

Prof Director Ludovic ORLANDO, PhD, HDR

Publication List (240, Updated Aug 2024)

220 Peer-reviewed

2024– Peer-reviewed

- 1) Nota K, **Orlando L**, Merchesini A, Girardi M, Bertilsson S, Vernesi C, Parducci L. 2024. Enriching barcoding markers in environmental samples utilising a phylogenetic probe design: insights from mock communities. **Environmental DNA** 6 :e593.
- 2) Dolenz S, van der Valk T, Jin C, Oppenheimer J, Sharif MB, **Orlando L**, Shapiro B, Dalén L, Heintzman PD. 2024. Unravelling reference bias in ancient DNA datasets. **Bioinformatics** 40:btac436.
- 3) Fegraeus K, Rosengren MK, Naboulsi R, **Orlando L**, Åbrink M, Jouni A, Velie BD, Raine A, Egner B, Mikael Mattsson C, Lång K, Zhigulev A, Björck HM, Franco-Cereceda A, Eriksson P, Andersson G, Sahle P, Meadows Lindgren G. 2024. An endothelial regulatory module links blood pressure regulation with elite athletic performance. **PLoS Genet** 20:e1011285.
- 4) Taylor WTT, Hart IA, Tuvshinjargal T, Bayarsaikhan J, Jarman NL, Bittner P, López Calle P, Blakeslee LA, Zhir M, Chauvey L, Tressières G, Tonasso-Calvière L, Schiavinato S, Cruaud C, Aury JM, Oliveira PH, Wincker P, **Orlando L**. 2024. High altitude horse use and early horse transport in eastern Eurasia: new evidence from melting ice. **The Holocene** doi: 10.1177/09596836241254484.
- 5) Librado P, Tressières G, Chauvey L, Fages A, Khan N, Schiavinato S, Calvière-Tonasso L, Kusliy MA, Gaunitz C, Liu X, Wagner S, Der Sarkissian C, Seguin-Orlando A, Perdereau A, Aury JM, Southon J, Shapiro B, Bouchez O, Donnadiou C, Running Horse Collin Y, Gregersen KM, Dengsø Jessen M, Christensen K, Claudi-Hansen L, Pruvost M, Pucher E, Vulic H, Novak M, Rimpf A, Turk P, Reiter S, Brem G, Schwall C, Barrey E, Robert C, Degueurce C, Kolska Horwitz L, Klassen L, Rasmussen U, Kveiborg J, Nørkjær N, Makowiecki D, Makarowicz P, Szeliga M, Ilchyshyn V, Rud V, Romaniszyn J, Mulin VE, Verdugo M, Bradley DG, Cardoso JL, Valente MJ, Telles Antunes M, Ameen C, Thomas R, Ludwig A, Marzullo M, Prato O, Bagnasco Gianni G, Tecchiati U, Granado J, Schlumbaum A, Deschler-Erb S, Schernig Mráz M, Boulbes N, Gardeisen A, Mayer C, Döhle HJ, Vicze M, Kosintsev PA, Kysely R, Peške L, O'Connor T, Ananyevskaya E, Shevnina I, Logvin A, Kovalev AA, Iderkhangai TO, Sablin MV, Dashkovskiy PK, Graphodatsky AS, Merts I, Merts V, Kasparov AK, Pitulko VV, Onar V, Ötzan A, Arbuckle BS, McColl H, Renaud G, Khaskhanov R, Demidenko S, Kadieva A, Atabiev B, Sundqvist M, Lindgren G, López-Cachero FJ, Albizuri S, Trbojević Vukičević T, Papeša AR, Burić M, Rajić Šikanjić P, Weinstock J, Asensio Vilaró D, Codina F, García Dalmau C, Morer de Llorens J, Pou J, de Prado G, Sanmartí J, Kallala N, Ramon Torres J, Maraoui-Telmini B, Belarte Franco MC, Valenzuela-Lamas S, Zazzo A, Lepetz S, Duchesne S, Alexeev A, Bayarsaikhan J, Houle JL, Bayarkhuu N, Turbat T, Crubézy E, Shingiray I, Mashkour M, Berezina NY, Korobov DS, Belinskiy A, Kalmykov A, Demoule JP, Reinhold S, Hansen S, Wallner B, Roslyakova N, Kuznetsov PF, Tishkin AA, Wincker P, Kanne K, Outram A, **Orlando L**. 2024. Widespread horse-based mobility arose around 2,200 BCE in Eurasia. **Nature** 631:819-825.
