

Supplementary Data

Table S1. Lists of specimens for morphological study, references for gene sequences, institutional abbreviations and description of landmarks

Specimens for morphological study

Taxon	Family	Age	Collection ID number	Institution
<i>Maiacetus inuus</i>	Protocetidae	Eocene (Lutetian)	UMMP VP 118197 (cast of GSP-UM 3551)	University of Michigan Museum of Paleontology
<i>Aegicetus gehennae</i>	Protocetidae	Eocene (Priabonian)	UMMP 118210 (cast of CGM 60584)	University of Michigan Museum of Paleontology
<i>Dorudon atrox</i>	Basilosauridae	Eocene (Priabonian)	UMMP VP 101222	University of Michigan Museum of Paleontology
Mysticeti indet.	Mysticeti	Oligocene (Chattian)	UABCS MNH sjMT	Autonomous University of Baja California Sur
<i>Balaena mysticetus</i>	Mysticeti	Extant	ZMUC 2x	Zoological Museum of Copenhagen University
<i>Cetotherium riabinini</i>	Mysticeti	Miocene	NMNHU-P 668/1	National Museum of Natural History of the National Academy of Sciences of Ukraine, Department of Paleontology
<i>Otradnocetus virodovi</i>	Mysticeti	Miocene	GNM CO 1-90	Georgian National Museum
<i>Balaenoptera acutorostrata</i>	Mysticeti	Extant	KhNU 6547	Karazin Kharkiv National University
<i>Eschrichtius robustus</i>	Mysticeti	Extant	n/a (specimen on the display)	Museo de la Ballena
<i>Balaenoptera edeni</i>	Mysticeti	Extant	n/a (specimen on the display)	Museo de la Ballena
<i>Balaenoptera musculus</i>	Mysticeti	Extant	n/a (specimen on the display)	Zoological Museum of Odessa I.I.Mechnikov National University
<i>Microzeuglodon caucasicum</i>	Odontoceti	Oligocene (Rupelian)	GNM 48	Georgian National Museum

<i>Sulacocetus dagestanicus</i>	Odontoceti	Oligocene (Rupelian)	GNM 118	Georgian National Museum
<i>Kelloggia barbarus</i>	Odontoceti	Oligocene (Chattian)	GNM 2/26	Georgian National Museum
<i>Oligodelphis azerbaijanicus</i>	Odontoceti	Oligocene (Chattian)	GNM 2/27	Georgian National Museum
<i>Ferecetotherium kelloggi</i>	Odontoceti	Oligocene (Rupelian)	GNM 2/29	Georgian National Museum
<i>Kogia sima</i>	Odontoceti	Extant	UABCS MNH 00/034	Autonomous University of Baja California Sur
<i>Physeter macrocephalus</i>	Odontoceti	Extant	KhNU 7353	Karazin Kharkiv National University
<i>Pachyacanthus suessii</i>	Odontoceti	Miocene	n/a	Georgian National Museum
<i>Hyperoodon planifrons</i>	Odontoceti	Extant	ONU 26	Mechnikov Odesa National University
<i>Ziphius cavirostris</i>	Odontoceti	Extant	ZMUC 1x	Zoological Museum of Copenhagen University
<i>Kentriodon fuchsii</i>	Odontoceti	Miocene	NMNERM 182	National Museum of Nature and Ethnography, Republic of Moldova
<i>Kentiodontidae indet</i>	Odontoceti	Miocene	P-135	Zaporizhzhia Regional Museum of Local Lore
<i>Phocoena phocoena</i>	Odontoceti	Extant	ZMUC CN 96	Zoological Museum of Copenhagen University
<i>Phocoena sinus</i>	Odontoceti	Extant	0139	Museo de la Ballena
<i>Monodon monoceros</i>	Odontoceti	Extant	ZMUC MCE 1358	Zoological Museum of Copenhagen University
<i>Delphinapterus leucas</i>	Odontoceti	Extant	ZMUC CN 4*	Zoological Museum of Copenhagen University
<i>Orcinus orca</i>	Odontoceti	Extant	ONU n/a	Mechnikov Odesa National University
<i>Leucopleurus acutus</i>	Odontoceti	Extant	ZMUC CN 4*	Zoological Museum of Copenhagen University
<i>Lagenorhynchus albirostris</i>	Odontoceti	Extant	ZMUC CN 898	Zoological Museum of

				Copenhagen University
<i>Globicephala melas</i>	Odontoceti	Extant	ZMUC CN 2*	Zoological Museum of Copenhagen University
<i>Orcaella brevirostris</i>	Odontoceti	Extant	ZMUC 310	Zoological Museum of Copenhagen University

References for gene sequences

Species	Reference
<i>Eubalaena glacialis</i>	Rhie A et al., "Towards complete and error-free genome assemblies of all vertebrate species.", Nature, 2021 Apr;592(7856):737-746 Dudchenko, O., Batra, S.S., Omer, A.D., Nyquist, S.K., Hoeger, M., Durand, N.C., Shamim, M.S., Machol, I., Lander, E.S., Aiden, A.P., Aiden, E.L., 2017. De novo assembly of the Aedes aegypti genome using Hi-C yields chromosome-length scaffolds. Science 356, 92–95. https://doi.org/10.1126/science.aal3327 . Dudchenko, O., Shamim, M.S., Batra, S., Durand, N.C., Musial, N.T., Mostofa, R., Pham, M., Hilaire, B.G.S., Yao, W., Stamenova, E., Hoeger, M., Nyquist, S.K., Korchina, V., Pletch, K., Flanagan, J.P., Tomaszewicz, A., McAloose, D., Estrada, C.P., Novak, B.J., Omer, A.D., Aiden, E.L., 2018. The Juicebox Assembly Tools module facilitates de novo assembly of mammalian genomes with chromosome-length scaffolds for under \$1000. bioRxiv 254797. https://doi.org/10.1101/254797 .
<i>Grampus griseus</i>	Senevirathna JDM et al., "Draft genome sequencing and assembly of Risso's dolphin, <i>Grampus griseus</i> .", J Genomics, 2023;11:9-13
<i>Platanista minor</i>	Johnson, J., Muren, E., Swofford, R., Turner-Maier, J., Marinescu, V., Genereux, D., Birren, B., Karlsson, E.K. and Lindblad-Toh, K. The 200 mammals project: sequencing genomes by a novel cost-effective method, yielding a high resolution annotation of the human genome. Unpublished. Submitted (07-SEP-2018) Vertebrate Genome Biology, Broad Institute, 75 Ames Street, Cambridge, MA 02142, USA
<i>Platanista gangetica</i>	Siddiki, A.Z., Kabir, A., Bhuiyan, M.A.B., Rahman, S.S. and Kibria, M.M. Whole genome sequencing of Ganges river dolphin (<i>Platanista gangetica</i>) and genome annotation to unveil genetic variations to explore the evolution and adaptation at genome level. Submitted (02-JAN-2021) Genomic Research Group, Chittagong Veterinary and Animal Sciences University; University of Chittagong (HRRL), Zakir Hossain Road, Chittagong 4225, Bangladesh
<i>Mesoplodon bidens</i>	Johnson, J., Muren, E., Swofford, R., Turner-Maier, J., Marinescu, V., Genereux, D., Birren, B., Karlsson, E.K. and Lindblad-Toh, K. The 200 mammals project: sequencing genomes by a novel cost-effective method, yielding a high resolution annotation of the human genome. Unpublished. Submitted (07-SEP-2018) Vertebrate Genome Biology, Broad Institute, 75 Ames Street, Cambridge, MA 02142, USA

