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Genomic evidence for the Pleistocene and recent population history of Native Americans

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Abstract

How and when the Americas were populated remains contentious. Using ancient and modern genome-wide data, we find that the ancestors of all present-day Native Americans, including Athabascans and Amerindians, entered the Americas as a single migration wave from Siberia no earlier than 23 thousand years ago (KYA), and after no more than 8,000-year isolation period in Beringia. Following their arrival to the Americas, ancestral Native Americans diversified into two basal genetic branches around 13 KYA, one that is now dispersed across North and South America and the other is restricted to North America. Subsequent gene flow resulted in some Native Americans sharing ancestry with present-day East Asians (including Siberians) and, more distantly, Australo-Melanesians. Putative 'Paleoamerican' relict populations, including the historical Mexican Pericúes and South American Fuego-Patagonians, are not directly related to modern Australo-Melanesians as suggested by the Paleoamerican Model.

It is generally agreed that ancestral Native Americans are descendants of Siberian peoples who traversed the Bering Land Bridge (Beringia) from northeast Asia in Late Pleistocene times, and though consensus has yet to be reached, it is mostly conceded that the Clovis archaeological complex, dating to ca. 13 KYA, does not represent the first migration as long supposed (1–7). Archaeological evidence accumulated over the last two decades indicates that people were south of the North American continental ice sheets more than a millennium earlier and had reached as far south as southern South America by at least ca. 14.6 KYA (1–3). Interpretations differ, however, regarding the precise spatio-temporal dynamics of the peopling process, owing to archaeological claims for a significantly earlier human presence pre-dating the Last Glacial Maximum (LGM; ca. 20 KYA) (8–10), and conflicting interpretations of the number and timing of migrations from Beringia based on anatomical and genetic evidence (11–16). Much of the genetic evidence is from studies of mitochondrial DNA (mtDNA) and Y-chromosome, which as single, uniparentally inherited

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SUPPLEMENTARY MATERIALS

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Materials and Methods

Supplementary Text

Figs. S1 to S41

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loci are particularly subject to genetic drift and sex-biased demographic and cultural practices.

Among the principal issues still to be resolved regarding the Pleistocene and recent population history of Native Americans are: (i) the timing of their divergence from their Eurasian ancestors; (ii) whether the peopling was in a single wave or multiple waves, and, consequently, if the genetic differences seen between major subgroups of Native Americans (e.g., Amerindian and Athabascan) result from different migrations or in situ diversification in the Americas (5, 6, 17, 18); (iii) if the migration involved ca. 15,000 years of isolation in the Bering Strait region, as proposed by the Beringian Incubation Model to explain the high frequency of unique and widespread American mitogenomes and private genetic variants (19–22); and, finally, (iv) if there was post-divergence gene flow from Eurasia and possibly even population replacement in the Americas, the latter suggested by the apparent differences in skull morphology between some early ('Paleoamerican') remains and those of more recent Native Americans (23–27). We address these issues using genomic data derived from modern populations, supplemented by ancient specimens that provide chronologically controlled snapshots of the genetics of the peopling process as it unfolded.

We sequenced 31 genomes from present-day individuals from the Americas, Siberia and Oceania to an average depth of ca. 20X: Siberians – Altai ($n = 2$), Buryat ($n = 2$), Ket ($n = 2$), Koryak ($n = 2$), Sakha ($n = 2$), Siberian Yupik ($n = 2$); North American Native Americans – Tsimshian ($n = 1$); southern North American and Central and South American Natives – Pima ($n = 1$), Huichol ($n = 1$), Aymara ($n = 1$), Yukpa ($n = 1$); and, Oceanians – Papuan ($n = 14$) (28) (Table S1). All the genome-sequenced present-day individuals were previously genotyped using single nucleotide polymorphism (SNP) chips (4, 29–35) except for the Aymara individual that was SNP chip genotyped in this study (tables S3 and S4). They were selected on the basis of their ancestry profiles obtained with *ADMIXTURE* (36) to best represent their respective populations, and to minimize recent genetic admixture from populations of western Eurasian origin (28). For populations represented by more than one individual, we also verified from the genotype data that the sequenced individuals did not represent close relatives (28). We additionally sequenced 23 genomes from ancient individuals dating between ca. 0.2–6 KYA from North and South America, with an average depth ranging between 0.003X and 1.7X, including specimens affiliated to putative relict Paleoamerican groups such as the Pericúes from Mexico and Fuego-Patagonians from the southernmost tip of South America (23, 26–28) (table S5). Finally, we generated SNP chip genotype data from 79 present-day individuals belonging to 28 populations from the Americas and Siberia (28) (table S4). All the aforementioned datasets were analyzed together with previously published genomes and SNP chip genotype data (Tables S1, S3, and S4), masking the data for recent European admixture in some present-day Native American populations (28).

The structure of Native American populations and the timing of their initial divergence

We explored the genetic structure of Native American populations in the context of worldwide populations using *ADMIXTURE* (36), employing a reference panel consisting of

3,053 individuals from 169 populations (table S3) (28). The panel included SNP chip genotype data from present-day individuals generated in this study and previously published studies, as well as the 4,000 year-old Saqqaq individual from Greenland (29) and the 12,600 year-old Anzick-1 (Clovis culture) individual from Montana (5) (table S3). When assuming four ancestral populations ($K=4$), we found a Native American-specific genetic component, indicating a shared genetic ancestry for all Native Americans including Amerindians and Athabascans (fig. S4). Assuming $K=15$, there is structure within the Native Americans. Athabascans and northern Amerindians (primarily from Canada) differ from the rest of the Native Americans in sharing their own genetic component (fig. S4). As reported previously, Anzick-1 falls within the genetic variation of southern Native Americans (5), while the Saqqaq individual shares genetic components with Siberian populations (fig. S4) (29).

To ascertain the population history of present-day American populations in relation to worldwide populations, we generated admixture graphs with *TreeMix* (28, 37). All the modern Siberian and Native American genomes sequenced in this study, except for the North American Tsimshian genome that showed evidence of recent western Eurasian admixture (28), were used for this analysis, together with previously published genomes from Africa (Yoruba) (38), Europe (Sardinian, French) (38), East Asia (Dai, Han) (38), Siberia (Nivkh) (39) and the Americas (Karitiana, Athabaskan, Greenlandic Inuit) (5, 38, 39) (table S1). The ancient individuals included in the analysis were Saqqaq, Anzick-1 and the 24,000 year-old Mal'ta child from south-central Siberia (4). *TreeMix* affirms that all Native Americans form a monophyletic group across all ten migration parameter values, with further diversification into two branches, one representing Amerindians (represented in this analysis by Amerindians from southern North America and Central and South America) and the other Athabascans (Fig. 1B and fig. S5). Paleo-Eskimos and Inuit were supported as a separate clade relative to the Native Americans, as reported previously (Fig. 1B and fig. S5) (29, 39). Our results show that the Siberian Yupik and Koryak are the closest Eurasian populations to the Americas, with the Yupik likely representing back-migration of the Inuit into Siberia (Fig. 1B and fig. S5).

To assess the pattern of the earliest human dispersal into the Americas, we estimated the timing of the divergence of ancestral Native Americans from East Asians (hereafter, including Siberians) using multiple methods. There is still some debate regarding mutation rates in the human genome (40), and this uncertainty could affect our estimates and results.

We applied *diCal2.0* (28) (Method 1), a new version of *diCal* (41) extended to handle complex demographic models involving multiple populations with migration (42), and an identity-by-state (IBS) tract method (43) (Method 2) to the modern genome dataset (28). With these, we first estimated divergence times between Native Americans and the Koryak of Siberia, one of the genetically closest sampled East Asian populations to Native Americans (fig. S5), using demographic models that reflect a clean split between the populations (28). With both *diCal2.0* and IBS tract method, the split of Native Americans (including Amerindians and Athabascans) from the Koryak dates to ca. 20 KYA (28) (tables S11A and S12 and fig. S15).

We further applied *diCal2.0* to models with gene flow post-dating the split between Native Americans and Koryak (Fig. 2A) and found that they provided a better fit to the data than the models without gene flow (28). Overall, simulated databases on the models inferred using *diCal2.0* and real data show very similar IBS tract length distributions (Fig. 2B) and relative cross coalescence rates (CCR) between pairs of individuals estimated using the Multiple Sequentially Markovian Coalescent (MSMC) method (Method 3) (28, 44) (Figs. 2, C and D). This serves as a confirmation for the model estimates from *diCal2.0*. We evaluated all the three methods using simulations under complex demographic models, and additionally investigated the effects of switch-errors in haplotype phasing on the estimates (28).

We then applied the *diCal2.0* model that allows for gene flow between populations after their split to estimate divergence times for Native Americans from more geographically and genetically distant East Asian groups, including the Siberian Nivkh and Han Chinese. As before, the divergence estimates for Amerindians and Athabascans were very similar to one another, ca. 23 KYA (table S11B and figs. S18 and S21).

Hence, our results suggest that Amerindians and Athabascans were, by three different methods, consistently equidistant in time to populations that were sampled from different regions of East Asia, including some proximate to Beringia, and with varied population histories. This suggests that these two major Native American sub-groups are descendants of the same source population that split off from ancestral East Asians during the LGM. It is conceivable that harsh climatic conditions during the LGM may have contributed to the isolation of ancestral Native Americans, ultimately leading to their genetic divergence from their East Asian ancestors.

We also modeled the peopling of the Americas using a climate-informed spatial genetic model (CISGeM), in which the genetic history and local demography is informed by paleoclimatic and paleovegetation reconstructions (28, 45), and found the results to be in accordance with the conclusion of a single migration source for all Native Americans. Using present-day and ancient high coverage genomes, we found that Athabascans and Anzick-1, but not Greenlandic Inuit and Saqqaq (29, 39), belong to the same initial migration wave that also gave rise to present-day Amerindians from southern North America and Central and South America (Fig. 3), and that this migration likely followed a coastal route, given our current understanding of the glacial geological and paleoenvironmental parameters of the Late Pleistocene (fig. S31).

In all cases, the best fit of the demographic models to the IBS tract distribution and relative CCR by MSMC required gene flow between Siberian and Native American populations after their initial split (Figs. 2, B to D). We also found strong evidence for gene flow between Athabascans and the Inuit (table S11B) supported by results from *ADMIXTURE* (fig. S4), *TreeMix* (fig. S5), *D*-statistics employing both whole genome and SNP chip genotype data (28, 46, 47) (figs. S6 and S8A), and outgroup f_3 statistics using whole genome data (28, 47) (Fig. S12). We attempted to estimate the divergence times between Inuit and Siberians as well as Inuit and Native Americans (table S11 and figs. S19 and S25 to S27),

but our analyses were complicated by gene flow between Inuit and Athabascans as well as complex admixture patterns among Arctic groups (fig. S5).

We tested the duration and magnitude of post-split gene flow between Native Americans and Siberians using *diCal2.0* by introducing stopping time of gene flow as a free parameter (28). We still obtained the highest likelihood for a divergence time of 22 KYA between Amerindians and Siberians as well as Athabascans and Siberians, although estimates for gene flow rate and end of the gene flow differ (table S11C and fig. S22). Significant gene flow between Athabascans and Siberians seems to have stopped ca. 12 KYA (Table S11C), suggesting a link to the breaching of the Beringian Land Bridge by rising sea levels (48).

Overall, our results support a common Siberian origin for all Native Americans, contradicting claims for an early migration to the Americas from Europe (49), with their initial isolation and entrance into the Americas occurring no earlier than 23 KYA, but with subsequent admixture with East Asian populations. This additionally suggests that the Mal'ta-related admixture into the early Americans (4), representing ancestors of both Amerindians and Athabascans (Fig. 1 and fig. S5), occurred sometime after 23 KYA, following the Native American split from East Asians.

Subsequent in situ diversification of Native American groups

That Amerindian and Athabaskan groups were part of the same migration implies that present-day genetic differences observed between them must have arisen later, after ca. 23 KYA. Using the clean-split model in *diCal2.0* on the modern genomes dataset, we estimated that Athabascans and Karitiana diverged ca. 13 KYA (95% confidence interval of ca. 11.5-14.5 KYA, estimated from parametric bootstrap results) (table S11A, fig. S16), which is consistent with results from MSMC (fig. S27) (28).

Where the divergence between Karitiana and Athabascans occurred is not known. However, several independent lines of evidence suggest that it is more likely to have occurred in lower latitude North America instead of eastern Beringia (Alaska). These include the equidistant split times of Amerindians and Athabascans to Asian populations, the relatively brief interval between their estimated divergence date range and the age of Anzick-1 (12.6 KYA) (5), and lastly, the geographic location of Anzick-1 to the south of the North American ice sheets and its clear affiliation with the 'southern branch' of Native Americans (taken broadly to include Amerindians from southern North America and Central and South America) (5), as determined with outgroup f_3 statistics using SNP chip genotype data from present-day worldwide populations (47) (Fig. 4 and figs. S13 and S14). Divergence in North America would also be consistent with the known pre-Clovis age sites in the Americas, such as Monte Verde (14.6 KYA) (50). The most parsimonious model would be that both Amerindians and Athabascans are descendants of the same ancestral Native American population that entered the Americas then subsequently diversified. However, we cannot discount alternative and more complex scenarios, which could be tested with additional ancient samples.

By the Clovis period (ca. 12.6 KYA), the ancestral Native American population had already diversified into 'northern' and 'southern' branches, with the former including ancestors of

present-day Athabascans and northern Amerindian groups such as Chipewyan, Cree and Ojibwa and the latter including Amerindians from southern North America and Central and South America (Fig. 4 and fig. S14). We tested whether later gene flow from East Asian sources, such as the Inuit, might explain the genetic differences between these two branches. Using *D*-statistics on SNP chip genotype data (47) masked for non-Native ancestry, we observed a signal of gene flow between the Inuit and northwest Pacific Coast Amerindians such as Coastal Tsimshian and Nisga'a, residing in the same region as the northern Athabascans (28) (fig. S8B). However, this signal of admixture with the Inuit, also detected in Athabascans (figs. S6 and S8A), was not evident among northern Amerindian populations located further east such as Cree, Ojibwa and Chipewyan (28) (fig. S8C). This suggests that the observed difference between the 'northern' and 'southern' branches is not a consequence of post-split East Asian gene flow into the 'northern branch', and also provides a possible explanation as to why the 'southern branch' Amerindians such as Karitiana are genetically closer to the northern Amerindians located further east than to northwest coast Amerindians and Athabascans (fig. S9).

In contrast to Anzick-1, several of the Holocene individuals from the Americas, including those sequenced in this study as well as the 8,500 year old Kennewick Man (51), are closely related to present-day Native American populations from the same geographical regions (Fig. 4 and figs. S13 and S14). This implies genetic continuity of ancient and modern populations in some parts of the Americas over at least the last 8.5 KYA, which is in agreement with recent results from Kennewick Man (51).

Evidence of more distant Old World gene flow into some Native Americans

When testing for gene flow between Athabascans and Inuit with masked SNP chip genotype data-based *D*-statistics (47) (fig. S8), we observed a weak tendency for the Inuit to be much closer to the Athabascans than to certain Amerindians like the North American Algonquin and Cree, and the Yaqui and Arhuaco of Central and South America (respectively), as compared to other Amerindians such as the Palikur and Surui of Brazil (fig. S8).