- 6) Pryor AJE, Ameen C, Liddiard R, Baker G, Kanne KS, Milton JA, Standish CD, Hambach B, **Orlando L**, Chauvey L, Schiavinato S, Calvière-Tonasso L, Tressières G, Wagner S, Southon J, Shapiro B, Pipe A, Creighton OH, Outram AK. 2024. Isotopic biographies reveal horse rearing and trading networks in medieval London. **Sci Adv** 10:eadj5782.
- 7) Wagner S, Seguin-Orlando A, Leplé JC, Leroy T, Lalanne C, Labadie K, Aury JM, Poirier S, Wincker P, Plomion C, Kremer A, **Orlando L**. 2024. Tracking population structure and phenology through time using ancient genomes from waterlogged white oak wood. **Mol Ecol** 33:e16859.
- 8) Lebrasseur O, More KD, **Orlando L**. 2024. Equine herpesvirus 4 infected domestic horses associated with Sintashta spoke-wheeled chariots around 4,000 years ago. **Virus Evol** 2024 10:vead087.
- 9) Allentoft ME, Sikora M, Refoyo-Martínez A, Irving-Pease EK, Fischer A, Barrie W, Ingason A, Stenderup J, Sjögren KG, Pearson A, Sousa da Mota B, Schulz Paulsson B, Halgren A, Macleod R, Jørkov MLS, Demeter F, Sørensen L, Nielsen PO, Henriksen RA, Vimala T, McColl H, Margaryan A, Ilardo M, Vaughn A, Fischer Mortensen M, Nielsen AB, Ulfeldt Hede M, Johannsen NN, Rasmussen P, Vinner L, Renaud G, Stern A, Jensen TZZ, Scorrano G, Schroeder H, Lysdahl P, Ramsøe AD, Skorobogatov A, Schork AJ, Rosengren A, Ruter A, Outram A, Timoshenko AA, Buzhilova A, Coppa A, Zubova A, Silva AM, Hansen AJ, Gromov A, Logvin A, Gotfredsen AB, Henning Nielsen B, González-Rabanal B, Lalueza-Fox C, McKenzie CJ, Gaunitz C, Blasco C, Liesau C, Martínez-Labarga C, Pozdnyakov DV, Cuenca-Solana D, Lordkipanidze DO, En'shin D, Salazar-García DC, Price TD, Borić D, Kostyleva E, Veselovskaya EV, Usmanova ER, Cappellini E, Brinch Petersen E, Kannegaard E, Radina F, Eylem Yediay F, Duday H, Gutiérrez-Zugasti I, Merts I, Potekhina I, Shevnina I, Altinkaya I, Guilaine J, Hansen J, Aura Tortosa JE, Zilhão J, Vega J, Buck Pedersen K, Tunia K, Zhao L, Mylnikova LN, Larsson L, Metz L, Yepiskoposyan L, Pedersen L, Sarti L, **Orlando L**, Slimak L, Klassen L, Blank M, González-Morales M, Silvestrini M, Vretemark M, Nesterova MS, Rykun M, Rolfo MF, Szymt M, Przybyła M, Calatini M, Sablin M, Dobisiková M, Meldgaard M, Johansen M, Berezina N, Card N, Saveliev NA, Poshekhonova O, Rickards O, Lozovskaya OV, Gábor O, Uldum OC, Aurino P, Kosintsev P, Courtaud P, Ríos P,

