
Supplementary information

Population genomics of the Viking world

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Supplementary Information

Supplementary Note 1. Ancient remains sampled for DNA

1.1. Historical background

1.1.1. The Viking Age: A definition

The Viking Age conventionally refers to the period c. 800-1050 CE in Scandinavia, the North Atlantic (including the British Isles), and the Baltic Sea area. Like most other historical time periods (e.g. the 'Middle Ages', 'Age of Crusades', 'Reformation Period', or 'Age of Enlightenment'), the term 'Viking Age' (hereinafter VA) does not refer to a naturally bounded time slice. Rather, it refers to a historical *durée* marked by the widespread and politically significant operation of seaborne warriors and colonists of Scandinavian descent in regions outside Scandinavia¹.

While the definition and naming of the period are debated², most researchers agree that it is a phase of rapid and profound economic and cultural changes^{3,4}. Many of these changes relate to the expansion and diversification of deep-sea seafaring, which had a number of knock-on effects. These include closer interactions and confrontations between groups around the Baltic and North Seas and further afield^{5,6}; an acceleration of cultural change and exchange, leading to, for example, the adoption of monetary systems of exchange and the spread of Christian religion in Scandinavian kingdoms⁷⁻⁹; an expansion of commercial exchange, focused on emerging maritime trading towns¹⁰⁻¹²; and the colonization of North Atlantic islands including Great Britain, Ireland, the Faroe Islands, Iceland, and Greenland, as well as brief ventures into Newfoundland^{13,14}. The demographic conditions and consequences of these events have been widely discussed^{4,15,16}, but many basic facts concerning both the size and development of populations and their interactions are poorly known from existing sources.

1.1.2. Populations and connectivity in first millennium CE Scandinavia

The VA does not mark a break from a previous state of isolation, and any genetic developments in the period must be considered on the basis of a long and changing history of interactions in northern Europe. Scandinavian societies were exposed to an increased cultural and probably also genetic exchange in the late Roman Period (c. 200-375 CE) with evidence of intense interactions between Scandinavian societies and the Roman Empire, especially along the latter's Rhine boundary¹⁷. In the succeeding Migration Period (c. 375-550 CE) written sources and archaeological evidence point to large scale migrations from northern Europe including parts of Scandinavia into western Europe and the Mediterranean area¹⁸. This includes the settlement of England by Anglo-Saxons from the areas that are now northern Germany and Denmark, which had a very significant cultural and genetic impact^{19,20}.

Recently there has been considerable interest in the period c. 530-550 CE. This is because evidence has accumulated for a period of climatic cooling in the northern hemisphere, the 'Late Antique Little Ice Age', when several major volcanic eruptions caused extreme weather events²¹. This led to widespread famine and a pandemic, the 'Justinian Plague', which is recorded across wide areas of Europe, probably including Scandinavia²². The effects in Scandinavia are suggested to have included a demographic drop through widespread death and migration²³. While little evidence currently exists

to illuminate the detailed sequence of events, it is possible that regions were affected differently, and this could have impacted the population genetics of the region.

The period c. 550-700 CE shows reduced archaeological evidence of migrations from, and supra-regional interaction between, Scandinavia and other regions²⁴, albeit punctuated by finds such as the Sutton Hoo boat burial in East Anglia, which dates to c. 630 CE and shows marked Scandinavian affinities in material culture and burial rituals^{7,25}.

As a historical dynamic, the 'Viking phenomenon' is considered to emerge gradually in the course of the 700s CE. This is suggested by various lines of evidence including the chronology of objects, which were likely brought into Scandinavia through the earliest raid and maritime trade²⁶⁻²⁸; evidence for the evolution of boat-building technology²⁹; and direct evidence of maritime warfare, such as the boat burial of warriors from a mid 8th century CE raiding party found in Salme, Estonia³⁰. In particular, the chronology is charted by the spread of maritime trading towns or *emporium* in the Baltic Sea area (e.g. Ribe in western Denmark c. 700 CE; Åhus in southeast Sweden and Truso in eastern Poland c. 725 CE; Birka in central Sweden and Staraja Ladoga in northeast Russia after c. 750 CE^{10,12}).

A first wave of raids, trade, and colonization culminated in the period c. 840-880 CE, when large Viking armies operated in France and the British Isles, while the earliest colonists settled in Iceland, and trading expeditions reached the Black Sea, and the Atlantic coast of Spain and Portugal, with occasional ventures into the Mediterranean³¹. This is followed by a period with less evidence of Viking activity in western Europe. Eventually this gave way to what is sometimes referred to as the 'second Viking Age' of c. 970-1020 CE, when raids resumed in the west, leading to the formation of a North Sea empire under King Cnut, who came to rule England, Denmark, Norway, and part of Sweden between c. 1016 and his death in 1035 CE³². While there is evidence for large-scale movement and migrations across the sea in both of these waves of Viking activity, it is not clear how they contributed to the demography and population genetics of the period.

The end of the VA is conventionally set to the mid 11th century CE, when Scandinavian seaborne armies ceased to be a primary political force in western Europe. However, in many regions this date is acknowledged to be an arbitrary convention, as the pattern of maritime activities and connections that marked out the VA continued to evolve in Scandinavia, the North Atlantic (including the British Isles), and the Baltic Sea area well into the following centuries¹.

1.1.3. The Viking Age burial record and DNA retrieval

Burial customs show marked regional and chronological variation in and around Scandinavia during the VA. While most regions see a gradual increase in the use of inhumation burials towards the end of the period, the early VA is represented mainly by cremation burials in many parts of Scandinavia. This implies that there is a limited record of relevant bone remains available for sampling in much of Sweden, for example^{33,34}. This problem is accentuated for the centuries immediately before the VA, because cremation burial was even more prevalent, leaving few human specimens to sample for DNA in most regions of Scandinavia.

The adoption of Christian burial practices in Scandinavia and the Baltic Sea area from the 10th century CE onwards meant that virtually all members of society from infants to adults were buried in designated burial areas around churches, leading to a much more comprehensive bioarchaeological

record. For all periods, the record of individuals given an archaeologically visible burial is highly selective and skewed towards social elites. This must be borne in mind when assessing evidence for mobility and diversity, as there is much to suggest that elites maintained wider networks and enjoyed higher degrees of mobility than the average person³³.

1.2. Ancient remains sampled for DNA

1.2.1. Overview of sample

In the present study, a total of 528 sets of ancient human remains were processed and screened (c. 15 million sequences per sample) for contamination levels and endogenous human DNA content. The remains spanned from the Bronze Age, c. 2400 BCE, to the early modern period, c. 1600 CE, but most of them were excavated in the major areas of Viking expansion and have been dated to between the late 8th and late 11th centuries CE. In the vast majority of cases, we targeted either teeth or petrous bones for DNA extraction.

After removing poorly preserved and contaminated samples the number of individuals was reduced to 442. These remains originated from over 80 archaeological sites, covering large parts of northern Europe and Greenland. The approximate locations of the archaeological sites are presented in Figure 1 in the main text. The details of sampled individuals with their unique IDs used throughout this study are presented in Supplementary Table 1.

The 442 ancient individuals were divided into five broad categories (Figure 1 in the main text) and the majority (n=376) were sequenced to between 0.1 and 11X average depth of coverage. The dataset includes Bronze Age (n=2) and Iron Age (n=10) individuals from Scandinavia; early VA (n=43) individuals from Estonia (n=34), Denmark (n=6), and Sweden (n=3); ancient individuals associated with Norse culture from Greenland (n=23), VA individuals from Denmark (n=78), the Faroe Islands (n=1), Iceland (n=17), Ireland (n=4), Norway (n=29), Poland (n=8), Russia (n=33), Sweden (n=118), the Isle of Man (n=1), Scotland (n=8), England (n=32), Wales (n=1), and Ukraine (n=3), as well as individuals from the medieval and early modern periods from the Faroe Islands (n=16), Italy (n=5), Norway (n=7), Poland (n=2), and Ukraine (n=1). The VA individuals were supplemented with published genomes from Sigtuna, Sweden (n=21, samples VK557-VK578)³⁵, and Iceland³⁶ (Supplementary Table 3).

Most of the specimens we sampled have been dated to the VA (8-12th centuries CE) or have direct relevance to the Viking period such as the ones from later Norse settlements in Greenland, medieval samples from the Faroe Islands, and noble family members of Ukrainian rulers of the 12-13th centuries CE as well as earlier pre-VA remains from Estonia and Iron Age samples. Two samples that were initially thought to belong to the VA were identified as late Neolithic/Bronze Age by radiocarbon dating.

1.2.2. Country-level catalogues of archaeological sites from which DNA samples were obtained

This section contains brief descriptions of most of the archaeological sites from which we obtained ancient samples. The section is organized as a series of country-level catalogues.

1.2.2.1. Denmark

(Prepared by Marie Louise Jørkov, Department of Forensic Medicine, University of Copenhagen and Søren M. Sindbæk, Centre for Urban Network Evolutions [UrbNet], Aarhus University)

This catalogue presents information on the skeletons from Danish collections included in the study. The information includes the nature and location of the site, the burial type, a brief report of any objects found with the skeleton, the date of the site and/or skeleton(s), plus notes about osteological and biochemical analyses carried out prior to the current project. The catalogue is based on information in the national database 'Fund og Fortidsminder', together with digests from published sources. The catalogue is organized geographically as per the National Sites and Monuments Numbers ('Stednummer'). First, the museum and the museum number of the find is given. After this, the site is indicated by place name, parish ('sogn'), shire ('herred'), and county ('amt'). The National Sites and Monuments number is then given, followed by the year of excavation. The project-specific 'VK'-numbers are listed after the descriptions of the sites/graves.

Bakkendrup

National Museum of Denmark RAS 45/83, Bakkendrup, Bakkendrup Sogn, Løve Herred, Holbæk Amt.

Nat. Sites and Monuments no.: 03.02.01-52 (sb. 52.)

Year of excavation: 1979

A cemetery with flat inhumation graves near Bakkendrup Bro. It was excavated in 1979 by the National Museum. Dated to the second half of the 9th century CE.

Samples used for DNA analysis:

VK294 Denmark_Bakkendrup losfund-2, conc.5

VK315 Denmark_Bakkendrup Grav 16

VK369 Denmark_Bakkendrup losfund-2, conc.1

Bårse

Museum Southeast Denmark SMV 28/86, Bårse, Tyvestensager, Bårse Sogn, Bårse Herred, Præstø Amt.

Nat. Sites and Monuments no.: 05.02.03-67.

Year of excavation: 1986

Excavated by Museum Southeast Denmark in 1986. A small VA burial ground with 11 inhumations located on a small hill. Cremation graves were found underneath the inhumations (it is not known whether the cremations were human or animal). We sampled the individual from Grave A, which was the deepest of the graves. Grave A was covered with three large stones, and included several objects: a strap-end mount, a buckle from a belt (same as the one found in Rantzausminde) dated to the 10th century CE, whetstones, and a pumice with abrasion marks.

Sample used for DNA analysis:

VK281 Denmark_Barse Grav A

Besser

National Museum of Denmark N01 353/41, C24368-83, Besser S, Samsø Herred, Holbæk Amt.

Nat. Sites and Monuments no.: 03.05.01-45

Year of excavation: 1941

Excavated by the National Museum in 1941. Six graves were found under a compact layer of stone on a small hill. The graves were originally constructed to fit wooden coffins, but fragments from a wood coffin were only recovered in one grave, Grave 1. Grave 1 was also the richest of the six burials. It contained a trefoil silver brooch, two oval brooches, a spindle whorl, four glass beads, a key, an iron knife, and a hemispherical vessel. Grave 4 contained a shield boss, a whet stone, a knife, a ring needle of bronze, and some undefined iron. The other graves only contained an iron knife. Grave 3 was the only inhumation grave. Grave 1, 5, and 6 were cremation graves but in man-length coffins. There were no human remains recovered in Grave 2 and 4. The graves have been dated to 750-1066 CE.

Sample used for DNA analysis:
VK298 Denmark_Besser Grav III

Bødker garden

Langlands Museum LMR 13372, Bødkgårds mark/Bødkergård, Tryggelev Sogn, Langlands Søndre Herred, Svendborg Amt.

Nat. Sites and Monuments no.: 09.03.07-40.

Year of excavation: 1997

Excavated by Langlands Museum in 1997. A small VA burial ground on a small hill containing five preserved inhumations. Three graves were oriented east-west and each had an iron knife as a grave good. Two adjacent graves in a north-south direction. One contained a small clay pot. Remains of settlement from the early Iron Age with postholes and pits. Burial D (adult male), southwest-northeast oriented. Cranium separate from postcranium, found adjacent to the lower part of torso. Mandible found upside down in "original head end". Buried in supine position. A knife was found underneath the skull. Grave H (adult male) right side hocker position in north-south direction with head north. Arms and legs bent. A small clay pot (14 cm diameter) next to the torso. Charcoal and burned animal bone found in fill. Entire cemetery dates broadly to 9th century CE based on the finding of buckles/pins (type P 42 after Ingmar Jansson 1985)³⁷. Grave D: younger than grave C. Difficult to date more precisely. Grave H did not have any stratigraphy that could be related to the other graves. It was buried with a clay jar. It has also been dated to the 9th century CE.

Samples used for DNA analysis:
VK289 Denmark_Bodker garden Grav H, sk 1
VK291 Denmark_Bodker garden Grav D, sk 1

Bogøvej

Langlands Museum LMR 12077, Bogøvej 21, Lindelse Sogn, Langlands Sønder Herred, Svendborg Amt.

Nat. sites and monuments no.: 09.03.04-28.

Year of excavation: 1987, 1988, 1989

Excavated in 1987, 1988, and 1989 by Langlands Museum. Burial ground from the VA. The cemetery is located on small drumlins of mixed moraine material with a high chalk content; there were thus varying, but often good, conditions for the preservation of skeletons³⁸. The burial ground is located on a small hill 500 m south of Lidelse Nor in an elongated area (70 m x 30 m in a northeast-southwest orientation). The burial ground was discovered in 1920, when four inhumation graves were uncovered. A total of 49 graves have been excavated, three of which were double graves. Excavations in 1987 and 1988 also revealed activity dated to the late Bronze Age, including 17 pits, some of which contained flint tools, large amounts of pottery, small fragments of bronze, and some tools made of

antler. The majority of the individuals had been buried in a supine position and a few in hocker. Some of the inhumation graves contained grave goods, e.g. knives, whetstones, buckles, and/or glass beads. Two stone-lined graves (Grave BA) had carriages (minus wheels) as coffins ('Vognfadning'), and a female burial had the remains of a wooden shrine containing an intact comb. A male burial contained an axe dated to the late VA, a strike-a-light, and an Arabic silver coin. One skeleton was decapitated (Grave T). Most graves were oriented east-west. Of the sexed individuals, 15 were male and 22 female. Only a few were subadults. Dated to the 10th century CE, possibly with a few graves dated to the early 11th century CE (unknown which ones).

Samples used for DNA analysis:

VK286 Denmark_Bogovej Grav BJ
VK288 Denmark_Bogovej Grav BA
VK292 Denmark_Bogovej Grav A.D.
VK320 Denmark_Bogovej Grav S
VK338 Denmark_Bogovej Grav BV
VK361 Denmark_Bogovej BX
VK362 Denmark_Bogovej LMR 12077
VK363 Denmark_Bogovej BT
VK364 Denmark_Bogovej BN
VK365 Denmark_Bogovej BS
VK366 Denmark_Bogovej BY
VK367 Denmark_Bogovej D
VK368 Denmark_Bogovej T

Galgedil

Odense City Museums OBM 4520, Galgedil, Otterup Sogn, Lunde Herred, Odense Amt.

Nat. Sites and Monuments no.: 080306 -08.

Year of excavation: 1999-2005

Excavated by Odense City Museums in 1999-2005. Galgedil is a VA cemetery (c. 800-1050 CE) located in the northern part of the Danish island of Funen. The site revealed 54 graves containing 59 inhumations and two cremation burials. Previous study of the remains has included light isotopes of carbon and nitrogen in collagen (10 samples) and the radiocarbon determination of the age of eight samples. In addition, aDNA was investigated in 10 samples from the cemetery by Melchior et al.³⁹ and strontium analysis was carried out by Price et al.⁴⁰ The cemetery is situated on the top, and down the southern and western slopes, of a small hill in a rolling, moraine landscape, 5 km from the former seacoast. The investigated skeletal material from Galgedil consisted of the human remains from 57 inhumations with varying degrees of preservation. The number of male and female skeletons was almost the same. There were 24 males (48%) and 19 females (38%). Sex could not be determined for six of the adult skeletons (14%) or for the eight subadult individuals of various ages. Several individuals seem to be non-locals based on strontium isotopes (samples Galgedil OU and Galgedil UD).

Samples used for DNA analysis:

VK133 Denmark_Galgedil KO
VK134 Denmark_Galgedil ALZ
VK135 Denmark_Galgedil ALY
VK138 Denmark_Galgedil AQQ
VK139 Denmark_Galgedil ANG

VK140 Denmark_Galgedil PT
VK141 Denmark_Galgedil OMB/BFQ
VK278 Denmark_Galgedil TQ
VK279 Denmark_Galgedil AXE
VK280 Denmark_Galgedil UO
VK370 Denmark_Galgedil ANO
VK371 Denmark_Galgedil UD-Vest
VK372 Denmark_Galgedil KM
VK373 Denmark_Galgedil BER
VK411 Denmark_Galgedil TT
VK446 Denmark_Galgedil LS

Gl. Lejre

Roskilde Museum ROM 641/85, Mysselhøjgård, Allerslev Sogn, Volborg Herred, København Amt

Nat. Sites and Monuments no.: 02.06.01-115.

Year of excavation: 2009

Excavated by Roskilde Museum in 2009. The archaeological site of Gl. Lejre is located on Sealand, c. 35 km west of Copenhagen. Seven inhumation graves or deposit finds were excavated at the hall area of an aristocratic residence⁴¹. One of the graves, A1636, was placed on the top of a hill in the centre of the residence, while a group of four burials—A1859, A1860, A1861, and A1896—were found 14 meters south of it, on a shallow slope. Grave A1880 was found in a disturbed area north of grave A1636, and 13 meters to the west in the northwestern corner of the residence another disturbed grave, A1697, was found. All but one of the skeletons were found lying in supine position with their heads to the west and in long, oval-shaped graves with no evidence of coffins. The exception was grave A1636. Grave A1896 was lying in hocker position. A total of five individuals could be sexed. Four were found to be male and one was determined to be female. All the individuals were estimated to be middle-aged adults or older. The only grave good recovered was a brass finger ring placed on the left fourth finger of the female A1861.

Samples used for DNA analysis:

VK94 Denmark_Gl Lejre-A1861

VK445 Denmark_Gl Lejre-A1896

Hesselbjerg

Moesgaard Museum FHM 1379, Hesselbjerg, Randlev Sogn, Hads Herred, Århus Amt

Nat. Sites and Monuments no.: 15.02.11-12.

Year of excavation: 1963-1970, 1997-2001

The cemetery has a distinct location on a narrow sand and gravel hill that stretches 300-400 m in a north-south direction. The surrounding landscape is flat with fertile agricultural land (UTM 574947 / 6200145). The cemetery is located approximately 1 km southeast of the parish village Over Randlev, and 3.8 km from the coast of Kattegat. The graves were positioned on the hilltop and on the east side of the hill. The graves were excavated by Moesgaard Museum in 1963-1970 and 1997-2001⁴²⁻⁴⁴. A total of 104 graves were recovered, of which 84 were inhumations and 20 were cremations. The preservation of the skeletons varied. More or less intact skeletons were recovered from 69 graves. Over 80% of those interred in the cemetery were women. There were only limited grave goods and these were mostly personal equipment such as knives, iron belt buckles, whetstones, pottery, and a few pieces of jewelry. Only a few graves contained elaborate artefacts. A single pit contained

numerous glass and amber beads and an elaborately decorated bronze gilt belt buckle. Based on the grave goods, the cemetery dates from the mid- 9th century CE to the 10th century CE. An associated building was excavated c. 200 m north-west of the cemetery. A well has been dated through dendrochronology to about 900 CE. An analysis of pollen from the bottom of the well shows that the nearby area consisted of fields for grazing animals.

Samples used for DNA analysis:

VK84 Denmark_Hesselbjerg Grav 3
VK86 Denmark_Hesselbjerg Grav 13
VK87 Denmark_Hesselbjerg Grav 41b, sk PC
VK300 Denmark_Hesselbjerg Grav 22, sk IR
VK339 Denmark_Hesselbjerg Grav 16, sk GO
VK340 Denmark_Hesselbjerg Grav 5, sk V
VK383 Denmark_Hesselbjerg Grav 11, sk DT
VK384 Denmark_Hesselbjerg Grav 14, sk EU

Hesselbjergmarken

Langlands Museum LMR 11163, Hesselbjergmarken, Magleby Sogn, Langelands Sønder Herred, Svendborg Amt.

Nat. Sites and Monuments no.: 09.03.06-35.

Year of excavation: 1982

Burials discovered in 1860 and in 1981. Excavated by Langlands Museum in 1982³⁸. VA burial ground. Grave B was buried with an iron knife, whetstone, and a silver Samanide coin dated to 903-913 CE (Museum no. 11163:6a). Buried in supine position with head in east end, feet in the west, and face turned north.

Sample used for DNA analysis:

VK318 Denmark_Hesselbjergmarken Grav B

Hessum

Odense City Museums/Nationalmuseet NM 818/50, Hessum, Skeby Sogn, Lunde Herred, Odense Amt.

Nat. Sites and Monuments no.: N/A

Year of excavation: 1950

A VA cemetery was identified during gravel digging and four of the graves were excavated and analyzed by Odense City Museums and the National Museum of Denmark in 1950. Two of the graves were relatively well preserved. Only limited grave goods in the form of an iron knife with wooden handle. It is not known which grave it belonged to.

Samples used for DNA analysis:

VK295 Denmark_Hessum sk 1
VK316 Denmark_Hessum sk II

Hundstrup Mose

National Museum of Denmark N01 673/47, C26290-91, C28241-51, Hundstrup Mose, Hammer Sogn, Hammer Herred, Præstø Amt.

Nat. Sites and Monuments no.: 05.04.01-12 (sb. 12)

Year of excavation: 1947

Sacrificed victims buried in the bog of Hundstrup. In total, two adults, two children, and two infants were recovered. The two children (7-11 and 11-13 years) were found lying together. They had been covered with branches and buried with an iron knife. The preservation was very good, but none of the skeletons was complete. Strontium analyses have been done on all of the individuals and show that Sk. 2 (VK297) was non-local. The graves date to Germanic Period rather than VA⁴⁵.

Samples used for DNA analysis:

VK296 Denmark_Hundrup Mose sk 1

VK297 Denmark_Hundrup Mose sk 2

Kaagården

Langelands Museum LMR 11563, Kaagården, Lindelse Sogn, Langelands Sønder Herred, Svendborg Amt.

Nat. Sites and Monuments no.: 09.03.04-60.

Year of excavation: 1984-1987

Excavated by Langelands Museum from 1984-1987³⁸. Cemetery on a small hill with 70 graves. The cemetery was in use from the late Germanic period to the late VA, but most of the graves date to the late VA. The richest graves were found on the top of the hill. The buried individuals included adults and subadults. Subadults were buried with iron knives. The presence of sand and the shells of marine mollusks in some of the graves strongly suggests that the bodies were cremated on the nearby beach.

Samples used for DNA analysis:

VK274 Denmark_Kaargarden 391

VK275 Denmark_Kaargarden 217

VK276 Denmark_Kaargarden BH

VK285 Denmark_Kaargarden Grav BZ

VK287 Denmark_Kaargarden Grav BS

VK317 Denmark_Kaargarden Grav BF99

Kumle høje

Langelands Museum LMR 12845, Kumle høje, Lindelse Sogn, Langelands Sønder Herred, Svendborg Amt.

Nat. Sites and Monuments no.: 09.03.04-41.

Year of excavation: 1998

Excavated by Langelands Museum in 1998. VA cemetery (date to 10th century CE) with a minimum of 11 adult individuals buried (males and females). A rare double grave with two males on top of each other, one on its back and the other facing down. Another male grave with healed cranial trauma. A female grave with a 17 cm long iron knife. One male grave with broken legs (perimortem). A female grave covered with large stone slabs. The richest grave was of a female in supine position with iron artefacts, amber, and part of a bronze belt buckle. Several other male graves showed trauma.

Sample used for DNA analysis:

VK290 Denmark_Kumle Høje Grav O

Ladby

National Museum of Denmark NM 182/34, Ladby, Kølstrup Sogn, Bjerger Herred, Odense Amt.

Nat. Sites and Monuments no.: 080106-06

Year of excavation: 1934-1935, 1938

The burial ground of Ladby was uncovered west of Nymarksgård near the ship-grave of Ladby, south of Kerteminde Fjord. It was found during the course of gravel digging. It was excavated by the National Museum in 1934-35 and 1938. Ten flat inhumation graves were unearthed. Traces of a wooden coffin were found in Grave 2 (VK319). The grave was oriented northwest-southeast. Grave 4 (VK301) was buried in a supine position with the head resting on a stone. The grave was oriented northwest-southeast. An iron knife was found in the grave. It has been difficult to determine the earliest and latest date for the use of the burial ground, because most of the graves were badly damaged and did not contain any objects that could yield specific dating. Most of the finds were iron knives. A C-14 dating of Grave 4 from 1997 yielded a date of 640-890 CE with +/- 1 standard deviation. Generally, the burial ground is thought to have been in use from about 700 CE to sometime into the 10th century CE⁴⁶⁻⁴⁸.

Samples used for DNA analysis:

VK301 Denmark_Ladby Grav 4

VK319 Denmark_Ladby Grav 2

Lejre

Roskilde Museum/National Museum of Denmark NM 194/45; NM 152/46, NM C29995-30150, Lejre, Kornerup Sogn, Sømme Herred, Københavns Amt.

Nat. Sites and Monuments no.: 02.06.01- 7.

Year of excavation: 1953-1968

A VA cemetery comprising 49 graves at the Gl. Lejre ship-burial site. Excavated by the National Museum in 1953-68. Four graves were cremation graves. The fill of several graves contained potsherds and cremated bones. No further archaeological information is available.

Samples used for DNA analysis:

VK90 Denmark_Lejre Grav 902

VK92 Denmark_Lejre Grav 935

VK247 Denmark_Lejre Grav 804

VK385 Denmark_Lejre Grav 321

Rantzausminde

Langelands Museum NM 288/27, Rantzausminde, Egense Sogn, Sunds Herred, Svendborg Amt.

Nat. Sites and Monuments no.: 09.05.04-66.

Year of excavation: 1926, 1927

A VA cemetery. Seven inhumations. No further metadata at Antrolab. There is no C-14 dating, but the few archaeological artefacts date the graves to the late 8th to early 9th century CE.

Samples used for DNA analysis:

VK312 Denmark_Rantzausminde Grav 1

VK313 Denmark_Rantzausminde Grav 2

VK314 Denmark_Rantzausminde Grav 5

Stengade

Langelands Museum LMR C195, Stengade I, Tullebølle Sogn, Langelands Nørre Herred, Svendborg Amt.

Nat. Sites and Monuments no.: 09.02.09-58.

Year of excavation: 1905-1923, 1963, 1972-1974

Excavated by Langelands Museum in 1972-1974. A VA cemetery constructed on a small bank and discovered during marl digging. The site comprises four inhumation graves, of which Grave 3 had a rich equipment of weapons and riding gear as well as the skeleton of a horse. Human remains were only preserved in Grave 4, a mature adult male buried with an iron knife. The site also had two inhumation graves from the early Roman Period, four cremation graves from the Roman period, and three undateable inhumation graves. Skeletal material has not been preserved from these graves. Grave LMR c195 (AS 36/78) likely stems from this site^{46,49,50}.

Sample used for DNA analysis:

VK282 Denmark_Stengade I, LMR c195

Tollemosegård

Tollemosen, Tollemosegård. Græse Sogn, Lyng-Frederiksborg Herred, Frederiksborg Amt. MFG 113/97.

Nat. Sites and Monuments no.: 01.03.03-61.

Year of excavation: 1997

A cemetery dated to the late Germanic period and early VA (700-1000 CE) based on grave goods. A total of 54 graves. Several double inhumations and a few cremations. Double graves in layers. Varying amounts of grave goods, from none to rich goods including sacrificed animals, knives, glass beads, amber beads, nails, and wooden buckets. Strontium analysis has been conducted on BQ (VK65), BT, and EW (VK 70) samples.

Samples used for DNA analysis:

VK65 Denmark_Tollemosegard-BQ

VK69 Denmark_Tollemosegard-DS

VK70 Denmark_Tollemosegard-EW

VK71 Denmark_Tollemosegard-BU

Trekroner

Roskilde Museum ROM 2285, Trekroner Øst-Grydehøj, Fløng Sogn, Sømme Herred, Roskilde Amt.

Nat. Sites and Monuments no.: 02.04.01-17.

Year of excavation: 2000

Grydehøj is a small hill east of Roskilde. The hill has been used as a burial site for approximately 3000 years. The west side of the hill was used during the early VA and 27 inhumations have been recovered there. At the time of excavation, the highest point of Trekroner--Grydehøj was approximately 39 m above sea level and thereby the highest point within a 1 km radius. At the foot of the east side there is a small lake today, but may have been a peat bog at that time. The burials dated to the VA represent burials from the very early part of the period (8th to 9th century CE). Only a few graves contained grave goods that could aid in the dating of the graves and all pointed towards the very early VA. Osteological examination indicates that there were 14 males, eight females, and ten unidentified individuals. Grave goods were found in 21 graves. Large stones were found in Grave A2058 and a stone was found on the left shoulder of the body⁵¹.

Sample used for DNA analysis:

VK284 Denmark_Grydehoj A2058

Kragehave Ødetofte

Kroppedal Museum TAK 1049, Høje Tåstrup Sogn, Smørum Herred, Københavns Amt.

Nat. Sites and Monuments no: 020207-115

Year of excavation: 2004

Excavated by Kroppedal Museum in 2004. Settlements including 42 houses, 11 fence-structures, and several wells were found dated to the later part of the Iron Age (3-8th century CE). Three inhumation graves were recovered. One was a female dated to early Roman Iron Age (0-200 CE), and the other two were a female and a male (x1718) dated to the late Roman Iron Age (C₂/C₃) (200-375 CE). The skeleton x1718 was of an old adult male (50+ years).

Sample used for DNA analysis:

VK532 Kragehave Odetofter XL718

Brøndsager

Kroppedal Museum SØL 941, Torslunde Sogn, Smørum Herred, Københavns Amt

Nat. Sites and Monuments no: 020213-41.

Year of excavation: 1997-1998

Excavated by Søllerød Museum in 1997-1998. A cemetery containing a minimum of 20 graves. The graves were found on a small plateau. Settlements were found on the south side of the plateau. Only three skeletons were excavated. They dated to the late Roman Iron Age (C₂) (200-380 CE). One grave (Grave 900) contained a male (25-30 years) buried in a supine position in a wooden coffin with his head to the south. The grave contained rich grave goods. A silver fibula was found next to his right shoulder, a comb of bone and bronze rivets was found next to his hip, and he had a small gold ring on his toe. A wooden bucket with bronze inlays and handle was found by his feet. Two smaller bowls were found inside the bucket as well as a glass. The remains of a slaughtered sheep were found in an upper layer of the grave. Another grave contained a subadult, c. 14-15 years old, possibly male (based on grave goods) buried in a wooden coffin with a wooden bucket with a bronze belt, four clay bowls, two Roman drinking glasses, a play board with red paint, 30 white and 29 black playing-pieces, a comb of bone with bronze rivets, a pearl necklace, and a gold Aureus with an eyelet. He had a gold coin in his mouth and a gold ornamented ring dated to the Late Roman Iron Age. He was buried with a pig and butchered sheep. The third grave contained a 4-5-year-old child who had also been buried in a wooden coffin. The individual was buried with a pearl necklace made of bronze and amber, a comb of bone with bronze rivets, two clay bowls, and a pig.

Sample used for DNA analysis:

VK521 Sol941 Grav900 Brøndsager Torslunde

Alken Enge

Skanderborg Museum SBM 1028, Torslunde Sogn, Smørum Herred, Københavns Amt

Nat. Sites and Monuments no: 020213-41.

Year of excavation: 2013-2014

Excavated by Skanderborg Museum in 2013-2014. The wet meadows of Alken Enge (Alken Meadows) at Lake Mossø are the site of a mass grave with skeletal remains of a minimum estimate of 380 defeated warriors. The specific bone sample was deposited in a natural channel between two sea basins. The tooth is from the mandible of a disarticulated male individual found centrally in the northern main field of the Alken Enge excavation. There were six remaining teeth; the rest had fallen out. In the absence of specimen-specific dating, the specimen must be attributed to the time frame of

the mass grave, which is 2 BCE-54 CE. Context and find data are presented in the publication and its supplementary data⁵².

Sample used for DNA analysis:

VK582 SBM1028 ALKEN ENGE 2013, X2244

Ribe

Sydvestjyske Museer ASR 13, Ribe, Ribe Domkirke sogn, Ribe Herred, Ribe Amt.

(Prepared by Morten Søvsø, Museum of Southwest Jutland, Denmark)

Nat. Sites and Monuments no.: 19.04.08-81.

Year of excavation: 2008-2011.

Between 2008 and 2011, excavations at the cathedral in Ribe (Fig. S1.1), Jutland, located a Christian cemetery sealed by settlement layers c. 1050 CE⁵³. ¹⁴C-dates combined with a large archaeological dataset including stratigraphy, preservation, grave customs, and coffin types date the burials to between c. 850 and 1050 CE leaving little doubt that the find documents the existence of Ansgar's church, founded c. 860 CE. Ribe is Scandinavia's first town. Founded around 700 CE, it became a major trading place/emporium with a controlled coin economy in the 8th century CE and declined from late 9th century CE. A church, the present-day Cathedral, was founded c. 860 CE. Samples used in the present study come from burials that predate 1050 CE.



Fig. S1.1: The Ribe site during excavation (left) and the skeleton K1586 sampled for aDNA analysis in this study. Photo: Museum of Southwest Jutland.

Samples used for DNA analysis:

VK322 K1568

VK323 K1563

VK324 K1552

VK325 K1572

VK326 K1578

VK327 K1586

VK328 K1594

VK329 K1600

VK330 K1582

Gerdrup

Roskilde Museum ROM 191/8, Gerdrup, Kirkerup Sogn, Sømme Herred, Københavns Amt.

(Prepared by Ole Kastholm, Roskilde Museum, Denmark)

Nat. Sites and Monuments no.: 02.04.08-67.

Year of excavation: 1981, 1983

In autumn 1981, the discovery of a Bronze Age sword was reported to the Roskilde Museum. The sword came from a field a few kilometers north of Roskilde, an area with many burial mounds, some still standing as visible monuments in the landscape, others more or less destroyed by ploughing and stone harvesting. Archaeologists from the museum visited the find place, and it was evident that the sword originated from a now-destroyed burial mound. Furthermore, a number of dark spots were observed in the newly ploughed field, which were thought to be cremation graves. Based on this, a small trial excavation was carried out, which confirmed the existence of such graves as well as an inhumation grave. Two graves were examined in 1981 and the museum returned for a larger campaign of excavation in 1983. The excavations unearthed a number of burials dating from the late Neolithic to the VA. In total c. 1800 m² was excavated. We sampled remains from two graves that were excavated in the museum's 1981 campaign: Grave A and Grave B. Grave A is a cremation grave without artefacts. The human remains it contains have been AMS-dated to c. 400 CE (sample A10) and c. 1800 BCE (sample A12). Grave B is a double inhumation grave containing an adult male and an adult female, contextually dated to the 9th century CE. The man (age 35-40 years) was lying with his head and neck in an awkward position, possibly indicating that his neck had been broken. Furthermore, his ankles were crossed, as if they had been tied together. He was buried with an iron knife. The woman (age 40-50 years) had given birth at least once and was buried with an iron knife, a bone case with iron needles, and a spear. The spearhead (Petersen's Type E)⁵⁴ dates the grave to the VA.

Samples used for DNA analysis:

VK213 Denmark_Gerdrup-A10

VK214 Denmark_Gerdrup-A12

VK215 Denmark_Gerdrup-B; sk 1

VK216 Denmark_Gerdrup-B; sk 2

1.2.2.2. Norway

(Prepared by Jan Bill, Museum of Cultural History, Oslo, Norway)

This catalogue presents information on the VA and earlier skeletons from Norwegian collections included in the study. The information includes the nature and location of the site, the burial type, a brief report of any objects found with the skeleton, and the date of the site and/or skeleton(s), plus notes about any osteological, pathological, or biochemical analyses that have been carried out prior to the current project. The catalogue is mainly based on information gathered from published sources, as well as the collection databases of Norwegian university museums and the database for the Schreiner Collection, where the skeletons are kept. The Schreiner Collection distinguishes between skeletons with crania of 'Nordic', 'Sami', 'Eskimoic', 'Other' or 'Unknown' type in order to avoid conflict with regulations for the sampling and use of Sami human material for research; all of the skeletons in the present catalogue have been categorized as having skulls of 'Nordic' type.

The catalogue is geographically organized, starting with skeletons found in southeast Norway, and ending with those found in northern Norway. First is given the museum number, the starting letters of which indicates to which museum collection the finds belong. The museum number serves as reference to information in the museum archives and registers. 'C' is the Museum of Cultural History at the University of Oslo; 'T' is the University Museum at the Norwegian University of Science and Technology in Trondheim; and 'Ts' is the University Museum at The Arctic University of Norway in Tromsø. Next, starting with A, is given the skeleton's number in the Schreiner Collection at the University of Oslo; the Schreiner Collection is today part of the Institute of Basic Medical Sciences, formerly the Anatomical Institute, and holds the majority of archaeological skeletons from the VA and earlier found in Norway. Next follows the project-specific 'VK'-number for Viking Genomics. After that are given the name of the region ('fylke'), the municipality ('kommune') and the farm ('gård'), followed by the farm number, the smallholding number and, if applicable, any local place name associated with the site. The next line shows the identification number in the National Register for Archaeological Monuments ('Askeladden'), where applicable (not all the finds are registered in this database). Geographical coordinates are given in EU89-UTM zone 33; if imprecise, the accuracy is stated as within the 'smallholding', 'farm', or 'municipality'. Following this, the year of excavation is stated.

Catalogue

Hedmark

C25552, A4005, VK448, Hedmark, Ringsaker, Berg øvre (619/9 «Breidablikk»)

Askeladden ID: None

Coordinates: EU89-UTM zone 33 N6746886 E275540 (smallholding)

Year of excavation: 1933

The skeleton was found in 1933 when a burial mound was being removed by the land user. It was found lying on two stone slabs, and had been covered by two or three further slabs; an accompanying sickle type R. 384 dates the burial to the VA. The site was inspected by Alf Söderholm from the Institute of Anatomy at the University of Oslo, and he concluded that the skeleton, which had been removed from the burial before his arrival, was female. The Schreiner database describes the skeleton to be from an adult woman. It also describes the position of the skeleton as 'atypical', and cites a letter from archaeologist Sigurd Grieg, University of Oslo, saying that the head was said to be found lying between the legs, and the body with its upper part to the north.

Sample used for DNA analysis:

VK448 Norway_Hedmark 4005

C26737, A4304, VK422, Hedmark, Åmot, Arnestad lille (25/1)

Askeladden ID: 41956-1

Coordinates: EU89-UTM zone 33 N6785034 E303152

Year of excavation: 1938

The burial, which was placed in a small mound, was found by a farmer in 1938 when he quarried the mound for stones. Apart from the skeleton, he found several objects: a double-edged sword of Petersen's M-type, a double-edged sword blade, an axe of Petersen's G-type, and an arrowhead of type R. 539. The grave was subsequently investigated by an archaeologist, Sverre Marstrander, but apart from another arrowhead, somewhat similar to type R. 538, this did not produce further finds. The human bones in the burial are reported to originate from two individuals, a young, strongly built man in his early twenties, and another person of around 50-60 years old. It is also stated that there are animal bones, including horse bones, among the osteological material. The M-type sword is dated by

Androschchuk⁵⁵ to around the mid-10th century CE, and is a common companion to the G-type axe⁵⁴. The Schreiner database describes the human material as a male. Russ⁵⁶ has examined the material and separated it into two individuals, A, and B. It was individual A that was sampled for DNA. The post-cranial bones were not possible to assign to either of the two individuals. The remains of individual A consist of a very fragmented cranium, to which two fragments of a mandible seemingly can be associated. The sex of this individual cannot be determined, but he/she is estimated to have been 17-30 years old at the time of death. Naumann⁵⁷ carried out isotopic analyses on both individuals.

Sample used for DNA analysis:
VK422 Norway_Hedmark 4304

C17564, A2813, VK420, Hedmark, Vang, Tommelstad (6/-)

Askeladden ID: None

Coordinates: EU89-UTM zone 33 N6747756 E287415 (bruk)

Year of excavation: c. 1893

The skeleton originates from a burial mound, where it was found together with three iron knives of a type different from those of the early Iron Age, an arrowhead of the type R. 539, a fire-steel of the common type R. 426, and an iron handle for a pot. These finds only allow the individual to be dated to the VA in general. The information in the Schreiner database is sparse. The skeleton is described as an adult, but no sex determination has been made.

Sample used for DNA analysis:
VK420 Norway_Hedmark 2813

C25720, A4006, VK393, Hedmark, Ringsaker, Mæhlum (752/1)

Askeladden ID: 29529

Coordinates: EU89-UTM zone 33 N6751636 E282299

Year of excavation: 1933

The skeleton was found during a professional excavation of a burial mound, 7.5 m in diameter, situated on a natural hummock c. 250 m west of the farm. The skeleton was situated in the middle of the mound, and oriented east-west. Six arrowheads—three type R. 358, two type R. 359, and one of undetermined design—were placed near the head, while other finds were made on the northern side of the torso and at the hips. These finds included an iron tool of unknown function, a possible fragment of an iron buckle, a fire-steel type R. 426, and a fragment of a three-layered bone or antler comb with an iron rivet. The R. 358 arrowheads date the burial to the 10th century, which is not in conflict with the presence of type R. 359 arrowheads⁵⁴ and a type R. 426 fire-steel⁵⁸. The Schreiner database describes the skeleton to be from an adult male. Russ⁵⁶ also suggests that the individual is male, and based on the teeth she posits that he was 33-45 years old at the time of death, while the cranial sutures indicate a somewhat greater age. Krzewińska, et al. (2015) estimated the mtDNA HVR1 sequence of this individual to represent haplogroup HV4a⁵⁹.

Sample used for DNA analysis:
VK393 Norway_Hedmark 4006

C27338, A4460, VK394, Hedmark, Åmot, Arnestad store (24/1)

Askeladden ID: 12709-1

Coordinates: EU89-UTM zone 33 N6784587 E303102

Year of excavation: c. 1943

During the demolition of a 1 m high, 5 m wide burial mound of mainly stones, a skeleton and several finds were unprofessionally recovered. A subsequent archaeological inspection of the site did not produce further finds. The finds included a poorly preserved axe resembling type R. 555, which is equivalent with Petersen's type H; four arrowheads of type R. 539; two arrowheads of type R. 540; and some unidentifiable iron objects. The R. 540 arrowheads indicate a Migration Period date for the burial, which is in contrast to the axe of type R. 555/Petersen's type H, which is datable to the first half of the 10th century CE, perhaps the entire century. The arrowheads of type R. 539 do not provide any clarity. The axe may be considered the more important dating element. The Schreiner database indicates that the skeleton is that of an adult, but gives no sex determination.

Sample used for DNA analysis:
VK394 Norway_Hedmark 4460

Oppland

A2808, VK417, Oppland, Gran, Sandeødegården on Nedre Hov (262/- or 263/-, Lindbak)

Askeladden ID: None

Coordinates: EU89-UTM zone 33 N6699700 E255988 farm

Year of excavation: 1868

Two inhumation burials in two mounds (No. 1 and 2) that were excavated in 1868 by Nicolay Nicolaysen. No objects were associated with the burials, and there were no indications of a construction of a grave chamber. Mound No. 1 was approximately 6.5 m in diameter and about 2 m high. A 1.5 m-high stone was found on top of the mound, where it had apparently earlier been placed in an upright position. Charcoal was found sparsely in the mound filling, and the skeleton was found, in a somewhat disturbed state, in the middle of the mound, at some distance above the base of the mound. Mound No. 2 was placed next to and northwest of Mound No. 1, and was about 1.2 m high and 7.8 m in diameter. Centrally in the mound was found a skeleton, lying on its back in an east-west orientation, with the head towards east. The graves can only be dated, by their burial type, to within the late Iron Age. The Schreiner database describes the two skeletons as brownish. It also mentions that there was at least one animal bone in the material turned over to the Schreiner Collection in 1885, but that was discarded along with other bones in 1924. The mound from which the skeleton (A2808, VK417) that we sampled originates is unknown.

Sample used for DNA analysis:
VK417 Norway_Oppland 2808-2

C35586, A5305, VK386, Oppland, Lesja, Skålgård søndre (131/1)

Askeladden ID: 11363

Coordinates: EU89-UTM zone 33 N6898881 E189426

Year of excavation: 1981

The grave was found next to a large stone during digging for the construction of a farm road in 1981. A subsequent controlled archaeological excavation produced no further information. Apart from the skeleton, the grave contained a sword of Petersen's Type L, the remains of a sword sheath, a whetstone of sandstone, a fragment of an iron knife blade, and an iron fragment of unknown use. Androschchuk⁵⁵ dates Petersen's L Type from the 870s CE into the 11th century CE. The Schreiner database describes the skeleton as that of a mature male, around 50 years old at the time of death.

Sample used for DNA analysis:

VK386 Norway_Oppland 5305

C24243 and 24297, A3777-3778, VK421 and VK387, Oppland, Jevnaker, Velo nordre (164/6)

Askeladden ID: None

Coordinates: EU89-UTM zone 33 N6694793 E247284

Year of excavation: 1928

Due to a mistake, the two skeletons VK421 and VK387 are recorded on two different farm numbers in the collection, but originate from the same grave on farm 164/6. VK421, alias C24243, was found June 1928 during construction of a roadbed from the farmhouse to the public road and sent to the Museum of Cultural History at the University of Oslo by the local sheriff. VK387, alias C24297, originates from the resulting archaeological investigation of the find site, carried out by the Anatomical Institute of the University of Oslo. Because of their different ways into the Museum of Cultural History and the recovery of ceramics during the archaeological investigation, they were considered two different graves. The find site is situated in the yard of the farm Velo Nordre, c. 20 southwest of the farmhouse. The initial finds were made 25-30 cm below the surface, and consisted of a skeleton oriented east-west, with the head to the west, and a small axe. The latter is of Petersen's L-type, which is datable to the mid-10th to 11th century⁵⁴. By the archaeological excavation of the remaining part of the grave some weeks later, remains of a further, female skeleton was found, along with unrecovered remains of two infants. The female skeleton was orientated in the same way as the first one found, and the infants were lying at her feet. The excavation also produced a ceramic shard identified to be from a vessel of type R. 361, two unidentifiable pieces of burned clay, and a small, unidentifiable piece of iron. The entire grave, with all four skeletons, had been lined with rather thick timbers, but no iron nails were found. The shard indicates an early Iron Age date, but may represent an earlier settlement on the site. The Velo farm has produced finds going back to the Bronze Age. The Schreiner database states that the VK387 skeleton (A3778) is that of an adult female. The VK421 skeleton (A3777) is described as an adult male. Russ⁵⁶ also concludes that A3777 is male, based on cranial features. The age is estimated to be >45 years old. Krzewińska, et al.⁵⁹ suggest haplogroup U5a/U5b2 for the individual's mtDNA HVR1 sequence.

Samples used for DNA analysis:

VK421 Norway_Oppland 3777

VK387 Norway_Oppland 3778

C14690-14692, A1517, VK414, Oppland, Skjåk, Nedre Hjeltar (59/1)

Askeladden ID: 51891

Coordinates: EU89-UTM zone 33 N6878623 E153537

Year of excavation: 1889

The skeleton was found in an east-west oriented burial, with the head towards the west, and the grave goods placed on either side of the cranium. The grave goods consisted of an axe, identified as a Type R. 555, four arrow heads, and some unidentifiable iron objects. The R. 555-type axe is the same as Petersen's H Type, and is dateable to the second half of the 10th century CE and the first part of the 11th century CE. The arrowheads cannot be identified. The Schreiner database lists the skeleton as that of an adult male. According to the description by Schreiner⁶⁰, substantial parts of the skeleton are preserved. Russ⁵⁶ estimates that the individual is male, and >45 years of age on the basis of degree of cranial suture closure. Krzewińska, et al.⁵⁹ find the mtDNA HVR1 sequence of this individual to represent haplogroup H6⁵⁹.

Sample used for DNA analysis:

VK414 Norway_Oppland 1517

C21852, A1520, VK415, Oppland, Lunner, Hov

Coordinates: EU89-UTM zone 33 N6691573 E258795

Year of excavation: 1910

The location of this find is slightly unclear, but is here located according to the place name 'Hov'. This skeleton was found approximately in the centre of a round mound, extended on its back and with the head towards the west. The right arm was bent over the breast. The only grave good found was a mosaic bead of black glass with milk-white and red decorations, dateable to the VA. The Schreiner database describes the skeleton as adult and female⁶⁰.

Sample used for DNA analysis:

VK415 Norway_Oppland 1520

Telemark

C21794, A1645, VK392, Telemark, Vinje, Særen (23/-)

Askeladden ID: None

Coordinates: EU89-UTM zone 33 N6626654 E100574 (farm)

Year of excavation: 1915

The information about the circumstances of this find is vague. It was found by an Olav Nykos during hunting on a scree slope 2 km north of the Særen farms. Two keys of type R. 459 date the grave to the VA, before the 11th century CE⁵⁸. No other finds were recovered. In the Schreiner database the skeleton is described as adult and of undetermined sex. Russ⁵⁶ estimates the skeleton to be female and, based on the fusion of the cranial sutures and the heavily worn teeth, to be >45 years old. Krzewińska, et al.⁵⁹ find the individual's mtDNA HVR1 sequence to represent haplogroup H*.

Sample used for DNA analysis:

VK392 Norway_Telemark 1645

C22242a-d, A1648A and A1648B, VK390 and VK391, Telemark, Skien, Søndre Mæla (4/76 Berg)

Askeladden ID: None

Coordinates: EU89-UTM zone 33 N6576689 E191488 (GÅRD)

Year of excavation: 1918

The two skeletons in this grave were found in 1918 during fence construction on the parcels Kveldro and Vesterbø on the smallholding Berg under Mæla Søndre. The skeletons were lying close together, and were accompanied by two non-cruciform brooches. These resemble the brooch in Shetelig⁶¹ and can be dated to the Migration Period (400-550/600 CE). In the Schreiner database, only the colour of the skeletons is mentioned. Russ⁵⁶ has separated the material into individual A (VK390) and B (VK391), but cannot exclude the presence of more individuals. Russ reports that individual A is male and c. 30-50 years old, while individual B, which has a more intact cranium, is female and c. 18-30 years old. Naumann et al.⁶² conducted isotopic analyses on the mandible.

Samples used for DNA analysis:

VK390 Norway_Telemark 1648-A

VK391 Norway_Telemark 1648-B

C23941a-f, A3697, VK389, Telemark, Skien, Bergsland (60/77 Lagmannsgårdshøyden)

Topografisk: Schreinerske arkiv: Schreiner 1927:

Askeladden ID: None

Coordinates: EU89-UTM zone 33 N6576540 E192556

Year of excavation: 1926

The finds were made during building work, at approximately 50 cm depth, below a layer of stone slabs. There were no traces or reports of a mound on the site. The finds consisted of skeletal remains plus a spearhead of Petersen Type I, a frostnail of Type R. 591 for a horse, and a few iron fasteners. Petersen Type I spearheads date to the first half of the 10th century CE, according to Peterson⁵⁴ Andrushchuk⁵⁵ dates some of the sword types that occur with the Peterson Type I spearhead into the second half of that century. The grave is therefore dated to within the 10th century CE. In the Schreiner database, the skeleton is described as adult and male.

Sample used for DNA analysis:

VK389 Norway_Telemark 3697

Sør-Trøndelag

T16298, A4481, VK516, Sør-Trøndelag, Ørlandet, Østråt (Austrått) (82/91)

Askeladden ID 56213-1

Coordinates: EU89-UTM zone 33 N7074267 E240441

Year of excavation: 1944

This grave find was made during road construction, and was sent to the Schreiner Collection from the Trondheim University Museum. No remains of a mound were reported, but the burial overlooked a small bay, where in modern times harbour structures were established. Two finds are reported: an iron spearhead of type R.521, with copper alloy knots, and a highly fragmented shield boss of type R.562. These date the grave to the 10th century CE. In the Schreiner database, the skeleton is described as originating from a burial site. Calvaria and remains of the facial bones are preserved together with a lower jaw, a left humerus, and fragments of other bones. The individual is estimated to be male and of adult age. The museum archive reports that Schreiner estimated the individual to be over 50 years old.

Sample used for DNA analysis:

VK516 Norway_Sor-Trondelag 4481

T13363, A3699, VK523, Sør-Trøndelag, Bjugn, Melem (Herstaen) (84/-)

Askeladden ID: None

Coordinates: EU89-UTM zone 33 N7089516 E239588

Year of excavation: 1926

Amateurs extracted these remains from a large, partly stone-lined chamber grave, oriented east-north-east to west-south-west, inside a cairn. Subsequently, the grave was excavated by a student, B. Irgens Larsen, and several shards of a very thin-walled ceramic vessel of possible Bronze Age type were recovered. The grave also contained an unusually thick-walled cranium, which was broken by the original finder. The Schreiner database states that the skeletal fragments consisted of a calvarium and minimal additional remains. The specimen is estimated to be an adult female.

Sample used for DNA analysis:

VK523 Norway_Sor-Trondelag 3699

Nord-Trøndelag

T2327, A3705, VK548, Nord-Trøndelag, Stjørdal, Kil søndre (220/-)

Coordinates: EU89-UTM zone 33 N7040131 E311368

Year of excavation: 1927

Askeladden ID: None

The remains were found during the construction of a railroad, in bog soil next to a creek. On the breast of the skeleton were found two well-preserved single shell oval brooches of copper alloy with riveted, plated knots (T-2293), a brown, opaque glass bead (T-2294), and a clay bead (T-2295). Bjørn⁶³ contends that the first of these beads is made of amber rather than glass. The oval brooches are of Type R. 649⁶⁴, which Petersen⁶⁵ dates to the 9th century CE, a dating that Bjørn agrees with. The Schreiner database states that the skeleton is well-preserved but not complete. Schreiner⁶⁰ lists 50 bones that are preserved, plus the cranium. The skeleton is female; no age is determined.

Sample used for DNA analysis:

VK548 Norway_Nord-Trondelag 3705

Nordland

TS7659, A5195, VK514, Nordland, Steigen, Vikran Nordre (71/2)

Coordinates: EU89-UTM zone 33 N7533257 E505595

Year of excavation: 1965-1966

Askeladden ID: 37739-1

The cranium was found while ploughing a field in 1965, and an archaeological excavation the following year produced additional parts of a skeleton. The individual was found lying on its left side with flexed legs and the head oriented south-south-west. The right arm was extended, with the fingers in front of the knees. A knife was lying at the hand, and another knife and a composite comb were positioned behind the hip. There is no indication that a mound had ever been present over the burial. The composite comb dates the burial to the between the 6th century CE and the 10th century CE. The Schreiner database describes the remains as well preserved. No sex determination is given, but the age is estimated to be 11-13 years old. Russ⁵⁶ states that sex determination is not possible due to the young age of the individual. The teeth indicate that the individual was 11 years old $\pm$ 30 months, while the rest of the skeleton suggests that s/he was 10-14 years old. Russ concludes that the individual's age was 11-12 years old. The remains have previously been sampled for isotope analysis⁶². Krzewińska, et al. determined the mtDNA HVR1 sequence of this individual to represent haplogroup K1a11⁵⁹.

Sample used for DNA analysis:

VK514 Norway_Nordland 5195

T20545 h:1, A5317, VK526, Nordland, Herøy, Sørherøy (Prestegården, 4/1)

Coordinates: EU89-UTM zone 33 N7319886 E376306

Year of excavation: 1983

Askeladden ID: 36189-1

The site is situated next to the Herøy Sound, only 80 m from the beach, and 300 m north of the large Romanesque Herøy church from the 12th century. A skeleton was found with one oval brooch 10 cm below the surface during construction works in an area that has yielded several other inhumation burials. During a control excavation after the discovery, remains of a further skeleton were found. This individual had been placed in an east-west direction, with the head towards the west. A 1.2 x 1.6 m large dark colouring of the sandy subsoil indicated the presence of a wooden coffin or grave lining.

It seemed that the deceased had been laying in a hocker position. There were no indications of a mound present. The finds from the excavation included wooden fragments, iron nails and rivets, animal bones, another oval brooch of the same type as found with the first individual (R.647 variant B⁶⁵), a knife, and textile fragments from the brooches. The two brooches differ in design, but may indicate that both skeletons came from the same burial, and dates them to the 9th century CE⁶⁵. According to the osteological investigation following the excavation, both skeletons were from young females. Schreiner estimated that the poorer preserved one (A5316) originated from a 17-18 year old woman, while the better preserved one (A5317) was judged to belong to a 12-13 year old female, an interpretation also found in the Schreiner database. Russ⁵⁶ found that A5317 belonged to a younger individual early in puberty, with an age of 12-17 years, most likely between 13-15 years. Russ concluded that, due to the individual's young age, it was not possible to determine sex with certainty, but that traits of the hip bone indicated female sex. The mtDNA HVR1 sequence of this individual was found to represent haplogroup J1d/J2b⁵⁹.

Sample used for DNA analysis:
VK526 Norway_Nordland 5317

T5105, A0642, VK529, Nordland, Steigen, Leines (6/-)

Coordinates: EU89-UTM zone 33 N7513575 E491831

Year of excavation: Before 1897

Askeladden ID: None

Sheriff Olaf Olsen gave this skeleton to Trondheim University Museum with the information that it had been found on the farm Leines in Ledingen parish, Nordland. The skeleton had been found with two single-edged swords of the types R. 491 and R. 500, a celt of type R. 401, two whetstones, and a possible sickle. The sword type R. 491 is equivalent to Petersens type C, which Androschuk⁵⁵ dates to the early VA, c. 750-870 CE. The celt and the R. 500 sword may indicate an earlier date. The Schreiner database describes the skeleton as well preserved, and indicates that the individual was an adult male. In 1927 Schreiner listed the preserved parts of the skeleton and suggested that the individual was a male⁶⁰. In 2013, Russ⁵⁶ described the remains as well preserved, and suggested that they belong to a male of 24-30 years of age. The remains have previously been subjected to isotope analysis⁵⁷. Krzewińska, et al.⁵⁹ found the mtDNA HVR1 sequence of this individual to represent haplogroup H*.

Sample used for DNA analysis:
VK529 Norway_Nordland 642

Ts5287, A4691B, VK519, Nordland, Steigen, Steigen Mellem (78/- Hagbartsholm)

Askeladden ID: 7944

Coordinates: EU89-UTM zone 33 N7535488 E498506

Year of excavation: 1954

This find is from an excavation of a Migration Period-VA burial site, carried out by H.E. Lund of Tromsø Museum in 1954. The individual is from Grave X, and the finds included fragments of a three-layered composite antler or bone comb with linear ornaments and five iron nails plus some adhering wood and charcoal. The comb dates the burial to between the 6th century CE and the 10th century CE. The Schreiner database describes the few remains as of adult age, but undetermined sex. A small iron ring is mentioned as a grave good, but this object is not noted in the archaeological record of the specimen. Russ⁵⁶ estimates the skeleton to be female, based on the crania and the femur joints. She concludes that the individual was 25-30 years old based on limited tooth wear. Naumann⁵⁷

measured several isotopes in the specimen⁵⁷.

Sample used for DNA analysis:
VK519 Norway_Nordland 4691b

Ts4306, A4511 and A4512, VK515 and VK530, Nordland, Bodø, Rønvik nedre (32/100, Rønvik)

Askeladden ID: None

Coordinates: EU89-UTM zone 33 N7462971 E473589

Year of excavation: c. 1946

These two graves were found about 20 m apart and c. 70 m from the beach, and it is unknown which skeleton belonged to which grave. One grave was very shallow, only 20 cm below the turf, and contained, apart from the human remains, a three-layered bone or antler comb and a bone needle house of type VGJ 492, a miniature sword of bone or wood of a shape like a Petersen type V sword, plus some possible chest mounts of iron. Androshchuk⁵⁵ dates the V-type sword to around 1000 CE, which might be a fair guess of the date of the chest mounts as well. The other burial, which was 180 cm deep and covered with stones, also contained human remains together with a sword of Petersen's Y-type, a spearhead of Petersen's G-type, and a shield boss of type R. 563. Androshchuk⁵⁵ dates the Y-sword to 900-975 CE, and Petersen⁵⁴ dates the spearhead to the second half of the tenth and the early 11th century CE. Thus, this grave can be dated to the middle or second half of the 10th century CE. Since the burials both date to the second half of the 10th century CE or perhaps slightly later, both skeletons can also be assigned to this date.

The Schreiner database states that skeleton VK 515 (A4512) originates from a young adult male. Russ⁵⁶ also determines the skeleton to be young and male on the basis of DSP of the coxae, less so of the cranium. On the basis of the teeth and the fusion of the epiphyses, the age is estimated to 18-20 years.. Naumann et al. measured the $\delta^{13}\text{C}$, $\delta^{15}\text{N}$, and $^{87}\text{Sr}/^{86}\text{Sr}$ values of VK 515 (A4512)⁶². Krzewińska, et al.⁵⁹ found that the mtDNA HVR1 sequence of this individual was estimated to represent haplogroup H*.

Skeleton VK 530 (A4511) is described in the Schreiner database as being from an adult male of 35-35 years of age. Some animal bones were found together with the human remains. Russ⁵⁶ found that the features of the cranium are indecisive, but that a humerus measurement indicates it to be a female. Based on tooth wear she suggested an age of 25-35 years, which is not contradicted by the state of the bones. Naumann et al.⁶² measured isotope values of this specimen. Krzewińska, et al.⁵⁹ found the mtDNA HVR1 sequence of this individual to represent haplogroup H*.

