurring base from all covering reads, discarding reads with a mapping quality score below 30 and a base quality score below 30.

For the data from (152) and (153), the informative SNPs are mutations on the branches of the phylogenetic tree relating the individuals sequenced in the respective studies. They therefore do not necessarily reflect diagnostic mutations for a particular haplogroup defined in ISOGG. Nevertheless, they allow us to determine the likely branching point of K14 simply by counting how often K14 matches the derived allele at each branch in the tree. Results for both of these datasets clearly show that K14 carries the derived alleles for all SNPs on branches ancestral to hg C, but ancestral alleles for the branches leading to more derived haplogroups (Fig. S13). Furthermore, K14 carries the derived allele for four hg C mutations in ISOGG (P255, V183, V199, V232) (Table S6). The MHG

individual from La Braña (22) carries the same derived mutations, suggesting that both are members of a closely related lineage within hg C.

S8: Array genotype and whole genome reference data

Array genotype data:

We included as reference dataset the HGDP data (155) and several other datasets (127, 156–162) that were publicly available from the Estonian Biocenter for download (<http://evolbio.ut.ee>). We restricted all analyses to populations that had at least 3 individuals. This joint dataset had 2061 individuals from 167 contemporary human populations, and, when combined, gave rise to 514,968 SNP sites.

Whole genomes:

For the modern genomes, we used the VCF files (called genotypes) from two studies (34, 127).

For the ancient genomes we combined data from (127, 163–165), i.e., data for the following individuals: MA1, Lorschbour, La Brana, Motala, Ajv58, Gok2, Iceman, Stuttgart.

When analyzing the whole genomes jointly, we discarded sites that were invariant in the high depth genomes.

Merged genotype and whole genome data:

For both array and whole genome datasets, we merged all ancient genomes with the genotype data by using SAMtools (147) and by sampling a random read for each ancient sample for each SNP position, discarding reads with a mapping quality score below 30 and a base quality score below 30, as well as alleles that did not match either of the observed alleles in the reference datasets.

These datasets were used for model-based clustering analyses (SOM section S10), Principal Component Analyses (SOM S11), the calculation of D -statistics, f_3 - and f_4 statistics (SOM section S9), TreeMix (SOM section S12), as well as for identifying genomic blocks of archaic hominin origin. (SOM section S13).

S9: Analysis of shared ancestry between K14 and modern populations with f_3 , f_4 and D statistics

“outgroup” f_3 and D -statistics reveal that K14 is most closely related to Northern Europeans

We computed an ‘outgroup f_3 -statistic’ to obtain a statistic that is informative of the genetic relatedness between a particular sample and each modern population in a reference set. A positive deviation from zero is a function of the shared genetic history of two populations A and B in their unrooted history with the outgroup O . We used the estimator suggested by (36)

$$f_3(O; A, B) = \frac{\sum[(k_O - k_A)(k_O - k_B) - \hat{h}_O/n_O]}{\sum 2\hat{h}_O}$$

where

$$\hat{h}_O = \frac{k_O(n_O - k_O)}{n_O(n_O - 1)}$$

and k_O is the count of allele 1 (arbitrarily chosen) in the outgroup, k_A and k_B are the counts in populations A and B , and n_O is the total number of alleles in the outgroup at a particular SNP, summed over all SNPs. Standard errors for the f_3 estimates were computed with a jackknife approach using blocks of 5Mb as suggested in (36).

We computed this statistic with the K14 individual as population A , one of 167 contemporary populations as B and an African population, Mbuti Pygmy as O . Europeans (Fig. 1C;1D), and in particular Northern Europeans, show the greatest affinity to K14, with a lesser degree of affinity in Central Asians (Fig. S14). When K14 is directly compared to other ancient individuals, using f_3 (Mbuti Pygmy; K14, Ancient), MHGs (Loschbour, La Braña) had the highest affinity to K14, suggesting shared ancestry of these ancient individuals with K14 (Fig S14). We also repeated the “outgroup” f_3 analysis for each ancient individual. Overall, the patterns of shared ancestry for K14 are similar to those observed for MHGs (La Brana, Ajv58, Loschbour) and MA1 (Fig. S15), except for the latter’s additional strong genetic affinity with Native Americans, which is unique to that genome.

We further explored the relationship between K14 and contemporary populations by computing D -statistics (36),

$$D(A, B; X, Y) = \frac{\sum[(p_A - p_B)(p_X - p_Y)]}{\sum(p_A + p_B - 2p_A p_B)(p_X + p_Y - 2p_X p_Y)}$$

where p_A , p_B , p_X , and p_Y are the frequencies of allele 1 (arbitrarily chosen from the two alleles present) in populations A , B , X , and Y , summed over all SNPs. Standard errors

for the D estimates were jackknifed over 5Mb blocks. Comparisons involving multiple ancient genomes were restricted to transversion polymorphisms.

We computed this statistic with Mbuti Pygmy as A , K14 as B , and all possible pairs of contemporary populations as X and Y . This analysis confirmed K14 to be significantly closer to Europeans than populations from other geographic regions (e.g., $Z = 12.1$, (Han, Lithuanians); Table S7), in all datasets (Table S7-S9). Within Europe, Northern Europeans also appear significantly closer to K14 than southern Europeans ($Z = 6.7$, (Sardinians, Lithuanians)) (Tables S7; Fig. S16).

f-statistics results are robust to contamination from modern humans

We used two complementary approaches to confirm that the key results described above are robust to contamination from modern DNA. First, we repeated the “outgroup” f_3 analysis on a dataset filtered for reads of likely ancient origin using PMDTools (166). The model implemented in PMDTools relies on post-mortem DNA damage substitutions (C>T / G>A) to calculate a score for the likelihood of a read to originate from an ancient DNA molecule. Since the K14 libraries were treated with USER to reduce the level of nucleotide misincorporations, we used an untrimmed BAM file to maximize the amount of data available for this analysis. Filtering reads with PMD scores > 3 , we obtain 49,050 SNPs for the merge with the reference dataset, corresponding to a ~ 10 fold reduction compared to the full dataset. Despite this significant reduction, we find that “outgroup” f_3 scores for the filtered BAM are highly correlated with the full dataset for all test populations. The only exception is specific to the Iceman, which appears slightly off the slope formed by the other populations (Fig. S17).

Second, we calculated contamination-corrected D -statistics of the form $D(\text{Mbuti Pygmy}, \text{K14}; \text{Sardinians}, \text{Lithuanians})$ following (127). Assuming that the contamination originated from an individual with Russian ancestry, we estimated $D_{\text{corrected}}$ as

$$D_{\text{corrected}} = \frac{D_{\text{K14}} - cD_{\text{Russian}}}{1 - c}$$

where c is the rate of contamination, D_{K14} is the statistic obtained with K14, and D_{Russian} is the statistic obtained using a randomly sampled individual from the Russian population instead of K14. Fig. S18 shows the result for $D_{\text{corrected}}$ for contamination rates up to 0.5, demonstrating that even substantially higher rates than the one observed have only marginal effects on the value of the statistic. Intuitively, the reason for the negligible effect is that the value of D_{Russian} (0.019) is not much greater than D_{K14} (0.011), which means that large values of c are necessary to cancel out the signal of D_{K14} .

Contemporary non-Africans are closer to MHGs and MA1 than K14.

We calculated D -statistics of the form $D(\text{Mbuti Pygmy}, \text{Modern}; \text{Ancient}, \text{K14})$, to test whether K14 and an ancient individual form a clade with respect to a modern population. We find that all contemporary non-Africans, except Australo-Melanesians, are closer to either Mal'ta (MA1) or MHGs than to K14, whereas they are equally distant to NEOL and K14 (Fig. S19; Tables S10-S11). A parsimonious explanation would be

gene flow from a previously suggested “basal Eurasian” lineage associated with Neolithic farmers into K14, consistent with results from the model-based clustering (SOM S10).

f_4 and “admixture f_3 ” statistics show HG ancestry in Siberians from Yenisei basin

We used f_4 statistics of the form $f_4(\text{Sardinian}, \text{Ancient}; \text{Modern}, \text{Papuan})$ to measure whether a modern population shares more alleles with contemporary Europeans or an ancient genome. We find that all Siberian and East Asians are equally distant from western MHGs (Fig. 3D, Table S12), supporting the postulated early split between East Asians and western Eurasians. In contrast to MHGs and MA1, many Siberian populations are genetically closer to contemporary Europeans (Sardinians) than to K14 ($3.1 < |Z| < 9.9$), particularly those from the Yenisei and Ob’ basins (e.g. Shors, $Z = 8.0$) (Table S12). Furthermore, these populations derive parts of their ancestry from a European “hunter-gatherer” (HG) component inferred in the ADMIXTURE analysis (Fig. S20), with populations showing higher “HG” ancestry proportion also being closer to contemporary Europeans using the f_4 statistic (Spearman $\rho = 0.96$, $p = 3.0 \times 10^{-18}$, Table S13).

To formally test for admixture in the modern Siberian populations, we calculated “admixture” f_3 statistics of the form $f_3(\text{Test}; A, B)$ as described above (replacing the outgroup with the test population). A significantly negative value of this statistic is evidence for admixture in the test population related to two source populations A and B. We calculated the statistic for all pairs of source populations A and B, which also allows to infer which pair of populations are the best proxies for the mixing populations, i.e. which pair shows the lowest value of f_3 (163).

For populations from the Yenisei and Ob basins, we find significant evidence for admixture with a variety of Siberian and European source populations (Table S14). The best pair of source populations (i.e., the most negative f_3 statistic) involves Swedish MHGs (Motala, Ajev58) and Evens (a northeast Siberian population) (e.g. $f_3(\text{Shors}; \text{Evens}, \text{Motala}) = -0.012$, $Z = -9.1$). Altogether, these results suggest that contemporary Siberian populations from the Yenisei basin derive part of their gene pool from a Eurasian HG population that shares ancestry with K14, but is more closely related to Scandinavian MHGs than to either MA1 or western European MHGs, indicating gene flow between their ancestors and Scandinavian Europe after K14 but prior to the Mesolithic ($36.3 > x > 7$ ka BP).

f_4 – ratio statistics for Neandertal ancestry

f_4 – ratio statistics were used as previously described by (34) to obtain estimates of Neandertal ancestry for all individuals (Table S15-S16), using Mbuti Pygmies as an African population without Neanderthal admixture. We estimate $< 2\%$ of Neandertal ancestry for most individuals, as previously reported (167). However, we found slightly elevated levels both in La Braña and K14, with an estimated $2.4 \pm 0.4\%$ in K14 (see also Fig. 4A). We then restricted this analysis to genomic regions without evidence for Neandertal introgressed haplotypes in modern humans, following the coordinates of

archaic tracts identified in (168) – labeled *akey* in Table S17-S18 - and (167) – labeled *reich* in the Table S17-S18 - and found 0% estimated ancestry for most individuals. For K14 we still detected $0.9 \pm 0.4\%$ Neandertal ancestry. Our interpretation is that this is the result if the presence of longer introgressed haplotypes in K14, due to its closer temporal proximity to the admixture event (see SOM S13).

S10: Model based clustering of K14 and other ancient individuals

Methods

We used a maximum likelihood based approach (ADMIXTURE, (169)) to reveal the relationships of K14 and other ancient genomes to modern human genetic diversity in Eurasia and the Americas (see section SOM8 for a description of data processing and data sources). We ran ADMIXTURE assuming 2 to 15 source populations ($K=2$ to $K=15$) with 10 replicates each using only the data from contemporary populations. The best of each set of 10 runs, based on the Log-likelihood estimates, is plotted in Fig. S20. Ancient individuals, including K14, were not included in the runs; the cluster membership proportions for these individuals were inferred afterwards using their genotypes and the ancestral allele frequencies for each cluster (see (170) for details).

K14 has four major components, two predominant in contemporary Europeans and two in contemporary Asians

At $K = 9$, K14 comprises four major components (Fig. 1B). The largest component belongs to the same ancestral cluster that is predominant in contemporary Eastern Europeans as well as all European MHGs. However, K14 also includes a sizeable component that characterizes contemporary Middle Eastern populations and Neolithic ancient genomes (Gok2, Iceman, Stuttgart), as well as two Asian components, one predominant in contemporary Central Asians and one in Southern Asians, analogous to the ones seen in MA1 (Fig. S20).

S11: Principal Component Analysis

Methods

Principal Component Analysis (PCA) was used to place K14 in the range of present-day and past human diversity. For each ancient genome, we randomly selected one read at positions that overlapped with SNPs present in the modern reference panel. We then randomly sampled a single haploid genotype from each modern individual to prepare a final matrix including only haploid genotype data across all individuals. For each ancient genome, Principal Component Analysis (PCA) was performed on the matrix of haploid genotypes for all SNPs with data in the ancient individual, using the R function `svd`. These individual PCAs were then combined using procrustes transformation, as implemented in the R package `vegan` (<http://cran.r-project.org/web/packages/vegan/index.html>). PCA plots were generated using R 3.0.2 (R Development Core Team 2011) and projections on the first 2 components are provided in Fig. S21-S23.

Results

We found that MHGs and Neolithic farmers cluster with Northern and Southern Europeans respectively, while the UP MA1 fell outside contemporary variation towards Native Americans, as previously described (127). K14 was also found to fall outside the range of contemporary European variation, but was distinct from MA1, clustering most closely with Central Asian populations. (Fig. S21-S23)

S12: Treemix

Methods

Admixture graphs for the whole genome datasets were inferred using TreeMix (171). We ran TreeMix considering up to 10 migration edges, choosing the best out of 5 replicates for each edge, and without sample size correction (-noss option). The block size for the estimation of the covariance matrix was 1000 SNPs. We forced two migration edges following the results from (127, 149), describing gene flow from MA1 into Native Americans and from Denisovans into Papuans (options -cor_mig and -climb). TreeMix output was plotted with the TreeMix R functions and the total fraction of the variance explained by each model was estimated using the get_f() R function. This ranged from 99.64% (m=2) to 99.85% (m=10).

Results

The tree topology resulting from TreeMix, including all ancient humans previously characterized at the genome level, places K14 basal to a pan-Eurasian group in the Prufer et al dataset, but as a sister group to MA1 in the (127) (Fig. S24-S25). For 4 migration edges and above, TreeMix identifies gene flow between Swedish / Western MHG and MA1, supporting genetic affinities between both groups, in line with previous reports (20) and our own analyses. Additionally, K14 showed evidence of gene flow into the ancestral node of the two Neandertal genomes currently available. This most likely reflects the presence of longer Neandertal tract identified in the K14 genome (SOM S13). For 6 migration edges and above, K14 grouped together with MA1, still occupying a basal position with respect to the modern populations listed above and all ancient human genomes. We note however that those results should be treated with caution, since we have not investigated thoroughly the effect of using genomes with heterogenous and high error rates (SOM S6). Furthermore, the variance explained is already high with the two forced migrations, and multiple population pairs are exhibiting increased residuals, which could indicate possible overfitting for the remaining migration edges.

S13: Archaic hominin genomic tracts

Genomic tracts from archaic hominin origin (Denisova, Altai Neandertal) were identified scanning ancient human genomes for runs of consecutive archaic alleles, restricting to sites where all African individuals present in our reference panel were homozygous ancestral. We furthermore required that the respective other archaic hominin was also homozygous ancestral, in order to minimize false positive tracts due to shared ancestry of Neandertal and Denisova. To ensure results are comparable between ancient and modern genomes, we randomly sampled a single allele at each site for each diploid modern genome. Archaic tracts were defined as runs of archaic alleles, allowing a maximum gap size of 100 kb between consecutive alleles. Furthermore, to allow for missing archaic alleles due to lack of read coverage or randomly sampling the ancestral allele at heterozygote genotypes, we allowed up to 13 ancestral alleles between consecutive archaic alleles (corresponding to a binomial sampling probability of $< 10^{-4}$) (Fig. S26).

S14: Testing for additional archaic introgression

A qualitative assessment of the low-coverage Kostenki genome suggests there are short (1-100 Kb) regions where the Kostenki 14 (K14) genome falls outside the range of contemporary human genetic variation. One potential explanation for this observation is prior admixture between an unknown (and unsampled) archaic human population and the ancestors of K14. To test this possibility, we sampled a randomly chosen read for each location where K14 had coverage. We then tabulated a list of all locations where the K14 allele did not match the human reference sequence (hg19). We then filtered out all locations where either hg19 or the ancestral allele had missing data, sites where the ancestral allele did not match either the K14 allele or the hg19 allele, and locations that contained SNPs in a panel of 42 unrelated high-coverage modern human genomes sequenced by Complete Genomics (<http://www.completegenomics.com/public-data>). This resulted in a list of 1.47 million potential K14-specific SNPs. The sites on this list could arise from four main causes:

1. Sequencing errors in the K14 reads
2. Errors caused by postmortem DNA modifications in the K14 reads
3. True private polymorphisms under a model without ancient admixture
4. Private polymorphisms due to introgression from a diverged archaic human population (i.e., ancient admixture)

While Illumina sequencing errors are known to correlate with local sequence content (172, 173) as a first-order approximation they are randomly distributed across the genome (see also below). Similarly, we know something about errors due to post-mortem DNA damage (31) but these too are roughly randomly distributed across the genome since each individual read is short.

To assess how K14-specific polymorphisms would be distributed under different demographic models, we modified a standard coalescent simulator (174) to allow for sampling of ancient and modern DNA sequences. We then ran simulations to quantify the correlation in locations of Kostenki-specific mutations under a simple demographic null model. In general, we found that beyond a scale of ~1 Kb, the locations of these mutations were essentially uncorrelated. In contrast, under models that included ancient admixture between modern humans and a diverged archaic human population, simulations produced clusters of K14-specific mutations, with the size of the clusters inversely related to the time of admixture. We then scanned the genome for short regions with elevated numbers of K14-specific mutations.

We partitioned the genome into non-overlapping 1 Kb windows and tabulated the number of K14-specific mutations for each window. We then tabulated all regions that were 5 Kb or longer that contained an average of 6 Kostenki-specific mutations or more per Kb. This led to the identification of 161 candidate regions (excluding the MHC), with an average length of 10.4 Kb. To assess the approximate significance of these regions, we repeatedly permuted the counts of the number of K14-specific mutations

across windows and tabulated how frequent it was to obtain regions that satisfied the criteria described above. We conservatively excluded windows with no K14-specific SNPs from these permutations to account for the uneven distribution of sites with no K14 sample coverage across the genome. In all, genome-wide simulations produced an average of 18.4 regions (average length 6.8 Kb) that fit the test criteria.

Finally, to further test whether our initial assumption that sequencing errors are randomly distributed across the genome, we compared the coordinates of our 161 candidate regions with a list of ~400,000 genomic locations where duplicate Illumina whole-genome sequence data from the same individual had discrepant genotype calls (without standard filters and with a genotype quality cutoff of $GQ \geq 20$; cf. (175)). We filtered out all candidate regions that contained one or more of these discrepant genotype calls. 121 regions failed this filter, with each containing an average of 97 discrepant genotype calls (null expectation of random locations for these Illumina sequencing errors would lead to ~1.2 per region). This left 40 candidates for ancient introgression, with an average length of 6.0 Kb. Given the uncertainty in our assumptions regarding the baseline distributions of sequencing errors and post-mortem DNA damage, and the small size of the identified regions, we do not believe these observations are necessarily inconsistent with a null model of no admixture.

We conclude that any introgression with an unsampled archaic human population, while theoretically possible, has left a negligible trace in the sampled K14 genome.

S15: Estimating Neandertal admixture time

We used a new Hidden Markov Model (HMM) method to estimate admixture times and admixture proportions using maximum likelihood (ML). This method will be described in detail in a forthcoming paper, together with extensive simulations evaluating the method. Here we provide a brief summary of the method:

The method is similar to previous methods (176, 177), but differ from these in several important aspects as detailed below. The HMM has two states, S_N and S_H , representing segments of the haploid genome of Neandertal and human origin, respectively. The objective is to estimate parameters of this two-state HMM and to use subsequent posterior decoding to infer admixture tracts. In contrast to some previous methods (167), the emission probabilities are not estimated using simulated training data, but are instead estimated directly from observed data. The algorithm therefore has two steps. In the first step emission probabilities are estimated from the 1000 Genomes Project (178). We consider only two possible type of emissions: (A) Sites variable in humans (phased 1000 Genomes v.2) in which the focal haplotype has a derived allele as determined by the 4-way EPO alignments, in which Neandertals contain at least one derived allele as well, and in which all reference African populations are invariant ancestral. (B) Variable sites (including Neandertals) that do not fulfill the conditions in (A). Invariable sites and sites that do not have information to determine if condition (A) is true are considered missing data. The HMM is then applied to these data, after removing sites in linkage disequilibrium, by multiplication of the likelihood function among individuals, using transition probabilities given by (179). The likelihood function is calculated using standard algorithms and optimized using the BFGS algorithm in (180). Notice that individuals may not be independent, they may share the same tracts. However, the estimator should still perform well as a composite likelihood estimator for obtaining point estimates. Using this method we obtain emission probabilities of 0.0155 and 6.67e-9 for observations of type A when in the Neandertal and human state, respectively.

The second step is then to estimate transition probabilities in K14 using maximum likelihood (ML) on the same set of sites as those used for estimating emission probabilities. The transition probability estimates directly provide ML estimates of the admixture proportion and the time of admixture in number of generations (by the invariance principle of maximum likelihood). In particular, the rate of transition from S_N to S_H , a_{NH} , can be converted to an estimate of the admixture time using the following equation:

$$a_{NH} = m(t-1) \text{ per Morgan,}$$

where m is the admixture proportion, and t is the admixture time in generations (179). There is an implicit assumption here of an exponential distribution of admixture tract lengths; an assumption that is not quite true but which should work reasonably well for the levels of divergence and admixture considered here (see (181) for a discussion of this issue). To enable application to the low-coverage, unphased aDNA, we consider a modified state space in which we only use at most one read for the K14 individual for each position. When more than one read is available for a position, we sample one uniformly at random. As a first approximation, we then assume that K14 is not homozygous for a Neandertal segment any place in the genome. The state space is then

reinterpreted as having two states: a state in which K14 is heterozygous for a Neandertal haplotype (S_N^*) and a state in which both alleles in K14 are of human origin (S_H^*). The emission probability for state S_H^* is then identical to the previously described emission probability for S_N . However, for state S_N^* , the emission probabilities are obtained as a 50:50 mixture between those of S_N and S_H in the previous analysis. Sites that are invariable in the 1000G data are considered missing data. This largely eliminates the effect of errors, and also eliminates the effect of unique mutations on the K14 lineage, ensuring that the previously estimated emission probabilities are applicable to the K14 individual. Using these methods we obtained an estimate of the admixture time of approx. 16,600 years before the sample was deposited, using a generation time of 29 years and a recombination rate of 1.26×10^{-8} bp/generation. The estimate for the age of the Neandertal admixture time is then approx. 54k years.