Mortensen P, Lotz P, Persson P, Bangsgaard P, de Barros Bamgaard P, Petersen PV, Martinez PP, Włodarczak P, Smolyaninov RV, Maring R, Menduïña R, Badalyan R, Iversen R, Turin R, Vasilyev S, Wählin , Borutskaya S, Skochina S, Sørensen SA, Andersen SH, Jørgensen T, Serikov YB, Molodin VI, Smrcka V, Merts V, Appadurai V, Moiseyev V, Magnusson Y, Kjær K, Lynnerup N, Lawson DJ, Sudmant PH, Rasmussen S, Korneliussen TS, Durbin R, Nielsen R, Delaëau O, Werge T, Racimo F, Kristiansen K, Willerslev E. 2024. Population genomics of post-glacial western Eurasia. **Nature** 625:301-311.

2023– Peer-reviewed

- 10) **Orlando L.** 2023. The history of the Coast Salish “wooly dogs”. **Science** 382:1236-1237.
- 11) Taylor WTT, Belardi JB, Barberena R, Coltrain JB, Marina FC, Borrero LA, Conner JL, Hodgins G, Admiraal M, Craig OE, Lucquin A, Talbot HM, Lundy J, Liu X, Chauvey L, Schiavinato S, Seguin-Orlando A, Le Roux P, Lucas M, **Orlando L**, Roberts P, Jones EL. 2023. Interdisciplinary evidence for early domestic horse exploitation in southern Patagonia. *Sci Adv* 9:eadk5201.
- 12) Jamsranjav B, Tsagaan T, Chinbold B, Tumurbaatar T, Wang J, Chechushkov I, Uetsuki M, Isahaya N, Hudson M, Shiraishi N, Li Y, Zhang C, Gelegdorj E, Caspari G, López-Calle P, Conner JL, Tressières G, Chauvey L, Birgel J, Nasan-Ochir EO, Bemmann J, Hodgins G, Richter KK, **Orlando L**, Warinner, C Taylor WTT. 2023. The origins of saddles and riding technology in East Asia: discoveries from the Mongolian Altai. **Antiquity** 1-17.
- 13) Klassen L, Rasmussen U, Kveiborg J, Richards M, **Orlando L**, Svenning JC, Ritchie K, Andreassen MH, Philippsen B, Iversen R, Johannsen NN. 2023. Ginnerup revisited. New excavations at a key Neolithic site on Djursland, Denmark. **J Neol Arc** 25:35-65.
- 14) **Orlando L.** 2023. A genetic window into the human social past. **PNAS** 120:e2312672120.
- 15) Todd ET, Fromentier A, Sutcliffe R, Running Horse Collin Y, Perdereau A, Aury JM, Èche C, Bouchez O, Donnadiou C, Wincker P, Kalbfleisch T, Petersen JL, **Orlando L.** 2023. Imputed genomes of historical horses provide insights into modern breeding. **iScience** 26:107104.
- 16) Bozlak E, Radovic L, Remer V, Rigler D, Allen L, Brem G, Stalder G, Castaneda C, Cothran G, Raudsepp T, Okuda Y, Moe KK, Moe HH, Kounnavongsa B, Keonouchanh S, Van NH, Vu VH, Shah MK, Nishibori M, Kazymbet P, Bakhtin M, Zhunushov A, Paul RC, Dashnyam B, Nozawa K, Almarzook S, Brockmann GA, Reissmann M, Antczak DF, Miller DC, Sadeghi R, von Butler-Wemken I, Kostaras N, Han H, Manglai D, Abdurasulov A, Sukhbaatar B, Ropka-Molik K, Stefaniuk-Szmukier M, Lopes MS, da Câmara Machado A, Kalashnikov VV, Kalinkova L, Zaitov AM, Novoa-Bravo M, Lindgren G, Brooks S, Rosa LP, **Orlando L**, Juras R, Kunieda T, Wallner B. 2023. Refining the evolutionary tree of the horse Y chromosome. **Sci Rep** 13:8954.
- 17) Clavel P, Louis L, Sarkissian C, Thèves C, Gillet C, Chauvey L, Tressières G, Schiavinato S, Calvière-Tonasso L, Telmon N, Clavel B, Jonvel R, Tzortzis S, Bouniol L, Fémolant JM, Klunk J, Poinar H, Signoli M, Costedoat C, Spyrou MA, Seguin-Orlando A, **Orlando L.** Improving the extraction of ancient *Yersinia pestis* genomes from the dental pulp. **iScience** 26:106787.
- 18) Taylor WTT, Librado P, American Horse CJ, Shield Chief Gover C, Arterberry J, Afraid of Bear-Cook AL, Left Heron H, Yellow Hair RM, Gonzalez M, Means B, High Crane S, Yellow Bull WW, Dull Knife B, Afraid of Bear A, Tecumseh Collin C, Ward C, Pasqual TA, Chauvey L, Tonasso-Calvière L, Schiavinato S, Seguin-Orlando A, Fages A, Khan N, Der Sarkissian C, Liu X, Wagner S, Leonard BG, Manzano BL, O'Malley N, Leonard JA, Bernáldez-Sánchez E, Barrey E, Charliquart L, Robbe E, Denoblet T, Gregersen K, Vershinina AO, Weinstock J, Rajić Šikanjić P, Mashkour M, Shingiray I, Aury JM, Perdereau A, Alquraishi S, Alfarhan AH, Al-Rasheid KAS, Trbojević Vukičević T, Buric M, Sauer E, Lucas M, Brenner-Coltrain J, Bozell JR, Thornhill CA, Monagle V, Perri A, Newton C, Hall WE, Conner JL, Le Roux P, Buckser SG, Gabe C, Belardi JB, Barrón-Ortiz CI, Hart IA, Ryder C, Sponheimer M, Shapiro B, Southon J, Hibbs J, Faulkner C, Outram A, Patterson Rosa L, Palermo K, Solé M, William A, McCrory W, Lindgren G, Brooks S, Eché C, Donnadiou C, Bouchez O, Wincker P, Hodgins G, Trabert S, Bethke B, Roberts P, Jones EL, Running Horse Collin Y, **Orlando L.** Early dispersal of domestic horses into the Great Plains and northern Rockies. **Science** 379:1316-1323.
- 19) **Orlando L.** 2023. The genomic history of ice-age Europeans. **Nature** 615:41-42.
- 20) Liu X, Seguin-Orlando A, Chauvey L, Tressières G, Schiavinato S, Tonasso-Calvière L, Aury JM, Perdereau A, Wagner S, Clavel P, Estrada O, Pan J, Ma Y, Enk J, Devault A, Klunk J, Lepetz S, Clavel B, Jiang L, Wincker P, Collin YRH, Sarkissian C, **Orlando L.** 2023. DNA methylation-based profiling of horse archaeological remains for age-at-death and castration. **iScience** 26:106144.
- 21) Wagner S, Seguin-Orlando A, Lepéle JC, Leroy T, Lalanne C, Labadie K, Aury JM, Poirier S, Wincker P, Plomion C, Kremer A, **Orlando L.** 2023. Tracking population structure and phenology through time using ancient genomes from waterlogged white oak wood. **Mol Ecol** doi: 10.1111/mec.16859.