To further investigate this trend, we tested for additional gene flow from Eurasian populations into the Americas with *D*-statistics using the masked SNP chip genotype dataset (47). We found that some American populations, including the Aleutian Islanders, Surui, and Athabascans are closer to Australo-Melanesians compared to other Native Americans, such as North American Ojibwa, Cree and Algonquin, and the South American Purepecha, Arhuaco and Wayuu (fig. S10). The Surui are, in fact, one of closest Native American populations to East Asians and Australo-Melanesians, the latter including Papuans, non-Papuan Melanesians, Solomon Islanders, and South East Asian hunter-gatherers such as Aeta (fig. S10). We acknowledge that this observation is based on the analysis of a small fraction of the whole genome and SNP chip genotype datasets, especially for the Aleutian Islander data that is heavily masked due to recent admixture with Europeans (28), and that the trends in the data are weak.

Nonetheless, if it proves correct, these results suggest there may be a distant Old World signal related to Australo-Melanesians and East Asians in some Native Americans. The

widely scattered and differential affinity of Native Americans to the Australo-Melanesians, ranging from a strong signal in the Surui to much weaker signal in northern Amerindians such as Ojibwa, points to this gene flow occurring after the initial peopling by Native American ancestors.

However, how this signal may have ultimately reached South America remains unclear. One possible means is along a northern route via the Aleutian Islanders, previously found to be closely related to the Inuit (39), who have a relatively greater affinity to East Asians, Oceanians and Denisovan than Native Americans in both whole genome and SNP chip genotype data-based *D*-tests (table S10 and figs. S10 and S11). On the basis of archaeological evidence and mtDNA data from ancient and modern samples, the Aleutian Islands are hypothesized to have been peopled as early as ca. 9 KYA by ‘Paleo-Aleuts’ who were succeeded by the ‘Neo-Aleuts’, with present-day Aleutian Islanders potentially resulting from admixture between these two populations (52, 53). Perhaps their complex genetic history included input from a population related to Australo-Melanesians through an East Asian continental route, and this genomic signal might have been subsequently transferred to parts of the Americas, including South America, through past gene flow events (Fig. 1). Evidence for this gene flow is supported by *diCal2.0* and MSMC analyses showing a weak but recent gene flow into South Americans from populations related to present-day Northeast Asians (Koryak) (Fig. 2C and table S11C), who might be considered a proxy for the related Aleutian Islanders.

Testing the Paleoamerican model

The detection of an Australo-Melanesian genetic signal in the Americas, however subtle, returns the discussion to the Paleoamerican model, which hypothesizes, on the basis of cranial morphology, that two temporally and source-distinct populations colonized the Americas. The earlier population reportedly originated in Asia in the Late Pleistocene and gave rise to both Paleoamericans and present-day Australo-Melanesians, whose shared cranial morphological attributes are presumed to indicate their common ancestry (23). The Paleoamericans were, in turn, thought to have been largely replaced by ancestors of present-day Amerindians, whose crania resemble modern East Asians and who are argued to be descendants of later arriving Mongoloid populations (14, 23, 26, 54). The presence of Paleoamericans is inferred primarily from ancient archaeological specimens in North and South America, and a few relict populations of more recent age, which include the extinct Pericúes and Fuego-Patagonians (24, 25, 55).

The Paleoamerican hypothesis predicts that these groups should be genetically closer to Australo-Melanesians than other Amerindians. Previous studies of mtDNA and Y chromosome data obtained from Fuego-Patagonian and Paleo-american skeletons have identified haplogroups similar to those of modern Native Americans (55–57). Although these results indicate some shared maternal and paternal ancestry with contemporary Native Americans, uniparental markers can be misleading when drawing conclusions about the demographic history of populations. To conclusively identify the broader population of ancestors who may have contributed to the Paleoamerican gene pool, autosomal genomic data are required.

We, therefore, sequenced 17 ancient individuals affiliated to the now-extinct Pericúes from Mexico and Fuego-Patagonians from Chile and Argentina (28), who, on the basis of their distinctive skull morphologies, are claimed to be relicts of Paleoamericans (23, 27, 58, 59). Additionally, we sequenced two pre-Columbian mummies from northern Mexico (Sierra Tarahumara) to serve as morphological controls, since they are expected to fall within the range of Native American morphological cranial variation (28). We found that the ancient samples cluster with other Native American groups and are outside the range of Oceanian genetic variation (28) (Fig. 5 and figs. S32, S33, and S34). Similarly, outgroup f_3 statistics (47) reveal low shared genetic ancestry between the ancient samples and Oceanians (28) (Figs. S36, S37), and genome-based and masked SNP chip genotype data-based D -statistics (46, 47) show no evidence for gene flow from Oceanians into the Pericúes or Fuego-Patagonians (28) (fig. S39).

As the Paleoamerican model is based on cranial morphology (23, 27, 58, 59), we also measured craniometric data for the ancient samples and assessed their phenotypic affinities to supposed Paleoamericans, Amerindians and world-wide populations (28). The results revealed that the analyzed Fuego-Patagonians showed closest craniometric affinity to Arctic populations and the Paleoamericans, while the analyzed female Pericúes showed closest craniometric affinities to populations from North America, the Arctic region and Northern Japan (table S15). More importantly, our analyses demonstrated that the presumed ancestral ancient Paleoamerican reference sample from Lagoa Santa, Brazil (24) had closest affinities to Arctic and East Asian populations (table S15). Consequently, for the Fuego-Patagonians, the female Pericúes and the Lagoa Santa Paleoamerican sample, we were not able to replicate previous results (24) that report close similarity of Paleoamerican and Australo-Melanesian cranial morphologies. We note that male Pericúes samples displayed more craniometric affinities with populations from Africa and Australia relative to the female individuals of their population (fig. S41). The results of analyses based on craniometric data are, thus, highly sensitive to sample structure and the statistical approach and data filtering used (51). Our morphometric analyses suggest that these ancient samples are not true relicts of a distinct migration, as claimed, and hence do not support the Paleo-american model. Similarly, our genomic data also provide no support for an early migration of populations directly related to Australo-Melanesians into the Americas.

Discussion

That Native Americans diverged from their East Asian ancestors during the LGM and no earlier than 23 KYA provides an upper bound, and perhaps the climatic and environmental context, for the initial isolation of their ancestral population, and a maximum estimate for the entrance and subsequent spread into the Americas. This result is consistent with the model that people entered the Americas prior to the development of the Clovis complex and had reached as far as southern South America by 14.6 KYA. As archaeological evidence provides only a minimum age for human presence in the Americas, we can anticipate the possible discovery of sites that approach the time of the divergence of East Asians and Native Americans. However, our estimate for the initial divergence and entry of Native American ancestors does not support archaeological claims for an initial peopling significantly earlier than the LGM (8–10).

While our data cannot provide the precise geographical context for the initial peopling process, it has allowed us to more accurately estimate its temporal dynamics. This, in turn, has enabled us to re-assess the Beringian Incubation Model, which, based on mtDNA data and the timing and geographical distribution of archaeological sites, hypothesized a ca. 15,000 year-long period of isolation of ancestral Native Americans in Beringia during the LGM (19–21). Our results, along with recent findings of mtDNA haplogroup C1 in Iceland and ancient northwest Russia (60), do not fit with the proposed 15,000-year span of the Beringian Incubation Model (19–21). It is possible that a shorter period of isolation occurred (ca. 8 KYA), but whether it occurred in Siberia or Beringia will have to be determined by future ancient DNA and archaeological findings. Given the genetic continuity between Native Americans and some East Asian populations (figs. S4 and S5), other demographic factors, such as surfing during population expansions into unoccupied regions (61), may ultimately need to be taken into account to better understand the presence of a large number of high frequency private variants in the indigenous populations of the Americas.

The data presented here are consistent with a single initial migration of all Native Americans and with later gene flow from sources related to East Asians and, more distantly, Australo-Melanesians. From that single migration, there was a diversification of ancestral Native Americans leading to the formation of ‘northern’ and ‘southern’ branches, which appears to have taken place ca. 13 KYA within the Americas. This split is consistent with the patterns of uniparental genomic regions of mtDNA haplogroup X and some Y chromosome C haplotypes being present in northern, but not southern, populations in the Americas (18, 62). This diversification event coincides roughly with the opening of habitable routes along the coastal and the interior corridors into unglaciated North America some 16 KYA and 14 KYA, respectively (63, 64), suggesting a possible role of one or both these routes in the isolation and subsequent dispersal of Native Americans across the continent.

Methods

DNA was extracted from 31 present-day individuals from the Americas, Siberia and Oceania and 23 ancient samples from the Americas, and converted to Illumina libraries and shotgun-sequenced (28). Three of the ancient samples were radiocarbon dated, of which two were corrected for marine reservoir offset (28). SNP chip genotype data was generated from 79 present-day Siberians and Native Americans affiliated to 28 populations (28). Raw data from SNP chip and shotgun sequencing were processed using standard computational procedures (28). Error rate analysis, DNA damage analysis, contamination estimation, sex determination, mtDNA and Y chromosome haplogroup assignment, ADMIXTURE analysis, ancestry painting and admixture masking, Principal Component Analysis using SNP chip genotype data, *TreeMix* analysis on genomic sequence data, *D*-statistic and outgroup f_3 -statistic tests on SNP chip genotype and genomic sequence data, divergence time estimation using *diCal2.0*, an IBS tract method and MSMC, Climate-Informed Spatial Genetic Model analysis, and, craniometric analysis were performed as described (28).

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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REFERENCES AND NOTES

1. Dillehay TD. The late Pleistocene cultures of South America. *Evol. Anthropol.* 1999; 7:206–216. doi:10.1002/(SICI)1520-6505(1999)7:6<206::AID-EVAN5>3.0.CO;2-G.
2. Jenkins DL, Davis LG, Stafford TW Jr, Campos PF, Hockett B, Jones GT, Cummings LS, Yost C, Connolly TJ, Yohe RM 2nd, Gibbons SC, Raghavan M, Rasmussen M, Paijmans JL, Hofreiter M, Kemp BM, Barta JL, Monroe C, Gilbert MT, Willerslev E. Clovis age Western Stemmed projectile points and human coprolites at the Paisley Caves. *Science.* 2012; 337:223–228. [PubMed: 22798611]

3. Meltzer, DJ. *First Peoples in a New World: Colonizing Ice Age America*. University of California Press; Berkeley: 2009.
4. Raghavan M, Skoglund P, Graf KE, Metspalu M, Albrechtsen A, Moltke I, Rasmussen S, Stafford TW Jr, Orlando L, Metspalu E, Karmin M, Tambets K, Rootsi S, Mägi R, Campos PF, Balanovska E, Balanovsky O, Khusnutdinova E, Litvinov S, Osipova LP, Fedorova SA, Voevoda MI, DeGiorgio M, Sicheritz-Ponten T, Brunak S, Demeshchenko S, Kivisild T, Villems R, Nielsen R, Jakobsson M, Willerslev E. Upper Palaeolithic Siberian genome reveals dual ancestry of Native Americans. *Nature*. 2014; 505:87–91.10.1038/nature12736 [PubMed: 24256729]
5. Rasmussen M, Anzick SL, Waters MR, Skoglund P, DeGiorgio M, Stafford TW Jr, Rasmussen S, Moltke I, Albrechtsen A, Doyle SM, Poznik GD, Gudmundsdottir V, Yadav R, Malaspina A-S, White SS 5th, Allentoft ME, Cornejo OE, Tambets K, Eriksson A, Heintzman PD, Karmin M, Korneliusen TS, Meltzer DJ, Pierre TL, Stenderup J, Saag L, Warmuth VM, Lopes MC, Malhi RS, Brunak S, Sicheritz-Ponten T, Barnes I, Collins M, Orlando L, Balloux F, Manica A, Gupta R, Metspalu M, Bustamante CD, Jakobsson M, Nielsen R, Willerslev E. The genome of a Late Pleistocene human from a Clovis burial site in western Montana. *Nature*. 2014; 506:225–229.10.1038/nature13025 [PubMed: 24522598]
6. Reich D, Patterson N, Campbell D, Tandon A, Mazieres S, Ray N, Parra MV, Rojas W, Duque C, Mesa N, García LF, Triana O, Blair S, Maestre A, Dib JC, Bravi CM, Bailliet G, Corach D, Hünemeier T, Bortolini MC, Salzano FM, Petzl-Erler ML, Acuña-Alonzo V, Aguilar-Salinas C, Canizales-Quinteros S, Tusié-Luna T, Riba L, Rodríguez-Cruz M, Lopez-Alarcón M, Coral-Vazquez R, Canto-Cetina T, Silva-Zolezzi I, Fernandez-Lopez JC, Contreras AV, Jimenez-Sanchez G, Gómez-Vázquez MJ, Molina J, Carracedo A, Salas A, Gallo C, Poletti G, Witonsky DB, Alkorta-Aranburu G, Sukernik RI, Osipova L, Fedorova SA, Vasquez R, Villena M, Moreau C, Barrantes R, Pauls D, Excoffier L, Bedoya G, Rothhammer F, Dugoujon JM, Larrouy G, Klitz W, Labuda D, Kidd J, Kidd K, Di Rienzo A, Freimer NB, Price AL, Ruiz-Linares A. Reconstructing Native American population history. *Nature*. 2012; 488:370–374. [PubMed: 22801491]
7. Waters MR, Forman SL, Jennings TA, Nordt LC, Driese SG, Feinberg JM, Keene JL, Halligan J, Lindquist A, Pierson J, Hallmark CT, Collins MB, Wiederhold JE. The Buttermilk Creek complex and the origins of Clovis at the Debra L. Friedkin site, Texas. *Science*. 2011; 331:1599–1603.10.1126/science.1201855 [PubMed: 21436451]
8. Santos GM, Bird MI, Parenti F, Fifield LK, Guidon N, Hausladen PA. A revised chronology of the lowest occupation layer of Pedra Furada Rock Shelter, Piauí, Brazil: The Pleistocene peopling of the Americas. *Quat. Sci. Rev.* 2003; 22:2303–2310.10.1016/S0277-3791(03)00205-1
9. Holen, SR.; Holen, K.; K. *Paleoamerican Odyssey*. Graf, KE.; Ketron, CV.; Waters, MR., editors. Texas A&M University Press; College Station: 2014. p. 429-444.
10. Boëda E, Clemente-Conte I, Fontugne M, Lahaye C, Pino M, Felice GD, Guidon N, Hoeltz S, Lourdeau A, Pagli M, Pessis A-M, Viana S, Da Costa A, Douville E. A new late Pleistocene archaeological sequence in South America: The Vale da Pedra Furada (Piauí, Brazil). *Antiquity*. 2014; 88:927–941.10.1017/S0003598X00050845
11. Owsley, DW.; Jantz, RL. *Kennewick Man: The Scientific Investigation of an Ancient American Skeleton*. Texas A&M University Press; College Station: 2014.
12. Achilli A, Perego UA, Bravi CM, Coble MD, Kong QP, Woodward SR, Salas A, Torroni A, Bandelt HJ. The phylogeny of the four pan-American mtDNA haplogroups: Implications for evolutionary and disease studies. *PLOS ONE*. 2008; 3:e1764.10.1371/journal.pone.0001764 [PubMed: 18335039]
13. Battaglia V, Grugni V, Perego UA, Angerhofer N, Gomez-Palmieri JE, Woodward SR, Achilli A, Myres N, Torroni A, Semino O. The first peopling of South America: New evidence from Y-chromosome haplogroup Q. *PLOS ONE*. 2013; 8:e71390.10.1371/journal.pone.0071390 [PubMed: 23990949]
14. Brace CL, Nelson AR, Seguchi N, Oe H, Sering L, Qifeng P, Yongyi L, Tumen D. Old World sources of the first New World human inhabitants: A comparative craniofacial view. *Proc. Natl. Acad. Sci. U.S.A.* 2001; 98:10017–10022.10.1073/pnas.171305898 [PubMed: 11481450]
15. Perego UA, Achilli A, Angerhofer N, Accetturo M, Pala M, Olivieri A, Kashani B, Hooshiar, Ritchie KH, Scozzari R, Kong Q-P, Myres NM, Salas A, Semino O, Bandelt H-J, Woodward SR,