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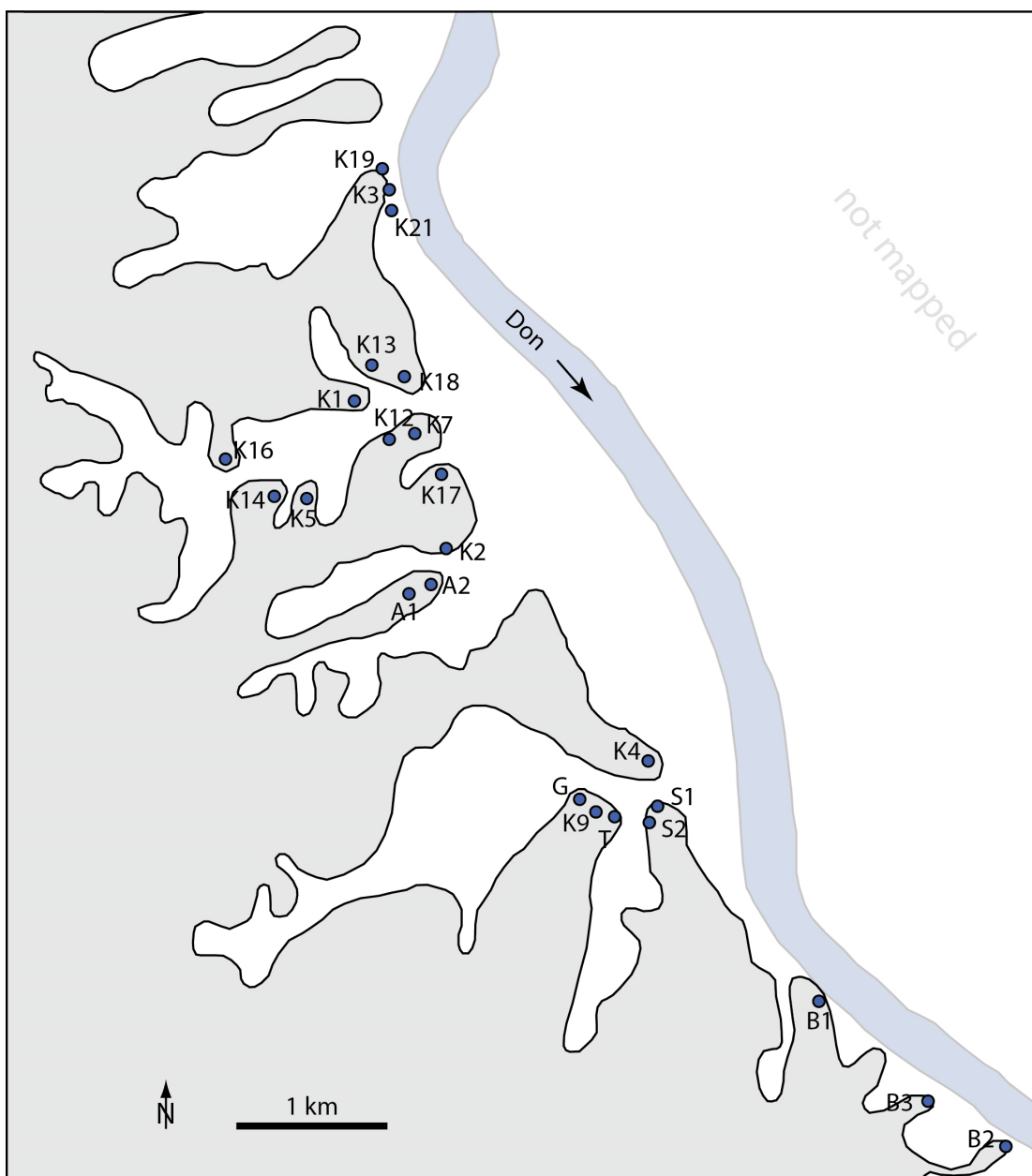


Fig. S1

Distribution of the archaeological sites that form the localities of Kostenki-Borshchevo the west bank of the river Don. Abbreviations: K: Kostenki, A: Anosovka, G: Gorodtsovskaya, S: Streletskaya, B: Borshchevo, T: Tel'manskaya. Redrawn after Klein (1969).

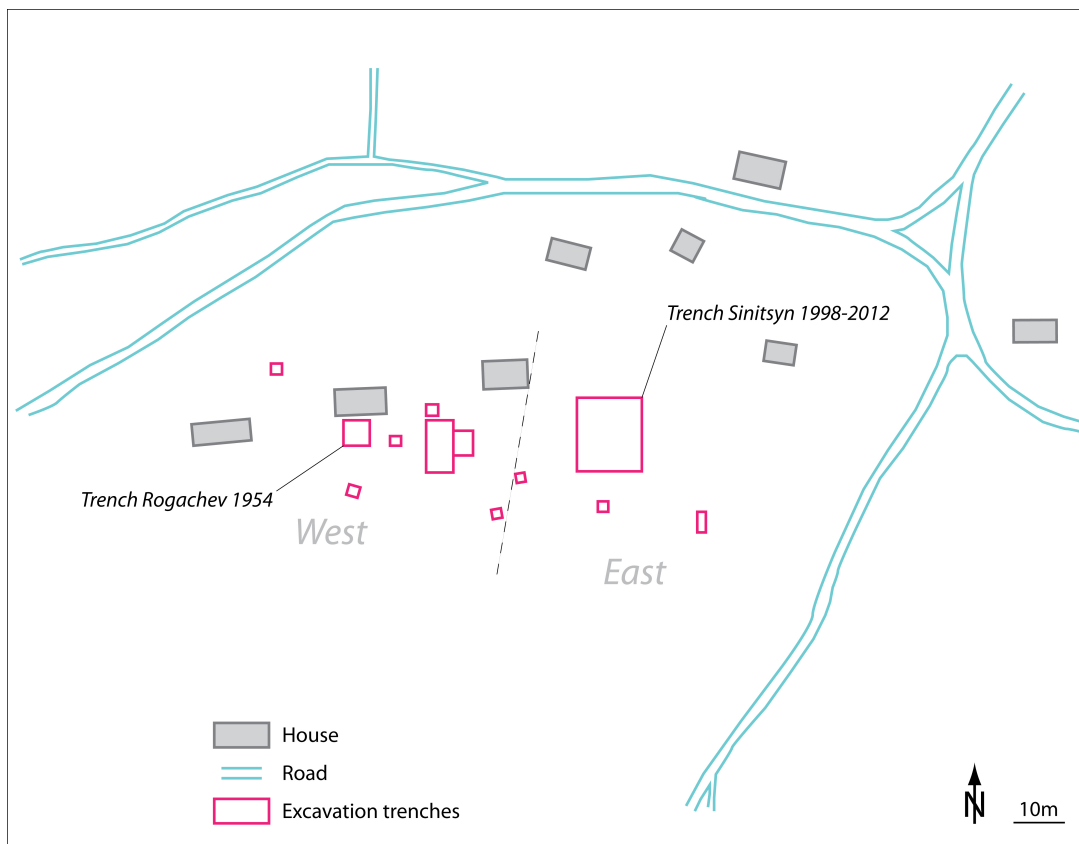


Fig. S2

Location of excavation trenches at Kostenki 14. The trenches on the western section of the site, which include that excavated by Rogachev in 1954 and where the skeleton was found, preserve a single horizon of Cultural Layer IV below the CI Y5 tephra, divided into two (IVa and IVb) in the eastern portion of the site.

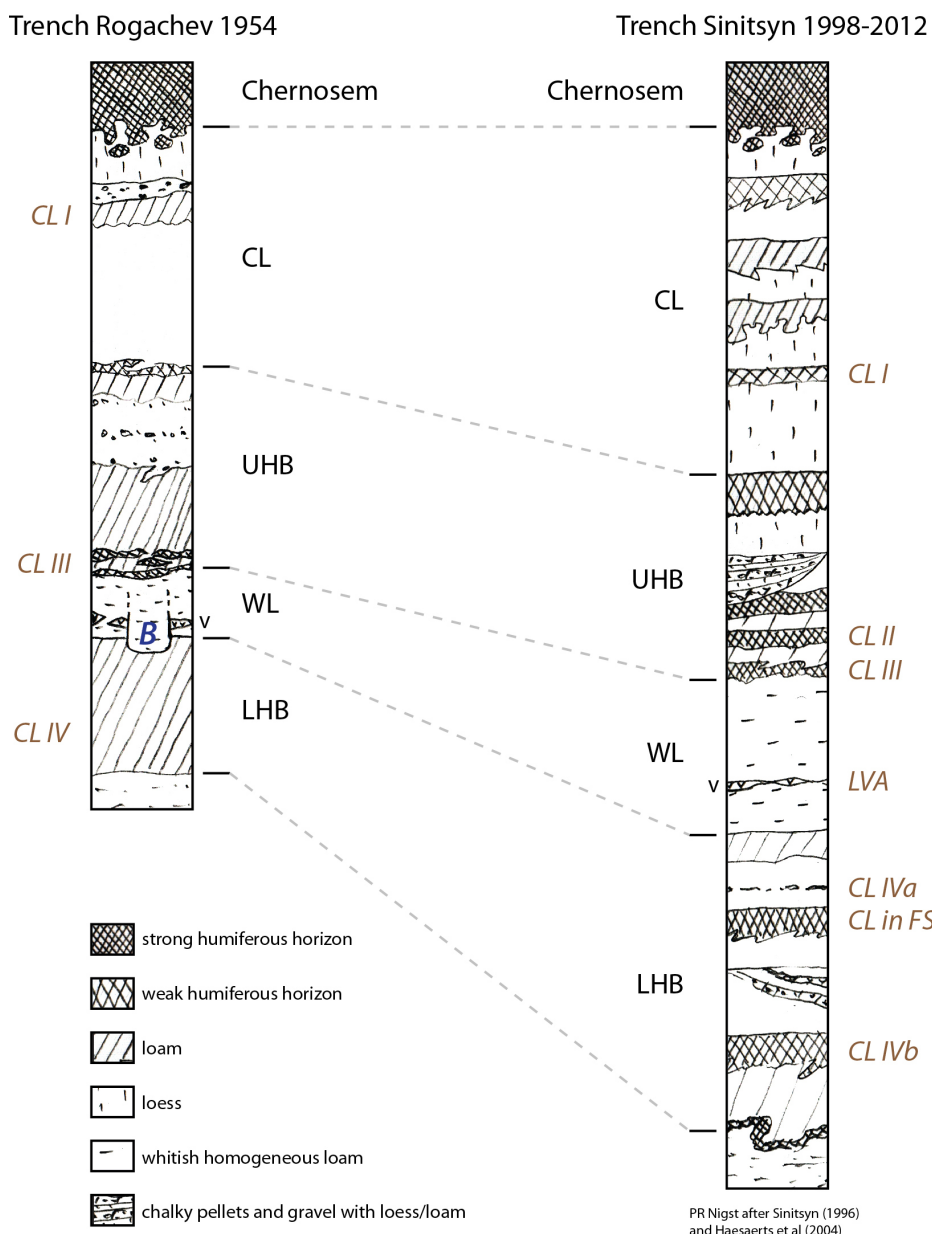


Fig. S3

Stratigraphic schema of Kostenki 14, showing Rogachev's 1954 section, where the human skeleton in the burial (B) was found, and the more recent section excavated by Sinitsyn 1998-2012 on the eastern part of the site and from where the detailed description of the cultural layers derives. Abbreviations: CL: Cover Loam, UHB: Upper Humic Bed, WL: Whitish Loam, LHB: Lower Humic Bed, v: volcanic ash. Cultural Layers (CL) are shown in brown and italic font. Stratigraphic logs not to scale. Figure: PR Nigst, compiled after Sinitsyn (1996) and Haesaerts et al. (2004).

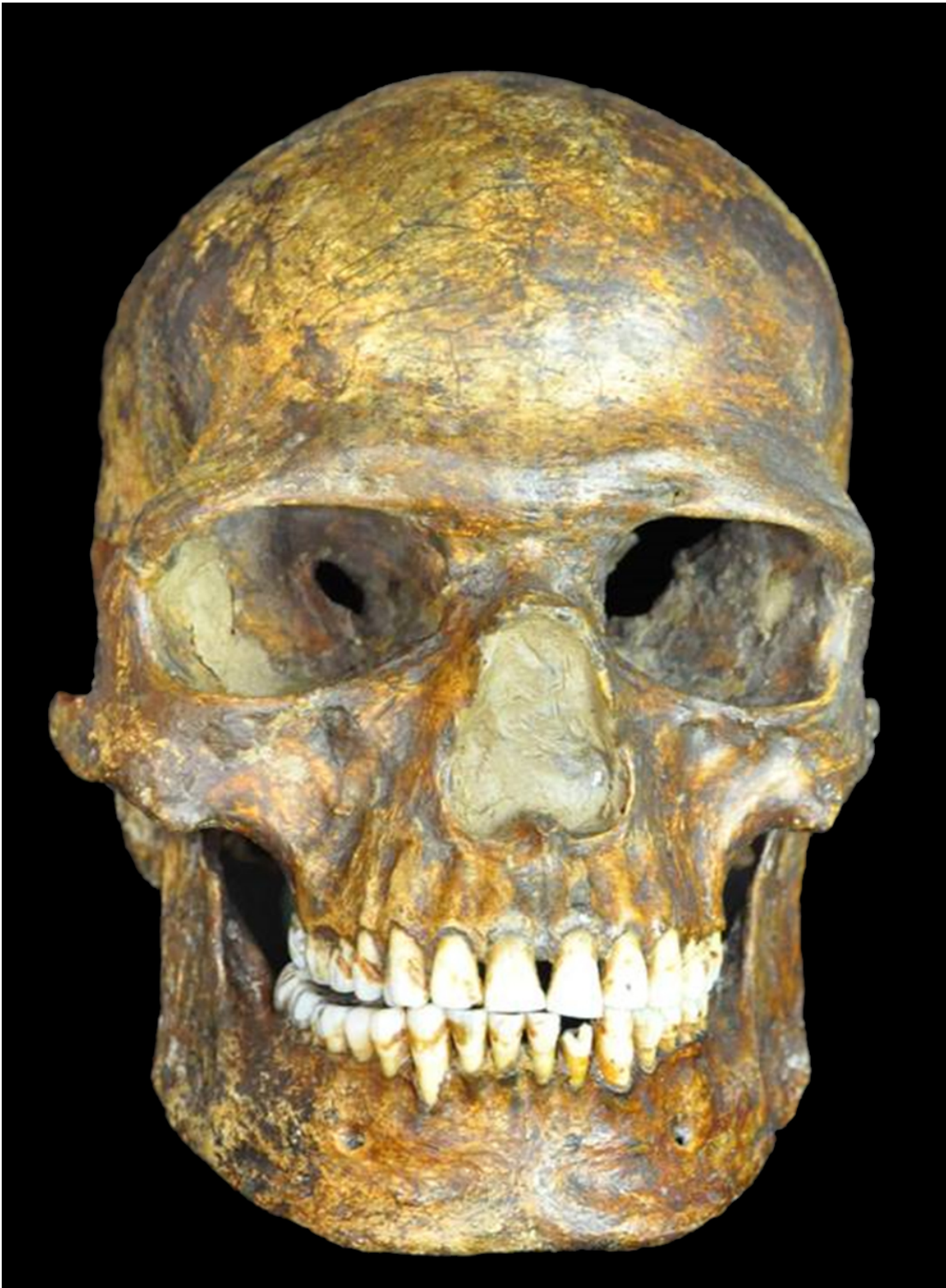


Fig. S4

Frontal view of the cranium of Kostenki 14. Courtesy of Vyacheslav Moiseyev, and Ethnography (Kunstkamera) Peter the Great Museum of Anthropology.

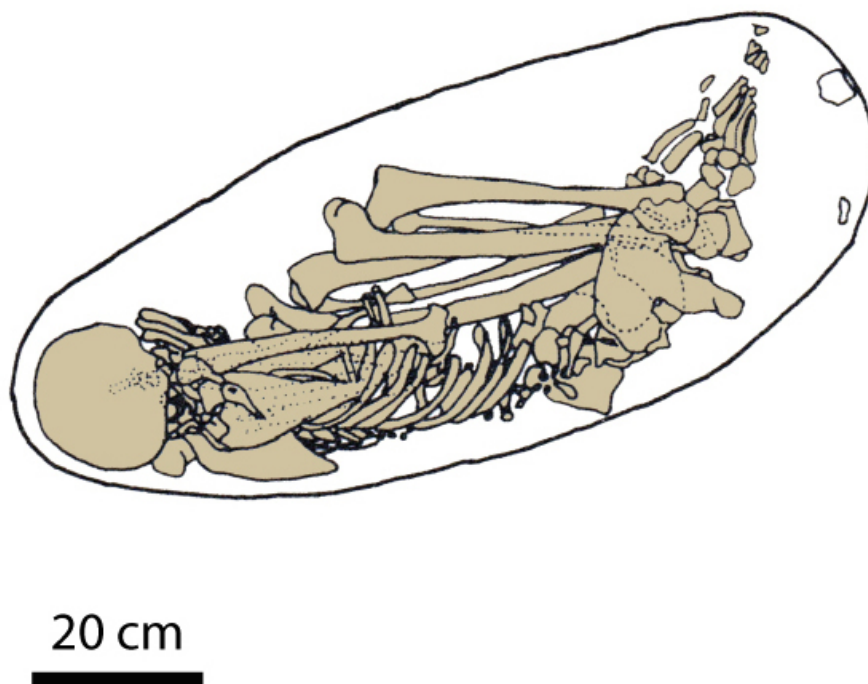


Fig. S5
Plan of the burial from Kostenki 14 (Markina Gora); redrawn and changed after Klein (1969, Fig. 23).

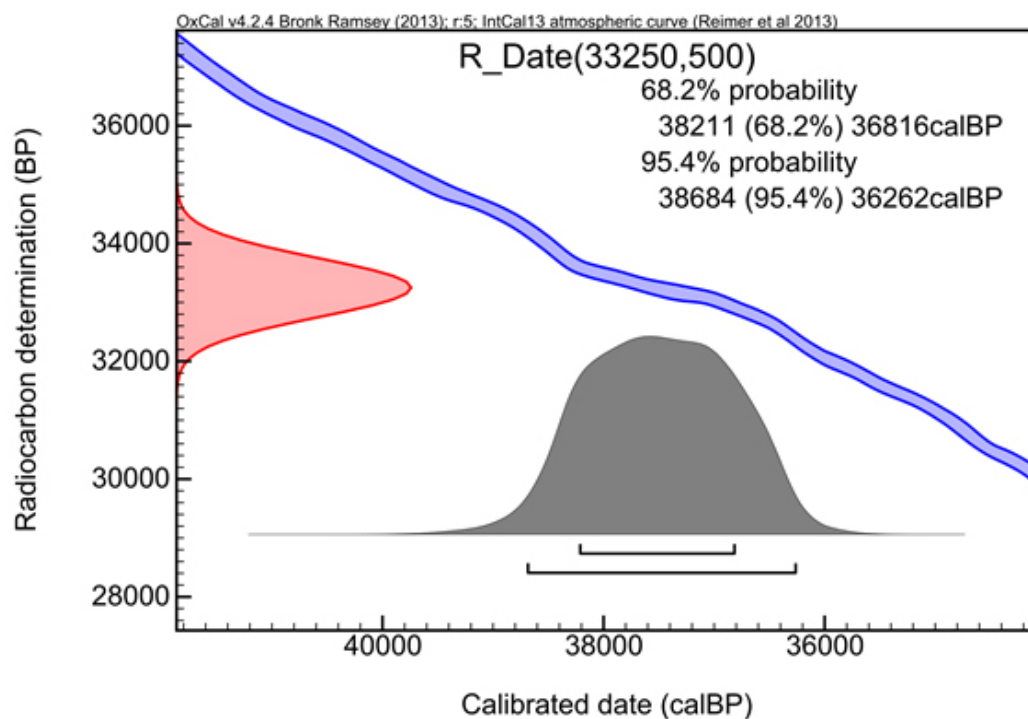


Fig. S6

Calibration graph of the radiocarbon date for Kostenki 14 published by Marom et al. 2006. Calibration curve: IntCal13 (Reimer et al 2013); software: OxCal 4.2.4 (Bronk Ramsey 2009).

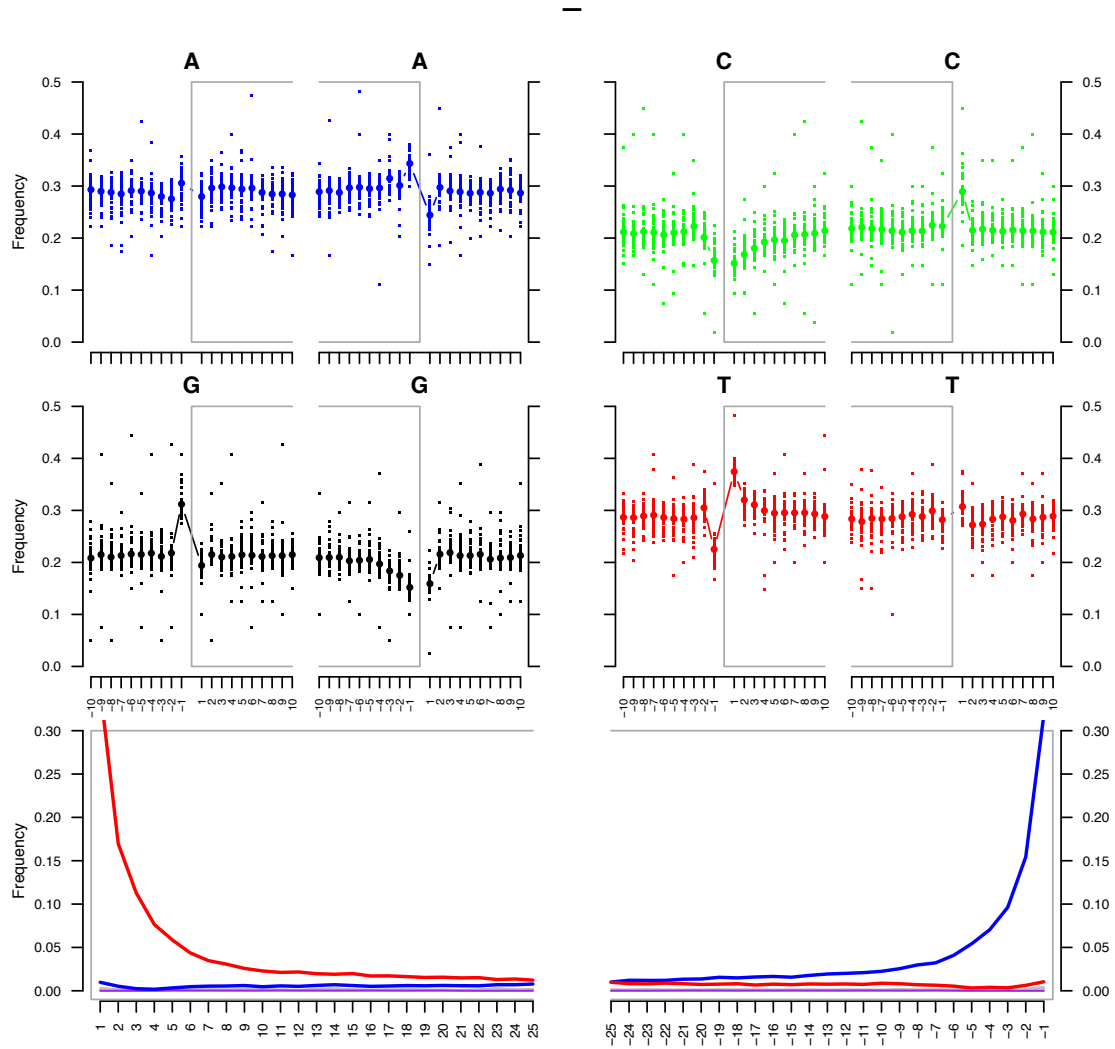


Fig. S7

An example of DNA fragmentation and mis-incorporation patterns observed on non-USER treated libraries. The sequence data corresponds to library ID K14_TGAACA (see Table S2 for further details).