2022– Peer-reviewed

- 22) Wang Y, Prohaska A, Dong H, Alberti A, Alsos IG, Beilman DW, Bjørk AA, Cao J, Cherezova AA, Coissac E, De Sanctis B, Denoëud F, Dockter C, Durbin R, Edwards ME, Edwards NR, Esdale J, Fedorov GB, Fernandez-Guerra A,

- Froese DG, Gusarova G, Haile J, Holden PB, Kjeldsen KK, Kjær KH, Korneliussen TS, Lammers Y, Larsen NK, Macleod R, Mangerud J, McColl H, Merkel MKF, Money D, Möller P, Nogués-Bravo D, **Orlando L**, Owens HL, Pedersen MW, Racimo F, Rahbek C, Rasic JT, Rouillard A, Ruter AH, Skadhauge B, Svendsen JI, Tikhonov A, Vinner L, Wincker P, Xing Y, Zhang Y, Meltzer DJ, Willerslev E. 2022. Reply to: When did mammoths go extinct? **Nature** 612:E4-E6.
- 23) Todd ET, Tonasso-Calvière L, Chauvey L, Schiavinato S, Fages A, Seguin-Orlando A, Clavel P, Khan N, Pardal LP, Patterson Rosa L, Librado P, Ringbauer H, Verdugo M, Southon J, Aury JM, Perdereau A, Vila E, Marzullo M, Prato O, Tecchiati U, Bagnasco Gianni G, Tagliacozzo A, Tinè V, Alhaique F, Cardoso JL, Valente MJ, Antunes MT, Frantz L, Shapiro B, Bradley DG, Boulbes N, Gardeisen A, Koska Horwitz L, Ötzan A, Arbuckle BS, Onar V, Clavel B, Lepetz S, Vahdati AA, Davoudi H, Mohaseb A, Mashjour M, Bouchez O, Donnadiou C, Wincker P, Brooks SA, Beja-Pereira A, Wu DD, **Orlando L**. 2022. The genomic history and global expansion of domestic donkeys. **Science** 377:1172-80.
- 24) Bergström A, Stanton DWG, Taron UH, Frantz L, Sinding MS, Ersmark E, Pfrengle S, Cassatt-Johnstone M, Lebrasseur O, Girdland-Flink L, Fernandes DM, Ollivier M, Speidel L, Gopalakrishnan S, Westbury MV, Ramos-Madriral J, Feuerborn TR, Reiter E, Gretzinger J, Münzel SC, Swali P, Conard NJ, Carøe C, Haile J, Linderholm A, Androsov S, Barnes I, Baumann C, Benecke N, Bocherens H, Brace S, Carden RF, Drucker DG, Fedorov S, Gasparik M, Germonpré M, Grigoriev S, Groves P, Hertwig ST, Ivanova VV, Janssens L, Jennings RP, Kasparov AK, Kirillova IV, Kurmaniyazov I, Kuzmin YV, Kosintsev PA, Lázníčková-Galetová M, Leduc C, Nikolskiy P, Nussbaumer M, O'Drisceoil C, **Orlando L**, Outram A, Pavlova EY, Perri AR, Pilot M, Pitulko VV, Plotnikov VV, Protopopov AV, Rehazek A, Sablin M, Seguin-Orlando A, Storå J, Verjux C, Zaibert VF, Zazula G, Crombé P, Hansen AJ, Willerslev E, Leonard JA, Götherström A, Pinhasi R, Schuenemann VJ, Hofreiter M, Gilbert MTP, Shapiro B, Larson G, Krause J, Dalén L, Skoglund P. 2022. Grey wolf genomic history reveals a dual ancestry of dogs. **Nature** 607:313-320.
- 25) Suchan T, Chauvey L, Pouillet M, Tonasso-Calvière L, Schiavinato S, Clavel P, Clavel B, Lepetz S, Seguin-Orlando A, **Orlando L**. 2022. Assessing the impact of USER-treatment on hyRAD capture applied to ancient DNA. **Mol Ecol Resour** 22:2262-64.
- 26) Cai D, Zhu S, Gong M, Zhanh N, Wen J, Liang Q, Sun W, Shao X, Guo Y, Cai Y, Zheng Z, Zhang W, Hu S, Wang X, Tian H, Li Y, Liu W, Yang M, Yang J, Wu D, **Orlando L**, Jiang Y. 2022. Radiocarbon and genomic evidence for the survival of *Equus Sussemionus* until the late Holocene. **Elife** 11:e73346.
- 27) Slimak L, Zanolli C, Higham T, Frouin M, Schwenninger JL, Arnold LJ, Demuro M, Douka K, Mercier N, Guérin G, Valladas H, Yvorra P, Giraud Y, Seguin-Orlando A, **Orlando L**, Lewis JE, Muth X, Camus H, Vandevelde S, Buckley M, Mallol C, Stringer C, Metz L. 2022. Modern human incursion into Neanderthal territories 54,000 years ago at Mandrin, France. **Sci Adv** 8:eabj9496.
- 28) Sharif M, Mohaseb AF, Zimmermann MI, Trixl S, Saliari K, Kunst GK, Cucchi T, Czeika S, Mashkour M, **Orlando L**, Schaefer K, Peters J, Mohandesan E. 2022. The mules that are not mules - metrics, morphology, archaeogenomics and mtDNA d-loop diversity in equids from Roman Switzerland. **J Arc Sci** 143:105624.
- 29) Liu X, **Orlando L**. 2022. mapDATAge: a ShinyRpackage to chart ancient DNA data through space and time. **Bioinformatics** 38:3992-4.
- 30) Librado P, **Orlando L**. 2022. Struct-f4: a Rccp package for ancestry profile and population structure inference from f4 statistics. **Bioinformatics** 38:2070-1.
- 31) Clavel B, Lepetz S, Chauvey L, Schiavinato S, Tonasso-Calvière L, Liu X, Fages A, Khan N, Seguin-Orlando A, Der Sarkissian C, Clavel P, Estrada O, Alioglu D, Gaunitz C, Aury JM, Barme M, Bodu P, Olive M, Bignong-Lau O, Castel JC, Boudadi-Maligne M, Boulbes N, Bourgeois A, Decanter F, Foucras S, Frère S, Gardeisen A, Jouanin G, Méla C, Morand N, Nieto Espinet A, Perdereau A, Putelat O, Rivière J, Robin O, Salin M, Valenzuela-Lamas S, Vallet C, Yvinec JH, Wincker P, **Orlando L**. 2022. Sex in the city: Uncovering sex-specific management of equine resources from prehistoric times to the Modern Period in France. **J Arc Sci Rep** 41:103341.
- 32) Liu X, Zhang Y, Liu W, Li Y, Pan J, Pu Y, Han J, **Orlando L**, Ma Y, Jiang L. 2022. A single-nucleotide mutation within the TBX3 enhancer increased body size in Chinese horses. **Curr Biol** 32:480-7.
- 33) Suchan T, Kusliy MA, Khan N, Chauvey L, Tonasso-Calvière L, Schiavinato S, Southon J, Keller M, Kitagawa K, Krause J, Bessudnov AN, Bessudnov AA, Graphodatsky AS, Valenzuela-Lamas S, Wilczyński J, Pospuła S, Tunia K, Nowak M, Moskal-delHoyo M, Tishkin AA, Pryor AJE, Outram AK, **Orlando L**. 2022. Performance and automation of ancient DNA capture with RNA hyRAD probes. **Mol Ecol Resour** 22:891-907