- Torroni A. Distinctive Paleo-Indian migration routes from Beringia marked by two rare mtDNA haplogroups. *Curr. Biol.* 2009; 19:1–8.10.1016/j.cub.2008.11.058 [PubMed: 19135370]
16. Perego UA, Angerhofer N, Pala M, Olivieri A, Lancioni H, Kashani B, Hooshiar, Carossa V, Ekins JE, Gómez-Carballea A, Huber G, Zimmermann B, Corach D, Babudri N, Panara F, Myres NM, Parson W, Semino O, Salas A, Woodward SR, Achilli A, Torroni A. The initial peopling of the Americas: A growing number of founding mitochondrial genomes from Beringia. *Genome Res.* 2010; 20:1174–1179.10.1101/gr.109231.110 [PubMed: 20587512]
 17. Fagundes NJR, Kanitz R, Bonatto SL. A reevaluation of the Native American mtDNA genome diversity and its bearing on the models of early colonization of Beringia. *PLOS ONE.* 2008; 3:e3157.10.1371/journal.pone.0003157 [PubMed: 18797501]
 18. Zegura SL, Karafet TM, Zhivotovsky LA, Hammer MF. High-resolution SNPs and microsatellite haplotypes point to a single, recent entry of Native American Y chromosomes into the Americas. *Mol. Biol. Evol.* 2004; 21:164–175.10.1093/molbev/msh009 [PubMed: 14595095]
 19. Tamm E, Kivisild T, Reidla M, Metspalu M, Smith DG, Mulligan CJ, Bravi CM, Rickards O, Martinez-Labarga C, Khusnutdinova EK, Fedorova SA, Golubenko MV, Stepanov VA, Gubina MA, Zhadanov SI, Ossipova LP, Damba L, Voevoda MI, Dipierri JE, VILLEMS R, Malhi RS. Beringian standstill and spread of Native American founders. *PLOS ONE.* 2007; 2:e829.10.1371/journal.pone.0000829 [PubMed: 17786201]
 20. Kitchen A, Miyamoto MM, Mulligan CJ. A three-stage colonization model for the peopling of the Americas. *PLOS ONE.* 2008; 3:e1596.10.1371/journal.pone.0001596 [PubMed: 18270583]
 21. Mulligan CJ, Kitchen A, Miyamoto MM. Updated three-stage model for the peopling of the Americas. *PLOS ONE.* 2008; 3:e3199.10.1371/journal.pone.0003199 [PubMed: 18797500]
 22. Schroeder KB, Schurr TG, Long JC, Rosenberg NA, Crawford MH, Tarskaia LA, Osipova LP, Zhadanov SI, Smith DG. A private allele ubiquitous in the Americas. *Biol. Lett.* 2007; 3:218–223.10.1098/rsbl.2006.0609 [PubMed: 17301009]
 23. González-José R, González-Martín A, Hernández M, Pucciarelli HM, Sardi M, Rosales A, Van Der Molen S. Craniometric evidence for Palaeoamerican survival in Baja California. *Nature.* 2003; 425:62–65.10.1038/nature01816 [PubMed: 12955139]
 24. Neves WA, Hubbe M. Cranial morphology of early Americans from Lagoa Santa, Brazil: Implications for the settlement of the New World. *Proc. Natl. Acad. Sci. U.S.A.* 2005; 102:18309–18314.10.1073/pnas.0507185102 [PubMed: 16344464]
 25. Neves, W., et al. *Paleoamerican Odyssey*. Graf, KE.; Ketron, CV.; Waters, MR., editors. Texas A&M University Press; College Station: 2014. p. 397-412.
 26. González-José R, Bortolini MC, Santos FR, Bonatto SL. The peopling of America: Craniofacial shape variation on a continental scale and its interpretation from an interdisciplinary view. *Am. J. Phys. Anthropol.* 2008; 137:175–187.10.1002/ajpa.20854 [PubMed: 18481303]
 27. Lahr MM. Patterns of modern human diversification: Implications for Amerindian origins. *Am. J. Phys. Anthropol.* 1995; 38(S21):163–198.10.1002/ajpa.1330380609
 28. Materials and methods are available as supplementary materials on *Science* Online.
 29. Rasmussen M, Li Y, Lindgreen S, Pedersen JS, Albrechtsen A, Moltke I, Metspalu M, Metspalu E, Kivisild T, Gupta R, Bertalan M, Nielsen K, Gilbert MT, Wang Y, Raghavan M, Campos PF, Kamp HM, Wilson AS, Gledhill A, Tridico S, Bunce M, Lorenzen ED, Binladen J, Guo X, Zhao J, Zhang X, Zhang H, Li Z, Chen M, Orlando L, Kristiansen K, Bak M, Tommerup N, Bendixen C, Pierre TL, Grønnow B, Meldgaard M, Andreasen C, Fedorova SA, Osipova LP, Higham TF, Ramsey CB, Hansen TV, Nielsen FC, Crawford MH, Brunak S, Sicheritz-Pontén T, VILLEMS R, Nielsen R, Krogh A, Wang J, Willerslev E. Ancient human genome sequence of an extinct Palaeo-Eskimo. *Nature.* 2010; 463:757–762.10.1038/nature08835 [PubMed: 20148029]
 30. Yunusbayev B, Metspalu M, Metspalu E, Valeev A, Litvinov S, Valiev R, Akhmetova V, Balanovska E, Balanovsky O, Turdikulova S, Dalimova D, Nymadawa P, Bahmanimehr A, Sahakyan H, Tambets K, Fedorova S, Barashkov N, Khidiyatova I, Mihailov E, Khusainova R, Damba L, Derenko M, Malyarchuk B, Osipova L, Voevoda M, Yepiskoposyan L, Kivisild T, Khusnutdinova E, VILLEMS R. The genetic legacy of the expansion of Turkic-speaking nomads across Eurasia. *PLOS Genet.* 2015; 11:e1005068.10.1371/journal.pgen.1005068 [PubMed: 25898006]

31. Cardona A, Pagani L, Antao T, Lawson DJ, Eichstaedt CA, Yngvadottir B, Shwe MT, Wee J, Romero IG, Raj S, Metspalu M, Villems R, Willerslev E, Tyler-Smith C, Malyarchuk BA, Derenko MV, Kivisild T. Genome-wide analysis of cold adaptation in indigenous Siberian populations. *PLOS ONE*. 2014; 9:e98076. . [PubMed: 24847810]
32. Li JZ, Absher DM, Tang H, Southwick AM, Casto AM, Ramachandran S, Cann HM, Barsh GS, Feldman M, Cavalli-Sforza LL, Myers RM. Worldwide human relationships inferred from genome-wide patterns of variation. *Science*. 2008; 319:1100–1104.10.1126/science.1153717 [PubMed: 18292342]
33. Moreno-Estrada A, Gravel S, Zakharia F, McCauley JL, Byrnes JK, Gignoux CR, Ortiz-Tello PA, Martínez RJ, Hedges DJ, Morris RW, Eng C, Sandoval K, Acevedo-Acevedo S, Norman PJ, Layrisse Z, Parham P, Martínez-Cruzado JC, Burchard EG, Cuccaro ML, Martin ER, Bustamante CD. Reconstructing the population genetic history of the Caribbean. *PLOS Genet*. 2013; 9:e1003925.10.1371/journal.pgen.1003925 [PubMed: 24244192]
34. Moreno-Estrada A, Gignoux CR, Fernández-López JC, Zakharia F, Sikora M, Contreras AV, Acuña-Alonzo V, Sandoval K, Eng C, Romero-Hidalgo S, Ortiz-Tello P, Robles V, Kenny EE, Nuño-Arana I, Barquera-Lozano R, Macín-Pérez G, Granados-Arriola J, Huntsman S, Galanter JM, Via M, Ford JG, Chapela R, Rodríguez-Cintron W, Rodríguez-Santana JR, Romieu I, Sienra-Monge JJ, del Rio Navarro B, London SJ, Ruiz-Linares A, Garcia-Herrera R, Estrada K, Hidalgo-Miranda A, Jimenez-Sanchez G, Carnevale A, Soberón X, Canizales-Quinteros S, Rangel-Villalobos H, Silva-Zolezzi I, Burchard EG, Bustamante CD. The genetics of Mexico recapitulates Native American substructure and affects biomedical traits. *Science*. 2014; 344:1280–1285.10.1126/science.1251688 [PubMed: 24926019]
35. Verdu P, Pemberton TJ, Laurent R, Kemp BM, Gonzalez-Oliver A, Gorodetzky C, Hughes CE, Shattuck MR, Petzelt B, Mitchell J, Harry H, William T, Worl R, Cybulski JS, Rosenberg NA, Malhi RS. Patterns of admixture and population structure in native populations of Northwest North America. *PLOS Genet*. 2014; 10:e1004530.10.1371/journal.pgen.1004530 [PubMed: 25122539]
36. Alexander DH, Novembre J, Lange K. Fast model-based estimation of ancestry in unrelated individuals. *Genome Res*. 2009; 19:1655–1664.10.1101/gr.094052.109 [PubMed: 19648217]
37. Pickrell JK, Pritchard JK. Inference of population splits and mixtures from genome-wide allele frequency data. *PLOS Genet*. 2012; 8:e1002967.10.1371/journal.pgen.1002967 [PubMed: 23166502]
38. Meyer M, Kircher M, Gansauge MT, Li H, Racimo F, Mallick S, Schraiber JG, Jay F, Prüfer K, de Filippo C, Sudmant PH, Alkan C, Fu Q, Do R, Rohland N, Tandon A, Siebauer M, Green RE, Bryc K, Briggs AW, Stenzel U, Dabney J, Shendure J, Kitzman J, Hammer MF, Shunkov MV, Derevianko AP, Patterson N, Andrés AM, Eichler EE, Slatkin M, Reich D, Kelso J, Pääbo S. A high-coverage genome sequence from an archaic Denisovan individual. *Science*. 2012; 338:222–226. [PubMed: 22936568]
39. Raghavan M, DeGiorgio M, Albrechtsen A, Moltke I, Skoglund P, Korneliussen TS, Grønnow B, Appelt M, Gulløv HC, Friesen TM, Fitzhugh W, Malmström H, Rasmussen S, Olsen J, Melchior L, Fuller BT, Fahrni SM, Stafford T Jr. Grimes V, Renouf MA, Cybulski J, Lynnerup N, Lahr MM, Britton K, Knecht R, Arneborg J, Metspalu M, Cornejo OE, Malaspina AS, Wang Y, Rasmussen M, Raghavan V, Hansen TV, Khusnutdinova E, Pierre T, Dneprovsky K, Andreasen C, Lange H, Hayes MG, Coltrain J, Spitsyn VA, Götherström A, Orlando L, Kivisild T, Villems R, Crawford MH, Nielsen FC, Dissing J, Heinemeier J, Meldgaard M, Bustamante C, O'Rourke DH, Jakobsson M, Gilbert MT, Nielsen R, Willerslev E. The genetic prehistory of the New World Arctic. *Science*. 2014; 345:1255832–1255832.10.1126/science.1255832 [PubMed: 25170159]
40. Scally A, Durbin R. Revising the human mutation rate: Implications for understanding human evolution. *Nat. Rev. Genet*. 2012; 13:745–753.10.1038/nrg3295 [PubMed: 22965354]
41. Sheehan S, Harris K, Song YS. Estimating variable effective population sizes from multiple genomes: A sequentially markov conditional sampling distribution approach. *Genetics*. 2013; 194:647–662.10.1534/genetics.112.149096 [PubMed: 23608192]
42. Steinrücken M, Paul JS, Song YS. A sequentially Markov conditional sampling distribution for structured populations with migration and recombination. *Theor. Popul. Biol*. 2013; 87:51–61.10.1016/j.tpb.2012.08.004 [PubMed: 23010245]

43. Harris K, Nielsen R. Inferring demographic history from a spectrum of shared haplotype lengths. *PLOS Genet.* 2013; 9:e1003521.10.1371/journal.pgen.1003521 [PubMed: 23754952]
44. Schiffels S, Durbin R. Inferring human population size and separation history from multiple genome sequences. *Nat. Genet.* 2014; 46:919–925.10.1038/ng.3015 [PubMed: 24952747]
45. Eriksson A, Betti L, Friend AD, Lycett SJ, Singarayer JS, von Cramon-Taubadel N, Valdes PJ, Balloux F, Manica A. Late Pleistocene climate change and the global expansion of anatomically modern humans. *Proc. Natl. Acad. Sci. U.S.A.* 2012; 109:16089–16094.10.1073/pnas.1209494109 [PubMed: 22988099]
46. Green RE, Krause J, Briggs AW, Maricic T, Stenzel U, Kircher M, Patterson N, Li H, Zhai W, Fritz MH, Hansen NF, Durand EY, Malaspina AS, Jensen JD, Marques-Bonet T, Alkan C, Prüfer K, Meyer M, Burbano HA, Good JM, Schultz R, Aximu-Petri A, Butthof A, Höber B, Höffner B, Siegemund M, Weihmann A, Nusbaum C, Lander ES, Russ C, Novod N, Affourtit J, Egholm M, Verna C, Rudan P, Brajkovic D, Kucan Z, Gusic I, Doronichev VB, Golovanova LV, Lalueza-Fox C, de la Rasilla M, Fortea J, Rosas A, Schmitz RW, Johnson PL, Eichler EE, Falush D, Birney E, Mullikin JC, Slatkin M, Nielsen R, Kelso J, Lachmann M, Reich D, Pääbo S. A draft sequence of the Neandertal genome. *Science.* 2010; 328:710–722.10.1126/science.1188021 [PubMed: 20448178]
47. Patterson N, Moorjani P, Luo Y, Mallick S, Rohland N, Zhan Y, Genschoreck T, Webster T, Reich D. Ancient admixture in human history. *Genetics.* 2012; 192:1065–1093.10.1534/genetics.112.145037 [PubMed: 22960212]
48. Hoffecker, JF.; Elias, SA. *Human Ecology of Beringia.* Columbia University Press; New York: 2007.
49. Oppenheimer S, Bradley B, Stanford D. Solutrean hypothesis: Genetics, the mammoth in the room. *World Archaeol.* 2014; 46:752–774.10.1080/00438243.2014.966273
50. Dillehay, TD. *Monte Verde, A Late Pleistocene Settlement in Chile: The archaeological context and interpretation.* Smithsonian Institution Press; Washington D.C.: 1997.
51. Rasmussen M, Sikora M, Albrechtsen A, Korneliussen TS, Moreno-Mayar JV, Poznik GD, Zollikofer CP, de León M, S. Ponce, Allentoft ME, Moltke I, Jónsson H, Valdiosera C, Malhi RS, Orlando L, Bustamante CD, Stafford TW Jr, Meltzer DJ, Nielsen R, Willerslev E. The ancestry and affiliations of Kennewick Man. *Nature.* 2015; 510:1038/nature14625.10.1038/nature14625 [PubMed: 26087396]
52. Davis RS, Knecht RA. Continuity and change in the eastern Aleutian archaeological sequence. *Hum. Biol.* 2010; 82:507–524. [PubMed: 21417882]
53. Crawford MH, Rubicz RC, Zlojutro M. Origins of Aleuts and the genetic structure of populations of the archipelago: Molecular and archaeological perspectives. *Hum. Biol.* 2010; 82:695–717. [PubMed: 21417890]
54. Hubbe M, Neves WA, Harvati K. Testing evolutionary and dispersion scenarios for the settlement of the new world. *PLOS ONE.* 2010; 5:e11105. . [PubMed: 20559441]
55. Chatters JC, Kennett DJ, Asmerom Y, Kemp BM, Polyak V, Blank AN, Beddows PA, Reinhardt E, Arroyo-Cabrales J, Bolnick DA, Malhi RS, Culleton BJ, Erreguerena PL, Rissolo D, Morell-Hart S, Stafford TW Jr. Late Pleistocene human skeleton and mtDNA link Paleoamericans and modern Native Americans. *Science.* 2014; 344:750–754.10.1126/science.1252619 [PubMed: 24833392]
56. García-Bour J, Pérez-Pérez A, Alvarez S, Fernández E, López-Parra AM, Arroyo-Pardo E, Turbón D. Early population differentiation in extinct aborigines from Tierra del Fuego-Patagonia: Ancient mtDNA sequences and Y-chromosome STR characterization. *Am. J. Phys. Anthropol.* 2004; 123:361–370.10.1002/ajpa.10337 [PubMed: 15022364]
57. Perez SI, Bernal V, Gonzalez PN, Sardi M, Politis GG. Discrepancy between cranial and DNA data of early Americans: Implications for American peopling. *PLOS ONE.* 2009; 4:e5746.10.1371/journal.pone.0005746 [PubMed: 19478947]
58. Hernández M, Fox CL, García-Moro C. Fuegian cranial morphology: The adaptation to a cold, harsh environment. *Am. J. Phys. Anthropol.* 1997; 103:103–117. doi:10.1002/(SICI)1096-8644(199705)103:1<103::AID-AJPA7>3.0.CO;2-X. [PubMed: 9185954]