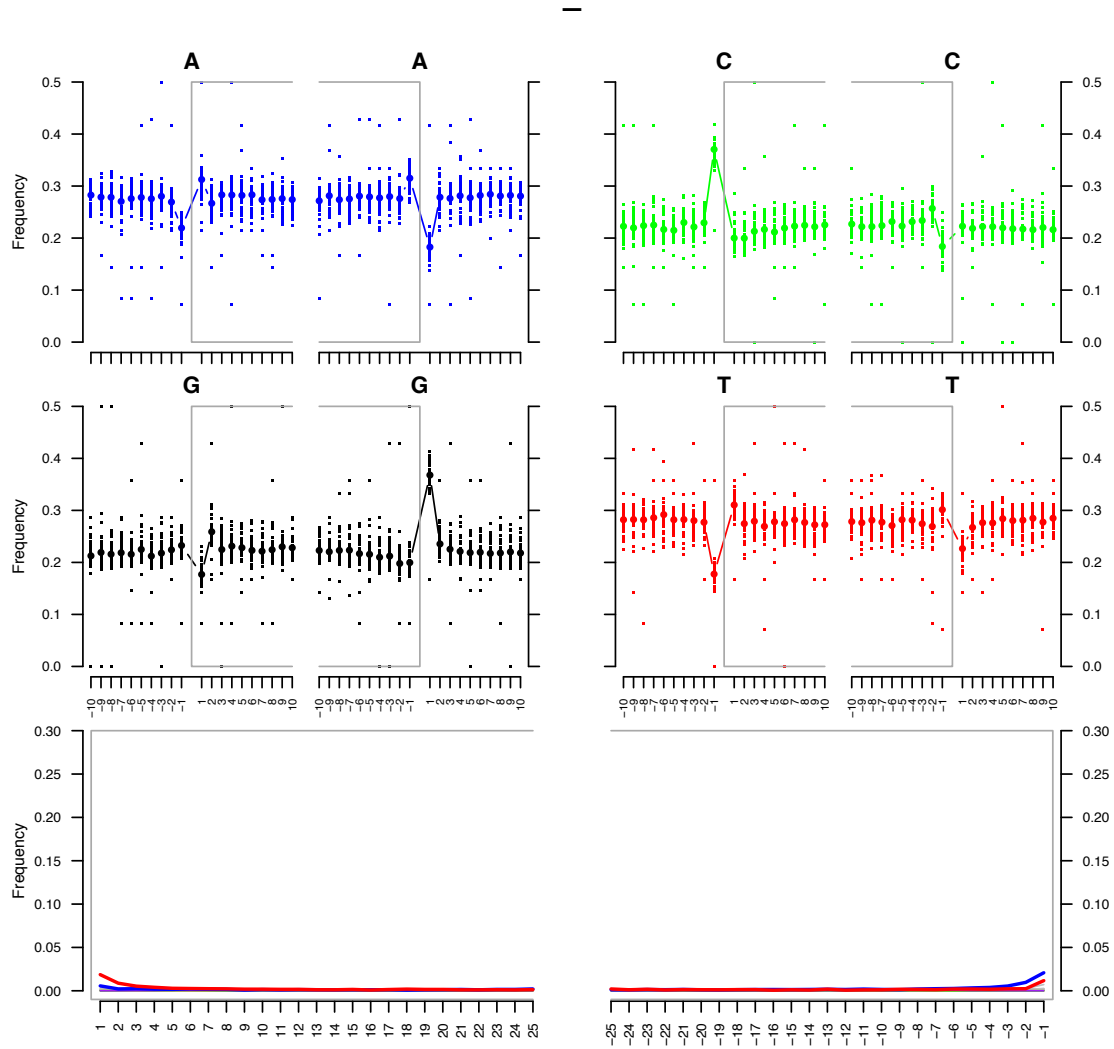


Fig. S8

An example of DNA fragmentation and mis-incorporation patterns observed on USER-treated libraries. The sequence data corresponds to library ID K14_14c_CGTAGT_USER (see table S2 for further details).



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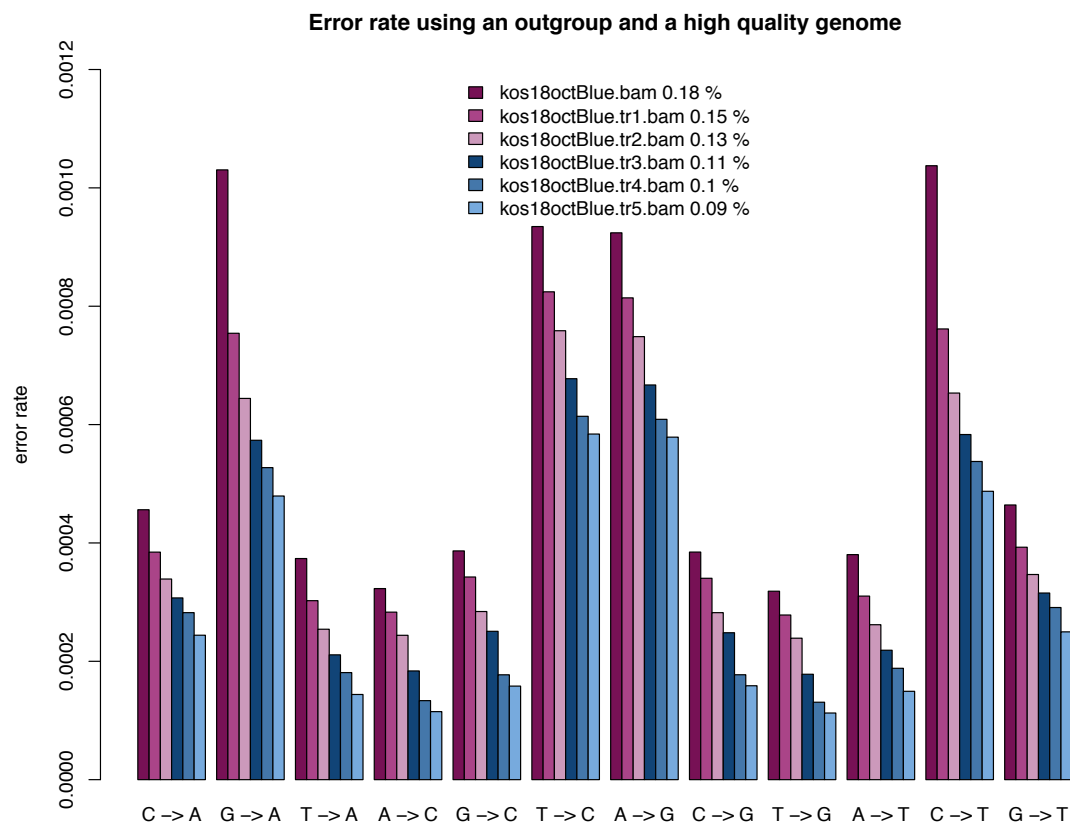


Fig. S10

Type specific error rates for different trimmings for all USER libraries. The overall error rates are shown in the legend.

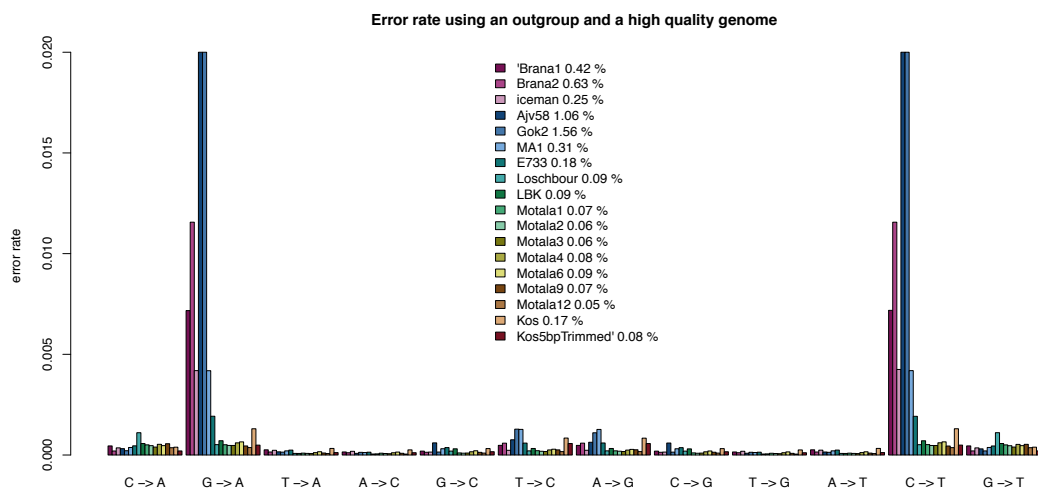


Fig. S11

Type specific error rates for all USER libraries. The type specific error rates for all libraries are seen in Fig. S6.

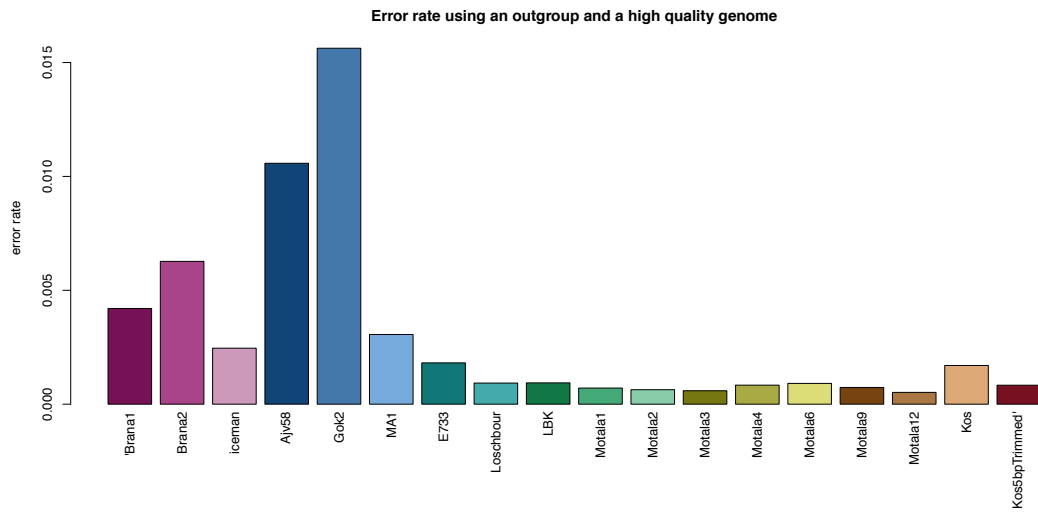


Fig. S12

Overall error rates for all ancient samples. We have included the untrimmed Kostenki K14 sample for comparison.

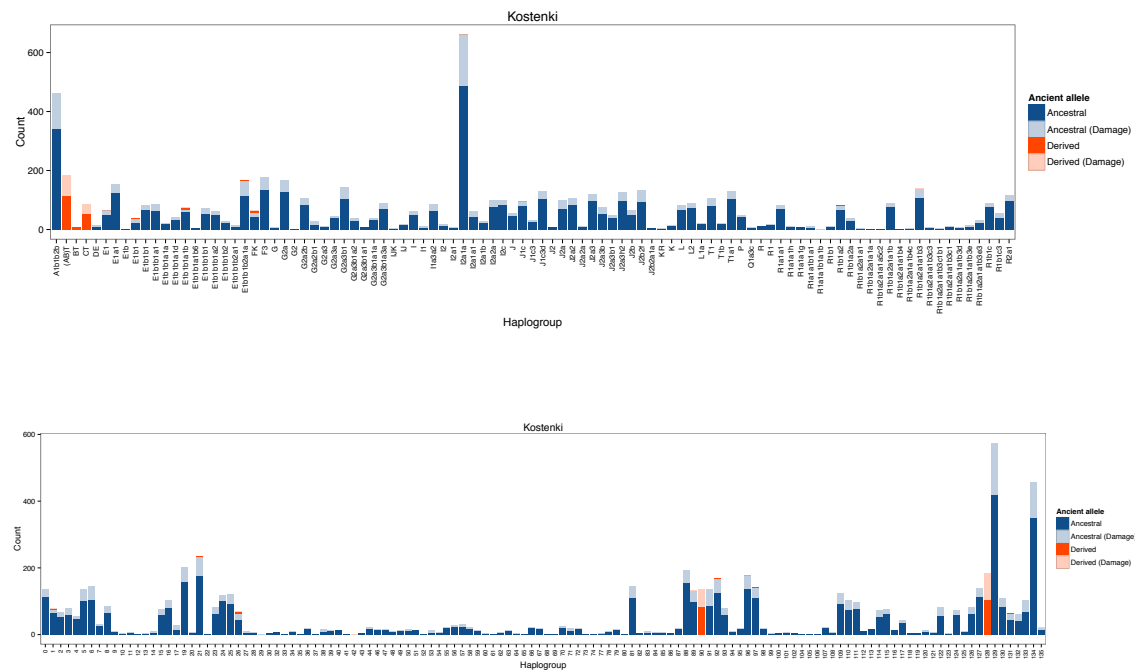
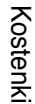


Fig. S13

Barplot of phylogenetically informative SNPs. The bars indicate the number of ancestral and derived mutations observed in K14 for each branch of the tree from (A) Table S1 in (152), and (B) (153) (http://www.popgen.dk/kostenki/figs_online/Poznik_tree.pdf).



f_3 outgroup plot for the K14 sample, compared to all modern and ancient populations.

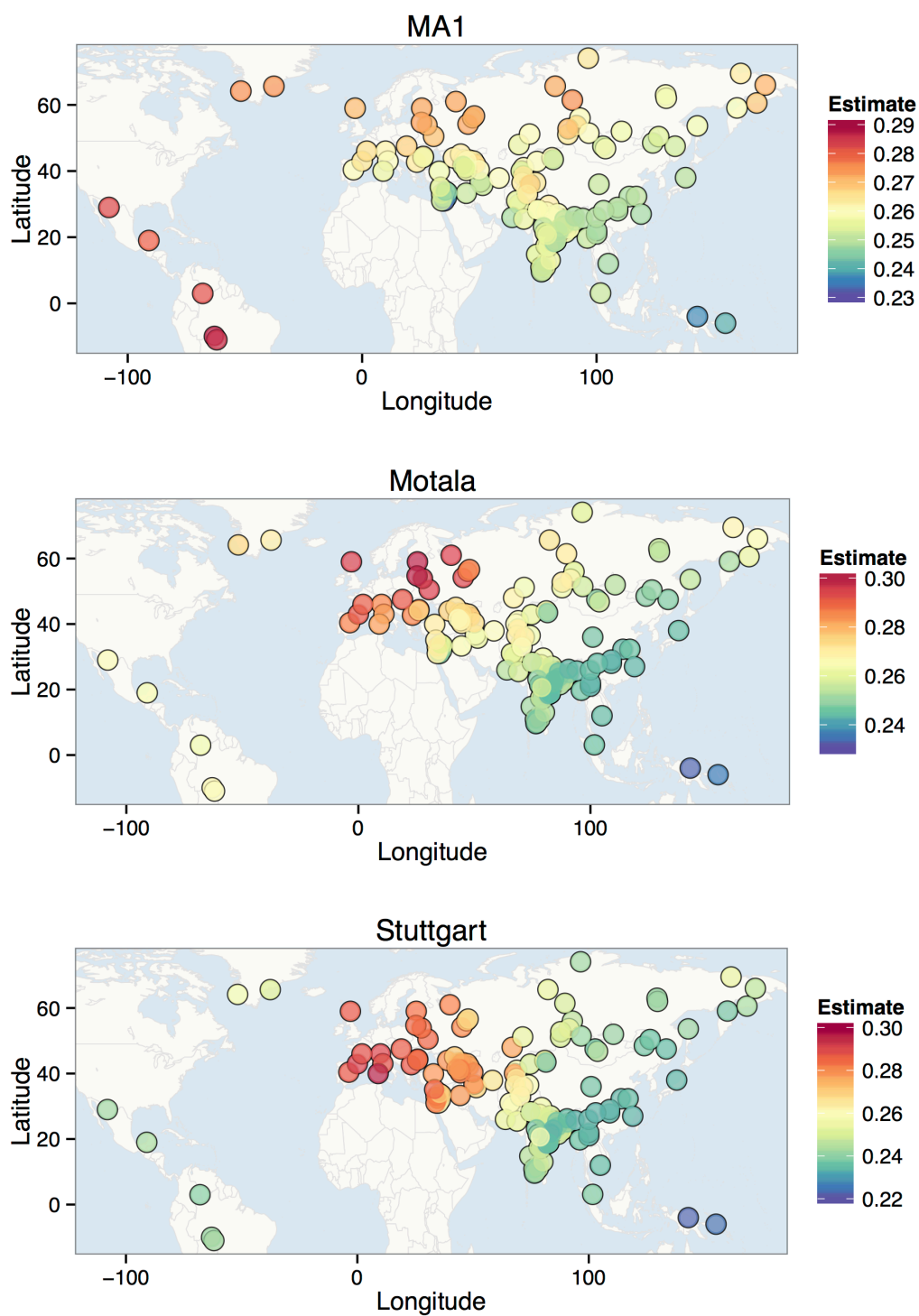


Fig. S15

f_3 outgroup maps of the form $f_3(\text{Mbuti}; \text{Ancient}, \text{Modern})$ for MA1, Motala, and Stuttgart genomes, compared to non-African modern populations.

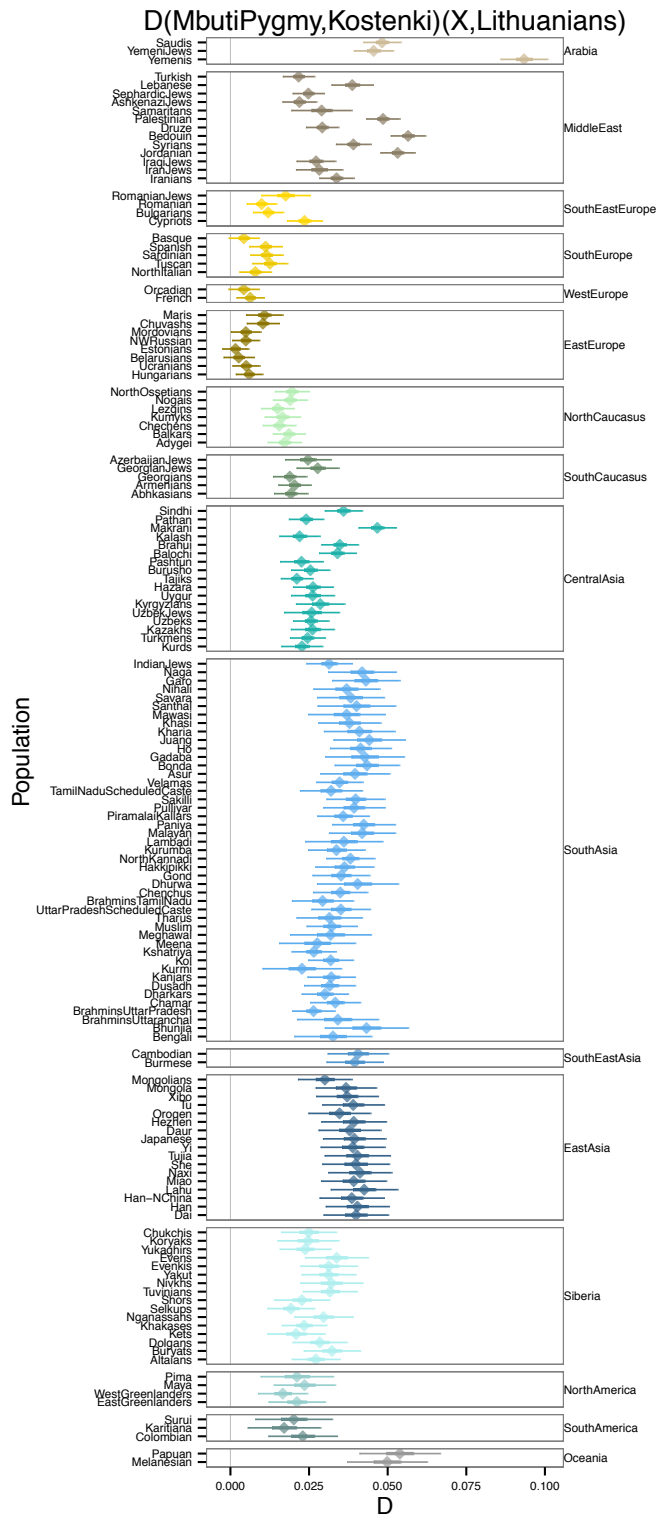


Fig. S16

D -statistics $D(\text{Mbuti}, \text{Kostenki})(X, \text{Lithuanians})$. Positive values indicate that K14 is closer to Lithuanians than to X.

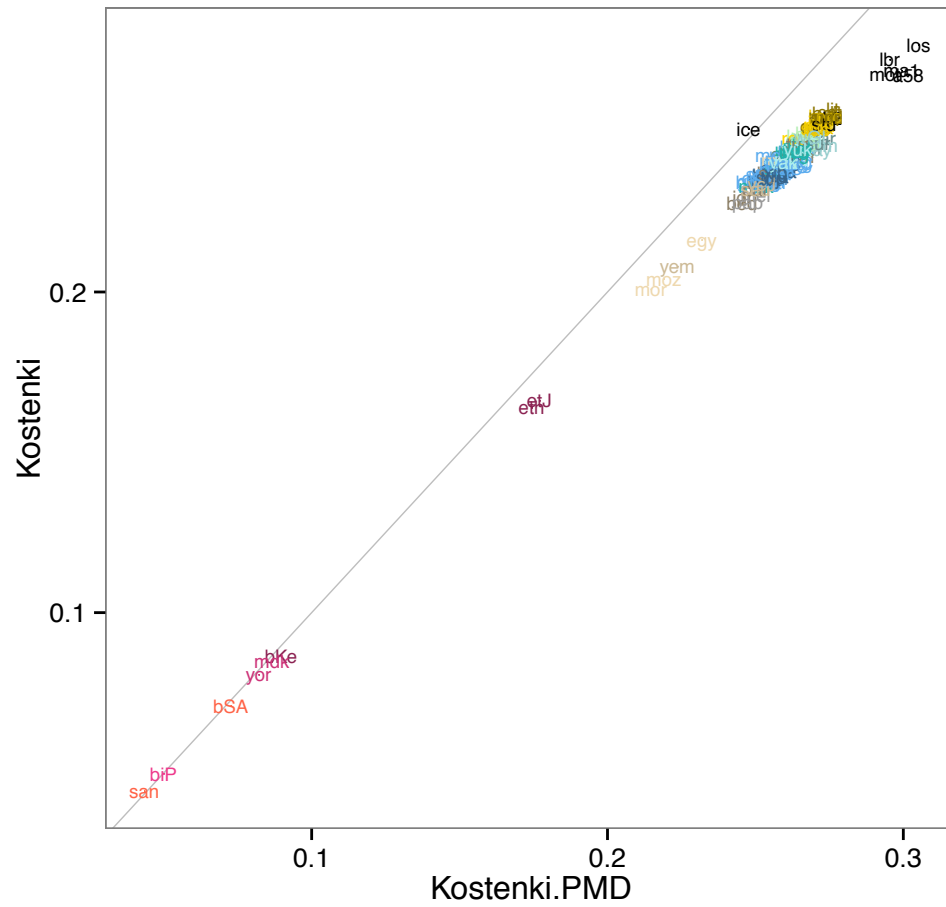


Fig. S17

Pairwise plot of “outgroup” f_3 statistics, for dataset filtered with PMD > 3 (x axis) compared to the full dataset (y axis).

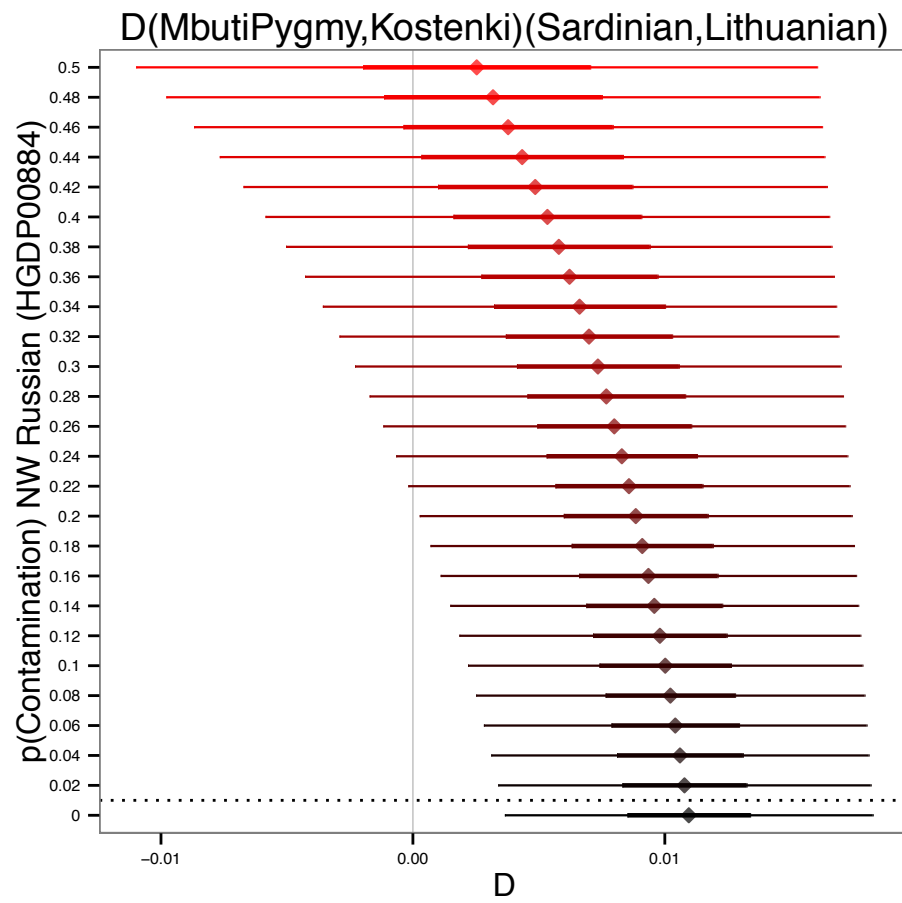


Fig. S18

Contamination-corrected D-statistics of the form $D(\text{Mbuti Pygmy}, K14; \text{Sardinian}, \text{Lithuanian})$, for different levels of contamination.