Mesoplodon densirostris	Dudchenko, O., Batra, S.S., Omer, A.D., Nyquist, S.K., Hoeger, M., Durand, N.C., Shamim, M.S., Machol, I., Lander, E.S., Aiden, A.P., Aiden, E.L., 2017. De novo assembly of the Aedes aegypti genome using Hi-C yields chromosome-length scaffolds. Science 356, 92–95. https://doi.org/10.1126/science.aal3327 . Dudchenko, O., Shamim, M.S., Batra, S., Durand, N.C., Musial, N.T., Mostofa, R., Pham, M., Hilaire, B.G.S., Yao, W., Stamenova, E., Hoeger, M., Nyquist, S.K., Korchina, V., Pletch, K., Flanagan, J.P., Tomaszewicz, A., McAloose, D., Estrada, C.P., Novak, B.J., Omer, A.D., Aiden, E.L., 2018. The Juicebox Assembly Tools module facilitates de novo assembly of mammalian genomes with chromosome-length scaffolds for under \$1000. bioRxiv 254797. https://doi.org/10.1101/254797 .
Ziphius cavirostris	Johnson, J., Muren, E., Swofford, R., Turner-Maier, J., Marinescu, V., Genereux, D., Birren, B., Karlsson, E.K. and Lindblad-Toh, K. The 200 mammals project: sequencing genomes by a novel cost-effective method, yielding a high resolution annotation of the human genome. Unpublished. Submitted (07-SEP-2018) Vertebrate Genome Biology, Broad Institute, 75 Ames Street, Cambridge, MA 02142, USA
Lipotes vexillifer	Zhou X et al., "Baiji genomes reveal low genetic variability and new insights into secondary aquatic adaptations.", Nat Commun, 2013;4:2708 Yan J et al., "Molecular phylogenetics of 'river dolphins' and the baiji mitochondrial genome.", Mol Phylogenet Evol, 2005 Dec;37(3):743-50
Pontoporia blainvillei	Pedro, S.L.S., Freitas, R.C., Barreto, A.S. and Lima, A.O.S. Submitted (22-MAY-2018) Centro de Ciencias Tecnológicas da Terra e do Mar (CTTMar), Universidade do Vale do Itajaí (UNIVALI), R. Uruguai, 458, Laboratório de Genética Molecular, Setor D7/Sala 212, Itajaí, Santa Catarina 88302-202, Brazil
Inia geoffrensis	Johnson, J., Muren, E., Swofford, R., Turner-Maier, J., Marinescu, V., Genereux, D., Birren, B., Karlsson, E.K. and Lindblad-Toh, K. The 200 mammals project: sequencing genomes by a novel cost-effective method, yielding a high resolution annotation of the human genome. Unpublished. Submitted (07-SEP-2018) Vertebrate Genome Biology, Broad Institute, 75 Ames Street, Cambridge, MA 02142, USA
Monodon monoceros	Damas J et al., "Evolution of the ancestral mammalian karyotype and syntenic regions.", Proc Natl Acad Sci U S A, 2022 Oct 4;119(40):e2209139119
Delphinapterus leucas	Jones SJM et al., "The Genome of the Beluga Whale (Delphinapterus leucas).", Genes (Basel), 2017 Dec 11;8(12)
Phocoena phocoena	Autenrieth M et al., "High-quality whole-genome sequence of an abundant Holarctic odontocete, the harbour porpoise (Phocoena phocoena).", Mol Ecol Resour, 2018 Nov;18(6):1469-1481
Phocoena sinus	Morin PA, Archer FI, Avila CD, et al. Reference genome and demographic history of the most endangered marine mammal, the vaquita. Mol Ecol Resour. 2021;21(4):1008-1020. doi:10.1111/1755-0998.13284
Sousa chinensis	Chao, B. Submitted (07-DEC-2018) BGI, BGI-SZ, Beishan, Shenzhen, Guangdong 518083, China
Hyperoodon ampullatus	Wellcome Sanger Tree of Life Programme. Submitted (24-MAR-2023) WELLCOME SANGER INSTITUTE, Tree of Life, Wellcome Genome Campus, Hinxton CB10 1SA, United Kingdom
Neophocaena asiaeorientalis	Yin, D., Chen, C., Lin, D., Zhang, J., Ying, C., Liu, Y., Liu, W., Cao, Z., Xu, R., Wang, C., Liang, L., Xu, P., Jian, J. and Liu, K. Gapless genome assembly of East Asian finless porpoise, Neophocaena asiaeorientalis sunameri. Submitted (03-AUG-

	2022) Key Laboratory of Freshwater Fisheries and Germplasm Resources Utilization, Freshwater Fisheries Research Center, Chinese Academy of Fishery Sciences, Binhu, Wuxi 214081, China
Globicephala melas	Wellcome Sanger Tree of Life Programme. Submitted (13-SEP-2023) WELLCOME SANGER INSTITUTE, Tree of Life, Wellcome Genome Campus, Hinxton CB10 1SA, United Kingdom
Orcinus orca	Wellcome Sanger Tree of Life Programme. Submitted (05-APR-2022) WELLCOME SANGER INSTITUTE, Tree of Life, Wellcome Genome Campus, Hinxton CB10 1SA, United Kingdom
Lagenorhynchus obliquidens	Culibrk,L., Leelakumari,S., Taylor,G.A., Tan,R., Tse,K., Cheng,D., Chuah,E., Kirk,H., Macleod,T., Pandoh,P., Troussard,A., Zhao,Y., Mungall,A.J., Moore,R., Marra,M.A., Haulena,M. and Jones,S.J.M. The genome of the whitesided dolphin. Submitted (15-OCT-2018) Genome Sciences Centre, BC Cancer Agency, Canada's Michael Smith Genome Sciences Centre, #100 - 570 West 7th Ave, Vancouver, BC V5Z-4S6, Canada
Tursiops truncatus	Karine A Martinez-Viaud, Cindy Taylor Lawley, Milmer Martinez Vergara, Gil Ben-Zvi, Tammy Biniashvili, Kobi Baruch, Judy St. Leger, Jennie Le, Aparna Natarajan, Marlem Rivera, Marbie Guillergan, Erich Jaeger, Brian Steffy, Aleksey Zimin, New de novo assembly of the Atlantic bottlenose dolphin (Tursiops truncatus) improves genome completeness and provides haplotype phasing, GigaScience, Volume 8, Issue 3, March 2019, giy168, https://doi.org/10.1093/gigascience/giy168
Tursiops aduncus	Moura AE et al., "Phylogenomics of the genus Tursiops and closely related Delphininae reveals extensive reticulation among lineages and provides inference about eco-evolutionary drivers.", Mol Phylogenet Evol, 2020 May;146:106756
Balaenoptera musculus	Arnason U et al., "Cetacean mitochondrial DNA control region: sequences of all extant baleen whales and two sperm whale species.", Mol Biol Evol, 1993 Sep;10(5):960-70 Arnason U et al., "Comparison between the complete mtDNA sequences of the blue and the fin whale, two species that can hybridize in nature.", J Mol Evol, 1993 Oct;37(4):312-22
Eubalaena japonica	Johnson,J., Muren,E., Swofford,R., Turner-Maier,J., Marinescu,V., Genereux,D., Birren,B., Karlsson,E.K. and Lindblad-Toh,K. The 200 mammals project: sequencing genomes by a novel cost-effective method, yielding a high resolution annotation of the human genome. Unpublished. Submitted (07-SEP-2018) Vertebrate Genome Biology, Broad Institute, 75 Ames Street, Cambridge, MA 02142, USA
Balaena mysticetus	Keane M, Semeiks J, Webb AE, Li YI, Quesada V, Craig T, Madsen LB, van Dam S, Brawand D, Marques PI, Michalak P, Kang L, Bhak J, Yim HS, Grishin NV, Nielsen NH, Heide-Jorgensen MP, Oziolor EM, Matson CW, Church GM, Stuart GW, Patton JC, George JC, Suydam R, Larsen K, Lopez-Otin C, O'Connell MJ, Bickham JW, Thomsen B, de Magalhaes JP (2015) Insights into the evolution of longevity from the bowhead whale genome. Cell Reports. 10, 112-120.
Balaenoptera physalus	Wolf M et al., "Genomic Impact of Whaling in North Atlantic Fin Whales.", Mol Biol Evol, 2022 May 3;39(5) Published online: Wolf M et al., "Genomic impact of whaling in North Atlantic fin whales.", Molecular Biology and Evolution, 2022;