59. González-José R, Dahinten SL, Luis MA, Hernández M, Pucciarelli HM. Craniometric variation and the settlement of the Americas: Testing hypotheses by means of R-matrix and matrix correlation analyses. *Am. J. Phys. Anthropol.* 2001; 116:154–165.10.1002/ajpa.1108 [PubMed: 11590587]
60. Der Sarkissian C, Brotherton P, Balanovsky O, Templeton JE, Llamas B, Soubrier J, Moiseyev V, Khartanovich V, Cooper A, Haak W, Genographic Consortium. Mitochondrial genome sequencing in Mesolithic North East Europe Unearths a new sub-clade within the broadly distributed human haplogroup C1. *PLOS ONE.* 2014; 9:e87612.10.1371/journal.pone.0087612 [PubMed: 24503968]
61. Excoffier L, Ray N. Surfing during population expansions promotes genetic revolutions and structuration. *Trends Ecol. Evol.* 2008; 23:347–351.10.1016/j.tree.2008.04.004 [PubMed: 18502536]
62. Achilli A, Perego UA, Lancioni H, Olivieri A, Gandini F, Kashani B, Hooshiar, Battaglia V, Grugni V, Angerhofer N, Rogers MP, Herrera RJ, Woodward SR, Labuda D, Smith DG, Cybulski JS, Semino O, Malhi RS, Torroni A. Reconciling migration models to the Americas with the variation of North American native mitogenomes. *Proc. Natl. Acad. Sci. U.S.A.* 2013; 110:14308–14313. [PubMed: 23940335]
63. Dixon EJ. Late Pleistocene colonization of North America from Northeast Asia: New insights from large-scale paleogeographic reconstructions. *Quat. Int.* 2013; 285:57–67.10.1016/j.quaint.2011.02.027
64. Mandryk CAS, Josenhans H, Fedje DW, Mathewes RW. Late Quaternary paleoenvironments of Northwestern North America: Implications for inland versus coastal migration routes. *Quat. Sci. Rev.* 2001; 20:301–314.10.1016/S0277-3791(00)00115-3
65. Purcell S, Neale B, Todd-Brown K, Thomas L, Ferreira MA, Bender D, Maller J, Sklar P, de Bakker PI, Daly MJ, Sham PC. PLINK: A tool set for whole-genome association and population-based linkage analyses. *Am. J. Hum. Genet.* 2007; 81:559–575.10.1086/519795 [PubMed: 17701901]
66. Cann HM, de Toma C, Cazes L, Legrand MF, Morel V, Piouffre L, Bodmer J, Bodmer WF, Bonne-Tamir B, Cambon-Thomsen A, Chen Z, Chu J, Carcassi C, Contu L, Du R, Excoffier L, Ferrara GB, Friedlaender JS, Groot H, Gurwitz D, Jenkins T, Herrera RJ, Huang X, Kidd J, Kidd KK, Langaney A, Lin AA, Mehdi SQ, Parham P, Piazza A, Pistillo MP, Qian Y, Shu Q, Xu J, Zhu S, Weber JL, Greely HT, Feldman MW, Thomas G, Dausset J, Cavalli-Sforza LL. A human genome diversity cell line panel. *Science.* 2002; 296:261b–262.10.1126/science.296.5566.261b [PubMed: 11954565]
67. Cui Y, Lindo J, Hughes CE, Johnson JW, Hernandez AG, Kemp BM, Ma J, Cunningham R, Petzelt B, Mitchell J, Archer D, Cybulski JS, Malhi RS. Ancient DNA analysis of mid-holocene individuals from the Northwest Coast of North America reveals different evolutionary paths for mitogenomes. *PLOS ONE.* 2013; 8:e66948.10.1371/journal.pone.0066948 [PubMed: 23843972]
68. Archer, D. The Lucy Island Archaeological Project. Victoria: 2011. Unpublished report on file with the British Columbia Archaeology Branch
69. McLaren, D. Sea level change and archaeological site locations on the Dundas Island Archipelago of North Coastal British Columbia. University of Victoria; 2008. PhD dissertation
70. Cybulski, JS. “Human Remains from Lucy Island, British Columbia, Site GbTp 1, 1984/85,” ms. 2360. Canadian Museum of Civilization Library Archives; Gatineau, Canada: 1986.
71. Chisholm BS, Nelson DE, Schwarcz HP. Marine and terrestrial protein in prehistoric diets on the British Columbia coast. *Curr. Anthropol.* 1983; 24:396–398.10.1086/203018 [PubMed: 20516186]
72. Cybulski, JS. Human Variation in the Americas: The Integration of Archaeology and Biological Anthropology. Auerbach, BM., editor. Center for Archaeological Investigations; Carbondale: 2010. p. 77-112.
73. Cybulski, JS. Violence and Warfare Among Hunter-Gatherers. Allen, MW.; Jones, TL., editors. Left Coast Press; Walnut Creek: 2014. p. 333-350.
74. Meyer M, Kircher M. Illumina sequencing library preparation for highly multiplexed target capture and sequencing. *Cold Spring Harb. Protoc.* 2010; 2010:t5448.10.1101/pdb.prot5448.1101/pdb.prot5448

75. Maricic T, Whitten M, Pääbo S. Multiplexed DNA sequence capture of mitochondrial genomes using PCR products. *PLOS ONE*. 2010; 5:e14004.10.1371/journal.pone.0014004 [PubMed: 21103372]
76. Arriaza, B. *Beyond Death: The Chinchorro Mummies of Ancient Chile*. Smithsonian Institution Press; 1995.
77. Arriaza BT, et al. Chemical and mineral characterization of gray sediments used to model Chinchorro bodies. *Chungara*. 2012; 44:177–194.
78. Arriaza B, Standen V, Reinhard K, Araújo A, Heukelbach J, Dittmar K. On head lice and social interaction in archaic Andean coastal populations. *Int. J. Paleopathol*. 2013; 3:257–268.10.1016/j.ijpp.2013.10.001
79. Orlando L, Ginolhac A, Zhang G, Froese D, Albrechtsen A, Stiller M, Schubert M, Cappellini E, Petersen B, Moltke I, Johnson PL, Fumagalli M, Vilstrup JT, Raghavan M, Korneliusen T, Malaspina AS, Vogt J, Szklarczyk D, Kelstrup CD, Vinther J, Dolocan A, Stenderup J, Velazquez AM, Cahill J, Rasmussen M, Wang X, Min J, Zazula GD, Seguin-Orlando A, Mortensen C, Magnussen K, Thompson JF, Weinstock J, Gregersen K, Røed KH, Eisenmann V, Rubin CJ, Miller DC, Antczak DF, Bertelsen MF, Brunak S, Al-Rasheid KA, Ryder O, Andersson L, Mundy J, Krogh A, Gilbert MT, Kjær K, Sicheritz-Ponten T, Jensen LJ, Olsen JV, Hofreiter M, Nielsen R, Shapiro B, Wang J, Willerslev E. Recalibrating Equus evolution using the genome sequence of an early Middle Pleistocene horse. *Nature*. 2013; 499:74–78.10.1038/nature12323 [PubMed: 23803765]
80. Clarke PD. A la recherche de La Petite-Rochelle: Memory and Identity in Restigouche. *Acadiensis (Fredericton)*. 1999; XXVIII:3–40.
81. Clarke PD. Land of East Wind: Mise en Forme d'une Memoire Mi'gmaq. *Can. Rev. Sociol*. 2000; 37:167–195.10.1111/j.1755-618X.2000.tb01263.x
82. Leonard, K. *Archaeology of the Restigouche River, New Brunswick: A Summary*. Mi'gmawei Mawiomis Secretariat; 2002. Wesgijinua'luet Research Title Project
83. Leonard, K. *Archaeology of the New Brunswick Sites of Gespegewagji*. Mi'gmawei Mawiomis Secretariat; 2002. Wesgijinua'luet Research Title Project
84. Martijn, C. *An Archaeological Survey of the Northeast Coast of New Brunswick 1968 (Restigouche and Gloucester Counties)*. Historical Resources Administration; Fredericton, New Brunswick: 1968.
85. Turnbull, CJ. *Old Mission Point 1973: Report for an Archaeological Survey of Canada Salvage Contract*. Archaeological Survey of Canada; Ottawa: 1974.
86. Turnbull, CJ. *The Richibucto Burial Site (CeDf-18), New Brunswick*. New Brunswick: 1981. Manuscript on file with Archaeological Services Unit
87. Garlie, TN. *An Ethnohistorical and Archaeological Review regarding Aboriginal Mortuary Remains reported from Nova Scotia and New Brunswick and the Potential for Future Research*. Memorial University; 1992. Unpublished Honours Essay
88. Pike, KA. *Bearing Identity: A Biocultural Analysis of Human Remains from Old Mission Point (CIDq-1), New Brunswick*. Memorial University; 2014. Unpublished Master of Arts Thesis
89. Turnbull, CJ.; Turnbull, SW. *Preliminary Report of the 1973 Excavations at Old Mission Point (CIDq-1) New Brunswick*. Archaeological Survey of Canada; Ottawa: 1973.
90. Petersen, JB.; Sanger, D. *Prehistory of the Maritime Provinces: Past and Present Research*. Deal, M.; Blair, S., editors. Council of Maritime Premiers; Fredericton: 1991. p. 113-170.
91. Svensson EM, Anderung C, Baubliene J, Persson P, Malmström H, Smith C, Vretemark M, Daugnora L, Götherström A. Tracing genetic change over time using nuclear SNPs in ancient and modern cattle. *Anim. Genet*. 2007; 38:378–383.10.1111/j.1365-2052.2007.01620.x [PubMed: 17596126]
92. Pijoan GV, Romero A, Mansilla J. Los Pericues de Baja California Sur en Perspectiva Tafonómica. *Colección Científica INAH*. 2010; 560:67.
93. García-Bour J, Pérez-Pérez A, Alvarez S, Fernández E, López-Parra AM, Arroyo-Pardo E, Turbón D. Early population differentiation in extinct aborigines from Tierra del Fuego-Patagonia: Ancient mtDNA sequences and Y-chromosome STR characterization. *Am. J. Phys. Anthropol*. 2004; 123:361–370.10.1002/ajpa.10337 [PubMed: 15022364]