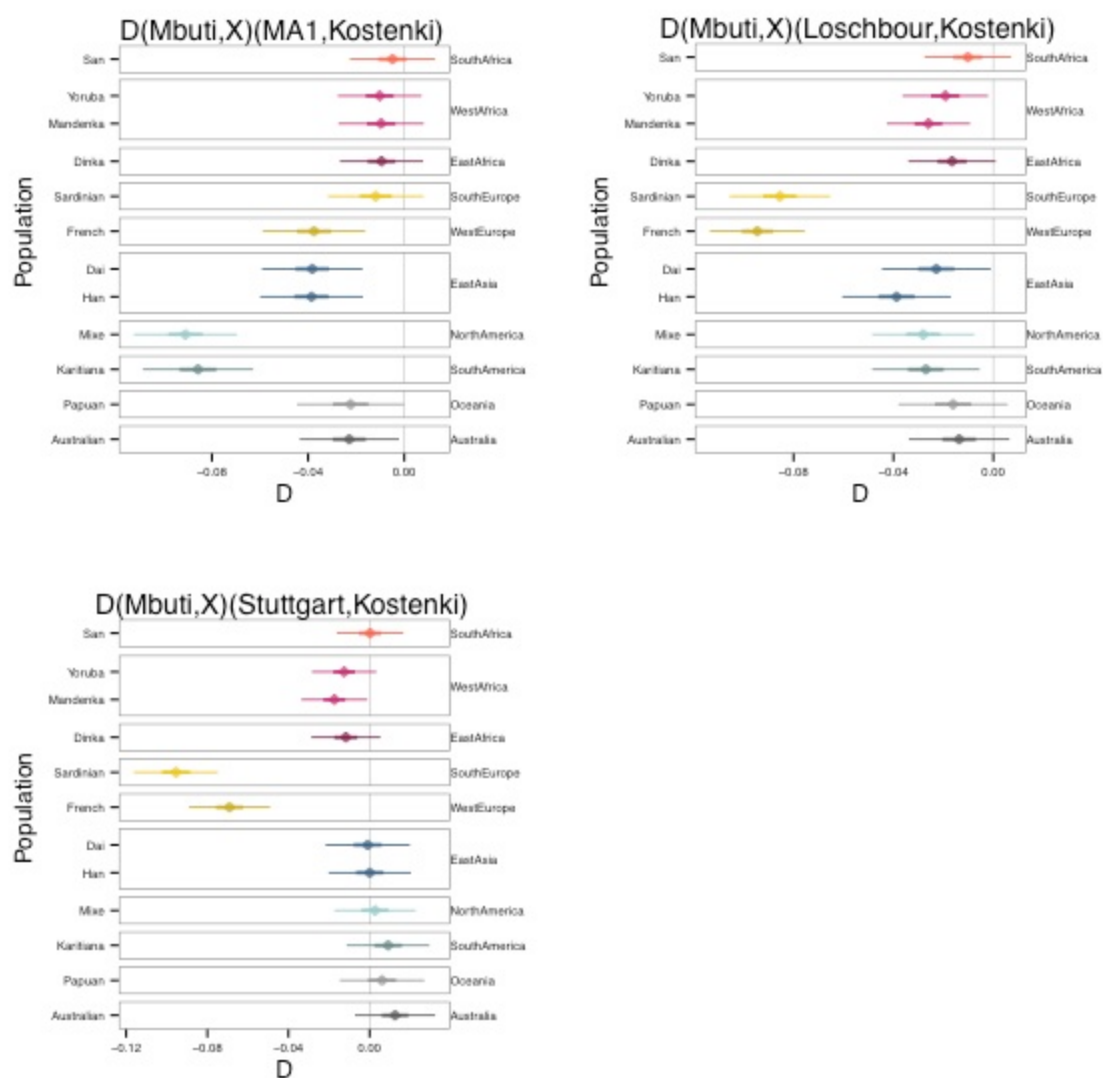


Fig. S19

Whole genome D-statistics of the form (Mbuti Pygmy, K14; Ancient₁, K14) for MA1 (UPHG), Loschbour (MHG), Stuttgart (NEOL) and MA1. Results are from the Prufer et al. (2014) genome, similar patterns for other MHGs and within NEOL (Tables S10-S11).

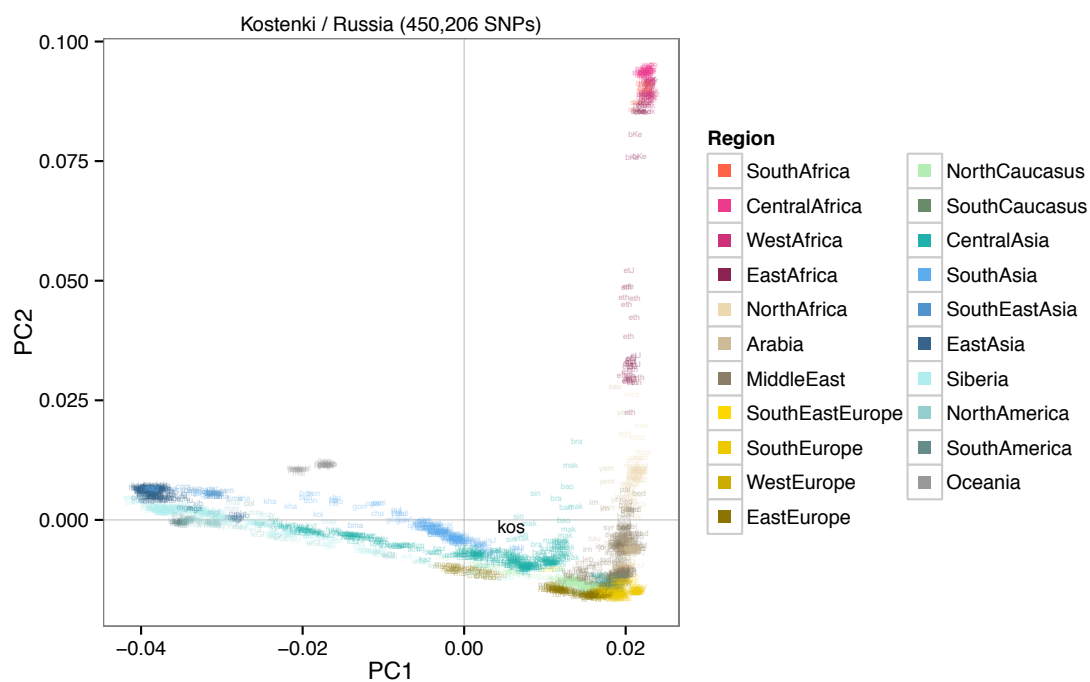


Fig. S21

PCA of K14 including a worldwide panel. PCAs were done using homozygous reference panel (randomly sampled hets) combined with K14 with a sample allele for each position.

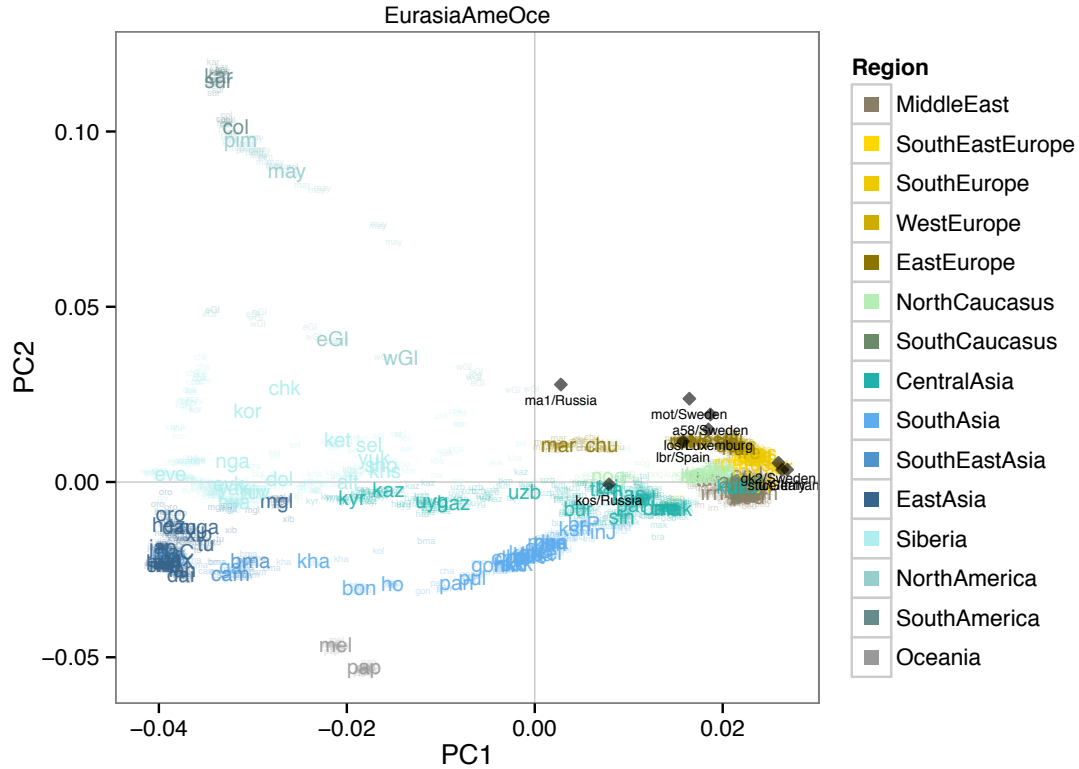


Fig. S22

Procrustes PCA of all ancient genomes on modern non-African populations. Bold letters indicate population average PC. Individual PCAs were done using homozygous reference panel (randomly sampled hets), then combined across ancient individuals using Procrustes.

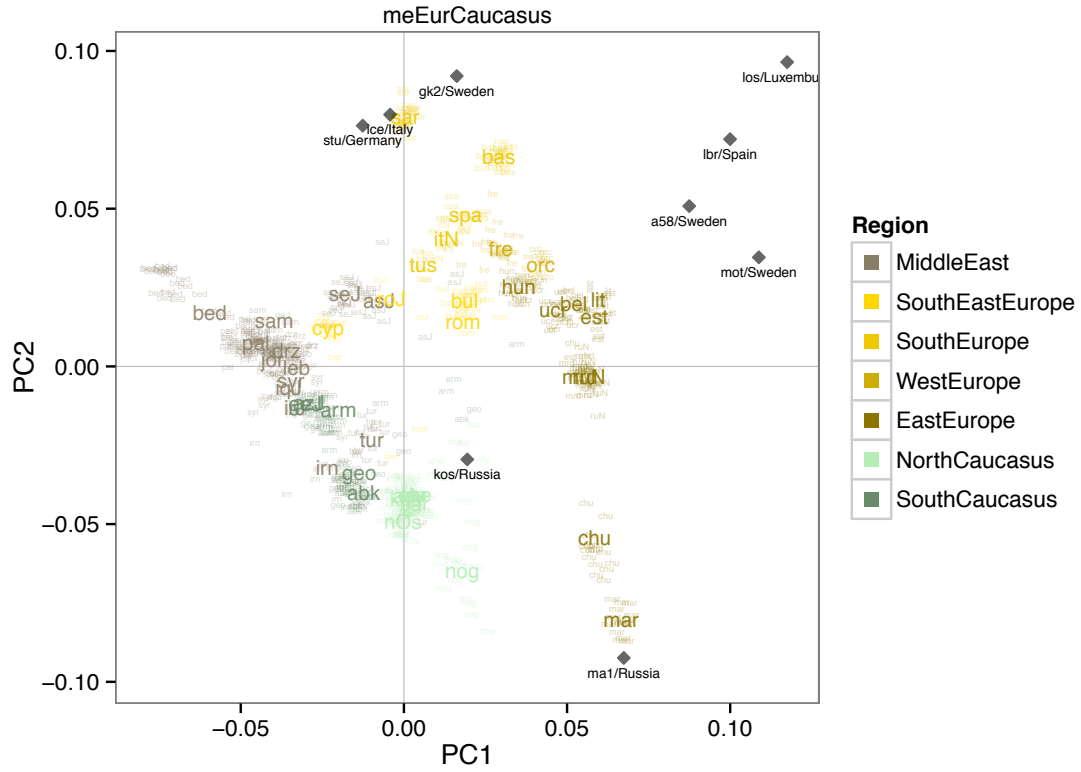


Fig. S23

Procrustes PCA of all ancient genomes on modern populations from Europe, Middle East and Caucasus. Bold letters indicate population average PC.

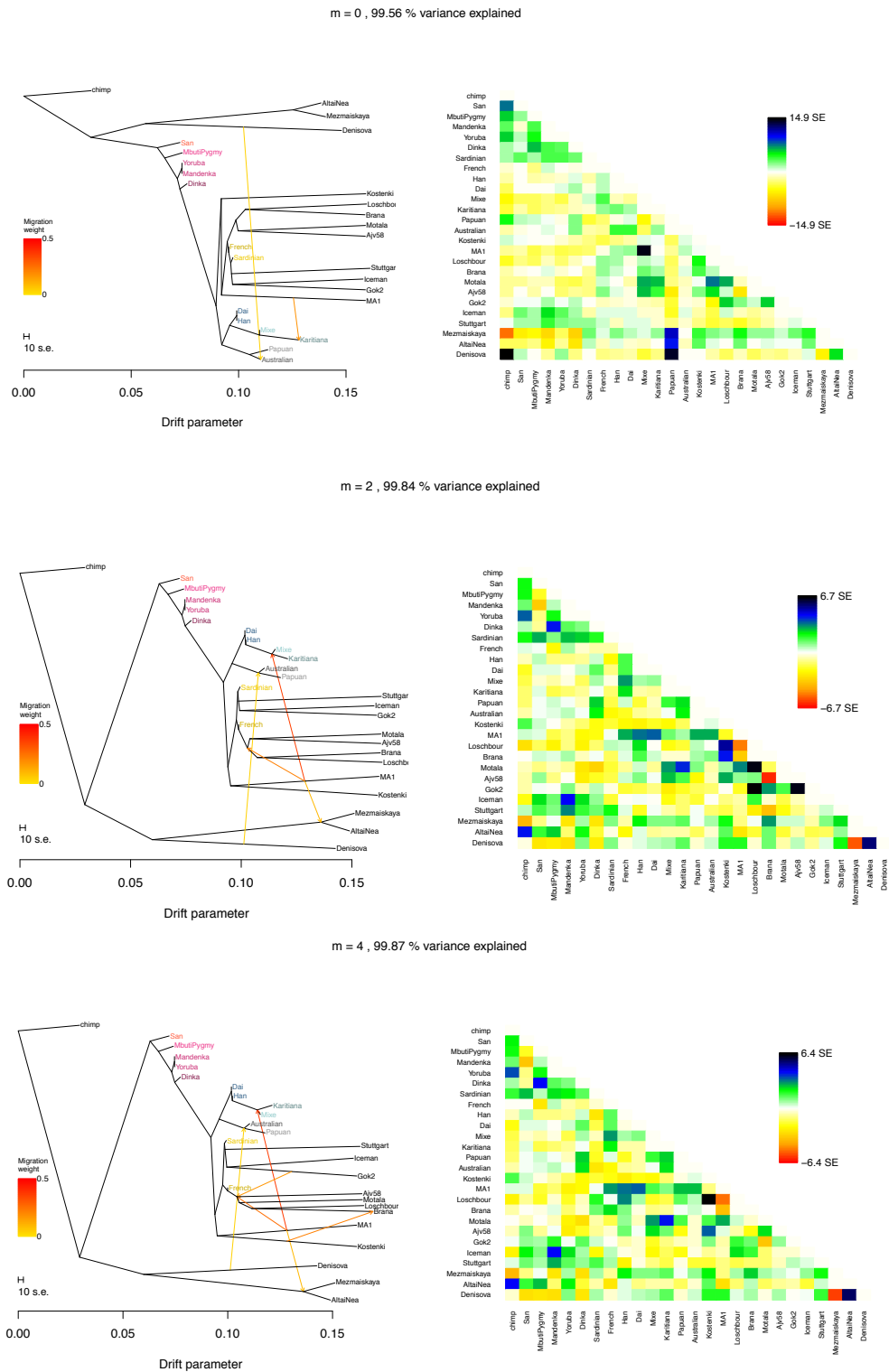


Fig. S24

Treemix on Prufer et al genomes. The first two migration edges were incorporated as known migrations in the tree building.

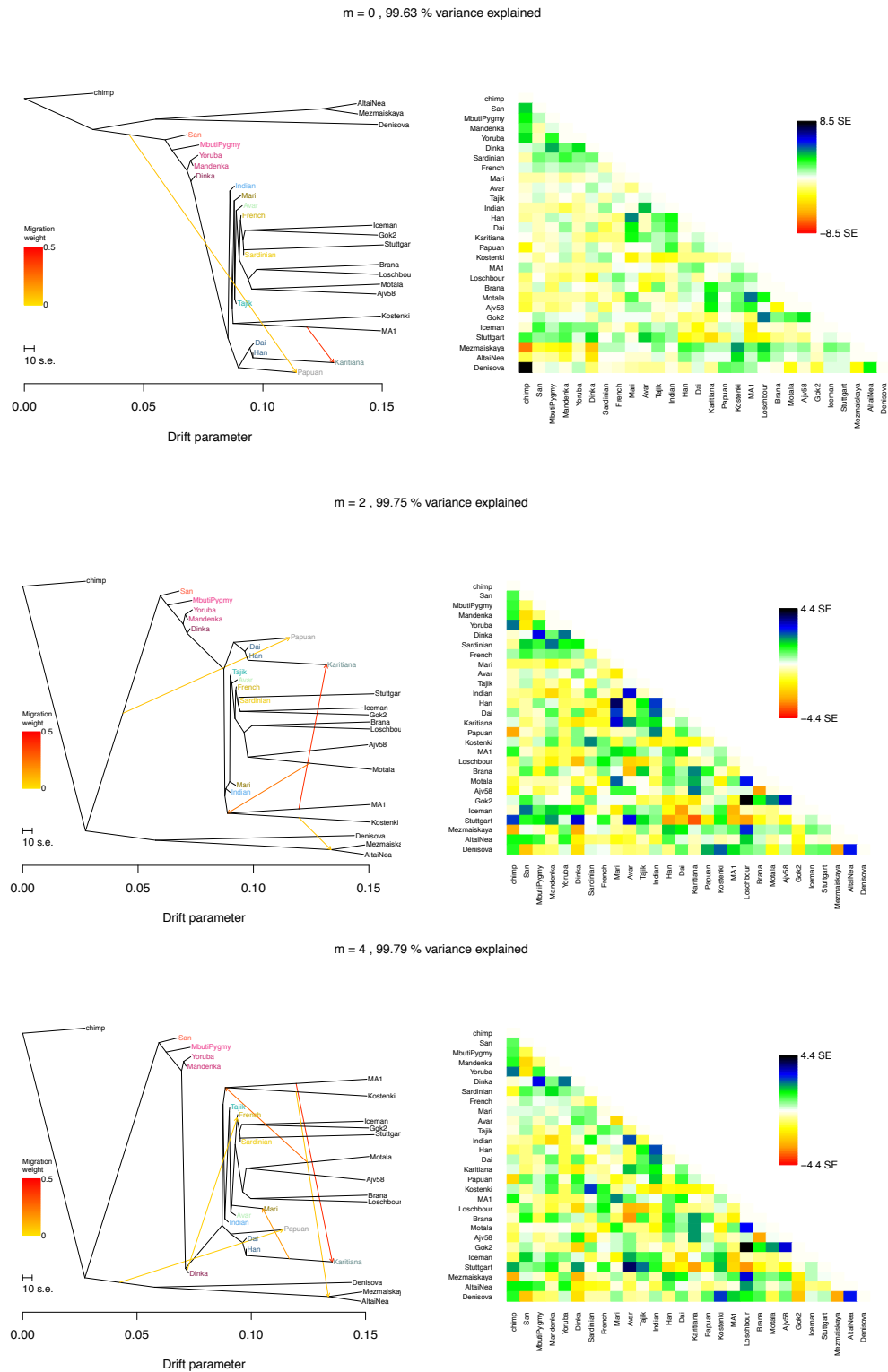


Fig. S25

Treemix on Raghavan et al genomes. The first two migration edges were incorporated as known migrations in the tree building.

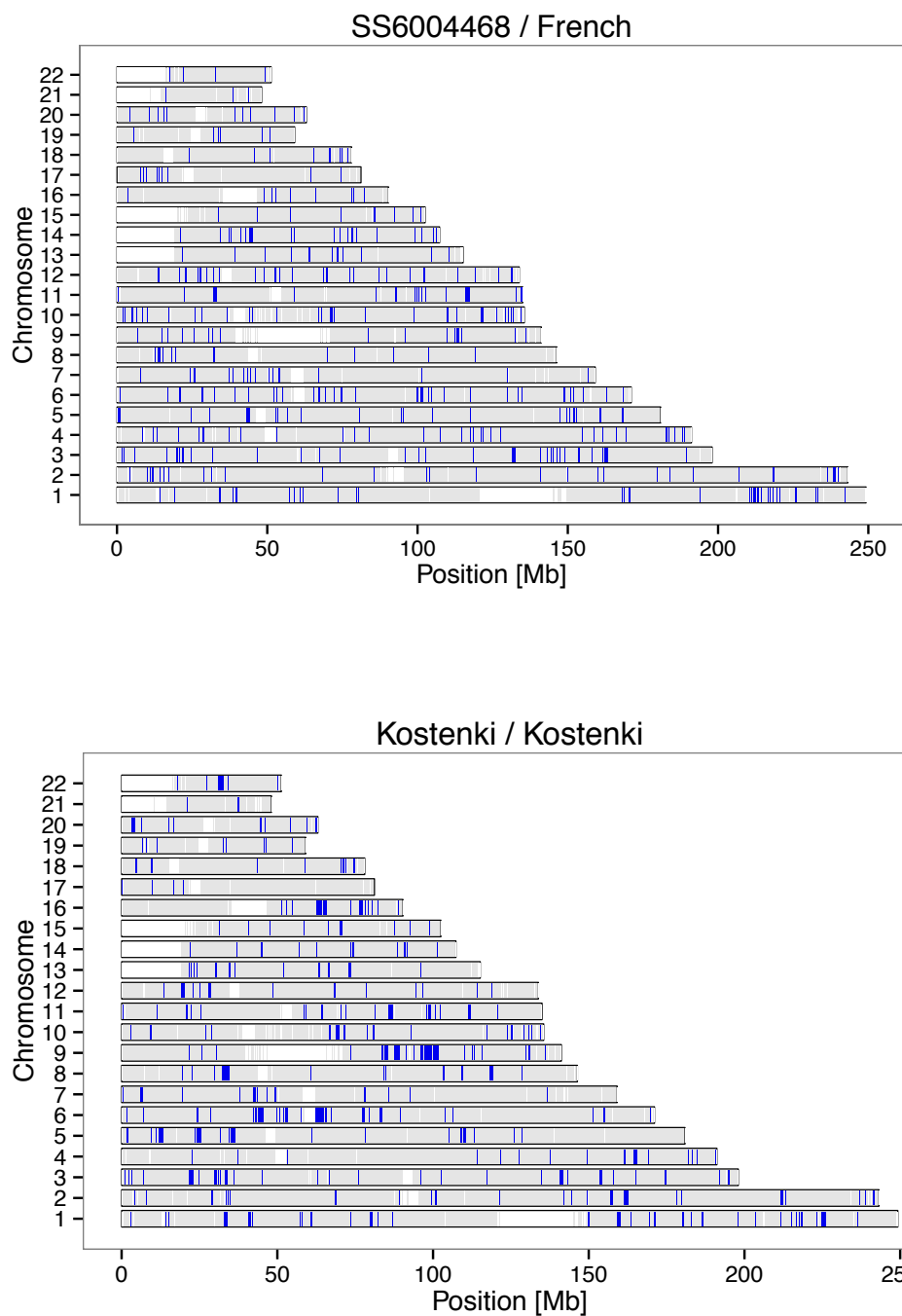


Fig. S26

Neanderthal chromosome painting. The tracts identified as Neanderthal (shown in blue) tend to be longer in K14 (lower panel) than a modern individual (e.g. French, upper panel).