<i>Balaenoptera ricei</i>	Dudchenko, O., Batra, S.S., Omer, A.D., Nyquist, S.K., Hoeger, M., Durand, N.C., Shamim, M.S., Machol, I., Lander, E.S., Aiden, A.P., Aiden, E.L., 2017. De novo assembly of the <i>Aedes aegypti</i> genome using Hi-C yields chromosome-length scaffolds. <i>Science</i> 356, 92–95. https://doi.org/10.1126/science.aal3327 . Dudchenko, O., Shamim, M.S., Batra, S., Durand, N.C., Musial, N.T., Mostofa, R., Pham, M., Hilaire, B.G.S., Yao, W., Stamenova, E., Hoeger, M., Nyquist, S.K., Korchina, V., Pletch, K., Flanagan, J.P., Tomaszewicz, A., McAloose, D., Estrada, C.P., Novak, B.J., Omer, A.D., Aiden, E.L., 2018. The Juicebox Assembly Tools module facilitates de novo assembly of mammalian genomes with chromosome-length scaffolds for under \$1000. <i>bioRxiv</i> 254797. https://doi.org/10.1101/254797 .
<i>Balaenoptera bonaerensis</i>	Published online: Kishida T et al., "Aquatic adaptation and the evolution of smell and taste in whales", <i>Zoological Letters</i> , 2015;1(1)
<i>Balaenoptera acutorostrata</i>	Wellcome Sanger Tree of Life Programme. Submitted (22-APR-2023) WELLCOME SANGER INSTITUTE, Tree of Life, Wellcome Genome Campus, Hinxton CB10 1SA, United Kingdom
<i>Megaptera novaeangliae</i>	Tollis M, Robbins J, Webb AE, et al. Return to the Sea, Get Huge, Beat Cancer: An Analysis of Cetacean Genomes Including an Assembly for the Humpback Whale (<i>Megaptera novaeangliae</i>). <i>Mol Biol Evol.</i> 2019;36(8):1746-1763. doi:10.1093/molbev/msz099
<i>Kogia breviceps</i>	Johnson,J., Muren,E., Swofford,R., Turner-Maier,J., Marinescu,V., Genereux,D., Birren,B., Karlsson,E.K. and Lindblad-Toh,K. The 200 mammals project: sequencing genomes by a novel cost-effective method, yielding a high resolution annotation of the human genome. Unpublished. Submitted (07-SEP-2018) Vertebrate Genome Biology, Broad Institute, 75 Ames Street, Cambridge, MA 02142, USA
<i>Physeter catodon</i>	Fan,G., Sun,Z., Sun,S., Wang,J., Zhang,H., Chen,J., Liu,X., Xu,X. and Liu,X. A high-quality reference genome of sperm whale reveals the chromosome-scale evolution of aquatic mammals. Submitted (09-NOV-2017) BGI-Qingdao, BGI, Tuanjie Road, Qingdao 266000, China
<i>Hippopotamus amphibius</i>	Li,Z., Zhou,B. Chen,L. Progressive evolution of secondary aquatic adaptation in hippos and cetaceans. Submitted (01-MAR-2022) College of Ecology and Environment, Northwestern Polytechnology University, Xian, Shan'xi Province 710129, China
<i>Delphinus delphis</i>	Wellcome Sanger Tree of Life Programme. Submitted (22-APR-2023) WELLCOME SANGER INSTITUTE, Tree of Life, Wellcome Genome Campus, Hinxton CB10 1SA, United Kingdom
<i>Eschrichtius robustus</i>	Johnson,J., Muren,E., Swofford,R., Turner-Maier,J., Marinescu,V., Genereux,D., Birren,B., Karlsson,E.K. and Lindblad-Toh,K. The 200 mammals project: sequencing genomes by a novel cost-effective method, yielding a high resolution annotation of the human genome. Unpublished. Submitted (10-SEP-2018) Vertebrate Genome Biology, Broad Institute, 75 Ames Street, Cambridge, MA 02142, USA
<i>Steno bredanensis</i>	
<i>Stenella coeruleoalba</i>	Wellcome Sanger Tree of Life Programme. Submitted (12-MAY-2023) WELLCOME SANGER INSTITUTE, Tree of Life, Wellcome Genome Campus, Hinxton CB10 1SA, United Kingdom
<i>Choeropsis liberiensis</i>	Li,Z., Zhou,B. Chen,L. Progressive evolution of secondary aquatic adaptation in hippos and cetaceans. Submitted (01-MAR-2022) College of Ecology and Environment, Northwestern Polytechnology University, Xian, Shan'xi Province 710129, China

Cephalorhynchus commersonii	Dudchenko, O., Batra, S.S., Omer, A.D., Nyquist, S.K., Hoeger, M., Durand, N.C., Shamim, M.S., Machol, I., Lander, E.S., Aiden, A.P., Aiden, E.L., 2017. De novo assembly of the Aedes aegypti genome using Hi-C yields chromosome-length scaffolds. Science 356, 92–95. https://doi.org/10.1126/science.aal3327. Dudchenko, O., Shamim, M.S., Batra, S., Durand, N.C., Musial, N.T., Mostofa, R., Pham, M., Hilaire, B.G.S., Yao, W., Stamenova, E., Hoeger, M., Nyquist, S.K., Korchina, V., Pletch, K., Flanagan, J.P., Tomaszewicz, A., McAloose, D., Estrada, C.P., Novak, B.J., Omer, A.D., Aiden, E.L., 2018. The Juicebox Assembly Tools module facilitates de novo assembly of mammalian genomes with chromosome-length scaffolds for under \$1000. bioRxiv 254797. https://doi.org/10.1101/254797.
Balaenoptera borealis	Dudchenko, O., Batra, S.S., Omer, A.D., Nyquist, S.K., Hoeger, M., Durand, N.C., Shamim, M.S., Machol, I., Lander, E.S., Aiden, A.P., Aiden, E.L., 2017. De novo assembly of the Aedes aegypti genome using Hi-C yields chromosome-length scaffolds. Science 356, 92–95. https://doi.org/10.1126/science.aal3327. Dudchenko, O., Shamim, M.S., Batra, S., Durand, N.C., Musial, N.T., Mostofa, R., Pham, M., Hilaire, B.G.S., Yao, W., Stamenova, E., Hoeger, M., Nyquist, S.K., Korchina, V., Pletch, K., Flanagan, J.P., Tomaszewicz, A., McAloose, D., Estrada, C.P., Novak, B.J., Omer, A.D., Aiden, E.L., 2018. The Juicebox Assembly Tools module facilitates de novo assembly of mammalian genomes with chromosome-length scaffolds for under \$1000. bioRxiv 254797. https://doi.org/10.1101/254797.
Lagenorhynchus acutus	Dudchenko, O., Batra, S.S., Omer, A.D., Nyquist, S.K., Hoeger, M., Durand, N.C., Shamim, M.S., Machol, I., Lander, E.S., Aiden, A.P., Aiden, E.L., 2017. De novo assembly of the Aedes aegypti genome using Hi-C yields chromosome-length scaffolds. Science 356, 92–95. https://doi.org/10.1126/science.aal3327. Dudchenko, O., Shamim, M.S., Batra, S., Durand, N.C., Musial, N.T., Mostofa, R., Pham, M., Hilaire, B.G.S., Yao, W., Stamenova, E., Hoeger, M., Nyquist, S.K., Korchina, V., Pletch, K., Flanagan, J.P., Tomaszewicz, A., McAloose, D., Estrada, C.P., Novak, B.J., Omer, A.D., Aiden, E.L., 2018. The Juicebox Assembly Tools module facilitates de novo assembly of mammalian genomes with chromosome-length scaffolds for under \$1000. bioRxiv 254797. https://doi.org/10.1101/254797.
Lagenorhynchus albirostris	Wellcome Sanger Tree of Life Programme. Submitted (29-MAR-2023) WELLCOME SANGER INSTITUTE, Tree of Life, Wellcome Genome Campus, Hinxton CB10 1SA, United Kingdom