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- 34) Lepetz S, Clavel B, Alioglu D, Chauvey L, Schiavinato S, Tonasso-Calvière L, Liu X, Fages A, Khan N, Seguin-Orlando A, Der Sarkissian C, Clavel P, Estrada O, Gaunitz C, Aury JM, Barme M, Boulbes N, Bourgeois A, Decanter F, Foucras S, Frère S, Gardeisen A, Jouanin G, Méla C, Morand N, Nieto Espinet A, Perdereau A, Putelat O, Rivière J, Robin O, Salin M, Valenzuela-Lamas S, Vallet C, Yvinec JH, Wincker P, **Orlando L**. 2021. Historical management of equine resources in France from the Iron Age to the Modern Period. **J Arc Sci Rep** 40:103250.

- 35) Taylor WTT, Hart I, Jones EL, Brenner-Coltrain J, Thompson Jobe J, Britt BB, McDonald G, Li Y, Zhang C, Le Roux P, Quinn Shield Chief Gover C, Schiavinato S, **Orlando L**, Roberts P. 2021. Interdisciplinary analysis of the Lehi horse: Implications for early historic horse cultures of the North American West. **Am Antiquity** 86:465-485.
- 36) Librado P, **Orlando L**. 2021. Genomics and the evolutionary history of equids. *Ann Rev Anim Biosci* 9:81-101.
- 37) Clavel P, Dumoncel J, Der Sarkissian C, Seguin-Orlando A, Calvière-Tonasso L, Schiavinato S, Chauvey L, Perdereau A, Aury JM, Wincker P, Onar V, Clavel B, Lepetz S, Braga J, **Orlando L**. 2021. Assessing the predictive taxonomic power of the bony labyrinth 3D shape in horses, donkeys and their F1-hybrids. **J Arc Sci** 131:105383.
- 38) **Orlando L**, Allaby R, Skoglund P, Der Sarkissian C, Stockhammer PW, Avila-Arcos MC, Fu Q, Krause J, Willerslev E, Stone AC, Warinner C. 2021. Ancient DNA analysis. **Nat Rev Methods Primers** 1:14.
- 39) Seguin-Orlando A, Donat R, Der Sarkissian C, Southon J, Thèves C, Manen C, Tchéremissinoff Y, Crubézy E, Shapiro B, Deleuze JF, Dalén L, Guilaine J, **Orlando L**. 2021. Heterogeneous Hunter-Gatherer and Steppe-Related Ancestries in Late Neolithic and Bell Beaker Genomes from Present-Day France. **Curr Biol** 31:1072-1083.e10.
- 40) Librado P, Khan N, Fages A, Kusliy MA, Suchan T, Tonasso-Calvière L, Schiavinato S, Alioglu D, Fromentier A, Perdereau A, Aury JM, Gaunitz C, Chauvey L, Seguin-Orlando A, Der Sarkissian C, Southon J, Shapiro B, Tishkin AA, Kovalev AA, Alquraishi S, Alfarhan AH, Al-Rasheid KAS, Seregély T, Klassen L, Iversen R, Bignon-Lau O, Bodu P, Olive M, Castel JC, Boudadi-Maligne M, Alvarez N, Germonpré M, Moskal-Del Hoyo M, Wilczyński J, Pospuła S, Lasota-Kuś A, Tunia K, Nowak M, Rannamäe E, Saarma U, Boeskorov G, Lõugas L, Kyselý R, Peške L, Bălăşescu A, Dumitraşcu V, Dobrescu R, Gerber D, Kiss V, Szécsényi-Nagy A, Mende BG, Gallina Z, Somogyi K, Kulcsár G, Gál E, Bendrey R, Allentoft ME, Sirbu G, Dergachev V, Shephard H, Tomadini N, Grouard S, Kasparov A, Basilyan AE, Anisimov MA, Nikolskiy PA, Pavlova EY, Pitulko V, Brem G, Wallner B, Schwall C, Keller M, Kitagawa K, Bessudnov AN, Bessudnov A, Taylor W, Magail J, Gantulga JO, Bayarsaikhan J, Erdenebaatar D, Tabaldiev K, Mijiddorj E, Boldgiv B, Tsagaan T, Pruvost M, Olsen S, Makarewicz CA, Valenzuela Lamas S, Albizuri Canadell S, Nieto Espinet A, Iborra MP, Lira Garrido J, Rodríguez González E, Celestino