Table S1.

Archeological layers in the western and eastern parts of Kostenki 14 (compiled after Sinitsyn 1996, Sinitsyn 2004, Sinitsyn 2010). Abbreviations explained in text.

Cultural Layer	Area	Geological Context	Age (in ka cal BP)	Archaeological association
CL I	West and East	CL	27.6-26.5 (minimum age?)	a large assemblage of mammoth bones and lithics attributed to the 'Kostenki-Avdeev' culture
CL II	West	UHB	33.6-31.5	'Gorodsovian' industry: The very rich lithic assemblage is flake based, typical 'Upper Paleolithic' blades are missing. Various 'Middle Paleolithic' tool types (sidescrapers, points, knives) are present. CL II also contains an extensive bone industry including mammoth bone spatulas, decorated bones and personal ornaments.
CL III	West and East	UHB	35.3-33.2	The lithic assemblage here is more blade based, but the level also contains a bone industry. It has been suggested that it has affinities to the Gordodsovian, a local Mid Upper Palaeolithic industry found in the overlying CL II.
Layer in Volcanic ash (LVA)	East	WL	39.3 (based on association with CI Y5 ash)	There is a small assemblage of artefacts (340) from within the volcanic ash. There are no cores, but evidence for unipolar striking with parallel dorsal scars, microblades, and micro-retouch. These have been interpreted as Dufour bladelets, and so provide an association with the Aurignacian (Sinitsyn 2003)
CL IV	West	LHB	Older than CI Y5 tephra	Blade dominated industry with unipolar blade production. Undiagnostic lithic tools including endscraper, burins and retouched flakes and blades. Some bone tools.
CL IVa	East	LHB	39.1-36 (minimum age?)	Few lithics, largely undiagnostic, with large numbers of horse bones.
CL in FS	East	LHB	40.8-37.5 (minimum age?)	Few, undiagnostic lithic and bone artefacts.
CL IVb	East	LHB	42.2-39.9 (minimum age?)	Rich lithic assemblage, distinctively Upper Palaeolithic, and unlike most assemblages in the region. Contains end scrapers, burins, prismatic cores, plus a bone industry and a possible carved ivory horse head, and has been assigned to the Initial Upper Palaeolithic (IUP) by Sinitsyn (2003) <i>sensu lato</i> . Human tooth remains from this level were provisionally assigned to modern humans

Table S2.

DNA extracts and summary statistics per library. P: silica pellets in solution approach (132).C: silica column-based approach (Dabney et al. 2013). USER: USER treated library (+). MBD: library enriched for methylated cytosines (+). %Endo: proportion of reads generated mapping uniquely against the human reference genome hg19 and passing quality filters. Cov.(X): average fold depth-of-coverage. The DNA libraries that have been selected for performing all downstream analyses based on contamination levels and error rates are indicated in bold. See details in SOM3-6.

	Extraction method	Extract #	USER	MBD	%Endo.	Cov.(X)	Length
All	NA	NA	NA	NA	1.58%	2.84542	50.3
K14_10c_ACAGAG_USER	P	1	+	-	0.98%	0.00552	50.2
K14_10c_AGTGAG_USER	P	1	+	-	0.70%	0.03294	51.9
K14_10c_CTCTGC_USER	P	1	+	-	0.99%	0.00214	50.7
K14_10c_GAGTAG_USER	P	1	+	-	0.73%	0.03553	51.3
K14_10c_GCTACT_USER	P	1	+	-	1.04%	0.00248	51.1
K14_10c_TAGCTG_USER	P	1	+	-	0.81%	0.02288	50.6
K14_14c_ACTGCG_USER	P	1	+	-	0.67%	0.03956	51.5
K14_14c_CAGCAC_USER	P	1	+	-	0.77%	0.03236	51.3
K14_14c_CGTAGT_USER	P	1	+	-	0.79%	0.02952	50.9
K14_14c_GTCGTC_USER	P	1	+	-	0.73%	0.02592	51.0
K14_14c_TACGAG_USER	P	1	+	-	0.73%	0.03290	51.4
K14_14c_TCGATG_USER	P	1	+	-	1.05%	0.00287	50.5
K14_TGAACA	P	1	-	-	1.70%	0.00611	55.3
K14_D1_2_CGTATA	C	2	-	-	0.45%	0.00278	49.9
K14_D1_3_TGATCG	C	2	-	-	0.43%	0.00237	50.5
K14_D1_CGCTAT	C	2	-	-	0.44%	0.00313	48.8
K14_D2_2_GTGTAT	C	3	-	-	0.57%	0.00263	48.3
K14_D2_3_TGCATA	C	3	-	-	0.49%	0.00296	49.6
K14_D2_TGAACA	C	3	-	-	0.58%	0.00234	48.5
K14_D3_USER_1_CGATGA	C	4	+	-	0.49%	0.00388	42.3
K14_D3_USER_2_TGCATA	C	4	+	-	0.46%	0.00485	42.8
K14_D3_USER_3_TCTCGC	C	5	+	-	0.30%	0.00283	43.0
K14_D3_USER_4_TGATGC	C	5	+	-	0.30%	0.00306	43.1
K14_A1_S2_1_USER_CAGCTA	P	6	+	-	1.22%	0.19670	57.6
K14_A2_S2_1_USER	P	6	+	-	1.15%	0.18102	56.7
K14_B1_S2_1_USER_ACAGTG	P	6	+	+	0.06%	0.00097	68.5
K14_B2_S2_1_USER_GCCAAT	P	6	+	+	0.01%	0.00075	66.6
K14_USER_Met1_ATCACG	P	6	+	+	0.15%	0.00083	67.5
K14_USER_Met2_TTAGGC	P	6	+	+	0.05%	0.00055	66.7
K14_S2_1_USER_36_TGCAGG	P	6	+	-	1.24%	0.17207	58.7
K14_S2_1_USER_37_ACTGCC	P	7	+	-	1.01%	0.22455	59.1
K14_A3_S2_2_USER	P	7	+	-	0.56%	0.01776	66.9

K14_A4_S2_2_USER	P	7	+	-	0.33%	0.01758	67.9
K14_B3_S2_2_MetCap_USER	P	7	+	+	0.05%	0.00112	69.2
K14_B4_S2_2_MetCap_USER	P	7	+	+	0.02%	0.00090	68.7
K14_USER_Met3_ACTTGA	P	7	+	+	0.14%	0.00091	67.7
K14_USER_Met4_GATCAG	P	7	+	+	0.10%	0.00064	66.9
K14_10_TAGCTT	P	8	+	-	0.12%	0.00030	50.1
K14_11_GGCTAC	P	8	+	-	0.13%	0.00036	50.6
K14_12_CTTGTA	P	8	+	-	0.12%	0.00066	51.0
K14_33_GACCGG	P	8	+	-	0.12%	0.00024	52.3
K14_34_GAGATA	P	8	+	-	0.12%	0.00038	50.1
K14_35_CTGACA	P	8	+	-	0.12%	0.00042	49.6
K14_46_CACGAA	P	8	+	-	0.12%	0.00040	51.2
K14_47_CATAGA	P	8	+	-	0.12%	0.00030	51.3
K14_48_ACAGTC	P	8	+	-	0.12%	0.00038	51.2
K14_49_CATCGT	P	8	+	-	0.12%	0.00065	52.8
K14_50_TTGAAC	P	8	+	-	0.12%	0.00071	50.9
K14_5_ACAGTG	P	8	+	-	0.12%	0.00063	49.7
K14_6_GCCAAT	P	8	+	-	0.12%	0.00080	50.9
K14_7_CAGATC	P	8	+	-	0.12%	0.00037	48.7
K14_8_ACTTGA	P	8	+	-	0.12%	0.00040	50.1
K14_9_GATCAG	P	8	+	-	0.12%	0.00021	50.4
K14_1_ATCACG	P	9	+	-	0.20%	0.00048	50.4
K14_24_CGATGA	P	9	+	-	0.20%	0.00066	48.1
K14_2_CGATGT	P	9	+	-	0.19%	0.00063	50.3
K14_31_GACACT	P	9	+	-	0.19%	0.00048	49.5
K14_36_TGCAGG	P	9	+	-	0.20%	0.00054	48.2
K14_37_ACTGCC	P	9	+	-	0.20%	0.00065	48.6
K14_38_GCAACG	P	9	+	-	0.19%	0.00054	48.3
K14_39_CGACCT	P	9	+	-	0.19%	0.00066	49.1
K14_3_TTAGGC	P	9	+	-	0.19%	0.00050	50.1
K14_40_TGACGT	P	9	+	-	0.19%	0.00058	49.5
K14_41_TGTCTG	P	9	+	-	0.19%	0.00055	49.1
K14_42_ACGTGC	P	9	+	-	0.19%	0.00045	49.3
K14_43_TGATCC	P	9	+	-	0.19%	0.00077	50.4
K14_44_CTCTAG	P	9	+	-	0.19%	0.00045	50.1
K14_45_GAGAAG	P	9	+	-	0.20%	0.00055	48.9
K14_4_TGACCA	P	9	+	-	0.19%	0.00061	51.5
K14_S5_1_A_ATCACG	P	10	+	-	2.46%	0.01581	39.3
K14_S5_2_B_TTAGGC	P	11	+	-	8.03%	0.03772	42.8
K14_S5_2_C_15_TGATCG	P	11	+	-	4.85%	0.56476	46.4
K14_S5_2_C_CAGATC	P	11	+	-	3.84%	0.78320	46.0

K14_S5_2_C_15_8_ACTTGA	P	11	+	-	3.62%	0.13211	53.6
K14_S5_2_C_15_6_GCCAAT	P	11	+	-	2.25%	0.16526	53.5
K14_S6_1_D_ACTTGA	P	12	+	-	0.97%	0.00586	39.0
K14_S6_2_E_GCCAAT	P	13	+	-	0.87%	0.00302	42.9
K14_S6_2_F_CTTGTA	P	13	+	-	0.92%	0.00343	44.0

Table S3.

Contamination estimates based on the MT for libraries selected for downstream analyses. We used a method described in Fu et al. 2013 (see SOM5 for details). The maximum a posteriori probability estimate (MAP) and the lower and upper bound of the 95% credible interval are shown.

	Contamination Estimate based on MT (MAP)	2.5%	97.5%
K14	3.8%	3.1%	4.5%
K14_A1_S2_1_USER_CAGCTA	1.0%	0.3%	3.1%
K14_A2_S2_1_USER	1.8%	0.7%	4.0%
K14_S2_1_USER_36_TGCAGG	3.0%	1.4%	5.7%
K14_S2_1_USER_37_ACTGCC	2.2%	0.9%	4.3%
K14_S5_2_C_15_TGATCG	2.8%	1.8%	4.3%
K14_S5_2_C_CAGATC	5.7%	4.5%	7.2%
K14_S5_2_C_15_8_ACTTGA	2.0%	0.6%	5.6%
K14_S5_2_C_15_6_GCCAAT	2.0%	0.6%	4.9%

Table S4.

Contamination estimates for the two X-based methods described in SOM S6.

X based contamination estimates for all libraries. See SOM6 for details. For some cases (“-”) contamination could not be estimated because either not enough data was available, or because the sample was a female.

Library	Method1	SE	Method2	SE
K14_10c_ACAGAG_USER	0.052	0.04	0.052	0.04
K14_10c_AGTGAG_USER	0.054	0.014	0.057	0.015
K14_10c_CTCTGC_USER	0.136	0.077	0.137	0.078
K14_10c_GAGTAG_USER	0.077	0.016	0.079	0.016
K14_10c_GCTACT_USER	0	0	0	0
K14_10c_TAGCTG_USER	0.047	0.016	0.047	0.015
K14_10_TAGCTT	0.409	0.406	0.409	0.406
K14_11_GGCTAC	0	0	0	0
K14_12_CTTGTA	0.64	0	0.64	0
K14_14c_ACTGCG_USER	0.068	0.015	0.065	0.014
K14_14c_CAGCAC_USER	0.083	0.017	0.086	0.017
K14_14c_CGTAGT_USER	0.056	0.014	0.061	0.015
K14_14c_GTCGTC_USER	0.067	0.017	0.07	0.018
K14_14c_TACGAG_USER	0.047	0.014	0.046	0.013
K14_14c_TCGATG_USER	0.034	0.034	0.034	0.034
K14_1_ATCACG	0.382	0.39	0.382	0.39
K14_24_CGATGA	0.347	0.191	0.347	0.191
K14_2_CGATGT	0.323	0.225	0.323	0.225
K14_31_GACACT	0.634	0.009	0.634	0.009
K14_33_GACCGG	0.435	NA	0.435	NA
K14_34_GAGATA	0.47	0.406	0.47	0.406
K14_35_CTGACA	0	0	0	0
K14_36_TGCAGG	0.217	0.251	0.217	0.251
K14_37_ACTGCC	0.535	0.099	0.535	0.099
K14_38_GCAACG	1	0	1	0
K14_39_CGACCT	0.358	0.195	0.358	0.195
K14_3_TTAGGC	0.448	0.241	0.448	0.241
K14_40_TGACGT	0.145	0.148	0.145	0.148
K14_41_TGTCTG	0.227	0.233	0.227	0.233
K14_42_ACGTGC	0.545	0.129	0.545	0.129
K14_43_TGATCC	0.769	0	0.769	0
K14_44_CTCTAG	0.426	0.426	0.426	0.426
K14_45_GAGAAG	0.534	0.162	0.534	0.162

K14_46_CACGAA	0	0	0	0
K14_47_CATAGA	0	0	0	0
k14_48_ACAGTC	0.38	0.393	0.38	0.393
K14_49_CATCGT	0	0	0	0
K14_4_TGACCA	0.901	0	0.901	0
K14_50_TTGAAC	0.389	0.27	0.389	0.27
K14_5_ACAGTG	0.34	0.371	0.34	0.371
K14_6_GCCAAT	0.433	0.292	0.433	0.292
K14_7_CAGATC	0	0	0	0
K14_8_ACTTGA	0	0	0	0
K14_9_GATCAG	0	NA	0	NA
K14_A1_S2_1_USER_CAGCTA	0.029	0.004	0.029	0.005
K14_A2_S2_1_USER	0.036	0.005	0.034	0.005
K14_A3_S2_2_USER	0.181	0.034	0.175	0.034
K14_A4_S2_2_USER	0.332	0.048	0.33	0.049
K14_B1_S2_1_USER_ACAGTG	0.403	0.157	0.383	0.141
K14_B2_S2_1_USER_GCCAAT	0.342	0.148	0.389	0.16
K14_B3_S2_2_MetCap_USER	0.738	0	0.787	0
K14_B4_S2_2_MetCap_USER	0.871	0	0.821	0
K14_Dabney_D3_USER_1_CGATGA	0.054	0.049	0.054	0.049
K14_Dabney_D3_USER_2_TGCATA	0.18	0.066	0.18	0.066
K14_Dabney_D3_USER_3_TCTCGC	0.042	0.042	0.042	0.042
K14_Dabney_D3_USER_4_TGATGC	0.126	0.071	0.126	0.071
K14_S5_1_A_ATCACG	0.03	0.016	0.03	0.016
K14_S5_2_B_TTAGGC	0.005	0.006	0.005	0.006
K14_S5_2_C_15_6_GCCAAT	0.019	0.004	0.02	0.004
K14_S5_2_C_15_8_ACTTGA	0.02	0.004	0.02	0.005
K14_S5_2_C_15_TGATCG	0.02	0.002	0.02	0.002
K14_S5_2_C_CAGATC	0.028	0.002	0.027	0.003
K14_S6_1_D_ACTTGA	0.049	0.036	0.049	0.036
K14_S6_2_E_GCCAAT	0	0	0	0
K14_S6_2_F_CTTGTA	0.106	0.063	0.106	0.063
K14_USER_Met1_ATCACG	0.691	0	0.691	0
K14_USER_Met2_TTAGGC	0.732	0	0.732	0
K14_USER_Met3_ACTTGA	0.424	0.149	0.441	0.152
K14_USER_Met4_GATCAG	0.224	0.15	0.248	0.157
S2_1_USER_36_TGCAGG	0.031	0.005	0.033	0.005
S2_1_USER_37_ACTGCC	0.04	0.005	0.041	0.005

Table S5.

X-based contamination estimates for ancient samples (SOM S6).

X based contamination estimates. See SOM6 for details. For some cases (“-“) contamination could not be estimated because either not enough data was available, or because the sample was a female.

<i>Sample</i>	Method 1		Method 2	
	<i>Estimate</i>	<i>SE</i>	<i>Estimate</i>	<i>SE</i>
K14	0.024	0.0011	0.021	0.0019
K14 5bp trimmed	0.020	0.0012	0.020	0.0019
Loschbour	0.0049	0.00028	0.0057	0.00089
Motala1	-	-	-	-
Motala2	0.010	0.010	6.6E-05	0
Motala3	0.0043	0.0021	0.0073	0.0039
Motala4	-	-	-	-
Motala6	6.6E-05	0.075	6.6E-05	0.075
Motala9	-	-	-	-
Motala12	0.0032	0.00053	0.0031	0.00091
Ajv58	0.012	0.0014	0.012	0.0022
Brana1	0.008	0.001	0.004	0.0018
Brana2	0.006	0.0012	0.004	0.0019
E733	0.030	0.0028	0.026	0.0040
Gok2	-	-	-	-
Iceman	0.012	0.00069	0.013	0.0013
LBK	-	-	-	-
MA1	0.013	0.002	0.0087	0.00289

Table S6.

ISOGG chromosome Y SNPs with derived allele in K14.

isoggId	haplogroup	position	mutation	K14	depth	isDamage
L990	A0	14001289	A->G	G	2	FALSE
L1085	A0-T	2790726	T->C	C	1	FALSE
L1089	A0-T	2887280	G->C	C	1	FALSE
L1105	A0-T	7590048	C->T	T	1	TRUE
L1116	A0-T	13888035	A->C	C	2	FALSE
L1120	A0-T	14496439	G->T	T	3	FALSE
L1121	A0-T	14496448	G->A	A	2	TRUE
L1123	A0-T	15425676	C->T	T	2	TRUE
L1128	A0-T	16428812	C->T	T	1	TRUE
L1129	A0-T	16596846	T->C	C	3	FALSE
L1130	A0-T	16661010	T->G	G	3	FALSE
L1132	A0-T	16718811	A->G	G	2	FALSE
L1137	A0-T	19047091	C->T	T	2	TRUE
L1145	A0-T	21739790	C->T	T	1	TRUE
L1150	A0-T	21903971	A->G	G	1	FALSE
L1155	A0-T	22191266	G->C	C	1	FALSE
L1002	A1	16392856	A->T	T	1	FALSE
L1004	A1	16773792	T->C	C	1	FALSE
L1009	A1	18180294	A->G	G	1	FALSE
L1013	A1	21646577	C->A	A	1	FALSE
L1053	A1	18759708	C->A	A	1	FALSE
L1084	A1	22957136	G->A	A	1	TRUE
L1112	A1	8466995	G->A	A	2	TRUE
L985	A1	7374927	A->C	C	1	FALSE
L989	A1	23551003	T->A	A	3	FALSE
V168	A1	17947672	G->A	A	1	TRUE
V238	A1	7651556	G->T	T	1	FALSE
V221	A1b	7589303	G->T	T	1	FALSE
M141	A1b1a1	21705977	T->A	A	2	FALSE
M118	A1b1b2b1	21763965	A->T	T	3	FALSE
V234	B (Investigation)	7644670	C->T	T	1	TRUE
V237	B (Investigation)	7647511	C->T	T	1	TRUE
50f2(P)	B2b1	23497067	G->C	C	2	FALSE
L1060	BT	21183571	C->T	T	4	TRUE
L1061	BT	22191243	G->A	A	1	TRUE
L957	BT	14079528	C->T	T	1	TRUE
L969	BT	21674225	T->C	C	1	FALSE

L977	BT	23302389	A->G	G	1	FALSE
M299	BT	22748506	T->G	G	1	FALSE
M42	BT	21866840	A->T	T	2	FALSE
M91	BT	21907538	del->T	T	1	FALSE
P97	BT	14886273	G->T	T	2	FALSE
Page65.1	BT	2657176	T->C	C	2	FALSE
PF1403	BT	2756519	T->C	C	4	FALSE
PF1411	BT	17037979	C->T	T	1	TRUE
V202	BT	2790584	G->C	C	1	FALSE
P255	C	8685038	G->A	A	1	TRUE
V183	C	14263271	G->A	A	1	TRUE
V199	C	2772928	C->A	A	2	FALSE
V232	C	7629098	T->C	C	1	FALSE
F3393	C1	23023974	C->A	A	1	FALSE
CTS3818	CF	15203676	A->G	G	3	FALSE
CTS6376	CF	16863259	C->G	G	2	FALSE
M168	CT	14813991	C->T	T	2	TRUE
M294	CT	22744945	C->T	T	2	TRUE
22457	D1b1a2	24464597	C->G	G	1	FALSE
Z1518	D1b2	8069557	C->T	T	4	TRUE
M5564	E	23463283	G->A	A	1	TRUE
Z15165	E1a2	23958822	T->C	C	2	FALSE
Z14907	E1a2b1a1a1	7787335	G->T	T	3	FALSE
Z16208	E1b1a1a1c2c3c	22542408	T->A	A	4	FALSE
CTS2590	E2	14376035	G->A	A	1	TRUE
P135	F	21618856	C->T	T	1	TRUE
Z14050	H1b1	14013176	G->A	A	1	TRUE
Z14173	H1b1	23004423	G->A	A	1	TRUE
P80	H1b1a	6739899	G->C	C	1	FALSE
P266	H1b1b	6739738	A->T	T	2	FALSE
Z14350	H1b2a	16314520	G->T	T	3	FALSE
Z13393	H3a	17248422	G->T	T	1	FALSE
CTS616	I2a2a1	6906332	C->G	G	1	FALSE
L1228	I2a2a2	15446045	C->G	G	1	FALSE
Z1842	J1a3a	21138032	C->T	T	1	TRUE
P329	L1a	8466781	G->A	A	1	TRUE
L58	N (Investigation)	6670461	T->G	G	1	FALSE
N10	O (Private)	21900347	C->G	G	1	FALSE
P103	O (Private)	15477831	G->C	C	5	FALSE
M199	Q1a2a1a1c	15031110	del->G	G	1	FALSE

Table S7.