Mesoplodon europaeus	Dudchenko, O., Batra, S.S., Omer, A.D., Nyquist, S.K., Hoeger, M., Durand, N.C., Shamim, M.S., Machol, I., Lander, E.S., Aiden, A.P., Aiden, E.L., 2017. De novo assembly of the Aedes aegypti genome using Hi-C yields chromosome-length scaffolds. Science 356, 92–95. https://doi.org/10.1126/science.aal3327. Dudchenko, O., Shamim, M.S., Batra, S., Durand, N.C., Musial, N.T., Mostofa, R., Pham, M., Hilaire, B.G.S., Yao, W., Stamenova, E., Hoeger, M., Nyquist, S.K., Korchina, V., Pletch, K., Flanagan, J.P., Tomaszewicz, A., McAloose, D., Estrada, C.P., Novak, B.J., Omer, A.D., Aiden, E.L., 2018. The Juicebox Assembly Tools module facilitates de novo assembly of mammalian genomes with chromosome-length scaffolds for under \$1000. bioRxiv 254797. https://doi.org/10.1101/254797.
Mesoplodon sejnegeri	Dudchenko, O., Batra, S.S., Omer, A.D., Nyquist, S.K., Hoeger, M., Durand, N.C., Shamim, M.S., Machol, I., Lander, E.S., Aiden, A.P., Aiden, E.L., 2017. De novo assembly of the Aedes aegypti genome using Hi-C yields chromosome-length scaffolds. Science 356, 92–95. https://doi.org/10.1126/science.aal3327. Dudchenko, O., Shamim, M.S., Batra, S., Durand, N.C., Musial, N.T., Mostofa, R., Pham, M., Hilaire, B.G.S., Yao, W., Stamenova, E., Hoeger, M., Nyquist, S.K., Korchina, V., Pletch, K., Flanagan, J.P., Tomaszewicz, A., McAloose, D., Estrada, C.P., Novak, B.J., Omer, A.D., Aiden, E.L., 2018. The Juicebox Assembly Tools module facilitates de novo assembly of mammalian genomes with chromosome-length scaffolds for under \$1000. bioRxiv 254797. https://doi.org/10.1101/254797.
Peponocephala electra	Dudchenko, O., Batra, S.S., Omer, A.D., Nyquist, S.K., Hoeger, M., Durand, N.C., Shamim, M.S., Machol, I., Lander, E.S., Aiden, A.P., Aiden, E.L., 2017. De novo assembly of the Aedes aegypti genome using Hi-C yields chromosome-length scaffolds. Science 356, 92–95. https://doi.org/10.1126/science.aal3327. Dudchenko, O., Shamim, M.S., Batra, S., Durand, N.C., Musial, N.T., Mostofa, R., Pham, M., Hilaire, B.G.S., Yao, W., Stamenova, E., Hoeger, M., Nyquist, S.K., Korchina, V., Pletch, K., Flanagan, J.P., Tomaszewicz, A., McAloose, D., Estrada, C.P., Novak, B.J., Omer, A.D., Aiden, E.L., 2018. The Juicebox Assembly Tools module facilitates de novo assembly of mammalian genomes with chromosome-length scaffolds for under \$1000. bioRxiv 254797. https://doi.org/10.1101/254797.

<i>Stenella attenuata</i>	Dudchenko, O., Batra, S.S., Omer, A.D., Nyquist, S.K., Hoeger, M., Durand, N.C., Shamim, M.S., Machol, I., Lander, E.S., Aiden, A.P., Aiden, E.L., 2017. De novo assembly of the <i>Aedes aegypti</i> genome using Hi-C yields chromosome-length scaffolds. <i>Science</i> 356, 92–95. https://doi.org/10.1126/science.aal3327. Dudchenko, O., Shamim, M.S., Batra, S., Durand, N.C., Musial, N.T., Mostofa, R., Pham, M., Hilaire, B.G.S., Yao, W., Stamenova, E., Hoeger, M., Nyquist, S.K., Korchina, V., Pletch, K., Flanagan, J.P., Tomaszewicz, A., McAloose, D., Estrada, C.P., Novak, B.J., Omer, A.D., Aiden, E.L., 2018. The Juicebox Assembly Tools module facilitates de novo assembly of mammalian genomes with chromosome-length scaffolds for under \$1000. <i>bioRxiv</i> 254797. https://doi.org/10.1101/254797.
<i>Stenella clymene</i>	Dudchenko, O., Batra, S.S., Omer, A.D., Nyquist, S.K., Hoeger, M., Durand, N.C., Shamim, M.S., Machol, I., Lander, E.S., Aiden, A.P., Aiden, E.L., 2017. De novo assembly of the <i>Aedes aegypti</i> genome using Hi-C yields chromosome-length scaffolds. <i>Science</i> 356, 92–95. https://doi.org/10.1126/science.aal3327. Dudchenko, O., Shamim, M.S., Batra, S., Durand, N.C., Musial, N.T., Mostofa, R., Pham, M., Hilaire, B.G.S., Yao, W., Stamenova, E., Hoeger, M., Nyquist, S.K., Korchina, V., Pletch, K., Flanagan, J.P., Tomaszewicz, A., McAloose, D., Estrada, C.P., Novak, B.J., Omer, A.D., Aiden, E.L., 2018. The Juicebox Assembly Tools module facilitates de novo assembly of mammalian genomes with chromosome-length scaffolds for under \$1000. <i>bioRxiv</i> 254797. https://doi.org/10.1101/254797.
<i>Stenella frontalis</i>	Dudchenko, O., Batra, S.S., Omer, A.D., Nyquist, S.K., Hoeger, M., Durand, N.C., Shamim, M.S., Machol, I., Lander, E.S., Aiden, A.P., Aiden, E.L., 2017. De novo assembly of the <i>Aedes aegypti</i> genome using Hi-C yields chromosome-length scaffolds. <i>Science</i> 356, 92–95. https://doi.org/10.1126/science.aal3327. Dudchenko, O., Shamim, M.S., Batra, S., Durand, N.C., Musial, N.T., Mostofa, R., Pham, M., Hilaire, B.G.S., Yao, W., Stamenova, E., Hoeger, M., Nyquist, S.K., Korchina, V., Pletch, K., Flanagan, J.P., Tomaszewicz, A., McAloose, D., Estrada, C.P., Novak, B.J., Omer, A.D., Aiden, E.L., 2018. The Juicebox Assembly Tools module facilitates de novo assembly of mammalian genomes with chromosome-length scaffolds for under \$1000. <i>bioRxiv</i> 254797. https://doi.org/10.1101/254797.