Samples used for DNA analysis:
VK515 Norway_Nordland 4512
VK530 Norway_Nordland 4511

Ts5252, A4689, VK518, Nordland, Værøy, Nordland, (17/- Vågehamn)

Askeladden ID: 59407

Coordinates: EU89-UTM zone 33 N7510519 E402848

Year of excavation: 1954

The site is situated at the north end of the small island Værøy, southern Lofoten, facing very rich fishing waters, but also one of the world's strongest whirlpools, Moskstraumen. The human remains originate from a grave with eight different individuals, buried at the same time. The grave was situated c. 50 m from the beach, 4-5 m ASL, and was first discovered through the digging of a trench for a

water pipe in August 1954. The remaining part of the grave was dug out in October the same year. It was reported that the remains of eight individuals were found, but detailed information is only available for the three of them. All remains were found inside a rectangular stone lining, which was oriented east-west and measured 3.1 m in length and about 1 m in width. The grave was not marked above ground. In the eastern part of the burial three parallel skeletons were found with their heads towards the east. On the northern side, a child was lying facing north with some animal bones at his/her breast. On the southern side, a male individual was lying on his back with his knees towards the south and an axe above his head. In the middle, a richly equipped female was placed with a number of dress accessories. In the western end of the burial another five persons with equipment were reported. The following burial goods date the burial: two axe heads of Petersen type D and E, which according to Petersen⁵⁴ appear with sword types that Androshchuk et al.⁵⁵ date to the mid-9th to 10th century CE; two further type C swords, which Androshchuk dates to the early VA, 750-870 CE. An oval brooch of type R. 647 is from the 9th century CE⁶⁵, and the same date—with an emphasis on the early part of that century is stipulated for a Berdal A type oval brooch also found in the grave⁶⁵. Thus, the burial seems to have taken place around the middle of the 9th century CE. The Schreiner database describes the find under number A4689a, while A4689b is unrelated. It states that post-cranial bones from A4684—but no cranium—have been intermixed with 4689a. Only one cranium is mentioned, and it is identified as female; this is the one that was sampled for VK518. Russ examined the human remains stored under A4689 in the Schreiner Collection and found the remains of four individuals, which probably reflects the three from the October 1954 excavation, plus the A4684 individual⁶⁶. She found one female—only represented through a cranium—and three males, one of these being only 16-20 years old. The female was, based on suture and teeth wear status, determined to be 25-40 years old.

Sample used for DNA analysis:
VK518 Norway_Nordland 4689

T9366-9379, A3708, VK524, Nordland, Nesna, Tommeidet (98/22)

Askeladden ID: 16512-1

Coordinates: EU89-UTM zone 33 N7351266 E397879

Year of excavation: c. 1910

This boat burial was found in one of several mounds overlooking a natural harbour on the west tip of the island Tomme. Remains of two individuals were found in the burial, placed side by side in the southwest-northeast orientated boat. Horse and cattle bones were found in the northeast end of the grave⁶⁶. Among the rather rich grave goods, the following datable items were found: two oval brooches of copper alloy, of the type R. 652, which Petersen dates from the late 9th century CE to the late 10th century CE⁶⁵; a trefoil brooch of type R. 671, a model which is also elsewhere found with R. 652⁶⁵; four beads of black glass with white bands and white, red, and green dots in glass added to the surface; a sword described as similar to type R. 495, but with a smaller top rather than a regular knob on the upper end (this sounds like a type P or Y sword, dated by Androshchuk⁵⁵ to the late 10th century CE); a shield boss of type R. 562, which dates to 850-950 CE according to Petersen⁵⁴; and an axe of type R. 552, which Petersen finds together with swords of the B, C, E, and H type—only the H-type of these continues into the 10th century CE. The grave can probably be dated to the middle of the 10th century CE.

The Schreiner database only describes the colour of the remains. The materials first came to the Anatomical Institute in 1927, probably when Schreiner was conducting his survey for the Oseberg publication. The preserved remains from a male and a female are listed by Schreiner⁶⁰. Russ could

not identify any remains of the woman⁵⁶. The surviving remains are from a male (cranium and DSP), 35-50 years old. Krzewińska, et al.⁵⁹ determines the mtDNA HVR1 sequence to represent haplogroup HV0.

Sample used for DNA analysis:
VK524 Norway_Nordland 3708

T12578, A3709, VK525, Nordland, Dønna, Hov (19/1, Løkta)

Askeladden ID: 73294

Coordinates: EU89-UTM zone 33 N7342211 E397137

Year of excavation: 1922

This site is situated only 50 m from the current beach, overlooking an open, stony bay facing east-north-east. The find was made during the digging of a trench for a water pipe to a farm building. The finds from this burial are few, including a knife and a sickle, plus two oval brooches of types R. 647 and R649, the latter datable to the 9th century⁶⁵. In the Schreiner database the remains are described as originating from an adult woman. They are more fully described by Schreiner⁶⁰. Russ⁵⁶ finds the skeleton belonged to a female, 25-30 years of age, based on tooth wear. The skeleton is described as poorly preserved, but very gracile. Some skeletal parts from the upper breast region are coloured green by copper alloy, demonstrating that at least one of the oval brooches most likely had been positioned there. The specimen was sampled for isotope analysis by Naumann et al.⁶².

Sample used for DNA analysis:
VK525 Norway_Nordland 3709

C18558, A253, VK388, Nordland, Lødingen, Ytterstad (17/-)

Askeladden ID: None

Coordinates: EU89-UTM zone 33 N7580530 E527347 (farm)

Year of excavation: 1889

The skeleton was found in a small mound at the farm Ytterstad, about 500 m from the beach. The farm is on the north side of a well sheltered bay facing east and overlooking the mouth of Tjeldsunde, a part of the inner sailing route along the Norwegian coast. The only accompanying object was an unidentified, ornamented antler tool. The ornaments indicate a date to the VA or Middle Ages, but the burial type excludes the latter. The skeleton was initially identified as female, but was later determined to be a young male by Schreiner⁶⁰. Russ⁵⁶ describes the skeleton as quite complete, but poorly preserved and belonging to a male age 15-17 years. The rearmost molar had erupted, but most epiphyses in the postcranial skeleton had not yet fused. Coxae could not be used for sex determination due to young age, but the cranium allowed an identification. The remains were sampled for isotope analysis by Naumann and colleagues⁶².

Sample used for DNA analysis:
VK388 Norway_Nordland 253

C14554-14557, A1522, VK419, Nordland, Bodø, Rønvik Øvre (31/-)

Askeladden ID: None

Coordinates: EU89-UTM zone 33 N7463888 E475796

Year of excavation: 1889

This burial was found in shell sand in what had earlier been a gentle slope towards the nearby beach, but which had been eroded at the time of discovery. There was no memory of a mound on the site. The grave itself was found below two stone slabs, 1.0 and 0.7 m long, which were lying in the topsoil.

Apart from the skeletal remains, the grave held an axe of early Iron Age type, but with similarities with Petersen's type C axe without a 'beard', a large scythe of type R. 386, and a sickle possibly of type R. 385. C-type axes are often found with H-type swords, which Androshchuk⁵⁵ dates to up to 950 CE. The burial cannot be dated more closely than the Migration Period to early VA. The Schreiner database states that the skeleton is from an adult male; the preserved bones are listed by Schreiner⁶⁰. Russ⁵⁶ suggests that the individual is most likely a young man, 17-25 years old, based on sutures, tooth wear, and epiphyses⁵⁶. Naumann et al.⁶² sampled a femur for isotope analysis. Krzewińska, et al.⁵⁹ estimated the mtDNA HVR1 sequence to represent haplogroup U1/U5a.

Sample used for DNA analysis:
VK419 Norway_Nordland 1522

C18035-18039, A1502, VK418, Nordland, Steigen, Steigen øvre (77/1)

Askeladden ID: None

Coordinates: EU89-UTM zone 33 N7535744 E499177

Year of excavation: c. 1894

The find was made during drainage work on the present-day cemetery of Steigen, only about 300 m from the rather marshy coast. There are several Iron Age cemeteries in the surrounding area. The burial produced weapon equipment that has been argued to be of eastern origin⁶⁷. A shield boss type of R. 221, two spearheads of Rygh's types 206 and 211, and a sword with a decorated scabbard mounting dates this find firmly in the early Iron Age, according to Sjøvold in the late 4th century CE. The Schreiner database describes the skeleton as from an adult male. The extent of the remains are described by Schreiner⁶⁰.

Sample used for DNA analysis:
VK418 Norway_Nordland 1502

Ts5656, A4727, VK547, Nordland, Tjelsund, Stokke (79/1)

Coordinates: EU89-UTM zone 33 N7604398 E557131 sogn Lødingen

Year of excavation: 1957

Askeladden ID: 47377-1

The burial was found through the digging of a cable ditch, straight downhill 15 m north of the main building of the farm and 1 m north of the road between Sandnes and Kjærstad. The site is situated c 150 m east of Hol church, at Tjelsundet. A professional excavation of the remaining part of the burial was conducted by a curator from Tromsø Museum. The grave was not marked on the surface, and the burial pit, dug in shell sand, was without stones and in the shape of a trough. It measured 30-50 cm in depth, and was 60 cm wide and 130 cm long. It was oriented east-west, and the body was lying on its side, with the head towards east, facing north, and with flexed legs. The sparse grave goods were found at the back of the legs, in the grave's southwest corner. They consisted of an auger of iron, a possible awl of iron with a wooden handle, and three iron tacks with wooden remains from an unidentified object. The finds can be dated no closer than to the VA. In the Schreiner database, the skeleton is described as well-preserved, and is suggested to be that of a male of around 45-55 years.

Sample used for DNA analysis:
VK547 Norway_Nordland 4727

Troms

Ts3639, A4184, VK520, Troms, Tromsø, Tussøy, (188/1)

Askeladden ID: None

Coordinates: EU89-UTM zone 33 N7729512 E621341

Year of excavation: 1935

The smallholder, Hjalmar Brox, and his son discovered this grave when digging in a small mound located c. 7 m ASL, c. 100 m west of the farmstead. On behalf of Tromsø Museum a student subsequently excavated a 7 m x 4 m section of the mound and found evidence of three individuals, of which A4184 is individual III. The other individuals, I and II, had apparently been buried simultaneously, and from the grave equipment (weapons and tools) they were identified as males who had been buried in the 8th century CE; no human remains were reported to have been salvaged. A4184 was in the grave first discovered by Brox, who had disturbed it severely, but the body had apparently been lying with the head towards the west. The cranium and a few other bones were recovered from the burial together with two oval brooches of the types Rygh 652 and Rygh 654⁶⁴, which were found in the breast region. According to Gjessing⁶⁸ the grave dates to the 10th century CE. In the Schreiner database, skeleton no. A4184 is described as well-preserved but incomplete. It is stated that it consists of a “very defect and deformed calva with associated right, defect upper jaw with cheek bone, plus a few further bones”. The skeleton is judged to be from an adult female. Russ⁵⁶ describes the skeleton as poorly preserved and with only a few skeletal parts present. Age determination based on the 3rd molar is 11-17 years, while the other material indicates 12-19 years, most likely 16-18 years. Due to the young age, sex determination is uncertain, but features of the cranium indicate female.

Sample used for DNA analysis:

VK520 Norway_Troms 4184

Ts3525, A4049, VK528, Troms, Tromsø, Tussøy, Trygstad i Bø (188/10)

Askeladden ID: 27358-1

Coordinates: EU89-UTM zone 33 N7730580 E622625

Year of excavation: 1933

A4049 was given to Tromsø Museum by a local from Tussøy, Tryggve Sletten, and he appears to be the source for the contextual information. The find was made 40-50 cm below the surface, at a place near a stream, 5-6 m ASL. The distance to the sea shore is c 50 m. The find included a skeleton in a supine position with the head towards the west. It had a sword of Petersen's type C⁵⁴ on its right hand side, and an axe on the left; supposed animal bones were also found at its side. The other finds from the grave included two arrowheads, a large, four-sided hone of slate, fragments of a knife, an iron staple, and a decorated bone comb of type Rygh 447⁶⁴. At the head and foot of the grave, stone heaps were found, and 5-10 m from the grave, towards the river, charcoal and other unspecified material were recovered. Gjessing⁶⁸ dates the grave to 800-850 CE, but Androschchuk⁵⁵ dates the C-type swords to the wider range of 750-870 CE and the comb falls into Ashby's Type 5, which broadly dates from the 8th century CE to the mid-10th century CE⁶⁹; Gjessing's⁶⁸ narrow dating interval may thus be expanded to 750-870 CE. In the Schreiner database A4049 is described as a well-preserved, incomplete skeleton. The skeleton is estimated to be that of a male of around 60 years of age. In her examination of the skeleton in 2013, Russ⁵⁶ estimated A4049 to be a male of 40-60 years of age. . The specimen has been included in two isotope studies^{57,62}. Naumann et al. point out that the ⁸⁷Sr/⁸⁶Sr value differs from known local values, indicating that the individual grew up at a different place than Tussøy. They further suggest a very significant change in diet from terrestrial to highly marine food in later part of life. Among 33 Merovingian and Viking age individuals from northern Norway, analysed by Naumann et al.⁶², A4049 was one of those digesting the most marine diet in his later years, while his childhood diet was among the most terrestrially dominated in the study. Krzewinska et al.⁵⁹ estimate the mtDNA HVR1 sequence of this individual to represent haplogroup K*.

Sample used for DNA analysis:
VK528 Norway_Troms 4049

Ts---- , A5001a, VK531, Troms, Lenvik, Skarsvåg (94/2)

Askeladden ID: 48876-1

Coordinates: EU89-UTM zone 33 N7709381 E617444

Year of excavation: 1964

No museum number is recorded for this skeleton, but information can be found in the archives of Tromsø Museum, in file 214/64 and under accession number 1964/104. The grave was situated above the natural harbour of Skarsvågen at the northwest end of the island of Senja, which overlooks the inner sailing route along the Norwegian coast. It was archaeologically excavated by P. Simonsen in 1964, who found no objects in the grave and no indications of a mound above. From the grave form, Simonsen dated it to VA, or perhaps a little earlier. However, recent ^{14}C dating results showed that the sample was much older than initially thought (^{14}C date: 3918 $\pm$ 36 uncal BP). In the Schreiner database, the skeleton is described as well-preserved but incomplete. It is said to be that of a male of 55-65 years of age.

Sample used for DNA analysis:
VK531 Norway_Troms 5001A

Medieval skeletons from the Public Library Site in Trondheim, Norway

(Prepared by Birgitte Skar and Lisa Mariann Strand, NTNU University Museum, Trondheim, Norway)

Seven skeletons originating from the early and high medieval periods in Norway, extending from 1030 to c. 1350 CE, are part of the foundation of the genetic research discussing demographics during the VA. The medieval churchyard from which the skeletons originate was located at The Public Library Site (Folkebibliotekstomten) in the central part of the town of Trondheim. After several minor excavations in the 19th and 20th centuries CE, the excavation of the St. Olav's churchyard was completed during a ten month period between 1984-85¹. The individuals that are included in the present analysis were between 11 and 50 years of age, and include both females and males. Each burial context shows distinct expressions of Christian ritualistic burial customs as they were inhumations, buried in an east-west direction, and were either buried in plank coffins, trunk coffins, or without a coffin. The seven individuals analysed in this study belong to the St. Olav's churchyard⁷⁰. This part of the churchyard lasted for approximately 100 years during which the churchyard was extended and an increased amount of burials were found. In addition to the clearly Christian burial customs, burial rods and hazel sticks were present in some of the graves. Five of the skeletons have been radiocarbon dated and display surprisingly old dates. Three of them except the sample from individual VK113 (SK223) are dated within the final Viking period, the VK113 individuals, however, is from the early medieval period. From the automated measure of stable carbon ($\delta^{13}\text{C}$) from the dating laboratory, it can be read that the stable carbon value is quite low. This indicates that the individuals have had a mixed diet potentially consisting primarily of marine resources. This is an issue that needs further investigation regarding stable carbon and nitrogen isotope values of the five dated individuals, which may again serve to clarify the obtained dates with reference to marine reservoir effect and thus shed light on the question of the dates being too old.

Samples used for DNA analysis:

VK113 Norway_Trondheim_SK223
VK114 Norway_Trondheim_SK332
VK116 Norway_Trondheim_SK372
VK117 Norway_Trondheim_SK328
VK118 Norway_Trondheim_SK271
VK124 Norway_Trondheim_SK356
VK125 Norway_Trondheim_SK367

1.2.2.3. Sweden

Sampling in Sweden targeted six sites: Varnhem (Skara) in Västergötland, Skämsta in Uppland, Ljungbacka in Scania, Karda in Småland, and Kopparsvik and Fröjel, both of which are on the island of Gotland. In addition, samples were included from 20 different sites on the island Öland.

Varnhem

Västergötlands Museum IM16-107025, RAÄ 60, Västergötland, Sweden

(Prepared by Maria Vretemark, Västergötlands Museum)

Varnhem in the central part of Västergötland is well known for its large church with the adjacent ruins of a Cistercian abbey. Less attention has been paid to the history of Varnhem before the abbey was founded in the middle of the 12th century CE. In order to learn more about this earlier period, the Museum of Västergötland started an archaeological research project in 2005 named '*Varnhem – innan munkarna kom*' (Varnhem – before the monks arrived). The archaeological excavations revealed a large settlement area and a VA church with a surrounding churchyard. Thick cultural layers, foundations of buildings, a church ruin, and hundreds of Christian VA graves were discovered. All of this presents an image of a prominent farmstead with roots going back into the Iron Age.

Varnhem is situated in an area with a great density of prehistoric sites. Graves and settlements dating from all periods are found here. Fertile soil, rich pasture and meadowland for harvesting and grazing, together with woodlands and lakes provided the right conditions for the emergence of a strong wealthy community. Among the rich archaeological finds discovered in the area, the large silver treasure found in 1873 deserves particular mention. This VA hoard consists of 476 silver coins from the early 11th century CE. Most of the coins are Anglo-Saxon and they point to contact with the west. Rune stones in the region bear witness to men killed in England. Several rune inscriptions also mention '*thegnar*' - a title of a follower of the Danish kings Sven Forkbeard and Cnut the Great, and as such a member of the English/Danish royal forces in England after the conquest in 1015 CE and the subsequent Danish occupation. Some of these *thegnar* obviously came from Västergötland, a region that had long been part of the Danish sphere of influence. The most successful Viking soldiers might have received a share of the taxes known as the *Danegeld*, which was paid in silver coins. They returned home after their service ended, and this could explain how the large number of Anglo-Saxon silver coins ended up in Varnhem.

The presence of a large Iron Age farmstead was confirmed through the discovery of the remains of houses, hearths, trenches, pits and postholes, along with pottery, animal bones, and other artefacts. A series of radiocarbon dates indicated that the site had been continuously settled for a thousand years, from the Roman Iron Age to the early medieval period. This was most likely an aristocratic manor. A church, built at the expense of the landowner, was included as one of the buildings on the prominent farm.

In past decades, remains of early churches and early Christian burial grounds have emerged in several places in central parts of Västergötland. The oldest churches in this region have been dated to the period around the year 1000 CE. They were privately built farm churches, predating the centralised church organisation of the 12th century with its system of parish churches based on a territorial division of the landscape. The foundations of this private church were excavated as part of the archaeological project at Varnhem (Extended Data Fig. 1d). The first church in Varnhem was built in the late 10th century CE. It was a small wooden church. Sometime during the period 1030-1050 CE the wooden church was replaced by a larger church built of locally quarried limestone. This church was probably one of the first stone buildings in Sweden.

Surrounding the foundations of the church in Varnhem, there is an extensive (nearly 4000 m²) Christian burial place containing at least 2000 graves and perhaps as many as 3000. Approximately 350 graves have been excavated so far and a well-preserved assemblage of human bones has been recovered for osteological analysis. The rest of the graves remain untouched under the grass of the park. The graves at Varnhem exhibit signs of a socially stratified society. Members of the family that owned the magnate's farm were buried closest to the church. This is indicated by the presence of limestone coffins. Further away from the church, the dead had been interred in wooden coffins or in simpler graves without a coffin. The social division of the churchyard is also reflected in the state of health that can be observed in the skeletons. There was also a division by gender. Men were buried to the south of the church and women to the north. The dating of the graves is interesting. The burial ground at Varnhem was used continuously for Christian burials from the first half of the 10th century CE to the end of the 12th century, a period of 250-300 years. Christianity was obviously established in the area by the middle of the 10th century CE at the latest⁷¹.

Samples used for DNA analysis:

VK29 Sweden_Skara 17
VK30 Sweden_Skara 105
VK31 Sweden_Skara 194
VK33 Sweden_Skara 175
VK34 Sweden_Skara 135
VK35 Sweden_Skara 118
VK39 Sweden_Skara 181
VK40 Sweden_Skara 106
VK42 Sweden_Skara 62
VK303 Sweden_Skara 27
VK304 Sweden_Skara 36
VK306 Sweden_Skara 33
VK308 Sweden_Skara 101
VK309 Sweden_Skara 53
VK395 Sweden_Skara 275
VK396 Sweden_Skara 166
VK397 Sweden_Skara 237
VK398 Sweden_Skara 231
VK399 Sweden_Skara 276
VK400 Sweden_Skara 236
VK401 Sweden_Skara 229
VK402 Sweden_Skara 38

VK403 Sweden_Skara 217
VK404 Sweden_Skara 277
VK405 Sweden_Skara 83
VK406 Sweden_Skara 203
VK407 Sweden_Skara 274
VK424 Sweden_Skara 273
VK425 Sweden_Skara 44
VK426 Sweden_Skara 216
VK427 Sweden_Skara 209

Skämsta, Uppland, Sweden

(Prepared by Caroline Ahlström Arcini, National Historical Museums, Lund)

Two Dwarfs: Upplandsmuseet, inventory number - UM36031_621 and UM36031_623b

In 1994 parts of a burial site were investigated in the small hamlet Skämsta north of Uppsala in Sweden. Six inhumation graves containing skeletons from seven individuals were excavated. In addition to the more intact graves, a pit of mixed bones was found in the northern part of the cemetery. These bones came from a damaged grave. The excavated graves were not visible above ground. Four of the graves were constructed of stone slabs of various sizes. Five of the individuals were orientated west-east and one was buried east-west. All of them were buried lying on their backs. They were all single graves, and in one of the graves bones from a newborn were found.

Different types of artefacts were found in the graves such as combs, pearls, and a ring for the hair. Regarding the ring there is one parallel found in Poland. The graves have, based on the finds, been dated to the later part of the VA and the beginning of the medieval period (1000-1100 CE). Estimation of age and sex has been done according to standards⁷² and the results indicate that five of the buried were adults, one was a sub-adult of 12-14 years of age, and one was a newborn. With respect to the adults, two died when they were 20-40 years of age and four died when they were between 40 and 60 years of age. Regarding the sex of the individuals, three of them were male (including the sub-adult), and three were female. The sex of the infant is unknown.

During the excavation, the archaeologists noticed that one of the graves (grave 41850, a.k.a. UM36031_623b) was unusual. It contained an adult of very short stature, about 130 cm. The osteological analysis of the skeletal material revealed that the individual was a dwarf. Further investigation of the rest of the skeletons showed that this was not the only dwarf. The individual in grave 33124 (UM36031_621), who was buried just north of the dwarf in grave 41850, was also abnormally short. A closer examination of the bones of these two individuals showed that in addition to very short limbs, their vertebrae were very short in the craniocaudal direction resulting in a short trunk⁷³. A radiologist was consulted at the hospital in Lund and X-rays were taken of several parts of the skeletons. The radiologist concluded that the two individuals suffered from a disease called *Spondyloepiphyseal dysplasia congenita (SED)*⁷⁴. In addition to short stature and deformed limbs, individuals affected by SED can have a flat face, and occasionally a cleft palate and/or club foot. Approximately 50 percent of those with the disease also have myopia and/or retinal detachment. *SED* is usually inherited as an autosomal dominant condition. It can either arise due to a mutation or appear in a child of an affected parent. If one parent is affected, the risk of inheritance is 50 percent and if both parents are affected the risk is 75 percent. There are three possible family relationships for the dwarfs at Skämsta. They are either brother and sister, mother and son or father and daughter.

Samples used for DNA analysis:

VK517 Sweden_Uppsala_UM36031_623b

VK527 Sweden_Uppsala_UM36031_621

Ljungbacka, Malmö Museum MHM 6031, Bronsdolken 7, Lockarp parish, Malmö, Sweden

(Prepared by Ingrid Gustin, Department of Archaeology and Ancient History, Lund University)

The burial ground of Ljungbacka is situated in southwest Scania, a few kilometres east of the coast. In the 1970s and 1980s parts of a major cemetery were excavated close to a Bronze Age burial mound. The total number of excavated burials reached 191; 31 were inhumations and 160 cremations. The cremations were dated to late Iron Age, while the inhumations were dated to the late Iron Age, most likely the VA. Six of the inhumation burials contained two or more individuals. The upper-lying individuals were often placed in the opposite direction to the underlying individual⁷⁵.

New grave number	MHM 6031: 26A	MHM 6031: 28
Old grave number	4A	0.250694444
Date	VA	Late Iron Age, probably VA
Grave type	inhumation	inhumation
Position	southwest-northeast	northeast-southwest
Age	55-75*	35-40
Sex	female*	male
Stature (cm)	167	170
Artefacts	keys, knife, whetstone	knife, whetstone, pottery
General comments	Individual placed in prone position, head facing south. Found above a coffin with a supine individual in east- west orientation.	The lower of two burials. This individual had supine position with head facing north. The filling of the grave contained unburned skeletal remains of a young man

Samples used for DNA analysis:

VK108 Grav4A_MHM 6031: 26A

VK217 Grave6_MHM 6031: 28

Öland, Sweden

(Prepared by Helene Wilhelmson, Sydsvensk arkeologi AB, Kristianstad, and Department of Archaeology and Ancient History, Lund University)

Many human remains from the late Iron Age (400-1050 CE) have been excavated from burials and other contexts on the island of Öland in the Baltic Sea. Throughout the period the burials are both cremations as well as inhumations. There is considerable variation in inhumation burial form (pit coffin, stone cist, etc.) during the VA⁷⁶⁻⁸⁰. The uncremated human remains from burials (and other contexts) were recently studied using an interdisciplinary bioarchaeological perspective⁸⁰ integrating new radiocarbon dates for many graves. The individuals studied for aDNA here are the majority of

the late Iron Age population discussed in that study.

The most recent dietary isotope analysis of human remains, show a great individual variation in diet⁵ supporting the archaeozoological finds and point towards a population with highly varied subsistence strategies. First generation migration to Öland was investigated through $^{87}\text{Sr}/^{86}\text{Sr}$ and $\delta^{18}\text{O}$ isotopes and the results were interpreted to show extensive immigration to the island with 68% non-local individuals in the late Iron Age. The immigrants appear to be both regional and interregional. The greater variation in individual diet could not be concluded to correlate to provenance of an individual. The people living in Öland during the late Iron Age have therefore been interpreted as a population of mixed provenance resulting in a creolized society with a combination of non-local and local traditions for burial and subsistence practices⁸⁰.

The 29 individuals we sampled were included in the study of Wilhelmson⁸⁰ and consist of all types of burials. They are from 20 sites in Öland, excavated on separate occasions between 1931 and 1975. About half of the individuals (n=15) are dated by ^{14}C and the rest are dated by typology. The burials are inhumations of varied type. They have different orientations (east-west, north-south or south-north), feature different architecture (lime stone cists, pits, coffins, full boat burial), and include single as well as multiple burials in one grave. Two more skeletons sampled in this study (id 1099, 1052) are from the early Iron Age. The table shown below presents details of the selected individuals.

Samples used for DNA analysis:

Sample	Id	Parish	SHM (grave field)	Grave id	^{14}C calib.	Year of excavation	local/non- local? (from provenance isotopes)	Age of death	Sex
VK332	Oland_1088	Smedby	23267	3	858 $\pm$ 68 CE	1944	local	45-60	Male
VK333	Oland_1028	Vickleby	22486		885 $\pm$ 69 CE	1939	non local	Mature	Male
VK334	Oland_1058	Gärdslösa	28364	134	1049 $\pm$ 58 CE	1964-66	gray	Mature	Female
VK335	Oland_1068	Långlöt	29352	18		1968	non local	Young-mature	Male
VK336	Oland_1075	Gärdslösa	28364	164	853 $\pm$ 67 CE	1965	local	Mature	Male
VK337	Oland_1064	Hulterstad	22394		858 $\pm$ 68 CE	1939	local	Mature	Male
VK342	Oland_1016	Hulterstad	25096			1954	non local	70+	female?
VK343	Oland_1021	Sandby	26454	3		1959	local	Young/mature	female?
VK 344	Oland_1030	Södra Möckleby	25657			1956	non local	Mature-old	Male?
VK345	Oland_1045	Långlöt	29352	24		1968-1969	non local	60+	Male
VK346	Oland_1057	Långlöt	29352	13		1968	local	Old	Male
VK347	Oland_1065	Köpinge	6393/75	3		1975	non local	Mature-old	Female?
VK348	Oland_1067	Köpinge	6393/75	20		1975	non local	Old	Male
VK349	Oland_1073	Kastlösa	27771	1	829 $\pm$ 57 CE	1960	non local	55-65	Male
VK350	Oland_1086	Långlöt	29352	25	799 $\pm$ 68 CE (1210 $\pm$ -45 uncal BP)	1968-73	non local	Ca 38	Female
VK352	Oland_1012	Runsten	28549			1966	non local	35-45	Male
VK353	Oland_1024	Smedby	25129		1049 $\pm$ 58 CE	1954	non local	16	Female
VK354	Oland_1026	Hulterstad	19726	1	986 $\pm$ 38 CE	1931	gray	60	Male

VK355	Oland_1046	Ventlinge	22291	-	847 ± 65 CE	1939	local	Ca 20	Male
VK357	Oland_1097	Kastlösa	22763	-	1053 ± 60 CE	1941	non local	mature	Female?
VK358	Oland_1105	Gårdslösa	28364	108:I:169	853 ± 71 CE	1965	non local	Young	Male?
VK359	Oland_1130	Böda	22231	A7	700-800 CE	1937	NA	Over 15	Undet.
VK379	Oland_1077	Böda	22231	A8	700-800 CE	1937	non local	juvenile- young	Undet.
VK380	Oland_1078	Böda	21367	A5		1935	gray	12-15y	Undet.
VK382	Oland_1132	Böda	22231	A7	700-800 CE	1937	NA	Over 15	Undet.
VK442	Oland_1008	Smedby	24542	I undre (=lower)	847 ± 65 CE	1951	non local	38 ± 10	Female
VK443	Oland_1101	Böda	21367	24		1935	non local	Ca 23	Male
VK444	Oland_1059	Smedby	23494	20	847 ± 65 CE	1945	gray	19	Male
VK522	Oland_1052	Stenåsa	24846	1	386 ± 80 CE	1953	local	19	Male
VK533	Oland_1076	Gårdslösa	28364	136	Viking age	1965	non local	50-60	Female
VK579	Oland_1099	Mörbylånga	1785/67	5	200-400 CE	1966-67	local	18-19	Female

Kärda

Nästa, Östbo hundred, Kärda parish, RAÄ 42, Småland, Sweden

(Prepared by Jörgen Gustafsson, Jönköpings Läns Museum)

Near the village of Nästa in Kärda parish, around 10 kilometers west of Värnamo in central Småland, several graves from the late Iron Age have been investigated on a number of occasions. In the surrounding area, there are other grave fields with a total of 100 mounds and 40 circular stone settings. There are also graves (mounds and large stone settings) from the Bronze Age and early Iron Age in the area, but they are much less common. The local ancient monument environment including the grave fields has been described from around the year 1800 CE onwards. In addition to these reports, sections of the grave field Kärda RAÄ 42b were partially investigated in connection with the building and widening of Road 27 on three occasions: 1936-1937, 1990, and 2015.

Most ancient monuments in the parish date back to the late Iron Age⁸¹. The parish, just as the region as a whole, is characterized by a large number of mounds and burial mound fields. Within the parish, there are 21 known grave fields comprising a total of 471 mounds and 158 circular stone settings.

When Road 27 was built between Värnamo and Smålandsstenar in November 1936, human bones were found, which led to an archaeological investigation of the site. During the excavations, 13 graves were found, of which nine held skeletons. Four were cremation graves, of which three were found in a mound with a central cairn dating back to the early Bronze Age. The age of the primary grave was determined by the discovery of a dagger-shaped fire-striking flint-stone. The grave field was located on a marked elevation along the old road. The southern part of the grave field was investigated and removed in 1936-1937. During the excavations in 1990, when the road was widened, the remaining parts of the grave field were removed on the southern and southwestern slope of the elevation, and a further nine graves containing skeletons were discovered. In 2015, in connection with the laying of a water supply pipe on the southwestern-most part of the grave field, a further grave with skeletal remains was found and investigated.

The graves consisted of slightly rounded mounds with shallow ditches around them, and inner stone packing that covered the skeletons. In some cases, it was found that the dead were buried in coffins.

All individuals were adults, with the exception of a boy of 7-11 years old. The graves contained a few artifacts. These included knives, a sandstone whetstone, a gold foil bead, and a bronze buckle from the 11th century CE. Only three ¹⁴C-dates have been obtained; one was of middle VA and two of late VA, around the year 1000 CE. It was possible to determine that the graves containing skeletons were oriented in an east-west direction and constructed according to Christian tradition. It is quite likely that they are from the era of overlap between pagan and Christian traditions. In Smålandsstenar, only some 30 kilometers from Kärda, investigated tumuli of approximately the same age were found to be cremation graves of the pagan tradition, which indicates that there were local differences when it came to the transition to Christian burial practices⁸². The samples used in the present study were taken from graves that were investigated in 1990.

Samples used for DNA analysis:

VK265 Sweden_Kärda 17

VK266 Sweden_Kärda 19

VK267 Sweden_Kärda 21

VK268 Sweden_Kärda 22

VK269 Sweden_Kärda 24

VK270 Sweden_Kärda 25

Kopparsvik

The Swedish History Museum in Stockholm SHM 16098/Gotland's Museum Inv.nr. GFC12675, Kopparsvik, Gotland, Sweden

(Prepared by Sabine Sten, Department of Archaeology and Ancient History, Uppsala University - Campus Gotland)

A large number of graves dated to the VA have been located on the coast of the Swedish island of Gotland, which has always held an important position as an island in the Baltic Sea. Archaeological finds show artefacts that are not locally manufactured on the island from as early as the Stone Age (7000-1800 CE). The VA was a very intense period for Gotland. Archaeological finds such as jewelry and coins, mainly manufactured from silver, but also from gold, show traces of trade and exchange contacts with countries to the east, south, and west. Perhaps visiting merchants who never returned home may have been buried on the island, and Gotlandic merchants may never have returned home from their travels.

One of the larger grave fields along the coast, just south of the Visby harbour, is Kopparsvik, Visby 76:1, (The Swedish History Museum in Stockholm SHM 16098, and Gotland's Museum Invnr. GFC12675). The area has been excavated a number of times—by Oscar Vilhelm Wennersten in 1917-1918, Greta Arwidsson in 1956, Erik Nylén in 1963, and Hilka Pettersson in 1964-1966. The grave field, which has been fully excavated, is estimated to have been approximately 120 m x 60 m and divided into two areas, a northern and a southern region (Fig. S1.2). Skeletal remains and archaeological artefacts have been collected from 330 graves. Based on the approximately 1000 archaeological artefacts, it has been possible to date the grave field to 900-1050 CE. The archaeological artefacts illustrate both Gotlandic manufacturing and traces of long distance trade. Among the papers that have been written on Kopparsvik are those by Pettersson⁸³, Westholm⁸⁴, Toplak⁸⁵ and Arcini^{86,87}.

No archaeological trace of settlements has been found in the vicinity of Kopparsvik, and the environment does not allow for farming. Kopparsvik has, therefore, been interpreted as a place of

commerce. In connection with a research project concerning health in the skeletal material, isotopic investigations were performed on 15 individuals from Kopparsvik, at the Archaeological Research Laboratory, Stockholm University. The measuring of carbon and nitrogen isotopes allowed us an insight of how the diet of the Kopparsvik population may have looked. Were they fishermen who lived mainly on a marine diet, such as fish and seal, or were they farmers who consumed terrestrial diet, such as cattle, sheep, pigs, or terrestrial wildlife? The isotopic analysis results showed an exclusively terrestrial diet (oral report from Professor Kerstin Lidén, Stockholm University).



Fig. S1.2: An overview of the site Kopparsvik (left) and skeletal remains (right).
Reproduced with permission from Riksantikvarieämbetet.

Samples used for DNA analysis:

VK48 Gotland_Kopparsvik-212/65
VK50 Gotland_Kopparsvik-53.64
VK51 Gotland_Kopparsvik-88/64
VK53 Gotland_Kopparsvik-161/65
VK232 Gotland_Kopparsvik-240.65
VK251 Gotland_Kopparsvik-30.64
VK450 Gotland_Kopparsvik-35
VK452 Gotland_Kopparsvik-111
VK453 Gotland_Kopparsvik-134
VK454 Gotland_Kopparsvik-140
VK467 Gotland_Kopparsvik-181
VK468 Gotland_Kopparsvik-235

VK469 Gotland_Kopparsvik-260
VK471 Gotland_Kopparsvik-63
VK472 Gotland_Kopparsvik-112
VK473 Gotland_Kopparsvik-126
VK474 Gotland_Kopparsvik-137
VK475 Gotland_Kopparsvik-187
VK476 Gotland_Kopparsvik-225
VK477 Gotland_Kopparsvik-228
VK478 Gotland_Kopparsvik-271
VK479 Gotland_Kopparsvik-272

Fröjel

Fröjel parish, RAÄ 188:1, Gotland, Sweden

(Prepared by Sabine Sten, Department of Archaeology and Ancient History, Uppsala University - Campus Gotland)

Gotland's position in the Baltic Sea and its long coasts (800 km) have been of great importance to the people on the island for centuries, especially in connection with fishing, seal and bird hunting, and marine commerce. A large number of fishing hamlets and larger harbors have been located along the coasts. Fröjel, Bottarve/Nymans, placed on the western coast of the island of Gotland, was one of the largest and most important harbours and commerce sites during the VA and early Middle Ages. Other important contemporary places of commerce in the Baltic Sea area were Birka in Uppland, Sweden, Hedeby in northern Germany, Wolin in northern Poland, and Grobin in south west Lithuania.



Fig. S1.3: Grave 8 (left) and the overview (right) of the Fröjel site it was excavated in. Reproduced with permission from Dan Carlsson.

Excavation of the Fröjel site was initiated in the late 1980s and proceeded for many years under the management of Dr. Dan Carlsson, Centre for Baltic Sea Studies, University of Gotland. The excavations revealed the remains of both a harbour and a place of commerce, with remnants of house structures from the 500s CE to the 1180s CE (Fig. S1.3). The archaeological finds include weight scales, balances, and silver coins, mainly Arabic and German, that indicated long distance trade. Other finds included raw materials and semi-manufactured objects of metal, bone, and antler, and others that imply the presence of handicrafts (e.g. combs and needles). Vast finds of animal bones indicate animal husbandry in the area, and finds of fish net sinkers indicate that the population engaged in fishing. A VA grave field was also excavated in the area, and contained finds of jewelry and fine details of garments. It is also evident that a church was built at the site in the early 1000s CE^{88,89}. The archaeological finds and the archaeological skeletal remains are stored at the County Museum Gotland.

Samples used for DNA analysis:

VK56 Gotland_Frojel-001A98
VK57 Gotland_Frojel-03601
VK58 Gotland_Frojel-03604
VK60 Gotland_Frojel-00702
VK63 Gotland_Frojel-01499
VK64 Gotland_Frojel-03504
VK428 Gotland_Frojel-00287
VK429 Gotland_Frojel-01599
VK430 Gotland_Frojel-00502
VK431 Gotland_Frojel-00487A
VK432 Gotland_Frojel-00303
VK433 Gotland_Frojel-01798
VK434 Gotland_Frojel-01288
VK435 Gotland_Frojel-02500
VK437 Gotland_Frojel-02303
VK438 Gotland_Frojel-04498
VK439 Gotland_Frojel-02498
VK440 Gotland_Frojel-003A88
VK441 Gotland_Frojel-032A98
VK455 Gotland_Frojel-03401
VK456 Gotland_Frojel-02404
VK457 Gotland_Frojel-03299_1
VK458 Gotland_Frojel-03299_3
VK459 Gotland_Frojel-02198
VK460 Gotland_Frojel-04898
VK461 Gotland_Frojel-025A89
VK462 Gotland_Frojel-025B89
VK463 Gotland_Frojel-019A89
VK464 Gotland_Frojel-019B89

1.2.2.4. Russia

(Prepared by Natalia Grigoreva, Institute for the History of Material Culture, Russian Academy of Sciences; Vyacheslav Moiseyev, Peter the Great Museum of Anthropology and Ethnography, Russian Academy of Sciences; Tamara Pushkina and Alexandra Buzhilova, Moscow State University)

Scandinavian artifacts are frequently found in settlements and burials between the 9th and 11th centuries CE in the northern territories occupied by the early Russian state known as ‘Old Rus’’. These finds and historical sources—specifically the earliest Russian chronicle, the Tale of Past Years, according to which Vikings (‘Varyagi’) took part in the foundation of the Rus’ state in 862—raise questions about the role of Scandinavians in the history of early Russia.

Regrettably, the pre-Christian burial tradition in the Baltic area involved cremation which limits the wide use of skeletal remains in genetic population studies. Most anthropological collections relevant to the problem are dated after the Christianization of the Rus’ at the end of the 10th century CE. Among the sites assemblages that can be closely linked with Vikings are those from Shestovitsy, Chernigov region, Ukraine; Gnezdovo, Smolensk region, Russia; and Staraya Ladoga, Leningrad region, Russia.

Staraya Ladoga (before 1701 CE - Ladoga)

Coordinates 59.999102, 32.295809

According to dendrochronological data, Ladoga (in the saga ‘Aldeigja’ or ‘Aldeigjuborg’) was founded no later than 753 CE. The place became the first residence of the military leader Rurik, possibly of Scandinavian origin in 862 CE before he moved to Novgorod and founded the first Russian royal dynasty. In the 11th-13th centuries CE, Staraya Ladoga functioned as a trade outpost of the Novgorod Republic on the way from the Baltic Sea to Novgorod and then to Constantinople or to Caspian Sea.

It is generally believed that medieval Ladoga was an important trade and handicraft centre that had a complex population structure, involving groups of different origin from all Baltic regions. The strongest Scandinavian influence in Staraya Ladoga is detected for the period from the middle of 9th century CE to the middle of the 10th century CE. In addition to a large number of Scandinavian imports, the presence of two large log buildings with galleries in Ladoga settlement was reported. It was suggested that these buildings served as inns and trade-storages of Scandinavian merchants⁹⁰.

Unfortunately, the Scandinavian-type burials of the 9th-10th centuries CE found at the Plakun site situated on the other bank of the Volkhov River, opposite to Ladoga settlement, consist only of cremations. The only early medieval skeletal collection available for genetic studies was excavated in 1938-1939 by V.I. Ravdonikas and G.P. Grozdilov on the so-called Zeml’yanoe Gorodische (earth hillfort) of Staraya Ladoga. All burials in the cemetery were made in graves without mounds according to Christian tradition. Skeletons lay on their backs with their heads to the west. According to stratigraphy, Ravdonikas suggested that the cemetery was used in two periods—the 11th-12th centuries CE and the 17th-18th centuries CE. Several burials from the lower horizon were dated by ¹⁴C to c. 880-1188 CE. According to strontium isotope analyses, the buried individuals have differences from the local fauna, which suggests that they may have migrated to the site. According to written sources in the first half of the 11th century CE, the Ladoga area was given by Grand Prince

of Rus', Yaroslav the Wise, to his wife, Swedish Princess Ingegerd Olofsdotter, as a dowry, and in turn one of her relatives, Earl Ragnvald Ulfsson, was made governor of the land. The Scandinavian Kings' Sagas testify to the presence of Viking Christians in the military troops of Ragnvald Ulfsson for defense against local pagan tribes.

The collection of skeletons from Staraya Ladoga are housed in the Peter the Great Museum of Anthropology and Ethnography (Kunstkamera), and consists of 65 individuals. Physical anthropological analyses suggest that the individuals from the southern part of the cemetery are likely related to VA populations from Scandinavia⁹¹ while those from the northern part of the cemetery possibly are a mixed Slavic, Finnish, and Scandinavian population.

Samples used for DNA analysis:

VK14 Russia_Ladoga_5680-12
VK15 Russia_Ladoga_5680-16
VK16 Russia_Ladoga_5680-2
VK17 Russia_Ladoga_5680-17
VK18 Russia_Ladoga_5680-3
VK19 Russia_Ladoga_5757-1
VK20 Russia_Ladoga_5680-1
VK21 Russia_Ladoga_5680-18
VK22 Russia_Ladoga_5680-13
VK23 Russia_Ladoga_5680-9
VK218 Russia_Ladoga_5680-4
VK219 Russia_Ladoga_5680-10
VK220 Russia_Ladoga_5680-11
VK221 Russia_Ladoga_5757-14
VK408 Russia_Ladoga_5757-18
VK409 Russia_Ladoga_5680-14
VK410 Russia_Ladoga_5680-15

Kurevanikha 2

Coordinates: 58.783533, 36.162257

The Kurevanikha 2 medieval cemetery is located on the Mologa River near Kurevanikha village, Ust'uzhna district, Vologda region. The cemetery was excavated by A.N. Bashenkin in 1990. The age of the burial place was estimated as 11th-13th centuries CE. It was suggested that the first Scandinavians appeared at the place in the 8th century CE due to its important role on the way from the Ladoga region to Volga trade route to the Caspian province. Again, although this suggestion is supported by Scandinavian artifacts found in graves, it cannot be proved by genetic research because of the widespread use of cremation burial before the Christian period.

Samples used for DNA analysis:

VK160 Russia_Kurevanikka_7283-3
VK161 Russia_Kurevanikka_7283-4

Pskov

Together with Gnezdovo and Staraya Ladoga, medieval Pskov was an area with clear evidence of Scandinavian presence. The main part of Pskov's Necropolis in the medieval period, situated on the

territory of Okol'ny Gorod (Outskirts City), is occupied by a kurgan (mound) burial ground. While most of the burials are very poor in artifacts, a few of them have rich assemblages of Scandinavian-type objects. Most of the burials are cremations, but several inhumations have also been found.

In 2003-2009, eight chamber burials with inhumations of 10th-11th centuries CE were found near Starovozenesenskiy monastery (Ancient Pskov necropolis of the 10th century CE to beginning of the 11th century CE). Originally these burials were covered by artificial mounds, which were later destroyed during subsequent construction. Nevertheless, these graves survived and were found during rescue archeological excavations. Chamber burials were also found in Kiev, Timerevo, Gnezdovo, Staraya Ladoga, and other sites. Basically, chamber burials are bigger than ordinary burial pits, with a size up to 3.4 X 3.2 m. Their walls, ceiling, and floor were made of logs. These burials were accompanied by numerous artifacts of northern European, including Scandinavian, origin. It has been suggested that the chamber burial tradition in early Russia is of Scandinavian origin. The socio-cultural group that practiced this rite in eastern Europe became part of the higher stratum of the Old Rus' population. The tradition subsided with the adoption of Christianity ⁹².

Samples used for DNA analysis:

VK158 Russia_Pskov_7283-18

VK159 Russia_Pskov_7283-20

Gnezdovo, Russia

The Gnezdovo complex of archaeological monuments (main period: early 10th - the early 11th centuries CE) is situated about 13 km west of present-day Smolensk. The complex occupies a large area on both banks of the Dnieper River and consists of two settlements and seven groups of burial mounds that surround the settlements⁹³. The complex includes 13 coin and coin-and-items hoards of the 10th century CE. The hoards were found mainly in the region of the Central settlement, the principal and the most thoroughly explored settlement⁹⁴.

At the present time, the Gnezdovo settlement that belongs to the 10th-early 11th century CE is designated as the only early town centre in the Smolensk part of the Dnieper basin and the biggest monument of the Old Rus state formation in eastern Europe. Many characteristics relate Gnezdovo to towns such as Birka and Hedeby. The monument's scope and its role were in many respects determined by Gnezdovo's geographical position at the junction of eastern Europe's river systems that connect the Baltic with the Black Sea and the Caspian Sea.

A small number of burials (about 1% of the collection) belong to the initial stage of the settlement's existence. This number of burials corresponds to the monument's initially modest scope. The heyday of Gnezdovo fell in the second half of the 10th century CE: the settlement area increased and attained its maximum (about 30 ha) due to expansion of building-up within the floodplain limits and development of new considerable area along the right bank of the Dnieper above the floodplain and of inland lands.

The majority of approximately 1,000 burial mounds explored in all five groups of mounds was built in the middle and the second half of the 10th century CE. Rare burial mounds with cremations (such mounds were built near the eastern, northwestern, and western boundaries of the settlement) are related to the earliest period of the settlement's existence. Some of the Forest mounds group and partially the Central mound group belong to such burials. The well-known mound L-13 is one of these mounds. The L-13 mound gave Gnezdovo's earliest find of Byzantine amphora with Slavic

graffiti. In the middle and the second half of the 10th century CE, the other mound groups (the Dnieper, the Ol'shanskaya and the Right-Bank Ol'shanskaya groups) were formed. These late mounds are situated along the Dnieper bank downstream. At the same time the Forest and the Central mound groups continued to grow.

Single and paired cremation burials under low mounds and so called 'big mounds' with a rather complicated cremation rite, as well as single inhumations in graves and chambers under mounds, belong to the late period of the settlement's existence. Male burials in chambers accompanied with riding horses belong to the same period. By the end of the late period, the total number of burial mounds reached 4,500-5,000.

Cremation is the predominant burial rite in the Gnezdovo mounds. Cremations comprise 52% of the investigated burials, while inhumations compose about one third (31%). The remaining 17% are so-called empty mounds, where remnants of burials have not been detected.

Based on the material obtained from the mound necropolis, the population of Gnezdovo may have comprised approximately 800-1100 persons. This population had a stable demographic structure and obvious social differentiation.

Exploration of the settlement territory has demonstrated its variegated structure and availability of different zones: residential and manufacturing zones as well as areas functioning as a river port. Traces of manufacturing activities—tools, rejected products, intermediate products, and raw material stocks—have been noted on all explored plots, from the earliest period of the settlement existence and onwards.

If judged by the concentration of Oriental silver, Gnezdovo is comparable with such northern European sites as Birka and Old Rus sites like Kiev, Rurikovo gorodishche (i.e. a place of abandoned old fortified settlement), and Novgorod (the earliest layers). Putative Byzantine imported goods (glazed pottery, precious textiles, etc.) comprise a considerable part of the finds. Abundance of Scandinavian items (adornments, items of everyday use, amulets etc.) is one of the most distinctive features of the Gnezdovo material culture. These findings are matched with data of burial rite analysis, which suggest that no less than 25% of the burials are Scandinavian.

The latest burials of Gnezdovo necropolis are few and can be dated by the turn of the 10th and 11th centuries CE. Archeological materials indicate that a rather active life continued in Gnezdovo in the early 11th century CE, but the site gradually lost its character as an urban center and became a feudal estate. The final stage connected with the town's extinction and the transfer of its functions to Smolensk are described in the chronicles. This fate brings Gnezdovo in line with certain early town centres in northern Europe. These reasons include the gradual cessation of the importation of Islamic coins in the 970s CE, changes in trade routes, and a conflict between local elite and the central power of the emerging state⁹⁴.

Samples used for DNA analysis:

VK222 Russia_Gnezdovo 60-95

VK223 Russia_Gnezdovo 75-140

VK224 Russia_Gnezdovo 78-249

VK252 Russia_Gnezdovo 78-258

VK253 Russia_Gnezdovo 78-262

VK254 Russia_Gnezdovo 81-287
VK255 Russia_Gnezdovo 81-292
VK272 Russia_Gnezdovo 77-241(g)
VK273 Russia_Gnezdovo 77-255
VK413 Russia_Gnezdovo 81-290
VK466 Russia_Gnezdovo 77-222
VK470 Russia_Gnezdovo 77-212

1.2.2.5. Ukraine

(Prepared by Inna Potekhina, Institute of Archaeology, National Academy of Sciences of Ukraine)

Samples from three sites in the Ukraine were selected for analysis: Chernihiv, Lutsk, and Shestovitsa.

Chernihiv city, Chernihiv oblast (region), Ukraine

Relevance for the Vikings: Rurik dynasty.

Gleb Svyatoslavich, ‘Gleb, son of Sviatoslav’ (in Ukrainian and Russian languages the endings ‘-ovych’ and ‘-evych’ in a name mean ‘son of’), was the 11th century CE prince of Tmutarakan/Novgorod, aged 25-35 according to anthropologist analysis.

Sources of information: Skull was found in 1967 in a stone sarcophagus near the Saviour’s Chernihiv cathedral. It was an accidental discovery during construction works on the territory of the state historical and cultural reserve ‘Chernihiv Starodavniy’ (Ancient Chernihiv).

Prior to the date of discovery there was no institution in Chernihiv (USSR) that could professionally gather archaeological data. Therefore, there are no archaeological reports of these findings in the archives. The skull was sent to Moscow and returned back in a wooden box. For many years, it lay in this box in the archives and was rediscovered for science only in 2016.

Coordinates: WGS84: 51° 29’ 20.45” N, 31° 18’ 28” E; 51.489014°, 31.307778°

Dating (archaeological only): The sarcophagus was found in the backyard of the cathedral. The depth of the upper plate of the sarcophagus was 1.9-2.0 m from the modern surface. The stratigraphy was slightly damaged by the later breach of the soil: water supply pipes are laid 0.2 m above the headboard of sarcophagus. Archaeologists date it to the 11th century CE.

Anthropological data: aged 25-35 years, traces of sword wounds are preserved on the skull. All anthropological measurements and indexes are in the article⁹⁵.

Sample used for DNA analysis:

VK542 Ukraine_Chernigov

Lutsk city, Volyn oblast (region), Ukraine

Relevance for the Vikings: Rurik dynasty

Izjaslav Ingwarevych, ‘Izjaslav, son of Ingvar’ (in Ukrainian and Russian languages the endings ‘-ovych’ and ‘-evych’ in a name mean ‘son of’) was a 13th century CE prince of Dorogobuzh, Principality of Volhynia/Galicia, aged 30-40 according to anthropological analysis.

Sources of information: Skull was found in 1989 in a tomb on the territory of Lutsk castle.

Archeology report is located in the scientific archive of Lutsk State historical and cultural reserve (Научный архив Государственного историко-культурного заповедника города Луцк). Archive number: 203, 51 pages.

Coordinates: WGS84: 50° 44' 20" N, 25° 19' 23" E; 50.738889°, 25.323056°

Dating (archeological only): given that the same church building material was used for the construction of the burial chamber and stratigraphy data, the burial can be dated to the end of the 12th century CE - beginning of the 13th century CE.

Anthropological data: aged 30-40, traces of stab wounds are preserved on the skeleton, at the moment of finding in 1989 archeologists observed an arrowhead stuck in the skull. All anthropological measurements and indexes are in the article⁹⁶.

Sample used for DNA analysis:
VK541 Ukraine_Lutsk

Shestovitsa, Ukraine

The site of Shestovitsa is an archaeological complex of the 9th century CE - 12th century CE that consists of a hillfort and numerous burial mounds. It is located in the Korovel tract, near the village of Shestovitsa, on the right bank of the Desna River (a tributary of the Dnieper River), 12 km southwest of the city of Chernigov⁹⁷. Coordinates are 51 ° 21'59.17 " N, 31 ° 10'46.04 " E, the altitude above the sea level is 116 m.

The first excavations of Shestovitsa were carried out in 1925-1927 by P.I. Smolichev. Research on the hillfort and the cemetery was resumed in 1948. The cemetery consists of several hundred burial mounds with a variety of funerary rites. By now, more than 160 burial mounds have been excavated, including more than 60 with the cremation rite, more than 50 with the inhumation rite, and the same number with cenotaphs. Most of the burial mounds date back to the 10th -11th centuries CE, and only a few to the 12th century CE. In many cases, collective burials containing from two to nine skeletons of men, women, and children have been found. Among the buried there are warriors with weapons and fighting horses. Rich burial inventories often included objects of Scandinavian origin: weapons (battle axes, swords, spearheads, daggers, quivers with arrows); ornaments and household items (knives, combs, stucco, and pottery); and remnants of clothing, fasteners, brooches. They often also included Arabic and Byzantine coins. In Shestovitsa, apparently, bodyguards of the Kiev prince were deployed, with the Varangian soldiers among them. Since the 1990s the Shestovitsa archaeological complex has been recognized by historians as one of the largest settlements of Vikings in Europe.

The presence of non-local groups from the Finno-Ugric lands in this region is consistent with the chronicles and archaeological data. It was also suggested that the Viking population is mixed here with the Slavic. Some researchers refer to the series from Shestovitsa to the Scandinavian cluster and find remote parallels in the synchronous population of Sweden and Britain.

Despite the multi-vector connections of the population of Shestovitsa, Slavic and Norman groups should probably be considered the dominant components in its composition. The real ratio is difficult to determine due to the low representativeness of the series, but there is every reason to believe that the role of each of them was different for the male and female population, and women evidently represented a more homogeneous group of Slavic origin.

For genetic analysis, samples of bone tissue from 12 burials excavated by D.I. Bliefeld in 1956-58 from various mounds of Shestovitsa were transferred. Unfortunately, materials from only two burials proved to be suitable for DNA isolation. These were a 25-30 year old male (kurgan 32(23)/ burial 2, pit B,) and a 35-40 year old female (kurgan 32(23)/ burial 1).

Samples used for DNA analysis:

VK539 Ukraine_Shestovitsa-8870-97

VK540 Ukraine_Shestovitsa-8871-96

1.2.2.6. Poland

Sandomierz

(Prepared by Monika Bajka, "Trzy Epoki" Archaeological Service, and Marek Florek, Institute of Archaeology, Maria Curie-Skłodowska University, Lublin)

The inhumation cemetery is situated on the left bank of the Vistula River, in the northern part of the Town Hill of Sandomierz (geo coordinates: N: 50°40'53,56''; E: 21°44'57,08''). The Town Hill occupies the edge of the Sandomierz upland loess area, which is c. 50 m above the level of the Vistula. In the medieval period (since the end of the 10th century CE), Sandomierz was the main centre of the Sandomierz Region, and constituted the second centre (after Cracow) of the historical Lesser Poland. In the 12th century CE, Sandomierz, together with Cracow and Wrocław, was called *sedes regni principalis*.

Recent work indicates that Sandomierz was established after the annexation of the northern part of Lesser Poland (Sandomierz Region) to the State of the Piasts (the family ruling the tribe of Polanie, which was from Greater Poland) in around the year 970 CE. The new incomers from Greater Poland (the centre of the Piast state) had the greatest influence on the creation of the town.

The cemetery encompasses the central and the northern part of the Town Hill. Because the site is mostly in a built-up area, the site is known mainly from casual findings. In the years 2013-2015, in the northern part of the Town Hill, nine graves were found. They represent the oldest part of the cemetery. Because of their shape (large, rectangular grave pits with walls covered with boards and wooden vaults, and with wooden coffins inside) some of them are associated with the 'chamber graves' from Scandinavia, northeastern Europe, and northern and central Poland (Pomerania, Kuyavia, Greater Poland). The chamber of grave No. 9 was additionally surrounded with a circular palisade. Some of the graves (including all the graves of chamber-like construction) were equipped with the following items: clay vessels, an iron axe, dress elements (horseshoe-shaped bronze buckles), silver and bronze decorations (silver rings, temple rings), and equipment for making fire (flint strike-a-lights, iron firesteels, etc.)⁹⁸⁻¹⁰⁰.

Chronology: Based on the equipment (pottery, metal objects), the graves discovered in the years 2013-2015 should be dated to the time between the end of the 10th century CE and the middle of the 11th century CE. Radiocarbon dating of bones from graves No. 8 and No. 9 was carried out. Grave 8 was dated to 1070±35 BP, which after calibration is 938-1022 CE; grave No. 9 was dated to 1090±35 BP, which after calibration is 888-1018 CE. These dates are in line with the date based on the artifacts.

There are several reasons to believe that some persons buried in the graves that were excavated in the

years 2013-2015 were of foreign origin:

- Some of the graves resemble chamber graves, which generally do not occur in the Sandomierz Region and in Lesser Poland.
- The vessels found in the graves have no analogies in the local pottery from the 10th and 11th centuries CE; their forms refer to the pottery from Greater Poland and central Poland
- Horseshoe-shaped bronze buckles (from graves Nos. 7 and 9) which represent a garment element characteristic mainly of the region of the Baltic coast and northeastern Europe (Rus').
- An axe from grave No. 7, which has the closest analogy to the finds from the cemeteries of the Varangian and Rus' cemeteries from eastern Europe.
- A key from grave No. 9 that was secondarily used as a firesteel; it has the closest analogy to finds from Scandinavian and Russian sites.
- The results of the analysis of strontium content in the teeth of the persons buried in the cemetery.

The furnishing of the graves is of high standard in comparison to other graves from the same period from Sandomierz and its neighbourhood. The form of the graves and their furnishing indicate that they were created for the local elites of foreign origin, who had arrived here from other territories, probably from Greater Poland, after the annexation of the Sandomierz Region to the State of Poland (the State of the Piasts). The equipment elements (horseshoe-shaped bronze buckles, axe, key used as firesteels) and the form of the graves might indicate that Varangians and Rus' people were also buried in the cemetery. They were at the service of the Piasts, e. g. as the members of the princely squads or as merchants.

Sample used for DNA analysis:
VK494 Poland_Sandomierz 1/13

Cedynia Site 2

(Prepared by Dariusz Błaszczuk, Institute of Archaeology, University of Warsaw)

Cedynia site 2 (Cedynia commune, Gryfino county, zachodniopomorskie voivodeship) is located on the Odra River (on the right bank) in Western Pomerania. The cemetery was situated at the top and slope of a hill, c. 200 m to the northeast of a fortified settlement (gród). In the cemetery 1308 inhumation and nine cremation graves were unearthed. The cemetery was partially excavated. It was used from the end of the 11th century CE and/or the beginning of the 12th century CE to the middle of the 14th century CE. Grave 558 was different from others graves in the cemetery owing to its grave goods, large burial pit, and traces of a wooden funeral construction (a chamber?).

Grave 558

An elite grave. Burial in a wooden chamber, adult male, oriented east-west^{101,102}. The individual was facing east (a typical Christian orientation of that time) and buried in a supine position, on his back, arms along the body, legs straight. The deceased was buried in a wooden coffin that was placed in a chamber made of timber 2.8 m (length) × 2.3 m (width) × 1.2 m (depth). The chamber was very poorly preserved; only traces of wood were visible. It was possibly built in a framework construction.

The grave goods were as follows: Iron double edged sword (type α according to Nadolski¹⁰³) at the left pelvic bone. The sword had a straight cross-guard, a relatively short handle and a lens-shaped pommel. Its total length was about 97 cm. On the blade under the cross-guard, x-ray examination revealed a sign in the form of an outline of a face. This type of sword was used at the end of 11th

century CE and at the beginning of the 12th century CE. In addition, an iron knife was found at the left pelvic bone, and a U-shaped belt fitting made of bronze plaque was found on the lumbar vertebrae.