D-statistics for *D*(Mbuti,K14)(X,Lithuanians). Positive values indicate K14 closer to Lithuanians.

p1	p2	p3	p4	D	sdJK	Z	nSites
MbutiPygmy	Kostenki	San	Lithuanians	0.356	0.004	101.3	359444
MbutiPygmy	Kostenki	BantuSouthAfrica	Lithuanians	0.314	0.003	93.3	370007
MbutiPygmy	Kostenki	MbutiPygmy	Lithuanians	0.446	0.003	144.2	375124
MbutiPygmy	Kostenki	BiakaPygmy	Lithuanians	0.345	0.003	105.8	373707
MbutiPygmy	Kostenki	Mandenka	Lithuanians	0.293	0.003	89.9	374355
MbutiPygmy	Kostenki	Yoruba	Lithuanians	0.299	0.003	93.0	374465
MbutiPygmy	Kostenki	BantuKenya	Lithuanians	0.291	0.003	90.8	373029
MbutiPygmy	Kostenki	Ethiopians	Lithuanians	0.170	0.003	66.0	372661
MbutiPygmy	Kostenki	EthiopianJews	Lithuanians	0.166	0.003	63.4	370132
MbutiPygmy	Kostenki	Egyptians	Lithuanians	0.078	0.002	36.7	366456
MbutiPygmy	Kostenki	Mozabite	Lithuanians	0.101	0.002	46.1	372678
MbutiPygmy	Kostenki	Moroccan	Lithuanians	0.106	0.002	45.3	367252
MbutiPygmy	Kostenki	MoroccanJews	Lithuanians	0.032	0.002	17.1	361083
MbutiPygmy	Kostenki	Yemenis	Lithuanians	0.093	0.002	37.5	365290
MbutiPygmy	Kostenki	YemeniJews	Lithuanians	0.046	0.002	21.7	361552
MbutiPygmy	Kostenki	Saudis	Lithuanians	0.048	0.002	24.3	366080
MbutiPygmy	Kostenki	Iranians	Lithuanians	0.034	0.002	18.4	364217
MbutiPygmy	Kostenki	IranJews	Lithuanians	0.028	0.002	11.4	349376
MbutiPygmy	Kostenki	IraqiJews	Lithuanians	0.027	0.002	13.2	356593
MbutiPygmy	Kostenki	Jordanian	Lithuanians	0.053	0.002	29.1	367766
MbutiPygmy	Kostenki	Syrians	Lithuanians	0.039	0.002	21.1	363528
MbutiPygmy	Kostenki	Bedouin	Lithuanians	0.056	0.002	30.7	372048
MbutiPygmy	Kostenki	Druze	Lithuanians	0.029	0.002	16.9	365393
MbutiPygmy	Kostenki	Palestinian	Lithuanians	0.049	0.002	27.4	370956
MbutiPygmy	Kostenki	Samaritans	Lithuanians	0.029	0.003	9.1	345872
MbutiPygmy	Kostenki	AshkenaziJews	Lithuanians	0.022	0.002	12.2	360331
MbutiPygmy	Kostenki	SephardicJews	Lithuanians	0.025	0.002	14.9	362002
MbutiPygmy	Kostenki	Lebanese	Lithuanians	0.039	0.002	17.6	356388
MbutiPygmy	Kostenki	Turkish	Lithuanians	0.022	0.002	12.9	361542
MbutiPygmy	Kostenki	Cypriots	Lithuanians	0.024	0.002	12.7	357847
MbutiPygmy	Kostenki	Bulgarians	Lithuanians	0.012	0.002	7.4	356986
MbutiPygmy	Kostenki	Romanian	Lithuanians	0.010	0.002	6.3	358900
MbutiPygmy	Kostenki	RomanianJews	Lithuanians	0.018	0.003	6.8	347244
MbutiPygmy	Kostenki	NorthItalian	Lithuanians	0.008	0.002	4.7	356188
MbutiPygmy	Kostenki	Tuscan	Lithuanians	0.013	0.002	6.8	353549

MbutiPygmy	Kostenki	Sardinian	Lithuanians	0.011	0.002	6.7	360703
MbutiPygmy	Kostenki	Spanish	Lithuanians	0.011	0.002	6.4	357028
MbutiPygmy	Kostenki	Basque	Lithuanians	0.004	0.002	2.7	358550
MbutiPygmy	Kostenki	French	Lithuanians	0.006	0.001	4.3	360938
MbutiPygmy	Kostenki	Orcadian	Lithuanians	0.004	0.002	2.6	356124
MbutiPygmy	Kostenki	Hungarians	Lithuanians	0.006	0.001	4.2	359039
MbutiPygmy	Kostenki	Ucranians	Lithuanians	0.005	0.001	3.5	358596
MbutiPygmy	Kostenki	Belarusians	Lithuanians	0.003	0.002	1.6	352836
MbutiPygmy	Kostenki	Estonians	Lithuanians	0.002	0.001	1.2	357377
MbutiPygmy	Kostenki	NWRussian	Lithuanians	0.005	0.001	3.4	360485
MbutiPygmy	Kostenki	Mordovians	Lithuanians	0.005	0.002	3.1	357522
MbutiPygmy	Kostenki	Chuvashs	Lithuanians	0.010	0.002	6.0	359426
MbutiPygmy	Kostenki	Maris	Lithuanians	0.011	0.002	5.6	357905
MbutiPygmy	Kostenki	Adygei	Lithuanians	0.017	0.002	9.6	359236
MbutiPygmy	Kostenki	Balkars	Lithuanians	0.019	0.002	10.9	360168
MbutiPygmy	Kostenki	Chechens	Lithuanians	0.016	0.002	8.9	359511
MbutiPygmy	Kostenki	Kumyks	Lithuanians	0.017	0.002	8.8	358920
MbutiPygmy	Kostenki	Lezgins	Lithuanians	0.015	0.002	8.6	359173
MbutiPygmy	Kostenki	Nogais	Lithuanians	0.019	0.002	10.4	360901
MbutiPygmy	Kostenki	NorthOssetians	Lithuanians	0.020	0.002	10.8	358941
MbutiPygmy	Kostenki	Abhkasians	Lithuanians	0.019	0.002	10.8	359704
MbutiPygmy	Kostenki	Armenians	Lithuanians	0.020	0.002	11.8	362558
MbutiPygmy	Kostenki	Georgians	Lithuanians	0.019	0.002	10.6	359307
MbutiPygmy	Kostenki	GeorgianJews	Lithuanians	0.028	0.002	12.4	354289
MbutiPygmy	Kostenki	AzerbaijanJews	Lithuanians	0.025	0.002	10.1	349140
MbutiPygmy	Kostenki	Kurds	Lithuanians	0.023	0.002	10.4	352564
MbutiPygmy	Kostenki	Turkmens	Lithuanians	0.025	0.002	13.2	361660
MbutiPygmy	Kostenki	Kazakhs	Lithuanians	0.026	0.002	11.4	361465
MbutiPygmy	Kostenki	Uzbeks	Lithuanians	0.026	0.002	13.5	363636
MbutiPygmy	Kostenki	UzbekJews	Lithuanians	0.026	0.003	8.8	344864
MbutiPygmy	Kostenki	Kyrgyzians	Lithuanians	0.029	0.003	11.1	361495
MbutiPygmy	Kostenki	Uygur	Lithuanians	0.026	0.002	11.4	358883
MbutiPygmy	Kostenki	Hazara	Lithuanians	0.026	0.002	12.3	363809
MbutiPygmy	Kostenki	Tajiks	Lithuanians	0.021	0.002	12.5	362577
MbutiPygmy	Kostenki	Burusho	Lithuanians	0.025	0.002	12.5	362829
MbutiPygmy	Kostenki	Pashtun	Lithuanians	0.023	0.002	9.9	352263
MbutiPygmy	Kostenki	Balochi	Lithuanians	0.034	0.002	17.4	365085
MbutiPygmy	Kostenki	Brahui	Lithuanians	0.035	0.002	17.8	365161
MbutiPygmy	Kostenki	Kalash	Lithuanians	0.022	0.002	10.3	357915
MbutiPygmy	Kostenki	Makrani	Lithuanians	0.047	0.002	23.5	368267
MbutiPygmy	Kostenki	Pathan	Lithuanians	0.024	0.002	13.1	362450

MbutiPygmy	Kostenki	Sindhi	Lithuanians	0.036	0.002	18.1	366118
MbutiPygmy	Kostenki	Bengali	Lithuanians	0.033	0.004	8.0	342446
MbutiPygmy	Kostenki	Bhunja	Lithuanians	0.043	0.004	9.8	343330
MbutiPygmy	Kostenki	BrahminsUttaranchal	Lithuanians	0.034	0.004	7.9	342633
MbutiPygmy	Kostenki	BrahminsUttarPradesh	Lithuanians	0.026	0.002	11.7	356502
MbutiPygmy	Kostenki	Chamar	Lithuanians	0.033	0.003	12.6	358148
MbutiPygmy	Kostenki	Dharkars	Lithuanians	0.030	0.002	12.2	358383
MbutiPygmy	Kostenki	Dusadh	Lithuanians	0.032	0.003	11.6	356551
MbutiPygmy	Kostenki	Kanjars	Lithuanians	0.032	0.003	12.7	356042
MbutiPygmy	Kostenki	Kurmi	Lithuanians	0.023	0.004	5.4	342529
MbutiPygmy	Kostenki	Kol	Lithuanians	0.032	0.002	13.3	361138
MbutiPygmy	Kostenki	Kshatriya	Lithuanians	0.026	0.002	11.3	355836
MbutiPygmy	Kostenki	Meena	Lithuanians	0.028	0.004	6.8	341479
MbutiPygmy	Kostenki	Meghawal	Lithuanians	0.032	0.004	7.4	341949
MbutiPygmy	Kostenki	Muslim	Lithuanians	0.032	0.003	12.1	353466
MbutiPygmy	Kostenki	Tharus	Lithuanians	0.031	0.003	9.0	346498
MbutiPygmy	Kostenki	UttarPradeshScheduledCaste	Lithuanians	0.035	0.003	11.3	349571
MbutiPygmy	Kostenki	BrahminsTamilNadu	Lithuanians	0.029	0.003	9.0	346282
MbutiPygmy	Kostenki	Chenchus	Lithuanians	0.035	0.003	12.1	351567
MbutiPygmy	Kostenki	Dhurwa	Lithuanians	0.040	0.004	9.4	343440
MbutiPygmy	Kostenki	Gond	Lithuanians	0.035	0.003	11.6	352138
MbutiPygmy	Kostenki	Hakkipikki	Lithuanians	0.036	0.003	11.7	351453
MbutiPygmy	Kostenki	NorthKannadi	Lithuanians	0.038	0.003	14.9	356844
MbutiPygmy	Kostenki	Kurumba	Lithuanians	0.034	0.003	11.2	350954
MbutiPygmy	Kostenki	Lambadi	Lithuanians	0.036	0.004	8.8	342283
MbutiPygmy	Kostenki	Malayan	Lithuanians	0.042	0.004	11.9	347312
MbutiPygmy	Kostenki	Paniya	Lithuanians	0.042	0.003	12.7	351634
MbutiPygmy	Kostenki	PiramalaiKallars	Lithuanians	0.036	0.003	13.0	356247
MbutiPygmy	Kostenki	Pulliyar	Lithuanians	0.039	0.003	12.0	351505
MbutiPygmy	Kostenki	Sakilli	Lithuanians	0.040	0.003	12.9	351439
MbutiPygmy	Kostenki	TamilNaduScheduledCaste	Lithuanians	0.032	0.003	9.7	346929
MbutiPygmy	Kostenki	Velamas	Lithuanians	0.035	0.002	14.1	357589
MbutiPygmy	Kostenki	Asur	Lithuanians	0.040	0.004	10.8	347577
MbutiPygmy	Kostenki	Bonda	Lithuanians	0.043	0.003	12.7	352230
MbutiPygmy	Kostenki	Gadaba	Lithuanians	0.043	0.004	10.2	343653
MbutiPygmy	Kostenki	Ho	Lithuanians	0.041	0.003	12.8	354336
MbutiPygmy	Kostenki	Juang	Lithuanians	0.044	0.004	11.6	348024
MbutiPygmy	Kostenki	Kharia	Lithuanians	0.041	0.004	10.9	347917
MbutiPygmy	Kostenki	Khasi	Lithuanians	0.038	0.003	11.4	350638
MbutiPygmy	Kostenki	Mawasi	Lithuanians	0.037	0.004	9.1	343209
MbutiPygmy	Kostenki	Santhal	Lithuanians	0.040	0.004	9.7	343460

MbutiPygmy	Kostenki	Savara	Lithuanians	0.038	0.004	10.8	347781
MbutiPygmy	Kostenki	Nihali	Lithuanians	0.037	0.004	10.5	347543
MbutiPygmy	Kostenki	Garro	Lithuanians	0.043	0.004	12.0	352544
MbutiPygmy	Kostenki	Naga	Lithuanians	0.042	0.004	11.6	351954
MbutiPygmy	Kostenki	IndianJews	Lithuanians	0.031	0.002	13.0	356340
MbutiPygmy	Kostenki	Burmese	Lithuanians	0.040	0.003	13.2	360473
MbutiPygmy	Kostenki	Cambodian	Lithuanians	0.041	0.003	12.6	357960
MbutiPygmy	Kostenki	Dai	Lithuanians	0.040	0.003	11.6	356965
MbutiPygmy	Kostenki	Han	Lithuanians	0.040	0.003	12.1	360719
MbutiPygmy	Kostenki	Han-NChina	Lithuanians	0.039	0.003	11.3	357277
MbutiPygmy	Kostenki	Lahu	Lithuanians	0.043	0.004	12.0	355253
MbutiPygmy	Kostenki	Miao	Lithuanians	0.039	0.003	11.3	356843
MbutiPygmy	Kostenki	Naxi	Lithuanians	0.041	0.003	12.3	355967
MbutiPygmy	Kostenki	She	Lithuanians	0.040	0.004	11.2	356395
MbutiPygmy	Kostenki	Tujia	Lithuanians	0.040	0.003	11.7	357262
MbutiPygmy	Kostenki	Yi	Lithuanians	0.039	0.003	11.4	357245
MbutiPygmy	Kostenki	Japanese	Lithuanians	0.039	0.003	11.8	360026
MbutiPygmy	Kostenki	Daur	Lithuanians	0.038	0.003	11.5	356631
MbutiPygmy	Kostenki	Hezhen	Lithuanians	0.039	0.003	11.4	355808
MbutiPygmy	Kostenki	Oroqen	Lithuanians	0.035	0.003	10.6	356246
MbutiPygmy	Kostenki	Tu	Lithuanians	0.039	0.003	11.9	357859
MbutiPygmy	Kostenki	Xibo	Lithuanians	0.037	0.003	11.3	356984
MbutiPygmy	Kostenki	Mongola	Lithuanians	0.037	0.003	11.4	357520
MbutiPygmy	Kostenki	Mongolians	Lithuanians	0.030	0.003	10.5	357174
MbutiPygmy	Kostenki	Altaians	Lithuanians	0.027	0.003	10.7	360439
MbutiPygmy	Kostenki	Buryats	Lithuanians	0.032	0.003	10.8	359419
MbutiPygmy	Kostenki	Dolgans	Lithuanians	0.028	0.003	9.9	356555
MbutiPygmy	Kostenki	Kets	Lithuanians	0.021	0.003	6.8	349915
MbutiPygmy	Kostenki	Khakases	Lithuanians	0.023	0.002	9.9	360383
MbutiPygmy	Kostenki	Nganassans	Lithuanians	0.030	0.003	9.5	356017
MbutiPygmy	Kostenki	Selkups	Lithuanians	0.019	0.002	7.7	358335
MbutiPygmy	Kostenki	Shors	Lithuanians	0.023	0.003	7.7	350789
MbutiPygmy	Kostenki	Tuvinians	Lithuanians	0.032	0.003	11.0	359116
MbutiPygmy	Kostenki	Nivkhs	Lithuanians	0.032	0.003	9.7	349377
MbutiPygmy	Kostenki	Yakut	Lithuanians	0.031	0.003	10.9	360251
MbutiPygmy	Kostenki	Evenkis	Lithuanians	0.031	0.003	10.4	357851
MbutiPygmy	Kostenki	Evens	Lithuanians	0.034	0.003	10.1	354634
MbutiPygmy	Kostenki	Yukaghirs	Lithuanians	0.024	0.003	8.8	354862
MbutiPygmy	Kostenki	Koryaks	Lithuanians	0.025	0.003	7.6	356354
MbutiPygmy	Kostenki	Chukchis	Lithuanians	0.025	0.003	8.5	356700
MbutiPygmy	Kostenki	EastGreenlanders	Lithuanians	0.021	0.003	7.0	353691

MbutiPygmy	Kostenki	WestGreenlanders	Lithuanians	0.017	0.003	6.3	354838
MbutiPygmy	Kostenki	Maya	Lithuanians	0.024	0.003	7.2	358417
MbutiPygmy	Kostenki	Pima	Lithuanians	0.021	0.004	5.5	351227
MbutiPygmy	Kostenki	Colombian	Lithuanians	0.023	0.004	6.3	350250
MbutiPygmy	Kostenki	Karitiana	Lithuanians	0.017	0.004	4.4	349416
MbutiPygmy	Kostenki	Surui	Lithuanians	0.020	0.004	4.9	347408
MbutiPygmy	Kostenki	Melanesian	Lithuanians	0.050	0.004	11.7	353923
MbutiPygmy	Kostenki	Papuan	Lithuanians	0.054	0.004	12.6	353787

Table S8.

D -statistics for $D(\text{Outgroup}, K14)(X, \text{French})$. Positive values indicate K14 closer to French. Altai Neanderthal whole modern genomes.

p1	p2	p3	p4	D	sdJK	Z	nSites
MbutiPygmy	Kostenki	San	French	0.393	0.005	77.1	1172844
MbutiPygmy	Kostenki	Mandenka	French	0.329	0.005	64.2	1145123
MbutiPygmy	Kostenki	Yoruba	French	0.335	0.005	63.5	1155436
MbutiPygmy	Kostenki	Dinka	French	0.321	0.005	62.1	1145195
MbutiPygmy	Kostenki	Sardinian	French	0.013	0.006	2.1	933558
MbutiPygmy	Kostenki	Han	French	0.047	0.006	7.4	970333
MbutiPygmy	Kostenki	Dai	French	0.044	0.006	7.0	969931
MbutiPygmy	Kostenki	Mixe	French	0.029	0.006	4.6	938306
MbutiPygmy	Kostenki	Karitiana	French	0.022	0.006	3.4	927792
MbutiPygmy	Kostenki	Papuan	French	0.058	0.007	8.5	953359
MbutiPygmy	Kostenki	Australian	French	0.056	0.006	8.6	1111101

Table S9.

D-statistics for $D(\text{Outgroup}, \text{Kostenki})(X, \text{French})$. Positive values indicate K14 closer to French. Mal'ta paper whole modern genomes.

p1	p2	p3	p4	D	sdJK	Z	nSites
MbutiPygmy	Kostenki	San	French	0.401	0.005	82.9	779767
MbutiPygmy	Kostenki	Mandenka	French	0.327	0.005	64.4	752632
MbutiPygmy	Kostenki	Yoruba	French	0.334	0.005	66.4	763508
MbutiPygmy	Kostenki	Dinka	French	0.309	0.005	59.0	759085
MbutiPygmy	Kostenki	Sardinian	French	0.008	0.006	1.4	615515
MbutiPygmy	Kostenki	Mari	French	0.010	0.006	1.6	132268
MbutiPygmy	Kostenki	Avar	French	0.013	0.006	2.2	330182
MbutiPygmy	Kostenki	Tajik	French	0.010	0.006	1.7	473285
MbutiPygmy	Kostenki	Indian	French	0.030	0.006	5.1	431881
MbutiPygmy	Kostenki	Han	French	0.043	0.006	7.0	647947
MbutiPygmy	Kostenki	Dai	French	0.042	0.006	7.1	648360
MbutiPygmy	Kostenki	Karitiana	French	0.009	0.006	1.4	614932
MbutiPygmy	Kostenki	Papuan	French	0.051	0.007	7.8	632657

Table S10:

D-statistics for *D*(Mbuti,Modern)(Ancient, K14); modern genomes from Prufer et al. (2014).

p1	p2	p3	p4	D	sdJK	Z	nSites
MbutiPygmy	San	MA1	Kostenki	-0.005	0.006	-0.8	115571
MbutiPygmy	San	Loschbour	Kostenki	-0.010	0.006	-1.8	166027
MbutiPygmy	San	Brana	Kostenki	0.000	0.006	0.1	120369
MbutiPygmy	San	Motala	Kostenki	0.000	0.006	-0.1	152012
MbutiPygmy	San	Ajv58	Kostenki	-0.007	0.006	-1.1	147098
MbutiPygmy	San	Gok2	Kostenki	-0.002	0.005	-0.4	98711
MbutiPygmy	San	Iceman	Kostenki	-0.005	0.006	-0.8	158243
MbutiPygmy	San	Stuttgart	Kostenki	0.000	0.005	0.0	171993
MbutiPygmy	Mandenka	MA1	Kostenki	-0.010	0.006	-1.6	123458
MbutiPygmy	Mandenka	Loschbour	Kostenki	-0.026	0.006	-4.7	177809
MbutiPygmy	Mandenka	Brana	Kostenki	-0.009	0.005	-1.8	129212
MbutiPygmy	Mandenka	Motala	Kostenki	-0.012	0.005	-2.2	163097
MbutiPygmy	Mandenka	Ajv58	Kostenki	-0.016	0.006	-2.8	158226
MbutiPygmy	Mandenka	Gok2	Kostenki	-0.015	0.005	-2.7	106163
MbutiPygmy	Mandenka	Iceman	Kostenki	-0.026	0.005	-4.8	170566
MbutiPygmy	Mandenka	Stuttgart	Kostenki	-0.017	0.005	-3.2	184602
MbutiPygmy	Yoruba	MA1	Kostenki	-0.010	0.006	-1.8	123626
MbutiPygmy	Yoruba	Loschbour	Kostenki	-0.019	0.006	-3.4	177200
MbutiPygmy	Yoruba	Brana	Kostenki	-0.006	0.006	-1.1	128420
MbutiPygmy	Yoruba	Motala	Kostenki	-0.007	0.005	-1.3	162582
MbutiPygmy	Yoruba	Ajv58	Kostenki	-0.014	0.006	-2.4	157238
MbutiPygmy	Yoruba	Gok2	Kostenki	-0.008	0.006	-1.5	105653
MbutiPygmy	Yoruba	Iceman	Kostenki	-0.018	0.005	-3.3	169431
MbutiPygmy	Yoruba	Stuttgart	Kostenki	-0.013	0.005	-2.4	182961
MbutiPygmy	Dinka	MA1	Kostenki	-0.009	0.006	-1.6	123931
MbutiPygmy	Dinka	Loschbour	Kostenki	-0.017	0.006	-2.8	177487
MbutiPygmy	Dinka	Brana	Kostenki	-0.008	0.006	-1.4	128916
MbutiPygmy	Dinka	Motala	Kostenki	-0.001	0.006	-0.1	163195
MbutiPygmy	Dinka	Ajv58	Kostenki	-0.012	0.006	-2.0	158204
MbutiPygmy	Dinka	Gok2	Kostenki	-0.020	0.006	-3.6	106048
MbutiPygmy	Dinka	Iceman	Kostenki	-0.013	0.006	-2.4	170270
MbutiPygmy	Dinka	Stuttgart	Kostenki	-0.012	0.006	-2.1	184627
MbutiPygmy	Sardinian	MA1	Kostenki	-0.012	0.007	-1.8	143868
MbutiPygmy	Sardinian	Loschbour	Kostenki	-0.085	0.007	-12.8	209554