S, Olària C, Arsuaga JL, Kotova N, Pryor A, Crabtree P, Zhumatayev R, Toleubaev A, Morgunova NL, Kuznetsova T, Lordkipanize D, Marzullo M, Prato O, Bagnasco Gianni G, Tecchiati U, Clavel B, Lepetz S, Davoudi H, Mashkour M, Berezina NY, Stockhammer PW, Krause J, Haak W, Morales-Muñiz A, Benecke N, Hofreiter M, Ludwig A, Graphodatsky AS, Peters J, Kiryushin KY, Iderkhangai TO, Bokovenko NA, Vasiliev SK, Seregin NN, Chugunov KV, Plasteeva NA, Baryshnikov GF, Petrova E, Sablin M, Ananyevskaya E, Logvin A, Shevnina I, Logvin V, Kalieva S, Loman V, Kukushkin I, Merz I, Merz V, Sakenov S, Varfolomeyev V, Usmanova E, Zaibert V, Arbuckle B, Belinskiy AB, Kalmykov A, Reinhold S, Hansen S, Yudin AI, Vybornov AA, Epimakhov A, Berezina NS, Roslyakova N, Kosintsev PA, Kuznetsov PF, Anthony D, Kroonen GJ, Kristiansen K, Wincker P, Outram A, **Orlando L**. 2021. The origins and spread of domestic horses from the Western Eurasian steppes. **Nature** 598:634-640.
- 41) Wang Y, Pedersen MW, Alsos IG, De Sanctis B, Racimo F, Prohaska A, Coissac E, Owens HL, Merkel MKF, Fernandez-Guerra A, Rouillard A, Lammers Y, Alberti A, Denoed F, Money D, Ruter AH, McColl H, Larsen NK, Cherezova AA, Edwards ME, Fedorov GB, Haile J, **Orlando L**, Vinner L, Korneliussen TS, Beilman DW, Bjørk AA, Cao J, Dockter C, Esdale J, Gusarova G, Kjeldsen KK, Mangerud J, Rasic JT, Skadhauge B, Svendsen JI, Tikhonov A, Wincker P, Xing Y, Zhang Y, Froese DG, Rahbek C, Nogués DB, Holden PB, Edwards NR, Durbin R, Meltzer DJ, Kjær KH, Möller P, Willerslev E. 2021. Late Quaternary dynamics of Arctic biota from ancient environmental genomics. **Nature** 600:86-92. Errata in: *Nature* 610:E5 and *Nature* 603:E31.
- 42) Seguin-Orlando A, Costedoat C, Der Sarkissian C, Tzortzis S, Kamel C, Telmon N, Dalén L, Thèves C, Signoli M, **Orlando L**. 2021. No particular genomic features underpin the dramatic economic consequences of 17th century plague epidemics in Italy. **iScience** 24:102383.
- 43) Vershinina AO, Heintzman PD, Froese DG, Zazula G, Cassatt-Johnstone M, Dalén L, Der Sarkissian C, Dunn SG, Ermini L, Gamba C, Groves P, Kapp JD, Mann DH, Seguin-Orlando A, Southon J, Stiller M, Wooller MJ, Baryshnikov G, Gimranov D, Scott E, Hall E, Hewitson S, Kirillova I, Kosintsev P, Shidlovsky F, Tong HW, Tiunov MP, Vartanyan S, **Orlando L**, Corbett-Detig R, MacPhee RD, Shapiro B. 2021. Ancient horse genomes reveal the timing and extent of dispersals across the Bering Land Bridge. **Mol Ecol** 30:6144-6161.
- 44) Kingsley NB, Hamilton NA, Lindgren G, **Orlando L**, Bailey E, Brooks S, McCue M, Kalbfleisch TS, MacLeod JN, Petersen JL, Finno CJ, Bellone RR. 2021. "Adopt-a-Tissue" Initiative Advances Efforts to Identify Tissue-Specific Histone Marks in the Mare. **Front Genet** 12:649959.
- 45) Taylor WTT, Pruvost M, Posth C, Rendu W, Krajcarz MT, Abydkanova A, Brancaloni G, Spengler R, Hermes T, Schiavinato S, Hodgins G, Stahl R, Min J, Alisher Kyzy S, Fedorowicz S, **Orlando L**, Douka K, Krivoshapkin A, Jeong C, Warinner C, Shnaider S. 2021. Evidence for early dispersal of domestic sheep into Central Asia. **Nat Hum Behav** 5:1169-1179.