Stenella longirostris	Dudchenko, O., Batra, S.S., Omer, A.D., Nyquist, S.K., Hoeger, M., Durand, N.C., Shamim, M.S., Machol, I., Lander, E.S., Aiden, A.P., Aiden, E.L., 2017. De novo assembly of the <i>Aedes aegypti</i> genome using Hi-C yields chromosome-length scaffolds. <i>Science</i> 356, 92–95. https://doi.org/10.1126/science.aal3327 . Dudchenko, O., Shamim, M.S., Batra, S., Durand, N.C., Musial, N.T., Mostofa, R., Pham, M., Hilaire, B.G.S., Yao, W., Stamenova, E., Hoeger, M., Nyquist, S.K., Korchina, V., Pletch, K., Flanagan, J.P., Tomaszewicz, A., McAloose, D., Estrada, C.P., Novak, B.J., Omer, A.D., Aiden, E.L., 2018. The Juicebox Assembly Tools module facilitates de novo assembly of mammalian genomes with chromosome-length scaffolds for under \$1000. <i>bioRxiv</i> 254797. https://doi.org/10.1101/254797 .
--------------------------	---

Museum abbreviations

GNM, Georgian National Museum, Tbilisi, Georgia

KhNU, Karazin Kharkiv National University, Kharkiv, Ukraine

MB, Museo de la Ballena, La Paz, Mexico

NMNERM, National Museum of Nature and Ethnography, Chisinau, Republic of Moldova

NMNHU-P, The National Museum of Natural History at the National Academy of Sciences of Ukraine, Kyiv, Ukraine

ONU, Mechnikov Odesa National University, Odesa, Ukraine

UABCS, Natural History Museum at Autonomous University of Baja California Sur, La Paz, Mexico

ZMUC, Zoological Museum, University of Copenhagen, Denmark

Landmarks

1: medial margin of tubercles complex; 2: posterior margin of tubercles; 3: anterior margin of tubercles; 4: posterior margin of the suture between the humeral head and diaphysis; 5: lateral margin of the suture between the humeral head and diaphysis; 6: anterior margin of the suture between the humeral head and diaphysis; 7: medial margin of the suture between the humeral head and diaphysis; 8: intersection between curves L4-L6 and L5-L7; 9: anterior margin of

the diaphysis at the level of L4; 10: posterior margin of the diaphysis at its proximal third of length (measured from suture between humeral head and diaphysis to suture between diaphysis and posterior end of the distal epiphysis); 11: anterior margin of the diaphysis at its proximal third of length; 12: mid-point of the curve L10-L11 on the lateral side; 13: mid-point of the curve L10-L11 on the medial side; 14: posterior margin of the diaphysis at its distal third; 15: anterior margin of the diaphysis at its distal third; 16: mid-point of the curve L14-L15 on the lateral side; 17: mid-point of the curve L14-L15 on the medial side; 18: posterior margin of the diaphysis at the middle level of the last third of diaphysis length; 19: anterior margin of the diaphysis at the middle level of the distal third of diaphysis length; 20: mid-point of the curve L18-L19 on the lateral side; mid-point of the curve L18-L19 on the medial side; 22: medial anterior margin of the distal epiphysis; 23: lateral anterior margin of the distal epiphysis; 24: lateral margin of the crest between facets of the distal epiphysis; 25: medial margin of the crest between facets of the distal epiphysis; 26: lateral posterior margin of the distal epiphysis; 27: medial posterior margin of the distal epiphysis; 28: mid-point between L22 and L23; 29: mid-point between L26 and L27; 30: mid-point between L18 and L29; 31: mid-point of the curve L5-L8; 32: mid-point of the curve L4-L8; 33: a pit between greater and lesser tubercles; 34: mid-point between L24 and L25.

Table S2. Angles (in degrees) between eigenvectors of the different component analyses. Significance (p) is the probability that angle between two random vectors is equal or less than the observed angle between components.

Test1 vs Test2	PC1	PC2
PCA vs phyPCA	12.59, p < 0.001	59.80, p < 0.001
PCA vs PaCA	18.40, p < 0.001	20.17, p < 0.001
phyPCA vs PaCA	27.67, p < 0.001	66.70, p < 0.001

Table S3. Contributions of the species (%) in principal component analyses.

	pca1	pca2	phy.pca1	phy.pca2	PaCA1	PaCA2
<i>Aegicetus gehennae</i>	11.35	2.98	1.07	4.17	9.57	10.84
<i>Azu</i>	7.71	0.08	2.42	0.14	7.77	1.89
<i>Balaena mysticetus</i>	0.80	12.67	14.74	2.37	0.13	11.01
<i>Balaenoptera acutorostrata</i>	0.84	13.36	7.89	0.01	0.14	13.74
<i>Balaenoptera edeni</i>	0.43	7.16	1.15	0.96	0.07	7.70
<i>Balaenoptera musculus</i>	1.97	10.70	2.95	14.22	0.83	12.23
<i>Cetotherium riabinini</i>	0.01	9.59	1.85	0.38	0.10	6.71
<i>Delphinapterus leucas</i>	0.43	0.45	7.51	0.51	0.74	0.05
<i>Dorudon atrox</i>	8.01	0.43	0.00	0.11	7.54	4.77
<i>Eschrichtius robustus</i>	0.00	1.93	0.65	0.06	0.04	1.36
<i>Ferecetotherium kelloggi</i>	1.77	3.01	0.75	6.45	2.28	0.19
<i>Globicephala melas</i>	3.98	2.29	7.78	2.49	4.86	0.00
<i>Hyperoodon planifrons</i>	0.08	0.34	0.50	1.25	0.13	0.10
<i>Kelloggia barbarus</i>	0.15	0.37	4.57	11.10	0.11	0.35
<i>Kentriodon fuchsii</i>	0.74	2.80	1.80	0.16	1.15	0.67
<i>Kentriodontidae indet</i>	0.01	1.81	0.72	0.09	0.01	1.32
<i>Kogia sima</i>	0.00	1.30	1.25	0.00	0.03	0.73
<i>Leucopleurus acutus</i>	10.36	2.96	9.85	0.44	11.24	0.27
<i>Lagenorhynchus albirostris</i>	8.19	1.97	3.03	0.06	8.91	0.22
<i>Maiacetus inuus</i>	19.42	1.02	2.61	0.43	17.87	11.44
<i>Microzeuglodon caucasicum</i>	2.69	0.01	0.10	0.10	2.76	0.94

Monodon_monoceros	0.08	5.02	1.58	15.72	0.43	2.07
Oligodelphis_azerbajdzanicus	1.38	0.48	0.00	0.84	1.20	1.59
Orcaella_brevirostris	0.07	5.08	12.61	0.00	0.39	2.41
Orcinus_orca	10.51	2.66	6.70	0.06	11.85	0.22
Otradnocetus_virodovi	0.03	2.70	0.67	2.63	0.01	2.38
Pachyacanthus_suessii	0.06	1.89	0.16	0.00	0.00	1.70
Phocoena_phocoena	2.89	3.56	1.78	0.10	3.83	0.36
Phocoena_sinus	1.70	0.26	0.04	34.99	2.00	0.04
Physeter_macrocephalus	0.13	0.60	1.28	0.08	0.06	0.21
Sulakocetus_dagestanicus	4.13	0.07	1.99	0.01	3.91	1.98
Ziphius_cavirostris	0.08	0.46	0.00	0.10	0.03	0.50

Table S4. Sum of contributions of x, y, and z coordinates of the landmarks (%) in principal component analyses.