MbutiPygmy	Sardinian	Brana	Kostenki	-0.062	0.007	-9.4	151515
MbutiPygmy	Sardinian	Motala	Kostenki	-0.067	0.007	-9.9	192016
MbutiPygmy	Sardinian	Ajv58	Kostenki	-0.069	0.007	-10.5	186194
MbutiPygmy	Sardinian	Gok2	Kostenki	-0.098	0.007	-14.9	125867
MbutiPygmy	Sardinian	Iceman	Kostenki	-0.083	0.006	-13.3	201173
MbutiPygmy	Sardinian	Stuttgart	Kostenki	-0.095	0.007	-13.8	219017
MbutiPygmy	French	MA1	Kostenki	-0.038	0.007	-5.3	147012
MbutiPygmy	French	Loschbour	Kostenki	-0.094	0.006	-14.9	213063
MbutiPygmy	French	Brana	Kostenki	-0.080	0.006	-13.2	154192
MbutiPygmy	French	Motala	Kostenki	-0.085	0.007	-12.4	196072
MbutiPygmy	French	Ajv58	Kostenki	-0.086	0.007	-12.6	189049
MbutiPygmy	French	Gok2	Kostenki	-0.077	0.006	-12.0	126985
MbutiPygmy	French	Iceman	Kostenki	-0.074	0.006	-12.3	203734
MbutiPygmy	French	Stuttgart	Kostenki	-0.069	0.007	-10.4	220632
MbutiPygmy	Han	MA1	Kostenki	-0.039	0.007	-5.4	140727
MbutiPygmy	Han	Loschbour	Kostenki	-0.039	0.007	-5.3	201566
MbutiPygmy	Han	Brana	Kostenki	-0.024	0.007	-3.5	146036
MbutiPygmy	Han	Motala	Kostenki	-0.026	0.007	-4.0	185194
MbutiPygmy	Han	Ajv58	Kostenki	-0.026	0.007	-3.7	179068
MbutiPygmy	Han	Gok2	Kostenki	-0.013	0.007	-1.9	119918
MbutiPygmy	Han	Iceman	Kostenki	-0.004	0.006	-0.6	192304
MbutiPygmy	Han	Stuttgart	Kostenki	0.000	0.007	0.0	208439
MbutiPygmy	Dai	MA1	Kostenki	-0.038	0.007	-5.5	141382
MbutiPygmy	Dai	Loschbour	Kostenki	-0.023	0.007	-3.1	202056
MbutiPygmy	Dai	Brana	Kostenki	-0.013	0.007	-1.9	146239
MbutiPygmy	Dai	Motala	Kostenki	-0.018	0.007	-2.6	185346
MbutiPygmy	Dai	Ajv58	Kostenki	-0.021	0.007	-3.1	179385
MbutiPygmy	Dai	Gok2	Kostenki	-0.009	0.007	-1.4	119918
MbutiPygmy	Dai	Iceman	Kostenki	-0.001	0.007	-0.1	191885
MbutiPygmy	Dai	Stuttgart	Kostenki	-0.001	0.007	-0.1	208671
MbutiPygmy	Mixe	MA1	Kostenki	-0.091	0.007	-12.7	140768
MbutiPygmy	Mixe	Loschbour	Kostenki	-0.028	0.007	-4.1	197906
MbutiPygmy	Mixe	Brana	Kostenki	-0.025	0.007	-3.6	143467
MbutiPygmy	Mixe	Motala	Kostenki	-0.048	0.007	-7.0	183071
MbutiPygmy	Mixe	Ajv58	Kostenki	-0.045	0.007	-6.5	176551
MbutiPygmy	Mixe	Gok2	Kostenki	-0.001	0.007	-0.2	117501
MbutiPygmy	Mixe	Iceman	Kostenki	0.001	0.007	0.1	188825
MbutiPygmy	Mixe	Stuttgart	Kostenki	0.003	0.007	0.4	204608
MbutiPygmy	Karitiana	MA1	Kostenki	-0.086	0.008	-11.2	138927

MbutiPygmy	Karitiana	Loschbour	Kostenki	-0.027	0.007	-3.8	195802
MbutiPygmy	Karitiana	Brana	Kostenki	-0.023	0.007	-3.4	142149
MbutiPygmy	Karitiana	Motala	Kostenki	-0.047	0.007	-6.6	181158
MbutiPygmy	Karitiana	Ajv58	Kostenki	-0.035	0.007	-4.8	174452
MbutiPygmy	Karitiana	Gok2	Kostenki	-0.001	0.007	-0.2	116412
MbutiPygmy	Karitiana	Iceman	Kostenki	0.006	0.007	0.8	186439
MbutiPygmy	Karitiana	Stuttgart	Kostenki	0.009	0.007	1.3	201830
MbutiPygmy	Papuan	MA1	Kostenki	-0.022	0.007	-3.0	134960
MbutiPygmy	Papuan	Loschbour	Kostenki	-0.016	0.007	-2.2	193181
MbutiPygmy	Papuan	Brana	Kostenki	-0.003	0.007	-0.4	139878
MbutiPygmy	Papuan	Motala	Kostenki	-0.012	0.007	-1.7	177496
MbutiPygmy	Papuan	Ajv58	Kostenki	-0.006	0.007	-0.8	171333
MbutiPygmy	Papuan	Gok2	Kostenki	0.002	0.007	0.2	114673
MbutiPygmy	Papuan	Iceman	Kostenki	0.008	0.007	1.2	184011
MbutiPygmy	Papuan	Stuttgart	Kostenki	0.006	0.007	0.9	199951
MbutiPygmy	Australian	MA1	Kostenki	-0.023	0.007	-3.3	158792
MbutiPygmy	Australian	Loschbour	Kostenki	-0.014	0.007	-2.0	226708
MbutiPygmy	Australian	Brana	Kostenki	-0.007	0.007	-1.1	164499
MbutiPygmy	Australian	Motala	Kostenki	-0.010	0.007	-1.5	208593
MbutiPygmy	Australian	Ajv58	Kostenki	-0.008	0.007	-1.2	201471
MbutiPygmy	Australian	Gok2	Kostenki	0.003	0.007	0.5	134531
MbutiPygmy	Australian	Iceman	Kostenki	0.007	0.006	1.2	215625
MbutiPygmy	Australian	Stuttgart	Kostenki	0.013	0.007	1.9	234191

Table S11.

D-statistics for *D*(Mbuti,Modern)(Ancient, K14); modern genomes from Raghavan et al. (2014).

p1	p2	p3	p4	D	sdJK	Z	nSites
MbutiPygmy	San	MA1	Kostenki	-0.003	0.006	-0.6	78821
MbutiPygmy	San	Loschbour	Kostenki	-0.004	0.006	-0.7	112712
MbutiPygmy	San	Brana	Kostenki	0.000	0.006	0.0	80913
MbutiPygmy	San	Motala	Kostenki	0.000	0.006	0.1	103026
MbutiPygmy	San	Ajv58	Kostenki	-0.008	0.006	-1.3	100277
MbutiPygmy	San	Gok2	Kostenki	-0.006	0.006	-1.0	65522
MbutiPygmy	San	Iceman	Kostenki	0.002	0.006	0.3	106426
MbutiPygmy	San	Stuttgart	Kostenki	-0.001	0.006	-0.2	116437
MbutiPygmy	Mandenka	MA1	Kostenki	0.008	0.006	1.4	83168
MbutiPygmy	Mandenka	Loschbour	Kostenki	-0.004	0.006	-0.6	118675
MbutiPygmy	Mandenka	Brana	Kostenki	-0.002	0.006	-0.3	85199
MbutiPygmy	Mandenka	Motala	Kostenki	0.001	0.006	0.2	108818
MbutiPygmy	Mandenka	Ajv58	Kostenki	-0.003	0.006	-0.5	105677
MbutiPygmy	Mandenka	Gok2	Kostenki	-0.006	0.006	-1.0	69105
MbutiPygmy	Mandenka	Iceman	Kostenki	0.006	0.005	1.1	112405
MbutiPygmy	Mandenka	Stuttgart	Kostenki	-0.007	0.006	-1.3	123312
MbutiPygmy	Yoruba	MA1	Kostenki	0.002	0.006	0.3	83661
MbutiPygmy	Yoruba	Loschbour	Kostenki	-0.010	0.006	-1.7	119761
MbutiPygmy	Yoruba	Brana	Kostenki	-0.010	0.006	-1.8	85981
MbutiPygmy	Yoruba	Motala	Kostenki	0.001	0.006	0.2	109603
MbutiPygmy	Yoruba	Ajv58	Kostenki	-0.015	0.006	-2.5	106470
MbutiPygmy	Yoruba	Gok2	Kostenki	-0.006	0.006	-1.1	69744
MbutiPygmy	Yoruba	Iceman	Kostenki	-0.001	0.006	-0.2	113172
MbutiPygmy	Yoruba	Stuttgart	Kostenki	-0.010	0.006	-1.7	124127
MbutiPygmy	Dinka	MA1	Kostenki	0.003	0.006	0.5	85002
MbutiPygmy	Dinka	Loschbour	Kostenki	-0.004	0.006	-0.6	122003
MbutiPygmy	Dinka	Brana	Kostenki	0.001	0.006	0.1	87082
MbutiPygmy	Dinka	Motala	Kostenki	-0.003	0.006	-0.4	111675
MbutiPygmy	Dinka	Ajv58	Kostenki	-0.009	0.006	-1.4	108309
MbutiPygmy	Dinka	Gok2	Kostenki	-0.003	0.006	-0.4	70654
MbutiPygmy	Dinka	Iceman	Kostenki	-0.003	0.006	-0.5	115579
MbutiPygmy	Dinka	Stuttgart	Kostenki	-0.003	0.006	-0.5	126353
MbutiPygmy	Sardinian	MA1	Kostenki	-0.012	0.007	-1.7	97338
MbutiPygmy	Sardinian	Loschbour	Kostenki	-0.083	0.007	-11.9	141445
MbutiPygmy	Sardinian	Brana	Kostenki	-0.064	0.007	-9.4	100800

MbutiPygmy	Sardinian	Motala	Kostenki	-0.057	0.007	-8.0	129081
MbutiPygmy	Sardinian	Ajv58	Kostenki	-0.070	0.007	-9.8	125246
MbutiPygmy	Sardinian	Gok2	Kostenki	-0.095	0.006	-14.7	82341
MbutiPygmy	Sardinian	Iceman	Kostenki	-0.078	0.007	-11.2	134599
MbutiPygmy	Sardinian	Stuttgart	Kostenki	-0.094	0.007	-13.7	147353
MbutiPygmy	French	MA1	Kostenki	-0.022	0.007	-3.1	99145
MbutiPygmy	French	Loschbour	Kostenki	-0.090	0.007	-13.2	143888
MbutiPygmy	French	Brana	Kostenki	-0.072	0.007	-10.3	102409
MbutiPygmy	French	Motala	Kostenki	-0.079	0.007	-11.6	131688
MbutiPygmy	French	Ajv58	Kostenki	-0.080	0.007	-11.8	127610
MbutiPygmy	French	Gok2	Kostenki	-0.082	0.007	-12.4	83617
MbutiPygmy	French	Iceman	Kostenki	-0.065	0.007	-9.4	136163
MbutiPygmy	French	Stuttgart	Kostenki	-0.069	0.007	-10.2	148652
MbutiPygmy	Mari	MA1	Kostenki	-0.043	0.010	-4.3	20424
MbutiPygmy	Mari	Loschbour	Kostenki	-0.068	0.009	-7.6	27386
MbutiPygmy	Mari	Brana	Kostenki	-0.050	0.009	-5.6	24704
MbutiPygmy	Mari	Motala	Kostenki	-0.072	0.009	-8.0	25429
MbutiPygmy	Mari	Ajv58	Kostenki	-0.063	0.009	-7.4	24378
MbutiPygmy	Mari	Gok2	Kostenki	-0.053	0.009	-5.9	23349
MbutiPygmy	Mari	Iceman	Kostenki	-0.028	0.009	-3.2	26575
MbutiPygmy	Mari	Stuttgart	Kostenki	-0.040	0.009	-4.6	28437
MbutiPygmy	Avar	MA1	Kostenki	-0.038	0.007	-5.4	52663
MbutiPygmy	Avar	Loschbour	Kostenki	-0.065	0.007	-9.5	71055
MbutiPygmy	Avar	Brana	Kostenki	-0.047	0.007	-6.8	60196
MbutiPygmy	Avar	Motala	Kostenki	-0.064	0.007	-9.2	65910
MbutiPygmy	Avar	Ajv58	Kostenki	-0.067	0.007	-10.1	63967
MbutiPygmy	Avar	Gok2	Kostenki	-0.062	0.007	-9.4	56412
MbutiPygmy	Avar	Iceman	Kostenki	-0.049	0.007	-7.3	70373
MbutiPygmy	Avar	Stuttgart	Kostenki	-0.063	0.007	-9.3	73683
MbutiPygmy	Tajik	MA1	Kostenki	-0.040	0.007	-5.8	75674
MbutiPygmy	Tajik	Loschbour	Kostenki	-0.049	0.007	-7.1	103790
MbutiPygmy	Tajik	Brana	Kostenki	-0.047	0.007	-6.6	82476
MbutiPygmy	Tajik	Motala	Kostenki	-0.055	0.007	-7.8	95973
MbutiPygmy	Tajik	Ajv58	Kostenki	-0.056	0.007	-8.4	92676
MbutiPygmy	Tajik	Gok2	Kostenki	-0.050	0.007	-7.4	73103
MbutiPygmy	Tajik	Iceman	Kostenki	-0.039	0.007	-5.8	102026
MbutiPygmy	Tajik	Stuttgart	Kostenki	-0.048	0.007	-7.3	107745
MbutiPygmy	Indian	MA1	Kostenki	-0.034	0.007	-4.8	67360
MbutiPygmy	Indian	Loschbour	Kostenki	-0.036	0.006	-5.7	92518

MbutiPygmy	Indian	Brana	Kostenki	-0.026	0.007	-3.7	72306
MbutiPygmy	Indian	Motala	Kostenki	-0.030	0.007	-4.3	85057
MbutiPygmy	Indian	Ajv58	Kostenki	-0.034	0.007	-4.9	82312
MbutiPygmy	Indian	Gok2	Kostenki	-0.030	0.007	-4.5	63444
MbutiPygmy	Indian	Iceman	Kostenki	-0.017	0.007	-2.5	89919
MbutiPygmy	Indian	Stuttgart	Kostenki	-0.022	0.007	-3.2	95204
MbutiPygmy	Han	MA1	Kostenki	-0.027	0.008	-3.5	96432
MbutiPygmy	Han	Loschbour	Kostenki	-0.021	0.007	-2.8	137766
MbutiPygmy	Han	Brana	Kostenki	-0.015	0.007	-2.1	98190
MbutiPygmy	Han	Motala	Kostenki	-0.020	0.007	-2.9	126212
MbutiPygmy	Han	Ajv58	Kostenki	-0.019	0.007	-2.7	122220
MbutiPygmy	Han	Gok2	Kostenki	-0.007	0.007	-0.9	79697
MbutiPygmy	Han	Iceman	Kostenki	0.015	0.007	2.1	129806
MbutiPygmy	Han	Stuttgart	Kostenki	0.000	0.007	0.0	141874
MbutiPygmy	Dai	MA1	Kostenki	-0.032	0.007	-4.4	96628
MbutiPygmy	Dai	Loschbour	Kostenki	-0.017	0.007	-2.3	137787
MbutiPygmy	Dai	Brana	Kostenki	-0.017	0.007	-2.4	98628
MbutiPygmy	Dai	Motala	Kostenki	-0.014	0.007	-2.0	126306
MbutiPygmy	Dai	Ajv58	Kostenki	-0.017	0.007	-2.4	122241
MbutiPygmy	Dai	Gok2	Kostenki	-0.006	0.007	-0.9	80226
MbutiPygmy	Dai	Iceman	Kostenki	0.015	0.007	2.2	130030
MbutiPygmy	Dai	Stuttgart	Kostenki	0.003	0.007	0.5	142047
MbutiPygmy	Karitiana	MA1	Kostenki	-0.076	0.008	-9.8	94637
MbutiPygmy	Karitiana	Loschbour	Kostenki	-0.018	0.007	-2.4	133143
MbutiPygmy	Karitiana	Brana	Kostenki	-0.015	0.007	-2.1	95149
MbutiPygmy	Karitiana	Motala	Kostenki	-0.037	0.007	-5.1	122668
MbutiPygmy	Karitiana	Ajv58	Kostenki	-0.032	0.007	-4.6	118349
MbutiPygmy	Karitiana	Gok2	Kostenki	0.006	0.007	0.8	76768
MbutiPygmy	Karitiana	Iceman	Kostenki	0.022	0.007	3.0	125104
MbutiPygmy	Karitiana	Stuttgart	Kostenki	0.017	0.007	2.4	136584
MbutiPygmy	Papuan	MA1	Kostenki	-0.010	0.008	-1.3	92223
MbutiPygmy	Papuan	Loschbour	Kostenki	-0.005	0.008	-0.6	131228
MbutiPygmy	Papuan	Brana	Kostenki	0.002	0.008	0.3	93872
MbutiPygmy	Papuan	Motala	Kostenki	-0.008	0.007	-1.1	120638
MbutiPygmy	Papuan	Ajv58	Kostenki	0.000	0.007	0.0	116730
MbutiPygmy	Papuan	Gok2	Kostenki	0.007	0.008	0.9	75952
MbutiPygmy	Papuan	Iceman	Kostenki	0.018	0.007	2.4	124203
MbutiPygmy	Papuan	Stuttgart	Kostenki	0.014	0.008	1.9	135598

Table S12. f_4 -statistics $f_4(\text{Sardinian, Ancient})(\text{Modern, Papuan})$ for Siberian populations.

p1	p2	p3	p4	f4	sdJK	Z	nSites
Sardinian	Kostenki	Altaians	Papuan	0.004	0.000	8.6	450206
Sardinian	Kostenki	Buryats	Papuan	0.002	0.000	5.3	450206
Sardinian	Kostenki	Dolgans	Papuan	0.003	0.000	6.4	450206
Sardinian	Kostenki	Kets	Papuan	0.003	0.000	6.1	450206
Sardinian	Kostenki	Khakases	Papuan	0.004	0.000	9.7	450206
Sardinian	Kostenki	Nganassans	Papuan	0.002	0.000	4.8	450206
Sardinian	Kostenki	Selkups	Papuan	0.004	0.000	8.0	450206
Sardinian	Kostenki	Shors	Papuan	0.004	0.000	8.0	450206
Sardinian	Kostenki	Tuvinians	Papuan	0.003	0.000	5.8	450206
Sardinian	Kostenki	Nivkhs	Papuan	0.003	0.000	5.9	450206
Sardinian	Kostenki	Yakut	Papuan	0.002	0.000	5.2	450206
Sardinian	Kostenki	Evenkis	Papuan	0.002	0.000	5.1	450206
Sardinian	Kostenki	Evens	Papuan	0.001	0.000	3.1	450206
Sardinian	Kostenki	Yukaghirs	Papuan	0.005	0.000	9.9	450206
Sardinian	Kostenki	Koryaks	Papuan	0.002	0.000	4.2	450206
Sardinian	Kostenki	Chukchis	Papuan	0.003	0.000	5.9	450206
Sardinian	MA1	Altaians	Papuan	0.000	0.000	1.1	361684
Sardinian	MA1	Buryats	Papuan	0.000	0.000	-0.5	361684
Sardinian	MA1	Dolgans	Papuan	0.000	0.000	0.3	361684
Sardinian	MA1	Kets	Papuan	-0.003	0.000	-5.1	361684
Sardinian	MA1	Khakases	Papuan	0.001	0.000	1.5	361684
Sardinian	MA1	Nganassans	Papuan	-0.002	0.000	-3.7	361684
Sardinian	MA1	Selkups	Papuan	-0.001	0.000	-2.1	361684
Sardinian	MA1	Shors	Papuan	-0.001	0.001	-1.1	361684
Sardinian	MA1	Tuvinians	Papuan	0.000	0.000	-1.2	361684
Sardinian	MA1	Nivkhs	Papuan	0.000	0.000	0.3	361684
Sardinian	MA1	Yakut	Papuan	0.000	0.000	-0.7	361684
Sardinian	MA1	Evenkis	Papuan	0.000	0.000	-1.0	361684
Sardinian	MA1	Evens	Papuan	-0.002	0.000	-3.6	361684
Sardinian	MA1	Yukaghirs	Papuan	0.002	0.000	3.9	361684
Sardinian	MA1	Koryaks	Papuan	-0.003	0.000	-5.6	361684
Sardinian	MA1	Chukchis	Papuan	-0.002	0.000	-5.4	361684
Sardinian	Loschbour	Altaians	Papuan	0.000	0.000	0.3	513262
Sardinian	Loschbour	Buryats	Papuan	0.000	0.000	0.7	513262
Sardinian	Loschbour	Dolgans	Papuan	0.000	0.000	-0.1	513262

Sardinian	Loschbour	Kets	Papuan	-0.001	0.000	-1.9	513262
Sardinian	Loschbour	Khakases	Papuan	0.000	0.000	0.1	513262
Sardinian	Loschbour	Nganassans	Papuan	-0.001	0.000	-1.2	513262
Sardinian	Loschbour	Selkups	Papuan	-0.001	0.000	-1.6	513262
Sardinian	Loschbour	Shors	Papuan	0.000	0.000	-0.6	513262
Sardinian	Loschbour	Tuvinians	Papuan	0.000	0.000	0.9	513262
Sardinian	Loschbour	Nivkhs	Papuan	0.000	0.000	-0.4	513262
Sardinian	Loschbour	Yakut	Papuan	0.000	0.000	0.6	513262
Sardinian	Loschbour	Evenkis	Papuan	0.000	0.000	-0.2	513262
Sardinian	Loschbour	Evens	Papuan	0.000	0.000	-0.4	513262
Sardinian	Loschbour	Yukaghirs	Papuan	0.000	0.000	-1.1	513262
Sardinian	Loschbour	Koryaks	Papuan	0.000	0.000	-0.8	513262
Sardinian	Loschbour	Chukchis	Papuan	-0.001	0.000	-1.4	513262
Sardinian	Brana	Altaians	Papuan	0.000	0.000	1.1	382865
Sardinian	Brana	Buryats	Papuan	0.000	0.000	0.6	382865
Sardinian	Brana	Dolgans	Papuan	0.000	0.000	0.3	382865
Sardinian	Brana	Kets	Papuan	-0.001	0.000	-1.5	382865
Sardinian	Brana	Khakases	Papuan	0.000	0.000	0.3	382865
Sardinian	Brana	Nganassans	Papuan	0.000	0.000	-1.0	382865
Sardinian	Brana	Selkups	Papuan	0.000	0.000	-1.0	382865
Sardinian	Brana	Shors	Papuan	0.000	0.000	0.0	382865
Sardinian	Brana	Tuvinians	Papuan	0.000	0.000	0.7	382865
Sardinian	Brana	Nivkhs	Papuan	0.000	0.000	-0.6	382865
Sardinian	Brana	Yakut	Papuan	0.000	0.000	0.5	382865
Sardinian	Brana	Evenkis	Papuan	0.000	0.000	0.5	382865
Sardinian	Brana	Evens	Papuan	-0.001	0.000	-1.3	382865
Sardinian	Brana	Yukaghirs	Papuan	0.000	0.000	0.0	382865
Sardinian	Brana	Koryaks	Papuan	-0.001	0.000	-1.4	382865
Sardinian	Brana	Chukchis	Papuan	0.000	0.000	-1.1	382865
Sardinian	Motala	Altaians	Papuan	0.000	0.000	-1.4	465565
Sardinian	Motala	Buryats	Papuan	0.000	0.000	0.1	465565
Sardinian	Motala	Dolgans	Papuan	0.000	0.000	-1.1	465565
Sardinian	Motala	Kets	Papuan	-0.002	0.000	-5.5	465565
Sardinian	Motala	Khakases	Papuan	-0.001	0.000	-2.1	465565
Sardinian	Motala	Nganassans	Papuan	-0.001	0.000	-2.6	465565
Sardinian	Motala	Selkups	Papuan	-0.002	0.000	-4.7	465565
Sardinian	Motala	Shors	Papuan	-0.001	0.000	-3.5	465565
Sardinian	Motala	Tuvinians	Papuan	0.000	0.000	-1.2	465565
Sardinian	Motala	Nivkhs	Papuan	0.000	0.000	0.1	465565