2020– Peer-reviewed

- 46) Gauthier J, Pajkovic M, Neuenschwander S, Kaila L, Schmid S, **Orlando L**, Alvarez N. 2020. Museomics identifies genetic erosion in two butterfly species across the 20th century in Finland. **Mol Ecol Resour** 20:1191-1205.

- 47) Fordham DA, Jackson ST, Brown SC, Huntley B, Brook BW, Dahl-Jensen D, Gilbert MTP, Otto-Bliesner BL, Svensson A, Theodoridis S, Wilmshurst JM, Buettel JC, Canteri E, McDowell M, **Orlando L**, Pilowsky, Rahbek, Nogues-Bravo D. 2020. Using paleo-archives to safeguard biodiversity under climate change. **Science** 369:eabc5654.
- 48) **Orlando L**. 2020. The evolutionary and historical foundation of the modern horse: lessons from ancient genomics. **Ann Rev Genet** 54:563-81.
- 49) Klumplerova M, Splichalova P, Oppelt J, Futas J, Kohutova A, Musilova P, Kubickova S, Vodicka R, **Orlando L**, Horin P. 2020. Genetic diversity, evolution and selection in the major histocompatibility complex DRB and DQB loci in the family Equidae. **BMC Genomics** 21:677.
- 50) Margaryan A, Lawson D, Sikora M, Racimo F, Rasmussen S, Moltke I, Cassidy L, Jørsboe E, Ingason A, Pedersen M, Korneliussen T, Wilhelmson H, Buś MM, de Barros Damgaard P, Martiniano R, Renaud G, Bhérer C, Moreno-Mayar JV, Fotakis A, Allen M, Allmæe R, Molak M, Cappellini E, Scorrano G, Buzhilova A, Fox A, Albrechtsen A, Schütz B, Skar B, Arcini C, Falys C, Hedenstierna Jonson C, Błaszczyk D, Pezhemsky D, Turner-Walker G, Gestsdóttir H, Lundstrøm I, Gustin I, Mainland I, Potekhina I, Muntoni IM, Cheng J, Stenderup J, Ma J, Gibson J, Peets J, Gustafsson J, Iversen KH, Simpson L, Strand L, Loe L, Sikora M, Florek M, Vretemark M, Redknap M, Bajka M, Pushkina T, Søvsø M, Grigoreva N, Christensen T, Kastholm O, Uldum O, Favia P, Holck P, Sten S, Arge SV, Ellingvåg S, Moiseyev V, Bogdanowicz W, Magnusson Y, **Orlando L**, Pentz P, Densø Jessen M, Pedersen A, Collard M, Bradley DG, Jørkov ML, Arneborg J, Lynnerup N, Price N, Gilbert MT, Allentoft M, Bill J, Sindbæk SM, Hedeager L, Kristiansen K, Nielsen R, Werge T, Willerslev E. 2020. Population genomics of the Viking World. **Nature** 585:390-6. Erratum in: *Nature* 591:E29.
- 51) Fages A, Seguin-Orlando A, Germonpré M, **Orlando L**. 2020. Horse males became over-represented in archaeological assemblages during the Bronze Age. **J Arc Sci Rep** 31:102364.
- 52) Granado JD, Dill N, Gaunitz C, Fages A, Khan N, Schernig Mrza M, Deschler-Erb S, **Orlando L**, Schlumbaum A. 2020. The mules that are not mules - metrics, morphology, archaeogenomics and mtDNA d-loop diversity in equids from Roman Switzerland. **J Arc Sci** 123:105253.
- 53) **Orlando L**. 2020. Filling Important Gaps in the Genomic History of Southwest Asia. **Cell** 181:966-8.
- 54) Frantz L, Bradley D, Larson G, **Orlando L**. 2020. Animal domestication in the era of ancient genomics. **Nat Rev Genet** 21:449-60.
- 55) Dolle D, Fages A, Mata X, Schiavinato S, Tonasso-Calvière L, Chauvey L, Wagner S, Der Sarkissia C, Fromentier A, Seguin-Orlando A, **Orlando L**. 2020. CASCADE: a Custom-made Archiving System for the Conservation of Ancient DNA Experimental Data. **Frontiers Ecol Evol** 8:185.
- 56) Pouillet M, **Orlando L**. 2020. Assessing DNA Sequence Alignment Methods for Characterizing Ancient Genomes and Methylomes. **Front Ecol Evol** 8:105.
- 57) Der Sarkissian C, Möller P, Hofman C, Ilsøe P, Rick T, Schiøtte T, Vinther Sørensen M, Dalén L, **Orlando L**. 2020. Unveiling the Ecological Applications of Ancient DNA From Mollusk Shells. **Front Ecol Evol** 8:37.
- 58) Wagner S, Plomion C, **Orlando L**. 2020. Uncovering signatures of DNA methylation in ancient plant remains from patterns of post-mortem DNA damage. **Front Ecol Evol** 8:11.
- 59) Wilkin S, Ventresca Miller A, Taylor W, Miller B, Hagan R, Bleasdale M, Scott A, Gankhuyg S, Ramsøe A, Ulziibayar S, Trachsel C, Nanni P, Grossmann J, **Orlando L**, Horton M, Stockhammer P, Myagmar E, Boivin N, Warinner C, Hendy J. 2020. Dairy pastoralism sustained Eastern Eurasian steppe populations for 5,000 years. **Nat Comms** 4:346-55.
- 60) **Orlando L**. 2020. Ancient Genomes Reveal Unexpected Horse Domestication and Management Dynamics. **Bioessays** 42:e1900164.