Landmark	Module	pca1	pca2	phy.pca 1	phy.pca 2	PaCA1	PaCA2
1	prox.epi.	5.72	14.87	5.56	6.08	9.85	10.21
2	prox.epi.	5.16	13.76	3.53	8.90	10.23	9.49
3	prox.epi.	4.00	2.15	6.50	15.93	1.63	3.55
4	prox.epi.	3.88	2.80	4.20	2.28	2.15	4.10
5	prox.epi.	5.14	0.78	5.02	0.29	4.46	2.03
6	prox.epi.	3.79	12.89	2.04	0.97	8.79	9.60
7	prox.epi.	0.02	14.29	0.20	3.07	1.59	14.38
8	prox.epi.	1.32	5.94	0.92	6.73	2.50	4.14
9	diaph.	2.38	6.20	4.62	0.94	0.95	6.64
10	diaph.	2.20	2.67	3.50	0.68	1.53	3.08
11	diaph.	0.92	1.12	2.68	3.14	0.38	0.80
12	diaph.	1.97	0.62	1.82	0.43	1.24	1.38
13	diaph.	3.68	1.48	3.39	2.50	3.57	2.37
14	diaph.	1.59	0.67	2.82	0.02	0.97	1.24
15	diaph.	0.86	0.44	1.75	1.72	0.82	0.36
16	diaph.	0.80	0.18	0.90	0.18	0.48	0.61

17	diaph.	2.27	1.66	1.80	1.51	2.16	2.08
18	diaph.	2.74	0.16	3.22	0.23	2.14	0.85
19	diaph.	4.76	0.94	4.57	1.71	5.17	0.36
20	diaph.	1.62	0.00	1.80	0.42	1.25	0.19
21	diaph.	1.92	1.90	1.49	1.33	1.73	1.96
22	dist.epi.	5.51	0.66	5.02	2.34	4.64	1.98
23	dist.epi.	4.70	1.42	4.62	6.03	3.51	2.21
24	dist.epi.	1.27	1.14	0.57	0.27	1.86	0.74
25	dist.epi.	1.06	0.34	1.19	0.57	0.86	0.76
26	dist.epi.	4.21	0.05	3.29	0.26	4.03	0.21
27	dist.epi.	3.32	0.22	3.83	5.54	2.37	0.53
28	dist.epi.	6.87	1.27	5.79	3.88	5.38	2.99
29	dist.epi.	4.60	0.94	3.35	2.72	3.78	1.68
30	diaph.	4.09	0.64	3.34	2.25	3.49	1.46
31	prox.epi.	3.37	1.83	2.84	1.57	3.13	1.92
32	prox.epi.	2.01	4.02	2.13	6.76	1.05	3.84
33	prox.epi.	1.15	0.62	0.70	5.81	0.76	1.55
34	dist.epi.	1.09	1.34	0.97	2.92	1.57	0.69

Table S5. Modularity analysis with CR index and phylogenetic correction

Groups		Statistic	Pair of modules			Total modularity
			proximal epiphysis – distal epiphysis	proximal epiphysis – diaphysis	distal epiphysis – diaphysis	
Mysticeti		CR	1.042	1.027	0.950	1.004
		p	0.447	0.474	0.006	0.208
		ES	-0.07	-0.04	-2.74	-0.83
Odontoceti		CR	0.934	1.006	0.960	0.966
		p	0.002	0.087	0.001	0.001
		ES	-2.74	-1.45	-3.52	-3.61
Paleogene Pelageceti		CR	0.811	0.831	1.036	0.892
		p	0.002	0.001	0.326	0.001
		ES	-3.49	-3.83	-0.28	-3.74
Significance of difference in effect sizes between groups (p-value)	Mysticeti - Paleogene Pelageceti		0.029	0.013	0.040	0.062
	Odontoceti - Paleogene Pelageceti		0.214	0.015	0.020	0.202
	Mysticeti - Odontoceti		0.176	0.505	0.911	0.311

Table S6. Integration analysis with PLS method with phylogenetic correction

Groups		Statistic	Pair of modules			Average integration
			proximal epiphysis – distal epiphysis	proximal epiphysis – diaphysis	distal epiphysis – diaphysis	
Mysticeti		r_{PLS}	0.960	0.964	0.919	0.948
		p	0.025	0.030	0.067	0.002
		ES	1.97	1.89	1.51	2.54
Odontoceti		r_{PLS}	0.881	0.962	0.924	0.922
		p	0.001	0.001	0.002	0.001
		ES	2.71	3.56	2.98	4.05
Paleogene Pelagiceti		r_{PLS}	0.823	0.835	0.981	0.880
		p	0.266	0.301	0.002	0.042
		ES	0.60	0.45	2.45	1.72
Significance of difference in effect sizes between groups (p-value)	Mysticeti - Paleogene Pelagiceti		0.630	0.541	0.244	0.481
	Odontoceti - Paleogene Pelagiceti		0.137	0.012	0.122	0.060
	Mysticeti - Odontoceti		0.183	0.018	0.021	0.119

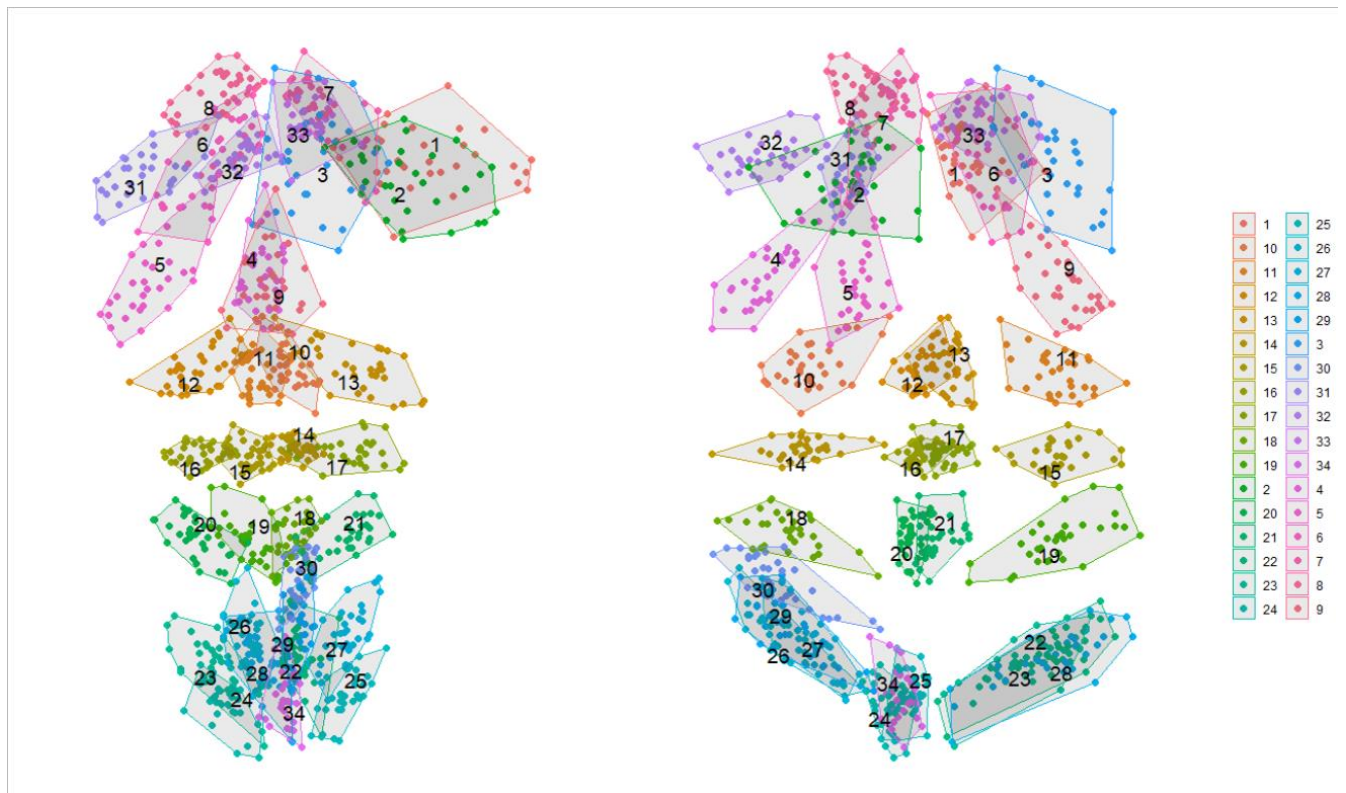


Figure S1. Variation of landmarks on cetacean humerus, XY and XZ coordinates. Clouds represent Procrustes aligned coordinates of different specimens of 32 species of Cetacea.

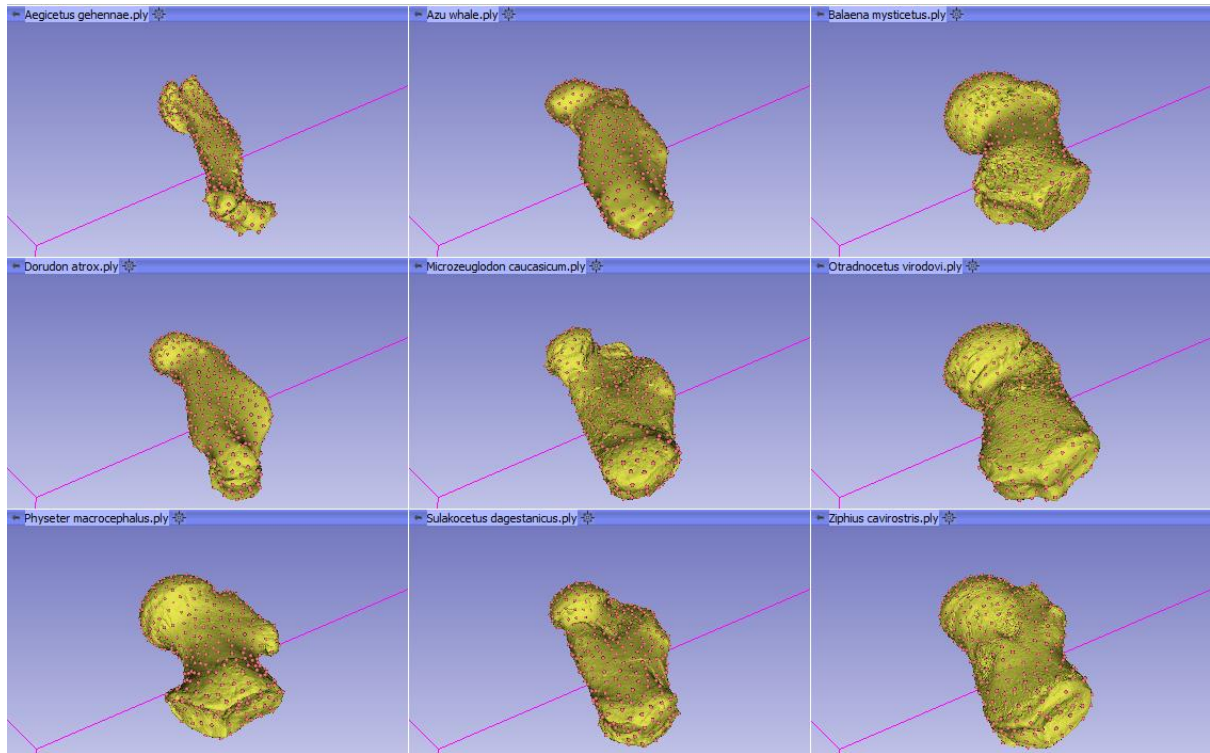


Figure S2. Distributions of 499 pseudolandmarks by taxa.

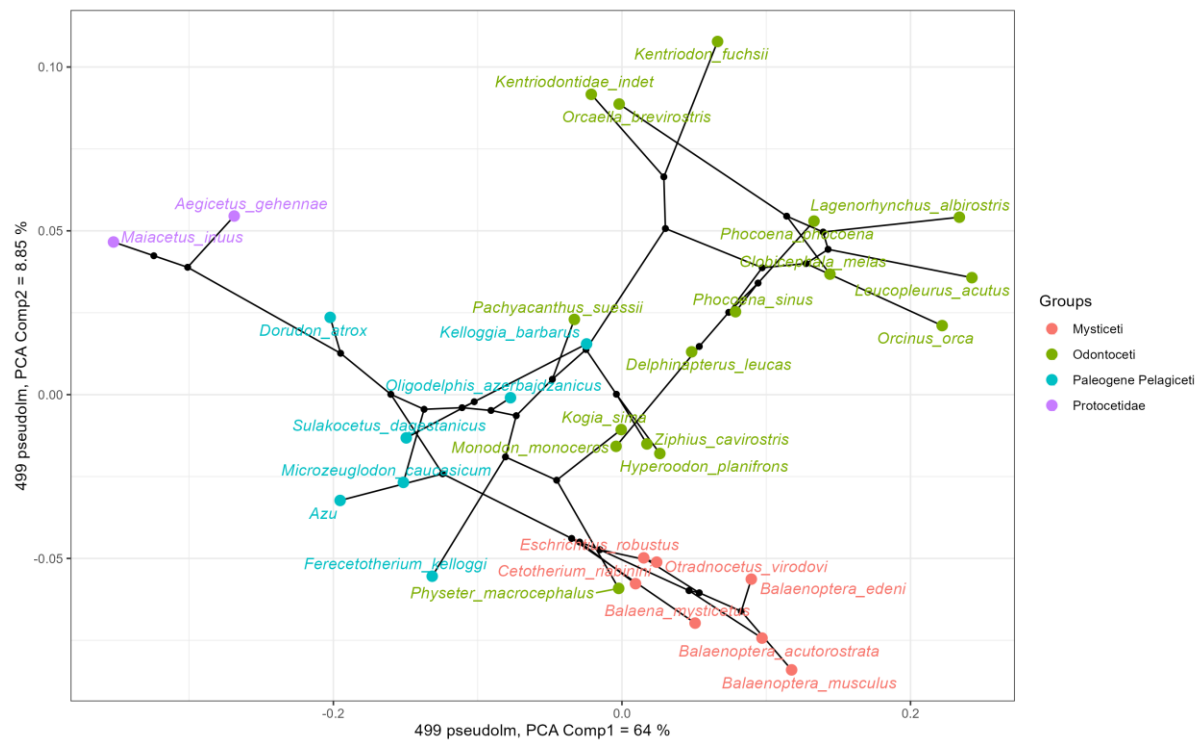


Figure S3. Multivariate analysis (PCA) of the shape of the humerus for the geometry of 499 pseudolandmarks.

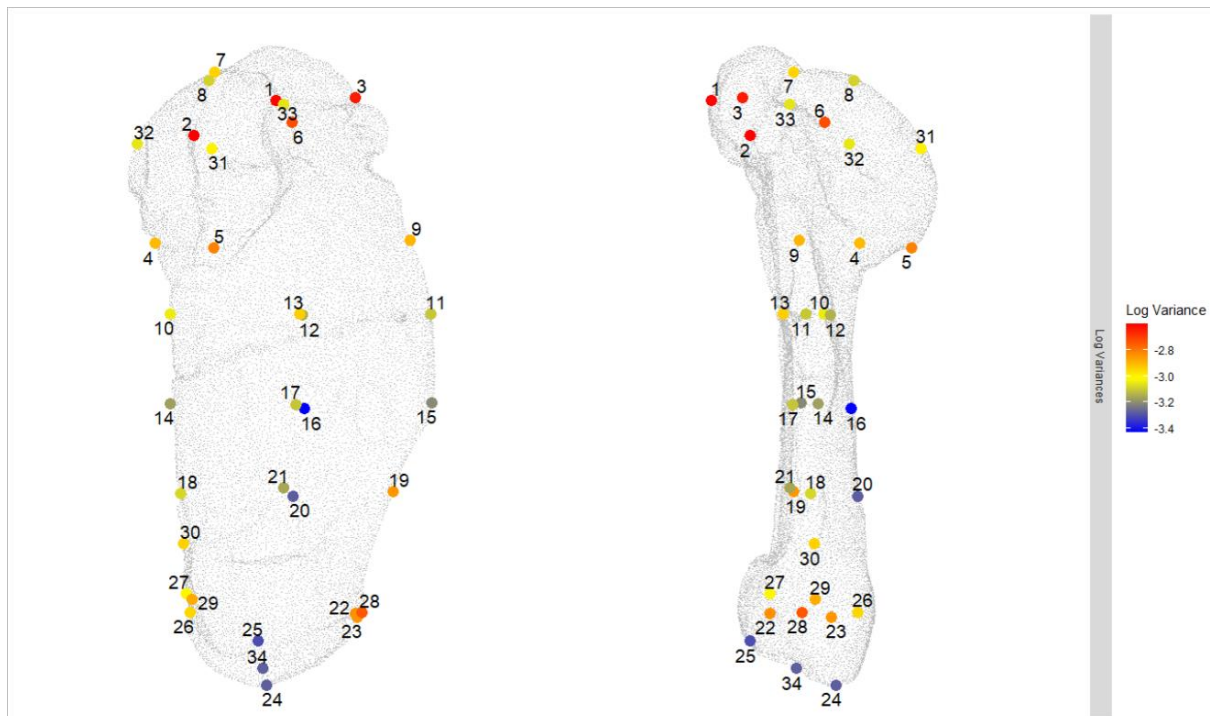


Figure S4. Variance of 34 fixed landmarks. Landmarks are colored by the value of $\log_{10}$ sum of coordinates variances.