Dating based on a typology of the sword suggests that the individual was buried at the end of the 11th century CE or in the first half of the 12th century CE. ¹⁴C analyses carried out at the Poznań Radiocarbon Laboratory returned a date of 1010±30 BP, which when calibrated is 973-1150 CE (Poz-75117). It should be noted that the ¹⁴C date may have been affected by the preservative that covers the whole skeleton.

The skeleton was covered with rodent bones; they were probably the result of post-depositional processes. Stones were found over the burial, but they were probably not connected with the grave but were possibly associated with the building of the nearby church¹⁰².

Carbon and Nitrogen isotope analyses of a rib sample indicated that the diet of the individual was based on C₃ plants (cereals, vegetables, and fruit) with some amount of animal products (meat, dairy, and eggs). He could also have consumed a small amount of freshwater fish. This type of diet was typical for the region and time period. The isotope analyses were carried out at the Stable Isotope Facility at the University of Bradford, UK.

The individual has also been subjected to a strontium isotope analysis. Its isotopic signature falls within the range of ⁸⁷Sr/⁸⁶Sr values occurring in the postglacial lowland areas of the southern shore of the Baltic Sea. It is likely therefore that the individual was of local origin, from Cedynia itself or from elsewhere in West Pomerania. This analysis was carried out at the Geochronology and Isotope Geochemistry Laboratory of the University of North Carolina.

Grave 435

We also sampled a post-VA grave, No. 435, for comparative purposes. Burial in a wooden coffin with no grave goods^{104,105}. An adult male, oriented east-west, facing east (a typical Christian orientation of that time) and buried in a supine position, on the back, arms along the body, legs straight. The individual dates to the Middle Ages (11th-13th centuries CE).

Samples used for DNA analysis:

VK211 Poland_Cedynia gr. 435

VK212 Poland_Cedynia gr. 558

Czersk, Poland

(Prepared by Dariusz Błaszczak, Institute of Archaeology, University of Warsaw)

The site of Czersk 1 is situated on the Vistula River (on the left bank) in the Masovia region of Poland (Góra Kalwaria commune, Piaseczno county, Masovia voivodeship). In the Middle Ages, Czersk was an important centre of political and ecclesiastical power. A burial ground was located around a church. The cemetery was partially excavated yielding 797 burials. The cemetery was used from the end of the 11th century CE or beginning of the 12th century CE to the 13th century CE¹⁰⁶.

Grave 609

An elite grave. Adult male of about 60 years old, oriented east-west, facing east (a typical Christian orientation of that time). The height of the individual was about 180 cm (according to M. Trotter and G. Gleser). The deceased was buried in a wooden coffin with iron ferrules. He was buried in a supine position, on the back, right hand straight along the body, left arm bent in the elbow and supported by hand on the pelvis, legs straight.

A double-edged iron sword (type α according to A. Nadolski¹⁰³) was found at the left pelvic bone. In addition, the following items were discovered: two bronze bowls (type VI according to T. Poklewski¹⁰⁷), an iron spearhead (type V according to Nadolski¹⁰³), a wooden bucket covered with decorated iron sheet, a golden ring, and a thin, silver, spirally wound wire (alloy of silver with copper and gold).

Archaeological dating based on a typology of the sword, the spearhead, and the bronze bowls puts the burial at the end of the 11th century CE or the first half of the 12th century CE (most probably the beginning of the 12th century). A ¹⁴C analysis of a bone sample carried out by the Poznań Radiocarbon Laboratory yielded a date of 1085±30 BP (Poz-68711). The date is affected by the reservoir effect as a result of significant consumption of marine fish (demonstrated by Nitrogen and Carbon isotope values). After correction, it can be calibrated to 1050-1200 CE, which is consistent with the typology-based date.

The grave was situated near the church. According to some scholars, grave 609 is the burial of Magnus Haroldson, one of three sons of Harold II Godwinson, the last Anglo-Saxon king of England^{108,109}.

Nitrogen and Carbon isotopes extracted from a rib sample suggested that sea fish and/or anadromous fish (e.g. sturgeon) were an important part of the diet of this individual. This type of diet was unusual for the region and time period and is very different from any known studied Polish populations. The Nitrogen and Carbon isotope analyses were carried out at the Stable Isotope Facility, University of Bradford, UK.

The result of a strontium isotope analysis were ambiguous in that it was not possible to determine whether the individual was of local origin or was a newcomer. The ⁸⁷Sr/⁸⁶Sr value obtained for the first molar is found in both areas with post-glacial deposits as well as areas with marine carbonate rocks or clastic rocks such as loess. Such values occur in northern Poland and other parts of Europe (e.g. southern Scandinavia). However, there was a difference in strontium values between the first molar (complete mineralization to about 4.5 years of age) and a rib (reflecting the last two to four years of life), which may indicate that the individual spent his adulthood (including the last years of his life) in a different place than his childhood. This would indicate that the man buried in the grave 609 changed his place of residence during his lifetime. The strontium analyses were carried out at the Geochronology and Isotope Geochemistry Laboratory of the University of North Carolina.

Sample used for DNA analysis
VK200 Poland_Czersk gr. 609

Kraków-Zakrzówek, Poland

(Prepared by Dariusz Błaszczyk, Institute of Archaeology, University of Warsaw)

The cemetery at Kraków-Zakrzówek was situated on the right bank of the Wisła River, on the sandy dune in the foothills of the Twardowski Rocks. The cemetery was a typical early Christian

inhumation, 'flat' burial ground with graves arranged in rows and oriented east-west. Seventy-five certain and 22 probable burials as well as two clusters of bones were unearthed¹¹⁰. The cemetery was used from the beginning of the 11th century CE to the beginning of the 13th century CE.

One grave attracted special attention because of its extraordinary form. This grave, number 19, was situated in the center of the cemetery and surrounded on three sides by a ditch with traces of nine postholes. It is possibly that a ditch also existed on the fourth side but was destroyed by post-depositional processes. The length of the entire structure was about 4 m, and its width was about 3.2 m. These traces indicate the existence on the surface of the grave of a monumental timber structure in the form of 'a house of the dead' or a fence. Grave 19 was different from the other graves in the cemetery with its central location, surrounding ditch, and grave goods. This sample, however, was not sequenced due to poor DNA preservation.

Grave 24

A commoner's grave. An adult male of about 40 years old, oriented east-west, facing west, and buried in a supine position, right hand along the body, left hand bent with a hand on the pelvis, legs straight. No traces of a coffin were discovered, but a whetstone was found in the grave. The grave dates to the Middle Ages, between the 11th century CE and the beginning of the 13th century CE. A strontium isotope analysis carried out by the Geochronology and Isotope Geochemistry Laboratory at the University of North Carolina indicated that the individual probably grew up in the place where he died and therefore was a local.

Sample used for DNA analysis:
VK210 Poland_Kraków gr. 24

Bodzia, Poland

(Prepared by Wiesław Bogdanowicz, Museum and Institute of Zoology, Polish Academy of Sciences)

Bodzia, located in the north-central part of Poland, approximately 40 km southeast of the city of Toruń, is one of the most fascinating archaeological sites dating back to the time of origin of the Polish state. The main discovery connected with this site relates to an early medieval cemetery found in 2007 during rescue excavations carried out by the Institute of Archeology and Ethnology of the Polish Academy of Sciences along the route of the A1 motorway. The discovery encompassed 50 chamber-like graves dated to the late 10th and early 11th centuries CE; along with eight belonging to a second phase dating to between the second half of the 11th century CE and the early 12th century CE. The unique character of this burial ground mainly lies in the fact that members of a small elite population were buried there. Furthermore, almost all the dead were orientated north-south, which was uncommon in Mediaeval Europe.

The layout of the cemetery has no analogies in Europe. It was formed of rows of graves with large burial pits placed in quadrangular burial spaces. The burial field was divided into rectangular sepulchral spaces, marked on the surface, and arranged into four rows oriented along the east-west axis. Some of these plots were adjacent, especially those in the northern row, with the shape of a trapezium narrowing down to the east. The others, located more to the south, were arranged in smaller clusters or individually, retaining the same orientation as the rest. The burials were located compactly and contiguously, thereby ensuring a clear delimitation of the cemetery boundaries.

Equally unique were the rich grave goods, which may be linked mainly with Scandinavia and Kievan Rus', but also with southern and western Europe. A characteristic feature of all the burials was the bountiful presence of a range of items, including weapons (e.g. sword, langsax, spearhead, Khazarian-type pickaxe) in the case of men, and numerous ornaments (e.g. rings, pendants, amulets, kaptorgas, necklaces) in the case of women. There were also abundant coins: 67 items from 58 graves. These relate to the Holy Roman Empire, England, the Premyslid State, and Poland. These and many other features make the cemetery at Bodzia a very specific example highlighting Europe's past.

Analyses of strontium isotopes¹¹¹ and aDNA¹¹² have indicated that a part of the population buried at Bodzia was not local, but was probably of Scandinavian and/or Rus-Varangian origin. A special role is played here by the tomb of a young warrior (E864/I) buried together with three young women; one of them was placed below him, in what is a two-level burial pit. In his tomb, a ceremonial sword was folded, ornamented in the Mammen style. On the strap-end there is a bident – the tamga of Prince Sviatopolk the Accursed (1015-1019 CE), who was the son of Vladimir the Great and husband of a daughter of Polish king Boleslav I (the Brave).

The cemetery extends back to the period when the Polish State originated, and also relates to unknown episodes in that state formation, and to the emergence of elites in the early state under the Piasts. The aforementioned features (as well as others) ensure this site's unique status where Europe's past is concerned.

Bone remains of five individuals were sample for the present study (see the inventory of the burials and their contents after Sobkowiak-Tabaka¹¹³; with dating after Buko and Kara¹¹⁴):

- E63 – Young adult male, incomplete skeleton, head of a Type 1 axe found near right femur; dated 978-1016 CE;
- E864/I – Adult male, weapons including an iron Petersen Type Z sword (swords of this type mainly date to the first half and middle of the 11th century CE, i.e. the late VA¹¹⁵; dated 1010-1020 CE;
- E58 – Adult male matusus, incomplete skeleton, weapons including a battle-knife of the langsax type, and tools and iron knife placed near the left arm, and another iron knife placed near the right femur;
- E37 – Young adult female, incomplete skeleton, iron bucket hoop near the feet; in a row of graves dated between 980/990 and 1030/1035 CE;
- E870 – Adult female (20-25 years old), incomplete skeleton, among grave goods are a few coins and a whorl made of Volhynian slate; dated 1017-1023 CE.

Samples used for DNA analysis:

VK153 Poland_Bodzia E63

VK154 Poland_Bodzia E37

VK155 Poland_Bodzia E870

VK156 Poland_Bodzia E58

VK157 Poland_Bodzia E864/I

1.2.2.7. United Kingdom

St John's College, Oxford

(Prepared by Ceri Falys, Thames Valley Archaeological Services)

In 2008, archaeological excavations in advance of development in the grounds of St John's College, Oxford, UK, revealed an unexpected sequence of deposits that shed new light on Oxford's prehistoric ritual past, a grisly episode in its history from the late Anglo-Saxon period (evidence of a massacre dating to around 1000 CE), and a more mundane but still interesting development from medieval occupation in three tenement plots to a post-medieval farm and then the arrival of the college.

Of interest to this study, the excavation led to the discovery of a mass grave containing a minimum of 35 human skeletons. The majority of individuals were articulated and relatively complete, although several disarticulated limbs and an isolated skull were also recovered. The remains were not deposited within a purposefully dug grave, but rather had been placed in a pre-existing depression in the landscape resulting from the incomplete infilling of a portion of a monumental Neolithic henge ditch. The skeletons were deposited in the grave in a disorganized manner and seemingly with little care or respect. There was no pattern to the positioning or orientation of individuals within the grave. Frequent intermingling of elements between individuals strongly suggests that all the skeletons had been deposited in a single episode. At the deepest portions of the grave, the bodies were piled four deep.

Osteological analysis found that all individuals, with the exception of two adolescents, were tall and robust adult males. All of them had met a violent death, as every man displayed evidence of perimortem sharp-force trauma (blade and puncture wounds), which was extensive and excessive in most cases. Many of the wounds were inflicted from behind, and few defensive wounds were observed. Most unusually, several skeletal elements had been partially burned. As a whole, the individuals in this assemblage appear to have an unusually high rate of non-fatal pathologies as well, both congenital and acquired through their lifestyle, and minimal evidence of antemortem trauma. It was concluded that this group, all robust adult males (bar the teenagers), mostly of the same generation, taller than average, sharing unusual pathologies, limited antemortem trauma, and extensive perimortem wounds, disposed of in this disorganized way, may well have been a physically distinct sub-group of the population, and had been massacred in a single event.

It was proposed that this is not a battle grave for fresh Vikings newly landed, but rather Danes who had been settled in Oxford for some years, possibly some of the younger ones may even have been second generation. The unusual occurrence of charring of some skeletal elements examined in context with historical documentation points strongly towards these men being the Danish victims of King Aethelred's decree ordering their extermination in 1002 CE, during the event known as the 'St Brice's Day Massacre'.

It was hoped that radiocarbon dating would confirm the possibility of these men being the victims of the known massacre, but, unfortunately, the results were inconclusive and difficult to interpret. The dating initially appeared to preclude associating all of the skeletons with the St Brice's Day massacre, with three of the radiocarbon results indicating a perfect fit with a date of 1002 CE. However, subsequent testing by a second laboratory returned three dates that appear much too early, which is puzzling and remains unresolved. Archaeologically, however, there is no possibility that the commingled human remains in the top of the Neolithic henge ditch could be interpreted as anything

other than a single mass grave.

Isotopic results suggested the possibility that several individuals, including three of the men with the earliest radiocarbon dates, had an unusually high seafood diet for the inland location. It has been suggested that this marine reservoir offset is a contributing factor for the apparent discrepancy in the dating. Other isotope results indicated the majority of men likely originated either in the British Isles or the nearer continent, including western Denmark and Germany. One man suggests an origin in a colder average climate than the rest of the group (e.g. Denmark or southern Scandinavia), while two have values well within the limits of the modern UK distribution, but could also be attributed to this northern region, and a further three men have values that would appear to be from somewhere warmer than the UK.

It is highly unusual for archaeology to capture evidence of a historically documented event, and archaeologists have usually been reluctant to make such connections, but it is here contended that, while there are some unresolved problems, the overwhelming probability is that this site presents just such an occasion. Of course other possibilities exist, but the nature of the extensive perimortem trauma (suggestive of attacks on defenseless victims rather than battle casualties), charring of severed limbs, unusual shared congenital defects, a diet unusually high in fish proteins for the local population, the assemblage comprised of solely tall, robust, hard-working males, with limited previous history of violence, the jumbled nature of their burial and the location of the burial outside of town in a prehistoric (pagan) monument all strongly support the hypothesis that these men were the Oxford victims of the St. Brice's Day Massacre¹¹⁶.

Samples used for DNA analysis:

VK163 UK_Oxford_sk 1870
VK146 UK_Oxford_sk 1785
VK147 UK_Oxford_sk 1864
VK148 UK_Oxford_sk 1787
VK149 UK_Oxford_sk 1852
VK150 UK_Oxford_sk 1866
VK151 UK_Oxford_sk 1963
VK172 UK_Oxford_sk 1968
VK173 UK_Oxford_sk 1978
VK174 UK_Oxford_sk 1984
VK175 UK_Oxford_sk 1996
VK164 UK_Oxford_sk 1872
VK176 UK_Oxford_sk 1990
VK177 UK_Oxford_sk 2056
VK178 UK_Oxford_sk 2057
VK165 UK_Oxford_sk 1876
VK166 UK_Oxford_sk 1891
VK167 UK_Oxford_sk 1898
VK168 UK_Oxford_sk 1899
VK143 UK_Oxford_sk 1951
VK144 UK_Oxford_sk 1756
VK145 UK_Oxford_sk 1783

Ridgeway Hill Mass Grave, Dorset

(Prepared by Louise Loe, Oxford Archaeology, UK)

The Ridgeway Hill mass grave was a multiple burial of executed Vikings that was created sometime in the 10th or 11th century CE on the crest of Ridgeway Hill, near Weymouth, on the south coast of England. The grave was discovered in 2009 by Oxford Archaeology during the construction of the Weymouth Relief Road. The skeletons, around 50 in total, were predominantly young adult males, all of whom had been decapitated: heads had been deposited in a pile located at the southern edge of the grave, while the beheaded bodies had apparently been thrown in with little care.

The burial was a one-off occurrence and took place at the time of, or shortly following, the men's execution, which probably occurred at the graveside. The grave itself was a disused Roman quarry, used by the executioners for convenience rather than specifically dug for the purpose. It was an irregular ovoid feature, which by the time it was used as a grave, had partially silted up. The individuals were buried to a maximum depth of less than one meter. In keeping with other Anglo-Saxon execution cemeteries, the proximity of the grave to a major road, a parish boundary, and prehistoric monuments, would all seem to have been important. It is conceivable that the executions were performed in front of a large crowd of spectators and as a formal event.

The men were buried in a variety of positions and without a particular orientation (Extended Data Fig. 1b). Most were lying prone (face down) on a west-east alignment, but there was a lot of variation and entanglement giving the overall impression of a jumble of bodies that had been thrown in with little care, with no consideration to how they lay and no attempt to bury them with their heads. This strongly suggests that they had been buried by their executioners and that, possibly, there had been more than one executioner. Site plans and digital survey data were scrutinized to explore the order in which the men had been buried, but no pattern could be discerned, which suggests that they may have been thrown into the grave from all sides.

It would seem that the men were stripped prior to their execution, because no dress fastenings or other remains of evidence for clothing were found. There was also no evidence to suggest that the men's hands had been tied, or that any other form of restraint had been used. The probable Icelandic Jomsvikings saga describes the execution by beheading of a number of warriors who did not have their hands tied, but were roped together. Perhaps this was also the case at Ridgeway Hill. .

Analysis was unable to determine exactly how many men were executed and buried in the grave, because of commingling and loss of bones as a result of modern disturbance. By employing counting and pair-matching exercises, it was estimated that between 47 and 52 individuals were present. There were more beheaded skeletons than skulls and this could mean that some heads were taken as trophies following the executions (Extended Data Fig. 1b).

All of the men suffered horrific ends, their executions an ugly affair involving excessive violence. The decapitations, probably performed with a sword, were evidenced by wounds that were concentrated in the region of the neck indicating that, in most cases, it had taken several attempts, from a variety of angles, to remove their heads. Blows intended to decapitate had been delivered from as high up as the back of the head to as low down as the shoulder blades, suggesting they had not been very well performed or organized. Approximately 188 wounds were observed on all of the skeletons, which is an average of almost four wounds per individual. In addition, sharp force lesions were present on the forearms and tops of skulls of some individuals and may have been defensive

injuries or incapacitating injuries.

Isotope analysis performed on a number of skeletons¹¹⁷ suggests they were a disparate group of people in terms of their origins, migratory histories, and dietary habits, although a general emphasis on Arctic and sub-Arctic areas of Scandinavia, northern Iceland, the Baltic States, Belarus, and Russia, and on terrestrial food sources, are suggested. It appears that the majority were not living in the British Isles in the years leading to their deaths.

Although most of the men were young adults (18-25 years old) when they died, the youngest was in their early or mid-teens and the oldest was over 50. They possessed features, particularly those relating to height and facial appearance, that were similar to Scandinavian populations of similar date. At least one individual had filed teeth, seen as horizontal grooves on his central, upper incisors, possibly as a status symbol or a marker of occupation. In addition, evidence for infection and physical impairment was frequent for a group of predominantly young individuals who had died in their prime of life, although none of the skeletons showed convincing evidence for previous war wounds¹¹⁸.

There are no historical records that directly link the mass grave with an event, but there are a number of possibilities, such as the ravaging of Portland in 982 CE, or Viking attacks in Dorset in 998, 1015, and 1016 CE. Although it seems very likely that these were Vikings executed by the English, the possibility that they were a group of mercenaries fighting for the English and executed by Vikings cannot be entirely ruled out. Other possible scenarios are that the men were merchants or recent settlers in England who were sentenced to judicial execution by the English authorities, were victims of the St Brice's Day massacre (1002 CE), or were hostages or combatants engaging in reprisals against previous enemies during the reign of Cnut (1016-35 CE).

In total, 10 skulls were sampled for DNA analysis for the present project. The skull with the filed teeth, 3736, is among them.

Samples used for DNA analysis:

VK256 UK_Dorset-3722
VK257 UK_Dorset-3723
VK258 UK_Dorset-3733
VK259 UK_Dorset-3734
VK260 UK_Dorset-3735
VK261 UK_Dorset-3736
VK262 UK_Dorset-3739
VK263 UK_Dorset-3742
VK264 UK_Dorset-3744
VK449 UK_Dorset-3746

Orkney Islands

(Prepared by Julie Gibson and Ingrid Mainland, University of the Highlands and Islands)

Newark, Deerness (HY 5746 0413)

Newark comprises a VA and medieval period chapel and cemetery located in the parish of Deerness on the island of Mainland, Orkney. The site was excavated in the late 1960s and early 1970s and although not fully published the osteological materials recovered have been subjected to ¹⁴C and isotopic analysis, providing a broad chronology for the cemetery and placing the human remains

within the cultural traditions of Scandinavian Scotland^{119,120}.

The site at Newark stands in a sand-blown landscape at the side of a bay. The deposits remain to a maximum of c. 1.3 m thick above glacial clay but were truncated by the construction of a grand post-medieval house. The cemetery has been eroding at least since the 1920s exposing over 100 m of graveyard associated with a medieval chapel.

The chapel was excavated by Don Brothwell between 1969 and 1972 in order to obtain a sequence of Norse skeletons; burials continue to be exposed from time to time in the coastal section. The recent find of a Pictish Type 2 decorated cross slab on this site by Hugo Anderson Whymark, introduces the possibility of the presence of an earlier 8th century CE chapel (see <https://sketchfab.com/models/6de93d22334a4b6da3098402e7e720b5>).

Three skeletons were selected for analysis, based on preservation and availability. Of these, only one (VK205) has a secure date: 930± 40 cal CE, but marine reservoir effect has been proposed by Barrett suggesting a date in early 11th century CE¹¹⁹. This individual is a female and was buried without grave goods.

Samples used for DNA analysis:

VK204 Orkney_Newark for Brothwell

VK205 Orkney_Newark 68/12

VK206 Orkney_Newark 71(13)

Buckquoy, Birsay (HY 243 282)

Buckquoy is a late Iron Age ('Pictish') and Norse period settlement site located in the parish of Birsay on the island of Mainland, Orkney. The settlement has been a key site in the discussion about Scandinavian first contact¹²¹, due to the mixture of Pictish- and Scandinavian-type material found within Pictish-style houses. Inhumations were associated with the structural remains, dating to both the Pre-Viking and Viking occupation. A full account of the archaeology can be found in Ritchie¹²² with additional information on the dating of the skeletal remains in Ashmore¹²³.

Excavations undertaken in the early 1970s at Point of Buckquoy¹²² revealed a somewhat disturbed inhumation inserted into the top of a multi-period settlement mound of the 8th to 10th centuries CE. Immediately beneath were the partial remains of a succession of Norse longhouses, overlying a Pictish multi-cellular dwelling. Identified by skeletal analysis as a male aged about 40, the burial (VK202) consisted of a simple scoop grave with the body thought to have been interred in a crouched position, laid on his right side and aligned south-north with his feet to the north. Grave goods consisted of a bronze ring-pin of the early 10th century CE, half of a silver penny of Edmund (940-946 CE), an iron knife, a whetstone, and an iron javelin-head. ¹⁴C dates are available but earlier than the artefactual assemblage; Brundle et al.¹²⁴ suggest the dated bone may be intrusive.

VK201 was an earlier, Pictish, unaccompanied long cist burial of an adult male dated to 404 - 596 cal CE¹²³.

Samples used for DNA analysis:

VK201 Orkney_Buckquoy, sk M12

VK202 Orkney_Buckquoy, sk 7B

Brough Road, Birsay (HY 2466 2807)

Archaeological remains from Brough Road are derived from excavation during the 1970s of a coastally eroding midden and associated structures dating to the late Iron Age and Norse periods. A full account of the archaeology can be found in Morris et al.¹²⁵ with additional information on the dating and isotopic analysis of human remains in Ashmore¹²³ and Barrett et al.¹²⁶. A pre-Viking long cist cemetery and later Viking or Norse inhumations were also recovered in this area, which overlooks the Brough of Birsay and Birsay village, important Pictish/Viking/Norse settlements and ecclesiastical centre.

Three individuals were sampled from Area A Brough Road. The primary use of the site is reflected by cairn-burials, comprising two long cist graves underlying stone cairns. VK203 is a long cist grave unaccompanied inhumation containing only one body. Two dates from this individual have resulted in two widely spaced ¹⁴C dates, 130-54 cal CE or 548-668 cal CE, but this individual represents in both cases a pre-Viking burial. Osteologically, this individual was probably a male and was elderly. The cairns were sealed by sand and midden layers into which were inserted two burials dating to the Viking/late Norse periods. VK208 is a rough cist grave cutting into the midden topping one of the cairns containing a disarticulated body of a probable male aged over 30 years. It was associated with iron artefacts, a complete antler comb, hog-backed in form and of a Viking period date. Two dates from this individual indicate a later Pictish to Viking date-range, 650-980 Cal CE or 890-1026 Cal CE. On top of one the cairns (above) lay a flexed inhumation (VK207), not contained within a cist and with no grave finds. This was an adult, aged c. 30-35 years, but sex could not be determined osteologically. A ¹⁴C date of 880 to 1160 cal CE¹²³ was obtained for this individual.

Samples used for DNA analysis:

VK203 Orkney_BY78, Ar. 1, sk 3

VK207 Orkney_BY78, Ar. 1, sk 1

VK208 Orkney_BY78, Ar. 1, sk 2

Glyn, Llanbedrgoch, Anglesey(Prepared by Mark Redknap, Amgueddfa Cymru – National Museum Wales)

Excavations by Amgueddfa Cymru – National Museum Wales at Glyn, Llanbedrgoch between 1994 and 2001, in 2004, and in 2012 uncovered a small early medieval settlement that by the late 9th century CE had developed into a large entrepôt and regional centre about one hectare in size serving the kingdom of Gwynedd. During the second half of the 9th century CE a stone rampart was built to provide additional security¹²⁷. In the second half of the 9th century rectangular timber buildings with ground-fast posts were remodelled, having sunken floors and sill-beam construction resting on low stone walls. A rich array of 9th/10th-century artefacts reflect an Insular mix of local, Anglo-Saxon, and Irish styles, as well as contact with the Scandinavian world (Hiberno-Norse hack-silver, fragments of Kufic silver coin, lead weights of different types, some capped with decorative metalwork, ringed pins, and a fragment of oval brooch).

The excavations have provided evidence for the organised use of space for activities such as iron working, baking, bronze smithing, waste disposal, sleeping, cooking, and burying. An unexpected bonus was the discovery in 1998 and 1999 of the remains of five people buried in a seemingly haphazard manner in the upper fill of the ditch outside the rampart. This raised questions about not only the identities of those buried so unceremoniously, but also the settlement's fate, who occupied it during the 10th century CE, and their status. The preliminary osteological report identified a young

adult female, a young adult male, a mature adult male, and two adolescents, and radiocarbon dates pointed to their deaths occurring in the mid- to second half of the 10th century CE, burial possibly later in the early 11th century CE¹²⁷.

The irregular disposition and orientation of the bodies and the observation that the wrists of one adult male (burial 3) appeared to have been tied behind the back, suggested a non-normative burial rite given that Christian burial within cemeteries was, by now, standard for the local population. Radiocarbon dates, stratification, and the absence of late 10th or early 11th century CE coins suggested that they had been buried during a final phase of occupation of the site in the 10th century CE¹²⁷.

During facial reconstruction work it was suggested that some of these features pointed to a genetic relationship between the skulls, either familial or more probably because the individuals originate from a small gene pool (Caroline Wilkinson, personal communication). Consequently it was considered possible that they represented local islanders, perhaps the victims of a Viking attack on the Anglesey¹²⁷. This view is no longer held¹²⁸.

Since 2004, the human remains from Llanbedrgoch have undergone a complete osteological reassessment by Alice Roberts in order to establish the demographic profile and health status of the individuals. This has refined the estimated age at death, and included a further inhumation found in 2012, just north of the 1998-1999 inhumations.

Multiple isotope analysis for palaeodietary reconstruction and to identify the childhood place of origin of these individuals has now been conducted on burials 1-7 by Katie Hemer as part of her PhD, the analytical work being undertaken at the NERC Isotope Geosciences Laboratory in Nottingham. Strontium results provide the most compelling evidence in the case of the Llanbedrgoch individuals because the signatures are distinctive. A full report on these burials is in preparation (Hemer, Roberts and Redknap, in prep.). Juvenile burial 4 (context 737) sampled for DNA analysis, provided two radiocarbon dates: Beta-150715: 1030+/-40 BP, CE 960-1040; OxA-33786: 1055+/- 40 BP, CE 892-1031. Stable isotope analysis (strontium and oxygen) of this juvenile (9.5-14 years old) by Katie Hemer suggests that he may have grown up between the ages of three and seven in parts of mid-Wales or on the border of England, while the other adult male (burial 3, with his wrists tied) in the same burial had strontium values consistent with old or radiogenic geologies found in parts of Scotland, Denmark or further afield in southwest Norway, and oxygen values within the range expected for the British Isles. None of the extra-mural burials grew up on Anglesey, and they appear to have grown up in places with diverse geologies and climate¹²⁸.

The archaeological context of this extra-mural cluster suggests that they may have been treated in death as incomers, outcasts because they were not local and perceived to be non-Christian, perhaps instilling fear or suspicion in the minds of those responsible for their burial. Bearing in mind the raids from the Isle of Man in the 970s and 980s CE, some may have been hostages or slaves of the Welsh, if not free traders. These results are still under discussion.

Sample used for DNA analysis:

VK171 Wales_Cardiff_burial#4_GL99

1.2.2.8. Isle of Man

Balladoole

(Prepared by Allison Fox, Manx National Heritage)

The Site: Around 900 CE, a Viking was buried in an oak ship at Balladoole, Arbory parish, in the south east of the Isle of Man. The site is on a low hill, with a wide panorama over the surrounding landscape and seascape. There is artefactual evidence for Mesolithic and Neolithic use of the area, and structural evidence for Bronze Age burials and Iron Age occupation. It was during the excavation of the latter hillfort that the Viking burial was discovered¹²⁹.

The ship had been placed in a shallow pit, which disturbed several existing Christian burials. Boulders were placed around the hull of the ship to hold it in place, and the dead man and his goods placed within (Extended Data Fig. 1c). The grave goods included jewelry of outstanding workmanship, as well as simpler, practical objects, but no sword, suggesting that his status was gained through trade. A low mound of earth and boulders was then raised over the ship and capped with the cremated remains of a horse, a dog, a pig, a sheep or goat, ox, and a cat that had been sacrificed as part of the burial rite. A marker post was set on the top of the mound.

By the time the site was excavated in the 1940s, the timber of the ship had almost completely rotted away in the soil, leaving only 300 of the iron nails that once held it together. The ship was about 10.5 m in length and was a trading vessel built for sailing short distances and landing on beaches to buy and sell goods, ideal for trading around the Irish Sea.

The human remains: The individual is estimated to have been about 45 years old when he died.. Isotope analyses of his diet and origin were undertaken by a team led by Leigh Symonds. The analyses suggested that the man was likely to have come directly from Scandinavia rather than from around the site of his burial¹³⁰.

Sample used for DNA analysis:
VK170 Isle-of-Man_Balladoole

1.2.2.9. Ireland

(Prepared by Maeve Sikora, National Museum of Ireland, and Linzi Simpson, Trinity College Dublin)

Islandbridge, Dublin NMI 08e0693:001 (Ireland_08e693)

This is the most recent discovery of a furnished Viking grave in Ireland. The grave, at Islandbridge in Dublin, is located close to the find spot of many Viking graves reported in the 19th century¹³¹. The human remains were discovered during an excavation in 2008 that took place as a response to the discovery of an iron sword and spearhead at the same location in 2004¹³². The in-situ human remains were discovered at a depth of 80-90 cm below ground level but most of the skeleton had been heavily disturbed and did not survive. The individual was lying in a supine position, and based on the position of the in-situ vertebrae, was oriented approximately north-south with the head at the north. The legs appear to have been flexed, as indicated by the portion of the left femur which was in situ. Portions of the right scapula and clavicle, fragments of seven right ribs, unsided fragments of radius and ulna, and fragments of vertebrae remains were recovered and have been identified by Barra Ó Donnabhain as those of a young adult male aged between 18 and 20 years at death¹³². Although the grave had

been heavily disturbed, a copper alloy ringed pin and two copper alloy objects that probably represent a scale pan were discovered associated with the remains. Copper staining on some of the rib bones suggests that these artefacts were originally placed on the torso. It is considered probable that the sword and spearhead found in the same area in 2004 were associated with this grave. Isotope analysis of the human remains indicate that this individual was not local to Dublin and likely spent most of his early life in a region of Scandinavia before coming to Ireland¹³². The burial has not been radiocarbon dated but based on the artefact typology dates to the first half of the 9th century CE. The main body of comparable material for this grave is found in the Islandbridge/Kilmainham/Inchicore area of Dublin. Graves from this area, the largest cemetery in the Viking west, have produced a rich array of artefacts with an impressive collection of weapons and trading material, among other objects. This grave was immediately northwest of the 'great gravel pit' that produced the rich collection of grave-goods in 1866¹³¹.

Sample used for DNA analysis:
VK546 Ireland_08E693

Eyrephort, County Galway NMI 1947:55 (Ireland_EP55)

This grave is one of the few graves of early VA date in Ireland to be discovered outside of Dublin. It was found in 1947 in west County Galway, in sand dunes in the townland of Eyrephort, close to the coast. It was not excavated at the time but a description of the burial was recorded based on the account of the finder who had uncovered and subsequently re-interred the remains. A full re-evaluation of the grave and contents was published recently¹³¹. The human remains were analysed by Barra Ó Donnabhain and represent a young adult male, probably aged between 20 and 25 years at death¹³¹. The burial was extended and supine with the head to the southwest and the feet to the northeast. The grave contained an iron sword, a spearhead, and a shield boss. Iron staining on the bones indicates that the sword probably lay along the left side, next to the arm. Both the spearhead and shield boss are of Scandinavian type and the sword is a double-edged sword of Petersen type K, which dates to the second half of the 9th century CE¹³¹.

Sample used for DNA analysis:
VK543 Ireland_EP55

Finglas, Co. Dublin, NMI 04E0900 (Ireland_FG254)

This grave was discovered during excavations in advance of construction works at Finglas, a suburb of Dublin, some 5.5km northwest of the city¹³³. Finglas was formerly a village outside of Dublin, and probably developed from an early medieval monastic centre. Although relatively little is recorded about the monastery, references to a scriptorium there in the 9th century CE suggest that it was considered a significant foundation¹³⁴. This report is based on Kavanagh's account of the excavation and Sikora's publication on the finds^{133,134}. The grave was located close to the church at Finglas, but outside of the boundary of the church grounds. It contained a single adult female who was buried with a pair of oval brooches, a casket decorated with bone plaques, and an antler comb, only a portion of which survived. The skeleton was extended and supine, with the head to the southwest. It had been damaged by previous groundworks and the lower legs and feet had been heavily disturbed. The remains are those of a woman aged between 25 and 35. She had been buried wearing a pair of oval brooches, one at each shoulder. The casket and comb had been placed by her right side. Only one brooch is intact; the second is very fragmentary. The brooches are single-shelled cast oval brooches of the Berdal type that have been gilded and inlaid with silver wire. The complete brooch is highly decorated with zoomorphic studs, some of which were cast with the brooch and some of which were

applied. These animals have eyes made of glass studs. This type of brooch dates to the mid-9th century, and it seems likely that the burial occurred around this time¹³⁴.

Finglas is not only unusual for the location of the burial and the high-status of some of the grave-goods. In Ireland 78 of the 107 Viking known graves are those of males¹³¹, so the discovery of a female grave is significant. The location of the grave, clearly a non-Christian burial, adjacent to a Christian church, is also interesting, and as Harrison and Ó Floinn point out, is “further evidence of the complex relationship between the ‘pagan’ Norse and ‘Christian’ Irish in the mid-ninth century”¹³¹.

Sample used for DNA analysis:
VK544 Ireland_FG254

Ship Street Great, Licence no. 01E0722, (Ireland_SSG12)

This Viking grave was located on the western side of Ship Street Great, close to the junction with Stephen Street Lower. The removal of a deep cellar exposed the remains of a very truncated skeleton lying approximately 3 m below the ground level, in boulder clay. The partial skeleton was in a supine position with the head to the west and was lying in a shallow grave-cut. All that survived was the intact lower mandible, crushed skull fragments, vertebrae, some ribs, the shoulder blades, the right collar bone, and part of the right arm. Analysis by Laureen Buckley revealed that this was probably a male aged 25-29. Four small artefacts were found in the neck area: a small silver finger ring, a corroded iron object, a glass bead, and a small twisted silver ring. A fragment of a pattern-welded sword was also found close to the skeleton but an examination of the surrounding boulder clay found no other features. A fragment of bone was sent to the Centrum Voor IsotopenOnderzoek in Groningen for dating, and this produced a 95% probability of the individual dating to between 665 and 865 CE (intercept date of 790 CE) with a 68% probability of dating to between 690 and 775 CE). The date range and the mode of burial suggest that this individual may have been a member of one of the groups of Viking warriors that descended on Ireland from the late 8th century CE onwards. That the skeleton formed part of a larger group of burials was also indicated by the subsequent excavations in Golden Lane by Edmond O'Donovan, where four additional Viking skeletons (including a female) were found, one of which lay just 5 m west of the Ship Street burial. These were interred in the environs of an early Christian cemetery and were all of a similar date. Four skeletons with some with weaponry had been found previously 150 m to the northeast, at South Great George's Street, and isotope analysis of these remains suggest that two were reared in the Scandinavian region while the other two were reared closer to the Atlantic, presumably in Viking colonies on the Western Isles or Northern Isles of Scotland^{131,135-137}.

Sample used for DNA analysis:
VK545 Ireland_SSG12

1.2.2.10. Iceland

(Prepared by Hildur Gestsdóttir, Institute of Archaeology, Iceland)

Hofstaðir, Mývatnssveit

The farm of Hofstaðir in Mývatnssveit in northern Iceland lies to the west of Lake Mývatn and is bordered to the west by the river Laxá (Fig. S1.4). A VA hall lies within the home-field of the Hofstaðir farm, west of the current farmhouses and up against a small scarp that demarcates the arable part of the home-field (the home-field boundary lies on top of the scarp). Excavations there, carried out under the direction of Gavin Lucas between 1996 and 2002, indicate that the hall was built in the middle of the 10th century CE. The site of the church and cemetery at Hofstaðir is within the home-field of the modern farm, 80 m southwest of the VA hall, up against the eastern edge of the old farm-mound, which was abandoned in the middle of the 20th century. The cemetery sits on the eastern edge of the farm-mound.

Excavations of the site were carried out in 2000-2004 and again in 2010-2015. The excavations revealed at least two, possibly three, phases of church structures in the center of an octagonal area bordered by a turf wall. Little remains of the earliest church, which appears to have been deliberately demolished, except post-foundations and the remains of a trampled floor. Radiocarbon and tephrochronology dating indicate that this earliest church was established in the mid 10th century CE. The later church was built on the same spot as the earlier one, although the later church was slightly smaller. Tephrochronology indicates that this later structure was built before the 1300 CE eruption in Katla, which also seals all burials within the cemetery. The earliest graves clearly respect the oldest structure on the site. Recent radiocarbon dating of six of the skeletons from the site returned dates between 695 and 1148 CE, although this range can be tightened in some instances as many of the burials clearly post-date the tephra from the 940 CE eruption in Veðivötn.

A total of 170 skeletons were excavated at Hofstaðir, mostly from in situ burials, although there are four examples of redeposited graves. There is a clear organization to the cemetery, as is seen in other medieval cemeteries in Iceland. Females are mostly buried in the northern half, males mostly in the southern half, and children up against the church; in particular, up against its southern wall. The burials are all inhumations. The grave-cuts are very tightly spaced with a lot of intercutting, especially in the area where the children are buried. All the burials are supine with the hands usually resting on the abdomen or alongside the body. About half of the adult burials were in simple wood-coffins of which nothing survived except wood-staining of the soil. The depth of the burials ranged between 30 cm (in areas where there had been levelling of the land for agricultural purposes in the middle of the 20th century) to about 80 cm (which represents the maximum depth of the burials while the cemetery was in use). Preservation in the cemetery was generally good and in most instances quite consistent although there were a couple of locations where variations had clearly caused the creation of micro-environments within the cemetery. An example of this is the small porch which had been added to the later church on top of three graves located immediately west of it. This resulted in poorer preservation of the skeletal material in these graves than in the rest of the cemetery. Bioarchaeological analysis of the skeletons from Hofstaðir have indicated a very high prevalence of inherited osteoarthritis, which suggests that the people buried within the cemetery were closely related^{138,139}.



Fig. S1.4: Aerial view of the Hofstaðir archaeological site.

Samples used for DNA analysis:

VK95 Iceland_HSM-A-127
 VK98 Iceland_HSM-A-083
 VK99 Iceland_HSM-A-104
 VK101 Iceland_HSM-A-125
 VK102 Iceland_HSM-A-128
 VK110 Iceland_HSM-A-115S
 VK111 Iceland_HSM-A-118
 VK122 Iceland_HSM-A-114
 VK123 Iceland_HSM-X-104
 VK225 Iceland_HSM-A-108
 VK226 Iceland_HSM-A-115N
 VK227 Iceland_HSM-A-117
 VK228 Iceland_HSM-A-120
 VK230 Iceland_HSM-A-123

Ingiríðarstaðir, Þegjandadalur

Þegjandadalur is a largely abandoned valley in northern Iceland, with limited areas of pasture towards the mouth of the valley, to the north. Elevation above sea level rises from circa 40 m at the valley mouth to circa 180 m at the head of the valley. The valley runs broadly north-south for approximately 7 km, and is up to 1.6 km at its widest. The area of lowland is approximately 7.3 km². The valley walls rise steeply to eroded heathland in the east, at circa 400 m, and more gently to better vegetated heathland in the west, at c. 230 m. At the southeastern limit of the valley a saddle gives access to Laxárdalur, at about 250 m above sea level. The grave field at Ingiríðarstaðir was discovered in 2008, as a result of a wider study of a complex and remarkably well preserved archaeological landscape in the valley of Þegjandadalur, in the county of Þingeyjarsýsla in northeastern Iceland.

Excavation of the grave field was carried out between 2008 and 2015. The excavation revealed eight adult inhumation burials as well as the remains of seven horses in six burials, all of which had been disturbed in antiquity. In addition, a single undisturbed neonatal skeleton inhumation burial was recovered. Radiocarbon and tephrochronological dating indicate a date of late 9th-early 11th century

CE. Recent isotope analysis has demonstrated that the individuals buried at Ingiríðarstaðir were born in the region¹⁴⁰.

Sample used for DNA analysis:
VK129 Iceland_ING08

Hringsdalur, Arnarfirði

In the summer of 2006 human remains and artefacts were discovered in an eroded sandbank on a small peninsula, Hreggnasi, which lies in the sea by the Hringsdalur valley in Arnarfjörður in the Westfjords in Iceland. This resulted in an archaeological investigation of the area between 2006 and 2011. The excavation revealed 4-5 burials, including one boat burial, which contained the disturbed remains of four adults, as well as a single undisturbed inhumation burial. A further 2-3 disturbed burials were located at the site. Dating of the site has mainly been based on artefact typology, which places it in the 10th century CE¹⁴¹.

Samples used for DNA analysis:
VK127 Iceland_HDR08
VK128 Iceland_HDR111

1.2.2.11. Greenland

(Prepared by Jette Arneborg, The National Museum of Denmark)

Sandnes, Kilaarsarfi V51

The Sandnes farm lies close to the shore at the head of Ameralla fjord and has an associated church. This site is the largest in the southern part of the Norse Western Settlement. The open valley behind the farm offered plenty of pasture while the nearby river supplied water for the farm. Today, the church is sanded up and flooded at high tide, clearly showing the dramatic changes of the landscape that has happened since the first Norse settlers arrived. Ten ruins have been recorded on the Kilaarsarfik plain during the course of multiple expeditions. An unknown number of ruins have been lost to the fjord¹⁴². The church and churchyard were excavated in 1930 and 1932. The recovered artefacts and radiocarbon dates indicate that the Sandnes farm was occupied from c. 1000 CE up until the time of the depopulation of the Western Settlement in the later part of the 14th century CE. Strontium isotopic analysis of skeletons from the church yard from the later settlement period suggest that they were raised in Greenland¹⁴³.

Samples used for DNA analysis:

VK74 Greenland_V051_0928

VK75 Greenland_V051_KAL-0929 / skeleton 11

VK76 Greenland_V051_KAL-0957 / skeleton 27

VK77 Greenland_V051_KAL-0959 /skeleton 31

VK78 Greenland_V051_KAL-0960 / skeleton 30

VK196 Greenland_V051_KAL-0947 /skeleton 22

Ujarassuit (Anavik) V7

The Anavik farm is situated on a raised beach terrace at Ujarassuit Fjord. The houses and the church lie spread over the large flat plateau where conditions for farming would have been excellent during the VA. Nine house ruins have been recorded at the site, including one of the best preserved stone houses in the Western Settlement. The main excavations of the site were carried out in 1932, when multiple buildings were identified. New excavations were conducted in 1982 when a small trench was opened in the churchyard to obtain human remains for $\delta^{13}\text{C}$ analysis. Radiocarbon dates and the positioning of the arms of the dead date the excavated burials to the 13th-14th century CE. The analysis of $\delta^{13}\text{C}$ indicated that the diet of the analyzed individuals was mainly marine^{144,145}.

Sample used for DNA analysis:

VK189 Greenland_V007_KAL-0992 / skeleton U04

Narsarsuaq Ø149

The Ø149 site is a Norse high-status farm with a connected church at Narsarsuaq in Uunartoq Fjord. It was first recorded in 1921 by Poul Nørlund and identified as the remains of a Benedictine nunnery. The farm is located on a peninsula between Lichtenau Fjord and Uunartoq Fjord in the southern region of the Eastern Settlement close to the hot springs on the island of Uunartoq. Twenty-one features, including the church, living houses, byres, stables, and barns have been recorded on the site. The first archaeological excavations were conducted in 1945-1946 and again in 1948 led by C.L. Vebæk. A few Norse ruins were investigated including the church and the churchyard, sections of the dwelling, a small stable, and the stable/barn complex. The church belongs to the later phase of the settlement from about 1300 CE but has had one or more predecessors. The human remains from the grave yard were radiocarbon dated to c. 14th century CE^{144,146}. Strontium isotope analysis of skeletons

from the church yard indicate that the individuals were local Greenlanders¹⁴³.

Samples used for DNA analysis:

VK190 Greenland_Ø149_KAL-0996 / skeleton 3, grave unit I

VK191 Greenland_Ø149_KAL-1000 /skeleton 7, grave unit I

Ruin group Ø64

The farm site of E64 is located in Igaliku Kujalleq, a small side branch of Igaliku Fjord in the Norse Eastern Settlement. Twelve features have been recorded on the site, among which are a small church belonging to the group of *landnam* churches that were established from the late 10th century CE, around 1000 CE. The church yard was excavated in 2007-2008 by a team led by Jette Arneborg. The excavated skeletons were radiocarbon dated within the period from late 10th century CE to about 1200 CE. A strontium isotope analysis indicated that several of the buried were immigrants from Iceland¹⁴³. Individuals X530, x532, x677 and x678 were all buried in the same grave.

Samples used for DNA analysis:

VK1 Greenland_Ø64_KNK2655x677

VK6 Greenland_Ø64_KNK2655x678

VK9 Greenland_Ø64_KNK2655x530

VK11 Greenland_Ø64_KNK2655x532

VK186 Greenland_Ø64_KNK2655#78

VK187 Greenland_Ø64_KNK2655#72

Brattahlid, Qassiarsuk, Ø29a

The site is located on the Qassiarsuk plain in Tunulliarfik Fjord, where 60 ruins were recorded and identified as the high-status farm Brattahlid, where one of the first Norse colonists, Erik the Red, settled with his family in the mid-980s CE.

The northernmost farm at Qassiarsuk identified as the ruin group Ø29a is thought to have been that of Erik the Red. According to Icelandic sagas Tjodhilde, the wife of Erik the Red had a church built on the farm around 1000 CE, and the remains of a small church found in the beginning of the 1960s have been identified with Tjodhildes' church. Radiocarbon dates of skeletons from the church yard indicate that the small church was built at the time of settlement in the late 10th century CE. The church yard was taken out of use in the beginning of the 1200s CE and the church site relocated¹⁴⁴.

There was a sex bias in the arrangement of the graves in the churchyard. The southern side of the church was mostly for high status men while many of the women were buried on the north side. A few high-status women were also buried on the south side, whereas a few low-status men were buried on the north side, and studies show that there were clear differences in both stature and teeth conditions between people buried on the south and north sides, likely reflecting the social structure of the Norse society¹⁴⁷.

A mass grave was also excavated on the south side of the church with 13 adult men and two boys of 10 and 17 years of age, respectively. This was determined to be a secondary grave because the bones of the skeletons did not lie in situ, indicating that the remains might have been moved to 'Tjodhildes' Church' from another grave or they may have died far away, and their bones were subsequently brought to Brattahlid for burial. Studies by Alexandersen and Prætorius¹⁴⁷ suggest that the individuals buried in the mass grave might have been relatives. Strontium isotope analyses suggested that some

of the individuals buried at Tjodhildes church were immigrants from Iceland¹⁴³. Samples F2, F3, F5, F6, F7, F8, and F9 are from the mass grave.

Samples used for DNA analysis:

VK513 Greenland_Ø029a_KAL-1088 / skeleton F8

VK179 Greenland_Ø029a_KAL-1092 /skeleton F2

VK180 Greenland_Ø029a_KAL-1091 /skeleton F3

VK182 Greenland_Ø029a_KAL-1085 /skeleton F5

VK183 Greenland_Ø029a_KAL-1086 /skeleton F6

VK184 Greenland_Ø029a_KAL-1087 / skeleton F7

VK185 Greenland_Ø029a_KAL-1089 /skeleton F9

VK193 Greenland_Ø029a_KAL-1061 /skeleton 75

1.2.2.12. Faroe Islands

(Prepared by Símun V. Arge, Tjóðsavnið, Faroe Islands National Museum)

The Church Site in Sandur, Sandoy

According to the Færeyingasaga, a man, Sniðálvur, lived in the village of Sandur in the Viking period. Local legends have it that he lived at á Krossi by the church, and that he had fled from the Hebrides because of a charge of manslaughter. Remains of ancient occupation have regularly been made visible by erosion of the coastline on both sides of the bay of Sandsvágur. Extensive Viking period settlements have now been revealed by and north of the ancient church site. At the site of á Sondum settlement activity has been dated to the 4th-6th centuries CE, which is the earliest dated evidence of human settlement in the islands. The village of Sandur is the largest agricultural area in the islands, which may have been especially attractive for the landnámsman when he should choose a site to settle. Settlement historical investigations and place-name studies indicate three larger farms in the village already in the Viking period¹⁴⁸.

Archaeological excavations within the church as well as at the church site at Sandur, við Kirkjugarð, have revealed some remarkable finds. Prior to professional excavations the only coin hoard in the islands so far turned up in 1863-1898. They comprised silver coins deriving from the Continent, Ireland, the UK and Scandinavia, and were hidden by the end of the 11th century CE. Archaeological investigations inside the church in 1969-1970 revealed five of the predecessors of the present church, which was built in 1839. The first church at the site was a small, plain wooden stave-church apparently dating from the 11th century CE. This church was replaced by a much larger church, Church 2. Both churches had a Romanesque plan. The church-typology and archaeological finds indicate that Church 2 was erected in the late 12th or early 13th century CE.

Excavations in the extended area of the churchyard to the south of the church during the period 1970-2009 revealed extensive settlement remains in the 3000 m² area. Rather than a proper habitation site, this area is interpreted as an activity area with the remains of different activities. Also, a Viking period burial ground was identified here, where 12 graves were found. Seven of the graves have been investigated. The dead were buried with personal belongings indicating a high-status society in the 10th century CE. The main settlement area is to be found to the north of the church site where archaeology has verified deep stratified layers along the eroding cliff edge from the period 8th-early 13th century CE.

Twenty-three burials were found in the nave of the second church at the site, Church 2; the individuals were interred in a planned manner below the wooden floor of the church (Fig. S4.3c). Most of the dead were buried in wooden coffins, but a few were interred in clothes only. The coffins were of the trapezoid medieval type. Seven of the buried were adults and 16 were children. Of the seven adults, three were women and four were men; all were over the age of 35 when they died. Child mortality in the medieval period was high, and of the 16 children all but one died before their first year and most just a few months after birth. This child was approximately four years old when it died. Generally, the skeletons are very well preserved.

It is surprising that men, women, and children were buried in the nave of the church. Usually only the priests were buried inside the church in the Middle Ages, at least outside the urban centers. This raises the question of whether the church may have had a special status, one that was different from a normal parish church. If the church was privately owned, it would have been reasonable to find members of the family of the owners amongst those buried within the church. Therefore, it is possible that the individuals buried below the nave were members of the family that occupied the main farm

in Sandur, to which the church belonged.

The archaeological context makes the church site in Sandur one of the most interesting and promising historical sites in the Faroe Islands¹⁴⁸.

Samples used for DNA analysis:

VK25 Sandoy_Church2_grave28
VK27 Sandoy_Church2_grave8
VK44 Sandoy_Church2_grave29
VK45 Sandoy_Church2_grave13
VK46 Sandoy_Church2_grave14
VK234 Sandoy_Church2_grave23
VK236 Sandoy_Church2_grave27
VK237 Sandoy_Church2_grave32
VK238 Sandoy_Church2_grave22
VK239 Sandoy_Church2_grave16
VK240 Sandoy_Church2_grave7
VK241 Sandoy_Church2_grave17
VK242 Sandoy_Church2_grave31
VK244 Sandoy_Church2_grave24
VK245 Sandoy_Church2_grave15
VK248 Sandoy_Church2_grave_B

The site of á Bønhúsfløtu, í Nesi, Hvalbøur, Suðuroy

The remains at the site of á Bønhúsfløtu in the village of Hvalbøur on the southernmost island of Suðuroy belong to a category of Faroese heritage that is attached to the specific place-name - bønhús, i.e. prayer houses or chapels. These are small ruins or mounds often with a circular dike surrounding the churchyard. The best preserved one, the Bønhústoft in Leirvík, is a 9 x 5.5 m ruin that is encircled by a nearly circular dike, 25 m in diameter. The place-name á Bønhúsfløtu— i.e. the chapel's plane—this indicates a chapel-site, and a local legend suggests an occupation by Irish monks a long time ago¹⁴⁹.

The site of á Bønhúsfløtu was surveyed for the first time in 2008-2009 by the staff from the Faroese National Museum. Some human bones had been found in the eroding cliff by this possible churchyard. One of these bones—a human tibia—was AMS-dated to 969-1020 CE (1 SD) and is indicative of the period of the activity at the site (AAR-13468). The remains that were surveyed at this site—low grass-grown ruins and dykes—are interpreted as an abandoned late Viking or Norse farm attached to which there was an enclosure—a semi-circular dike—that most likely could indicate a churchyard with the presence of a possible chapel, and referring to the place-name a chapel site as well¹⁵⁰.

Sample used for DNA analysis:

VK24 Á Bønhúsfløtu_Nesi_Hvalba_grave1

1.2.2.13. Estonia

(Prepared by Jüri Peets, Tallinn University)

Salme

In autumn 2008 human skeletal remains and ancient artefacts (sword fragments, rivets, gaming pieces, dice, etc.) were brought to light during the creation of an electrical cable trench for the lighting of a cycling track near the Salme borough on the island of Saaremaa in Estonia. Archaeological rescue excavations revealed that the finds came from a partly destroyed boat burial (Salme I). It was probably a rowing ship c. 11.5 m long and c. 2 m wide. Fragments of three swords and other weapons, and a lot of gaming pieces, were found as grave goods¹⁵¹. Skeletal remains of seven individuals were found, including some *in situ* partial skeletons. Numerous bones of domestic animals, and the remains of goshawk (*Accipiter gentilis*) and sparrow hawk (*Accipiter nisus*) were also found¹⁵².

As a result of fieldwork during two summers (2010-2011) a second ship of Salme (Salme II) was discovered; practically the whole ship contour, which in the middle part could be observed to the height of 5-6 rivet rows, together with the remains of 34 warriors was unearthed^{153,154}. The skeletons lay in three layers mostly in an area of about 3 m x 4 m in the central part of the ship. In the two upper layers the perished warriors had been placed with their heads pointing northeast, in the same direction as the ship. In the bottom layer they had been placed between the ribs, transverse with the longitudinal axle of the ship, heads pointing alternately east and west. The dead had been provided with rich grave goods, which mostly consisted of weapons, including more than 50 arrowheads, some spears, and about 40 swords (whole and broken). At least five swords had hilts of gilded bronze, among them one ring-hilt sword with a blade of pattern-welded steel. One sword had a blade ornamented with an inlay of golden wire and a handle decorated with garnets. Other items included nearly 300 gaming pieces of whale bone, antler combs, small padlocks, whetstones of schist, and beads. The dead had been covered with shields with iron bosses. In addition to the remains of terrestrial animals, some bones of goshawk and peregrine falcon (*Falco peregrinus*) as well as mallard (*Anas platyrhynchos*) were recovered. At least five or six dogs had been buried in the ship, all in the top layer at the boards of the ship. The original length of the vessel, considering the proportions of the preserved remains, could have been 17-17.5 m or more¹⁵⁵. Unlike the ship discovered in 2008, this ship may have moved by sail¹⁵⁴.

Apparently the most important individual was the man (skeleton XII (L)) who was buried in the middle of the first row of the second layer in the mass burial of the Salme II ship. He had a valuable ring sword (blade broken in several pieces), and warriors with shouldered swords placed at each side. Most likely the fallen warriors in the Salme I ship had been buried with as much homage and weapons as those in the second one. Apparently, they had been also covered with shields, of which, unfortunately, only shield rivets with domed heads survived. Artefact typologies and ¹⁴C dating of some of the human bones suggest that the burials were part of the same 'event', and that that event took place c. 750 CE. The 'event' may have been an armed conflict and the dead warriors-seafarers were buried in two mass graves in the ships on the seashore. The shape of the weapons and other artefacts of both ships allow us to date them to the late Vendel Period. Most of the finds belong to the Vendel Age period VII: 4 (c. 700-750 CE)¹⁵⁶ or earlier. Several human bones from the two ships (four samples from Salme I and nine samples from Salme II) were dated by ¹⁴C (94,5%). Most of the bones yielded dates in the time range 650-780 cal CE, but some samples gave results up to 940 cal CE^{151,153}. At the same time the earliest and the latest dates for the samples from the two ships are practically identical. For Salme I the earliest date is from skull SaI: 3., This individual is dated to 1320±30 BP or 650-780 cal CE (Hela-1915). The latest date for Salme I is from the skeleton SaI: 4. This specimen

is dated to 1200±30 BP or 700-940 cal CE (Beta-509634). The comparable dates of the samples from Salme II are from skeleton XV (O), which is dated to 1330±30 BP or 649–767 cal CE (Poz-109002), and skeleton XII (L), which is dated to 1199±32 BP or 700-940 CE (Ua-50746) (both skeletons originated from the second burial layer; Extended Data Fig. 1a). Most results of the analyses of animal bones remain within these limits. The reason for the relatively large variation in the dates is unclear. All analyzed samples were taken from materials without any later impact, i.e. all samples were taken from bones that were not disturbed after burial. Resolving this phenomenon is of utmost importance, not least because our analyses indicate that four of the individuals were brothers and the dates for these individuals differ considerably. In addition to the above mentioned skeleton XV (O), dated as the oldest (1330±30 BP), skeletons of two other brothers were dated—skeleton XIV (N) 1295±32 BP (Ua-50747) and skeleton XXII (V) 1250±30 BP (Beta-509632). The skeleton XXVI (Ö), the fourth brother, is currently not dated. Results of isotope analyses ($^{87}\text{Sr}/^{86}\text{Sr}$, $^{18}\text{O}/^{16}\text{O}$, and $^{13}\text{C}/^{12}\text{C}$ in human dental enamel and bones) suggest that the warriors buried in the mass graves in the ships came from central Sweden³⁰.

Samples used for DNA analysis:

VK480 Estonia_Salme_II-VI(E)
 VK481 Estonia_Salme_II-IV(F)
 VK482 Estonia_Salme_II-XVI(P)
 VK483 Estonia_Salme_II-XXII(V)
 VK484 Estonia_Salme_II-XVII(Q)
 VK485 Estonia_Salme_II-XV(O)
 VK486 Estonia_Salme_II-VII(G)
 VK487 Estonia_Salme_II-I(A)
 VK488 Estonia_Salme_II-VIII(H)
 VK489 Estonia_Salme_II-XXXV(Ä)
 VK490 Estonia_Salme_II-XIV(N)
 VK491 Estonia_Salme_II-XXIV(Ö)
 VK492 Estonia_Salme_II-II(B)
 VK493 Estonia_Salme_II-XXXIV(Š)
 VK495 Estonia_Salme_II-III(C)
 VK496 Estonia_Salme_II-XXIII(W)
 VK497 Estonia_Salme_II-XXVI(Ö)
 VK498 Estonia_Salme_II-XXXII(Z)
 VK504 Estonia_Salme_I-1
 VK505 Estonia_Salme_I-2
 VK506 Estonia_Salme_I-3
 VK507 Estonia_Salme_I-4
 VK508 Estonia_Salme_I-5
 VK509 Estonia_Salme_I-6
 VK510 Estonia_Salme_I-7
 VK511 Estonia_Salme_II-XXVIII(X)
 VK512 Estonia_Salme_II-XXVII(Ü)
 VK549 Estonia_Salme_II-X(J)
 VK550 Estonia_Salme_II-V(D)
 VK551 Estonia_Salme_II-XXI(U)
 VK552 Estonia_Salme_II-XI(K)
 VK553 Estonia_Salme_II-XIII(M)

VK554 Estonia_Salme_II-XII(L)

VK555 Estonia_Salme_II-IX(I)

1.2.2.14. Italy

(Prepared by Gabriele Scorrano, University of Copenhagen, Enrico Cappellini University of Copenhagen, Pasquale Favia, University of Foggia, and Italo M. Muntoni, Soprintendenza Archeologia)

San Lorenzo in Carminiano, Foggia

The medieval settlement of San Lorenzo in Carminiano (then Carmignano) was the main village in northern Apulia between the late Middle Ages and the modern period. It is located in the central area of the Tavoliere delle Puglie plain, just outside the city of Foggia. The settlement had three subdivisions, bounded by ditches—a northern trapezoidal one (enclosure I), probably surrounded by walls and extending over seven hectares and dating to c. 13th-16th centuries CE; another in the northwestern position (enclosure II), which is smaller in size and has a half-circular morphology; and a third southern one (enclosure III), which is elliptical and very broad (up to 15 ha). In the site only a small church dedicated to San Lorenzo has been found. Outside the church, along the bottom wall, various paving slabs have been discovered, both in cobwebs (USR 932-841) covered with a combustion ground, in tessellato, with stone tiles and brick sections and finally a wider lacer with brick remains¹⁵⁷. Some post holes have also been found and they may perhaps refer to a late medieval stage. The excavation in the area in front of the church identified at least four phases: the first three referring to the Middle Ages, the latter probably to the 17th-18th century CE¹⁵⁷. The oldest traces of a funeral attendance are represented by a simple burial in the ground (t.2), hosting three individuals.