2019– Peer-reviewed

- 61) Cappellini E, Welker F, Pandolfi L, Ramos-Madriral J, Samodova D, Rütther PL, Fotakis AK, Lyon D, Moreno-Mayar JV, Bukhsianidze M, Rakownikow Jersie-Christensen R, Mackie M, Ginolhac A, Ferring R, Tappen M, Palkopoulou E, Dickinson MR, Stafford TW Jr, Chan YL, Götherström A, Nathan SKSS, Heintzman PD, Kapp JD, Kirillova I, Moodley Y, Agusti J, Kahlke RD, Kiladze G, Martínez-Navarro B, Liu S, Sandoval Velasco M, Sinding MS, Kelstrup CD, Allentoft ME, **Orlando L**, Penkman K, Shapiro B, Rook L, Dalén L, Gilbert MTP, Olsen JV, Lordkipanidze D, Willerslev E. 2019. Early Pleistocene enamel proteome from Dmanisi resolves Stephanorhinus phylogeny. **Nature** 574:103-107.
- 62) **Orlando L**, Librado P. 2019. Origin and Evolution of Deleterious Mutations in Horses. **Genes (Basel)** 10(9) pii: E649.
- 63) Liu X, Zhang Y, Li Y, Pan J, Wang D, Chen W, Zheng Z, He X, Zhao Q, Pu Y, Guan W, Han J, **Orlando L**, Ma Y, Jiang L. 2019. EPAS1 gain-of-function mutation contributes to high-altitude adaptation in Tibetan horses. **Mol Biol Evol** 36: 2591-2603.
- 64) Renaud G, Hanghøj K, Korneliussen TS, Willerslev E, **Orlando L**. 2019. Joint Estimates of Heterozygosity and Runs of Homozygosity for Modern and Ancient Samples. **Genetics** 212:587-614.
- 65) Fages A, Hanghøj K, Khan N, Gaunitz C, Seguin-Orlando A, Leonardi M, McCrory Constantz C, Gamba C, Al-Rasheid KAS, Albizuri S, Alfarhan AH, Allentoft M, Alquraishi S, Anthony D, Baimukhanov N, Barrett JH, Bayarsaikhan J, Benecke N, Bernaldez-Sánchez E, Berrocal-Rangel L, Biglari F, Boessenkool S, Boldgiv B, Brem G, Brown D, Burger

- J, Crubézy E, Daugnor L, