

The ice sheets were at that time still a substantial barrier to movement that would have helped to maintain separation from the Ancient Beringian population. Although members of the SNA branch have not been documented in regions that were once north of the Pleistocene glaciers^{1,18}, NNA groups (including Athabascan speakers) are present in Alaska today. Therefore, NNA are likely to be descendants of a population that moved north sometime after 11.5 ka²⁵.

The USR1 results provide direct genomic evidence that all Native Americans can be traced back to the same source population from a single Late Pleistocene founding event. Descendants of that population were present in eastern Beringia until at least 11.5 ka. By that time, however, a separate branch of Native Americans had already established itself in unglaciated North America, and diverged into the two basal groups that ultimately became the ancestors of most of the indigenous populations of the Americas.

Online Content Methods, along with any additional Extended Data display items and Source Data, are available in the online version of the paper; references unique to these sections appear only in the online paper.

Received 29 March; accepted 26 November 2017. Published online 3 January 2018.

- Reich, D. et al. Reconstructing Native American population history. Nature 488, 370–374 (2012).
- 2. Raghavan, M. et al. Genomic evidence for the Pleistocene and recent population history of Native Americans. Science **349**, aab3884 (2015).
- Skoglund, P. et al. Genetic evidence for two founding populations of the Americas. Nature 525, 104–108 (2015).
- von Cramon-Taubadel, N., Strauss, A. & Hubbe, M. Evolutionary population history of early Paleoamerican cranial morphology. Sci. Adv. 3, e1602289 (2017).
- Hoffecker, J. F., Elias, S. A., O'Rourke, D. H., Scott, G. R. & Bigelow, N. H. Beringia and the global dispersal of modern humans. Evol. Anthropol. 25, 64–78 (2016).
- Potter, B. A., Irish, J. D., Reuther, J. D. & McKinney, H. J. New insights into Eastern Beringian mortuary behavior: a terminal Pleistocene double infant burial at Upward Sun River. *Proc. Natl Acad. Sci. USA* 111, 17060–17065 (2014).
- Rasmussen, M. et al. The genome of a Late Pleistocene human from a Clovis burial site in western Montana. Nature 506, 225–229 (2014).
- Raghavan, M. et al. Upper Palaeolithic Siberian genome reveals dual ancestry of Native Americans. Nature 505, 87–91 (2014).
- Tamm, E. et al. Beringian standstill and spread of Native American founders. PLoS ONE 2, e829 (2007).
- Flegontov, P. et al. Na-Dene populations descend from the Paleo-Eskimo migration into America. Preprint at https://doi.org/10.1101/074476 (2016).
- Dillehay, T. D. et al. Monte Verde: seaweed, food, medicine, and the peopling of South America. Science 320, 784–786 (2008).
- 12. Goebel, T. & Potter, B. A. in *The Oxford Handbook of the Prehistoric Arctic* (eds Friesen, T. M. & Mason, O. K.) 223–252 (Oxford Univ. Press, 2016).
- 13. Llamas, B. et al. Ancient mitochondrial DNA provides high-resolution time scale of the peopling of the Americas. Sci. Adv. 2, e1501385 (2016).
- Rasmussen, M. et al. The ancestry and affiliations of Kennewick Man. Nature 523, 455–458 (2015).
- 15. Raghavan, M. et al. The genetic prehistory of the New World Arctic. Science 345, 1255832 (2014).
- Rasmussen, M. et al. Ancient human genome sequence of an extinct Palaeo-Eskimo. Nature 463, 757–762 (2010).
- Tackney, J. C. et al. Two contemporaneous mitogenomes from terminal Pleistocene burials in eastern Beringia. Proc. Natl Acad. Sci. USA 112, 13833–13838 (2015).
- Verdu, P. et al. Patterns of admixture and population structure in native populations of northwest North America. PLoS Genet. 10, e1004530 (2014).

- Patterson, N. et al. Ancient admixture in human history. Genetics 192, 1065–1093 (2012).
- Alexander, D. H., Novembre, J. & Lange, K. Fast model-based estimation of ancestry in unrelated individuals. *Genome Res.* 19, 1655–1664 (2009).
- Skotte, L., Korneliussen, T. S. & Albrechtsen, A. Estimating individual admixture proportions from next generation sequencing data. *Genetics* 195, 693–702 (2013).
- Malaspinas, A.-S. et al. bammds: a tool for assessing the ancestry of low-depth whole-genome data using multidimensional scaling (MDS). Bioinformatics 30, 2962–2964 (2014).
- Pickrell, J. K. & Pritchard, J. K. Inference of population splits and mixtures from genome-wide allele frequency data. *PLoS Genet.* 8, e1002967 (2012).
- Dyke, A. S., Moore, A. & Robertson, L. Deglaciation of North America. (Natural Resources Canada, 2003).
- Pedersen, M. W. et al. Postglacial viability and colonization in North America's ice-free corridor. Nature 537, 45–49 (2016).
- 26. Kari, J. M. & Potter, B. A. (eds) *The Dene–Yeniseian Connection* (Univ. Alaska, 2011)
- Steinrücken, M., Kamm, J. A. & Song, Y. S. Inference of complex population histories using whole-genome sequences from multiple populations. Preprint at https://doi.org/10.1101/026591 (2015).
- Kamm, J. A., Terhorst, J. & Song, Y. S. Efficient computation of the joint sample frequency spectra for multiple populations. J. Comput. Graph. Stat. 26, 182–194 (2017).
- Terhorst, J., Kamm, J. A. & Song, Y. S. Robust and scalable inference of population history from hundreds of unphased whole genomes. *Nat. Genet.* 49, 303–309 (2017).
- Goebel, T. The 'microblade adaptation' and recolonization of Siberia during the late Upper Pleistocene. Archaeol. Pap. Am. Anthropol. Assoc. 12, 117–131 (2002).

Supplementary Information is available in the online version of the paper.

Acknowledgements The Upward Sun River excavations and analysis were conducted under a Memorandum of Agreement (MOA) signed by the State of Alaska, the National Science Foundation, the Healy Lake Tribal Council and the Tanana Chiefs Conference. We appreciate the cooperation of all parties. We thank M. Allentoft, S. Gopalakrishnan, T. Korneliussen, P. Librado, J. Ramos-Madrigal, G. Renaud and F. Vieira for discussions, and the Danish National High-throughput Sequencing Centre for assistance with data generation. GeoGenetics members were supported by the Lundbeck Foundation and the Danish National Research Foundation (DNRF94) and KU2016. J.V.M.-M. was supported by Conacyt (Mexico). Samples were recovered during excavations by B.A.P. supported by NSF Grants 1138811 and 1223119. Research was supported in part by NIH grant R01-GM094402 (M.St., J.T., J.A.K. and Y.S.S.) and a Packard Fellowship for Science and Engineering (Y.S.S.). Y.S.S. is a Chan Zuckerberg Biohub investigator. D.J.M. is supported by the Quest Archaeological Research Fund. A.-S.M. is supported by the Swiss National Science Foundation and the ERC.

Author Contributions The project was conceived by E.W. and B.A.P. and headed by E.W. L.V. processed ancient DNA. J.V.M.-M. and S.R. assembled datasets. J.V.M.-M., M.St., J.T., J.A.K. and A.A. analysed genetic data. B.A.P. led the USR field investigation and B.A.P. and D.J.M. provided anthropological contextualization. B.A.P., J.D.R. and J.D.I. conducted archaeological and bioanthropological work. R.N., Y.S.S., M.Si., A.-S.M., and L.O. supervised bioinformatic and statistical analyses. B.A.P. engaged with indigenous communities. J.V.M.-M., B.A.P., D.J.M. and E.W. wrote the manuscript with input from L.V., A.-S.M., M.Si., R.S.M., L.O., Y.S.S. R.N. and the other authors.

Author Information Reprints and permissions information is available at www.nature.com/reprints. The authors declare no competing financial interests. Readers are welcome to comment on the online version of the paper. Publisher's note: Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations. Correspondence and requests for materials should be addressed to E.W. (ewillerslev@snm.ku.dk).