94. Lalueza C, Pérez-Pérez A, Prats E, Cornudella L, Turbón D. Lack of founding Amerindian mitochondrial DNA lineages in extinct aborigines from Tierra del Fuego-Patagonia. *Hum. Mol. Genet.* 1997; 6:41–46.10.1093/hmg/6.1.41 [PubMed: 9002668]
95. Moraga ML, Rocco P, Miquel JF, Nervi F, Llop E, Chakraborty R, Rothhammer F, Carvalho P. Mitochondrial DNA polymorphisms in Chilean aboriginal populations: Implications for the peopling of the southern cone of the continent. *Am. J. Phys. Anthropol.* 2000; 113:19–29. doi: 10.1002/1096-8644(200009)113:1<19::AID-AJPA3>3.0.CO;2-X. [PubMed: 10954617]
96. Yang DY, Eng B, Wayne JS, Dudar JC, Saunders SR. Improved DNA extraction from ancient bones using silica-based spin columns. *Am. J. Phys. Anthropol.* 1998; 105:539–543. doi:10.1002/(SICI)1096-8644(199804)105:4<539::AID-AJPA10>3.0.CO;2-1. [PubMed: 9584894]
97. Rohland N, Hofreiter M. Ancient DNA extraction from bones and teeth. *Nat. Protoc.* 2007; 2:1756–1762.10.1038/nprot.2007.247 [PubMed: 17641642]
98. Gilbert MTP, Wilson AS, Bunce M, Hansen AJ, Willerslev E, Shapiro B, Higham TF, Richards MP, O'Connell TC, Tobin DJ, Janaway RC, Cooper A. Ancient mitochondrial DNA from hair. *Curr. Biol.* 2004; 14:R463–R464.10.1016/j.cub.2004.06.008 [PubMed: 15203015]
99. Behar DM, Yunusbayev B, Metspalu M, Metspalu E, Rosset S, Parik J, Rootsi S, Chaubey G, Kutuev I, Yudkovsky G, Khusnutdinova EK, Balanovsky O, Semino O, Pereira L, Comas D, Gurwitz D, Bonne-Tamir B, Parfitt T, Hammer MF, Skorecki K, Vilems R. The genome-wide structure of the Jewish people. *Nature.* 2010; 466:238–242.10.1038/nature09103 [PubMed: 20531471]
100. Behar DM, Metspalu M, Baran Y, Kopelman NM, Yunusbayev B, Gladstein A, Tzur S, Sahakyan H, Bahmanimehr A, Yepiskoposyan L, Tambets K, Khusnutdinova EK, Kushniarevich A, Balanovsky O, Balanovsky E, Kovacevic L, Marjanovic D, Mihailov E, Kouvatsi A, Triantaphyllidis C, King RJ, Semino O, Torroni A, Hammer MF, Metspalu E, Skorecki K, Rosset S, Halperin E, Vilems R, Rosenberg NA. No evidence from genome-wide data of a Khazar origin for the Ashkenazi Jews. *Hum. Biol.* 2013; 85:859–900.10.3378/027.085.0604 [PubMed: 25079123]
101. Fedorova SA, Reidla M, Metspalu E, Metspalu M, Rootsi S, Tambets K, Trofimova N, Zhadanov SI, Kashani B, Hooshiar, Olivieri A, Voevoda MI, Osipova LP, Platonov FA, Tomsy MI, Khusnutdinova EK, Torroni A, Vilems R. Autosomal and uniparental portraits of the native populations of Sakha (Yakutia): Implications for the peopling of Northeast Eurasia. *BMC Evol. Biol.* 2013; 13:127.10.1186/1471-2148-13-127 [PubMed: 23782551]
102. Kenny EE, Timpson NJ, Sikora M, Yee MC, Moreno-Estrada A, Eng C, Huntsman S, Burchard EG, Stoneking M, Bustamante CD, Myles S. Melanesian blond hair is caused by an amino acid change in TYRP1. *Science.* 2012; 336:554.10.1126/science.1217849 [PubMed: 22556244]
103. Migliano AB, Romero IG, Metspalu M, Leavesley M, Pagani L, Antao T, Huang DW, Sherman BT, Siddle K, Scholes C, Hudjashov G, Kaitokai E, Babalu A, Belatti M, Cagan A, Hopkinshaw B, Shaw C, Nelis M, Metspalu E, Mägi R, Lempicki RA, Vilems R, Lahr MM, Kivisild T. Evolution of the pygmy phenotype: Evidence of positive selection for genome-wide scans in African, Asian, and Melanesian pygmies. *Hum. Biol.* 2013; 85:251–284.10.3378/027.085.0313 [PubMed: 24297229]
104. Pierron D, Razafindrazaka H, Pagani L, Ricaut FX, Antao T, Capredon M, Sambo C, Radimilahy C, Rakotoarisoa JA, Blench RM, Letellier T, Kivisild T. Genome-wide evidence of Austronesian-Bantu admixture and cultural reversion in a hunter-gatherer group of Madagascar. *Proc. Natl. Acad. Sci. U.S.A.* 2014; 111:936–941.10.1073/pnas.1321860111 [PubMed: 24395773]
105. Rasmussen M, Guo X, Wang Y, Lohmueller KE, Rasmussen S, Albrechtsen A, Skotte L, Lindgreen S, Metspalu M, Jombart T, Kivisild T, Zhai W, Eriksson A, Manica A, Orlando L, De La Vega FM, Tridico S, Metspalu E, Nielsen K, Ávila-Arcos MC, Moreno-Mayar JV, Muller C, Dortch J, Gilbert MT, Lund O, Wesolowska A, Karmin M, Weinert LA, Wang B, Li J, Tai S, Xiao F, Hanihara T, van Driem G, Jha AR, Ricaut FX, de Knijff P, Migliano AB, Romero I, Gallego, Kristiansen K, Lambert DM, Brunak S, Forster P, Brinkmann B, Nehlich O, Bunce M, Richards M, Gupta R, Bustamante CD, Krogh A, Foley RA, Lahr MM, Balloux F, Sichert-Pontén T, Vilems R, Nielsen R, Wang J, Willerslev E. An Aboriginal Australian genome reveals

- separate human dispersals into Asia. *Science*. 2011; 334:94–98.10.1126/science.1211177 [PubMed: 21940856]
106. Reich D, Thangaraj K, Patterson N, Price AL, Singh L. Reconstructing Indian population history. *Nature*. 2009; 461:489–494.10.1038/nature08365 [PubMed: 19779445]
 107. Verdu P, Pemberton TJ, Laurent R, Kemp BM, Gonzalez-Oliver A, Gorodezky C, Hughes CE, Shattuck MR, Petzelt B, Mitchell J, Harry H, William T, Worl R, Cybulski JS, Rosenberg NA, Malhi RS. Patterns of admixture and population structure in native populations of Northwest North America. *PLOS Genet*. 2014; 10:e1004530. [PubMed: 25122539]
 108. Yunusbayev B, Metspalu M, Järve M, Kutuev I, Rootsi S, Metspalu E, Behar DM, Varendi K, Sahakyan H, Khusainova R, Yepiskoposyan L, Khusnutdinova EK, Underhill PA, Kivisild T, Villems R. The Caucasus as an asymmetric semipermeable barrier to ancient human migrations. *Mol. Biol. Evol*. 2012; 29:359–365.10.1093/molbev/msr221 [PubMed: 21917723]
 109. Altshuler DM, Gibbs RA, Peltonen L, Altshuler DM, Gibbs RA, Peltonen L, Dermitzakis E, Schaffner SF, Yu F, Peltonen L, Dermitzakis E, Bonnen PE, Altshuler DM, Gibbs RA, de Bakker PI, Deloukas P, Gabriel SB, Gwilliam R, Hunt S, Inouye M, Jia X, Palotie A, Parkin M, Whittaker P, Yu F, Chang K, Hawes A, Lewis LR, Ren Y, Wheeler D, Gibbs RA, Muzny DM, Barnes C, Darvishi K, Hurler M, Korn JM, Kristiansson K, Lee C, McCarroll SA, Nemesh J, Dermitzakis E, Keinan A, Montgomery SB, Pollack S, Price AL, Soranzo N, Bonnen PE, Gibbs RA, Gonzaga-Jauregui C, Keinan A, Price AL, Yu F, Anttila V, Brodeur W, Daly MJ, Leslie S, McVean G, Moutsianias L, Nguyen H, Schaffner SF, Zhang Q, Ghorji MJ, McGinnis R, McLaren W, Pollack S, Price AL, Schaffner SF, Takeuchi F, Grossman SR, Shlyakhter I, Hostetter EB, Sabeti PC, Adebamowo CA, Foster MW, Gordon DR, Licinio J, Manca MC, Marshall PA, Matsuda I, Ngare D, Wang VO, Reddy D, Rotimi CN, Royal CD, Sharp RR, Zeng C, Brooks LD, McEwen JE, International HapMap 3 Consortium. Integrating common and rare genetic variation in diverse human populations. *Nature*. 2010; 467:52–58. [PubMed: 20811451]
 110. Kent WJ, Sugnet CW, Furey TS, Roskin KM, Pringle TH, Zahler AM, Haussler D. The human genome browser at UCSC. *Genome Res*. 2002; 12:996–1006. Article published online before print in May 2002. 10.1101/gr.229102 [PubMed: 12045153]
 111. Johnson AD, Handsaker RE, Pulit SL, Nizzari MM, O'Donnell CJ, de Bakker PI. SNAP: A web-based tool for identification and annotation of proxy SNPs using HapMap. *Bioinformatics*. 2008; 24:2938–2939.10.1093/bioinformatics/btn564 [PubMed: 18974171]
 112. Manichaikul A, Mychaleckyj JC, Rich SS, Daly K, Sale M, Chen WM. Robust relationship inference in genome-wide association studies. *Bioinformatics*. 2010; 26:2867–2873.10.1093/bioinformatics/btq559 [PubMed: 20926424]
 113. Moorjani P, Thangaraj K, Patterson N, Lipson M, Loh PR, Govindaraj P, Berger B, Reich D, Singh L. Genetic evidence for recent population mixture in India. *Am. J. Hum. Genet*. 2013; 93:422–438.10.1016/j.ajhg.2013.07.006 [PubMed: 23932107]
 114. Thornton T, Tang H, Hoffmann TJ, Ochs-Balcom HM, Caan BJ, Risch N. Estimating kinship in admixed populations. *Am. J. Hum. Genet*. 2012; 91:122–138.10.1016/j.ajhg.2012.05.024 [PubMed: 22748210]
 115. Skoglund P, Malmström H, Raghavan M, Storå J, Hall P, Willerslev E, Gilbert MT, Götherström A, Jakobsson M. Origins and genetic legacy of Neolithic farmers and hunter-gatherers in Europe. *Science*. 2012; 336:466–469. [PubMed: 22539720]
 116. Li H, Handsaker B, Wysoker A, Fennell T, Ruan J, Homer N, Marth G, Abecasis G, Durbin R, 1000 Genome Project Data Processing Subgroup. The Sequence Alignment/Map format and SAMtools. *Bioinformatics*. 2009; 25:2078–2079.10.1093/bioinformatics/btp352 [PubMed: 19505943]
 117. Lindgreen S. AdapterRemoval: Easy cleaning of next-generation sequencing reads. *BMC Res. Notes*. 2012; 5:337.10.1186/1756-0500-5-337 [PubMed: 22748135]
 118. Quinlan AR, Hall IM. BEDTools: A flexible suite of utilities for comparing genomic features. *Bioinformatics*. 2010; 26:841–842.10.1093/bioinformatics/btq033 [PubMed: 20110278]
 119. DePristo MA, Banks E, Poplin R, Garimella KV, Maguire JR, Hartl C, Philippakis AA, del Angel G, Rivas MA, Hanna M, McKenna A, Fennell TJ, Kernysky AM, Sivachenko AY, Cibulskis K, Gabriel SB, Altshuler D, Daly MJ. A framework for variation discovery and genotyping using

- next-generation DNA sequencing data. *Nat. Genet.* 2011; 43:491–498.10.1038/ng.806 [PubMed: 21478889]
120. Delaneau O, Marchini J, Zagury J-F. A linear complexity phasing method for thousands of genomes. *Nat. Methods.* 2012; 9:179–181.10.1038/nmeth.1785 [PubMed: 22138821]
 121. Wigginton JE, Cutler DJ, Abecasis GR. A note on exact tests of Hardy-Weinberg equilibrium. *Am. J. Hum. Genet.* 2005; 76:887–893.10.1086/429864 [PubMed: 15789306]
 122. Gronau I, Hubisz MJ, Gulko B, Danko CG, Siepel A. Bayesian inference of ancient human demography from individual genome sequences. *Nat. Genet.* 2011; 43:1031–1034.10.1038/ng.937 [PubMed: 21926973]
 123. Andrews RM, Kubacka I, Chinnery PF, Lightowlers RN, Turnbull DM, Howell N. Reanalysis and revision of the Cambridge reference sequence for human mitochondrial DNA. *Nat. Genet.* 1999; 23:147.10.1038/13779 [PubMed: 10508508]
 124. Schubert M, Ginolhac A, Lindgreen S, Thompson JF, Al-Rasheid KA, Willerslev E, Krogh A, Orlando L. Improving ancient DNA read mapping against modern reference genomes. *BMC Genomics.* 2012; 13:178.10.1186/1471-2164-13-178 [PubMed: 22574660]
 125. Daley T, Smith AD. Predicting the molecular complexity of sequencing libraries. *Nat. Methods.* 2013; 10:325–327.10.1038/nmeth.2375 [PubMed: 23435259]
 126. Briggs AW, Stenzel U, Johnson PL, Green RE, Kelso J, Prüfer K, Meyer M, Krause J, Ronan MT, Lachmann M, Pääbo S. Patterns of damage in genomic DNA sequences from a Neandertal. *Proc. Natl. Acad. Sci. U.S.A.* 2007; 104:14616–14621.10.1073/pnas.0704665104 [PubMed: 17715061]
 127. Sawyer S, Krause J, Guschanski K, Savolainen V, Pääbo S. Temporal patterns of nucleotide misincorporations and DNA fragmentation in ancient DNA. *PLOS ONE.* 2012; 7:e34131.10.1371/journal.pone.0034131 [PubMed: 22479540]
 128. Allentoft ME, et al. The half-life of DNA in bone: measuring decay kinetics in 158 dated fossils. *Proc. R. Soc. B Biol. Sci.* 2012.10.1098/rspb.2012.1745
 129. Pedersen JS, Valen E, Velazquez AM, Parker BJ, Rasmussen M, Lindgreen S, Lilje B, Tobin DJ, Kelly TK, Vang S, Andersson R, Jones PA, Hoover CA, Tikhonov A, Prokhortchouk E, Rubin EM, Sandelin A, Gilbert MT, Krogh A, Willerslev E, Orlando L. Genome-wide nucleosome map and cytosine methylation levels of an ancient human genome. *Genome Res.* 2014; 24:454–466.10.1101/gr.163592.113 [PubMed: 24299735]
 130. Korneliusson TS, Albrechtsen A, Nielsen R. ANGSD: Analysis of Next Generation Sequencing Data. *BMC Bioinformatics.* 2014; 15:356.10.1186/s12859-014-0356-4 [PubMed: 25420514]
 131. Abecasis GR, Auton A, Brooks LD, DePristo MA, Durbin RM, Handsaker RE, Kang HM, Marth GT, McVean GA, 1000 Genomes Project Consortium. An integrated map of genetic variation from 1,092 human genomes. *Nature.* 2012; 491:56–65. [PubMed: 23128226]
 132. Fu Q, Mittnik A, Johnson PL, Bos K, Lari M, Bollongino R, Sun C, Giemsch L, Schmitz R, Burger J, Ronchitelli AM, Martini F, Cremonesi RG, Svoboda J, Bauer P, Caramelli D, Castellano S, Reich D, Pääbo S, Krause J. A revised timescale for human evolution based on ancient mitochondrial genomes. *Curr. Biol.* 2013; 23:553–559.10.1016/j.cub.2013.02.044 [PubMed: 23523248]
 133. Gelman A, Rubin DB. Inference from Iterative Simulation Using Multiple Sequences. *Stat. Sci.* 1992; 7:457–472.10.1214/ss/1177011136
 134. Plummer M, Best N, Cowles K, Vines K. CODA: Convergence diagnosis and output analysis for MCMC. *R. News.* 2006; 6:7–11.
 135. Skoglund P, Storå J, Götherström A, Jakobsson M. Accurate sex identification of ancient human remains using DNA shotgun sequencing. *J. Archaeol. Sci.* 2013; 40:4477–4482.10.1016/j.jas.2013.07.004
 136. Kloss-Brandstätter A, Pacher D, Schönherr S, Weissensteiner H, Binna R, Specht G, Kronenberg F. HaploGrep: A fast and reliable algorithm for automatic classification of mitochondrial DNA haplogroups. *Hum. Mutat.* 2011; 32:25–32.10.1002/humu.21382 [PubMed: 20960467]
 137. van Oven M, Kayser M. Updated comprehensive phylogenetic tree of global human mitochondrial DNA variation. *Hum. Mutat.* 2009; 30:E386–E394.10.1002/humu.20921 [PubMed: 18853457]