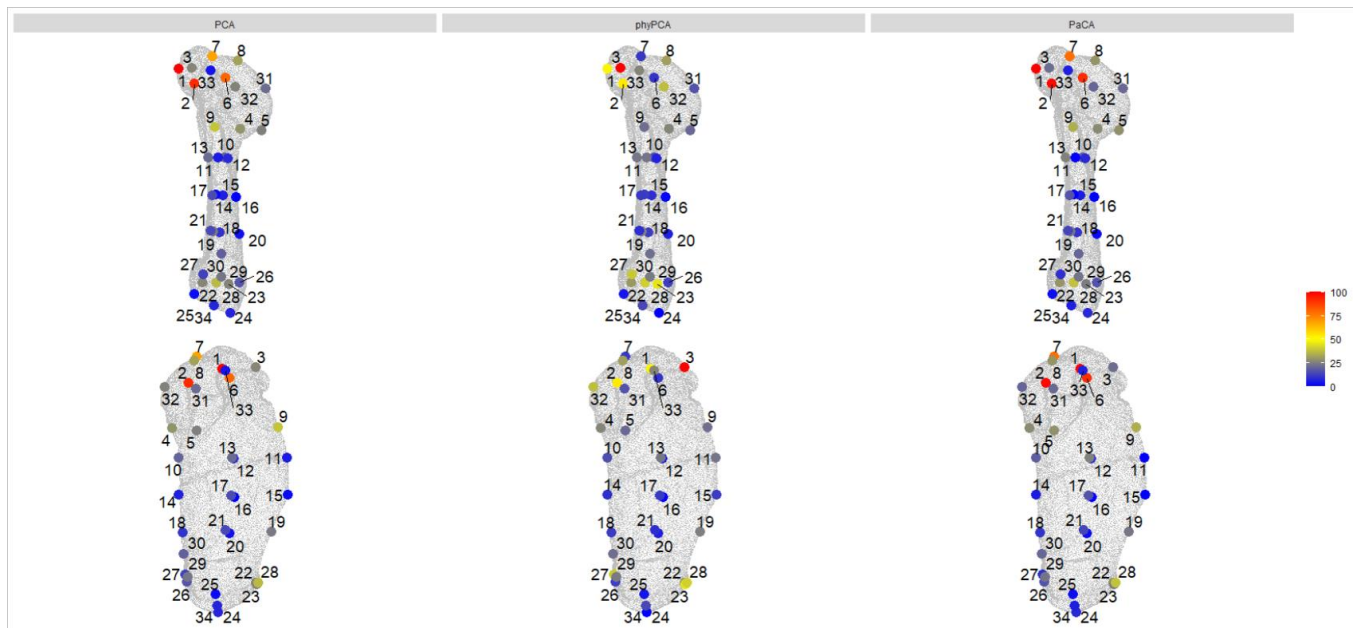


Figure S5. Summarized contribution of the landmarks (sum of contributions of the x, y, z coordinates and first two components) for different ordinations. Color of points for each analysis rescaled to range from 0 to 100. Most contributing landmarks in standard PCA and PaCA: 1, 2, 6, 7; in phyPCA: 3, 2, 1, 23, 28, 27.

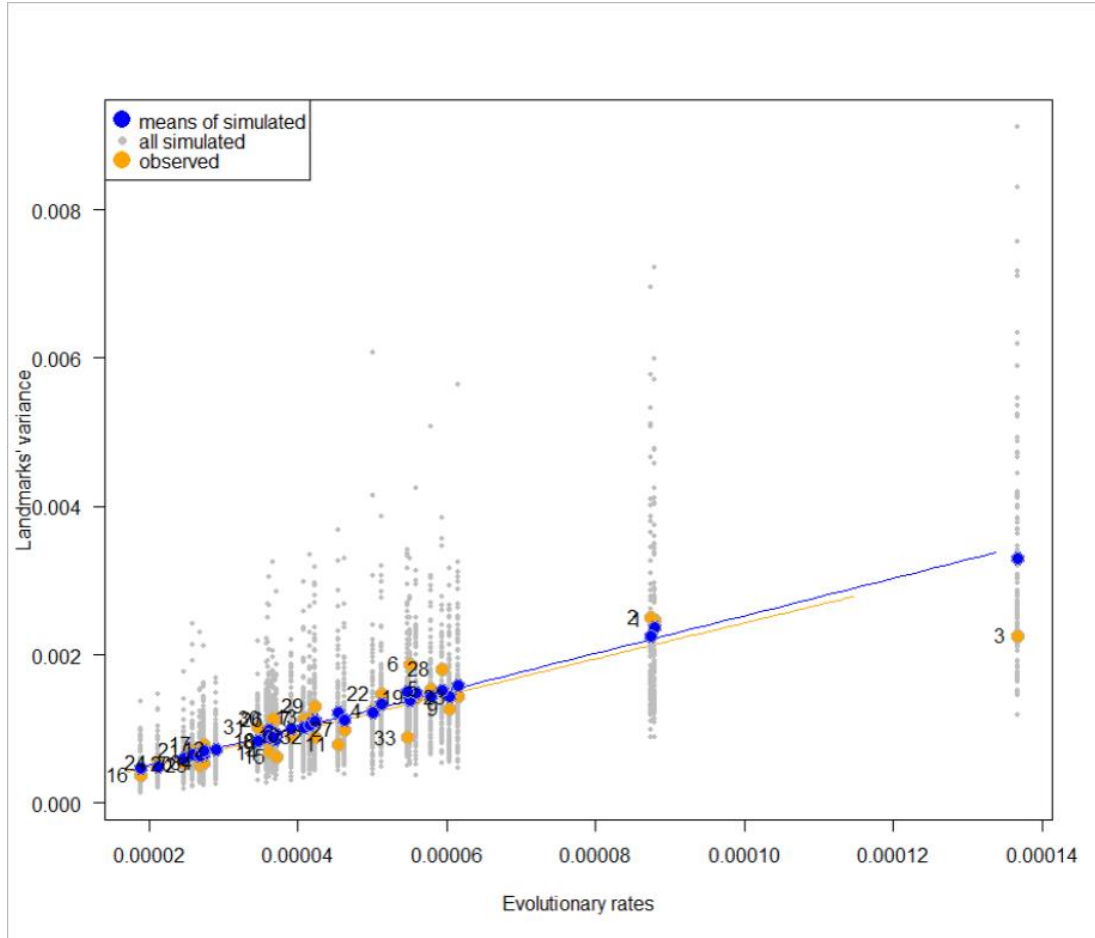


Figure S6. SMA regression of variance and evolutionary rates of simulated (blue) and observed (orange) data. Grey dots are all simulated variances under Brownian motion for the given evolutionary rates; null hypothesis of equal slopes between the observed and simulated data was supported in 65% of SMA regression tests, predicted for the Brownian motion.