Samples used for DNA analysis:

VK534 Italy_Foggia-869

VK535 Italy_Foggia-891

Cancarro, Troia, Foggia

The church of Cancarro is situated 3.5 km southwest of Troia, at 430 m ASL. The city of Troia was built on the ruins of the Roman town of Aecae, which occupied a strategic position on the Via Traiana. The church was used between the 11th and the 13th centuries CE¹⁵⁸. Next to the church archaeologists unearthed a cemetery with 54 well-preserved burials, often overlying each other. Two graves held two individuals and five pits were ossuaries¹⁵⁸. A minimum of 79 skeletons, mainly women, were confidently identified from reused graves¹⁵⁸. Based on artifacts, the cemetery was used between the late 11th century CE (Norman Age) and the second half of the 13th century CE (Swabian-Angevin Age)¹⁵⁸.

Samples used for DNA analysis:

VK536 Italy_Foggia-1240

VK537 Italy_Foggia-1248

VK538 Italy_Foggia-1249

Supplementary Note 2. Ancient DNA laboratory procedures and sample selection

2.1. Ancient DNA extraction

All aDNA laboratory procedures were conducted in the special aDNA clean-room facilities at the Centre for GeoGenetics, Natural History Museum, University of Copenhagen, according to strict aDNA standards^{159,160}. The overwhelming majority of ancient samples were petrous bones and teeth (Supplementary Table 1). To maximize the yield of endogenous DNA from ancient human samples we targeted the cementum (the hard and relatively well preserved outer layer of the tooth roots)¹⁶¹ or the otic capsule of the petrous bones¹⁶².

The drilled bone sample (ranging from 100 to 400 mg) was briefly digested in digestion buffer (4.65 ml 0.5 M EDTA, 50 µl recombinant Proteinase K, 50 µl 100x TE and 250 µl 10% N-Laurylsarcosyl) for 45 minutes at 40 °C (pre-digestion step)¹⁶¹. After this, the samples were centrifuged for 2 minutes at 2000g and the resulting supernatant was removed. To the bone material, an identical digestion buffer was added for a full 24-hour digestion at 40 °C. After this digestion step, the samples were centrifuged for 5 minutes at 2000g and the remaining undigested pellets were stored for later re-extraction. Silica-powder-based DNA extraction protocol was used to extract the aDNA from 2 ml digested solution. The water based suspension of silica was prepared by mixing 6g of SiO₂ with 50 ml H₂O. After 1 hour of sedimentation, the top 48 ml supernatant was transferred to a new 50 ml tube. This was followed by another 5-hour sedimentation after which the top 43 ml of the supernatant was discarded and the silica was re-suspended and activated by 60 µl 37% HCL. To each of 2 ml digested sample, 20 ml of the binding buffer (19.54 ml Qiagen buffer PB, 360 µl 5M sodium acetate, 100 µl 5M sodium chloride) and 100 µl silica suspension was added and adjusted to pH 4-5 with 37% HCl¹⁶³. This was followed by a 1-hour incubation at room temperature, after which the supernatant was removed by a brief centrifugation step for 2 minutes at 2000×g. The silica was re-suspended in a 1 ml binding buffer, transferred to 2ml Eppendorf tubes, centrifuged, and then washed twice with 80% ice-cold ethanol. The DNA was released from silica particles by 70 µl Qiagen EB buffer. With each round of extractions, negative controls were used.

2.2. NGS library preparation and sequencing of ancient samples

From 20 µl double-stranded DNA extracts blunt-end DNA libraries were prepared using Illumina-specific adapters and NEBNext DNA Sample Pre Master Mix Set 2 (E6070) kit according to the manufacturer's instructions with a few modifications. The end-repair step was conducted in 25 µl reactions using 20 µl of DNA extract. This was incubated for 20 mins at 12°C and 15 mins at 37°C, purified using PB buffer with Qiagen MinElute spin columns, and eluted in 17 µl EB buffer. This was followed by ligation (25 µl reactions) of the Illumina-specific sequencing adapters prepared according to Meyer and Kircher 2010¹⁶⁴. This step was carried out for 15 mins at 20°C and the resulting DNA-adaptor complex was purified using PB buffer and Qiagen MinElute columns, before eluting in 20 µl EB Buffer. The last, adapter fill-in reaction was conducted in 30 µl volume and incubated for 20 mins at 65°C, followed by 20 mins at 80°C to inactivate the Bst enzyme. qPCR was conducted using SYBR green MIX (Roche) according to manufacturer's instructions and the same forward and reverse primers used for the subsequent index PCR step in order to calculate the total amount of DNA library in each sample and assess the optimal number of PCR cycles required for DNA library amplification at the subsequent step. After that, the 12µl DNA library was index-amplified in a 50 µl PCR reaction by mixing with 25 µl 2X Kapa U+, 1 µl of each primer (10 µM,

inPE forward primer + indexed reverse primer) and 11 µl H₂O. The PCR thermocycling conditions were 45s at 98°C, followed by number of cycles (based on qPCR values) of 15s at 98°C, 30s at 65°C and 30s at 72°C, and a final 60s elongation step at 72°C. The amplified DNA library was purified with PB buffer using Qiagen MinElute columns and eluted in 50 µl EB buffer. Negative library controls, based on EB as well as negative extraction controls were included for each batch. To quantify the amount of the purified DNA libraries, Agilent Bioanalyzer 2100 was used. The library pools were sequenced (80 bp single read) on Illumina HiSeq 2500 machines at the Danish National High-throughput DNA Sequencing Centre. The base-calling and sequence sorting by sample-specific indices were produced by the Sequencing Centre using CASAVA v1.8.2.

2.3. Sample selection

A total of 528 ancient human remains were processed and screened (c. 15 million sequences per sample) for contamination levels and endogenous human DNA content. After removing contaminated and poorly preserved samples, the number reduced to 442. Many of the remaining samples were prioritized based on their endogenous human DNA content and relevance to the project and were sequenced deeper resulting in 376 samples between 0.1 and 11.7X coverage, of which 216 were above 1X. A total of 64,786,513,002 DNA reads from 442 different samples were generated for this study, out of which 23,149,730,287 uniquely mapped to the human reference genome (Supplementary Table 2).

Supplementary Note 3 - Data quality assessment, contamination, error profiles, sex determination, and mitochondrial and Y chromosome analyses

3.1. Data quality assessment

AdapterRemoval v2.1.3¹⁶⁵ was used for removing Illumina adapter sequences and stretches of Ns at both ends of the aDNA reads, keeping only sequences with a minimum length of 30 bp. We mapped the adapter-free sequences against the human reference genome build 37 using BWA v0.7.10 aligner¹⁶⁶ with the seed (-l parameter) disabled for higher sensitivity of aDNA reads¹⁶⁷. DNA sequences were processed with samtools v1.3.1¹⁶⁶ and only aligned sequences with mapping quality of at least 30 were kept. Picard v1.127 (<http://broadinstitute.github.io/picard>) was used to sort the reads and remove duplicates. DNA libraries were combined at sample level and realigned using GATK v3.3.0¹⁶⁸ with Mills and 1000G gold standard indels. At the end, realigned bam files had the md-tag updated and extended BQs calculated using samtools calmd. Read depth and coverage were determined using pysam (<http://code.google.com/p/pysam/>) and BEDtools¹⁶⁹. The mapping statistics for the ancient samples are summarized in Supplementary Table 2.

DNA damage is one of the most characteristic features of ancient DNA molecules and is usually manifested in the form of single or double stranded breaks resulting in fragmented DNA molecules (usually <100 bp) and single-stranded overhangs, as well as cytosine deamination towards the 5' end of DNA fragments leading to the typical C→T transitions in the sequenced DNA reads. We used mapDamage v2.0 to obtain approximate bayesian estimates of damage parameters¹⁷⁰. Three main parameters were assessed: (i) the C→T transitions rates at the first position of the 5' end of DNA reads, (ii) λ , the proportion of nucleotides in single-stranded overhang regions, and (iii) δ_s , which shows the estimated C→T transition rate for the single-stranded overhang segments.

Of the 442 ancient samples, the C → T transition rates at the first position of the 5' end of the DNA fragments ranged from 1.5% to 42.4% when compared with the human reference genome (Figure S3.1). Both the lambda (λ) and DeltaS (δ_s) parameters showed a significant deviation from zero, indicating that the bulk of the recovered DNA molecules were damaged and degraded, which suggested that the majority of DNA molecules were of ancient origin. The DNA damage parameters of each ancient sample from this study are presented in Supplementary Table 4.

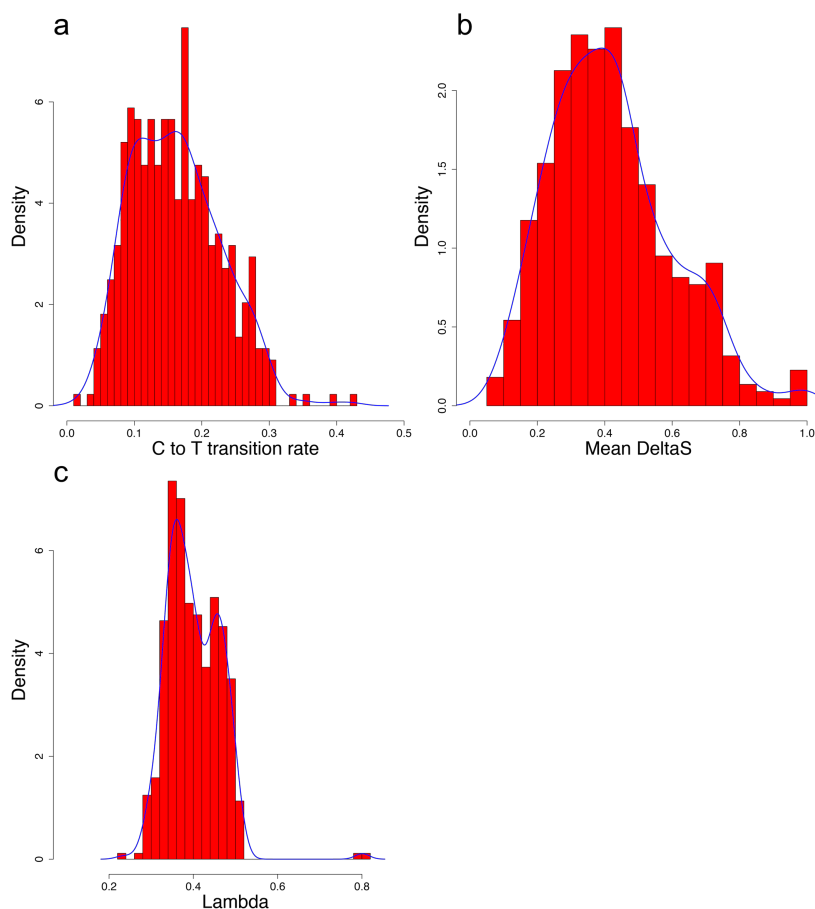


Fig. S3.1: Distribution of the ancient samples according to the DNA damage levels. (a) C→T transition rates; (b) transition rates in single-stranded overhangs; (c) fraction of bases in single stranded overhangs.

3.2. Contamination

ContamMix: This method relies on the reconstructed consensus mtDNA sequences of ancient samples; the contamination should not exceed 50% for this method to work. The details of ContamMix are described elsewhere¹⁷¹. It also assumes that the sequenced mtDNA reads originate from a mixture of the reconstructed consensus sequence and 311 whole mitochondrial genomes, representing possible contaminant sequences from present-day worldwide populations. By comparing the mapping affinity of each ancient mtDNA read to the reconstructed consensus sequence and to the 311 possible contaminants, ContamMix reports the total fraction of non-endogenous reads as the contamination rate with a Bayesian estimate of the posterior probability of the contamination proportion.

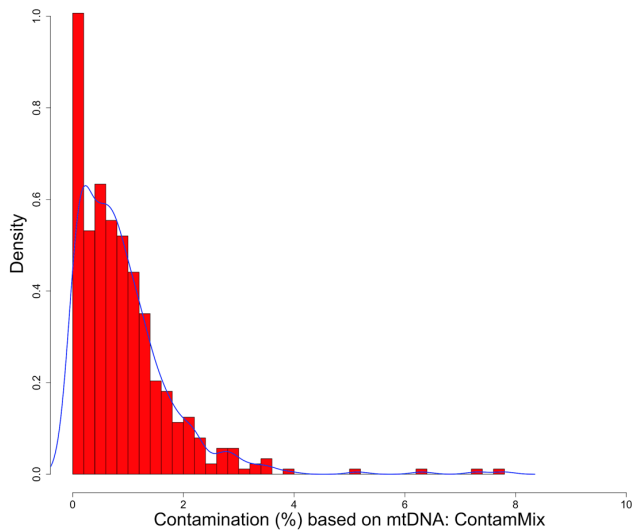


Fig. S3.2: Distribution of the ancient samples according to the contamination levels. All ancient samples have >9X sequencing depth (n=442) on mtDNA. The four samples with more than 5% contamination on the plot did not show significant contamination based on Schmutzi, therefore were kept for downstream analysis.

For this approach, we aligned all trimmed reads from ancient samples to the human mitochondrial reference genome: revised Cambridge Reference Genome (rCRS) with the same parameters as for the whole genome mapping. The sequencing depth of coverage for the mtDNA ranged 9-538X, the details are provided in the Supplementary Table 2. To construct the endogenous mtDNA sequence of ancient samples required for ContamMix we used an in-house perl script. mtDNA sites with base quality <20 and reads with mapping quality <30 were discarded. Only SNPs and sites with at least 3X coverage were considered for consensus calling. At each mtDNA position a base was called only if it was observed in at least 70% of the reads covering that site. The distribution of the ancient samples based on contamination levels assessed by ContamMix are shown in Figure S3.2. The contamination estimates are presented in Supplementary Table 4.

Schmutzi: The amount of present-day human contamination was also estimated in each sample with Schmutzi¹⁷². This estimate was performed without the inclusion of the predicted contaminant in the database of putative present-day human contaminant mitogenomes used by Schmutzi (option ‘--notusepredC’). Unlike ContamMix, it does not estimate a parameter for error but instead uses input mis-incorporation rates due to deamination and uses base quality scores. Schmutzi also assumes a single contaminant source unlike ContamMix.

Both methods were applied to our dataset and only samples with contamination levels greater than 5% detected with both methods were removed.

Schmutzi was also used to infer the endogenous consensus sequences by mitigating the impact of deamination-induced nucleotide mis-incorporations and the presence of present-day human contamination. The former is achieved by incorporating the rates of mis-incorporations into a Bayesian model that considers every possible 4 bases for the endogenous and the contaminant. Each aDNA fragment is assigned a probability of being endogenous given the contamination prior provided above. This probability is computed using the distribution of fragment lengths and the rate of base

mis-incorporations due to deamination. The most likely base is produced along with a per-base error probability on a PHRED scale.

Male X-chromosome based contamination analysis: Since male individuals carry only 1 X chromosome inherited from the mother, any heterozygous position of that chromosome (outside the pseudoautosomal regions) would be either due to sequencing errors or contamination. In case of sequencing errors, the heterozygous positions are expected to be randomly distributed across the chromosome, while in case of contamination heterozygous positions should be restricted to mainly diagnostic positions (sites on the X chromosome that are known to be polymorphic). The difference of mismatch rates between these positions and adjacent sites indicates the contamination levels. This method is described in more detail in previous work¹⁷³ using the package ANGSD¹⁷⁴. For this analysis, we removed the pseudoautosomal regions of the X chromosome and used mapping quality ≥ 30 and base quality ≥ 20 filters. The reported values are based on the maximum likelihood estimator using the unbiased sampling-based approach, i.e. ‘Method1’ in ANGSD (Figure S3.3).

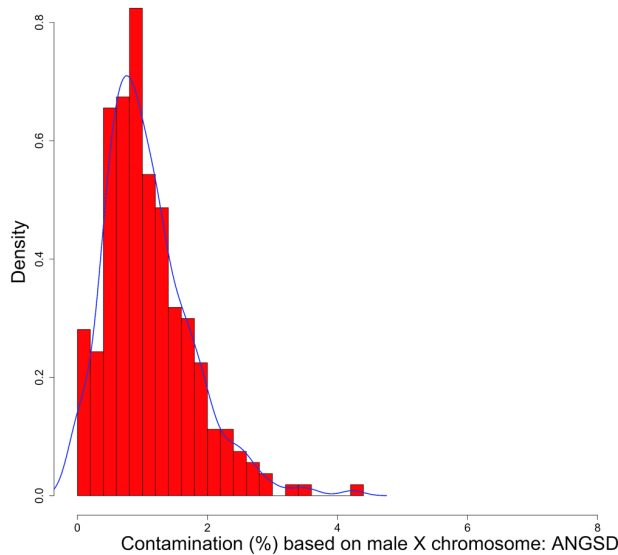


Fig. S3.3: Distribution of the ancient samples according to the X-chromosome based contamination levels. Only male individuals with $>0.1X$ average genomic depth of coverage were used for the analysis (n=267).

3.4. Sex determination

The sex of ancient individuals was determined by calculating the R_y parameter, which reflects the ratio of the fraction of Y chromosome reads to the fraction mapped to both X and Y chromosomes¹⁷⁵. According to this method, individuals with R_y values above 0.077 are considered as male, while the ones lower than 0.016 as female.

We assessed the sex of all the ancient samples in this study, regardless of the sequencing depth. We identified 141 females and 296 males (Supplementary Table 5) while the biological sex for the rest of the five samples was not identified (four of which due to low coverage). This strong male bias was expected, since in many of the famous sites such as Dorset-UK (executed c. 50 males) and Salme-Estonia (two ship burials of male warriors), only male individuals were buried. Moreover, whenever feasible (with all other factors being equal - e.g. age of the sample or preservation), males were prioritised due to the extra genetic information carried in the Y-chromosome. Interestingly, one of

the ancient samples with unidentified biological sex (VK204) had c. 1X average genomic coverage. The inability of this method to identify the sex of this individual may indicate that this person was affected by some form of Klinefelter syndrome and had one of the non-usual karyotypes (e.g. XXY or XXXY). Given the relatively high rate of occurrence of this syndrome with roughly 1 in 576 males¹⁷⁶, it is not unlikely to observe one case in such a large number of ancient samples.

3.5. Mitochondrial DNA analysis

For mtDNA haplogroup assignment we used the mtDNA consensus sequences created by Schmutzi. The mitochondrial haplogroups of the ancient VA individuals were assigned using haplogrep¹⁷⁷.

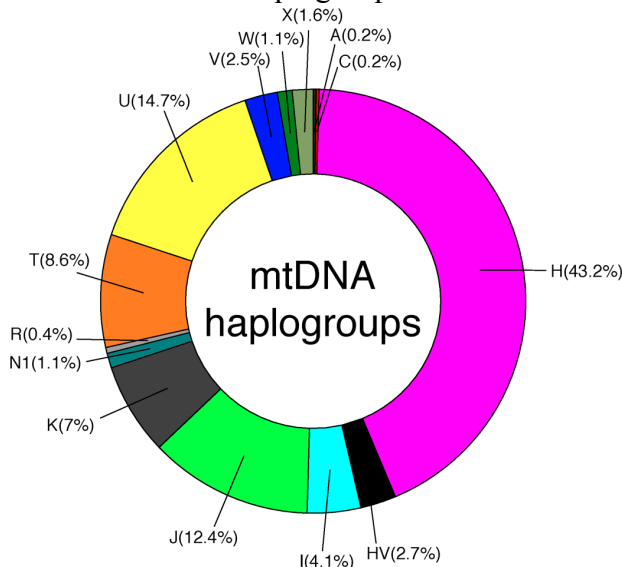


Fig. S3.4: The distribution of mtDNA haplogroups across the 442 ancient samples from this study. The haplogroup frequencies should be interpreted with caution since there are a few related individuals in this study especially from Faroe Islands and Salme boat burials (see the genetic relatedness section) which were not removed for the frequency estimation of the whole dataset.

The overall distribution of the mtDNA haplogroups of the ancient VA samples (Figure S3.4) is quite similar to the diversity of mtDNA lineages found in modern northern European populations. The frequently encountered (>5%) major mtDNA haplogroups were Hg H (43%), followed by Hgs U, J, T and K (http://www.eupedia.com/europe/european_mtdna_haplogroups_frequency.shtml). Interestingly, we found two individuals VK548 (a female individual from Norway; Nord-Trøndelag 3705) and VK160 (a male individual from Russia; Kurevanikka_7283-3) who had mtDNA haplogroups commonly found in Asian populations: haplogroups A12a and C4a1a, respectively. The VK548 sample was previously suggested to have had the haplogroup A4b based on mtDNA HVR1 data⁵⁹.

The haplogroup frequencies in Figure S3.5 should be interpreted with caution since there are a few related individuals in this study especially from Faroe Islands and Salme boat burials (see Supplementary Note 4) that were not removed for the frequency estimation of the whole dataset.

The aligned whole mtDNA sequences of VA samples (roughly dating 1000 CE) were used as an input for BEAST v1.8.4¹⁷⁸ to uncover the trajectory of the effective female population size (N_e) through time using the Bayesian skyline plot (BSP) method. The MCMC chains were run for 10E8 states and

sampled every 10E4 states with the first 10E6 states discarded as burn-in. We used the CIPRES open-access server for phylogenetic studies¹⁷⁹ to run the BEAST analysis. We checked the output data for convergence to a stationary distribution and sufficient effective sample size estimates using Tracer v1.7¹⁸⁰. We used the GTR model with gamma plus invariant sites and a strict clock with a normal prior of 2.2E-8/site/year as the mean value with standard deviation of 2.2E-9. The resulting trees were annotated with TreeAnnotator 1.8.4 (BEAST package) and visualised by FigTree (<http://tree.bio.ed.ac.uk/software/figtree/>).

A Bayesian Skyline plot analysis is shown in Figure S3.5. Even though the 95% confidence intervals are large, it shows an increase in female population size for the last 10-15,000 years with a mean female population size of c. 100,000, assuming a generation time of 25 years. The increase in female population size after the Last Glacial Maximum (LGM) is in accordance with previously published data¹⁸¹.

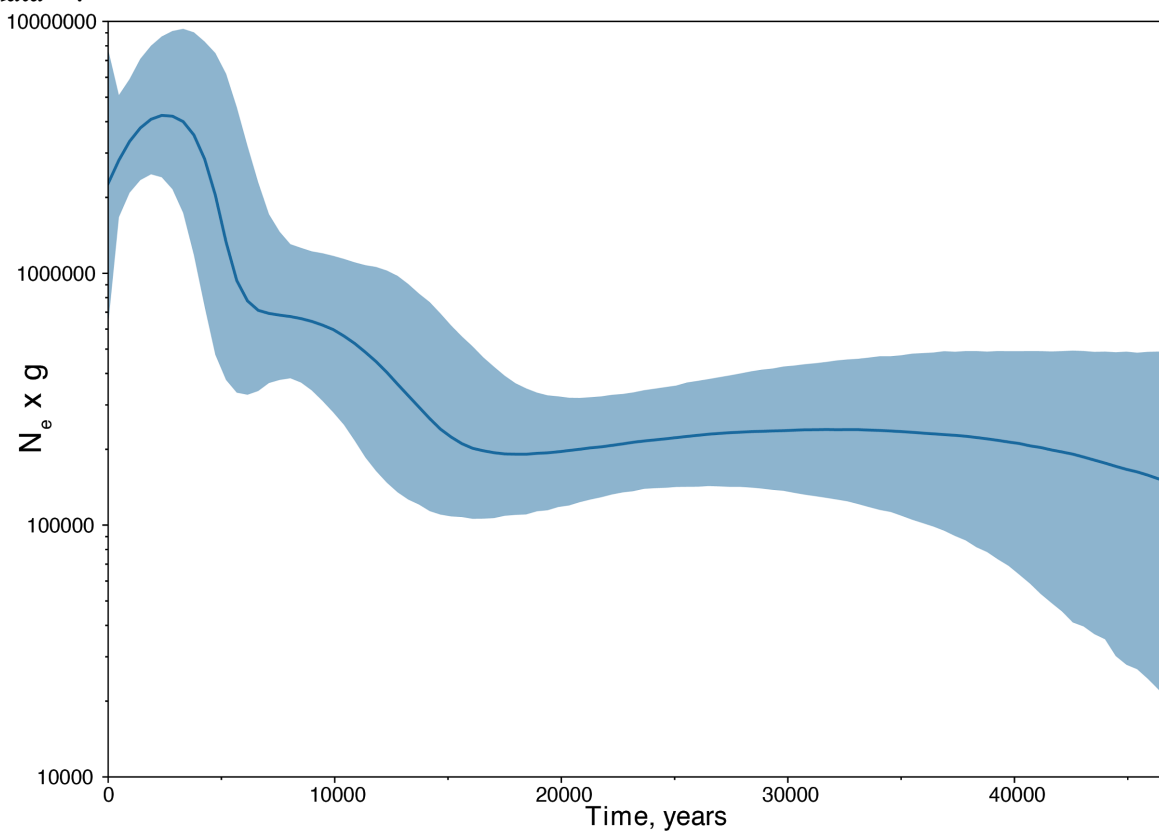


Figure S3.5: Bayesian skyline plot based on the ancient samples. Values on the y axis represent the effective female population size (N_e) x generation time (g). $n=442$ mtDNA sequences were used. The shaded region indicates the 95% highest posterior density intervals.

A Bayesian phylogenetic tree of mtDNA sequences of all 442 ancient samples is presented in Figure S3.6.

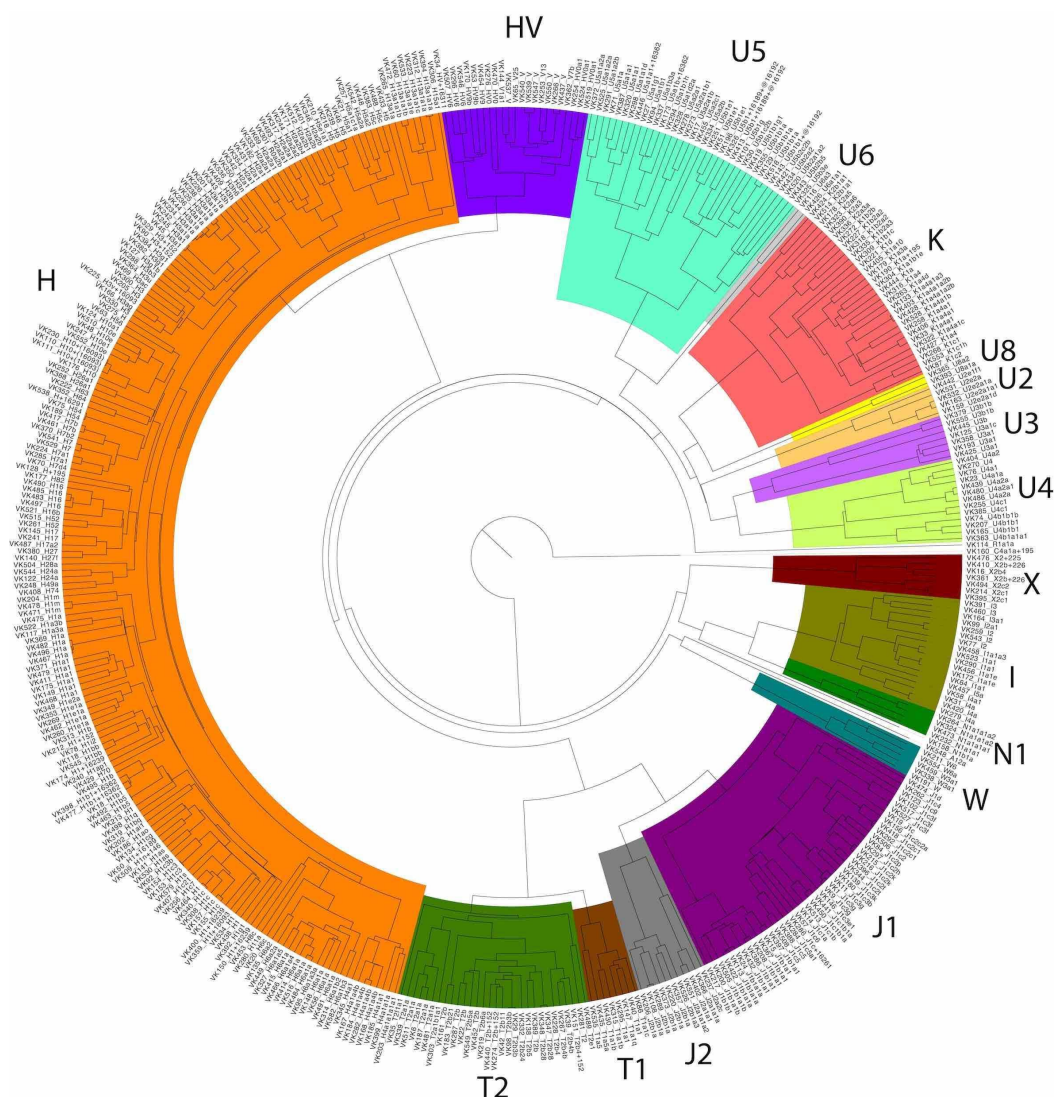


Figure S3.6: Phylogenetic tree of ancient samples from this study based on whole mtDNA sequences. The tip labels indicate the ancient sample IDs and mtDNA haplogroups.

3.6. Y chromosome analyses

We assigned Y chromosome haplogroups to the ancient male samples with Yleaf v2¹⁸², restricting our analysis to 26,083 biallelic SNPs from the ISOGG (International Society of Genetic Genealogy) 2019 database (https://isogg.org/tree/ISOGG_YDNA_SNP_Index.html) confidently placed within the Y-chromosome tree (i.e. excluding those annotated with '~', of uncertain placement, to avoid inconsistencies in the determination of haplogroups). The distribution of the Y chromosome haplogroups is presented in Figure S3.7.

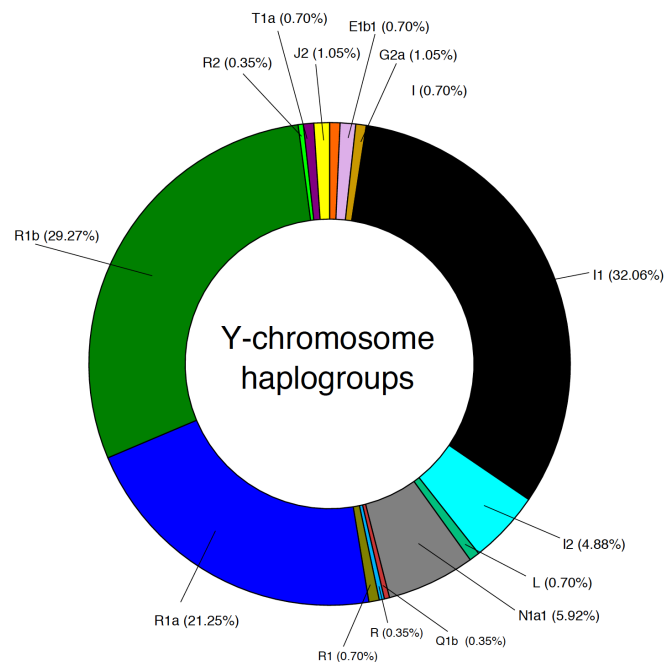


Fig. S3.7: Distribution of Y chromosome haplogroups in 276 ancient (mostly VA) male individuals.

The assigned haplogroups are provided in the Supplementary Table 5. As with the mitochondrial DNA haplogroups, the overall distribution profile of the Y chromosomal haplogroups in the VA samples was similar to that of the modern northern European populations. The most frequently encountered male lineages were the haplogroups I1, R1b, and R1a.

Among the ancient samples, two individuals had derived haplogroups identified as E1b1b1-M35.1, which are frequently encountered in modern southern Europe, the Middle East, and North Africa¹⁸³. Interestingly, the individuals carrying these haplogroups had much less Scandinavian ancestry compared to the most samples inferred from haplotype-based analysis. A similar pattern was also observed for less frequent haplogroups in our ancient dataset, such as G (n=3), J (n=3) and T (n=2), indicating a possible non-Scandinavian male genetic component in VA northern Europe. Interestingly, individuals carrying these haplogroups were from the later VA (10th century CE and younger), which might indicate some male gene influx into the Viking population during the Viking period. It is worth mentioning that due to the small sample size of the rare haplogroups, these differences might be of stochastic nature and therefore the results based on uniparental markers should be interpreted with caution.

pathPhynder Analysis: The highly degraded nature of aDNA data poses considerable challenges for combining ancient and modern samples for phylogenetic analyses. Typical analyses of ancient Y-chromosome data focus on a curated set of known markers (ISOGG). However, many more markers exist and will continuously be generated as more sequencing studies emerge. By making use of this additional Y-chromosome variation, we can increase the probability of overlap of ancient DNA reads with branch-defining markers and use this information to place ancient samples into more detailed phylogenies.

Using the pathPhynder workflow (<https://github.com/ruidlpm/pathPhynder>), we first assigned 56,246 variants from the 1000 Genomes Project to the branches of the Y-chromosome tree¹⁸⁴. Next, for each aDNA sample, we generated a pileup at these informative sites, excluding C/T and G/A sites covered

by a single read to minimise the impact of post-mortem deamination ('conservative' mode). Next, for each ancient sample, we determined the number of ancestral and derived alleles at each branch and traversed the 1000 Genomes Y-chromosome tree, using this information to map ancient samples to their most likely place in the phylogeny (Figure S3.8).

In the 1000 Genomes Project Y-chromosome phylogeny, haplogroup N is split into two main clades, one composed of mostly East Asian individuals (CHB) and one of Finnish individuals (FIN). The Viking and early Viking samples from Estonia and Sweden are positioned within the FIN clade, more specifically at the branch defined by the marker VL29/CTS2929-N1a1a1a1a, or at branches downstream of it. A large study of Y chromosomes revealed that the VL29 lineage occurs at highest frequencies in present-day Estonians, Latvians, Lithuanians, Finns, and other northern European populations¹⁸⁵.

Haplogroup I1, previously described as showing the signature of a star-like expansion¹⁸⁴, occurs in present-day Scandinavians at a frequency of 25–35%¹⁸⁶. In the 1000 Genomes Project dataset, this clade is mostly composed of FIN, GBR, and CEU populations. I1 is the best represented haplogroup in our ancient dataset, and most regions contained individuals belonging to this lineage (especially Estonia, Russia, Denmark, and Greenland), with the exception of the Isle of Man, Ireland, and Italy (these regions have comparatively small sample sizes which may not allow the detection of this haplogroup). The ancient samples in the present study are mainly distributed in two clades, I1a1b1-L22, which accounts for 71% of the I1 haplotypes in a Y chromosome survey of Finland¹⁸⁷, and I1a2a-S246. Of particular interest, the clade I1a2a1a1d1a-S247 is especially well represented in Estonian samples, and is found mostly in present-day Finnish and northern Scandinavian groups.

While it is likely that many I1 lineages dispersed into the British Isles from Scandinavia during the Viking period, it is also probable that earlier Anglo-Saxon migrations also played a role, as suggested by the east to west decreasing frequency cline of I lineages¹⁸⁸ and the presence of the I1 lineage in an individual from this period excavated in England¹⁸⁹.

Within haplogroup I2, two Viking samples from Sweden and Ukraine, fall within the L621-I2a1a2b and its downstream I2a1a2b1-CTS10936 clade, together with a FIN individual. This lineage has a mostly eastern European distribution¹⁹⁰, occurring more frequently in Slavic peoples. Other I2 ancient samples fall within the clade defined by I2a1b1-M223, with highest frequencies in Germanic and Scandinavian peoples¹⁸⁶. A subset of these individuals from Sweden, Orkney, and England was positioned in the I2a1b1a2b-Z161 branch, a lineage present in northern Europe, especially in Denmark, Germany, the Netherlands, and England.

In terms of haplogroup R, only a single R2-M9710 individual was found in Iceland (VK123), and this individual was positioned together with mostly South Asian populations of the 1000 Genomes project. All the other ancient samples assigned to haplogroup R belonged to R1 subclades.

Within Europe, the subclades of R1, R1a-M420, and R1b-M343 reach higher frequencies in the east and west, respectively. In broad terms, the distribution of R1 lineages in our ancient dataset is consistent with this, with the Isle of Man and Italy carrying exclusively R1b derived lineages, and Ukraine and Estonia R1a derived lineages.

Focusing on R1a, two major lineages exist, one more common in Central and South Asian populations (R1a1a1b2-Z93) and the other in Europe (R1a1a1b1a-Z282)¹⁹¹. As expected, the R1a derived ancient

samples analysed here fall within the European Z282 clade, and are positioned near Great British (GBR), European (CEU), and Finnish (FIN) individuals in the Y chromosome tree, rather than with the South Asian individuals in the Z93 clade. Many of the ancient Norwegian and Swedish samples were determined to be derived for the R1a1a1b1a3a-S221/Z284 marker, of nearly exclusive distribution within Scandinavian populations and occurring at approximately 20% in Norway¹⁹¹.

In terms of R1b lineages, the R1b1a1b1b-Z2105 and R1b1a1b1a-L11 clades have distinct distributions, with the first being typically associated with the Yamnaya^{163,192,193} and distributed today around the Caucasus and Volga-Uralic regions¹⁹⁰, and the latter more commonly found in the late Neolithic, Bronze Age, and later periods in central and western Europe. A derived status at R1b1a1b1b-Z2105 was found in a single sample from Italy (VK535). The vast majority of other R1b samples belonged instead to the R1b1a1b1a-L11 clade, and were mostly distributed within its two main subclades: P312/S116-R1b1a1b1a1a2 and U106/M405-R1b1a1b1a1a1¹⁹⁴, of western and eastern distribution relative to the Rhine river basin¹⁹⁵.

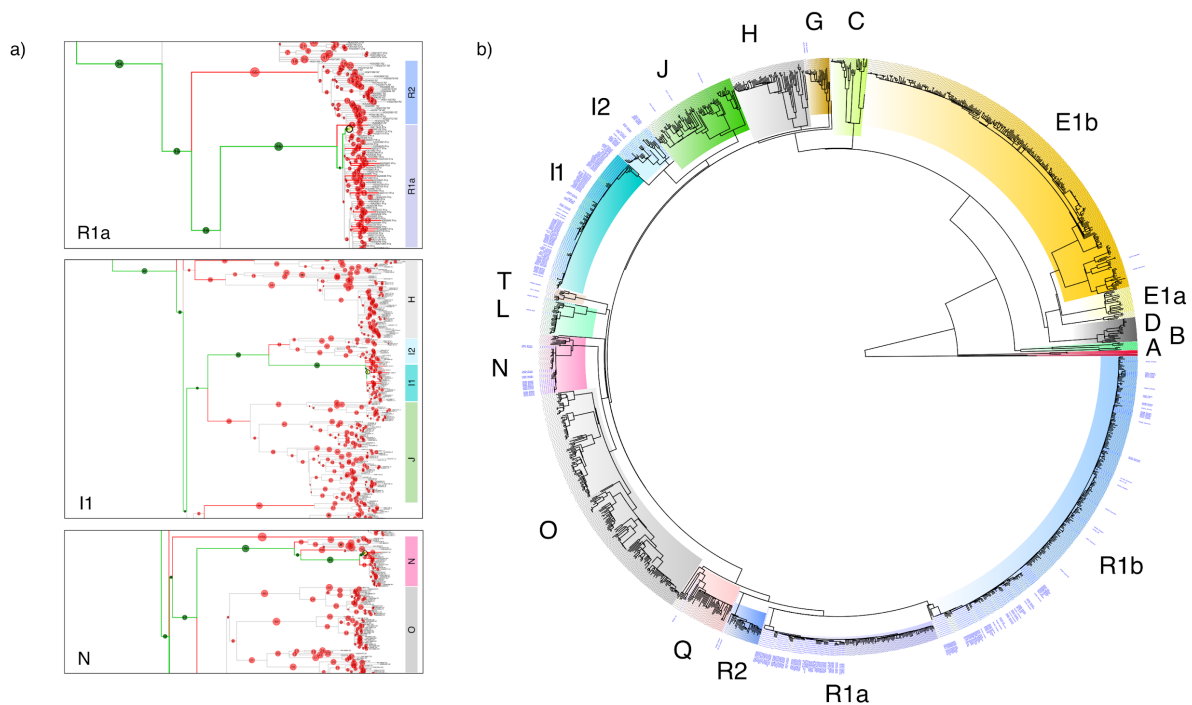


Fig. S3.8: Placing ancient DNA samples within the 1000 Genomes Y-chromosome tree: a) Examples of the identification of the best path within the Y-chromosome tree for 3 representative ancient samples. The phylogeny is traversed and the number of derived (green circles) and ancestral (red circles) markers present in a given ancient sample are evaluated in order to identify the best path (green branches) and position (yellow circle) where this individual can be placed. b) 1000 Genomes Y-chromosome phylogeny with 284 ancient samples (labelled in blue) added to the most likely place of the tree according to the number of derived and ancestral markers carried at each branch.

Supplementary Note 4 - Kinship analysis

4.1. Introduction

Because many of the ancient samples were sampled from the same archaeological sites, it seemed possible that there would be some level of genetic relatedness between certain pairs of individuals across our dataset. To assess to what extent this was the case we used two different methods implemented in the programs NgsRelate¹⁹⁶ and READ¹⁹⁷, which have previously been shown to be relatively robust for low coverage NGS data. Specifically we used NgsRelate to detect family relationships between all pairs of samples and double checked all detected first and second degree relationships with READ.

4.2. Methods

READ (Relationship Estimation from Ancient DNA): Because genetic relatedness analysis can be difficult with low coverage data, we used the program READ, which has been shown to successfully work with ancient NGS data as low as 0.1X sequencing depth for determining up to second degree relationships¹⁹⁷. This method estimates the proportion of non-matching alleles for each pair of individuals and uses the same statistic from unrelated individuals for normalization purposes. Based on the normalised proportions of shared alleles the degree of genetic relatedness between pairs of individuals is assigned as first degree (parent-offspring or siblings), second degree (half-siblings or nephew/niece-uncle/aunt, or grandparent-grandchild), unrelated, or identical. All the sites in the vcf files were assumed as homozygous (by only taking the majority allele for each polymorphic site) and low frequency alleles (<1%) were removed from the resulting plink files with `-maf 0.01`.

NgsRelate: We also used the program NgsRelate to infer relatedness¹⁹⁶. NgsRelate is a maximum-likelihood based program that for a pair of individuals estimates the three coefficients, k_0 , k_1 and k_2 , from genotype likelihoods (GLs) instead of called genotypes and through the GLs it takes into account the uncertainty of the true genotypes, which is inherent to low-depth data. The coefficients, k_0 , k_1 and k_2 , denote the proportions of the genome where the pair of analyzed individuals share 0, 1, and 2 alleles identical by descent, respectively. Importantly, they can be used to infer relatedness, e.g. the expected values for a full sibling pair is $k_0=0.25$, $k_1=0.5$, and $k_2=0.25$, and, in general, the more related a pair of individuals is the lower k_0 is expected to be.

Because it has not been shown that NgsRelate works for sequencing data of ultra-low depth, we only included the 376 samples with sequencing depth above 0.1X in the analyses. From these we estimated GLs and allele frequencies with ANGSD¹⁷⁴ using the SAMtools GL model (`-gl 1`). For this we only used reads with `MapQ>30` and bases with `baseQ>20` and excluded sites where the minor allele frequency across the analysed samples was below 0.05. To minimize potential issues caused by high error rates caused by the samples being ancient, we only estimated GLs and allele frequencies for the autosomal sites where 1000 Genomes CEU population has a minor allele frequency of 0.05 and are not transitions, and we used the minor and major alleles from this CEU population as input to ANGSD (`-doMajorMinor 3`). Across all samples this resulted in a dataset, GLs and allele frequencies, from 1,752,719 sites.

We applied NgsRelate to the dataset and used an accelerated EM algorithm to obtain maximum likelihood estimates (`-m 1`). As a stopping criterion for the EM algorithm, we used a log-likelihood difference of less than 10^{-6} between two consecutive EM-steps (`-t 1e-06`), and set the maximum number of steps to 10000 (`-i 10000`). To be able to assess whether the EM algorithm converged, we

ran ten NgsRelate analyses with different starting seeds. For each pair of samples in the dataset, we used the estimates from the analysis run with the highest likelihood and for all pairs the likelihood difference among the top 5 runs were less than 0.15, suggesting that convergence was reached.

PRIMUS: The pedigree reconstructions based on the kinship coefficients were conducted using PRIMUS - Pedigree Reconstruction and Identification of a Maximum Unrelated Set¹⁹⁸.

4.3. Results

The results of kinship analysis of all pairs based on the NgsRelate analysis are depicted in Figure S4.1 and the estimated relatedness coefficients for pairs estimated to have $k_0 < 0.875$ are listed in Table S4.1. The results for first and second degree relationships obtained by READ were identical with that of NgsRelate.

Pairwise relatedness estimates for samples with >0.1X data

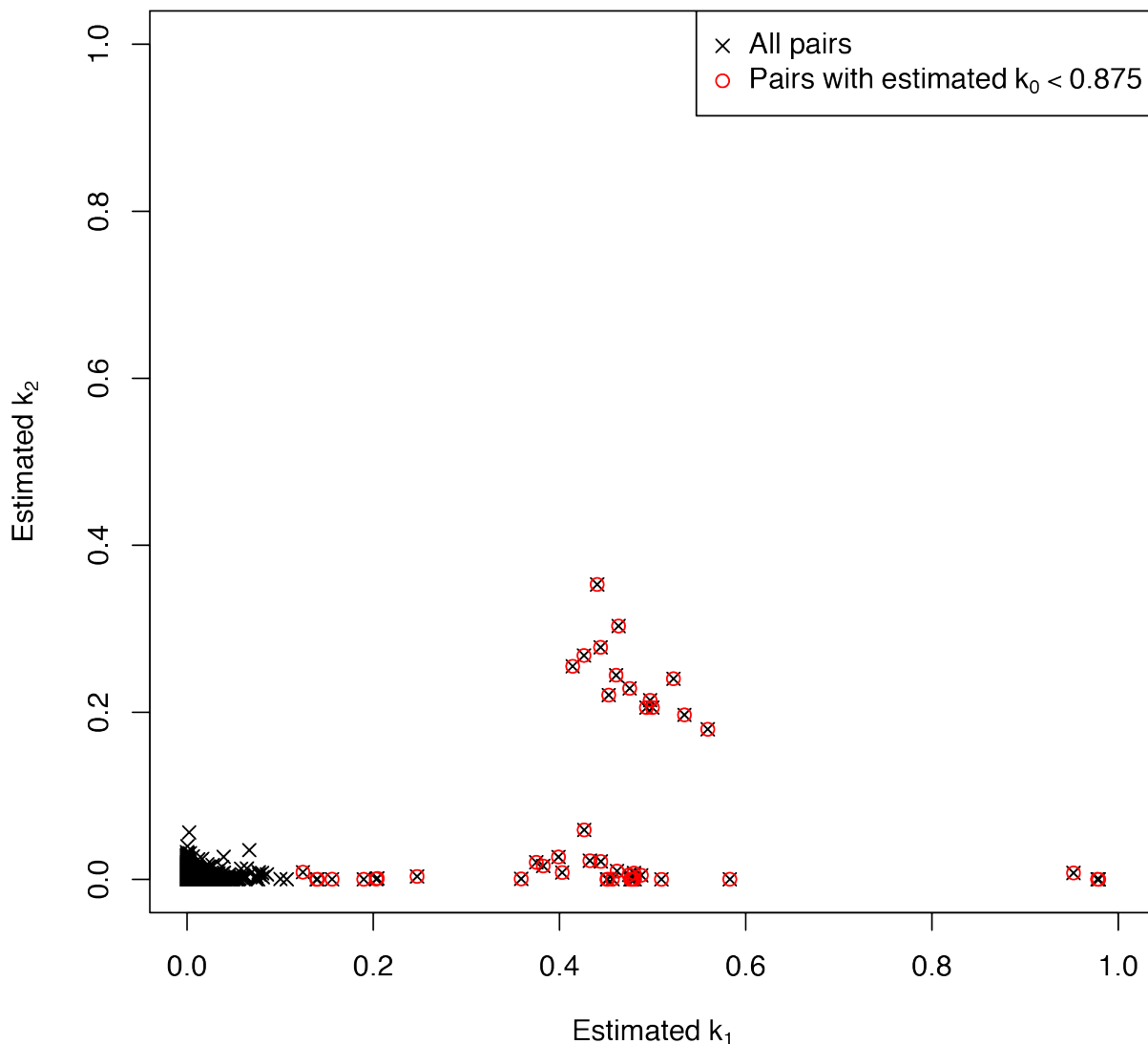


Fig. S4.1: Estimated relatedness coefficients for all pairs of samples with more than 0.1X data. The estimates for each pair is shown with black crosses and the ones with estimated k_0 below 0.875 are marked with a red circle.

These results suggest that a large number of individuals are closely related in our ancient dataset, in particular the individuals from the Faroe Islands, Iceland, and Salme ship burial.

Table S4.1: Estimated relatedness coefficients for pairs of ancient individuals with more than 0.1X data with k_0 below 0.875.

IDs		Origin		Relatedness estimates			
Sample 1	Sample 2	Sample 1	Sample 2	# of sites	k_0	k_1	k_2
VK46	VK245	Faroe Islands	Faroe Islands	1144972	0.491	0.509	0.000
VK46	VK45	Faroe Islands	Faroe Islands	189451	0.574	0.399	0.027
VK154	VK156	Poland	Poland	1023563	0.522	0.478	0.000
VK230	VK110	Iceland	Iceland	1331502	0.306	0.426	0.268
VK230	VK111	Iceland	Iceland	1036610	0.021	0.979	0.000
VK279	VK144	Denmark_Fyn	Oxford	250669	0.528	0.462	0.010
VK25	VK236	Faroe Islands	Faroe Islands	1136739	0.296	0.475	0.229
VK25	VK238	Faroe Islands	Faroe Islands	1117599	0.641	0.359	0.001
VK25	VK234	Faroe Islands	Faroe Islands	791012	0.301	0.493	0.206
VK25	VK242	Faroe Islands	Faroe Islands	702498	0.507	0.488	0.005
VK25	VK44	Faroe Islands	Faroe Islands	567811	0.513	0.480	0.007
VK179	VK183	Greenland	Greenland	640061	0.860	0.140	0.000
VK110	VK111	Iceland	Iceland	962379	0.022	0.978	0.000
VK483	VK497	Salme	Salme	1130328	0.206	0.440	0.353
VK483	VK490	Salme	Salme	942642	0.288	0.497	0.214
VK483	VK485	Salme	Salme	795096	0.261	0.559	0.180
VK237	VK244	Faroe Islands	Faroe Islands	645056	0.867	0.124	0.009
VK539	VK540	Shestovitsa	Shestovitsa	853398	0.331	0.414	0.255
VK497	VK490	Salme	Salme	876836	0.295	0.500	0.206
VK497	VK485	Salme	Salme	739597	0.327	0.453	0.221
VK236	VK238	Faroe Islands	Faroe Islands	1034784	0.549	0.451	0.000
VK236	VK234	Faroe Islands	Faroe Islands	734873	0.269	0.534	0.197
VK236	VK242	Faroe Islands	Faroe Islands	655170	0.602	0.382	0.016

VK236	VK44	Faroe Islands	Faroe Islands	529445	0.543	0.457	0.000
VK342	VK527	Öand	Uppsala	909447	0.861	0.139	0.000
VK342	VK354	Öland	Öland	682763	0.548	0.452	0.000
VK238	VK234	Faroe Islands	Faroe Islands	718915	0.545	0.433	0.022
VK238	VK242	Faroe Islands	Faroe Islands	640593	0.524	0.476	0.000
VK238	VK44	Faroe Islands	Faroe Islands	515690	0.519	0.481	0.000
VK406	VK33	Skara	Skara	805059	0.040	0.952	0.008
VK168	VK167	Oxford	Oxford	746748	0.520	0.475	0.005
VK527	VK517	Uppsala	Uppsala	816579	0.233	0.463	0.303
VK555	VK490	Salme	Salme	770828	0.844	0.156	0.000
VK245	VK240	Faroe Islands	Faroe Islands	636199	0.534	0.444	0.021
VK245	VK45	Faroe Islands	Faroe Islands	132706	0.278	0.444	0.278
VK157	VK155	Poland	Poland	248596	0.237	0.522	0.240
VK490	VK485	Salme	Salme	619501	0.295	0.461	0.244
VK187	VK183	Greenland	Greenland	460045	0.797	0.203	0.000
VK241	VK244	Faroe Islands	Faroe Islands	436861	0.749	0.247	0.003
VK240	VK45	Faroe Islands	Faroe Islands	107208	0.514	0.426	0.059
VK234	VK242	Faroe Islands	Faroe Islands	454640	0.605	0.375	0.020
VK234	VK44	Faroe Islands	Faroe Islands	367567	0.523	0.476	0.000
VK19	VK408	Ladoga	Ladoga	141229	0.417	0.583	0.000
VK242	VK44	Faroe Islands	Faroe Islands	329339	0.589	0.403	0.008

In the Salme II ship burial, four male siblings , i.e. brothers, were discovered (VK483, VK485, VK490, VK497; Figure S4.2a), which was additionally supported by the identical mtDNA and Y chromosome profiles (Supplementary Table 5). It is worth mentioning here that the slight differences in Y chromosomal haplogroup assignments in this case are likely due to the presence of ancient DNA damaged sites or insufficient genomic coverage. As one would expect, the four brothers were buried relatively close to each other in the same layer of the Salme II ship burial.

In Iceland, we identified a female individual (VK111) with her two children (one male VK110 and one female VK230, Figure S4.2b).

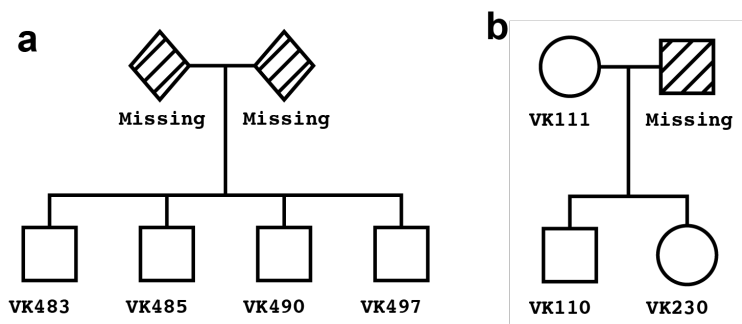
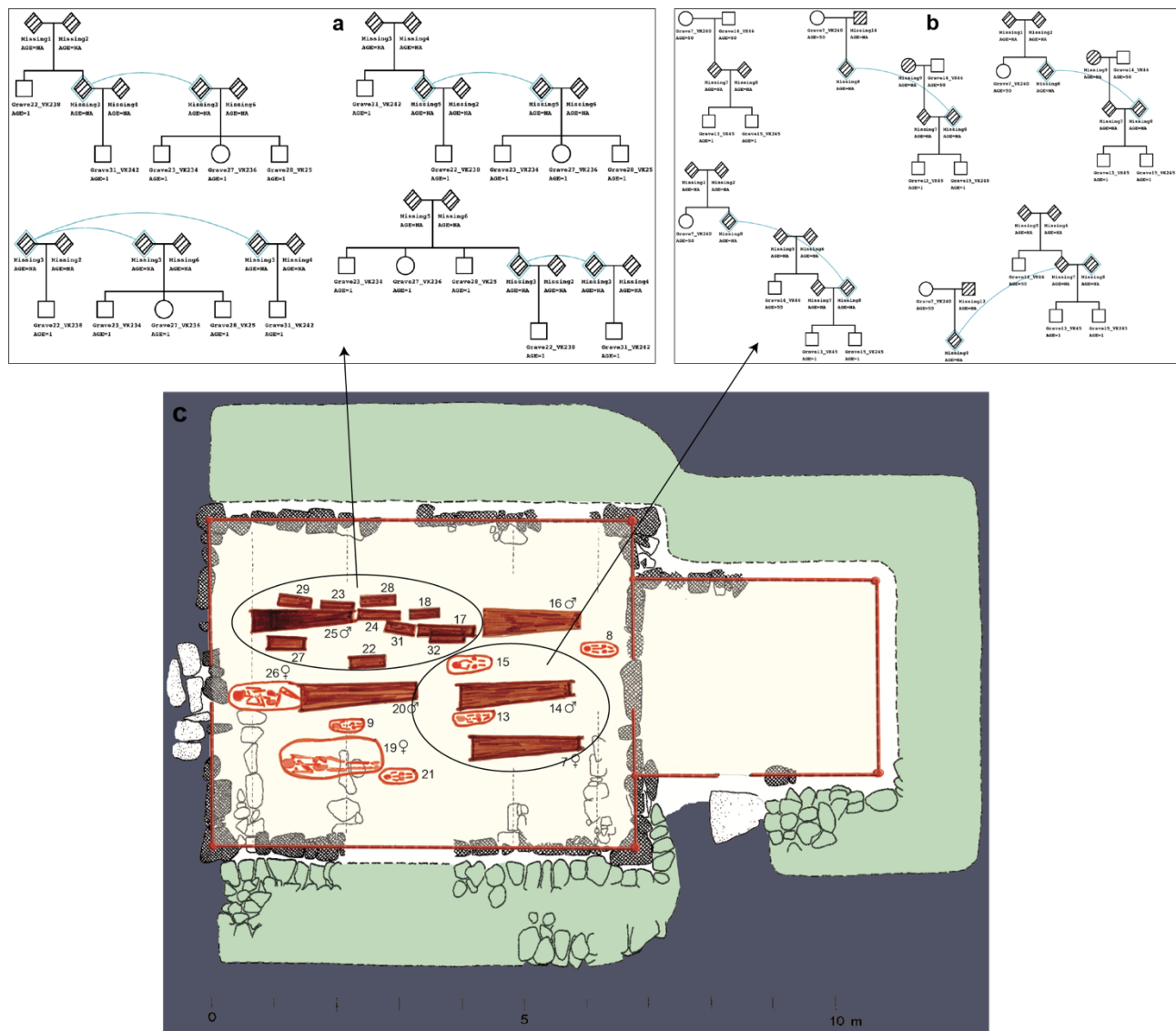


Fig. S4.2: Genealogy networks for individuals from Salme (a) and Iceland (b).

The largest number of related individuals were identified in Faroe Islands. Three family groups were identified in the Church burial in Faroe Islands, but only two groups are analysed here due to the relative closeness of family members within the two groups. Even though we could not see a significant degree of relationship between the groups, we cannot exclude the genetic ties between these groups due to missing individuals in our dataset. The first family included five infants—grave22 (VK238), grave31 (VK242), grave23 (VK234), grave27 (VK236) and grave28 (VK25). The possible four pedigree networks are shown in Figure S4.3a. The second family included four related individuals (Figure S4.3b). The most parsimonious network likely reflects the true genetic relationship among the individuals also considering the grave locations in the churchyard, i.e. two infants in graves 13 (VK45) and 15 (VK245) buried close to their (likely) grandparents in graves 7 (VK240) and 14 (VK46).

Fig. S4.3: Kinship analysis of ancient samples from Sandur Church 2 site in Faroe Islands.



a, Reconstruction of four most likely pedigree networks for one (Family-1) of the three families in Sandur Church 2 site in Faroe Islands. **b**, Five most likely pedigree networks for the Family-2: the most parsimonious network (top left) is likely to represent the true family relationship between the individuals (i.e. grandparents and grandsons) based on the burial pattern of the graves as shown at the bottom image (c). Ages of the individuals are approximate to help pedigree reconstructions. Blue diamond shapes and lines in each possible pedigree reconstruction represent the same individual.

Intriguingly, we identified several additional pairs of kin among the other Viking genomes. One is a pair of 2nd degree male relatives (i.e. half-brothers, nephew-uncle, or grandson-grandfather) from two locations separated by the North Sea: one of the samples (VK279) was excavated in Denmark (Galgedil site on Funen; this cemetery was also analyzed for strontium with a group of non-locals there), while the other individual (VK144) was found in the UK (Oxford site). Another pair of individuals with 3rd or 4th degree relatedness (e.g. cousins) was discovered in Sweden, namely a male sample excavated on the island of Öland (VK342) and a female individual from Skämsta, Uppsala (VK527), some 300-400 km apart.

Interestingly, in our dataset we also identified VK527's brother in Uppsala (VK517). Based on the anthropological analysis both siblings displayed a rare genetic disorder of abnormal skeletal development: spondyloepiphyseal dysplasia. Given the very low frequency of this disorder, the close family ties between these individuals were expected by the archaeologists¹⁹⁹. These long-distance relationships in our dataset underscore the degree of individual-level mobility during the Viking era.

Supplementary Note 5 - Imputation

Genotype imputations were conducted for 298 ancient samples (289 from this study plus nine from the study by Krzewińska et al.³⁵) that had a sequencing depth greater than 0.5X. Because these ancient samples were sequenced at low depth of coverage, we used Beagle v4.1²⁰⁰ for imputations based on the genotype likelihood data, which was first estimated by GATK v3.7.0 UnifiedGenotyper. To generate the genotype data we only called biallelic sites present in the 1000G dataset and only the observed alleles (--genotyping_mode GENOTYPE_GIVEN_ALLELES). The resulting VCF files were filtered by setting genotype likelihoods to 0 for all three genotypes (e.g. hom ref, het, and hom alt) for sites with potential deamination (C>T and G>A) as described by Martiniano et al.²⁰¹. Following this, the per-individual vcfs were merged using bcftools-v1.3.1. The combined VCF were then split into 15,000 markers each and imputed separately using beagle-4.0 using the 1000G phase3 map included with beagle (*.phase3.v5a.snps.vcf.gz and plink.chr*.GRCh37.map) with input through the genotype likelihood option. Run time for imputing using beagle was approximately 280,000 core hours.