Sardinian	Motala	Yakut	Papuan	0.000	0.000	-0.7	465565
Sardinian	Motala	Evenkis	Papuan	0.000	0.000	-0.5	465565
Sardinian	Motala	Evens	Papuan	-0.001	0.000	-1.7	465565
Sardinian	Motala	Yukaghirs	Papuan	0.000	0.000	-1.1	465565
Sardinian	Motala	Koryaks	Papuan	-0.001	0.000	-3.2	465565
Sardinian	Motala	Chukchis	Papuan	-0.001	0.000	-3.8	465565
Sardinian	Ajv58	Altaians	Papuan	-0.001	0.000	-2.8	460091
Sardinian	Ajv58	Buryats	Papuan	-0.001	0.000	-1.5	460091
Sardinian	Ajv58	Dolgans	Papuan	-0.001	0.000	-2.3	460091
Sardinian	Ajv58	Kets	Papuan	-0.002	0.000	-5.7	460091
Sardinian	Ajv58	Khakases	Papuan	-0.001	0.000	-2.7	460091
Sardinian	Ajv58	Nganassans	Papuan	-0.002	0.000	-4.5	460091
Sardinian	Ajv58	Selkups	Papuan	-0.002	0.000	-5.2	460091
Sardinian	Ajv58	Shors	Papuan	-0.001	0.000	-3.0	460091
Sardinian	Ajv58	Tuvinians	Papuan	-0.001	0.000	-2.5	460091
Sardinian	Ajv58	Nivkhs	Papuan	-0.001	0.000	-1.7	460091
Sardinian	Ajv58	Yakut	Papuan	-0.001	0.000	-2.3	460091
Sardinian	Ajv58	Evenkis	Papuan	-0.001	0.000	-1.9	460091
Sardinian	Ajv58	Evens	Papuan	-0.001	0.000	-3.0	460091
Sardinian	Ajv58	Yukaghirs	Papuan	-0.001	0.000	-2.6	460091
Sardinian	Ajv58	Koryaks	Papuan	-0.001	0.000	-3.8	460091
Sardinian	Ajv58	Chukchis	Papuan	-0.002	0.000	-4.5	460091
Sardinian	Gok2	Altaians	Papuan	0.000	0.000	1.2	317281
Sardinian	Gok2	Buryats	Papuan	0.000	0.000	1.4	317281
Sardinian	Gok2	Dolgans	Papuan	0.000	0.000	0.9	317281
Sardinian	Gok2	Kets	Papuan	0.000	0.000	1.0	317281
Sardinian	Gok2	Khakases	Papuan	0.000	0.000	1.3	317281
Sardinian	Gok2	Nganassans	Papuan	0.000	0.000	0.1	317281
Sardinian	Gok2	Selkups	Papuan	0.000	0.000	0.4	317281
Sardinian	Gok2	Shors	Papuan	0.000	0.000	1.2	317281
Sardinian	Gok2	Tuvinians	Papuan	0.000	0.000	1.2	317281
Sardinian	Gok2	Nivkhs	Papuan	0.000	0.000	-0.1	317281
Sardinian	Gok2	Yakut	Papuan	0.000	0.000	1.3	317281
Sardinian	Gok2	Evenkis	Papuan	0.000	0.000	1.2	317281
Sardinian	Gok2	Evens	Papuan	0.000	0.000	1.2	317281
Sardinian	Gok2	Yukaghirs	Papuan	0.000	0.000	0.3	317281
Sardinian	Gok2	Koryaks	Papuan	0.000	0.000	1.3	317281
Sardinian	Gok2	Chukchis	Papuan	0.000	0.000	1.3	317281
Sardinian	Iceman	Altaians	Papuan	0.001	0.000	2.1	495464

Sardinian	Iceman	Buryats	Papuan	0.001	0.000	2.4	495464
Sardinian	Iceman	Dolgans	Papuan	0.001	0.000	2.3	495464
Sardinian	Iceman	Kets	Papuan	0.001	0.000	2.4	495464
Sardinian	Iceman	Khakases	Papuan	0.001	0.000	2.5	495464
Sardinian	Iceman	Nganassans	Papuan	0.001	0.000	1.9	495464
Sardinian	Iceman	Selkups	Papuan	0.000	0.000	1.6	495464
Sardinian	Iceman	Shors	Papuan	0.001	0.000	1.8	495464
Sardinian	Iceman	Tuvinians	Papuan	0.001	0.000	2.8	495464
Sardinian	Iceman	Nivkhs	Papuan	0.001	0.000	1.8	495464
Sardinian	Iceman	Yakut	Papuan	0.001	0.000	2.6	495464
Sardinian	Iceman	Evenkis	Papuan	0.001	0.000	2.5	495464
Sardinian	Iceman	Evens	Papuan	0.001	0.000	2.5	495464
Sardinian	Iceman	Yukaghirs	Papuan	0.001	0.000	2.4	495464
Sardinian	Iceman	Koryaks	Papuan	0.001	0.000	1.5	495464
Sardinian	Iceman	Chukchis	Papuan	0.001	0.000	2.1	495464
Sardinian	Stuttgart	Altaians	Papuan	0.001	0.000	1.7	513224
Sardinian	Stuttgart	Buryats	Papuan	0.000	0.000	1.4	513224
Sardinian	Stuttgart	Dolgans	Papuan	0.000	0.000	1.5	513224
Sardinian	Stuttgart	Kets	Papuan	0.001	0.000	1.8	513224
Sardinian	Stuttgart	Khakases	Papuan	0.000	0.000	1.5	513224
Sardinian	Stuttgart	Nganassans	Papuan	0.001	0.000	1.6	513224
Sardinian	Stuttgart	Selkups	Papuan	0.001	0.000	1.6	513224
Sardinian	Stuttgart	Shors	Papuan	0.001	0.000	2.5	513224
Sardinian	Stuttgart	Tuvinians	Papuan	0.001	0.000	2.0	513224
Sardinian	Stuttgart	Nivkhs	Papuan	0.001	0.000	2.4	513224
Sardinian	Stuttgart	Yakut	Papuan	0.001	0.000	1.9	513224
Sardinian	Stuttgart	Evenkis	Papuan	0.001	0.000	1.6	513224
Sardinian	Stuttgart	Evens	Papuan	0.000	0.000	1.3	513224
Sardinian	Stuttgart	Yukaghirs	Papuan	0.001	0.000	1.5	513224
Sardinian	Stuttgart	Koryaks	Papuan	0.001	0.000	1.6	513224
Sardinian	Stuttgart	Chukchis	Papuan	0.001	0.000	1.9	513224

Table S13.

Correlation of f_4 (Sardinian, Ancient)(Modern, Papuan) with admixture proportion of “HG” ancestral cluster

individual	rho	p
Kostenki	0.96	3.04E-18
MA1	-0.08	6.68E-01
Ajv58	-0.77	1.42E-07
Motala	-0.85	6.17E-10
Brana	-0.04	8.29E-01
Loschbour	-0.63	7.43E-05

Table S14.

“admixture” f_3 for Siberian populations. For each population, the ten source population pairs with the lowest statistic are shown..

p1	p2	p3	f3	sdJK	Z	nSites
Altaians	Evens	Iceman	-0.021	0.001	-31.4	454086
Altaians	Evens	Gok2	-0.021	0.001	-28.9	291421
Altaians	Basque	Evens	-0.021	0.000	-53.7	476000
Altaians	Sardinian	Evens	-0.020	0.000	-50.8	476077
Altaians	Hezhen	Ajv58	-0.020	0.001	-30.7	421937
Altaians	NorthItalian	Evens	-0.020	0.000	-49.6	475581
Altaians	Lithuanians	Evens	-0.020	0.000	-49.6	475188
Altaians	Orcadian	Evens	-0.020	0.000	-51.6	475712
Altaians	Evens	Stuttgart	-0.020	0.001	-28.8	470609
Altaians	Tuscan	Evens	-0.020	0.000	-48.8	475140
Buryats	Evens	Iceman	-0.007	0.001	-9.6	438197
Buryats	Evens	Gok2	-0.007	0.001	-8.8	281364
Buryats	Evens	Stuttgart	-0.007	0.001	-9.3	454149
Buryats	Sardinian	Evens	-0.007	0.000	-13.7	461963
Buryats	Tuscan	Evens	-0.007	0.001	-12.9	460782
Buryats	Cypriots	Evens	-0.007	0.001	-13.1	461247
Buryats	Georgians	Evens	-0.006	0.000	-13.6	461650
Buryats	NorthItalian	Evens	-0.006	0.001	-12.9	461363
Buryats	Druze	Evens	-0.006	0.000	-13.3	462225
Buryats	Spanish	Evens	-0.006	0.001	-12.7	461366
Chukchis	Koryaks	EastGreenlanders	-0.003	0.000	-7.9	458150
Chukchis	Koryaks	WestGreenlanders	-0.003	0.000	-6.8	460322
Chukchis	Koryaks	Loschbour	-0.002	0.001	-2.2	447305
Chukchis	Koryaks	Ajv58	-0.001	0.001	-2.1	400993
Chukchis	Koryaks	Motala	-0.001	0.001	-1.9	405670
Chukchis	Koryaks	Gok2	-0.001	0.001	-1.9	277335
Chukchis	Lithuanians	Koryaks	-0.001	0.000	-2.6	464586
Chukchis	Koryaks	Surui	-0.001	0.001	-1.9	450143
Chukchis	Belarusians	Koryaks	-0.001	0.000	-2.1	464397
Chukchis	Orcadian	Koryaks	-0.001	0.000	-2.0	466576
Dolgans	Evens	Gok2	-0.012	0.001	-14.7	271143
Dolgans	Evens	Iceman	-0.012	0.001	-14.7	422451
Dolgans	Sardinian	Evens	-0.012	0.001	-20.7	452492
Dolgans	Basque	Evens	-0.011	0.001	-21.3	452205
Dolgans	Evens	Stuttgart	-0.011	0.001	-14.0	437819

Dolgans	Belarusians	Evens	-0.011	0.001	-19.7	450172
Dolgans	Spanish	Evens	-0.011	0.001	-20.3	451341
Dolgans	Tuscan	Evens	-0.011	0.001	-20.3	449998
Dolgans	NorthItalian	Evens	-0.011	0.001	-19.9	451264
Dolgans	Lithuanians	Evens	-0.011	0.001	-19.4	450406
Evenkis	Evens	Iceman	-0.007	0.001	-8.8	428009
Evenkis	Evens	Gok2	-0.006	0.001	-8.3	274896
Evenkis	Sardinian	Evens	-0.006	0.000	-12.8	453730
Evenkis	Basque	Evens	-0.006	0.000	-12.4	453585
Evenkis	Spanish	Evens	-0.006	0.001	-12.3	452974
Evenkis	Evens	Stuttgart	-0.006	0.001	-8.5	443624
Evenkis	Belarusians	Evens	-0.006	0.000	-12.4	452326
Evenkis	Evens	Loschbour	-0.006	0.001	-8.0	443638
Evenkis	Tuscan	Evens	-0.006	0.001	-11.7	452171
Evenkis	French	Evens	-0.006	0.000	-12.5	453936
Evens	Nganassans	Nivkhs	0.008	0.001	13.2	415903
Evens	Hezhen	Nganassans	0.009	0.001	15.3	423279
Evens	Japanese	Nganassans	0.009	0.001	16.5	432185
Evens	Daur	Nganassans	0.010	0.001	17.4	426299
Evens	She	Nganassans	0.010	0.001	15.6	424197
Evens	Tujia	Nganassans	0.010	0.001	16.1	425845
Evens	Xibo	Nganassans	0.010	0.001	17.9	428999
Evens	Han	Nganassans	0.010	0.001	17.6	434447
Evens	Miao	Nganassans	0.010	0.001	17.2	425274
Evens	Naga	Nganassans	0.010	0.001	16.6	415507
Kets	Evens	Motala	-0.005	0.001	-3.8	338072
Kets	Evens	Ajv58	-0.004	0.001	-2.9	334402
Kets	Lithuanians	Evens	-0.002	0.001	-2.4	421906
Kets	Evens	MA1	-0.002	0.001	-1.6	262682
Kets	Orcadian	Evens	-0.002	0.001	-1.8	425530
Kets	Evens	Loschbour	-0.002	0.001	-1.2	373547
Kets	Belarusians	Evens	-0.002	0.001	-1.5	421650
Kets	Oroqen	Motala	-0.001	0.001	-0.9	338981
Kets	French	Evens	-0.001	0.001	-1.2	429059
Kets	Ucranians	Evens	-0.001	0.001	-1.2	427739
Khakases	Basque	Evens	-0.022	0.000	-55.2	477854
Khakases	Evens	Motala	-0.022	0.001	-27.9	428624
Khakases	Orcadian	Evens	-0.022	0.000	-53.1	477598
Khakases	Evens	Iceman	-0.022	0.001	-32.0	455875

Khakases	Lithuanians	Evens	-0.022	0.000	-52.3	477070
Khakases	Oroqen	Motala	-0.022	0.001	-31.3	428640
Khakases	French	Evens	-0.022	0.000	-55.4	478139
Khakases	Evens	Gok2	-0.022	0.001	-28.4	292389
Khakases	Evens	Stuttgart	-0.022	0.001	-31.1	472427
Khakases	Hezhen	Motala	-0.022	0.001	-30.7	428577
Koryaks	Evens	Chukchis	0.016	0.001	29.1	450588
Koryaks	Oroqen	Chukchis	0.017	0.001	32.3	452831
Koryaks	Nivkhs	Chukchis	0.018	0.001	30.2	447583
Koryaks	Hezhen	Chukchis	0.018	0.001	33.6	452168
Koryaks	Nganassans	Chukchis	0.018	0.001	33.0	456451
Koryaks	Daur	Chukchis	0.018	0.001	34.4	453800
Koryaks	Japanese	Chukchis	0.018	0.001	34.9	457166
Koryaks	Evenkis	Chukchis	0.018	0.001	35.6	458155
Koryaks	Tujia	Chukchis	0.019	0.001	33.9	453696
Koryaks	Naga	Chukchis	0.019	0.001	31.0	448441
Nganassans	Evens	Ajv58	0.007	0.001	8.0	388147
Nganassans	Evens	Gok2	0.008	0.001	8.1	268343
Nganassans	Evens	Motala	0.008	0.001	8.0	392871
Nganassans	Evens	Loschbour	0.008	0.001	8.5	433037
Nganassans	Lithuanians	Evens	0.008	0.001	12.4	446603
Nganassans	Evens	Iceman	0.008	0.001	9.8	417811
Nganassans	Belarusians	Evens	0.008	0.001	12.9	446463
Nganassans	Orcadian	Evens	0.008	0.001	13.0	447777
Nganassans	Hungarians	Evens	0.009	0.001	13.6	448516
Nganassans	Ucranians	Evens	0.009	0.001	13.7	448607
Nivkhs	Evens	Gok2	0.000	0.001	0.1	216081
Nivkhs	Evens	Iceman	0.001	0.001	1.0	335331
Nivkhs	Evens	Loschbour	0.002	0.001	1.4	347894
Nivkhs	Sardinian	Evens	0.002	0.001	1.9	419671
Nivkhs	Belarusians	Evens	0.002	0.001	1.9	412685
Nivkhs	Tuscan	Evens	0.002	0.001	2.1	411353
Nivkhs	Basque	Evens	0.002	0.001	2.2	419005
Nivkhs	NorthItalian	Evens	0.002	0.001	2.2	415874
Nivkhs	Cypriots	Evens	0.003	0.001	2.4	415869
Nivkhs	Oroqen	Gok2	0.003	0.001	2.1	216932
Selkups	Evens	Motala	-0.018	0.001	-22.4	419613
Selkups	Evens	Ajv58	-0.017	0.001	-22.0	414678
Selkups	Lithuanians	Evens	-0.016	0.000	-34.3	469068

Selkups	Orcadian	Evens	-0.016	0.000	-35.1	470037
Selkups	Evens	Loschbour	-0.016	0.001	-19.0	462518
Selkups	Belarusians	Evens	-0.015	0.000	-34.2	469013
Selkups	Evens	Iceman	-0.015	0.001	-20.8	446373
Selkups	Evens	Gok2	-0.015	0.001	-19.5	286467
Selkups	Basque	Evens	-0.015	0.000	-34.8	470400
Selkups	French	Evens	-0.015	0.000	-34.6	470859
Shors	Evens	Motala	-0.012	0.001	-9.1	347812
Shors	Oroqen	Motala	-0.011	0.001	-9.0	348475
Shors	Hezhen	Motala	-0.011	0.001	-8.6	347920
Shors	Japanese	Motala	-0.011	0.001	-8.8	350077
Shors	Tujia	Motala	-0.010	0.001	-7.8	348424
Shors	Daur	Motala	-0.010	0.001	-8.0	348791
Shors	She	Motala	-0.010	0.001	-7.6	348015
Shors	Basque	Evens	-0.010	0.001	-10.8	433463
Shors	Orcadian	Evens	-0.010	0.001	-10.9	431660
Shors	Lithuanians	Evens	-0.010	0.001	-10.5	428328
Tuvinians	Evens	Gok2	-0.011	0.001	-13.9	281243
Tuvinians	Evens	Iceman	-0.010	0.001	-14.7	438139
Tuvinians	Basque	Evens	-0.010	0.000	-21.5	462473
Tuvinians	Sardinian	Evens	-0.010	0.000	-21.4	462627
Tuvinians	Cypriots	Evens	-0.010	0.000	-21.4	461850
Tuvinians	Spanish	Evens	-0.010	0.001	-20.4	461932
Tuvinians	NorthItalian	Evens	-0.010	0.000	-20.9	461968
Tuvinians	Tuscan	Evens	-0.010	0.001	-19.8	461256
Tuvinians	French	Evens	-0.010	0.000	-21.2	462811
Tuvinians	Orcadian	Evens	-0.010	0.000	-20.5	462188
Yakut	Evens	Gok2	-0.007	0.001	-10.0	286746
Yakut	Evens	Iceman	-0.007	0.001	-10.3	447040
Yakut	Sardinian	Evens	-0.007	0.000	-14.9	468274
Yakut	Basque	Evens	-0.007	0.000	-15.0	468250
Yakut	Tuscan	Evens	-0.007	0.000	-14.6	467548
Yakut	Spanish	Evens	-0.007	0.000	-14.4	467908
Yakut	Belarusians	Evens	-0.007	0.000	-14.4	467615
Yakut	Cypriots	Evens	-0.007	0.000	-14.4	467825
Yakut	NorthItalian	Evens	-0.007	0.000	-14.1	467942
Yakut	Georgians	Evens	-0.007	0.000	-14.6	468133
Yukaghirs	Evens	Gok2	-0.017	0.001	-18.7	267036
Yukaghirs	Evens	Loschbour	-0.017	0.001	-18.4	431021

Yukaghirs	Lithuanians	Evens	-0.016	0.001	-27.7	448486
Yukaghirs	Evens	Iceman	-0.016	0.001	-19.1	415742
Yukaghirs	Sardinian	Evens	-0.016	0.001	-28.3	451497
Yukaghirs	Evens	Stuttgart	-0.016	0.001	-18.1	431259
Yukaghirs	Basque	Evens	-0.016	0.001	-28.3	451099
Yukaghirs	Belarusians	Evens	-0.015	0.001	-27.8	448330
Yukaghirs	Orcadian	Evens	-0.015	0.001	-26.8	450271
Yukaghirs	Evens	Ajv58	-0.015	0.001	-17.8	386510

Table S15. f_4 -ratio for Neanderthal ancestry proportion with modern individuals from (34).

a	b	c	o	x	pNeanderthal	sdJK	Z	nSites
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Sardinian	0.017	0.003	5.81	1004976
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	French	0.016	0.003	5.53	1004799
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Han	0.018	0.003	5.90	1004026
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Dai	0.015	0.003	5.28	1003078
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Kostenki	0.024	0.004	6.69	897672
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	MA1	0.018	0.004	5.07	711123
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Loschbour	0.019	0.003	6.04	1008232
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Brana	0.025	0.003	7.61	780227
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Motala	0.019	0.003	6.33	913741
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Ajv58	0.020	0.003	5.95	894481
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Gok2	0.016	0.003	4.87	669789
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Iceman	0.017	0.003	5.78	964143
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Stuttgart	0.019	0.003	5.89	1007448

Table S16.*f*₄-ratio for Neanderthal ancestry proportion with modern individuals from (183).

a	b	c	o	x	pNeanderthal	sdJK	Z	nSites
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Sardinian	0.017	0.003	6.01	677063
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	French	0.016	0.003	5.43	684069
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Mari	0.016	0.004	3.74	178064
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Avar	0.015	0.003	4.74	424430
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Tajik	0.017	0.003	5.69	562447
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Indian	0.016	0.003	5.06	505542
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Han	0.022	0.003	6.95	683309
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Dai	0.017	0.003	5.66	685412
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Kostenki	0.023	0.004	6.27	617147
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	MA1	0.016	0.004	4.27	488737
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Loschbour	0.023	0.003	6.64	692763
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Brana	0.026	0.004	7.22	534776
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Motala	0.022	0.003	6.37	628033
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Ajv58	0.022	0.003	6.35	615002
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Gok2	0.018	0.003	5.25	457380
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Iceman	0.017	0.003	5.49	659874
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Stuttgart	0.019	0.003	5.65	692220

Table S17.

f_4 -ratio for Neanderthal ancestry proportion with modern individuals from (34); stratified by introgressed regions detected in modern individuals.

a	b	c	o	x	pNeanderthal	sdJK	Z	nSites	mask
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Sardinian	0,012	0,003	3,55	760521	akey
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Sardinian	0,002	0,003	0,48	590808	reich
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	French	0,010	0,003	2,88	760442	akey
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	French	0,001	0,003	0,43	590711	reich
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Han	0,009	0,004	2,28	759829	akey
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Han	-0,003	0,004	-0,74	590238	reich
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Dai	0,006	0,003	1,67	759150	akey
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Dai	-0,003	0,003	-0,89	589696	reich
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Kostenki	0,016	0,004	4,01	678656	akey
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Kostenki	0,009	0,004	2,19	528550	reich
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	MA1	0,009	0,004	2,18	537658	akey
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	MA1	-0,002	0,004	-0,46	418394	reich
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Loschbour	0,014	0,004	3,77	763076	akey
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Loschbour	0,004	0,004	1,09	592803	reich
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Brana	0,015	0,004	3,97	589266	akey
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Brana	0,004	0,004	0,96	460529	reich
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Motala	0,010	0,004	2,86	691658	akey
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Motala	-0,001	0,004	-0,21	537548	reich
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Ajv58	0,013	0,004	3,22	676605	akey
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Ajv58	-0,001	0,004	-0,25	525607	reich
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Gok2	0,006	0,004	1,71	504954	akey
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Gok2	-0,004	0,004	-0,96	396489	reich
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Iceman	0,013	0,003	3,83	728952	akey
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Iceman	0,003	0,003	0,79	566745	reich
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Stuttgart	0,011	0,004	2,85	762518	akey
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Stuttgart	0,001	0,004	0,21	592314	reich

Table S18.

f_4 -ratio for Neanderthal ancestry proportion with modern individuals from (183); stratified by introgressed regions detected in modern individuals.

a	b	c	o	x	pNeanderthal	sdJK	Z	nSites	mask
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Sardinian	0,011	0,003	3,22	512216	akey
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Sardinian	0,004	0,004	1,00	399938	reich
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	French	0,008	0,003	2,42	517563	akey
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	French	0,002	0,004	0,53	404314	reich
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Mari	0,009	0,005	1,81	133052	akey
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Mari	0,000	0,006	-0,02	109600	reich
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Avar	0,008	0,004	2,02	318007	akey
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Avar	-0,001	0,004	-0,17	254814	reich
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Tajik	0,010	0,004	2,76	423368	akey
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Tajik	0,001	0,004	0,27	334278	reich
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Indian	0,007	0,004	1,93	380613	akey
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Indian	0,001	0,004	0,32	300566	reich
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Han	0,013	0,004	3,57	517017	akey
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Han	0,003	0,004	0,81	403867	reich
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Dai	0,007	0,003	2,13	518513	akey
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Dai	-0,001	0,004	-0,20	405055	reich
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Kostenki	0,015	0,004	3,60	466502	akey
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Kostenki	0,007	0,004	1,64	365357	reich
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	MA1	0,005	0,004	1,12	369742	akey
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	MA1	-0,003	0,004	-0,68	289663	reich
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Loschbour	0,018	0,004	4,62	524276	akey
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Loschbour	0,008	0,004	1,96	409648	reich
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Brana	0,015	0,004	3,70	403610	akey
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Brana	0,006	0,004	1,35	317686	reich
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Motala	0,014	0,004	3,50	475259	akey
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Motala	0,003	0,004	0,61	371481	reich
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Ajv58	0,013	0,004	3,35	465111	akey
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Ajv58	0,002	0,004	0,37	363451	reich
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Gok2	0,006	0,004	1,63	344322	akey
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Gok2	-0,002	0,004	-0,50	272486	reich
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Iceman	0,011	0,004	3,13	498660	akey
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Iceman	0,002	0,004	0,60	390061	reich
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Stuttgart	0,010	0,004	2,66	523853	akey
Denisova	Mezmaiskaya	MbutiPygmy	AltaiNea	Stuttgart	0,002	0,004	0,38	409283	reich

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