138. Behar DM, van Oven M, Rosset S, Metspalu M, Loogväli EL, Silva NM, Kivisild T, Torroni A, Villems R. A “Copernican” reassessment of the human mitochondrial DNA tree from its root. *Am. J. Hum. Genet.* 2012; 90:675–684.10.1016/j.ajhg.2012.03.002 [PubMed: 22482806]
139. Derenko MV, Malyarchuk BA, Dambueva IK, Shaikhaev GO, Dorzhu CM, Nimaev DD, Zakharov IA. Mitochondrial DNA variation in two South Siberian Aboriginal populations: Implications for the genetic history of North Asia. *Hum. Biol.* 2000; 72:945–973. [PubMed: 11236866]
140. Derenko M, Malyarchuk B, Grzybowski T, Denisova G, Dambueva I, Perkova M, Dorzhu C, Luzina F, Lee HK, Vanecek T, Villems R, Zakharov I. Phylogeographic analysis of mitochondrial DNA in northern Asian populations. *Am. J. Hum. Genet.* 2007; 81:1025–1041.10.1086/522933 [PubMed: 17924343]
141. Pimenoff VN, Comas D, Palo JU, Vershubsky G, Kozlov A, Sajantila A. Northwest Siberian Khanty and Mansi in the junction of West and East Eurasian gene pools as revealed by uniparental markers. *Eur. J. Hum. Genet.* 2008; 16:1254–1264.10.1038/ejhg.2008.101 [PubMed: 18506205]
142. Derbeneva OA, Starikovskaya EB, Wallace DC, Sukernik RI. Traces of early Eurasians in the Mansi of northwest Siberia revealed by mitochondrial DNA analysis. *Am. J. Hum. Genet.* 2002; 70:1009–1014.10.1086/339524 [PubMed: 11845409]
143. Derbeneva OA, Starikovskaia EB, Volod'ko NV, Wallace DC, Sukernik RI. [Mitochondrial DNA variation in Kets and Nganasans and the early peoples of Northern Eurasia]. *Genetika.* 2002; 38:1554–1560. [PubMed: 12500682]
144. Karmin M, Saag L, Vicente M, Sayres M. A. Wilson, Järve M, Talas UG, Rootsi S, Ilumäe AM, Mägi R, Mitt M, Pagani L, Puurand T, Faltyskova Z, Clemente F, Cardona A, Metspalu E, Sahakyan H, Yunusbayev B, Hudjashov G, DeGiorgio M, Loogväli EL, Eichstaedt C, Eelmeets M, Chaubey G, Tambets K, Litvinov S, Mormina M, Xue Y, Ayub Q, Zoraqi G, Korneliussen TS, Akhatova F, Lachance J, Tishkoff S, Momynaliev K, Ricaut FX, Kusuma P, Razafindrazaka H, Pierron D, Cox MP, Sultana GN, Willerslev R, Muller C, Westaway M, Lambert D, Skaro V, Kova evic L, Turdikulova S, Dalimova D, Khusainova R, Trofimova N, Akhmetova V, Khidiyatova I, Lichman DV, Isakova J, Pocheshkhova E, Sabitov Z, Barashkov NA, Nymadawa P, Mihailov E, Seng JW, Evseeva I, Migliano AB, Abdullah S, Andriadze G, Primorac D, Atramentova L, Utevska O, Yepiskoposyan L, Marjanovic D, Kushniarevich A, Behar DM, Gilissen C, Vissers L, Veltman JA, Balanovska E, Derenko M, Malyarchuk B, Metspalu A, Fedorova S, Eriksson A, Manica A, Mendez FL, Karafet TM, Veeramah KR, Bradman N, Hammer MF, Osipova LP, Balanovsky O, Khusnutdinova EK, Johnsen K, Remm M, Thomas MG, Tyler-Smith C, Underhill PA, Willerslev E, Nielsen R, Metspalu M, Villems R, Kivisild T. A recent bottleneck of Y chromosome diversity coincides with a global change in culture. *Genome Res.* 2015; 25:459–466.10.1101/gr.186684.114 [PubMed: 25770088]
145. van Oven M, Van Geystelen A, Kayser M, Decorte R, Larmuseau MH. Seeing the wood for the trees: A minimal reference phylogeny for the human Y chromosome. *Hum. Mutat.* 2014; 35:187–191.10.1002/humu.22468 [PubMed: 24166809]
146. ISOGG. <http://www.isogg.org>
147. Karafet TM, Mendez FL, Meilerman MB, Underhill PA, Zegura SL, Hammer MF. New binary polymorphisms reshape and increase resolution of the human Y chromosomal haplogroup tree. *Genome Res.* 2008; 18:830–838.10.1101/gr.7172008 [PubMed: 18385274]
148. Karafet TM, Osipova LP, Gubina MA, Posukh OL, Zegura SL, Hammer MF. High levels of Y-chromosome differentiation among native Siberian populations and the genetic signature of a boreal hunter-gatherer way of life. *Hum. Biol.* 2002; 74:761–789.10.1353/hub.2003.0006 [PubMed: 12617488]
149. Dulik MC, Zhadanov SI, Osipova LP, Askapuli A, Gau L, Gokcumen O, Rubinstein S, Schurr TG. Mitochondrial DNA and Y chromosome variation provides evidence for a recent common ancestry between Native Americans and Indigenous Altaians. *Am. J. Hum. Genet.* 2012; 90:229–246.10.1016/j.ajhg.2011.12.014 [PubMed: 22281367]
150. Rootsi S, Kivisild T, Benuzzi G, Help H, Bermisheva M, Kutuev I, Bara L, Per i M, Balanovsky O, Pshenichnov A, Dion D, Grobei M, Zhivotovsky LA, Battaglia V, Achilli A, Al-Zahery N, Parik J, King R, Cinnio lu C, Khusnutdinova E, Rudan P, Balanovska E, Scheffrahn

- W, Simonescu M, Brehm A, Goncalves R, Rosa A, Moisan J-P, Chaventre A, Ferak V, Füredi S, Oefner PJ, Shen P, Beckman L, Mikerezi I, Terzi R, Primorac D, Cambon-Thomsen A, Krumina A, Torroni A, Underhill PA, Santachiara-Benerecetti AS, Villems R, Magri C, Semino O. Phylogeography of Y-chromosome haplogroup I reveals distinct domains of prehistoric gene flow in Europe. *Am. J. Hum. Genet.* 2004; 75:128–137.10.1086/422196 [PubMed: 15162323]
151. Pritchard JK, Stephens M, Donnelly P. Inference of population structure using multilocus genotype data. *Genetics.* 2000; 155:945–959. [PubMed: 10835412]
152. Jakobsson M, Rosenberg NA. CLUMPP: A cluster matching and permutation program for dealing with label switching and multimodality in analysis of population structure. *Bioinformatics.* 2007; 23:1801–1806.10.1093/bioinformatics/btm233 [PubMed: 17485429]
153. Maples BK, Gravel S, Kenny EE, Bustamante CD. RFMix: A discriminative modeling approach for rapid and robust local-ancestry inference. *Am. J. Hum. Genet.* 2013; 93:278–288.10.1016/j.ajhg.2013.06.020 [PubMed: 23910464]
154. Frazer KA, Ballinger DG, Cox DR, Hinds DA, Stuve LL, Gibbs RA, Belmont JW, Boudreau A, Hardenbol P, Leal SM, Pasternak S, Wheeler DA, Willis TD, Yu F, Yang H, Zeng C, Gao Y, Hu H, Hu W, Li C, Lin W, Liu S, Pan H, Tang X, Wang J, Wang W, Yu J, Zhang B, Zhang Q, Zhao H, Zhao H, Zhou J, Gabriel SB, Barry R, Blumenstiel B, Camargo A, Defelice M, Faggart M, Goyette M, Gupta S, Moore J, Nguyen H, Onofrio RC, Parkin M, Roy J, Stahl E, Winchester E, Ziaugra L, Altshuler D, Shen Y, Yao Z, Huang W, Chu X, He Y, Jin L, Liu Y, Shen Y, Sun W, Wang H, Wang Y, Wang Y, Xiong X, Xu L, Wayne MM, Tsui SK, Xue H, Wong JT, Galver LM, Fan JB, Gunderson K, Murray SS, Oliphant AR, Chee MS, Montpetit A, Chagnon F, Ferretti V, Leboeuf M, Olivier JF, Phillips MS, Roumy S, Sallée C, Verner A, Hudson TJ, Kwok PY, Cai D, Koboldt DC, Miller RD, Pawlikowska L, Taillon-Miller P, Xiao M, Tsui LC, Mak W, Song YQ, Tam PK, Nakamura Y, Kawaguchi T, Kitamoto T, Morizono T, Nagashima A, Ohnishi Y, Sekine A, Tanaka T, Tsunoda T, Deloukas P, Bird CP, Delgado M, Dermitzakis ET, Gwilliam R, Hunt S, Morrison J, Powell D, Stranger BE, Whittaker P, Bentley DR, Daly MJ, de Bakker PI, Barrett J, Chretien YR, Maller J, McCarroll S, Patterson N, Pe'er I, Price A, Purcell S, Richter DJ, Sabeti P, Saxena R, Schaffner SF, Sham PC, Varilly P, Altshuler D, Stein LD, Krishnan L, Smith AV, Tello-Ruiz MK, Thorisson GA, Chakravarti A, Chen PE, Cutler DJ, Kashuk CS, Lin S, Abecasis GR, Guan W, Li Y, Munro HM, Qin ZS, Thomas DJ, McVean G, Auton A, Bottolo L, Cardin N, Eyheramendy S, Freeman C, Marchini J, Myers S, Spencer C, Stephens M, Donnelly P, Cardon LR, Clarke G, Evans DM, Morris AP, Weir BS, Tsunoda T, Mullikin JC, Sherry ST, Feolo M, Skol A, Zhang H, Zeng C, Zhao H, Matsuda I, Fukushima Y, Macer DR, Suda E, Rotimi CN, Adebamowo CA, Ajayi I, Aniagwu T, Marshall PA, Nkwodimmah C, Royal CD, Leppert MF, Dixon M, Peiffer A, Qiu R, Kent A, Kato K, Niikawa N, Adewole IF, Knoppers BM, Foster MW, Clayton EW, Watkin J, Gibbs RA, Belmont JW, Muzny D, Nazareth L, Sodergren E, Weinstock GM, Wheeler DA, Yakub I, Gabriel SB, Onofrio RC, Richter DJ, Ziaugra L, Birren BW, Daly MJ, Altshuler D, Wilson RK, Fulton LL, Rogers J, Burton J, Carter NP, Clee CM, Griffiths M, Jones MC, McLay K, Plumb RW, Ross MT, Sims SK, Willey DL, Chen Z, Han H, Kang L, Godbout M, Wallenburg JC, L'Archevêque P, Bellemare G, Saeki K, Wang H, An D, Fu H, Li Q, Wang Z, Wang R, Holden AL, Brooks LD, McEwen JE, Guyer MS, Wang VO, Peterson JL, Shi M, Spiegel J, Sung LM, Zacharia LF, Collins FS, Kennedy K, Jamieson R, Stewart J, International HapMap Consortium. A second generation human haplotype map of over 3.1 million SNPs. *Nature.* 2007; 449:851–861.10.1038/nature06258 [PubMed: 17943122]
155. Reich D, Green RE, Kircher M, Krause J, Patterson N, Durand EY, Viola B, Briggs AW, Stenzel U, Johnson PL, Maricic T, Good JM, Marques-Bonet T, Alkan C, Fu Q, Mallick S, Li H, Meyer M, Eichler EE, Stoneking M, Richards M, Talamo S, Shunkov MV, Derevianko AP, Hublin JJ, Kelso J, Slatkin M, Pääbo S. Genetic history of an archaic hominin group from Denisova Cave in Siberia. *Nature.* 2010; 468:1053–1060.10.1038/nature09710 [PubMed: 21179161]
156. Durand EY, Patterson N, Reich D, Slatkin M. Testing for ancient admixture between closely related populations. *Mol. Biol. Evol.* 2011; 28:2239–2252.10.1093/molbev/msr048 [PubMed: 21325092]
157. Busing FMTA, Meijer E, van der Leeden R. Delete-m Jackknife for Unequal m. *Stat. Comput.* 1999; 9:3–8.10.1023/A:1008800423698

158. Paul JS, Song YS. A principled approach to deriving approximate conditional sampling distributions in population genetics models with recombination. *Genetics*. 2010; 186:321–338.10.1534/genetics.110.117986 [PubMed: 20592264]
159. Paul JS, Steinrücken M, Song YS. An accurate sequentially Markov conditional sampling distribution for the coalescent with recombination. *Genetics*. 2011; 187:1115–1128.10.1534/genetics.110.125534 [PubMed: 21270390]
160. Wiuf C, Hein J. Recombination as a point process along sequences. *Theor. Popul. Biol.* 1999; 55:248–259.10.1006/tpbi.1998.1403 [PubMed: 10366550]
161. McVean GA, Cardin NJ. Approximating the coalescent with recombination. *Philos. Trans. R. Soc. Lond. B Biol. Sci.* 2005; 360:1387–1393.10.1098/rstb.2005.1673 [PubMed: 16048782]
162. Marjoram P, Wall JD. Fast “coalescent” simulation. *BMC Genet.* 2006; 7:16.10.1186/1471-2156-7-16 [PubMed: 16539698]
163. Liu S, Lorenzen ED, Fumagalli M, Li B, Harris K, Xiong Z, Zhou L, Korneliusson TS, Somel M, Babbitt C, Wray G, Li J, He W, Wang Z, Fu W, Xiang X, Morgan CC, Doherty A, O’Connell MJ, McInerney JO, Born EW, Dalén L, Dietz R, Orlando L, Sonne C, Zhang G, Nielsen R, Willerslev E, Wang J. Population genomics reveal recent speciation and rapid evolutionary adaptation in polar bears. *Cell*. 2014; 157:785–794.10.1016/j.cell.2014.03.054 [PubMed: 24813606]
164. Harris K, Nielsen R. Error-prone polymerase activity causes multinucleotide mutations in humans. *Genome Res.* 2014; 24:1445–1454.10.1101/gr.170696.113 [PubMed: 25079859]
165. Staab PR, Zhu S, Metzler D, Lunter G. scrm: Efficiently simulating long sequences using the approximated coalescent with recombination. *Bioinformatics*. 2015; 31:1680–1682.10.1093/bioinformatics/btu861.10.1093/bioinformatics/btu861 [PubMed: 25596205]
166. Harritt RK. Paleo-Eskimo beginnings in North America: A new discovery at Kuzitrin Lake, Alaska. *Etud. Inuit.* 1998; 22:61–81.
167. Kong A, Thorleifsson G, Gudbjartsson DF, Masson G, Sigurdsson A, Jonasdottir A, Walters GB, Jonasdottir A, Gylfason A, Kristinsson KT, Gudjonsson SA, Frigge ML, Helgason A, Thorsteinsdottir U, Stefansson K. Fine-scale recombination rate differences between sexes, populations and individuals. *Nature*. 2010; 467:1099–1103.10.1038/nature09525 [PubMed: 20981099]
168. Dyke AS, Moore A, Robertson L. Deglaciation of North America. Geological Survey of Canada Open File. 2003:1574.
169. Wegmann D, Leuenberger C, Neuenschwander S, Excoffier L. ABCtoolbox: A versatile toolkit for approximate Bayesian computations. *BMC Bioinformatics*. 2010; 11:116.10.1186/1471-2105-11-116 [PubMed: 20202215]
170. Liu H, Prugnolle F, Manica A, Balloux F. A geographically explicit genetic model of worldwide human-settlement history. *Am. J. Hum. Genet.* 2006; 79:230–237.10.1086/505436 [PubMed: 16826514]
171. Rosenberg NA, Mahajan S, Ramachandran S, Zhao C, Pritchard JK, Feldman MW. Clines, clusters, and the effect of study design on the inference of human population structure. *PLOS Genet.* 2005; 1:e70.10.1371/journal.pgen.0010070 [PubMed: 16355252]
172. Price AL, Patterson NJ, Plenge RM, Weinblatt ME, Shadick NA, Reich D. Principal components analysis corrects for stratification in genome-wide association studies. *Nat. Genet.* 2006; 38:904–909.10.1038/ng1847 [PubMed: 16862161]
173. Patterson N, Price AL, Reich D. Population structure and eigenanalysis. *PLOS Genet.* 2006; 2:e190. [PubMed: 17194218]
174. Oksanen, J., et al. vegan: Community Ecology Package. 2013. <http://cran.r-project.org/web/packages/vegan/index.html>
175. Home. RStudio. available at <http://www.rstudio.com/>
176. Sikora M, Carpenter ML, Moreno-Estrada A, Henn BM, Underhill PA, Sánchez-Quinto F, Zara I, Pitzalis M, Sidore C, Busonero F, Maschio A, Angius A, Jones C, Mendoza-Revilla J, Nekhrizov G, Dimitrova D, Theodossiev N, Harkins TT, Keller A, Maixner F, Zink A, Abecasis G, Sanna S, Cucca F, Bustamante CD. Population genomic analysis of ancient and modern genomes yields

- new insights into the genetic ancestry of the Tyrolean Iceman and the genetic structure of Europe. *PLOS Genet.* 2014; 10:e1004353.10.1371/journal.pgen.1004353 [PubMed: 24809476]
177. Neves W. The origin of the first Americans: An analysis based on the cranial morphology of early South American human remains. *Am. J. Phys. Anthropol.* 1990; 81:274.
 178. Neves W, Blum M. “Luzia” is not alone: Further evidence of a non-mongoloid settlement of the new world. *Curr. Res. Pleistocene.* 2001; 18:73–77.
 179. González-José R, Neves W, Lahr MM, González S, Pucciarelli H, Martínez M, Hernández, Correal G. Late Pleistocene/Holocene craniofacial morphology in Mesoamerican Paleoindians: Implications for the peopling of the New World. *Am. J. Phys. Anthropol.* 2005; 128:772–780.10.1002/ajpa.20165 [PubMed: 16028226]
 180. Neves WA, Hubbe M, Correal G. Human skeletal remains from Sabana de Bogotá, Colombia: A case of Paleoamerican morphology late survival in South America? *Am. J. Phys. Anthropol.* 2007; 133:1080–1098.10.1002/ajpa.20637 [PubMed: 17554759]
 181. Perez SI, Bernal V, Gonzalez PN, Sardi M, Politis GG. Discrepancy between cranial and DNA data of early Americans: Implications for American peopling. *PLOS ONE.* 2009; 4:e5746.10.1371/journal.pone.0005746 [PubMed: 19478947]
 182. Pucciarelli HM, Perez SI, Politis GG. Early Holocene human remains from the Argentinean Pampas: Additional evidence for distinctive cranial morphology of early South Americans. *Am. J. Phys. Anthropol.* 2010; 143:298–305.10.1002/ajpa.21347 [PubMed: 20623674]
 183. Neves W, Pucciarelli H. The Zhoukoudian Upper Cave skull 101 as seen from the Americans. *J. Hum. Evol.* 1998; 34:219–222.10.1006/jhev.1997.0183 [PubMed: 9503095]
 184. Powell JF, Neves WA. Craniofacial morphology of the first Americans: Pattern and process in the peopling of the New World. *Am. J. Phys. Anthropol.* 1999; 110(Suppl 29):153–188. doi:10.1002/(SICI)1096-8644(1999)110:29+<153::AID-AJPA6>3.0.CO;2-L. [PubMed: 10601986]
 185. Steele DG, Powell JF. Paleobiology of the first Americans. *Evol. Anthropol. Issues News Rev.* 1993; 2:138–146.10.1002/evan.1360020409
 186. Powell, JF. *The first Americans: race, evolution and the origin of native Americans.* Cambridge University Press; Cambridge: 2005.
 187. Gonçalves VF, Stenderup J, Rodrigues-Carvalho C, Silva HP, Gonçalves-Dornelas H, Líryo A, Kivisild T, Malaspina AS, Campos PF, Rasmussen M, Willerslev E, Pena SD. Identification of Polynesian mtDNA haplogroups in remains of Botocudo Amerindians from Brazil. *Proc. Natl. Acad. Sci. U.S.A.* 2013; 110:6465–6469.10.1073/pnas.1217905110 [PubMed: 23576724]
 188. Neves W, Pucciarelli H. Morphological affinities of the first Americans: An exploratory analysis based on early South American human remains. *J. Hum. Evol.* 1991; 21:261–273.10.1016/0047-2484(91)90107-7
 189. Dillehay TD. Probing deeper into first American studies. *Proc. Natl. Acad. Sci. U.S.A.* 2009; 106:971–978.10.1073/pnas.0808424106 [PubMed: 19164556]
 190. van Vark GN, Kuizenga D, Williams FL. Kennewick and Luzia: Lessons from the European Upper Paleolithic. *Am. J. Phys. Anthropol.* 2003; 121:181–184. discussion 185–188. 10.1002/ajpa.10176 [PubMed: 12740961]
 191. Jantz RL, Owsley DW. Reply to Van Vark et al.: Is European Upper Paleolithic cranial morphology a useful analogy for early Americans? *Am. J. Phys. Anthropol.* 2003; 121:185–188.10.1002/ajpa.10188
 192. Bookstein, FL. *Morphometric Tools for Landmark Data.* Cambridge University Press; Cambridge: 1991.
 193. Roseman CC, Weaver TD. Multivariate apportionment of global human craniometric diversity. *Am. J. Phys. Anthropol.* 2004; 125:257–263.10.1002/ajpa.10424 [PubMed: 15386236]
 194. Betti L, Balloux F, Amos W, Hanihara T, Manica A. Distance from Africa, not climate, explains within-population phenotypic diversity in humans. *Proc. R. Soc. B-Biol. Sci.* 2009; 276:809–814.
 195. Hubbe M, Hanihara T, Harvati K. Climate signatures in the morphological differentiation of worldwide modern human populations. *Anat. Rec.* 2009; 292:1720–1733.10.1002/ar.20976 [PubMed: 19718714]
 196. Betti L, Balloux F, Hanihara T, Manica A. The relative role of drift and selection in shaping the human skull. *Am. J. Phys. Anthropol.* 2010; 141:76–82. [PubMed: 19582777]

197. Howells, WW. *Skull Shapes and the Map: Craniometric Analyses in the Dispersion of Modern Homo*. Harvard University Press; Cambridge: 1989. Peabody Museum of Archaeology and Ethnology
198. Howells, WW. *Cranial Variation in Man: A Study by Multivariate Analysis of Patterns of Difference Among Recent Human Populations*. Harvard University Press; 1973.
199. Morimoto N, de León M. S. Ponce, Zollikofer CP. Phenotypic variation in infants, not adults, reflects genotypic variation among chimpanzees and bonobos. *PLOS ONE*. 2014; 9:e102074.10.1371/journal.pone.0102074 [PubMed: 25013970]
200. Howells WW. Howells' craniometric data on the Internet. *Am. J. Phys. Anthropol.* 1996; 101:441–442.10.1002/ajpa.1331010302 [PubMed: 8922187]
201. Neves WA, Hubbe M, Okumura MM, González-José R, Figuti L, Eggers S, De Blasis PA. A new early Holocene human skeleton from Brazil: Implications for the settlement of the New World. *J. Hum. Evol.* 2005; 48:403–414.10.1016/j.jhevol.2004.12.001 [PubMed: 15788186]
202. Neves WA, Hubbe M, Piló LB. Early Holocene human skeletal remains from Sumidouro Cave, Lagoa Santa, Brazil: History of discoveries, geological and chronological context, and comparative cranial morphology. *J. Hum. Evol.* 2007; 52:16–30.10.1016/j.jhevol.2006.07.012 [PubMed: 16996575]
203. Roseman CC. Detecting interregionally diversifying natural selection on modern human cranial form by using matched molecular and morphometric data. *Proc. Natl. Acad. Sci. U.S.A.* 2004; 101:12824–12829.10.1073/pnas.0402637101 [PubMed: 15326305]
204. Prüfer K, Racimo F, Patterson N, Jay F, Sankararaman S, Sawyer S, Heinze A, Renaud G, Sudmant PH, de Filippo C, Li H, Mallick S, Dannemann M, Fu Q, Kircher M, Kuhlwilm M, Lachmann M, Meyer M, Ongyerth M, Siebauer M, Theunert C, Tandon A, Moorjani P, Pickrell J, Mullikin JC, Vohr SH, Green RE, Hellmann I, Johnson PL, Blanche H, Cann H, Kitzman JO, Shendure J, Eichler EE, Lein ES, Bakken TE, Golovanova LV, Doronichev VB, Shunkov MV, Derevianko AP, Viola B, Slatkin M, Reich D, Kelso J, Pääbo S. The complete genome sequence of a Neanderthal from the Altai Mountains. *Nature*. 2014; 505:43–49.10.1038/nature12886 [PubMed: 24352235]
205. Greenberg JH, Turner CG, Zegura SL. The settlement of the Americas: A comparison of the linguistic, dental, and genetic evidence. *Curr. Anthropol.* 1986; 27:477–497.10.1086/203472

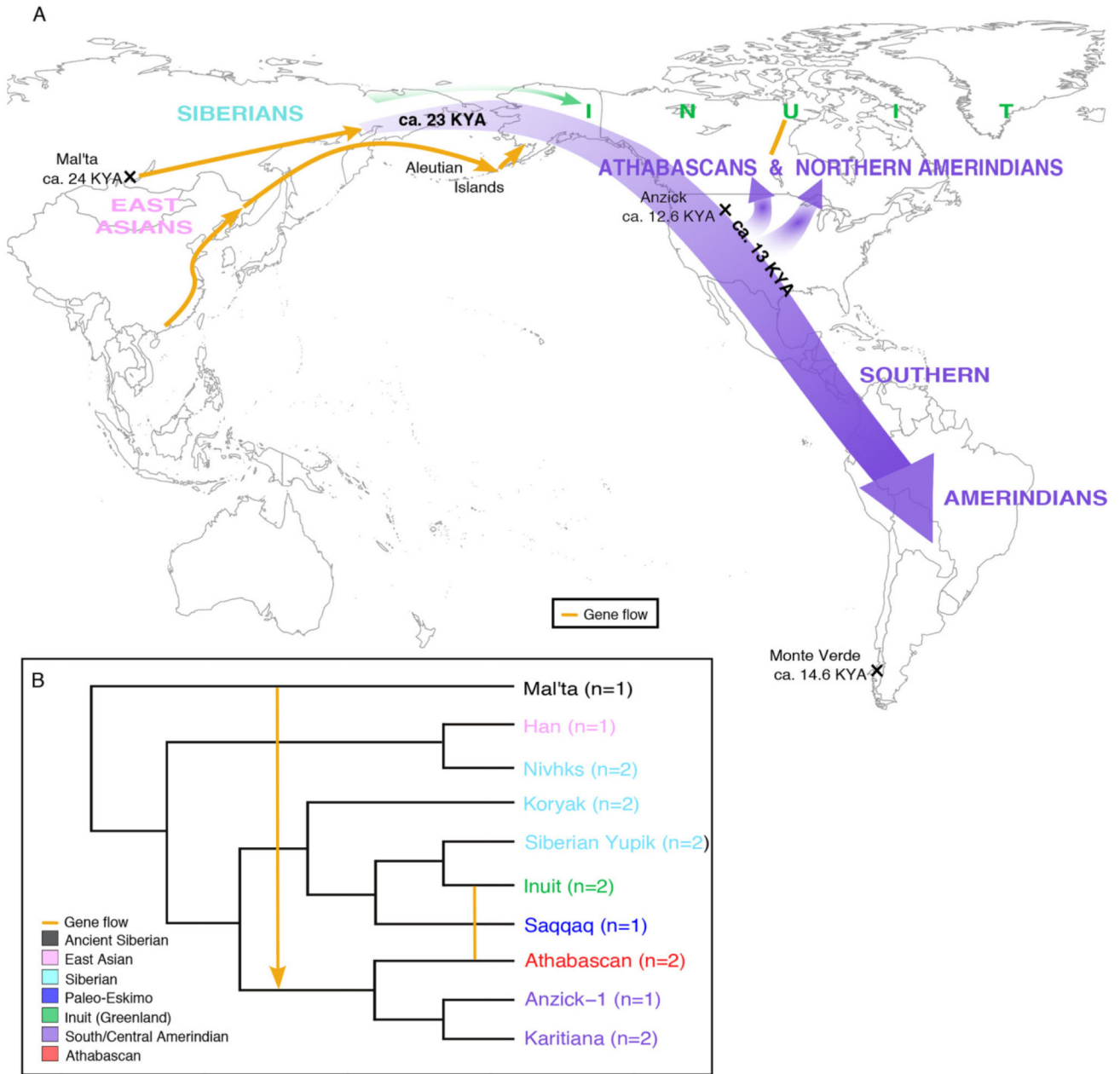


Fig. 1. Origins and population history of Native Americans

(A) Our results show that the ancestors of all present-day Native Americans, including Amerindians and Athabascans, derived from a single migration wave into the Americas (purple), separate from the Inuit (green). This migration from East Asia occurred no later than 23 KYA and is in agreement with archaeological evidence from sites such as Monte Verde (50). A split between the northern and southern branches of Native Americans occurred ca. 13 KYA, with the former comprising Athabascans and northern Amerindians and the latter consisting of Amerindians in northern North America and Central and South America including the Anzick-1 individual (5). There is an admixture signal between Inuit and Athabascans and some northern Amerindians (yellow line); however, the gene flow

direction is unresolved due to the complexity of the admixture events (28). Additionally, we see a weak signal related to Australo-Melanesians in some Native Americans, which may have been mediated through East Asians and Aleutian Islanders (yellow arrows). Also shown is the Mal'ta gene flow into Native American ancestors some 23 KYA (yellow arrow) (4). It is currently not possible for us to ascertain the exact geographical locations of the depicted events; hence, the positioning of the arrows should not be considered a reflection of these. B. Admixture plot created on the basis of *TreeMix* results (fig. S5) shows that all Native Americans form a clade, separate from the Inuit, with gene flow between some Native Americans and the North American Arctic. The number of genome-sequenced individuals included in the analysis is shown in brackets.

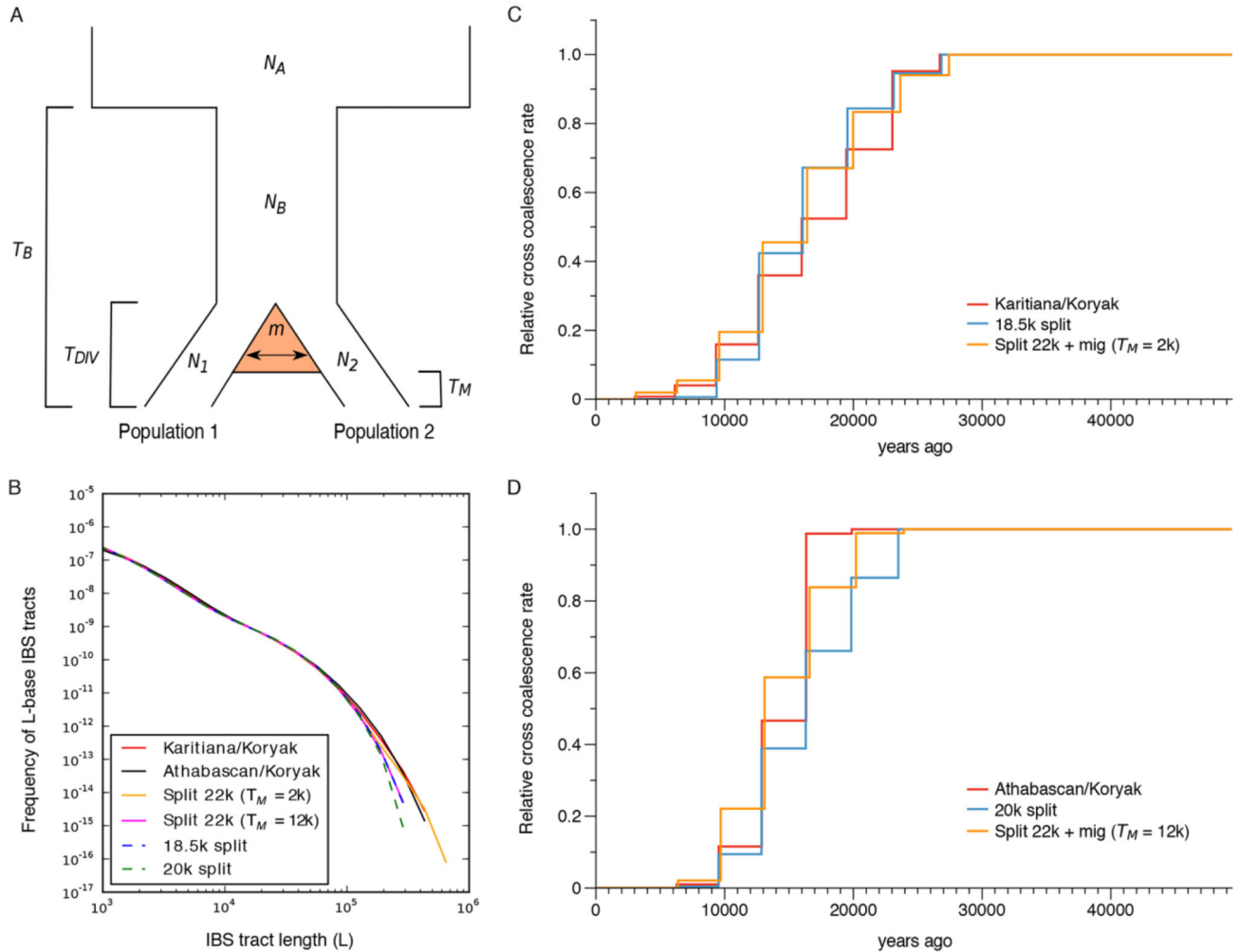


Fig. 2. Divergence estimates between Native Americans and Siberian Koryak

(A) The demographic model used allows for continuous gene flow between populations 1 and 2, starting from the time T_{DIV} of divergence and ending at T_M . The backward probability of migration per individual per generation is denoted by m . The bottleneck at T_B captures the out-of-Africa event. (B) The red and black solid curves depict empirical distributions of IBS tracts shared between Karitiana-Koryak and Athabascan-Koryak, respectively. The orange, pink, dashed blue and dashed green curves depict IBS tracts shared between the two population pairs, simulated under two demographic models based on results from *diCal2.0*. Overall, for Karitiana-Koryak and Athabascan-Koryak, the migration scenarios (orange and pink, respectively) match the empirical curves (red and black, respectively) better than the clean split scenarios (dashed blue and dashed green, respectively), with more long IBS tracts showing evidence of recent common ancestry between Koryaks and Native Americans. (C and D) Relative cross-coalescence rates (CCR) for the Karitiana-Koryak and Athabascan-Koryak divergence (red), respectively, including data simulated under the two demographic models in panel B. In both cases, the model with gene flow (orange) fits the data (red) better than the clean split model (blue). The migration model explains a broader CCR tail in the

case of Karitiana-Koryak and the relatively late onset of the CCR decay for Athabascan-Koryak.

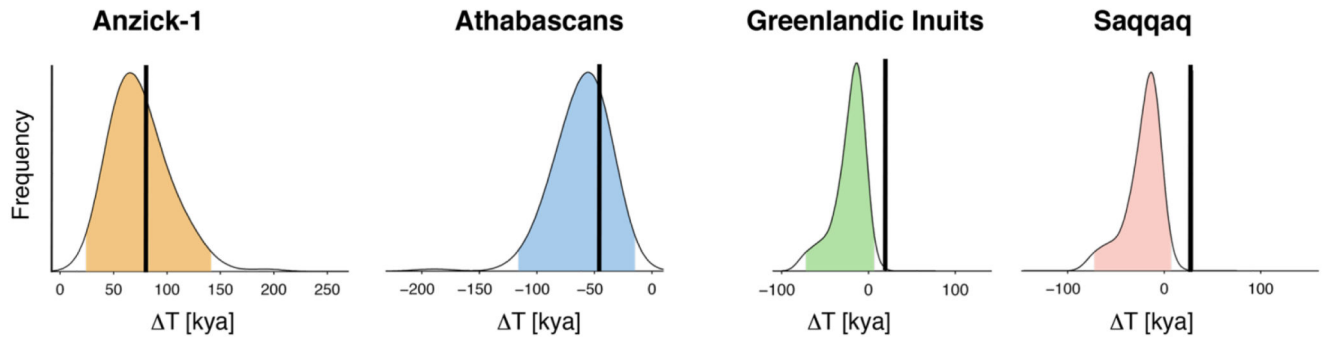


Fig. 3. Testing migrations into the Americas using a climate-informed model

Estimates of difference in genetic divergence between Amerindians (from southern North America and Central and South America) or Koryak versus Athabascan and Greenlandic Inuit and the ancient Saqqaq and Anzick-1 genomes (black vertical lines), compared to posterior probability distribution predicted from a climate-informed spatial genetic model reconstructing a single wave into the Americas (curves, the colored part represents the 95% credibility interval). T for population X is defined as $T(X, \text{Koryak}) - T(X, \text{Central and South Amerindians})$ (28). Both Anzick-1 and the Athabascans were part of the same wave into the Americas to which other Amerindian populations from southern North America and Central and South America belonged, while the Inuit and Saqqaq are the descendants of different waves (observed values outside the 95% credibility interval).

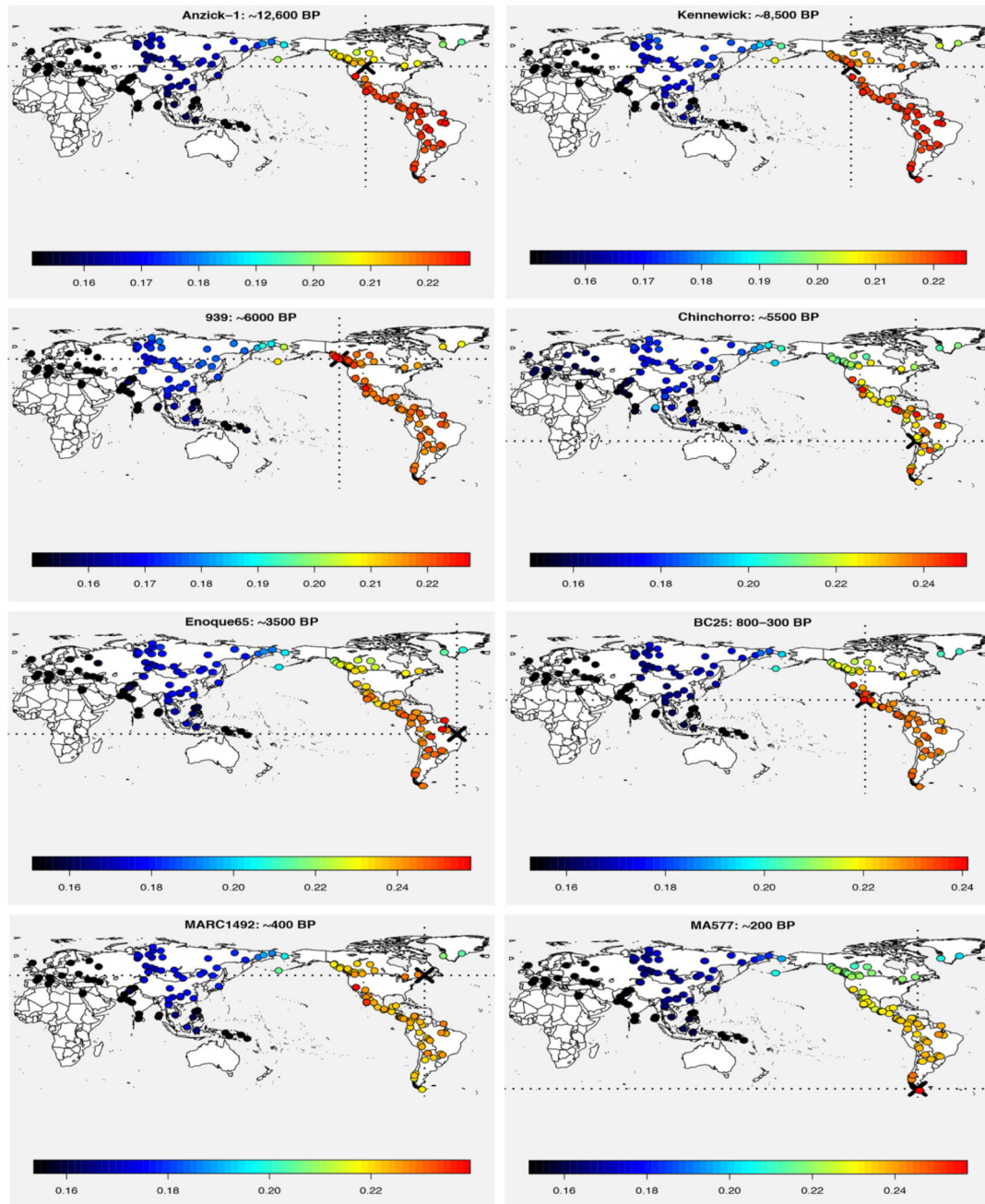


Fig. 4. Diversification within the Americas

SNP chip genotype data-based outgroup f_3 statistics (47) of the form $f_3(X, \text{Ancient}; \text{Yoruba})$ were used to estimate the shared ancestry between ancient samples from the Americas and a large panel of worldwide present-day populations (X), including Athabascan and Amerindian groups from North America (table S3), some of which were masked for non-Native ancestry prior to the analysis (28). The outgroup f_3 statistics are depicted as heat maps with the sampling location of the ancient sample marked by the dotted lines, and corresponding ranked plots with error bars are shown in fig. S14. BP refers to time before

present. We find the Anzick-1 sample to share most ancestry with the ‘southern’ branch of Native Americans when using multiple northern Native Americans sequenced in this study, consistent with (5). The seven Holocene aged samples share most ancestry with Native Americans, with a general tendency to be genetically closer to present-day Native American populations from the same geographical region.

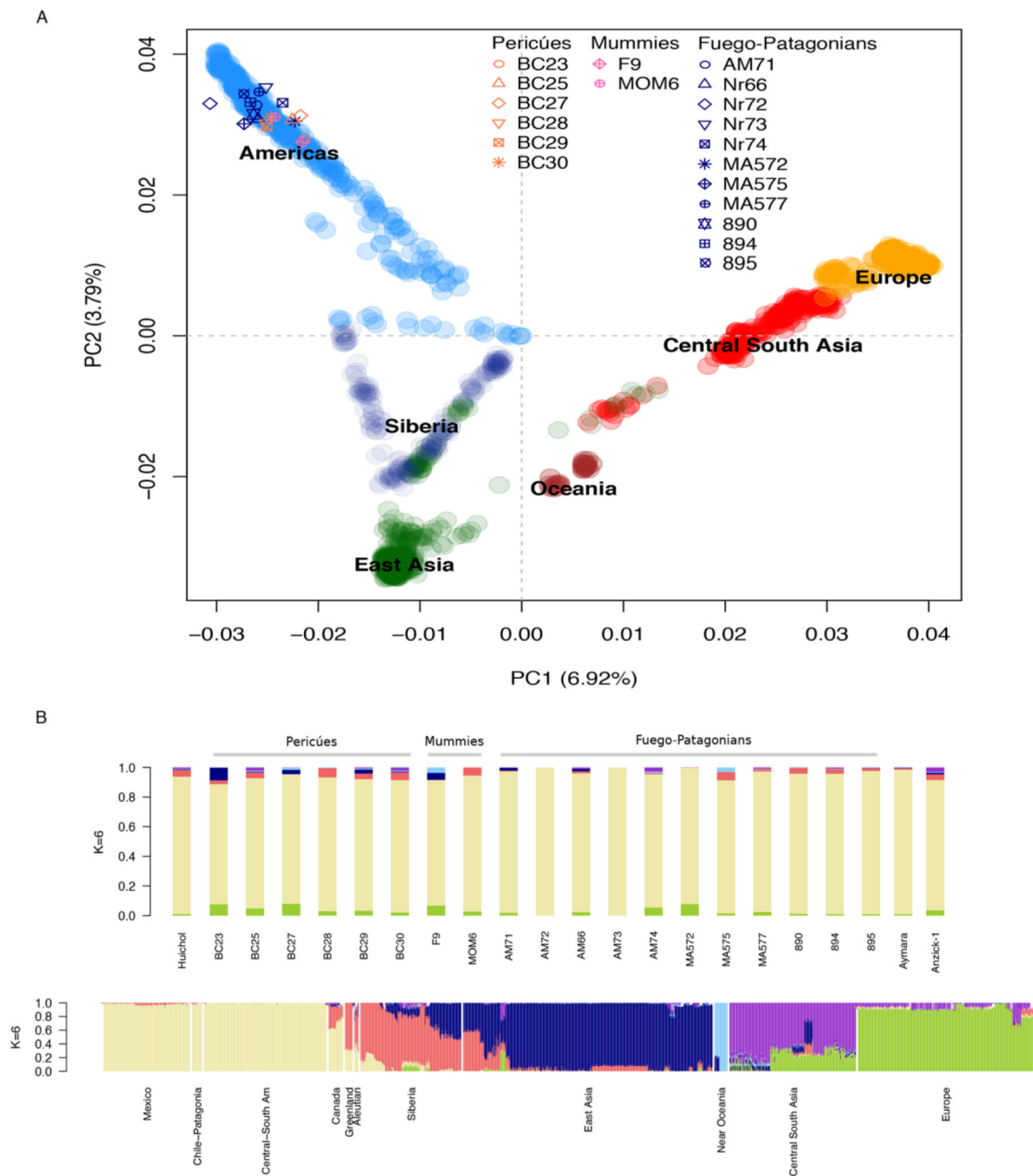


Fig. 5. The Paleoamerican model

(A) Principal Component Analysis plot of 19 ancient samples combined with a worldwide reference panel, including 1,823 individuals from (6). Our samples plot exclusively with American samples. For plots with other reference panels consisting of Native American populations, see fig. S32. (B) Population structure in the ancient Pericú, Mexican mummy and Fuego-Patagonian individuals from this study. Ancestry proportions are shown when assuming six ancestral populations ($K = 6$). The top bar shows the ancestry proportions of the 19 ancient individuals, Anzick-1 (5), and two present-day Native American genomes

from this study (Huichol and Aymara). The plot at the bottom illustrates the ancestry proportions for 1,823 individuals from (6). Our samples show primarily Native American (ivory, >92%) and Siberian (red, ca. 5%) ancestry. For the plot with $K=13$, see fig. S33.