Supplementary Note 6 - Merge with existing panels

To assess the genetic relationship between the ancient Viking samples and other populations (both modern and ancient) we merged the whole-genome shotgun data of the Vikings with two different SNP array datasets of modern worldwide and ancient populations. Because most ancient samples from this study were low coverage, to obtain the genotypes of the ancient samples (mostly VA) the ‘samtools mpileup’ command was used followed by a single read sampling of the majority allele for each of the sites present in the relevant reference dataset, with mapping and base quality ≥ 30 .

6.1. Scandinavian panel - SNP array of European populations enriched for Scandinavians

A new reference panel was constructed based on three published datasets for which we conducted quality control (QC) analysis: the EGAD00010000632 dataset from Leslie et al.²⁰² (UK dataset), the EGAD00010000124 dataset from Genetic Analysis of Psoriasis Consortium & the Wellcome Trust Case Control Consortium 2²⁰³ (IRE dataset), and the EGAD00000000120 dataset from The International Multiple Sclerosis Genetics Consortium & The Wellcome Trust Case Control Consortium 2²⁰⁴ (EU dataset). The UK dataset was genotyped on the Human1-2M-DuoCustom SNPchip and contained 1,115,428 sites and 2,912 individuals. The IRE and EU datasets were genotyped on the Human670-QuadCustom SNPchip with 580,030 sites and included 2,622 and 11,376 individuals, respectively. The UK dataset consist of only UK individuals, the IRE dataset has both UK and Irish individuals, and the EU dataset contains individuals from Australia, Belgium, Denmark, Finland, France, Germany, Italy, New Zealand, Norway, Poland, Spain, Sweden, the UK, and the US.

The datasets were converted from their original genotype (.gen) file format to binary plink files using GTOOL and plink²⁰⁵, the GTOOL default cut-off of 0.9 for genotype probabilities was used, this included all autosomal + the X and Y chromosomes. The datasets included a list of both SNPs and individuals that passed QC which we used, leaving 870,170 markers and 2,578 individuals for the UK dataset, 535,475 markers and 2,178 individuals for the IRE dataset and 475,806 markers and 10,299 individuals for the EU dataset.

All the datasets were checked to be on the TOP strand as specified by the SNPchip manifest. Then the datasets were put on the plus strand using plink and strand files (detailing for each SNPchip which strand TOP refers to for each individual site, from: <http://www.well.ox.ac.uk/~wrayner/strand/>). Then using liftOver²⁰⁶ the datasets were lifted from hg18 to hg19. Sites that deviated from Hardy-Weinberg equilibrium were filtered away, using a cutoff P-value of 1×10^{-6} . The three datasets were then merged, and sites where none of the alleles agreed with the hg19 reference sequence were removed along with duplicated sites, based on genomic position. Non-autosomal sites were removed. SNPs in the MHC/HLA region on chromosome 6 were removed, due to the fact that it is hard to map to this region because of the high degree of recombination and the observed big differences in frequencies between the datasets for markers in this region. In the end, we only kept the seven most relevant populations for this study from Denmark, Sweden, Norway, Finnland, Poland, UK, and Italy with a total number of 414,264 SNPs. The obvious outliers from each group were removed if their outgroup- f_3 statistics estimates were different from the population mean ($Z > 3$), resulting in 1464 individuals. The CHB (Han Chinese) and YRI (Yoruba) populations from the 1000 Genomes project phase 3 database were merged to this panel as outgroups.

6.2. Human Origins panel - Affymetrix Human Origins SNP array panel of worldwide populations

This dataset of modern individuals consists of 2180 individuals from 213 worldwide populations^{207,208}. We extracted autosomal genotypes at a subset of 593,102 SNPs that were also included in the ‘1240K’ capture panel²⁰⁹.

6.3. 1000 Genomes panel

We used a set of 1,995 individuals from 20 populations (excluding individuals from the AMR super-population as well as admixed ASW and ACB populations) of the 1000 Genomes project phase 3 release 5 (<ftp.1000genomes.ebi.ac.uk/vol1/ftp/release/20130502/>). We restricted the dataset to a set of 12,731,663 biallelic transversion SNPs located within the ‘strict’ mappability mask regions (ftp.1000genomes.ebi.ac.uk/vol1/ftp/release/20130502/supporting/accessible_genome_masks/).

Analyses of phenotype associated SNPs were carried out using five European-ancestry populations (IBS/Spanish; TSI/Tuscan; CEU/Utah Residents with northern and western European ancestry; GBR/British; FIN/Finnish) along with CHB (Han Chinese) and YRI (Yoruba) as outliers. These were used to assess genome-wide allele frequencies for various SNPs associated with pigmentation phenotypes and lactose intolerance.

6.4. Ancient panels

We constructed datasets for population genetic analyses by merging the newly sequenced VA individuals as well as other previously published ancient individuals^{20,162,163,189,192,193,201,209–231} with the two modern reference panels described above. Ancient individuals were represented with ‘pseudo-haploid’ genotypes, obtained by randomly sampling an allele passing filters (mapping quality ≥ 30 and base quality ≥ 30), further requiring that it matched one of the two alleles observed in the reference panel (Supplementary Table 3). For high coverage ancient and modern individuals, we used diploid genotypes obtained using samtools / bcftools as previously described.

Supplementary Note 7 - Latent ancestry modelling

Based on the pseudohaploid individuals from the ‘ancient panels’ and ‘Human Origins panel’ (see Supplementary Note 6) we ran ADMIXTURE²³² by thinning the dataset for linkage disequilibrium using plink with recommended settings (--indep-pairwise 50 10 0.1). This dataset contained 1324 samples for 151,235 markers for the autosomal chromosomes. Only samples with >20,000 SNPs overlapping with the ‘Human Origins panel’ were kept in the analysis, resulting in 378 samples from this study. We did 50 replicates with different seeds for $k=2$ to $k=10$. For each replicate, we calculated the cross-validation error using the --cv option of ADMIXTURE. The distribution is shown as boxplots in Figure S7.1. We used pong²³³ to identify the best run for each K and similar components between different K s. Due to increasing cross-validation error estimates we have limited the admixture plot up to $K=5$ (Figure S7.2). In the Extended Data Fig. 2 we chose the 567 most relevant individuals representing 71 different populations and visualized this for $K=2$ to $K=5$.

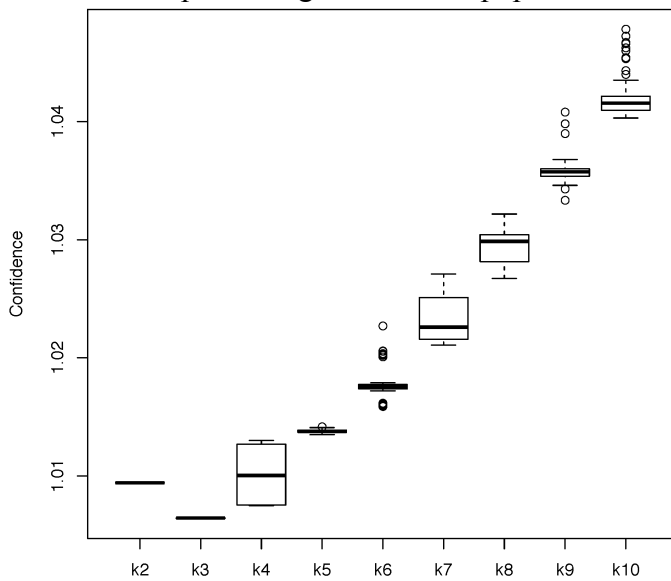


Fig. S7.1: Boxplots of the cross-validation error for our dataset with 1324 individuals and 151,235 markers. The actual cross validation was done with 50 replicates using the --cv option of admixture runs for $K=2$ to $K=20$ with different seed values.

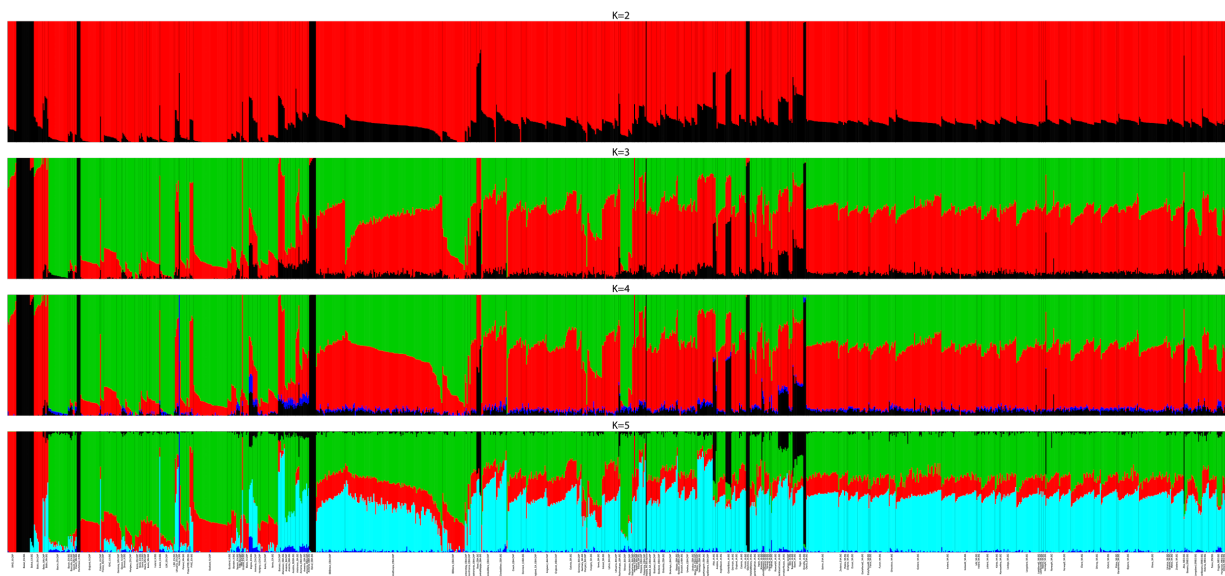


Fig. S7.2: Model-based clustering analysis of 1324 individuals: K=2 to K=5. This dataset includes 946 published and 378 ancient samples from this study (mostly VA). See the Extended Data Fig. 2 for a subset of most relevant populations from this dataset.

Supplementary Note 8 - Genetic clustering

The large number of ancient individuals included in the analysis panels facilitates genetic clustering using the ancient individuals themselves, rather than projecting them on axes of variation inferred from modern populations. We carried this out using multi-dimensional scaling (MDS) on a distance matrix obtained from pairwise identity-by-state (IBS) sharing between individuals.

8.1. Batch effects

Genetic clustering using genetic similarity among the ancient individuals themselves provides a more accurate picture of their genetic differentiation than projecting them on axes of variation inferred from modern populations. However, a potential pitfall of this approach is that it is more susceptible to biases due to batch effects between sets of individuals, e.g. those with differences in sample processing. The dataset used in this study includes large numbers of individuals, compiled from heterogenous sample origins (e.g. shotgun sequencing vs in-solution capture), both of which are expected to exaggerate this potential issue.

To investigate this issue, we first assessed dimensions inferred from genetic clustering of 1,265 ancient western Eurasians using multi-dimensional scaling (MDS) on a pairwise identity-by-state (IBS) sharing matrix. While the first two dimensions differentiate samples with respect to their genetic ancestry, we observe a possible batch effect separating capture and shotgun samples along dimension 3 (Figs. S8.1 and S8.2).

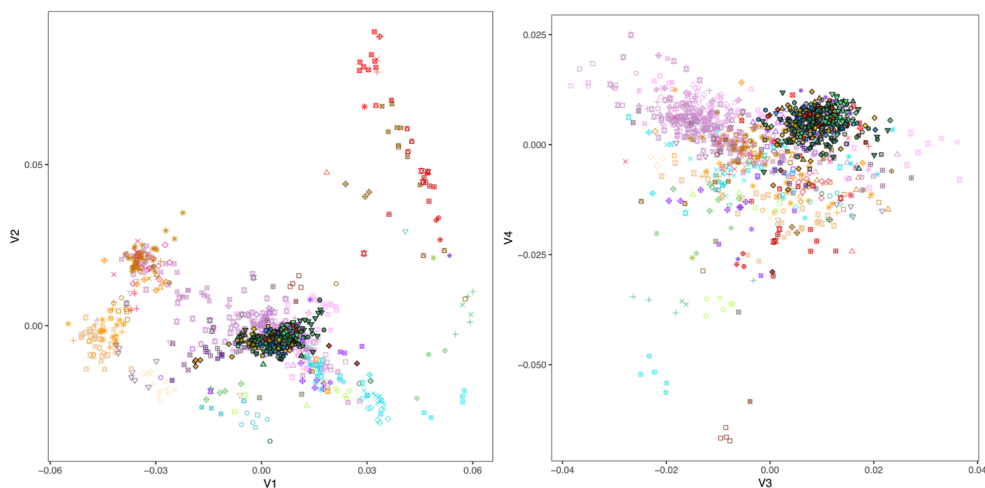


Fig. S8.1: MDS on 1,265 ancient western Eurasian individuals, showing dimensions 1 and 2 (left) and 3 and 4 (right). Plot symbols indicate population grouping as used throughout the study.

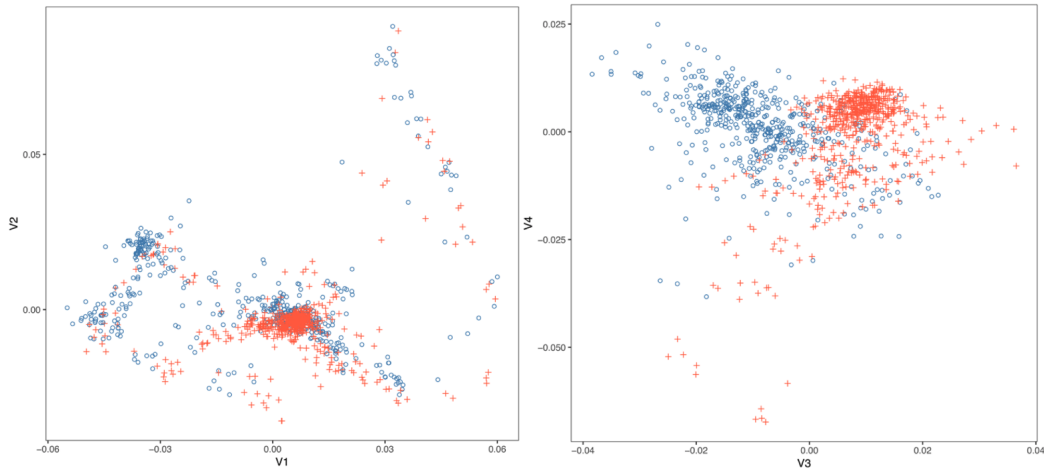


Fig. S8.2: MDS as in Fig. S8.1, but with plot symbols indicating samples processing using shotgun sequencing (red crosses) or in-solution capture (blue circles).

To further investigate, we included data from a total of 36 previously published individuals which were generated using both shotgun and capture approaches. We then carried out principal component analysis (PCA) on different subsets of individuals and investigated the loadings of each SNP along the inferred components, using the algorithms implemented in the GCTA package²³⁴. Performing PCA on the full dataset of 1,265 individuals as well as the shotgun/capture paired individuals recovers structure that closely resembles the MDS results (Fig. S8.3).

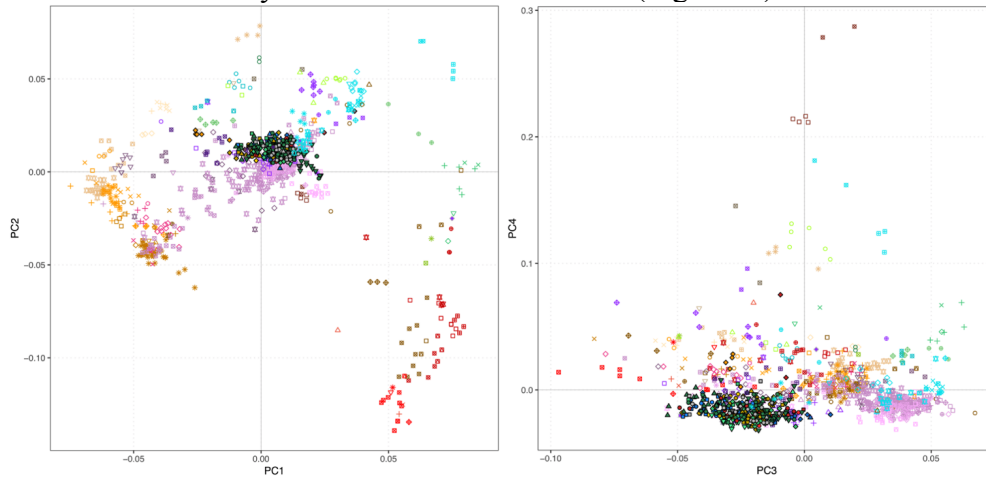


Fig. S8.3: PCA on 1,265 ancient western Eurasian individuals and shotgun/capture pairs, showing dimensions 1 and 2 (left) and 3 and 4 (right).

We confirmed batch effects using the shotgun/capture pairs, which showed clear and consistent separation along PC3 as well as a subtler effect along PC2 (Fig. S8.4).

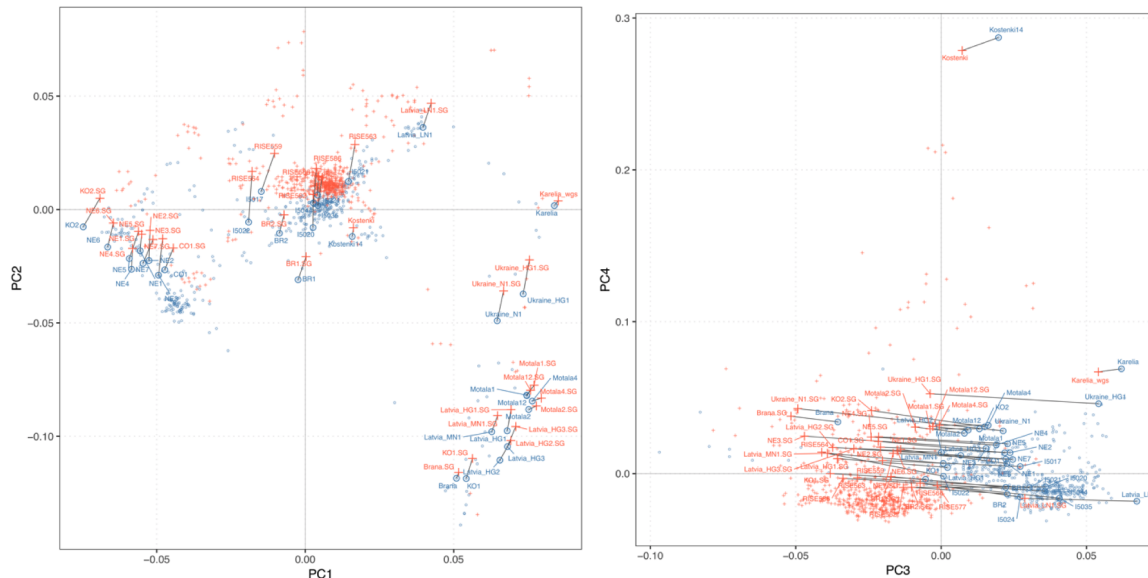


Fig. S8.4: PCA as in Fig. S8.3, but with plot symbols indicating sample processing using shotgun sequencing (red crosses) or in-solution capture (blue circles). Pairs of individuals with data from both approaches are joined with black lines and indicated by sample name.

However, inspection of the distribution of SNPs with high loadings along PC3 revealed a more complex pattern, with batch effects appearing to be confounded with a biological effect due to SNPs within genomic regions previously reported to show evidence for recent positive selection in West Eurasians ²⁰⁹ (Fig. S8.5).

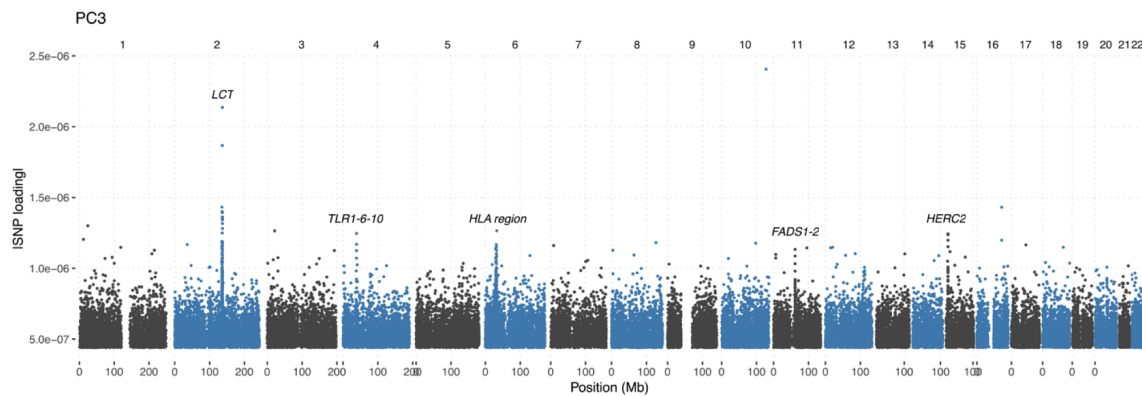


Fig. S8.5: Manhattan plot of SNP loadings along PC3. Peaks of high SNP loadings overlapping genes previously reported as targets of recent positive selection in western Eurasians are indicated.

The observed confounding is not entirely surprising as the investigated ancestry and age groups are not evenly distributed across the two sample processing groups. The bulk of the shotgun data originates from VA and later individuals from northern Europe, in contrast to a large fraction of earlier Bronze Age individuals from western and southern Europe in the capture data. We therefore repeated the PCA analysis on a subset excluding any Iron Age or later individuals. Similar to the analysis with all individuals, we find evidence for shotgun/capture batch effects along PC3, but without strong effects of individual gene regions under selection as seen before (Fig. S8.6, S8.7)

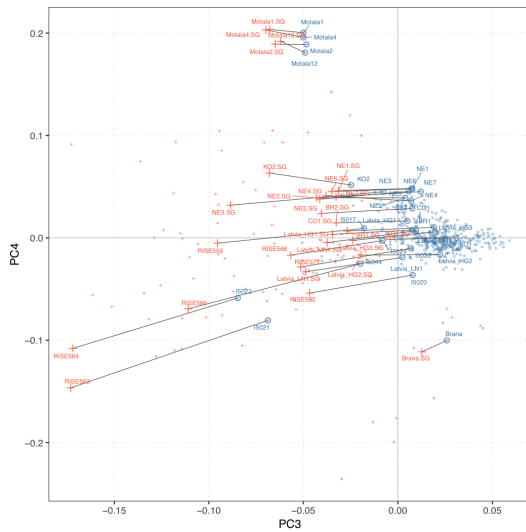


Fig. S8.6: PCA on a subset of $n=585$ pre-Iron Age individuals, with plot symbols indicating samples processing using shotgun sequencing (red crosses) or in-solution capture (blue circles). Pairs of individuals with data from both approaches are joined with black lines and indicated by sample name.

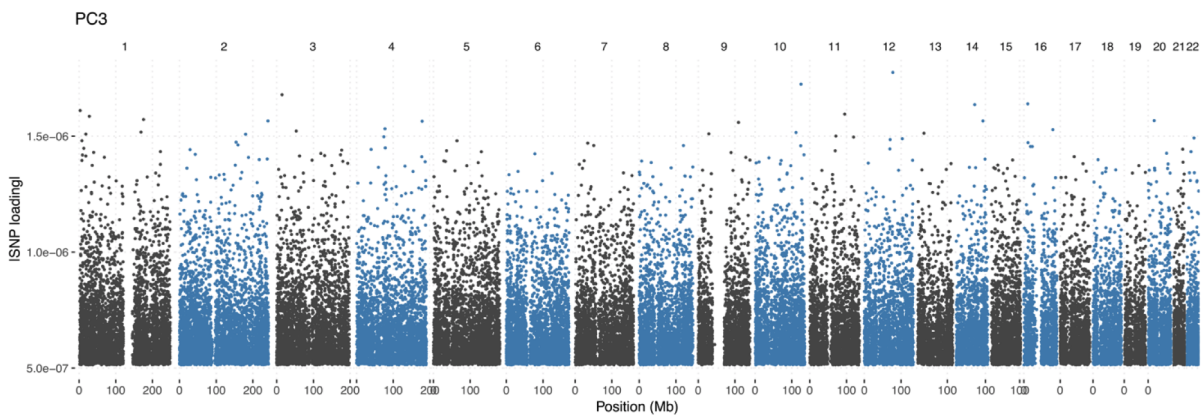


Fig. S8.7: Manhattan plot of SNP loadings along PC3 for a subset of $n=585$ pre-Iron Age individuals.

Based on these results, we tested two subsets of SNPs for batch effect removal. For each of the PCA analyses above (Fig. S8.6. and Fig. S8.8), we identified the subset of SNPs with the highest loadings along PC3 (absolute value > 1 standard deviation from the mean), and removed those from the dataset. Results for PCA on the full set of individuals using the two SNP subsets are shown in Fig. S8.8.

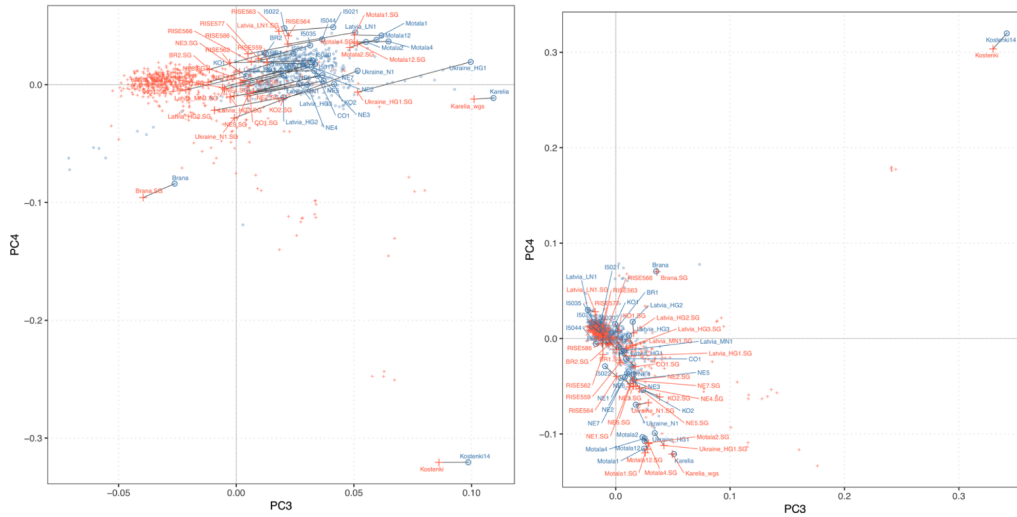


Fig. S8.8: Biplot of PC3 and PC4 from a PCA on all $n=1,265$ individuals, using two different subsets of SNPs for batch effect correction: SNPs with high loadings in pre-Iron Age individual dataset (left) or in the full dataset (right).

We found that batch effects were reduced but still visible along PC3 removing the SNPs identified using the pre-Iron Age individuals (Fig. S8.8 left), whereas they were removed from PC3 and PC4 when excluding the set of SNPs identified in the full set (Fig. S8.8. left). Investigating the loadings along PC3 in the pre-Iron Age corrected SNP set revealed that effects of genomic regions under selection were still present and even amplified compared to the full set of SNPs (Fig. S8.9).

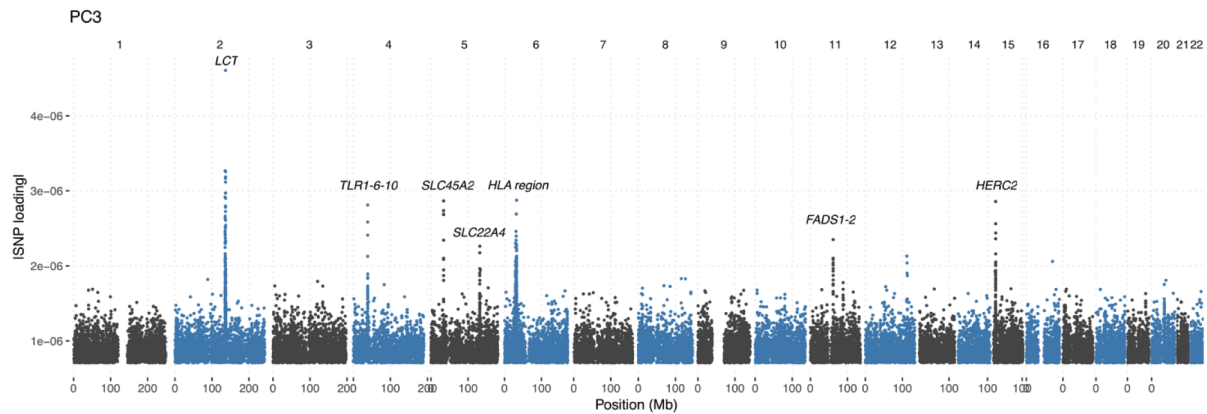


Fig. S8.9: Manhattan plot of SNP loadings along PC3 for the full set of $n=1,265$ individuals, using batch correction by removing SNPs identified in the pre-Iron Age individuals.

In summary, we found that both differences in sample processing and genuine biological differences due to regions affected by recent positive selection impacted genetic affinities between individuals in subtle and complex ways. The larger sample sizes available of western Eurasians from the Bronze Age onwards, combined with their greater genetic homogeneity compared to earlier individuals, facilitated the detection of these previously hidden effects. As neither of the two effects is desirable in analyses of population history, we restricted all analyses of population history that use both shotgun

and capture individuals to the subset of SNPs identified using the full dataset (i.e. all outliers in Figure S8.5).

8.2. Clustering analysis

We performed the main genetic clustering on a set of 1,305 ancient Eurasian individuals with >50,000 SNPs with genotype data, restricting to the batch-corrected SNP set described above. Results from the batch-corrected MDS were combined with further dimensionality reduction using uniform manifold approximation and projection (UMAP), an approach that has recently been shown to effectively visualize population structure among individuals across multiple scales²³⁵. We explored the influence of three parameters on the resulting projection:

- The number of dimensions to retain from the initial MDS.
- UMAP hyperparameter ‘n_neighbors’, which controls the balance between preserving local or global structure.
- UMAP hyperparameter ‘min_dist’, which controls how tightly points are packed in the projection.

Figures S8.10-S8.13 provide examples of the resulting projections for combinations of the two hyperparameters across three different input matrices. We found that all parameter settings yielded qualitatively similar clustering, the major differences being more isolated smaller clusters observed at low values for ‘n_neighbors’ and ‘min_dist’. The parameter combination for the results presented in Figure 2 and Extended Data Figure 3 (eight MDS dimensions, n_neighbors = 5, min_dist = 0.4) were chosen with the aim to reveal fine-scale local structure while preserving the global relationship among the major ancestry clusters in the dataset. Genetic structure not evident from the first two dimensions of the MDS is easily recognizable in this projection—for example among different groups of Neolithic individuals or among Bronze Age and Iron Age groups from the Baltic region (Fig 2b, Extended Data Fig. 3).

Overall, we found that the majority of our samples broadly clustered within the range of other European Bronze Age (BA) and Iron Age (IA) populations, characterized by an ancestry component that is related to pastoralist populations from the Pontic-Caspian steppe (Fig. 2a, Extended Data Fig. 2 and 3) entering Europe around 3000 BCE^{163,192}. The UMAP analysis revealed additional structure among the VA individuals, distributed within a broad area anchored by three ancestry clusters: Pre-Neolithic European hunter-gatherers (Fig. 2b, top right); Neolithic farmers from Anatolia and Europe (Fig. 2b, bottom right); and early BA Steppe pastoralists (Fig. 2b, left).

We also identify some clear outliers: A late Neolithic / early BA individual from northern Norway who clusters with pre-Neolithic hunter-gatherers from Norway (VK531); an individual with East Asian-related ancestry who groups with ancient Saami individuals from Finland (VK518); and four medieval individuals from Foggia in southern Italy with affinities to BA Mycenaean individuals from Greece (Fig. 2 and Extended Data Fig. 3).

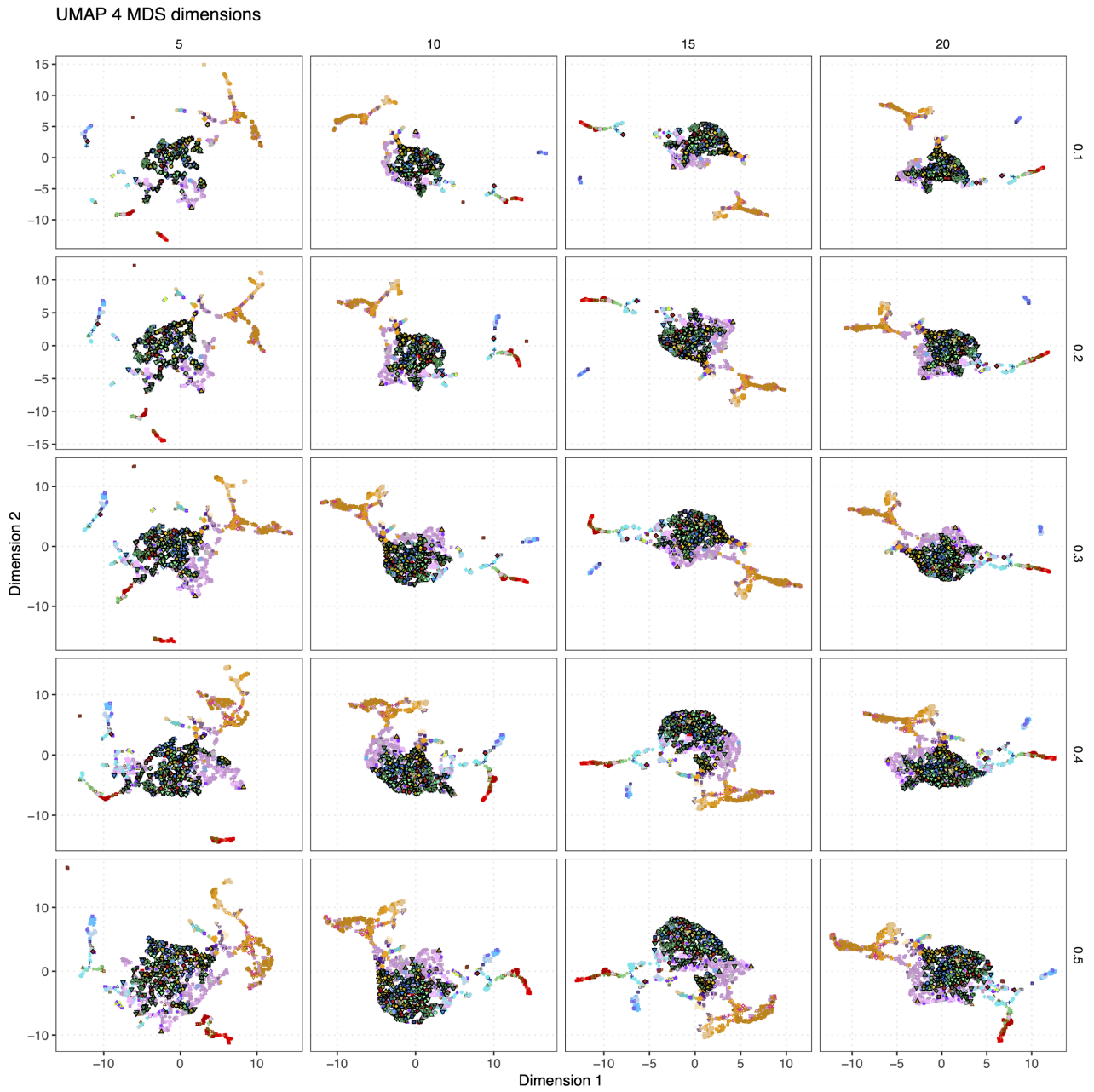


Fig. S8.10: Effect of hyperparameters on genetic clustering of $n=1,305$ ancient genomes using IBS-UMAP. Panels show clustering results for combinations of hyperparameters 'n_neighbors' (columns) and 'min_dist' (rows), using the first four MDS dimensions as input matrix.

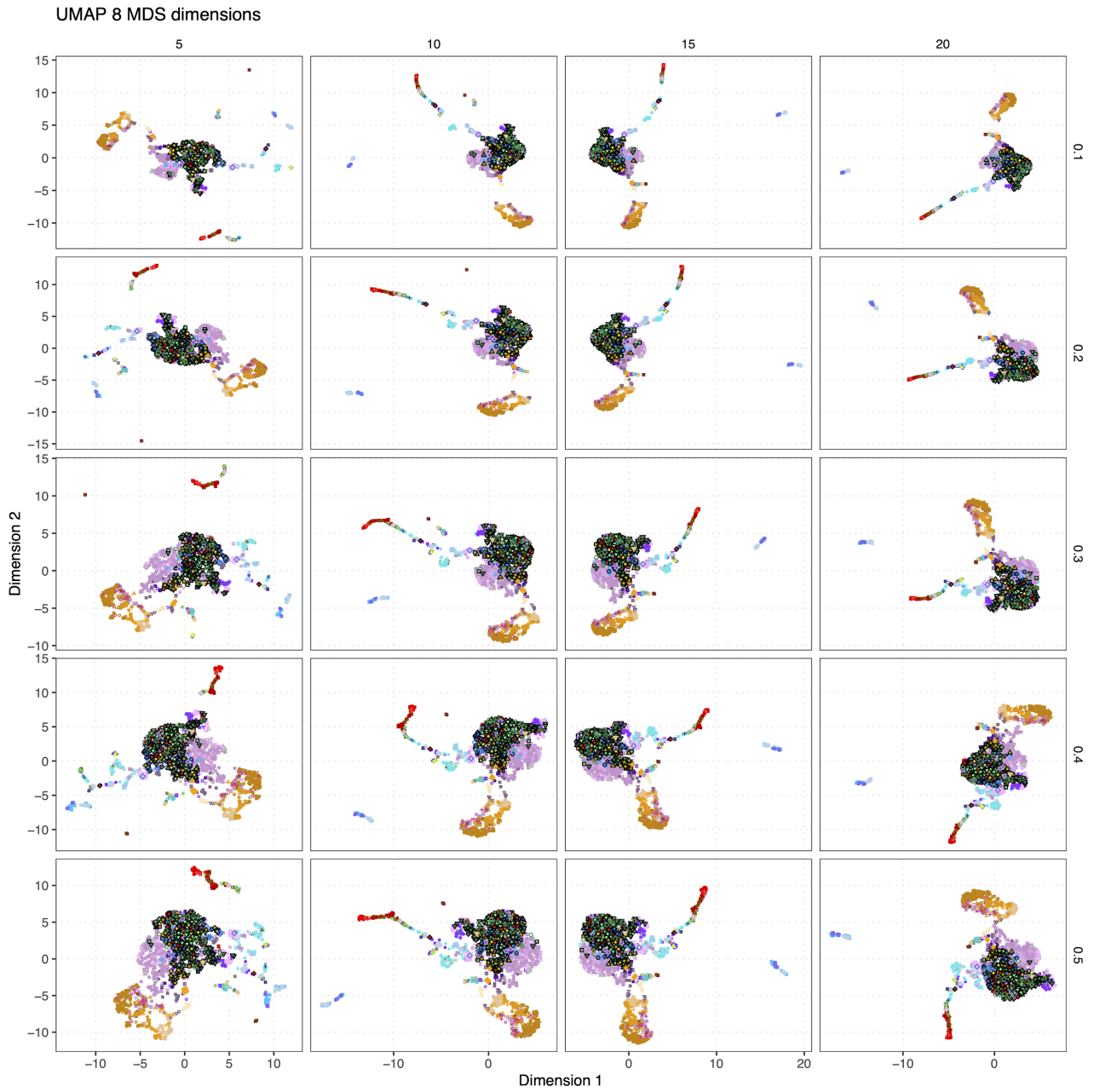


Fig. S8.11: Effect of hyperparameters on genetic clustering of $n=1,305$ ancient genomes using IBS-UMAP. Panels show clustering results for combinations of hyperparameters 'n_neighbors' (columns) and 'min_dist' (rows), using the first eight MDS dimensions as input matrix.

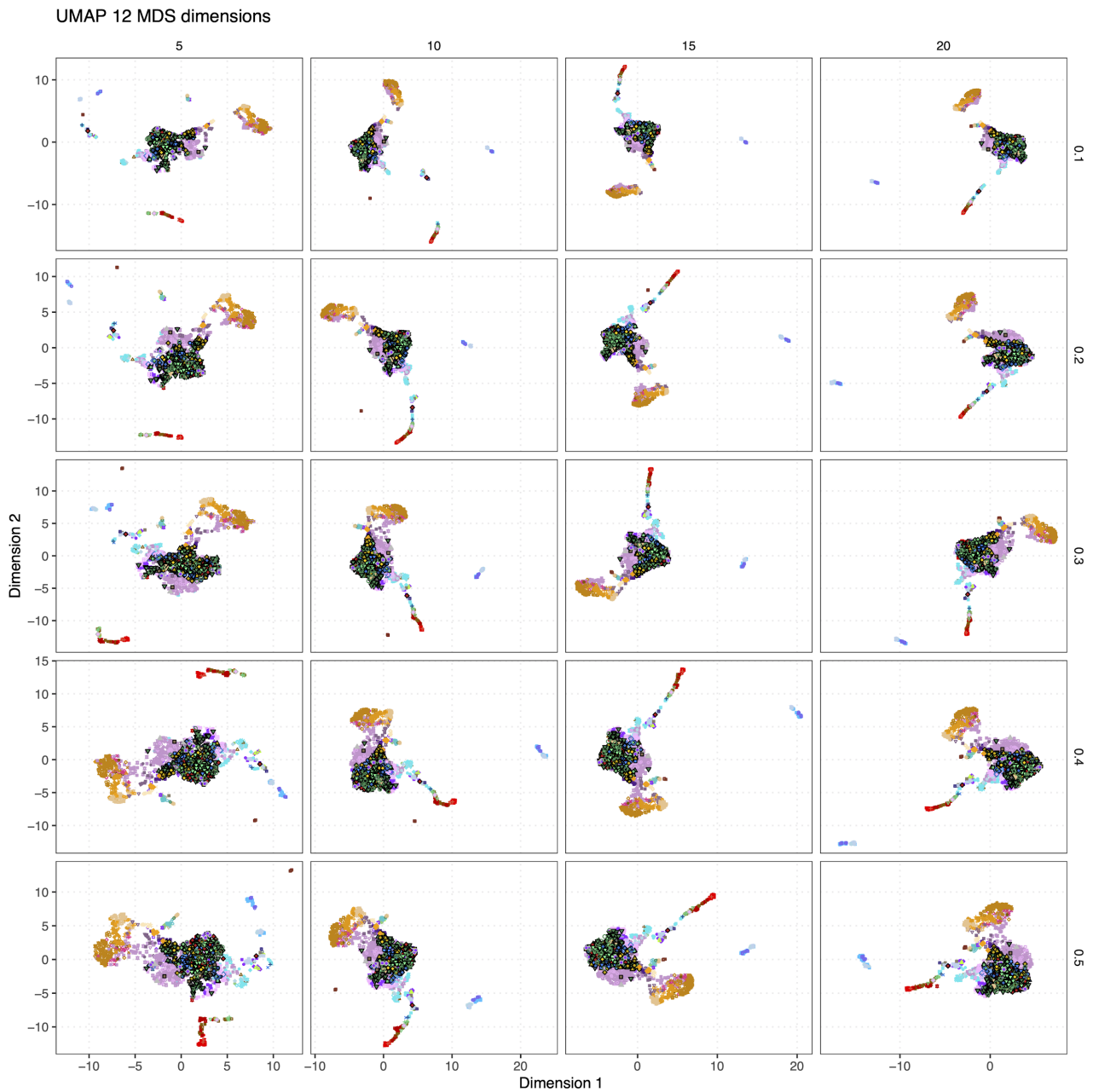


Fig. S8.12: Effect of hyperparameters on genetic clustering of $n=1,305$ ancient genomes using IBS-UMAP. Panels show clustering results for combinations of hyperparameters ‘n_neighbors’ (columns) and ‘min_dist’ (rows), using the first twelve MDS dimensions as input matrix.

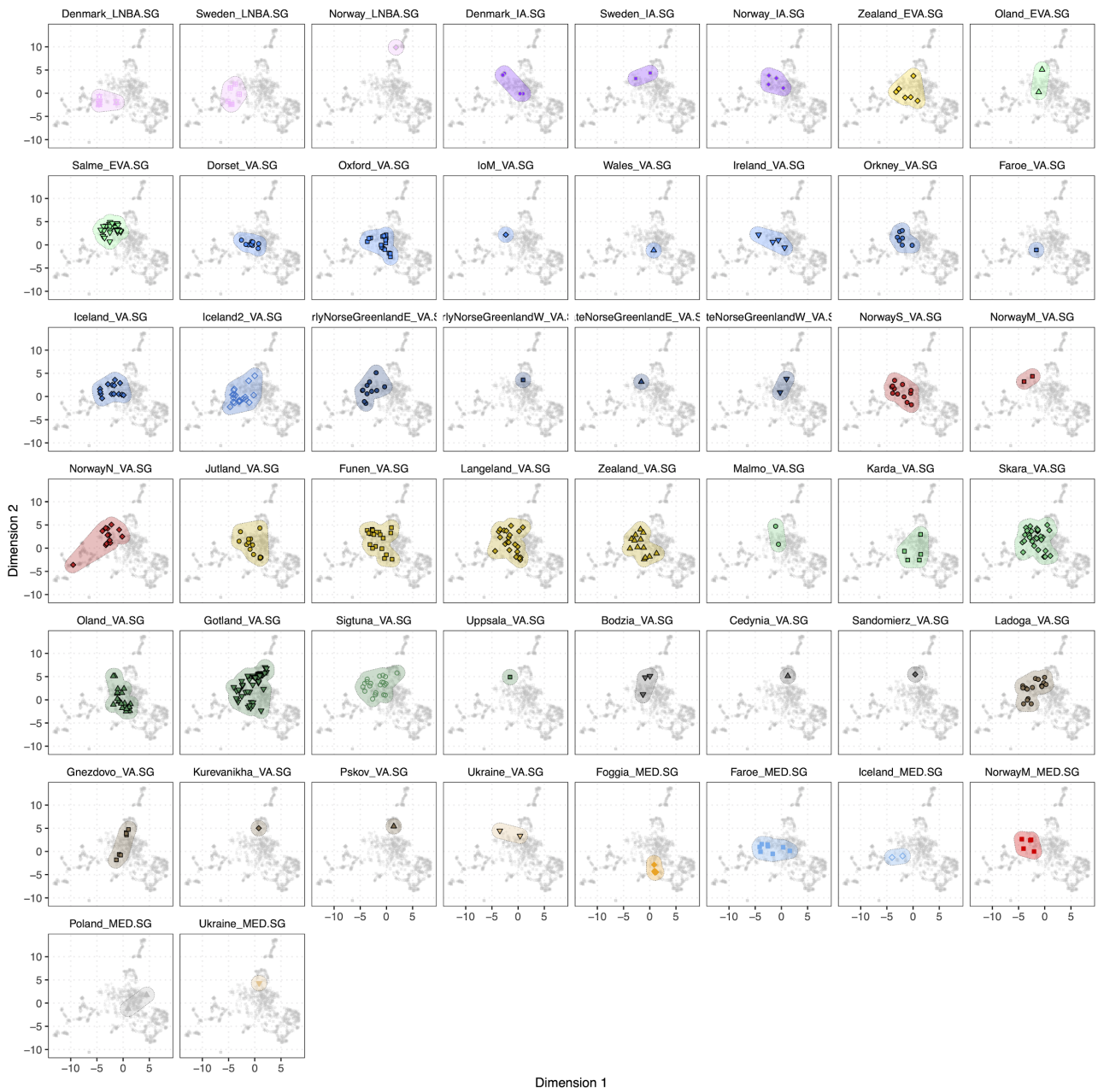


Fig. S8.13: Genetic clustering of $n=1,305$ study individuals using IBS-UMAP. Each panel highlights the position of individuals from indicated groups over the full set of individuals. UMAP was carried out on the first eight MDS dimensions, using hyperparameters $n_neighbors=5$ and $min_dist=0.4$

Supplementary Note 9 – Population genetics

9.1. Individual-level allele sharing

We used f_4 statistics to investigate allele sharing between sets of test individuals and different modern and ancient groups. To characterize the deep ancestry relationship of the study individuals we calculated f_4 (YRI, Test individual; Barcin_EN.SG, Yamnaya_EBA.SG) for all ancient Europeans from the BA onwards (1000 Genomes panel merge; Extended Data Fig. 4a; Supplementary Table 7). This statistic contrasts genetic affinities of the test individuals with two major ancestry groups contributing to the gene pool of ancient Europeans from the Bronze Age onwards: Anatolian farmers and Steppe pastoralists. Genetic continuity with Scandinavian Iron Age groups was investigated using f_4 (YRI, Test group; Test individual, Scandinavia IA group) (1000 Genomes panel merge). This statistic measures whether a test individual is consistent with forming a clade with Scandinavian IA groups to the exclusion of a test group from outside of Scandinavia. We tested each Scandinavian IA group (Denmark_IA.SG, Sweden_IA.SG, Norway_IA.SG) against a set of IA and other groups from outside (Estonia_BA.SG; England_IA.SG; AngloSaxon_IA.SG; Saami_IA.SG; SarmatianRussia_IA.SG; Longobard_EMED.SG). Results for this analysis are given in Supplementary Table 8 and represented as quantile-quantile plots in Fig. S9.1. We found that most test individuals are consistent with the expectation for a clade-like relationship for most configurations (points on diagonal in Fig. S9.1).

The sets of outlier individuals fall into three main categories: Individuals from Foggia who show affinities to the outgroup with respect to the test groups (positive f_4 values in all configurations); Individual VK518 from Norway who shows excess allele sharing with ancient Saami (negative outlier in Saami_IA.SG panel); and a group of individuals including a substantial number of VA individuals from Gotland who show excess allele sharing with Baltic BA individuals (outliers with negative values in panel Baltic_BA.SG).

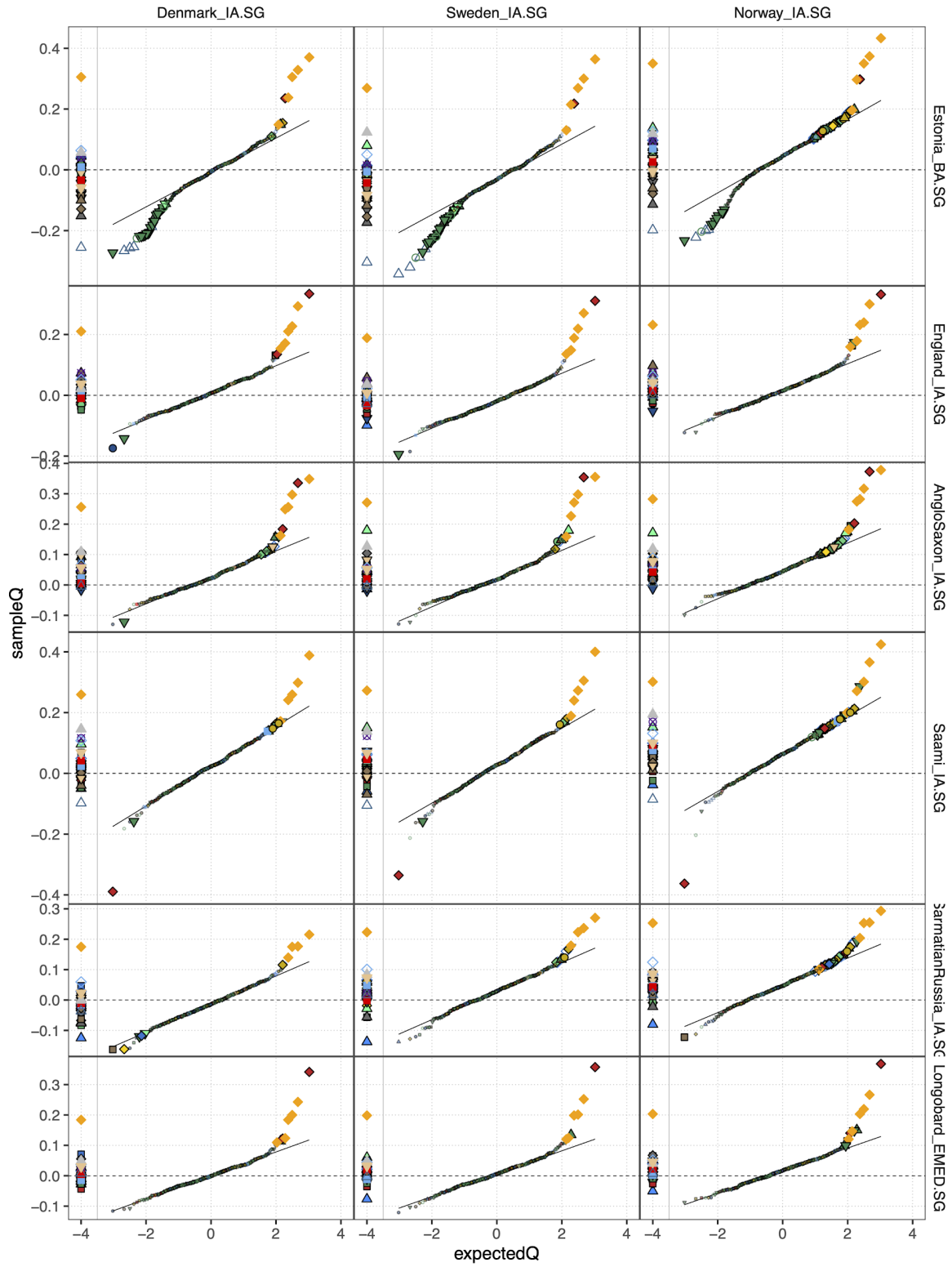


Fig. S9.1. Quantile-quantile (QQ) plots of individual statistics f_4 (YRI, Test group; Test individual, Scandinavia IA group) for different Scandinavian IA groups (columns) and test groups from outside of Scandinavia (rows). Insets on the left of QQ-plots show median values of observed f_4 statistics for the respective groups of ancient test individuals.

Genetic affinities between ancient groups and present-day populations were investigated using $f_4(\text{YRI}, \text{Test individual}; \text{Present-day test population}, \text{present-day reference population})$ (Scandinavian panel). Results are given in Supplementary Table 9, as well as Extended Data Fig. 5b (Denmark as present-day reference population) and Figures S9.2-S9.3 (Sweden, Norway reference populations).

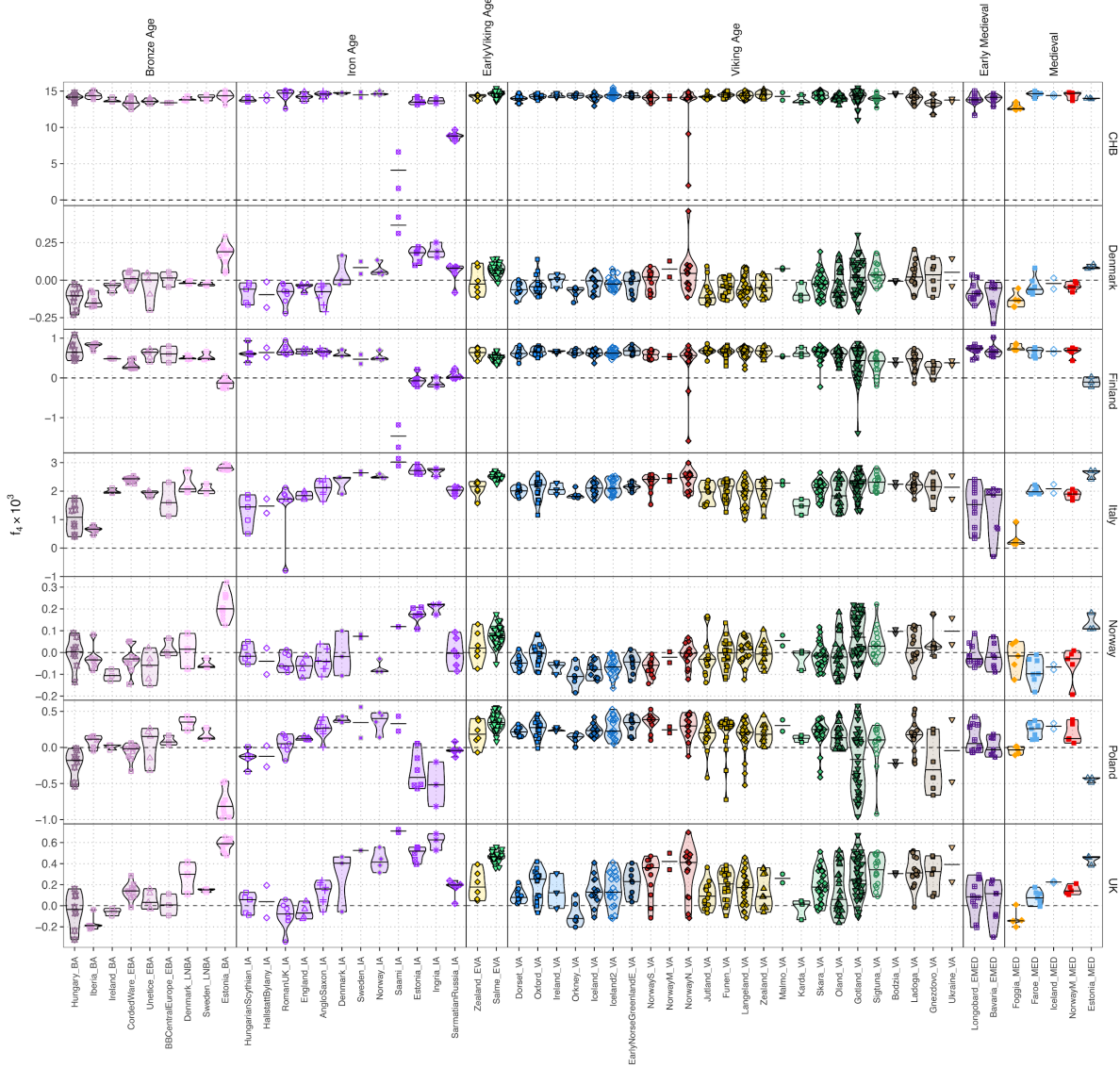


Fig. S9.2. Contrasting allele sharing between present-day Sweden and other populations. Violin plots showing distributions of statistics $f_4(\text{YRI}, \text{test individual}; \text{Panel population}, \text{Sweden})$ for $n=489$ individuals with a minimum of 50,000 SNPs with genotypes and groups with at least two such individuals.

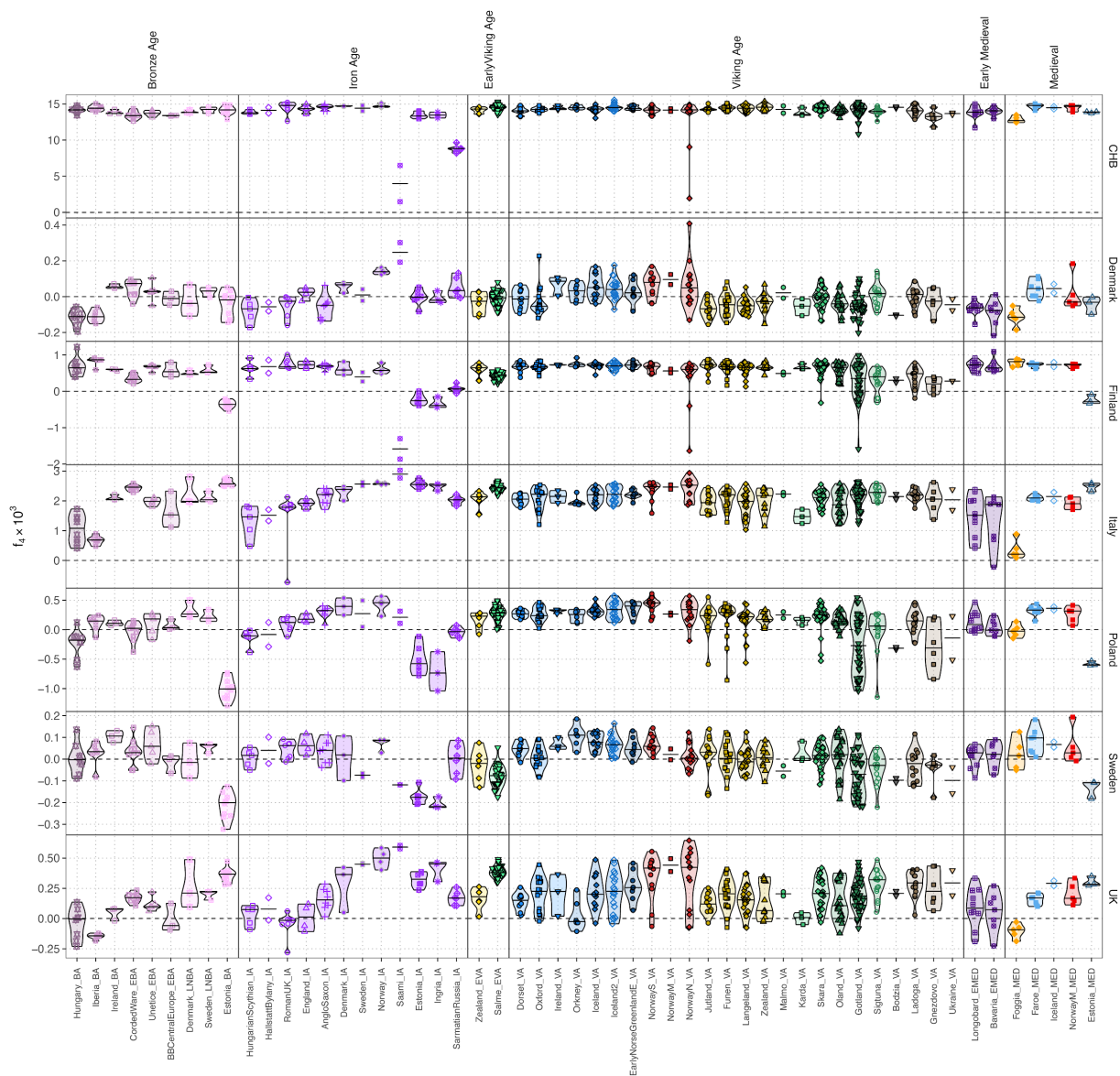


Fig. S9.3. Contrasting allele sharing between present-day Norway and other populations. Violin plots showing distributions of statistics $f_4(\text{YRI, test individual; Panel population, Norway})$ for $n=489$ individuals with a minimum of 50,000 SNPs with genotypes and groups with at least two such individuals.

Lastly, we tested for evidence of gene flow between Native American or Inuit populations and Greenland individuals using $f_4(\text{YRI, Alaska_LP.SG/Kolyma_M.SG; Greenland test individual, Salme_EVA.SG})$. We found no evidence for excess allele sharing for any Greenland individuals and either Native Americans (Alaska_LP.SG) or Paleosiberians (Kolyma_M.SG) (Fig. S9.4)

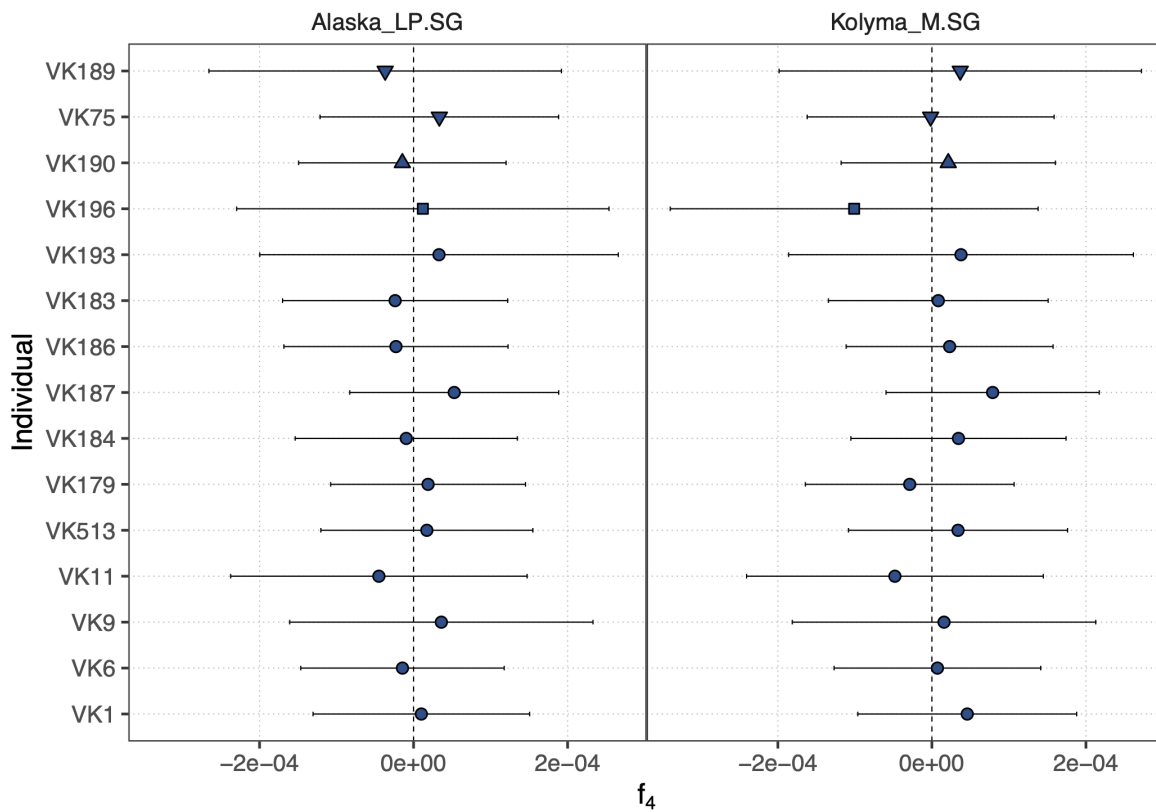


Fig. S9.4. Panels are showing point estimates and three standard errors of statistic f_4 (YRI, Alaska_LP.SG/Kolyma_M.SG; Greenland test individual, Salme_EVA.SG) for $n=15$ Greenland individuals.

9.2. Ancestry modelling using qpAdm

We performed estimation of ancestry proportions for ancient groups using *qpAdm*²³⁶. Ancestry proportion estimation using *qpAdm* is based on f_4 -statistics of the form $f_4(X, O1; O2, O3)$, where X is either the source or target population, and $O1/O2/O3$ are triplets of outgroups to the source/target groups. As such, they are susceptible to batch effects described above, e.g. if both source/target groups and the set of outgroups are composed from different sample processing schemes. To minimize batch effects and/or biases due to ancient DNA damage or SNP ascertainment, we conducted this analysis on a dataset restricted to shotgun sequenced individuals, on a set of 1,800,038 transversion-only sites that were found polymorphic with minor allele frequency $\geq 0.5\%$ and missing genotype rate of $\leq 15\%$ in the 1000 Genomes panel merge.

We first investigated the ancestry of ancient groups from the Bronze Age and later using a distal ancestry model with three deep ancestral lineages previously identified as major sources of European genetic variation: West Eurasian hunter-gatherers (Loschbour_M.SG); Anatolian farmers (Barcin_EN.SG); and Steppe pastoralists (Yamnaya_EBA.SG). For this analysis we used the following set of nine outgroups

Ust_UP.SG
Yana_UP.SG
Sunghir_UP.SG
Bichon_LP.SG
Zagros_EN.SG

DevilsCave_N.SG
Baikal_EN.SG
Alaska_LP.SG

Results of these analyses are shown in Extended Data Fig. 4 and Supplementary Tables 10 and 11. While the three source groups provide a good fit for most ancient groups, a number of them reject the fit at $p < 0.01$. We attempted to model those groups by adding the following additional distal source groups in turn in a four-way model:

CaucasusHG_M.SG (Caucasus hunter-gatherer-related ancestry)
Botai_EBA.SG ('Ancient northern Eurasian' [ANE] ancestry)
XiongNu_IA.SG (East Asian-related ancestry)

All target groups except Oland.SG_VA were successfully modelled this way ($p \geq 0.01$), and can be broadly grouped into two patterns. For northern and eastern VA groups, models with low levels of additional East Asian-related ancestry (XiongNu_IA.SG) provide good model fits. For the remaining groups including Kärda_VA.SG and Foggia_MED.SG, only models including additional ancestry contribution from a Caucasus hunter-gatherer-related source cannot be rejected (Extended Data Fig. 4). Similar ancestry compositions have been previously documented in Greek Bronze Age individuals²²³ and contemporary southern Italians²³⁷. However, the presence of such ancestry (~20% using Nordic_IA and Anatolia_BA as sources.) in Kärda in the Småland area (southern Sweden) is more surprising, suggesting either descendants of a remnant group from an earlier expansion of southeastern groups (e.g. during the Migration Period) or ongoing contacts during the VA. Interestingly, VA burial customs suggest that the Småland area was characterized by locally restricted cultural groups³³, which stands in marked contrast to contemporary coastal and island communities. Consistent with this, individuals from Kärda have reduced nucleotide diversity compared to other VA groups (Fig. S9.5).

We next investigated the relationship of VA groups with temporally more proximate source groups from the Iron Age and early medieval periods. To achieve this, we added the three source groups from the distal analysis as well as additional Bronze Age groups from Europe to the outgroup set:

Barcin_EN.SG
Yamnaya_EBA.SG
Loschbour_M.SG
Nordic_LNBA.SG
CordedWare_EBA.SG
Unetice_EBA.SG

First, we tested for continuity with European Iron Age groups in one-way ancestry model using the following groups with ≥ 3 individuals as putative sources:

England_IA.SG
RomanUK_IA.SG
AngloSaxon_IA.SG
Denmark_IA.SG
Norway_IA.SG
Longobard_EMED.SG

We found that a single source model with at least one of these putative sources could not be rejected ($p \geq 0.01$) for the majority of the VA groups, highlighting the low genetic differentiation of ancient Europeans after the Bronze Age. Nevertheless, systematic differences in the possible source groups were observed between VA groups from different geographic regions (Extended Data Fig. 5). We then investigated two-way models for test groups with marginal or rejected one-way model fits ($p < 0.05$), by adding the following proximate source groups in turn:

Anatolia_MLBA.SG
SarmatianRussia_IA.SG
Saami_IA.SG
Tagar_IA.SG
Estonia_BA.SG

These two-way models provide good fits for all remaining VA groups with a number of possible source group combinations (Extended Data Fig. 5, Supplementary Tables 12 and 13).

Overall, these observations are consistent with archaeological claims of wide-ranging demographic turmoil in the aftermath of the Roman Empire with consequences for the Scandinavian populations during the late Iron Age^{18,238}. We caution, however, that sampling for the periods preceding the VA is still sparse, and hence our samples may not provide a full picture of the genetic diversity across Scandinavia or in the rest of Europe during that period. Furthermore, methods based on shared genetic drift such as *qpAdm* are expected to have low power to disentangle fine-scale differences among groups with low genetic differentiation such as those observed in ancient Europeans from the BA onwards.

9.3. Genetic diversity

We quantified genetic diversity for ancient groups using ‘conditional nucleotide diversity’ as previously described²³⁹. For this analysis, pairwise differences between individuals were calculated using SNPs polymorphic in an outgroup population (YRI) and with a minor allele count ≥ 5 in the 1000 Genomes merge. Results of this analysis are shown in Fig. S9.5.

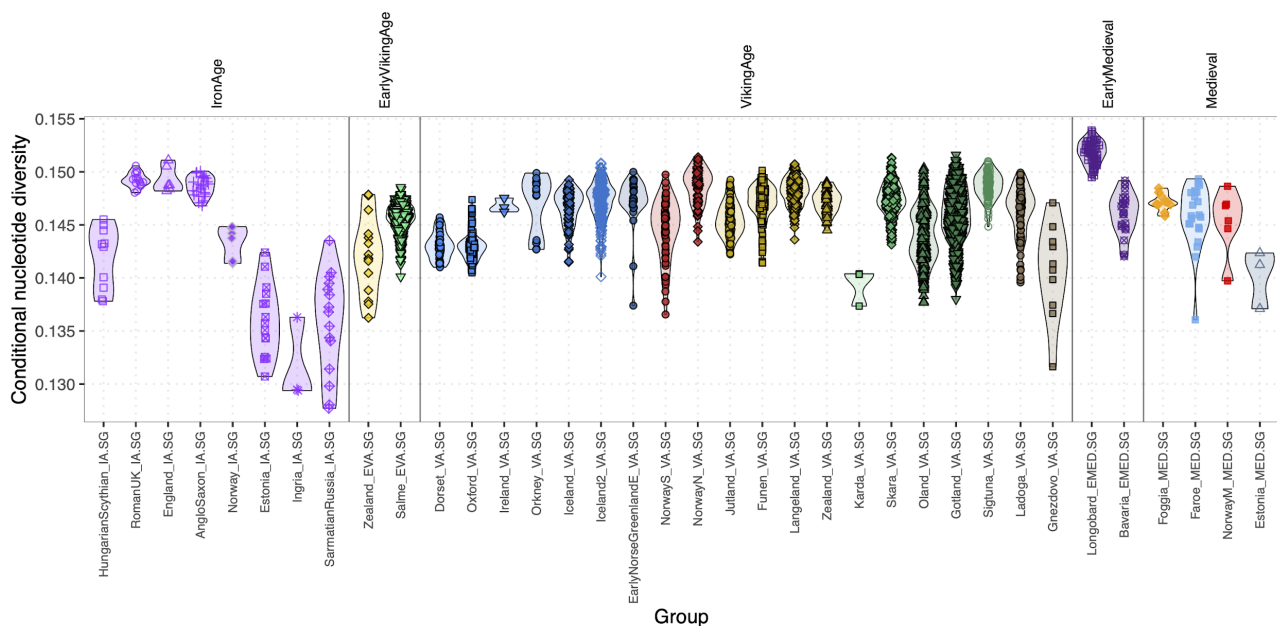


Fig. S9.5: Conditional nucleotide diversity for pairs of individuals from Iron Age and later ancient groups. Violin plots showing distributions of statistics for $n=3,321$ pairs of individuals across $n=36$ groups. Only individuals with a minimum of 2,000,000 SNPs with genotypes were included, and only groups with at least three such individuals are plotted.

Supplementary Note 10 – Identity-by-descent

By the end of the Iron Age in the 8th century CE, Scandinavia formed a patchwork of conflicting and competing kingdoms with a shared cultural background. For centuries, a political economy based on raiding, trading, and gifts had been common²⁴⁰. However, the causes for the development of this economic and political system into the more organized maritime society of the VA remain debated²⁴⁰. It is commonly argued that seafaring^{241,242} contributed to the creation of the densely interlinked Scandinavia of the VA^{1,243,244}.

To disentangle the fine-scale population structure within VA Scandinavia, we performed genotype imputation on a subset of 298 individuals with sufficient ($>0.5X$) coverage (289 from this study plus 9 published³⁵) and inferred genomic segments shared via identity-by-descent (IBD) within the context of a reference panel of 1,464 present-day Europeans, using IBDseq. Genetic clustering by MDS on a distance matrix obtained from pairwise IBD sharing and UMAP revealed fine-scale population structure among VA individuals invisible from allele-frequency-based IBS analyses (Figs. 3 and S10.1).

We find that VA Scandinavians generally cluster into three groups according to their geographic origin and have close affinities with their respective present-day counterparts in Denmark, Sweden, and Norway (Fig. 3a). Closer inspection of the distributions for the different groups reveals additional complexity in their genetic structure (Fig. S10.1). We find that the 'Norwegian' cluster includes Norwegian IA individuals, who are distinct from both Swedish and Danish IA individuals. The latter two groups of individuals cluster with the majority of central and eastern Swedish VA individuals. Many individuals from southwestern Sweden (e.g. Skara) cluster with Danish present-day individuals from the eastern islands (Funen, Zealand), skewing towards the 'Swedish' cluster with respect to early and more western Danish VA individuals (Jutland). Some individuals have strong affinities with eastern Europeans, particularly those from the island of Gotland in eastern Sweden. The latter likely reflects individuals with Baltic ancestry, as clustering with Baltic BA individuals is evident in the IBS-UMAP analysis (Fig. 2b) and through f_4 -statistics (Fig S9.1).

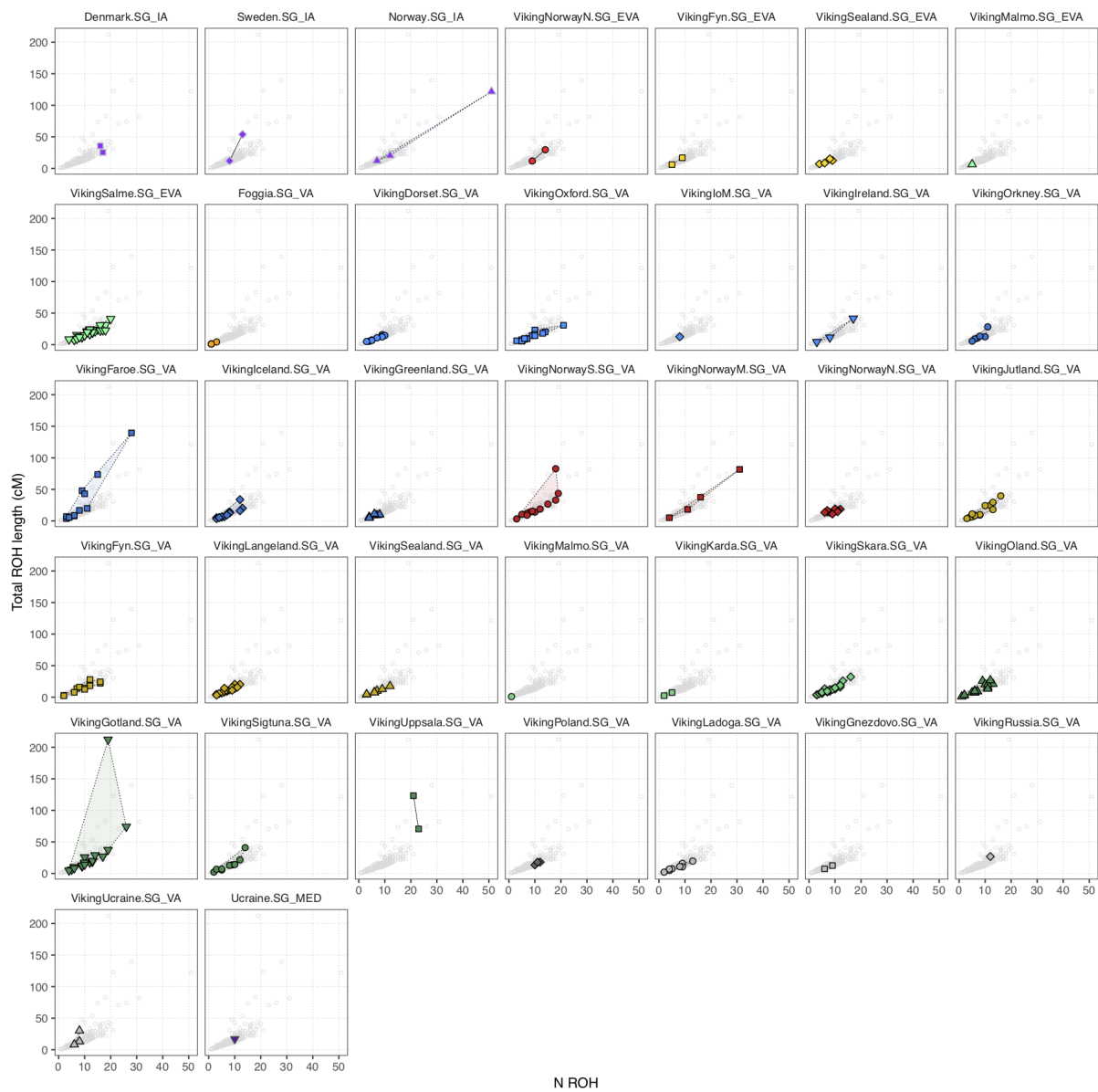


Fig. S10.2: Number and total length of genomic segments homozygous-by-descent in VA individuals.

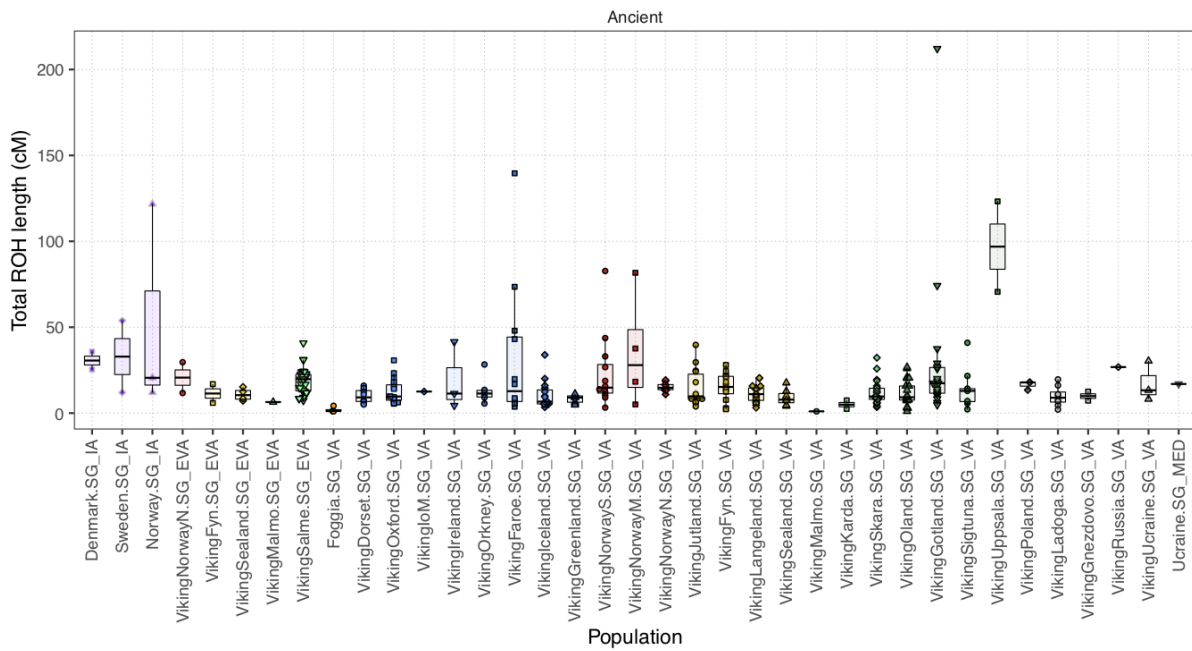


Fig. S10.3: Distributions of total length of genomic segments homozygous-by-descent in n=295 VA individuals. Box plots show the median, 25th and 75th percentile of the distributions, with whiskers showing the smallest/largest value at most 1.5 times the inter-quartile range from the lower/upper hinges.

Supplementary Note 11 - Chromosome Painting

11.1. Introduction

When examining the sequence data of the VA genomes sequenced to 0.1X or higher, we found that standard analyses were largely inadequate in extracting population structure within Scandinavia. We therefore used a fine-scale method called Chromosome Painting²⁴⁵ to extract maximum signal from the ancient DNA.

To understand our analysis, it is important to define the terminology:

- 'Recipient': an individual whose genetics we wish to describe.
- 'Donor individuals': a set of individuals who we will 'paint' the recipient from, that together form a 'Panel'.
- 'Paint': Use a model, ChromoPainter²⁴⁵, to estimate the total amount of genome that each donor is the closest relative to the recipient in the panel.
- 'Palette': a grouping of the donors into clusters, to obtain the amount of genome that the recipient has a closest relative from each donor population.
- 'Surrogate population': a population that we will use to represent a named population of interest.

Briefly, we used ancient DNA to create a set of K high-quality surrogate populations that are compared to a palette of M donor populations, with $M > K$ to allow us to retain as many individuals as possible. We will then be able to describe each modern or ancient individual by painting them against the donor populations (to form a palette vector of length M) and describing them as a mixture of the K surrogate populations' palettes. This procedure is a refinement of that used by the GLOBETROTTER method²⁴⁶.

This approach has the advantage that it is robust to batch effects of modern and ancient samples, because we focus on comparing all individuals to only one panel. The chromosome painting method contains an error rate parameter that is unique to each sample. Therefore, batch effects will be treated as noise, which will be higher in the non-reference batch, and should not produce systematic bias.

11.2. Chromosome Painting Procedure:

1. **Unsupervised Ancient Sample Analysis.** We first tried ChromoPainter and FineSTRUCTURE²⁴⁵ in its default, unsupervised approach. However, unsupervised, there was not clear population structure in this data for the clustering method to identify strong structure (Figure S11.1).
2. **Create Modern Reference.** Create a modern reference panel using 1675 modern individuals sampled from northern Europe, using the standard FineSTRUCTURE pipeline:
 - a. Apply ChromoPainter to paint all modern individuals using the remaining individuals as donors;
 - b. Cluster with FineSTRUCTURE;
 - c. Assign geographical meaning to the clusters using the known labels;
 - d. Call the resulting clustering the 'Modern Reference Panel', which consists of 23 Modern Surrogate populations and 23 Modern Donor populations.
3. **Create Ancient Reference.** Create an 'ancient reference panel' using the modern reference panel:
 - a. Apply ChromoPainter to paint all ancient individuals using the 'Modern Population Palette';

- b. Create a supervised 'Ancient Population Palette' consisting of populations that: A: 'represent' a modern ancestry direction, or B: are 'best associated with' a modern ancestry direction, using an iterated Mixture Model;
 - c. Create an 'Ancient Population Surrogate' for each modern population, consisting of the individuals that 'represent' each modern population. For $K=7$ modern populations, this results in a matrix of $K=7$ rows (surrogate populations) and $2K=14$ columns (donor palette populations) which captures the ancient population structure.
4. **Infer Ancestry.** Learn about population structure in either modern individuals or ancient individuals by painting them with respect to the 'ancient population panel' and fitting them as a mixture using the 'ancient population surrogates'.
- After the panels are constructed, there are additional steps to be performed:
5. **Check Ancient Reference.** We perform a range of checks and sensitivity analyses to ensure that the inference procedure performs as expected.
 6. **Principal Components Analysis.** As a sensitivity and triangulation exercise, we also consider the PCA of the ancient population panel as well as an all-vs-all ChromoPainter analysis including modern and ancient populations.
 7. **Interpretation.** We then interpret the ancestry results.

11.3. Ancient Sample Analysis

We used fs2.0.8 (www.paintmychromosomes.com) using the protocol described with the software²⁴⁵ to paint the 298 individuals whose aDNA will form the 'ancient sample'. Each is painted using all other ancient samples to create the 'coancestry matrix', which is the number of independent segments or 'chunks' or genome for which individual j (columns) is the closest match to individual i (rows). This allowed us to identify related individuals who share more and longer chunks than do unrelated individuals; after removal of one of each related pair we were left with 255 unrelated ancient individuals who will be used to create the 'ancient panel'. The coancestry matrix is then used by FineSTRUCTURE to perform unsupervised clustering, as shown in Figure S11.1.

Whilst there is population structure visible in these results, it is insufficient to clearly define useful population labels. This is because a) there are relatively few ancient samples, b) the ancient populations come from very similar populations, and c) many individuals are not in fact representatives of ancient population groups.

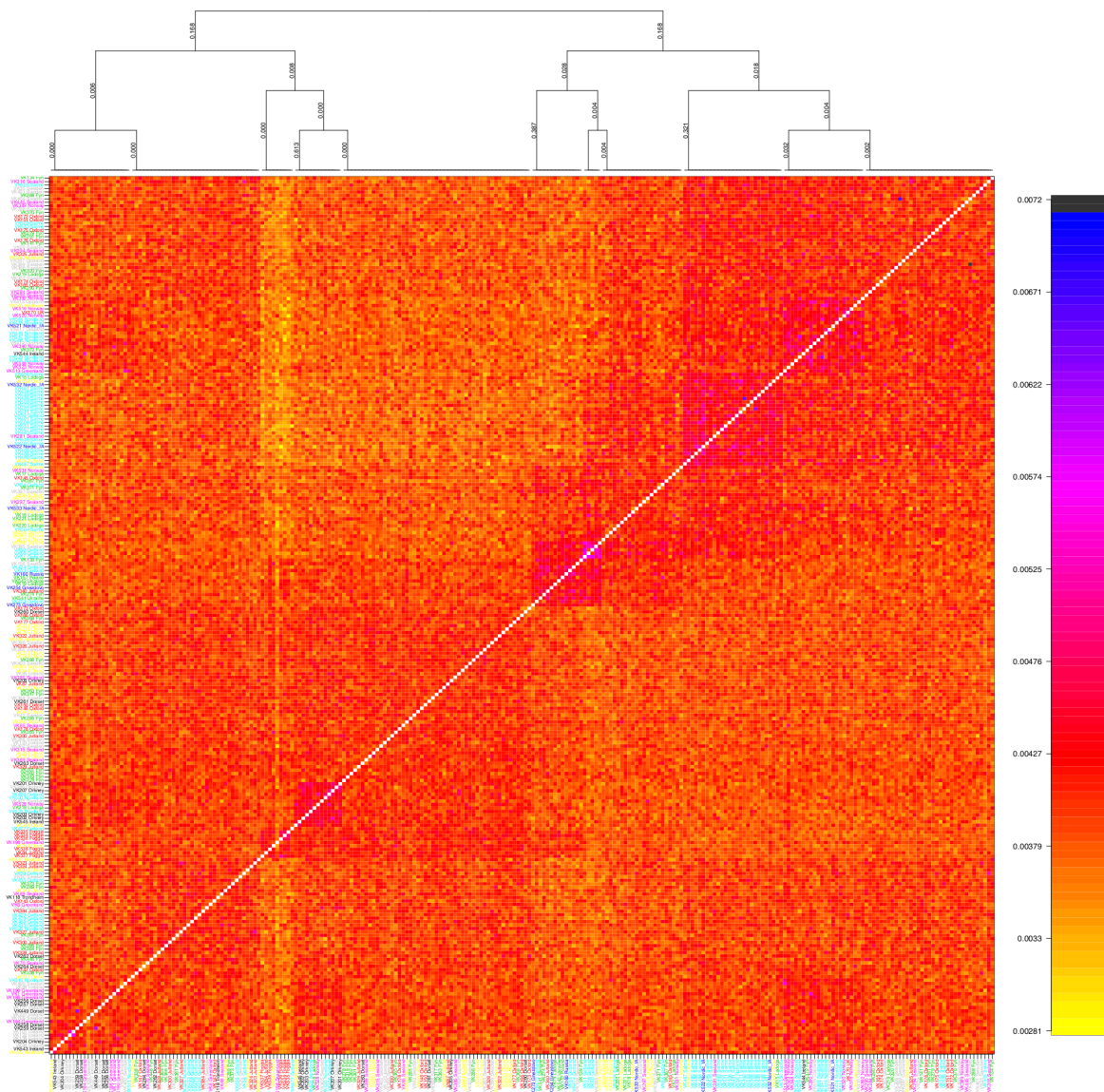


Fig. S11.1: Unsupervised ChromoPainter and FineSTRUCTURE results for 255 unrelated ancient individuals. The tree shows the clustering and relationship between clusters as inferred by FineSTRUCTURE, whilst the heatmap shows the Coancestry Matrix output by ChromoPainter.

11.4. Modern References

We used fs2.0.8 (www.paintmychromosomes.com) with the protocol described with the software²⁴⁵ to paint 1675 modern individuals primarily from across Europe (UK, Italy, Poland, Denmark, Sweden, Finland, Norway, as well as China and Africa) who together form the 'modern sample'. FineSTRUCTURE identified 40 populations which after removal of small populations and merging of the Chinese (CHB) and African (YRI) sub-populations created 23 modern populations consisting of the 1554 unrelated individuals who could be associated with a modern population label. These together will form the 'modern reference panel'. Painting against this 'Modern Population Palette' was done by simply summing the contribution from each individual in each donor population.

These results are shown in Figure S11.2. The clustering is strong and perfectly stratified by population label. Each population is characterized by receiving higher ancestry from its own population, implying that each represents a unique aspect of genetic drift.

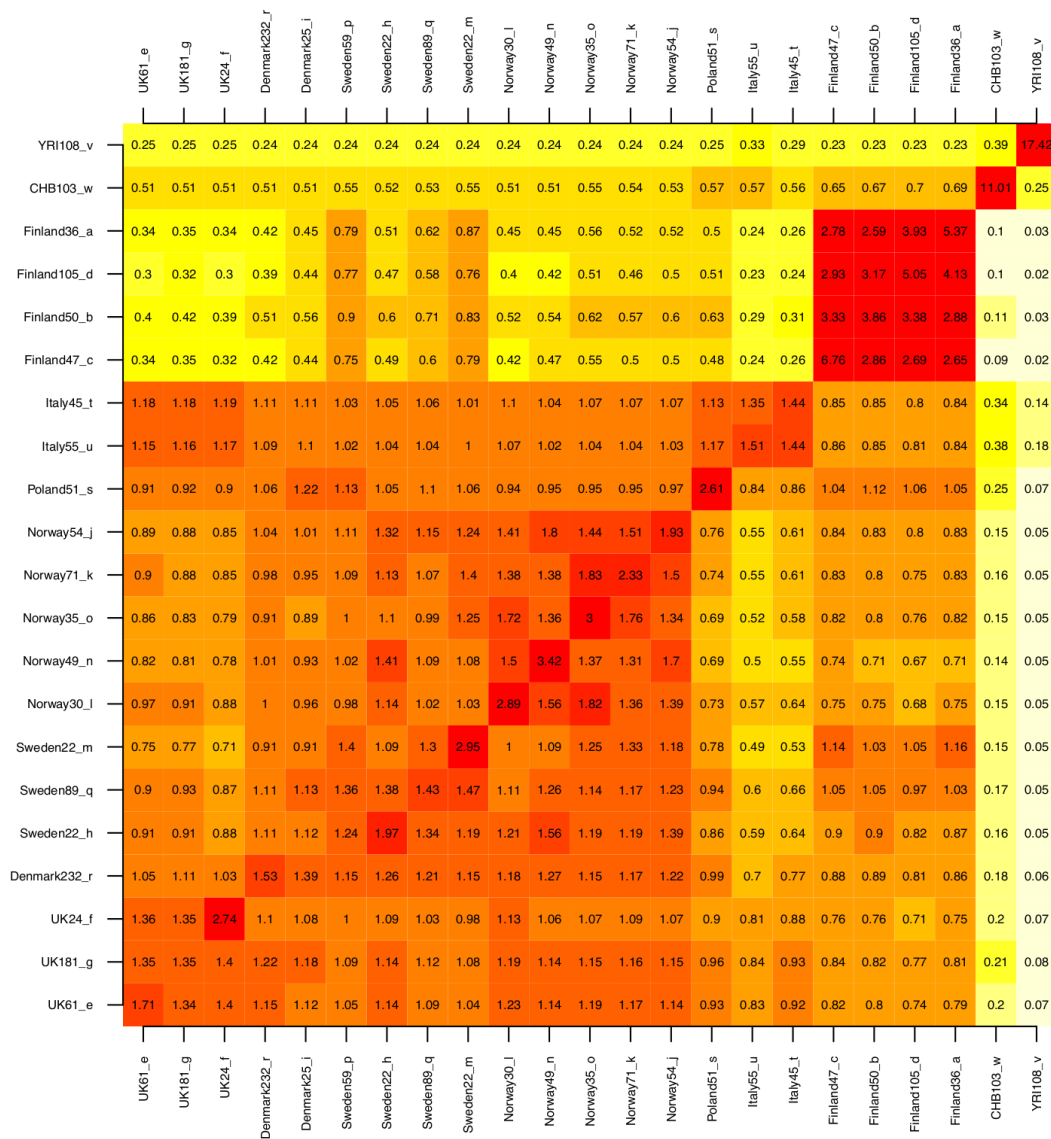


Fig. S11.2: Unsupervised ChromoPainter and FineSTRUCTURE results for 1554 unrelated modern individuals, where all donor individuals in the same population (i.e. columns) have been summed to create a 'population donor palette', which is averaged over all individuals in the same 'recipient population' (i.e. rows). The tree shows the relationship between the populations as inferred by FineSTRUCTURE.

11.5. Ancient References

This stage is more involved. We first:

a. Apply ChromoPainter to paint all ancient individuals using the 'Modern Population Palette'. We used ChromoPainter v2 to paint each ancient sample against each modern sample. Unlike above, where fs2 automatically learns parameters (which measures recombination rate and which measures

error rate), we had to manually learn these using ChromoPainter v2's Expectation-Maximisation procedure, as performed in the GLOBETROTTER method²⁴⁶. We then reran ChromoPainter v2 with these parameters fixed for all individuals. We obtained a painting for each ancient sample in the ancient panel, described as a K=23 long palette as shown in Figure S11.3.

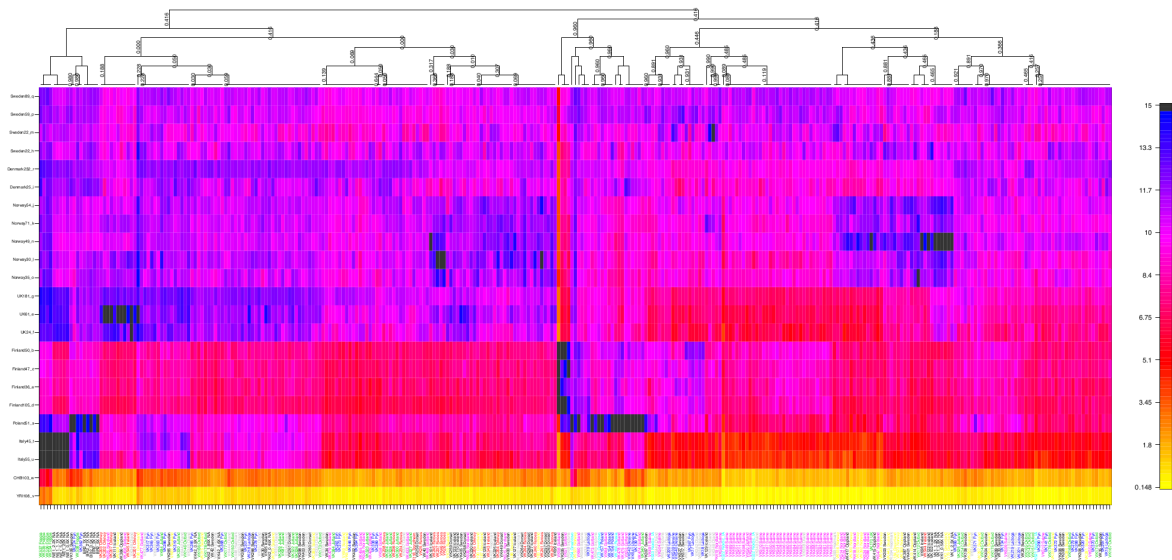


Fig. S11.3: Ancient panel (n=255) painted against the Modern Population Palette (n=1554). The palette is ordered as in Figure S11.2, whilst the ancient individuals are ordered according to the FineSTRUCTURE clustering.

There are three advantages of using the modern palette, i.e. using Figure S11.3 over Figure S11.1:

1. Because the donor populations are much larger, there is reduced statistical noise in the painting.
2. The donor populations are readily interpretable.
3. The ancient individuals naturally separate into populations that share a lot of drift with specific modern populations – i.e. they are 'representative' of them, and those that do not.

Furthermore—and perhaps surprisingly—most modern European populations (at the level of the 7 labels, not the 23 inferred populations) look to be effectively represented.

In terms of difficulty of assigning populations, Denmark is one. The individuals that best match a Denmark population also match well the 'UK181_g' population. The UK populations contain individuals from the PoBI study and so we can confirm that these are English and hence contain a high proportion of Anglo-Saxon ancestry. The 'UK61_e' population, which is well-matched by the ancient Orkney individuals, contains individuals from Scotland and Northern Ireland, whilst 'UK_24f' contains individuals from Wales. Another difficult population is Sweden, for which ancient individuals often well-associate with significant Finland or Norwegian ancestry.

We exploited these labels by creating an initial labelling of the ancient populations. To do this we normalised the ancient-vs-modern coancestry by a) calculating the amount of ancestry received per donor individual from the 7 labelled countries; and b) normalising each donor label to have mean 1. Figure S11.4 shows how this normalisation changes the matrix. This normalisation was chosen to move from a representation that asks 'which populations are important for an individual' to one that asks 'which individuals are important for a population'?

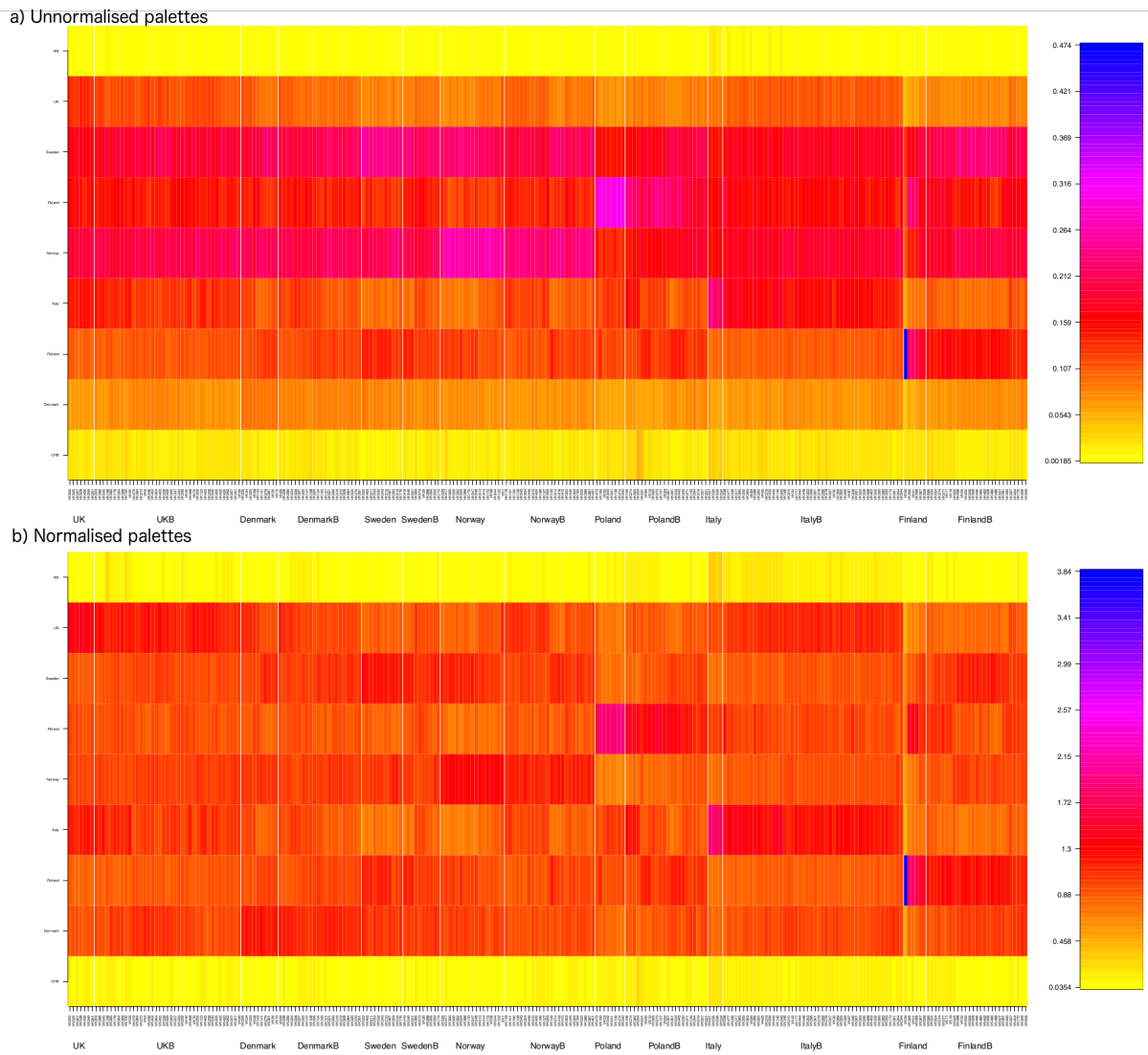


Fig. S11.4: a) the ancient individuals ($n=255$) represented by their palettes, in unnormalised form, for which each column represents the importance of each population to a specific individual from the modern panel ($n=1554$). b) the normalised coancestry matrix on which selection of individuals is performed, for which each row represents the importance that each individual has to a specific population.

For each of the 7 European labels, we then used the following criteria to select 'potential representative individuals':

- Individuals score population X more than any other population in the normalised coancestry;
- Additionally, they are in the top x_k for population k , where x is chosen to represent the first change-point in the density of scores (Figure S11.5).

The remaining individuals were then assigned to their best-matching population as 'potential non-representative donors'.

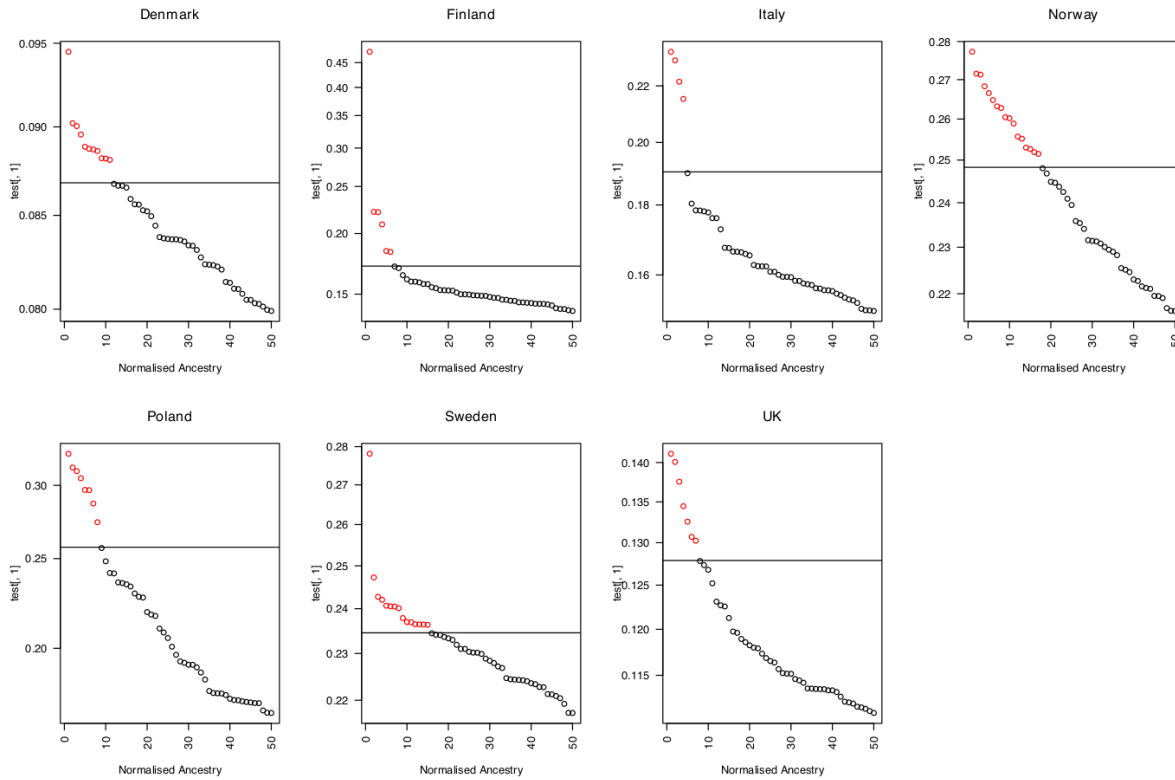


Fig. S11.5: Thresholds for defining the most important individuals for each modern population. All individuals above the line are chosen as representative, whilst those below may be assigned to their best scoring population as 'non-representative donors'.

11.6. Ancient Population Palette

We are now in the position of having a well-chosen set of populations. The next task is to create an ancient population palette that can be used as a reference. This stage follows the procedure used in GLOBETROTTER²⁴⁶.

First we repaint each ancient individual using the 14 donor populations, this time 'leaving out' themselves as donors from their own population, and one random individual from each of the other populations²⁴⁶. This is done three times: once to learn the painting parameters N_e and μ ; a second time to learn a genome-wide prior for the donor palette, conditional on the parameters; and a final time using a shared N_e , μ , and an individual-specific donor-prior, to obtain a high-quality palette. For each of the 7 surrogate populations (defined by the 'representative individuals' above) we learn the average amount of genome received from each donor individual in each donor population. This K by M=2K matrix is the 'ancient population palette' for the ancient population panel. The results from this are shown in Figure S11.6, for both the ancient panel and the modern panel.

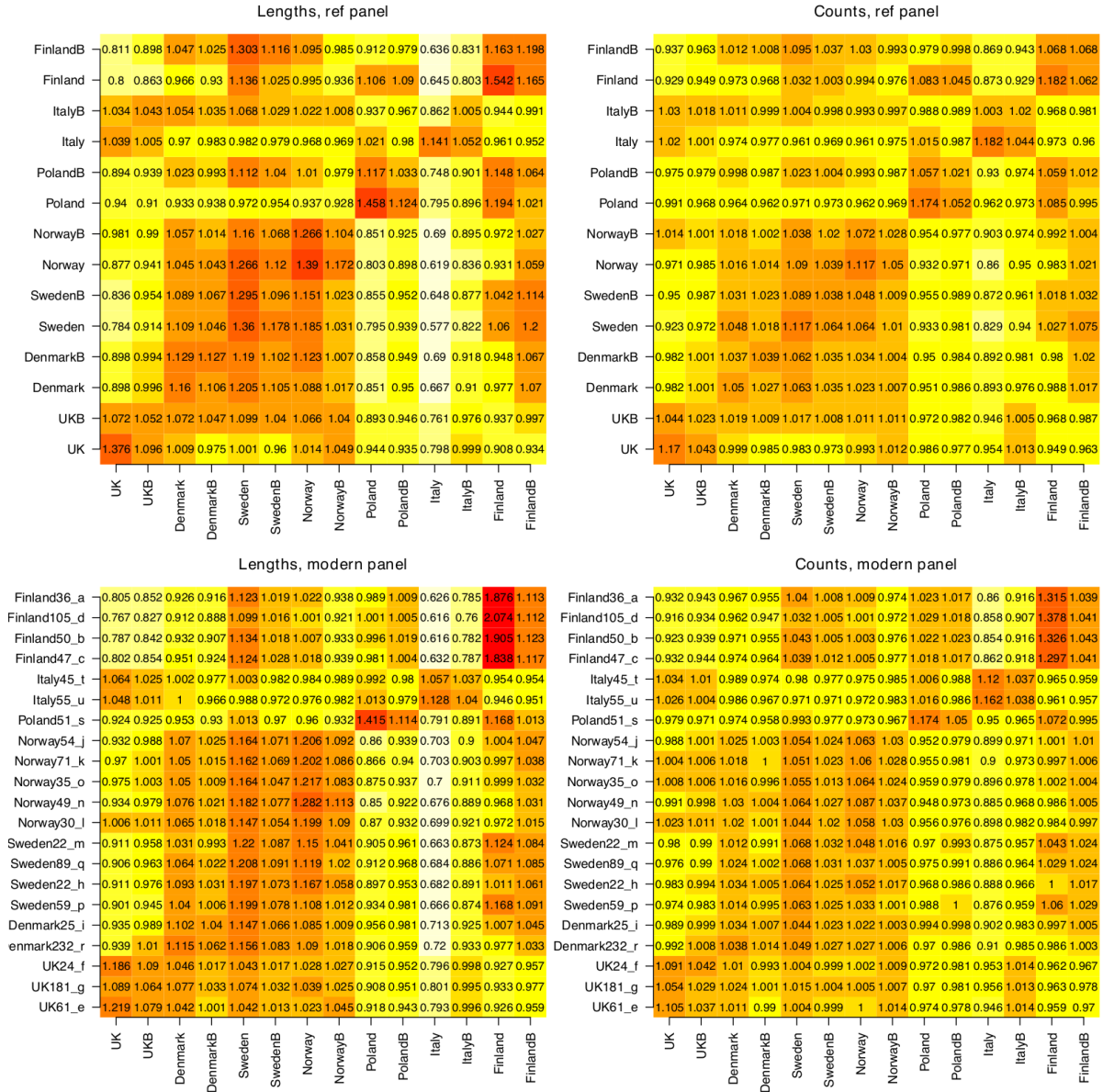


Fig. S11.6: Ancient DNA painting palette (top) and modern panel painted against the ancient panel (bottom). We show both the total genome shared (lengths) and inferred number of shared recombination events (counts). We use the lengths data for onward analysis. The plots show the average of each score, per donor individual, normalised to have mean value of 1. The rows show the average for each recipient individual in a population, when painted against the populations in the columns. Based on $n=255$ unrelated ancient individuals and $n=1554$ unrelated modern individuals.

The importance of the leave-one-out procedure is that now the individuals used in the donor populations (who cannot share genome with themselves) are now exchangeable with the individuals in the modern populations. That is because they are all painted against exactly $n_k - 1$ donor individuals, where n_k is the number of individuals in population k , regardless of whether the individual itself is in the panel.

11.7. Ancestry learning

The target of inference is an admixture profile for each modern and ancient individual. We use the first stage of the admixture estimation method as implemented in the software GLOBETROTTER²⁴⁶. To quantify uncertainty, we bootstrap over chromosomes, i.e. resample with replacement the per-chromosome palettes for each individual, normalise the chromosome length, and reapply admixture estimation. We report the average and confidence interval over 100 random samplings as performed by ²⁴⁶. Supplementary Table 6 gives the per-individual estimates of ancestry.

Given that we have performed imputation and the ancient genomes have variable coverage, it is important to test how this will affect inference. We first check whether sequence depth is driving any broad scale painting structures. Figure S11.7 shows that the results of the Unsupervised Ancient Sample Analysis are not associated with sequence depth.

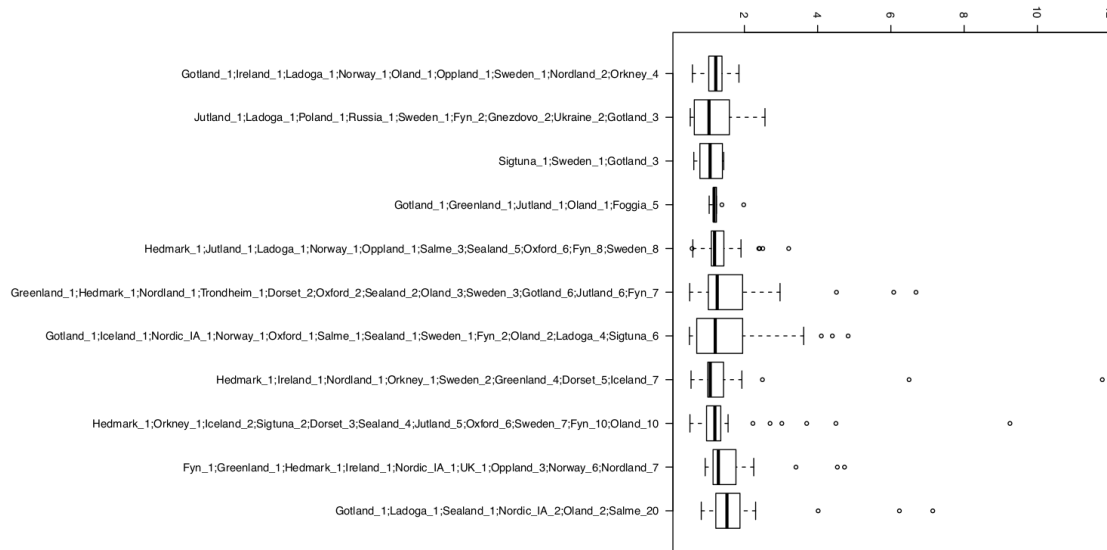


Fig. S11.7: The labels of the individuals in the unsupervised cluster membership (see Unsupervised Ancient Sample Analysis) showing the sequence depth of members. There is no association between membership and sequence depth. Based on $n=255$ unrelated ancient individuals. Boxes show the 1st-3rd quantiles with the whiskers extending to 1.5x the interquartile range, or the last point, whichever is closer to the median.

Next, we examined the fine-scale effects of sequence depth by downsampling two high quality genomes, VK1 (Greenland East Settlement; sequence depth 11.8 X) and VK50 (Gottland; sequence depth 6.2 X), at the raw read level, to an average sequence depth of 1, 2, or 4. We repeated the analysis as if these individuals were only available at the specified sequence depth. Figure S11.8 shows how the inference changes as a function of sequence depth, along with the bootstrap samples. In general, there is surprisingly little variation as a function of sequence depth, with some evidence that 1X is biased towards a more mixed solution but not dramatically worse than the variation induced by changing depth. There is no evidence that a) wrong ancestry components are added, or b) major changes in ancestry can occur. All changes are within Scandinavian ancestries and the correct components are always recovered.

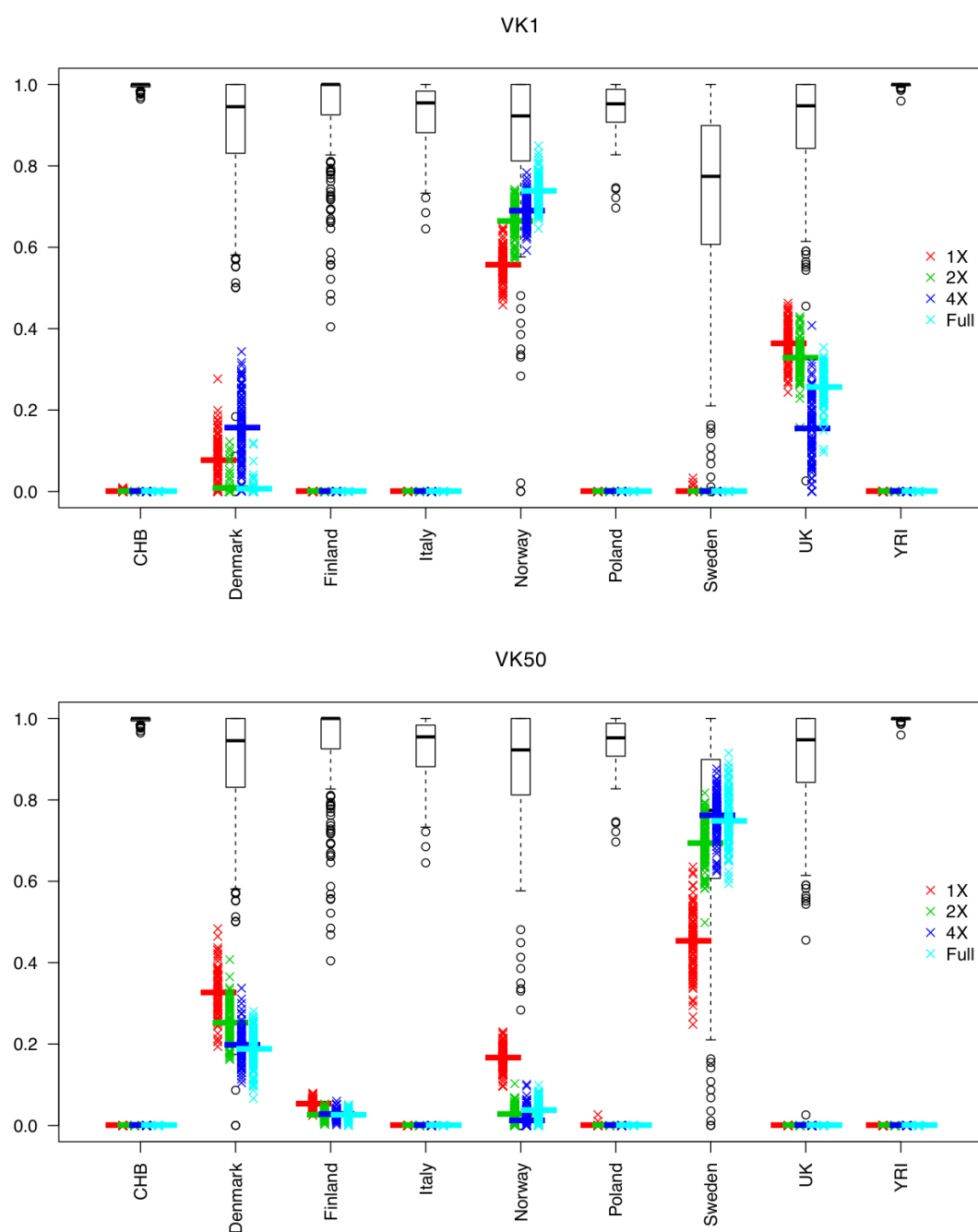


Fig. S11.8: Top: VK1, Bottom: VK50. The mean results along with 100 bootstrap resamples of the painting are shown for ancestry reconstruction from the 7 populations. Results are shown for each sequence depth (crosses of different colours: red/blue/green/cyan). Also shown is the distribution of each component within the specified population (black boxplots/circles); e.g. the 'Denmark' boxplot shows the distribution of Denmark ancestry for individuals from the Denmark population. Based on $n=1000$ bootstrap resampling. Boxes show the 1st-3rd quartiles with the whiskers extending to 1.5x the interquartile range, or the last point, whichever is closer to the median.

11.8. Spatio-temporal Regression Model

To assess the spatio-temporal structure in the data, we use a simple regression model:

$$a_{ik} = \alpha_{jk}t_i + \beta_{jk}x_i + \gamma_{jk}y_i + \varepsilon_{ijk},$$

where a_{ik} is the amount of ancestry individual i possesses from population j , t_i is the 'age category' of the individual (1=Iron Age, 2=early VA, 3=VA, 4=Medieval), and (x_i, y_i) are the longitude and latitude of the death location of the individual. We choose to analyse the samples by region, hence restricting to a subset of individuals $i \in P_r$ found in that region r (UK, Scandinavia, whole Europe including UK and Scandinavia). The results of the inference are a time-effect α_{jk} , a longitude effect β_{jk} and a latitude effect γ_{jk} . We perform time-tests in Scandinavia and Europe, and lat-long tests in Scandinavia, UK, and Europe, for a total of eight tests each run for seven ancestries.

Table S11.2: Regression results for spatio-temporal structure in ancestries. Each row shows the value for a region (named in the columns) of α_{jk} (for age), β_{jk} (for longitude) and γ_{jk} (for latitude) in the model described in Spatio-temporal Regression Model. Significance thresholds: *: $p < 0.05$, **: $p < 0.005$, ***: $p < 0.0005$, given precisely in Table S11.3 from a 2-sided t-test. Based on n=255 unrelated ancient individuals.

	Scandinavia Age	Scandinavia Lat	Scandinavia Long	Europe Age	Europe Lat	Europe Long	UK Lat	UK Long
UK	0.106	0.008	-0.004	0.07*	0.008*	-0.004*	0.06***	-0.027
Denmark	0.193**	-0.022***	-0.003	0.073*	-0.012*	2.4e-4*	-0.022	0.061**
Sweden	-0.613***	-0.001	0.001	-0.374***	0.001***	0.003***	-0.005	0.016
Norway	-0.173**	0.037***	-0.04***	0.047	0.018	-0.005	-0.017	-0.068**
Poland	0.188***	-0.007	0.018**	0.069*	-0.003*	0.003*	-0.001	0.003
Italy	0.136**	-0.015***	-0.002	0.129***	-0.015***	0.001***	-0.012	0.012
Finland	0.163*	-0.002	0.025***	-0.014	0.003	0.003	-0.003	0.004

Table S11.3: p-values for spatio-temporal structure in ancestries. Each row shows the p-value for the corresponding quantity from Table S11.2. from a 2-sided t-test. Based on n=255 unrelated ancient individuals.

	Scandinavia Age	Scandinavia Lat	Scandinavia Long	Europe Age	Europe Lat	Europe Long	UK Lat	UK Long
UK	3.8e-02	4.5e-02	4.0e-01	5.5e-03	5.5e-03	5.5e-03	1.0e-04	4.0e-01
Denmark	3.0e-03	5.6e-03	1.5e-01	9.3e-04	9.3e-04	9.3e-04	7.0e-02	4.1e-03
Sweden	4.9e-09	3.4e-01	5.0e-06	1.1e-21	1.1e-21	1.1e-21	4.8e-01	2.4e-01
Norway	3.9e-02	7.6e-08	9.8e-10	7.6e-01	7.6e-01	7.6e-01	1.9e-01	1.6e-03
Poland	9.2e-02	1.3e-01	3.9e-01	3.8e-03	3.8e-03	3.8e-03	7.3e-01	2.5e-01
Italy	3.1e-03	9.6e-03	7.5e-01	2.8e-03	2.8e-03	2.8e-03	1.1e-01	2.8e-01
Finland	2.8e-01	8.1e-01	1.4e-02	6.4e-01	6.4e-01	6.4e-01	2.7e-01	4.5e-01

Such regression analyses are dependent on the sample locations and choice of geographical region. They are therefore intended as a guide to formalise the spatio-temporal relationships that are clear by-eye in the maps smoothing ancestry estimates. They are helpful to understand what the inferred ancestry components mean. The within-Scandinavia results make it clear that the group called 'Sweden' represents a historical population that once existed in Sweden, replaced by more southern populations containing more continental European ancestry. Similarly, Norwegian ancestry has declined but is still higher in the northwest of Scandinavia (i.e. Norway). Italian and Danish ancestry both increase over time and are higher in the south of Scandinavia, consistent with a migration flow. Similarly, the UK analysis shows that the population labelled 'UK' was at the time of sampling predominant in the north, with 'Danish-like' ancestry found in the east and Norwegian in the west.

11.9. Principal Components Analysis of Painting

We performed a Principal Components Analysis of the covariance of the painting which (if the data were treated as containing no linkage-disequilibrium) is equivalent under some theoretical conditions²⁴⁵. Specifically, we formed an N_{M+A} by M matrix of the ancient and modern combined palette painting, calculated the N_{M+A} by N_{M+A} matrix of covariance, and computed the eigenvalue decomposition using the function 'eigen' in R. Figure S11.9 shows the results of this analysis.

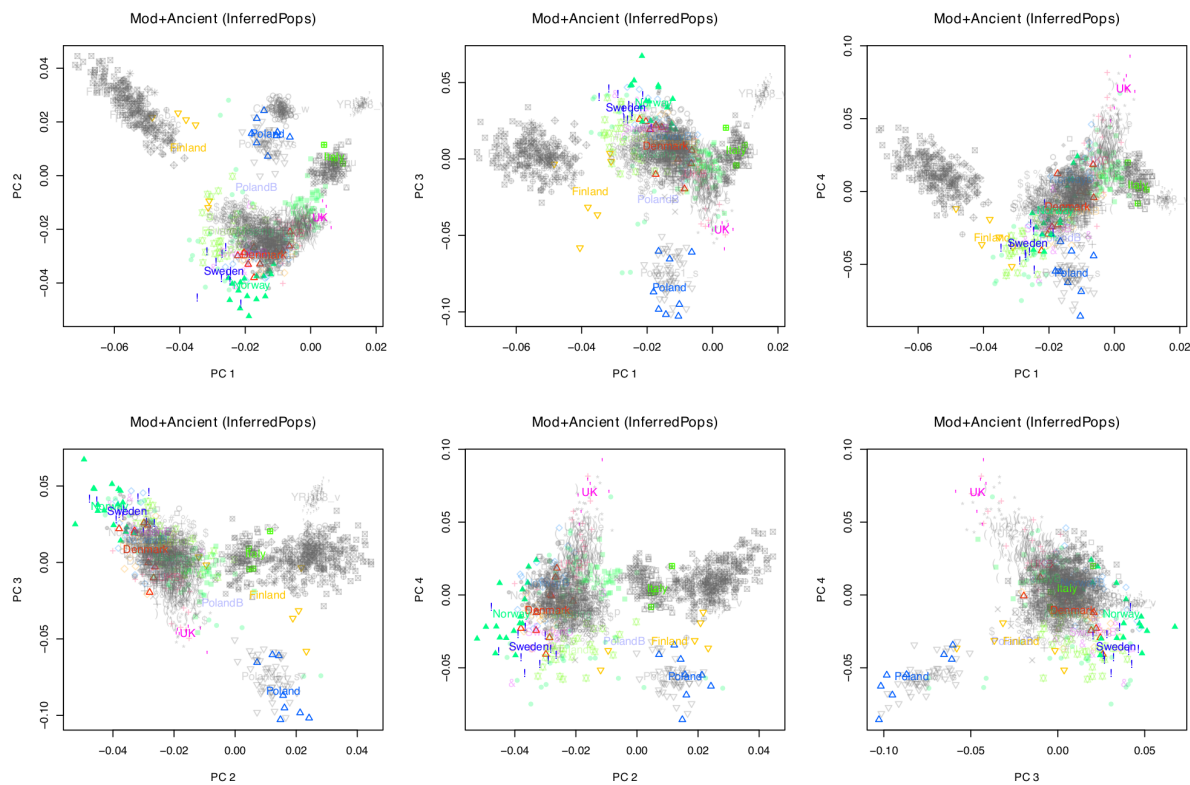


Fig. S11.9: PCA of the ancient and modern samples using the ancient palette, showing different PCs. Modern individuals are grey and the $K=7$ ancient panel surrogate populations are shown in strong colors, whilst the remaining $M-K=7$ ancient populations are shown in faded colors. Based on $n=255$ ancient + 1675 modern samples.

Several features are clear from Figure S11.9. First, modern Finnish individuals are not like ancient Finnish individuals, because the modern individuals have ancestry of a population not in the

reference; this is most likely Steppe/Russian ancestry, as Chinese are in the reference and do not share this direction. Second, ancient Swedes and Norwegians are more extreme than modern individuals on PC2 and 4. Third, ancient UK individuals are more extreme than Modern UK individuals on PC3 and 4. Lastly, ancient Danish individuals look rather similar to modern individuals from all over Scandinavia.

By using a supervised ancient panel, we removed recent drift from the signal, which would have affected modern Scandinavians and Finnish populations especially. This is in general a desirable feature but it is important to check that it has not affected inference. As a sensitivity analysis, we therefore repeated the analysis but this time used the modern and ancient samples together in 'all-vs-all mode', employing the same label annotations as above. This leads to a N_{M+A} by N_{M+A} 'coancestry matrix' which we normalise²⁴⁵ in the standard way (zero mean rows, standardize variance), before removing African and Chinese individuals from the rows, so that their ancestry is represented but they are not projected. We then used the R function 'svd' to perform a Singular Value Decomposition (theoretically and practically equivalent to computing the Principal Components). This is shown in Figure S11.10.

As expected, variation in the large modern dataset dominates the picture. Further, the early PCs are dominated by within-population structure. While PC1 describes similarity with Africa for high values, PC2 describes Finnish ancestry, PC3 reflects variation within Finnish ancestry, PC4 describes Norwegian ancestry, and PC5 describes variation within Norway at one end of its range. PC8 describes the first batch effect between modern and ancient samples; that it is a relatively small effect compared to the population structure is an additional indicator that the imputation procedure has not biased inference.

The story for Modern-vs-ancient Finnish ancestry is consistent, with ancient Finns looking much less extreme than the moderns. Conversely, ancient Norwegians look like less-drifted modern Norwegians; the Danish admixture seen through the use of ancient DNA is hard to detect because of the extreme drift within Norway that has occurred since the admixture event. PC4 vs PC5 is the most important plot for the ancient DNA story: Sweden and the UK (along with Poland, Italy, and to an extent also Norway) are visibly extremes of a distribution the same 'genes-mirror-geography'⁴ that was seen in the Ancient-palette analysis. PC1 vs PC2 tells the same story—and stronger, since this is a high variance-explained PC—for the UK, Poland, and Italy.

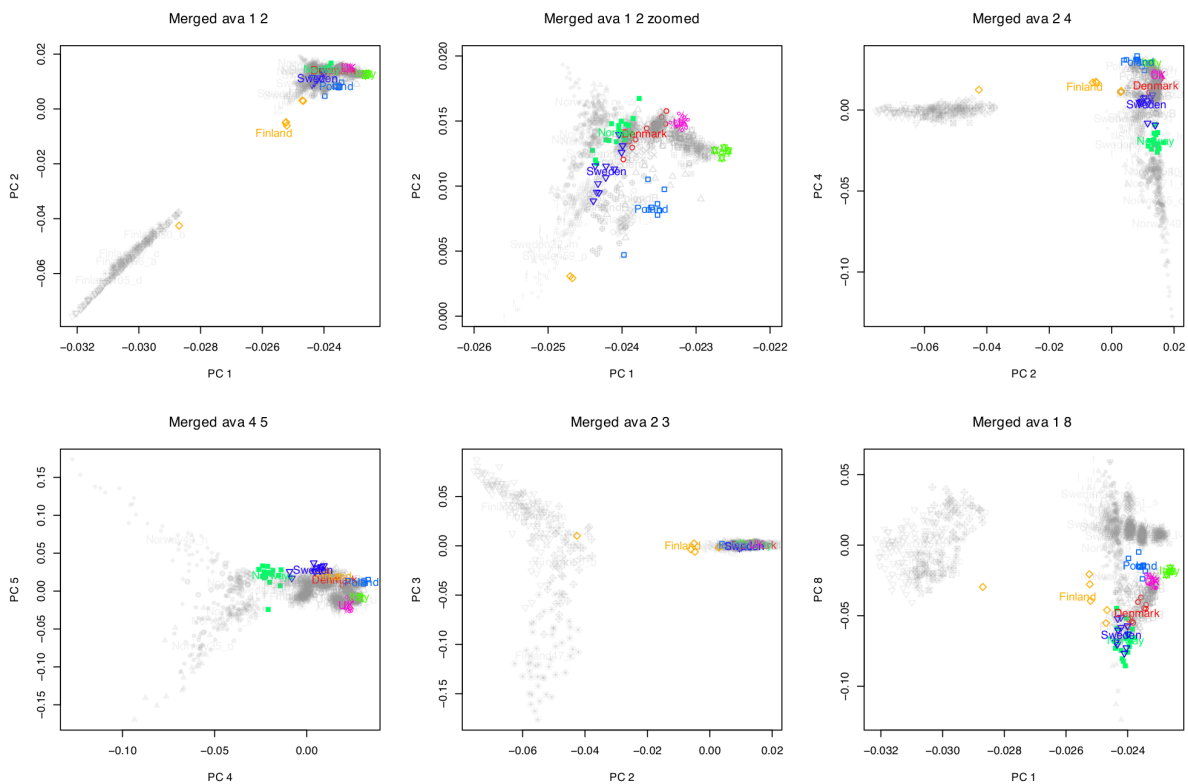


Fig. S11.10: PCA of the ancient and modern samples using no palette (see text), showing selected PCs to illustrate the salient features. Modern individuals are grey and the $K=7$ ancient panel surrogate populations are shown in strong colors. Based on $n=255$ ancient + 1675 modern samples.

PCA should be carefully interpreted as it can easily be misleading^{3,5}. For example, individuals from very different populations can be mapped to the same location in some PCs if they do not differ in their variation in the directions displayed. The PCs are also dominated by variance components that represent a large number of individuals (e.g. modern variation), or a few individuals that share a large fraction of the variance (e.g. Finnish). Despite these problems, the PC analysis provides support for the inferences described through the chromosome painting admixture analysis.

11.10. Interpretation: Inference of historical ancestry sharing using Chromosome Painting

The first summary of the data to consider is the population averages of ancestry by population, commonly called the confusion matrix. This is shown in Figure S11.11, which as a sensitivity analysis includes an analysis based on 'chunk counts' as used by FineSTRUCTURE as well as the total amount of genome shared, called chunk lengths, on which all other inference is based.

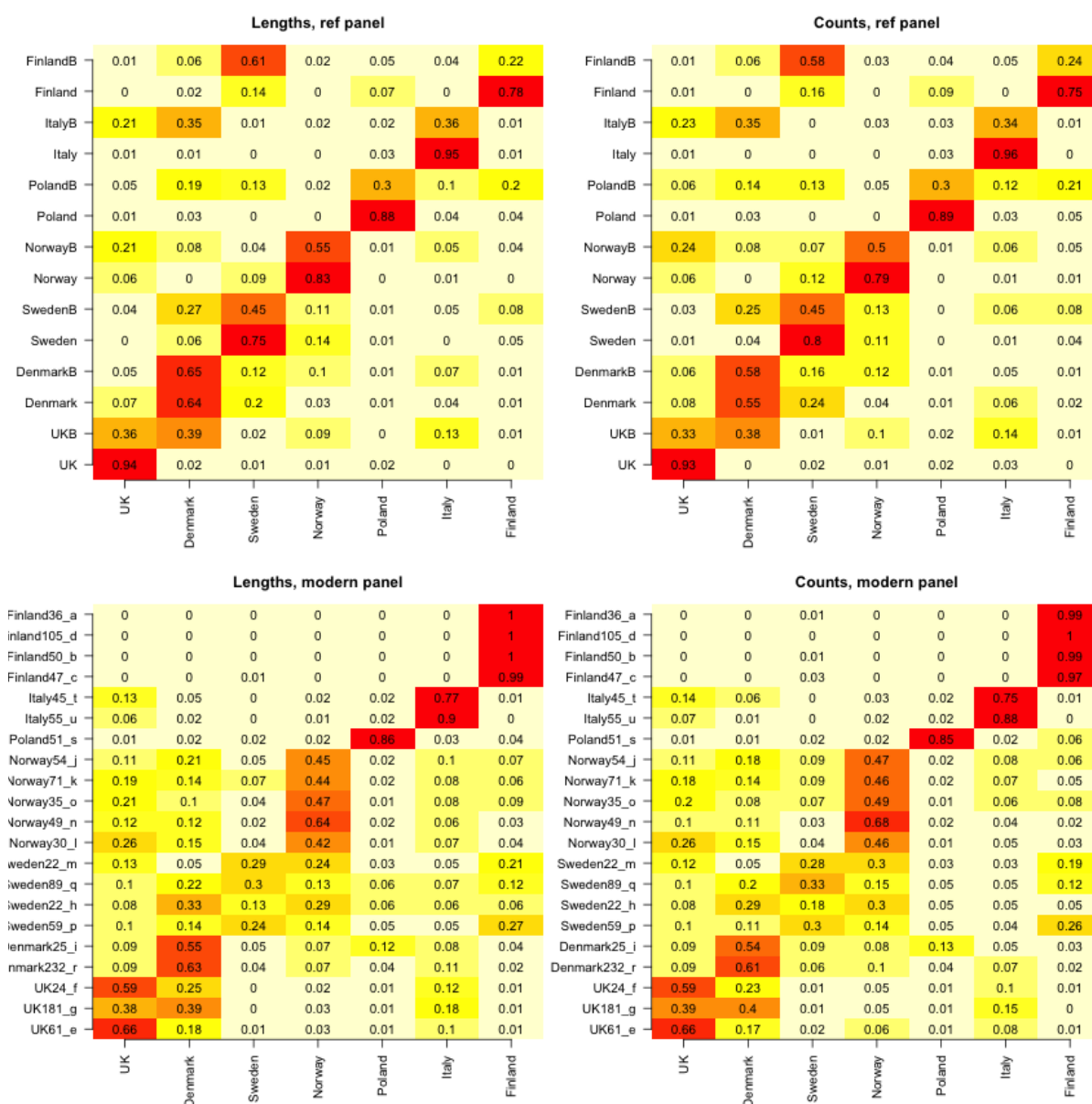


Fig. S11.11: Left: results based on inference using the total length of genome shared with individuals from each donor population. Right: results based on inference using the total number of 'chunks' (most recent recombination events). Top: ancient panel (n=255). Bottom: modern panel (n=1554).

The general structure of this inference is:

- We can recover the representative donors' reference populations well.
- Lengths perform slightly better than counts for this problem.
- The populations labelled 'B', who are 'non-representative donors' are always more of a mixture than the 'representative donors'.
- Norwegian ancestry is found primarily in Scandinavia, with small amounts in UKB.
- Swedish ancestry is found primarily in Sweden and Scandinavia, though is also found in Finland and PolandB.
- UK ancestry is found primarily in the UK but also in the ItalyB and NorwayB populations.
- Denmark ancestry is found in nearly every B population though is lowest in NorwayB and FinlandB.

- h) Poland ancestry is restricted to Poland and Finland.
- i) Italy ancestry is found in all B populations and no representative populations.
- j) Finland ancestry is found in Finland, PolandB and SwedenB only.

These are inferred populations that were labelled based on which ancestral population 'was closest to them', rather than which they were closest to. Empirically this is symmetric for all cases except FinlandB, who are more related to Sweden than Finland on average.

Figure S11.12 shows the same results as Figure S11.11 (for admixture) and Figure S11.6 (for palettes) but presented by labels, that is, the region, country and age of each set of samples. It must be remembered that the individuals concerned were found in heterogeneous locations and where there are multiple individuals, may be heterogeneous genetically. To explore diversity of sites explicitly, we devised a measure of diversity that could characterise highly diverse vs homogeneous sample labels, shown in Extended Data Fig. 5.

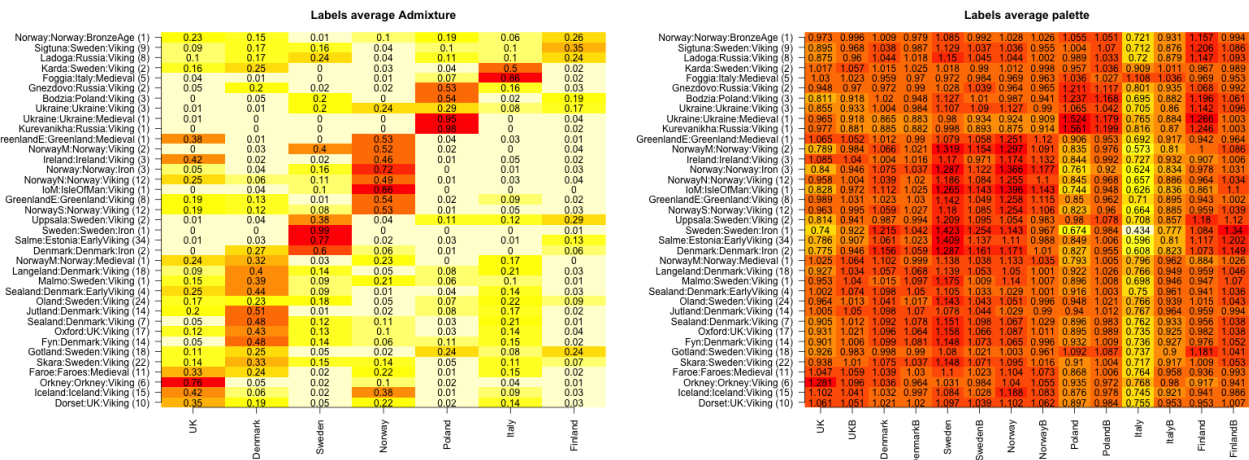


Fig. S11.12: Results presented in terms of the labels, which are shown in 'Region:Country:Age (sample size)' format. Left: Inferred ancestry. Right: Average painting palettes. Based on n=255 ancient unrelated individuals.

For the purpose of characterising diversity there is not a ready off-the-shelf measure. The data consist of a diversity of probability vectors. We quantify their diversity by computing the average Kullback-Leibler (KL) Divergence for each individual label from the average of that label:

$$D(A^{(l)}) = \frac{1}{n_l} \sum_{i=1}^{n_l} KL(A_i^{(l)} || p^{(l)})$$

where $A^{(l)}$ is the n_l by K matrix of ancestry estimates in label l , $p^{(l)}$ is the length K vector of average ancestries in that label, and $KL(Q || P) = \sum_{k=1}^K q_k \log_2 \left(\frac{q_k}{p_k} \right)$. This therefore classifies a population as 'diverse' if there is a large deviation of individual ancestry estimates away from the average ancestry in that population.

We confirm that this score is well-calibrated using simulations. We simulated from a hierarchical dirichlet setup where we make a random 'population mean' $\alpha \sim \text{Dirichlet}(\text{rep}(\alpha_0, K))$ and then sample individuals $x_i \sim \text{Dirichlet}(\alpha)$. This is shown in Figure S11.13 (right), with a search of good

choices of α_0 (left) being guided by the fit to the data under a normal distribution approximation. This simulation confirms that the diversity measure is appropriate for the data.

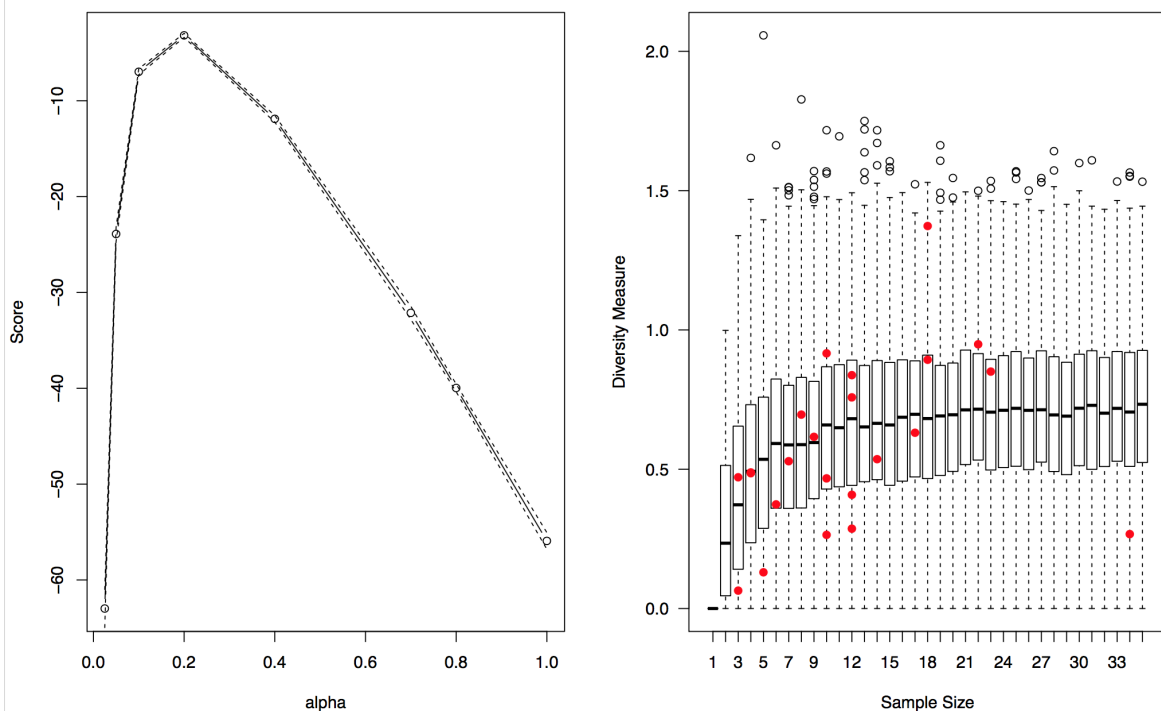


Fig. S11.13: Simulated diversity measures for labels. Left: quality of fit of simulations to the data as a function of a tuning parameter α_0 (see text). Right: simulated data (boxplots) and observed data (red dots) as a function of sample size, to check model fit. Note that the distribution is testing model fit, not statistical significance of diversity. Based on $n=1000$ simulations per sample size. Observed data is based on $n=255$ unrelated ancient samples. Boxes show the 1st-3rd quantiles with the whiskers extending to 1.5x the interquartile range, or the last point, whichever is closer to the median.

This exploration of diversity raises several points. First, Bodzia (associated with our ‘Poland’ population), Foggia (associated with our ‘Italy’ population), and Salme (associated with our ‘Sweden’ population) are relatively homogeneous. Dorset is also homogeneous, containing primarily ‘Norway’ or ‘UK’ ancestry.

Extreme diversity is seen in Gotland, a well-known trading location. Other locations such as Skara and northern Norway are diverse due to the presence of UK, Danish, Swedish, and Norwegian ancestry. The overall picture is of high-diversity—and high heterogeneity—in Scandinavia, brought in from outside. Sampling must be considered for the peripheral regions, which were sampled to target Viking cultural burial.

11.11. Modern interpretation: Inference of historical ancestry sharing using Chromosome Painting

The estimates in Figure S11.11 of ancestry in modern populations from historical populations is a mean, and therefore does not separate ancestry contributions from recent admixture from that which is typical of the population. The median is not affected by some individuals with relatively recent ancestry, but instead produces estimates that do not sum to 1. To estimate ancestry of populations,

we therefore consider the *spatial median* of the individual ancestry estimates using the R package 'ICSNP'²⁴⁷, which is a multivariate extension of the median that preserves the sum.

We estimate confidence intervals by using the *same* bootstrap resampled individuals as described above and recomputing the spatial median for each population. We report the 95% confidence range (2.5% and 97.5% quantiles).

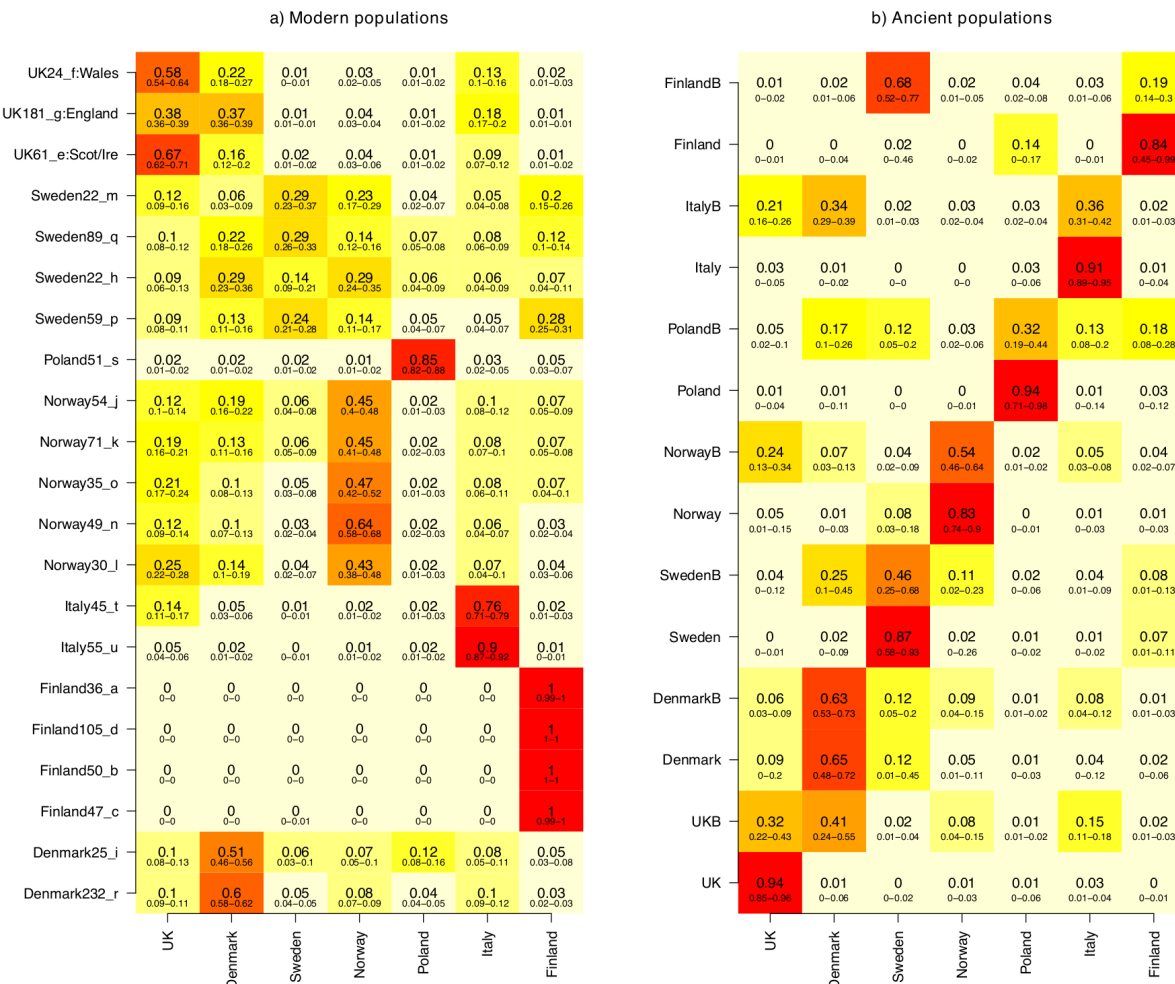


Fig. S11.14: Population-based admixture estimates based on the spatial median, as described in the text. a) estimates of the proportion of ancient populations in modern populations. b) estimates of the proportion of ancient populations in ancient samples. Based on n=255 ancient unrelated individuals and n=1554 unrelated modern individuals.

Figure S11.15 shows our best estimates for modern populations, and the ancient sample groupings, based on this spatial median approach. The ancient reference populations are all seen as broadly their own population. The ancient non-reference populations may not be meaningful as they are not expected to be homogenous. However, the modern populations are relatively homogeneous and the spatial median should represent the typical individual from these populations.

From this, we can see the spread of ancestry during and around the Viking era:

- UK populations all have high 'Denmark' ancestry. Although Anglo-Saxon and Danish Viking ancestry are hard to distinguish, Viking-era Danes have too much 'Sweden' ancestry to have

contributed more than around 6% ancestry into England, whereas they could plausibly have contributed all (up to 16%) of the Scottish and Irish signal. Anglo-Saxon samples are needed to explore this further.

- The ‘Norway’ ancestry signal in the British Isles cannot be explained via Danish or Anglo-Saxon contribution. These fractions (4% in England, Scotland, and Ireland, 3% in Wales) likely correspond to the Norwegian Viking legacy in Britain.
- Modern UK individuals contain around 9-18% ‘Italian’ ancestry, plausibly associated with the Normans and associated increase in population movement during that era. This is a two-way process, with high fractions of the ‘UK-like’ ancestry in a sub-population of Italians.
- Modern Norwegians are structured by their proportion of ‘UK’ and ‘Danish’ ancestry.
- Modern Swedes are structured by a ‘Finland’-like group, a ‘Denmark’ plus ‘Norway’ group, and a ‘UK’ group.
- Modern Danes are structured into high and low ‘Polish’ ancestry groups, both with similar amounts of ‘Norway’ and ‘UK’ ancestry, suggesting that these admixtures occurred earlier. Indeed, the ancient panel implies that this process started in the Viking era, where the high confidence interval is explained by high inter-individual variation.

To understand the biases involved in the use of spatial.median we plot the estimates from this procedure compared to the individual data in Figure S11.15. From this it is clear that small estimates are biased upwards from the sample median for each ancestry, due to the constraint that ancestries should sum to 1. This has been accounted for in the discussion above.

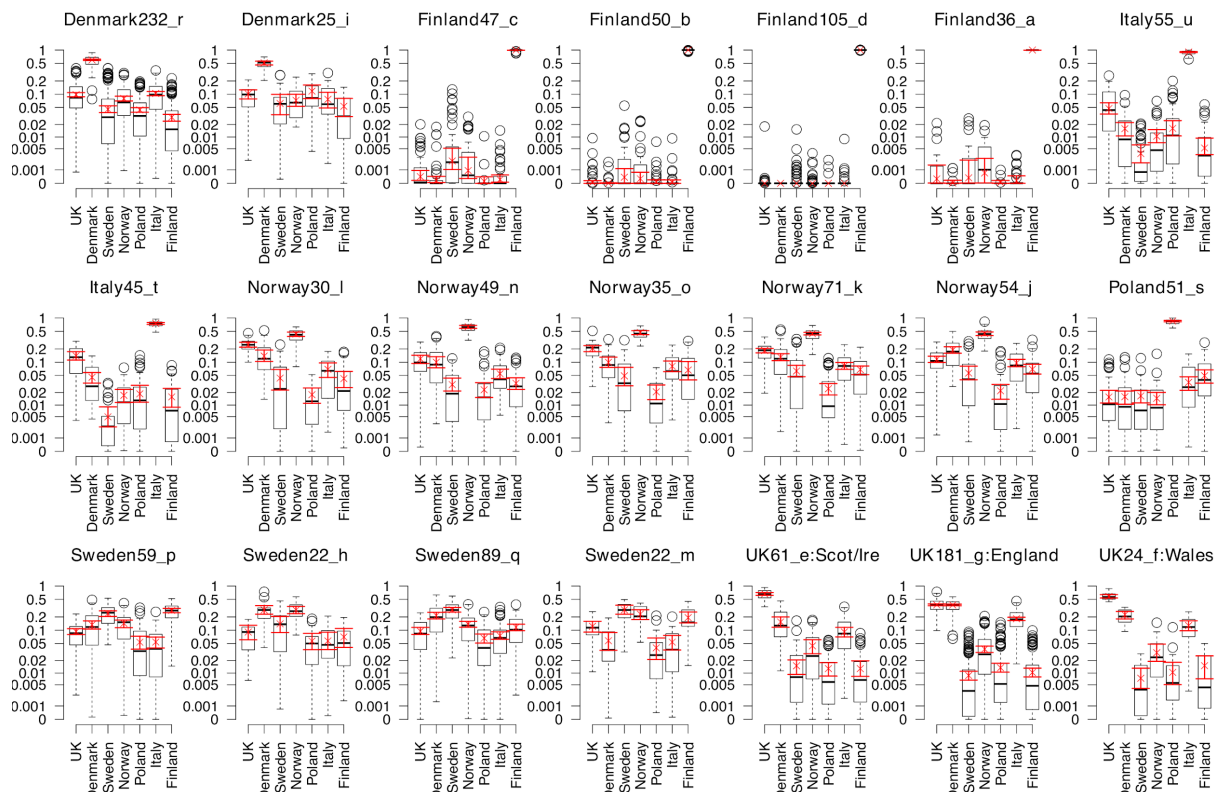


Fig. S11.15: Spatial median estimates (red; crosses for best estimate with range shown) and individual estimates (black; reported as a boxplot) for each modern population using the 7 ancient reference

populations. Black horizontal bars denote the median for each sample. Based on 1554 unrelated modern individuals.

11.12. The Pictish Genomes

The Viking identity was not necessarily always associated with Scandinavian genetic ancestry. Archaeological evidence indicates that four higher-coverage VA individuals from three different archaeological sites in the Orkney Islands have Scandinavian cultural links^{122,125}. However, two of these samples, VK202 and VK207, have over 85% ‘North Atlantic’ ancestry and are genetically similar to present-day Irish and Scottish populations (Figs S11.3, S11.12, S11.14, Supplementary Table 6), which is in contrast to the available isotopic evidence²⁴⁸. Haplotype-based analyses corroborate that two of these samples possess local genetic ancestries, with little Scandinavian contribution, aligning them with two local Pictish skeletons. The other two individuals, VK204 and VK205, displayed c. 50% ‘Norwegian-like’ and ‘Danish-like’ ancestries (Supplementary Table 6), respectively, which may indicate admixture between the locals and Scandinavians in Orkney during the VA. Our interpretation of the Orkney samples can be summarised as follows. First, they represent ‘native British’ ancestry rather than an unusual type of Scandinavian ancestry. Second, that this ‘British’ ancestry was found in Britain before the Anglo-Saxon migrations. Lastly, that in Orkney, the VA individuals would have descended from Pictish populations. The evidence for this interpretation is:

1. In Figure S11.10 showing modern and ancient samples painted together and analysed using PCA without any supervision, the ‘UK’ cluster is far from Scandinavia in PC1-2 and PC4-5, and PC3 describes drift inside modern Finland.
2. In Figure S11.9 showing modern and ancient samples painted together and analysed using PCA after projection into our supervised clusters, the ‘UK’ cluster is further outlying. In PC1-3 it clusters with nothing but is closest to ‘Italy’ and ‘Poland’. In PC4 it is an extreme point opposite Poland and Finland.
3. In Figure S11.3 showing ancient individuals painted against modern populations, the Orkney individuals best match modern Scottish populations (UK61_e), and show no particular affinity to modern Scandinavian ancestry. In Figure S11.4 showing the importance of modern populations for ancient samples, the modern UK populations do not well describe this variation.
4. In Figure S11.6a-b showing the painting of ancient population clusters against one another, the UK population is rarely used to describe Scandinavians (low values in the ‘UK’ column), whereas the Italians do. Conversely, the ‘UK’ population does use an excess of Norway ancestry, implying a degree of contemporary admixture into that population (likely due to low sample sizes of un-admixed individuals).
5. In Figure S11.6c-d showing the painting of modern population clusters against ancients, the Irish and Scottish (UK61_e) and Welsh (UK24_f) populations receive the most ‘UK’ ancestry. This is followed by Italy, and then some Norwegian subpopulations into which British is known to have been taken.
6. In Figure S11.11 showing the inferred ancestry of ancient populations, ‘UK’ ancestry is little seen in other main clusters, and appears in known admixtures including ‘NorwayB’ and ‘ItalyB’.
7. In Figure S11.12 showing the inferred ancestry of ancient sampling locations, ‘UK’ ancestry is found at highest proportions in Orkney, Iceland, Ireland, Dorset in England, and medieval Faroe Islands.
8. Of the 10 individuals with more than 80% ‘UK’ ancestry (Supplementary Table 6) only four are in Orkney and one in Ireland. Of these four, two were archaeologically identified as

Pictish. The rest are in Scandinavia during the Viking period: Norway (VK386, VK525, VK528) and Sweden (VK456, VK405). These populations are sampled more heavily and the overall rate of 'UK' ancestry in those locations is low. This is consistent with the migration of individuals with 'UK' ancestry into Scandinavia rather than a population present in Scandinavia.

9. In Figure S11.14-15 showing modern admixture estimates, the 'UK' fraction is ordered: Scotland and Ireland, Wales, England, Norway³⁰, rest of Norway, northern Italy, Denmark, and Sweden. This indicates that this ancestry is located in the UK today, though widely distributed throughout Europe. Note that we have not shown whether the signal in Italy is due to post-Viking era admixture or a signal of ancient population structure.

Therefore 'UK' represents a group from which modern British and Irish people all receive an ancestry component. This information together implies that within the sampling frame of our data, they are proxying the 'Briton' component in UK ancestry; that is, a pre-Roman genetic component present across the UK. Given the location that the VA individuals were found in Orkney, this makes it very likely that they were descended from a Pictish population.

Modern genetic variation within the UK²⁰² sees variation between 'native Briton' populations in Wales, Scotland, Cornwall, and Ireland as large compared to that within the more 'Anglo-Saxon' English. This is despite subsequent gene flow into those populations from English-like populations. We have not attempted to disentangle modern genetic drift from historically distinct populations. Roman-era period people in England, Wales, Ireland, and Scotland may not have been genetically close to these Orkney individuals, but our results show that they have a shared genetic component as they represent the same direction of variation.

Supplementary Note 12 - Spatiotemporal patterns of ancestry in the Viking World

Viking society is particularly famous for its ship technology, allowing for fast transport of large numbers of individuals in a single vessel²⁴⁹. These vessels enabled the Vikings not only to carry out lucrative raids and extend trade routes across western Eurasia, but also to reach and settle lands in the North Atlantic^{250–253}. Based on historical and archaeological data, Vikings were present in both western and eastern Europe, reaching perhaps as far as the Pontic Steppe and the Middle East^{254,255}. It is commonly believed that the westward migrations and raids were mainly carried out by people from what are now Norway and Denmark in the 9th and 10th centuries CE. In contrast to the western movements, the eastward expansions are commonly believed to have been carried out by Swedish Vikings, trading along navigable river systems and overland caravan routes²⁵⁵. These people formed a major component in the complex ethnic group known as the Rus', and are also credited for being active in the formation of the first Russian state^{256,257}.

To visualise the migration patterns of the Vikings we used inverse distance weighting interpolation implemented in the function 'idw' of the R package *gstat* to interpolate the proportion of each ancient genome that was attributed by our fineStructure analysis (Supplementary Table 6) to one of the pre-defined ancestry groups: 'UK', 'Denmark', 'Norway', 'Sweden', 'Italy', 'Poland', and 'Finland'. We used the Shepard method of interpolation^{258,259} with the weight for a given interpolation location x equal to $1/(d(x,v)^2)$ where v is the location of an observed sample and $d(a,b)$ is the distance between two points a and b . For plotting maps, we used a Mercator projection and downloaded coastal contours at 1:50m scale from Natural Earth: <https://www.naturalearthdata.com/>. We chose to plot a Europe-wide (including Greenland) map (Figure S12.1) and smaller maps of particular regions of interest: Scandinavia (Figures S12.2-S12.4), the British Isles (Figure S12.5), and the Baltic region (Figure S12.6). For the Europe-wide map, we used an interpolation point grid size of $0.2^\circ \times 0.2^\circ$. For all other maps, we used a grid size of $0.1^\circ \times 0.13^\circ$. As our densest temporal sampling was for Scandinavia, we made separate Scandinavian maps for the Iron Age (Figure S12.2), the early VA (Figure S12.3) and the entire VA (Figure S12.4). For all other maps, we combined samples across time periods, but the vast majority of our samples were from the VA, so our signal was dominated by this particular period: we only have VA samples from the British Isles, while for the Baltic region we only have Viking and early VA samples. In addition, we also present the non-interpolated version of Figure 4 in the main text to visualize the results without possible distortions due to interpolation (Figure S12.7).

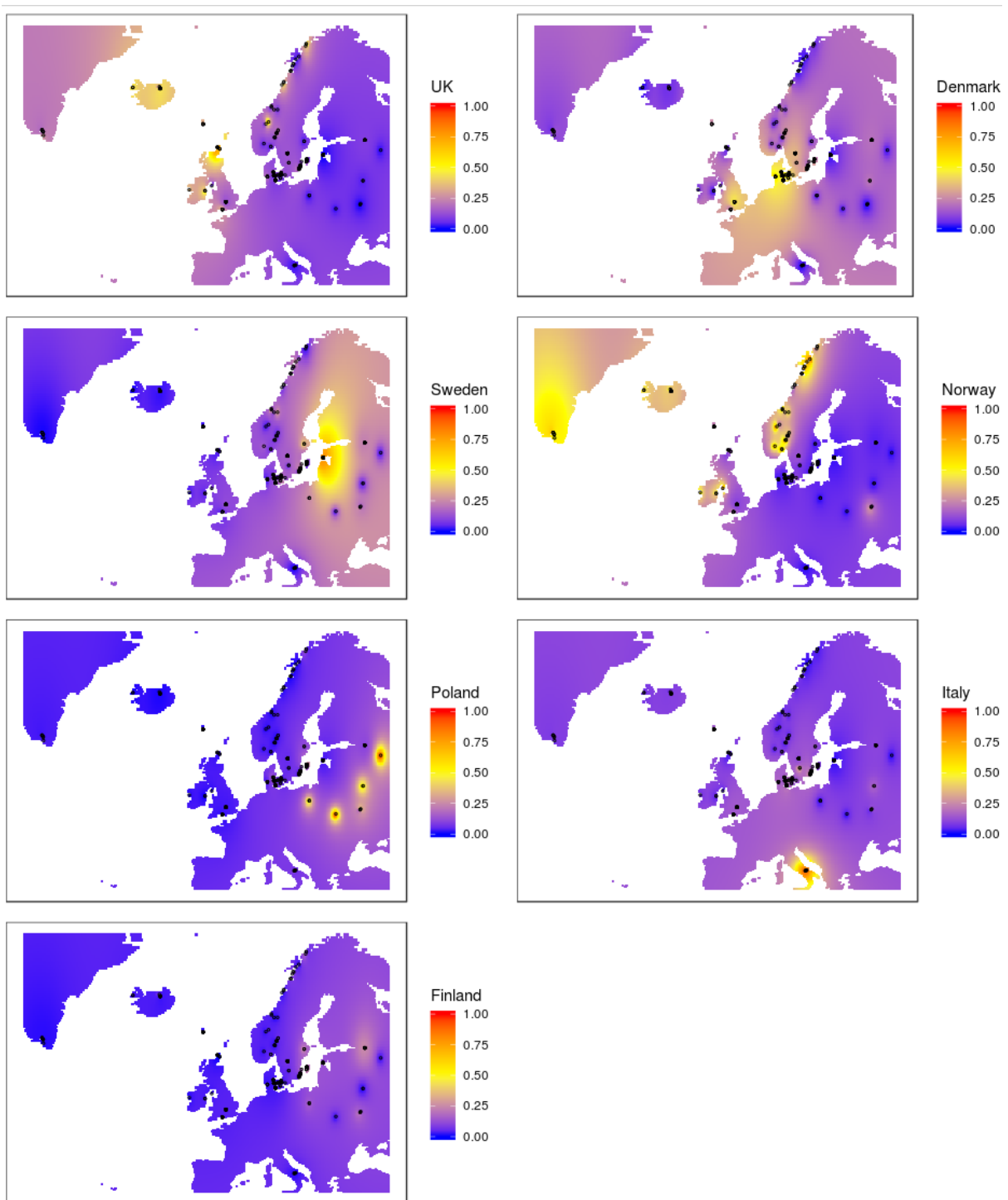


Fig. S12.1: Maps of interpolated *fineStructure* ancestries for Europe and Greenland, combining Iron Age, early VA, VA, and early medieval samples. $n = 289$ genomes used for interpolation.

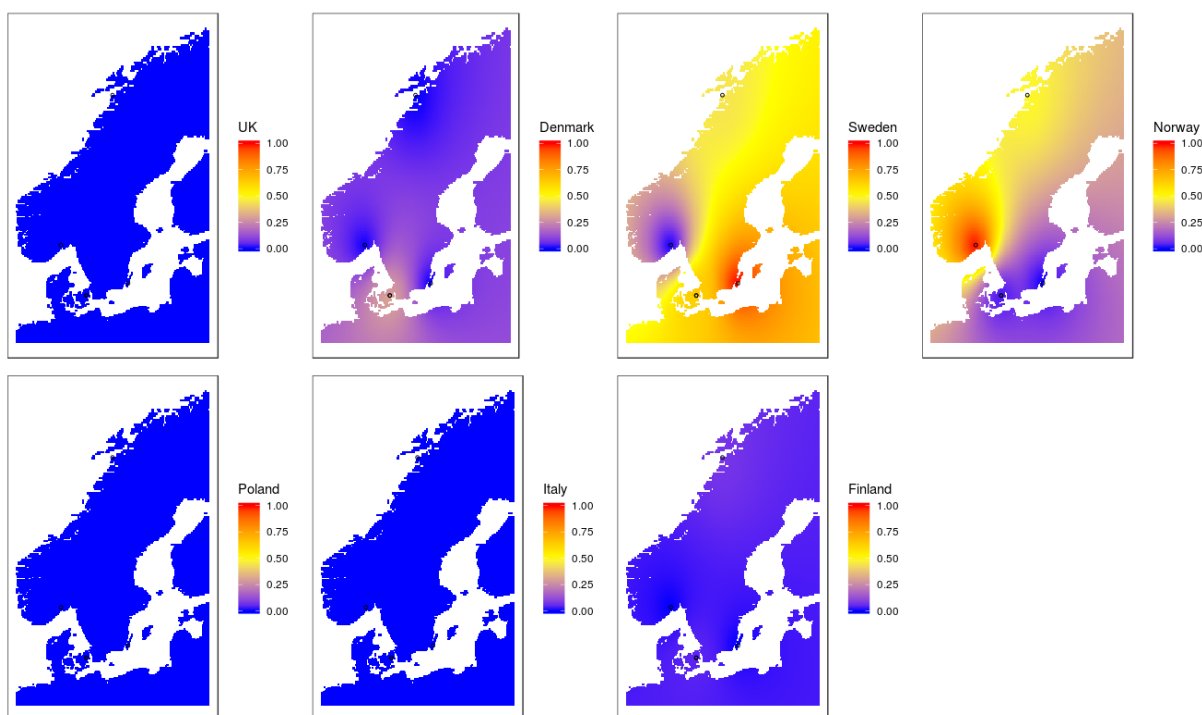


Fig. S12.2: Maps of interpolated *fineStructure* ancestries for Iron Age samples, focusing on the Scandinavian part of the map. $n = 7$ genomes used for interpolation.

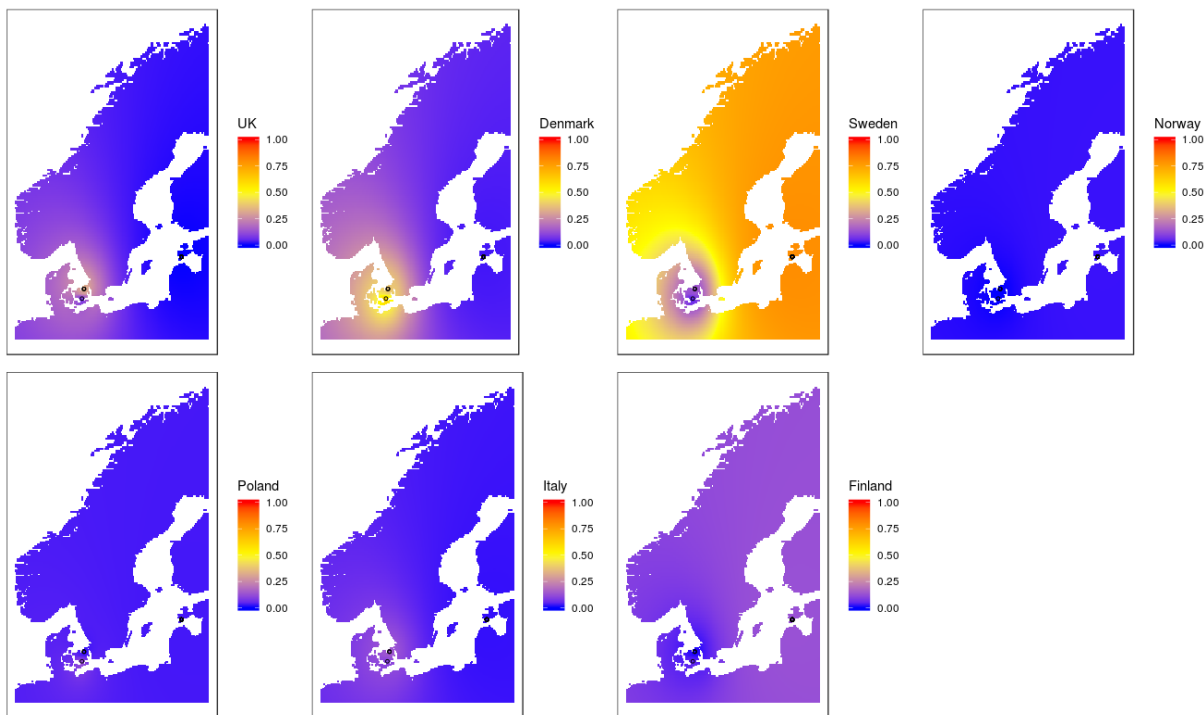


Fig. S12.3: Maps of interpolated *fineStructure* ancestries for early VA samples, focusing on the Scandinavian part of the map. $n = 38$ genome used for interpolation.

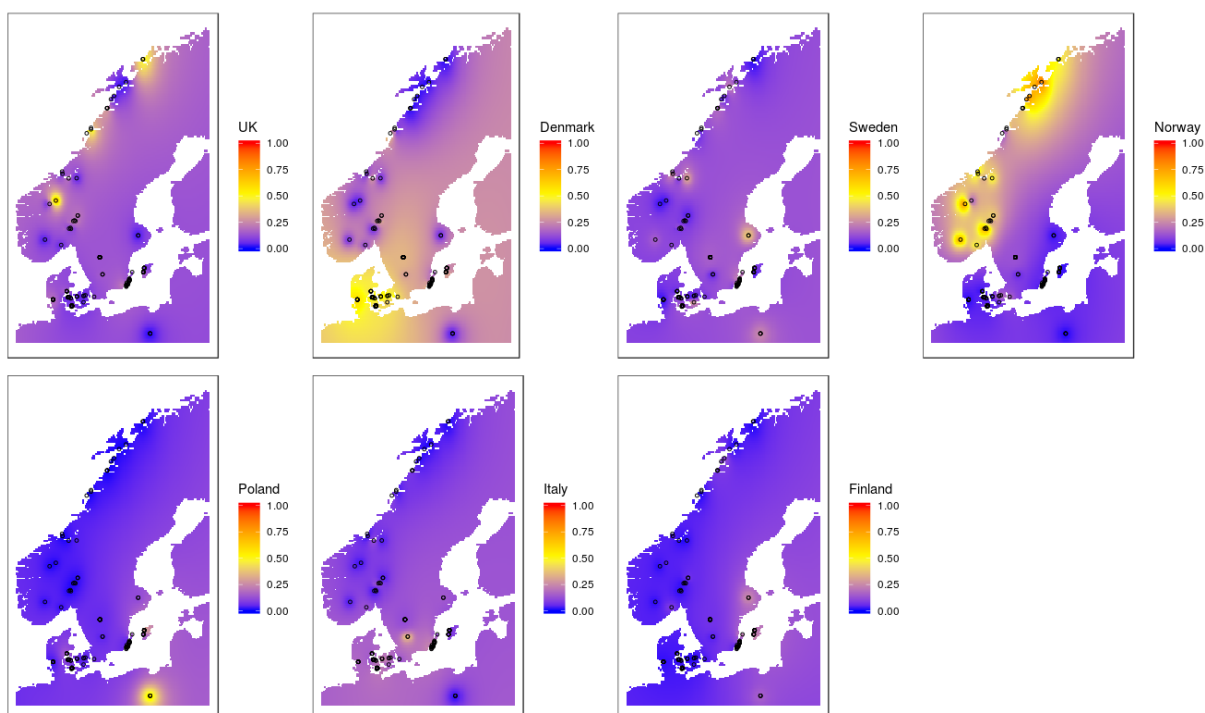


Fig. S12.4: Maps of interpolated *fineStructure* ancestries for VA samples, focusing on the Scandinavian part of the map. $n = 230$ genomes used for interpolation

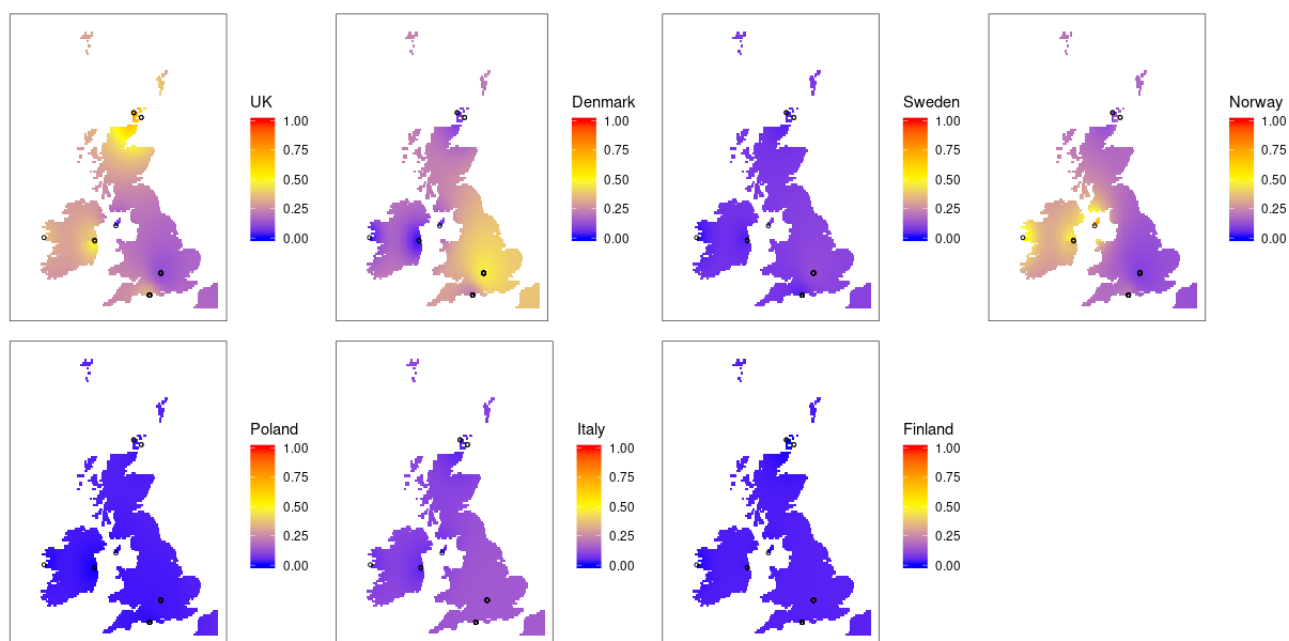


Fig. S12.5: Maps of interpolated *fineStructure* ancestries for VA samples, focusing on the section of the map containing the British Isles. $n = 230$ genomes used for interpolation.

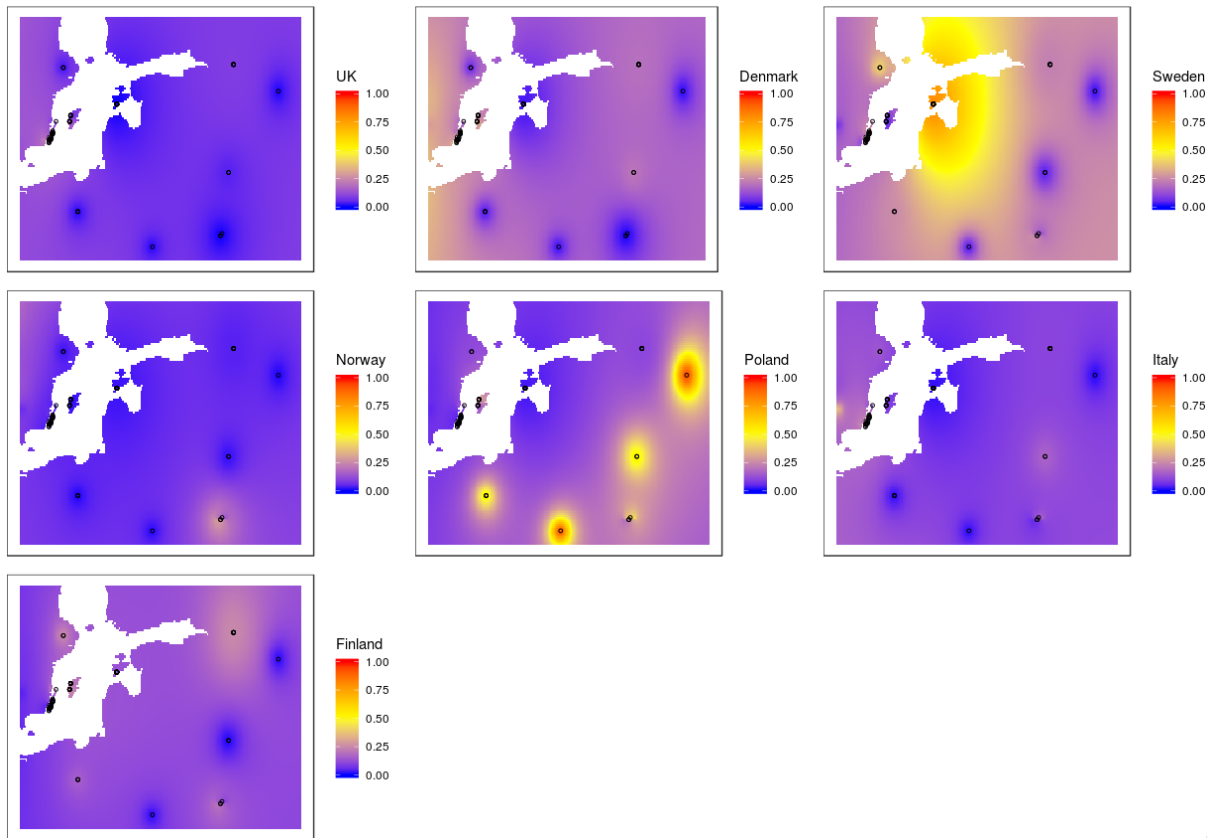


Fig. S12.6: Maps of interpolated *fineStructure* ancestries for early Viking and VA samples, focusing on the Baltic region. $n = 268$ genomes used for interpolation.

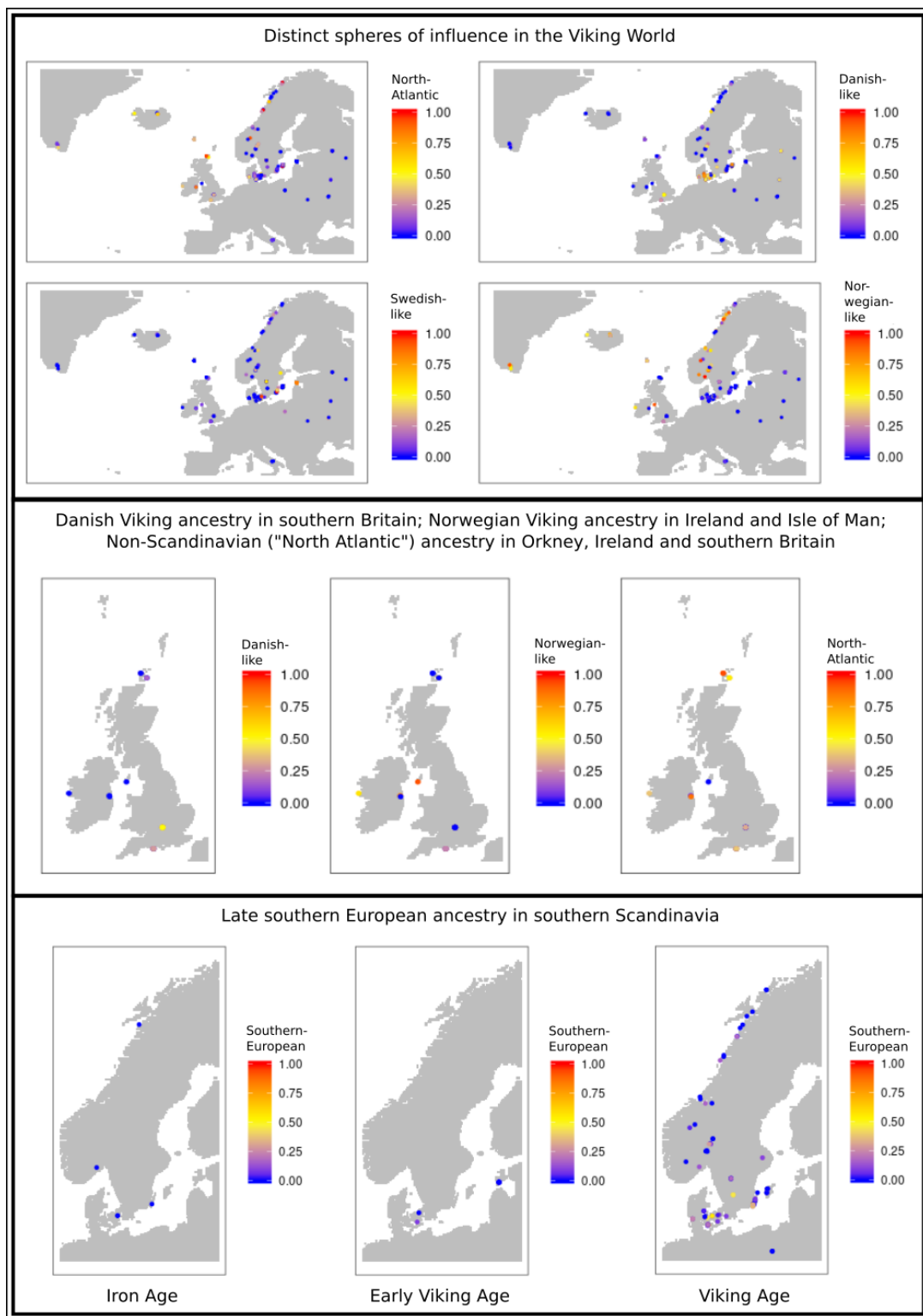


Fig. S12.7: Spatiotemporal patterns of Viking and non-Viking ancestry in Europe during the IA, EVA and VA. This figure is the non-interpolated version of Figure 4. $n = 289$ genomes.

Supplementary Note 13 - Lactase persistence and pigmentation SNPs

13.1. Lactase persistence

To investigate the level of lactase persistence in the ancient population we estimated the derived 'A' allele frequency of the SNP rs4988235 known to affect expression of the lactase LCT gene. The ancestral 'G' allele is responsible for lactase intolerance in adult Europeans²⁶⁰. Because most of the ancient samples were sequenced at low depth of coverage, the ANGSD software package was used to estimate the allele frequencies of the ancient population based on the genotype likelihood data. We used the five European populations (CEU – northern European, FIN – Fins, GBR – British, TSI – Italy, IBS – Spain) and two outgroups (Yoruba – YRI; Chinese – CHB) from the 1000 Genomes Project as comparative groups as well as the modern Danish population from the IPSYCH case-cohort study²⁶¹. We also included geographically proximate Iron and Bronze Age populations to trace frequency shifts of SNP rs4988235 through time. The results are presented in Extended Data Fig. 8b.

13.2. Pigmentation

Having a large number of ancient individuals allowed us to assess the frequencies of SNPs responsible for pigmentation phenotypes of the ancient dataset (Vikings) at population level. For this analysis we used ancient individuals from the whole VA (i.e. early VA plus VA) from Scandinavia.

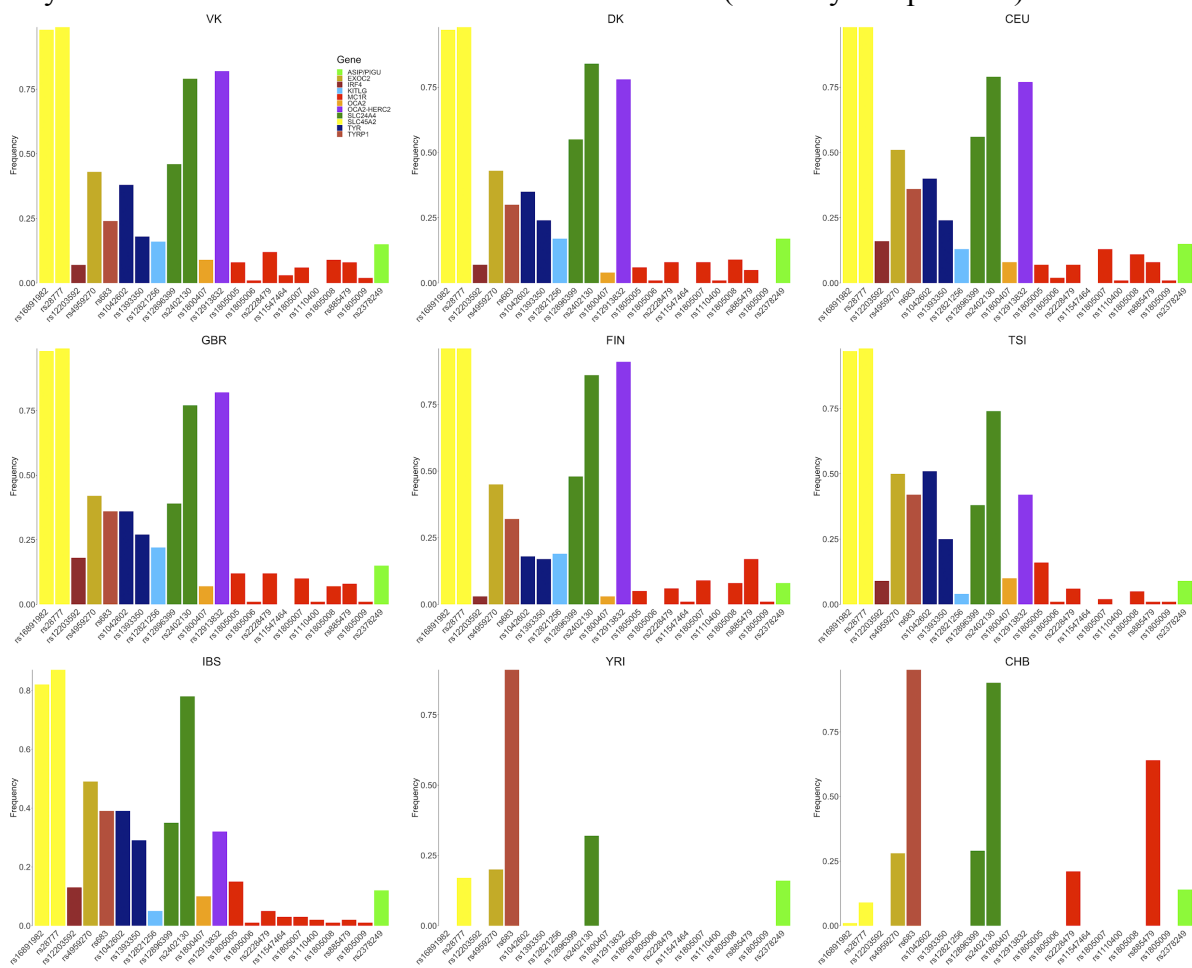


Fig. S13.1: The frequencies of derived SNPs with strongest influence on human pigmentation phenotype in Viking ('VK') and comparative groups. The rs IDs of the SNPs are indicated on the X

axis. The genes that contain these SNPs are mentioned in the figure legend. Eight additional populations are also included for comparison: CEU, FIN, GBR, TSI, IBS; YRI; CHB from the 1000 Genomes project and 'DK' representing the modern Danish population from IPSYCH case-cohort study.

The SNPs with strongest association with lighter hair and eye pigmentation phenotypes such as the ones in *HERC2*, *OCA2*, and *TYR* genes in humans are elevated in the Viking population, and the profile of allele frequency distribution is close to the present-day northern European population represented here by the 'CEU' (1000 Genomes Project) and the modern Danish population ('DK') from IPSYCH case-cohort study. The frequencies of informative SNPs associated with pigmentation are presented in Figure S13.1. This suggests that the genetic profile of pigmentation SNPs we observe in northern Europeans today had been largely formed at the onset of the Viking period. Nevertheless, it is important to stress that the genotypes of these SNPs are not fixed across the sequenced individuals, and that there is therefore not a single 'Viking phenotype'. For example, we have applied the HIrisPlex²⁶² model to predict the hair and eye colour for two ancient individuals with highest average sequencing depth of coverage, i.e. VK1 and VK42, using imputed genotypes for both individuals. Both have different pigmentation phenotypes: VK42 from Skara, Sweden, has alleles associated with brown eyes and dark hair coloration, while VK1 from Greenland has alleles associated with blue eyes and lighter hair.

Table S13.1: The list of SNPs used for the HIrisPlex model for the VK1 and VK42 samples.

Chromosome	Pos	SNP ID	Gene	Ref	Alt	VK1	VK42
5	33951693	rs16891982	SLC45A2	C	G	G/G	G/G
5	33958959	rs28777	SLC45A2	C	A	A/A	A/A
6	396321	rs12203592	IRF4	C	T	C/C	C/C
6	457748	rs4959270	EXOC2- LOC105374875	C	A	C/C	C/A
9	12709305	rs683	TYRP1	C	A	A/A	A/A
11	88911696	rs1042602	TYR	C	A	C/A	C/A
11	89011046	rs1393350	TYR	G	A	G/G	G/G
12	89328335	rs12821256	KITLG	T	C	T/T	T/T
14	92773663	rs12896399	SLC24A4- LOC105370627	G	T	G/G	T/T
14	92801203	rs2402130	SLC24A4	G	A	A/A	A/A
15	28230318	rs1800407	OCA2	C	T	C/C	C/C
15	28365618	rs12913832	HERC2	A	G	G/G	A/A
16	89985844	rs1805005	MC1R	G	T	G/G	G/G

16	89985918	rs1805006	MC1R	C	A	C/C	C/C
16	89985940	rs2228479	MC1R	G	A	G/A	G/G
16	89986091	rs11547464	MC1R	G	A	G/G	G/G
16	89986117	rs1805007	MC1R	C	T	C/C	C/C
16	89986130	rs1110400	MC1R	T	C	T/T	T/T
16	89986144	rs1805008	MC1R	C	T	C/C	C/C
16	89986154	rs885479	MC1R	G	A	G/A	G/G
16	89986546	rs1805009	MC1R	G	C	G/G	G/G
20	33218090	rs2378249	ASIP-PIGU	G	A	G/A	A/A

Table S13.1 summarizes the genotypes of each of the 22 SNPs used for phenotype analysis. For individual VK1: the estimated probability of having blue eyes was 0.85, while the hair color probabilities were blond (0.63), brown (0.29), red (0.01) and black (0.07). For individual VK42, the estimated probability of having brown eyes was 0.98, while the hair color probabilities were blond (0.15), brown (0.6), red (0.001) and black (0.25).

Supplementary Note 14 - Finding signatures of selection in Europe in the past ten millennia

14.1. Introduction

We aimed to find SNPs whose allele frequencies changed significantly in the last 10,000 years, using our ancient human genomes to look at the frequencies of alleles in the past. We combined our VA and IA genomes with previously published present-day, Bronze Age, Neolithic, and Mesolithic sequence data typed at the Human Origins array (see Supplementary Note 6). We filtered for genomes that were younger than 8,000 BCE and that were located within a bounding box encompassing the European continent: $30 < \text{latitude} < 75$ and $-15 < \text{longitude} < 45$. We then used neoscan in Ohana^{263,264} to look for variants whose allele frequencies were strongly associated with time, after controlling for genome-wide changes in ancestry that might have also occurred over time. We only analyzed sites with a minor allele frequency $> 1\%$.

14.2. Methods

Briefly, Ohana works by modelling the allele frequencies across a specific number (K) of ancestry components via a multivariate Gaussian distribution. Each genome is modeled as a mixture of 1 or more components. For more details see Cheng et al.^{263,264}. After genome-wide ancestry component estimation via qpas, the neoscan method implemented in Ohana²⁶⁵ tests a model in which the frequency of an allele at a site is determined by the genome-wide-estimated ancestry components against a model in which the frequency is also influenced by a free parameter (alpha) that determines the dependence of this frequency on the time at which a genome was sampled. Thus, at each SNP, neoscan computes a log-likelihood ratio that is equal to $2 \cdot (\text{best local log likelihood} - \text{global log likelihood})$. The global log likelihood is:

$$H_0 : \ln(L_j) = \sum_i \left(g_{ij} \cdot \ln \left(\sum_k \left(q_{ik} \cdot f_{kj}^{\text{est}} \right) \right) + (2 - g_{ij}) \cdot \ln \left(\sum_k \left(q_{ik} \cdot (1 - f_{kj}^{\text{est}}) \right) \right) \right)$$

In turn, the local log likelihood is:

$$H_a : \ln(L_j) = \sum_i \left(g_{ij} \cdot \ln \left(\sum_k \left(q_{ik} \cdot f_{kj}^{\text{alt}_i} \right) \right) + (2 - g_{ij}) \cdot \ln \left(\sum_k \left(q_{ik} \cdot (1 - f_{kj}^{\text{alt}_i}) \right) \right) \right)$$
$$f_{kj}^{\text{alt}_i} = \min \left(1, \max \left(0, f_{kj}^{\text{est}} + \alpha \cdot \frac{(t_i - t_{\text{ave}})}{t_{\text{ave}}} \right) \right)$$

The notation here follows from Cheng et al.²⁶³. It is the total number of sites. g_{ij} is the called genotype for individual i at SNP j , where 0 is homozygous major, 1 is heterozygous, and 2 is homozygous minor. q_{ik} is the estimated genome-wide proportion of ancestry from component k in individual i . f_{kj} is the estimated frequency in component k at site j . The local log likelihood is maximized with respect to the parameter alpha, which interacts with the time of sampling of individual i (t_i) normalized by the average of all the sampling times (t_{ave}). This means that SNPs that are not well-modeled by the genome-wide mixture of ancestries, and whose deviations from this mixture depend strongly on time, will have large likelihood ratios.

Sampling times were set as 2000 before present (BP) for all Iron Age samples, 1200 BP for all early VA samples, 1000 BP for all VA and early Norse samples, 750 BP for all medieval and Norse samples, and 500 BP for all late medieval samples. The sampling times for all other ancient published samples were obtained from the midpoint of their radiocarbon date range. In our final scan, we used $K=3$, but also verified that our top candidate SNPs were largely robust to the choice of K , by repeating

the analysis with higher K, ranging from 4 to 7. The resulting likelihood ratios for all genotyped SNPs in the autosomes are displayed in Figure S14.1.

We call the above described scan the ‘general’ scan (Figure S14.2, Table S14.1), but we also performed two additional scans, focusing on either ‘ancient’ positive selection (older than 4,000 BP, Figure S14.5, Table S14.2) or ‘recent’ positive selection (younger than 4,000 BP, Figure S14.8, Table S14.3). For the recent scan, we set all times older than 4,000 BP to be equal to 4,000 BP, so that ancient selection would not affect the local log-likelihood. Conversely, for the ancient scan, we set all times younger than 4,000 BP to be equal to 4,000 BP.

For each analysis, we selected candidate SNPs whose log-likelihood ratio was larger than the 99.9% empirical quantile of the genome-wide distribution of log-likelihood ratios, and that had at least two nearby SNPs (in a +/- 500kb region) that had a ratio score larger than the same quantile. We note, however, that because we are working with a dataset intersected with the Human Origins SNPs, the highest scoring SNP in a given region may not be the causal one, as the latter may have not been selected for SNP capture. We plotted allele frequency time series for candidate SNPs (Figures S14.3, S14.6, S14.9 for the ‘general’, ‘ancient’, and ‘recent’ scans, respectively), grouping ancient genomes into five different periods: a period ranging from 10,000 to 8,000 BP, one ranging from 8,000 to 6,000 BP, one ranging from 6,000 BP to 4,000 BP, one ranging from 4,000 BP to 2,000 BP, one ranging from 2,000 BP to the present (excluding present-day samples) and one containing present-day samples only. We used Jeffreys priors to obtain 95% Bayesian credible intervals for the allele frequency of each time period. For each candidate SNP, we also plotted the scores in the local region surrounding the SNP (Figure S14.4, S14.7, S14.10 for the ‘general’, ‘ancient’, and ‘recent’ scans, respectively). Lastly, we visually verified whether any of the top selection candidates could appear as SNPs due to sequencing or mapping errors in the gnomAD browser²⁶⁶.

14.3. Results

In the general scan, we mostly find previously described candidate regions for positive selection in Europe: the LCT/MCM6 region, the TLR region, the HLA region, SLC45A2 and SLC22A4, all of which have been previously reported to be under selection in Europe^{163,209}.

In the ‘ancient’ selection scan, we find several new candidates for selection, including a region overlapping COL27A1, DNFB31 and AKNA. The region is centered around AKNA, which codes for a transcription factor that regulates CD40 and its ligand. It is expressed by B and T lymphocytes, natural killer cells, and dendritic cells, and plays an important role in the secondary immune response²⁶⁷. Another candidate region includes the DCC gene, implicated in colorectal cancer²⁶⁸. A third new candidate region overlaps the DFFB and CEP104 genes. DFFB codes for a nuclease involved in apoptosis²⁶⁹ while CEP104 codes for a protein involved in ciliary structural integrity and may be involved in Joubert syndrome²⁷⁰. In this scan, we also find a strong candidate for selection in a region overlapping the CXCR4 gene, though this one is close to the LCT/MCM6 region and shows similar allele frequency dynamics in time, so we cannot discount the possibility that it is part of the same selective event.

In the ‘recent’ selection scan, we again recover the LCT/MCM6 region (with the highest score by far), the TLR region and the HLA region, suggesting that positive selection on these regions either began (for the LCT/MCM6 region) or persisted (for the other two regions) in recent times. However, the SLC45A2 region is not recovered in this scan, in agreement with the previously inferred history of allele frequency change in this region^{163,209}.

14.4. Tables

Table S14.1: Top candidate SNPs from 'general' neoscan temporal scan with K=3. SNPs are listed if they had a log-likelihood ratio score than the 99.9% quantile of the empirical distribution of log-likelihood ratios, and at least two neighboring SNPs (+/- 500kb) with a score larger than the same quantile. n = 1,185 genomes used in the selection scan.

CHR	POSITION (hg19)	LIKELIHOOD RATIO	GENES (+/- 200 kb)
2	136557319	66.053	R3HDM1,UBXN4,LCT,MCM6,DARS
6	31348164	31.690	POU5F1,HCG27,HLA-C,HLA-B,MICA,MICB,MCCD1,ATP6V1G2-DDX39B,DDX39B,ATP6V1G2,NFKBIL1,LTA,TNF
4	38859799	24.450	KLF3,TLR10,TLR1,TLR6,FAM114A1,TMEM156,KLHL5
5	131586598	18.257	PDLIM4,SLC22A4,SLC22A5,C5orf56,IL3,CSF2,P4HA2
5	33954511	11.715	ADAMTS12,RXFP3,SLC45A2,AMACR,C1QTNF3

Table S14.2: Top candidate SNPs from 'ancient' neoscan temporal scan with K=3. SNPs are listed if they had a log-likelihood ratio score than the 99.9% quantile of the empirical distribution of log-likelihood ratios, and at least two neighboring SNPs (+/- 500kb) with a score larger than the same quantile. n = 1,185 genomes used in the selection scan.

CHR	POSITION (hg19)	LIKELIHOOD RATIO	GENES (+/- 200 kb)	NOTES
9	117102046	41.088	COL27A1,ORM1,ORM2,AKNA,DFNB31	
2	136976255	39.16	CXCR4	Near LCT/MCM6 region
18	50686991	30.029	DCC	
1	3776166	27.294	TP73,CCDC27,SMIM1,LRRC47,CEP104, DFFB,C1orf174	
5	131586598	26.997	PDLIM4,SLC22A4,SLC22A5,C5orf56,IL3, CSF2,P4HA2	
6	29732302	23.505	GABBR1,OR2H2,MOG,ZFP57,HLA-F,HLA-G,HLA-A	
1	61115790	21.933	N/A	
5	33958910	20.607	ADAMTS12,RXFP3,SLC45A2,AMACR,C1QTNF3	
16	83508437	18.912	CDH13	
4	38886293	18.04	KLF3,TLR10,TLR1,TLR6,FAM114A1,TMEM156,KLHL5	

1	163837511	17.854	N/A	
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Table S14.3: Top candidate SNPs from 'recent' neoscan temporal scan with K=3. SNPs are listed if they had a log-likelihood ratio score than the 99.9% quantile of the empirical distribution of log-likelihood ratios, and at least two neighboring SNPs (+/- 500kb) with a score larger than the same quantile. n = 1,185 genomes used in the selection scan.

CHR	POSITION (hg19)	LIKELIHOOD RATIO	GENES (+/- 200 kb)	NOTES
2	135631400	52.517	TMEM163,ACMSD,CCNT2,MAP3K19,RAB3GAP1	Near LCT/MCM6 region
6	31348164	17.39	POU5F1,HCG27,HLA-C,HLA-B,MICA,MICB,MCCD1,ATP6V1G2-DDX39B,DDX39B,ATP6V1G2,NFKBIL1,LTA,TNF	
4	38859799	12.357	KLF3,TLR10,TLR1,TLR6,FAM114A1, TMEM156,KLHL5	
8	140922006	11.382	TRAPPC9,C8orf17	May not be a true SNP: no rs ID
13	34067497	8.713	STARD13	May not be a true SNP: no rs ID

14.5. Figures

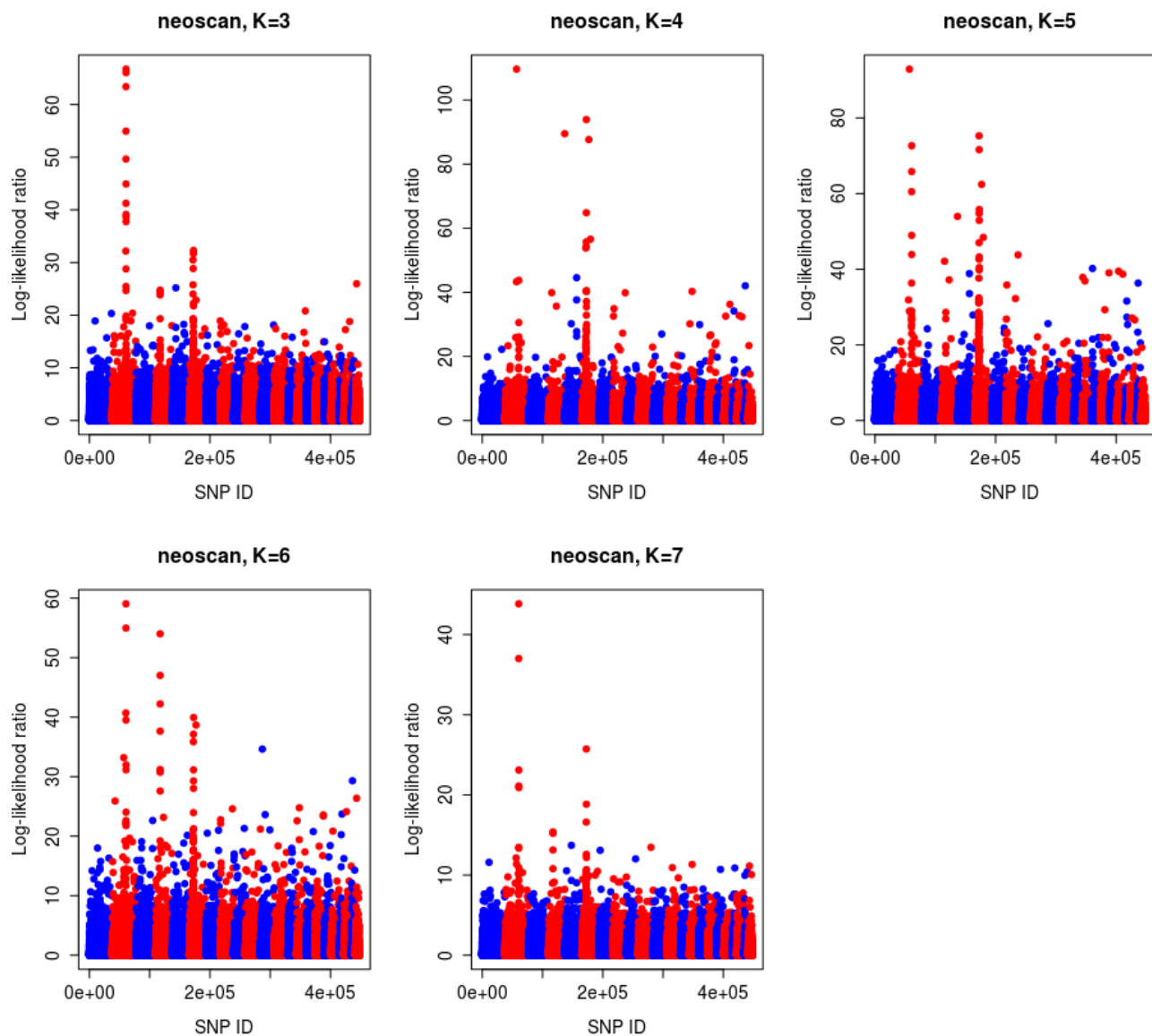


Fig. S14.1: Manhattan plots of Ohana neoscan with a latent ancestry fitting ranging from K=3 to K=7. $n = 1,185$ genomes used in the selection scan.

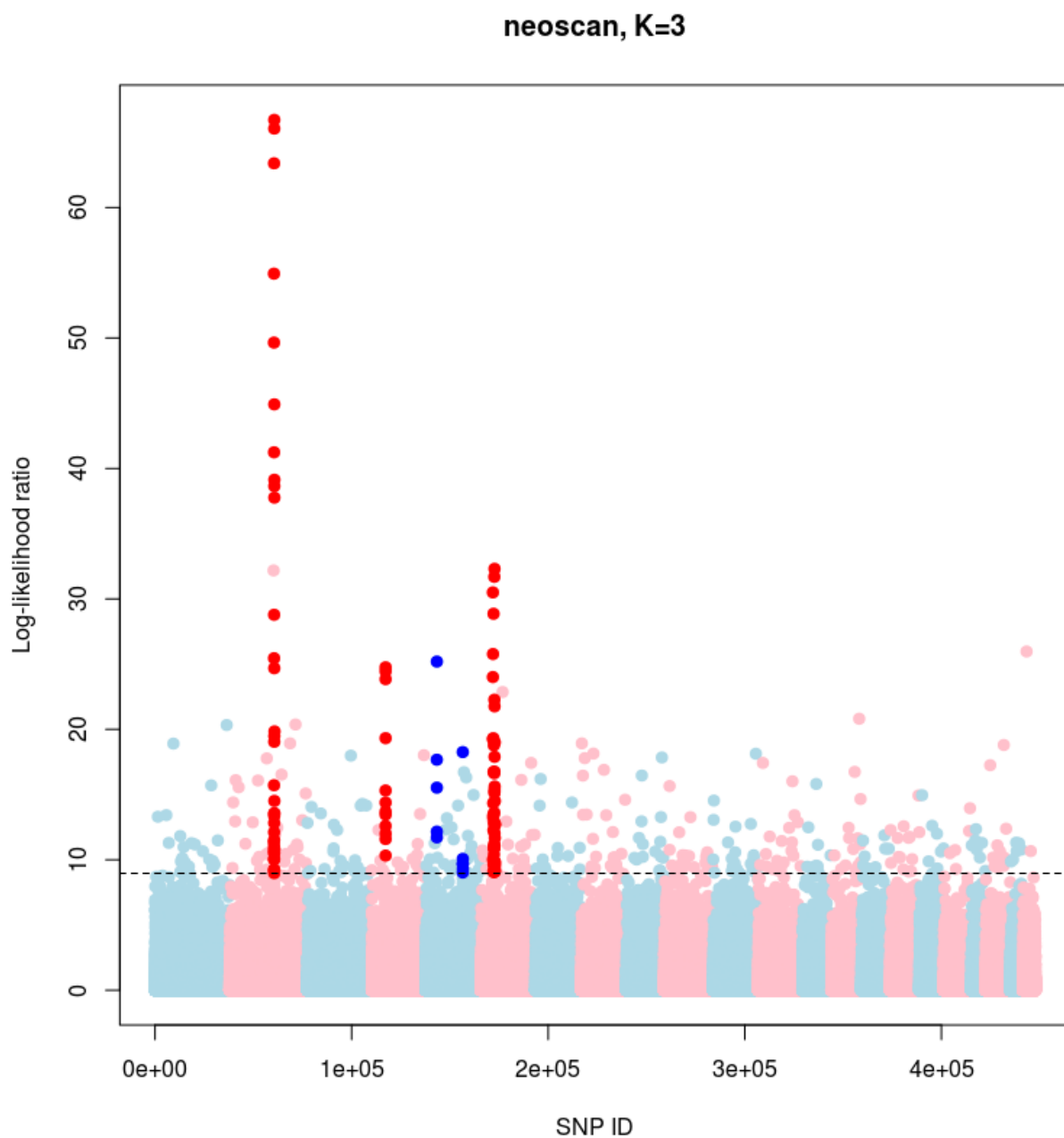


Fig. S14.2: Manhattan plot of Ohana 'general' neoscan (K=3) looking for SNPs whose allele frequencies were strongly associated with time over the entire 10,000 BP period, after accounting for genome-wide changes in ancestry over time. The highlighted SNPs have a score larger than the 99.9% quantile of the empirical distribution of log-likelihood ratio, and have at least two neighboring SNPs ($\pm 500\text{kb}$) with a score larger than the same quantile. $n = 1,185$ genomes used in the selection scan.

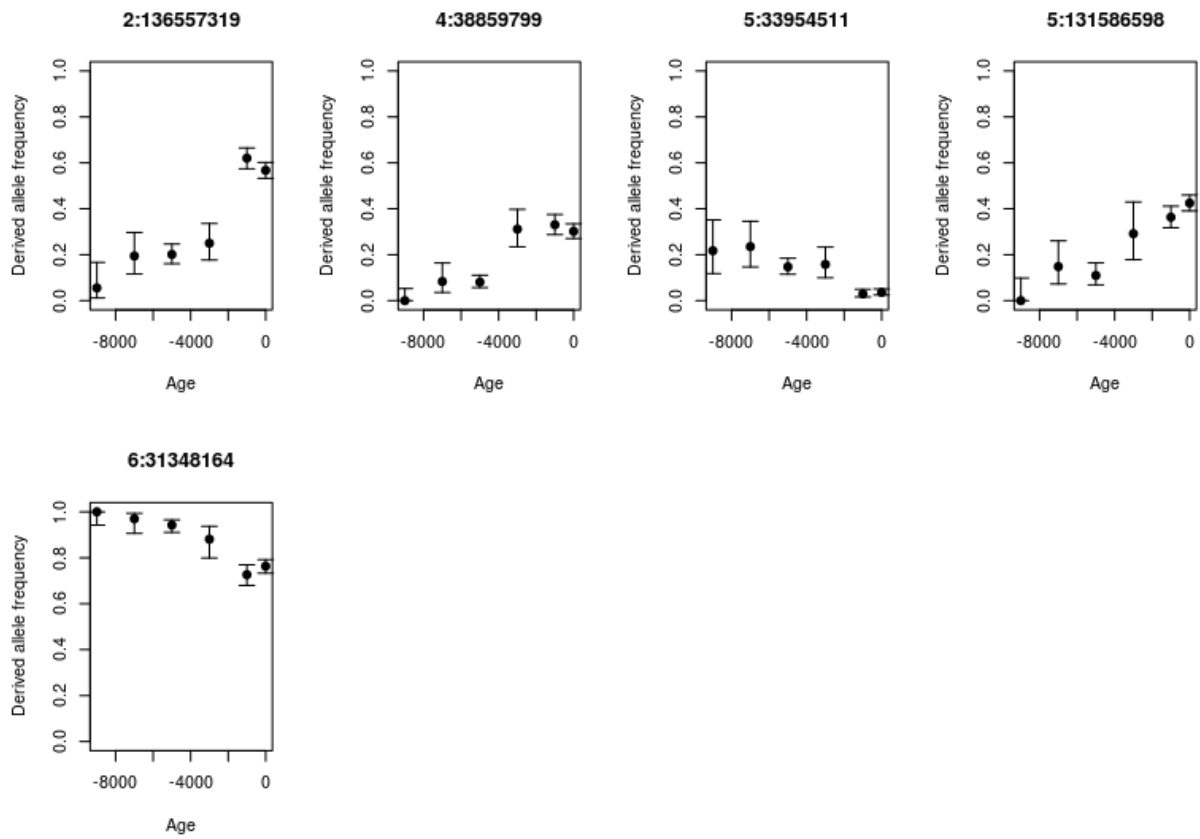


Fig. S14.3: Derived allele frequencies of top candidate SNPs from 'general' scan with $K=3$, as a function of age, after aggregating ages of ancient samples into 2,000-year bins. 95% Bayesian credible intervals (error bars) were computed using a Jeffreys prior. $n = 1,185$ genomes used in the computation of allele frequencies.

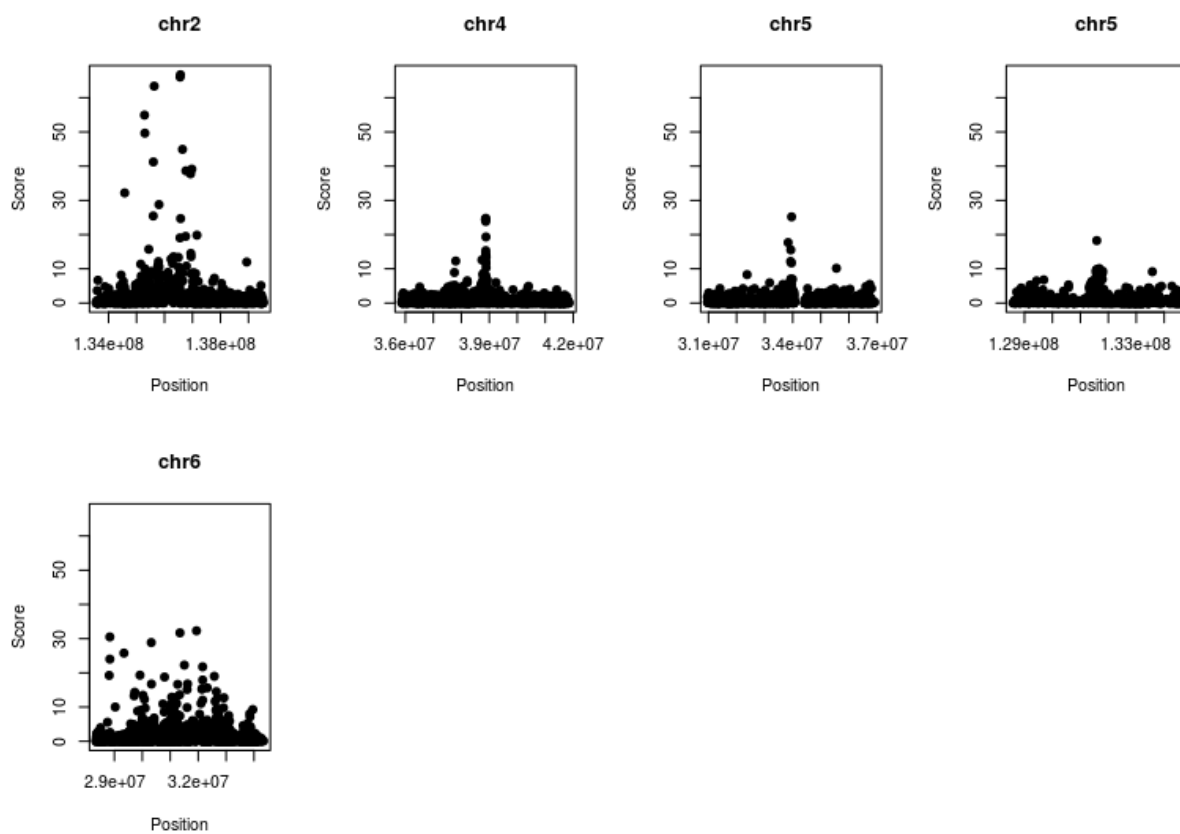


Fig. S14.4: Zoomed-in plots of regions (± 3 Mb) surrounding the candidate SNPs from the 'general' scan. $n = 1,185$ genomes used in the selection scan.

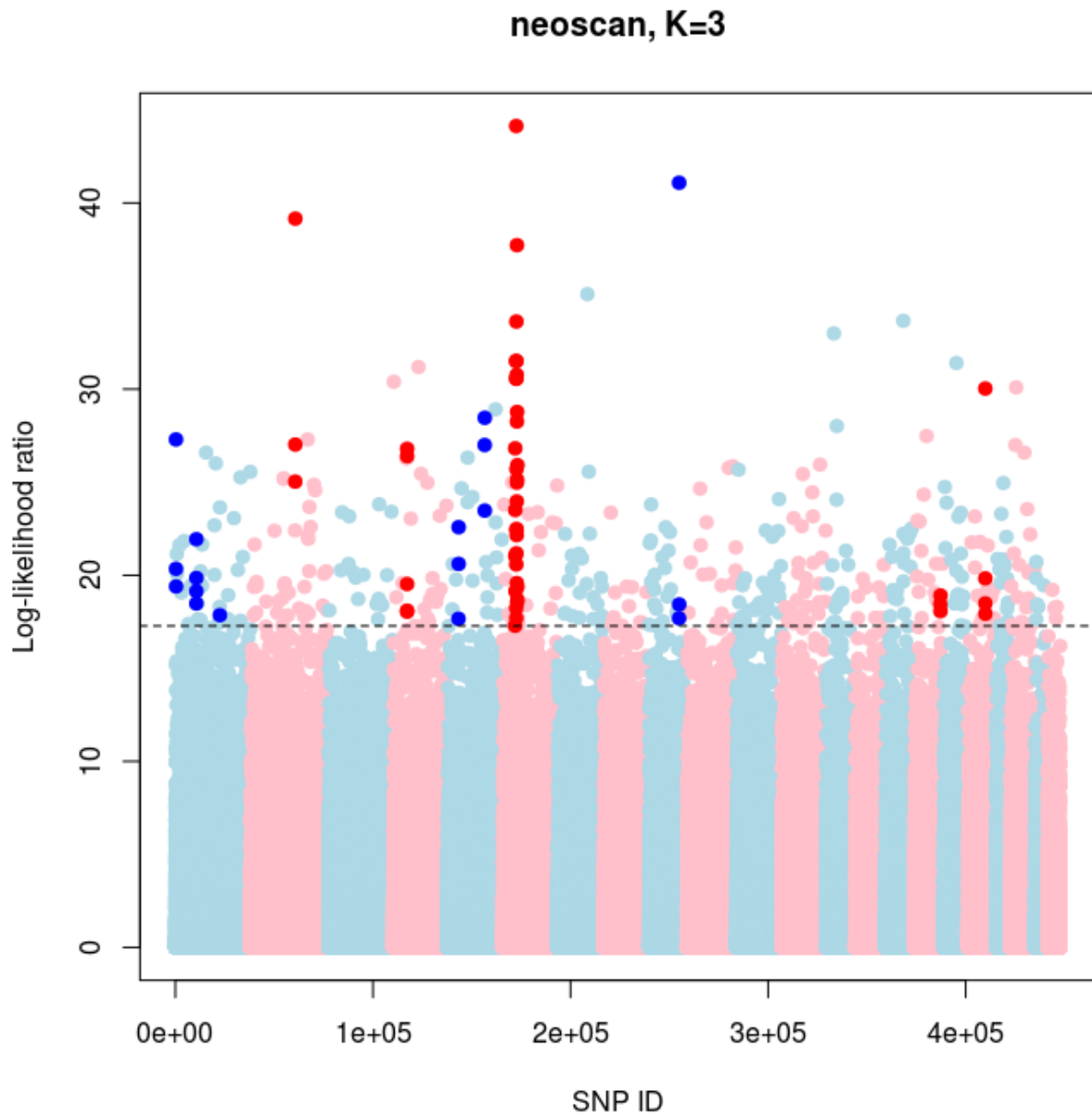


Fig. S14.5: Manhattan plot of Ohana ‘ancient’ neoscan (K=3) looking for SNPs whose allele frequencies were strongly associated with time after 4,000 BP, after accounting for genome-wide changes in ancestry over time. The highlighted SNPs have a score larger than the 99.9% quantile of the empirical distribution of log-likelihood ratio, and have at least two neighboring SNPs ($\pm 500\text{kb}$) with a score larger than the same quantile. $n = 1,185$ genomes used in the selection scan.

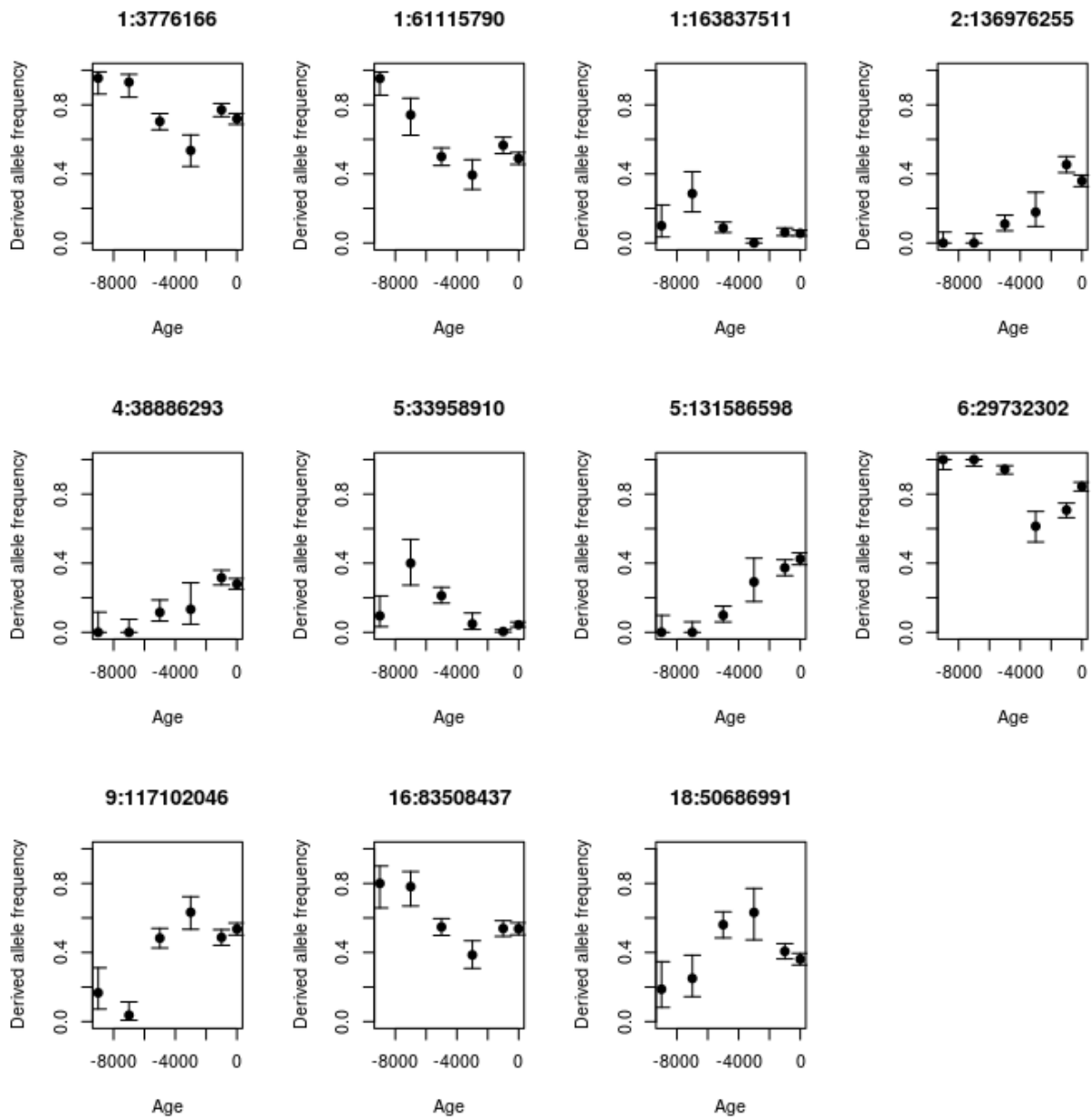


Fig. S14.6: Derived allele frequencies of top candidate SNPs from ‘ancient’ scan, as a function of age, after aggregating ages of ancient samples into 2,000-year bins. 95% Bayesian credible intervals (error bars) were computed using a Jeffreys prior. $n = 1,185$ genomes used in the computation of allele frequencies.

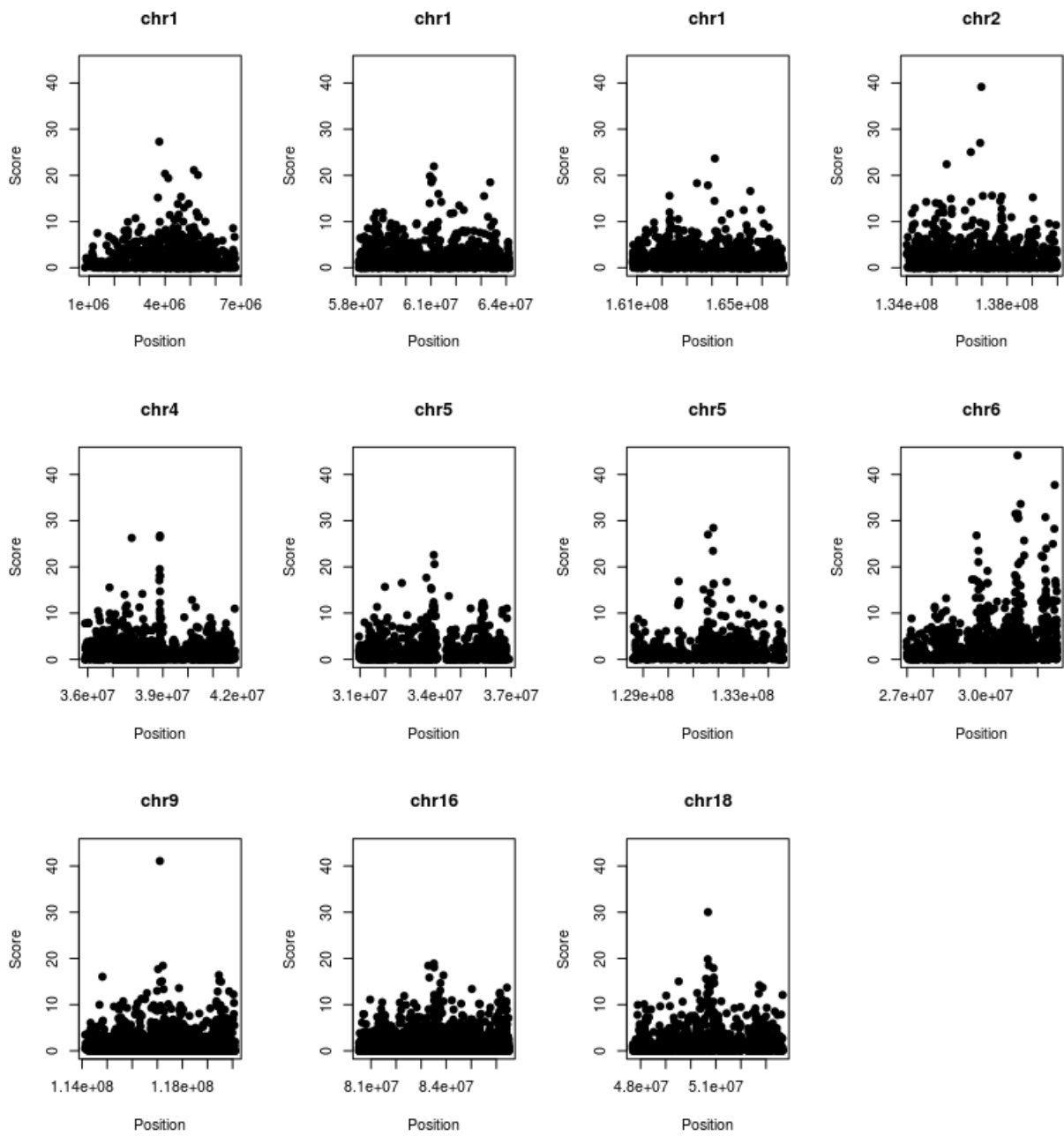


Fig. S14.7: Zoomed-in plots of regions (± 300 kb) surrounding the candidate SNPs from the ‘ancient’ scan. $n = 1,185$ genomes used in the selection scan.

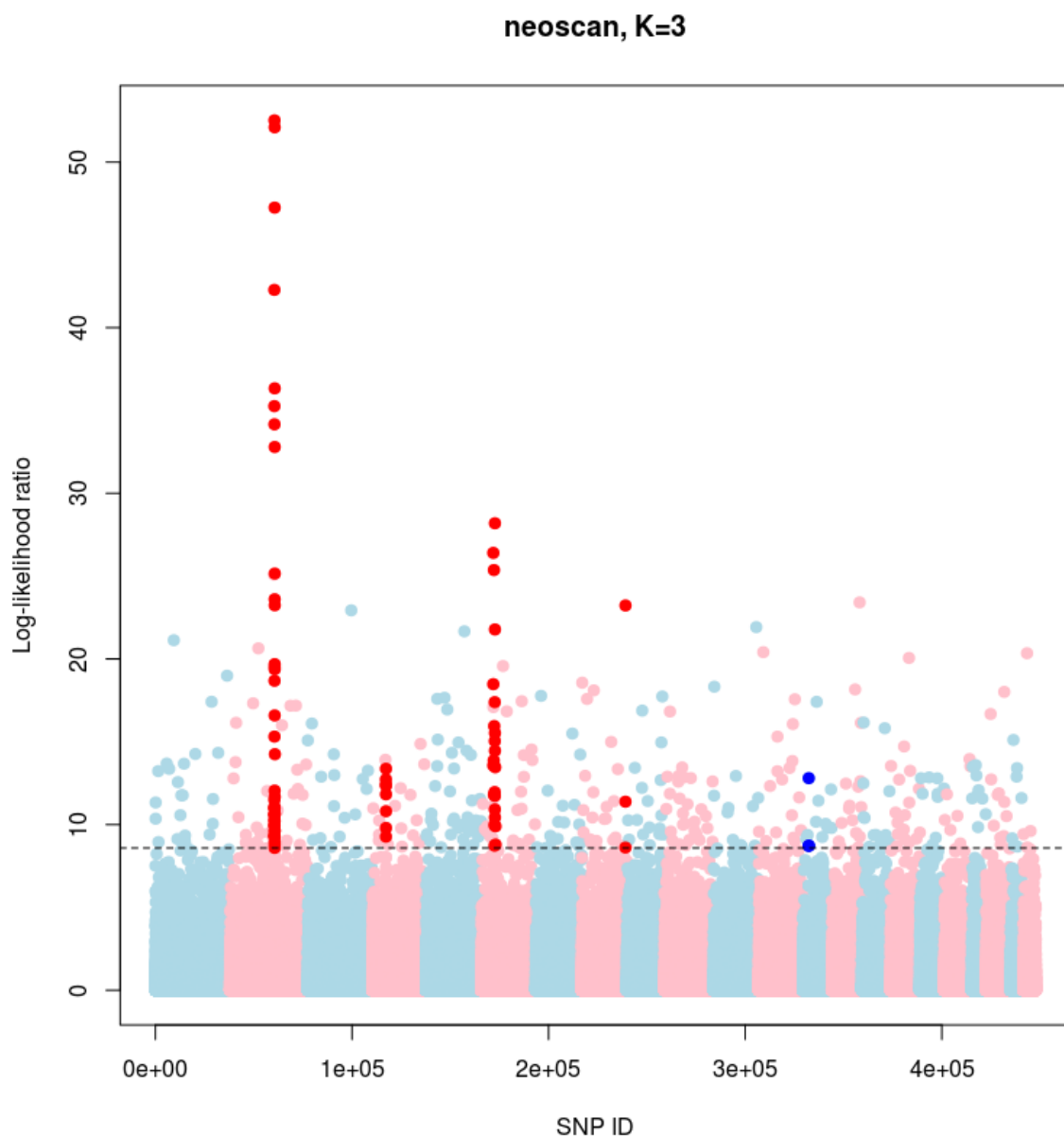


Fig. S14.8: Manhattan plot of Ohana ‘recent’ neoscan (K=3) looking for SNPs whose allele frequencies were strongly associated with time after 4,000 BP, after accounting for genome-wide changes in ancestry over time. The highlighted SNPs have a score larger than the 99.9% quantile of the empirical distribution of log-likelihood ratio, and have at least two neighboring SNPs ($\pm 500\text{kb}$) with a score larger than the same quantile. $n = 1,185$ genomes used in the selection scan.

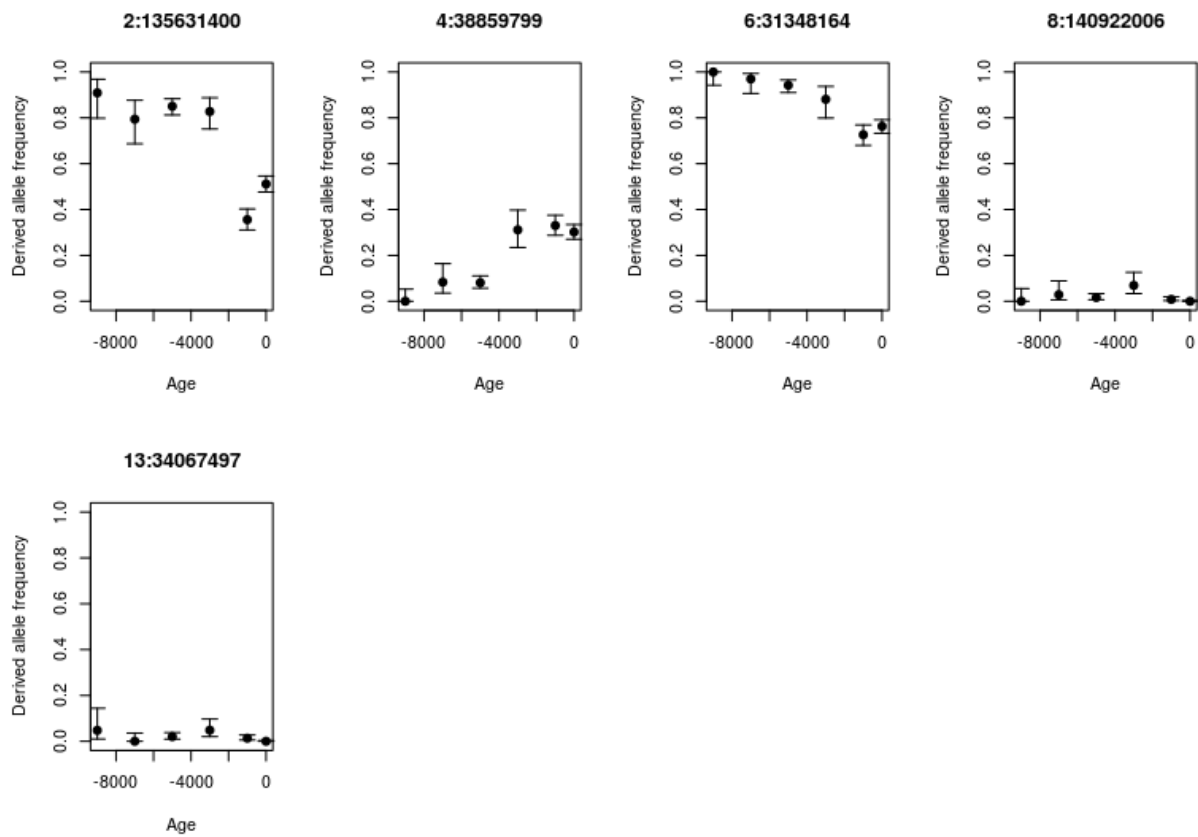


Fig. S14.9: Derived allele frequencies of top candidate SNPs from ‘recent’ scan, as a function of age, after aggregating ages of ancient samples into 2,000-year bins. 95% Bayesian credible intervals (error bars) were computed using a Jeffreys prior. $n = 1,185$ genomes used in the computation of allele frequencies.

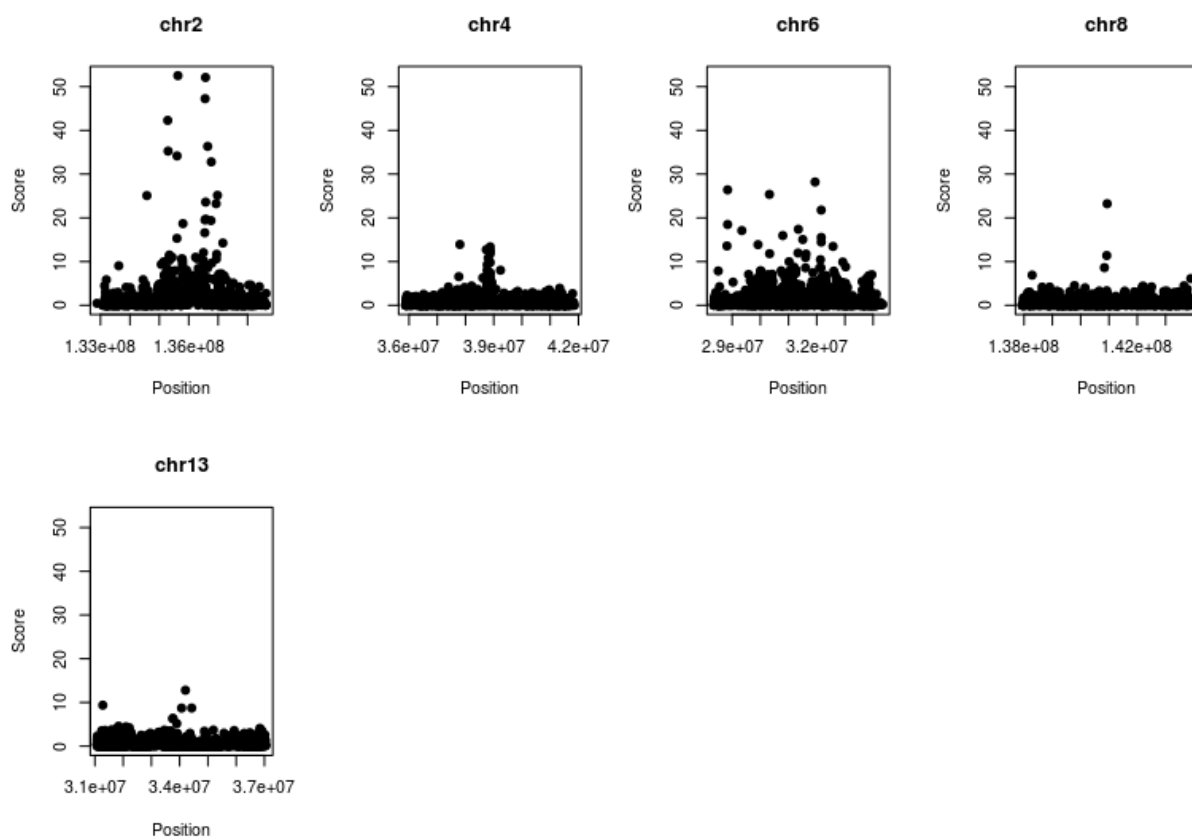


Fig. S14.10: Zoomed-in plots of regions (± 3 Mb) surrounding the candidate SNPs from the ‘recent’ scan. $n = 1,185$ genomes used in the selection scan.

Supplementary Note 15

15.1. Tracking the evolution of complex traits in Scandinavia

We wanted to examine whether we could identify signals of recent population differentiation of complex traits by comparing genotypes of VA samples excavated in Denmark, Sweden, and Norway with those of a present-day Scandinavian population. We chose to focus on traits for which summary statistics from well-powered genome-wide association studies (GWAS) were available.

15.2. Samples and genotyping

For comparison with the VA samples we used imputed genotypes from subjects born in Denmark between 1981-2005 from the IPSYCH case-cohort study²⁶¹. To minimize potential bias from sample source and genotyping platform (the IPSYCH samples are genotyped on Illumina PsychArray and imputed with SHAPEIT3²⁷¹ and IMPUTE2²⁷² using 1000 Genomes as reference) we filtered both datasets on markers' imputation info (>0.98) and minor allele frequency (>0.1) before merging the datasets on c. 1.3M SNP markers present in both datasets. We then further filtered the merged dataset to include only samples and markers with >0.98 genotype yield.

15.3. Principal component analysis

To prevent the large present-day Danish sample from dominating the weights of the principal components, we used a subset of samples to estimate principal components, and then the rest of the sample was projected onto these components. We pruned genotypes iteratively with respect to LD ($R^2 < 0.1$ within a window of 100 adjacent SNPs) to a set of 21,013 uncorrelated autosomal SNPs and used all unrelated VA samples and a subset of unrelated IPSYCH samples enriched for ethnic diversity ($\approx 1,000$ random population samples with both parents born in Denmark and further $\approx 3,000$ samples with both parents born outside Denmark, including $\approx 2,000$ with both parents born outside Europe) and derived 25 ancestry-sensitive principal components (PC) with SMARTPCA²⁷³.

15.4. Polygenic score analysis

We downloaded summary statistics from the Genome wide association study ATLAS webpage (<https://atlas.ctglab.nl>)²⁷⁴ for studies of 16 disease and anthropometric traits (excluding those related to cognition) published in 2017 or later with SNP heritability estimated at >0.1 , sample size of $>100,000$, and >100 identified genome-wide significant loci. We calculated polygenic risk scores based on independent ($R^2 < 0.1$ within 10Mb range) genome-wide significant allelic effects and standardized them to a unit representing the standard deviation of the mean of their distribution. We then removed outliers (anyone with a value for any of the 25 PCs falling more than 4 standard deviations away from the group mean) iteratively from within each ancestry group (treating the Scandinavian VA samples as one ancestry group), and subsequently tested for difference in PRS distribution between VA samples and Danish ancestry IPSYCH random population samples using a linear regression model correcting for sex and the 25 principal components. The analysis was done in R (version 3.5.0) and we use the *ggplot* function of the *ggplot2* package, and the *forest* function of the *metafor* package to plot the results in figure S15.1 and Extended Data Fig. 7.

15.5. Results

A plot of the first two PCs (Figure S15.1) shows clustering of the present-day IPSYCH random sample (before removing PC outliers) according to ancestry (as determined by parents' country/region of birth), and that the VA samples cluster together with the Danish ancestry IPSYCH random sample. PRS for three of the 16 traits showed difference between PRS of VA samples ($N = 148$) and the Danish ancestry IPSYCH random population sample ($N = 20,551$) (Extended Data Fig.

7); these were PRS for black hair colour and standing height from GWAS of the UK biobank ($N \approx 385,000$), and for schizophrenia from a GWAS meta-analysis of the Psychiatric Genomics Consortium ($N = 105,318$). However, the difference in PRS for height and schizophrenia between the VA and present-day Danish random sample did not remain significant after taking into account the number of tests.

To test whether the observed difference in PRS for black hair colour was driven by a few large effect loci, or otherwise dependent on the estimated allelic effects from the respective GWA studies, we performed a binomial test of the number of risk alleles found in higher frequency in the VA sample ($n = 65$) and the present-day sample ($n = 41$), respectively, which showed a significant difference from a 50/50 distribution ($P = 0.025$). To further test whether this difference could be explained by the frequency distribution of the risk alleles, we performed a permutation test, in which we replaced the actual risk alleles for black hair colour 1,000 times with randomly drawn alleles matched on ancestral allele frequency. In 17 of the 1,000 permutations the distribution of risk alleles (according to whether the frequency was higher in the VA or present-day sample) deviated as much, or more, from a 50/50 distribution, than we had observed with the actual risk alleles (adjusted $P = 0.017$). Hence, we conclude that the observed PRS difference is neither explained by a few large effect loci, nor by a general tendency of alleles with the same frequency distribution as the risk alleles to be found at differing frequencies between the VA and present-day sample.

Thus, it appears that frequencies of established common alleles affecting hair colour have significantly changed in the Danish population since the VA, whereas we do not observe any significant change for alleles affecting other common anthropometric traits and a few complex disorders. At the moment, we cannot conclude whether this difference is due to selection acting on these alleles between the VA and the present time, or to some other factor, or whether a similar change in allele frequencies affecting hair colour has occurred in the other Scandinavian populations.

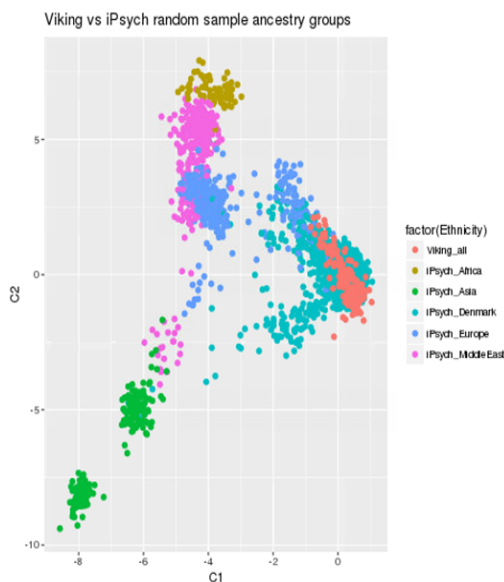


Fig. S15.1: A cluster plot of the two first principal components (prior to removal of outliers) across VA samples ($n = 149$, red) and IPSYCH randomly drawn Danish population sample grouped by parents' birthplace (only

using samples where both parents are born either in Denmark ($n = 21,824$) or one of the other respective regions; Africa ($n = 74$), Asia ($n = 193$), the Middle East ($n = 358$), Europe ($n = 461$)). The VA samples fall mostly within the cluster of Danish ancestry.

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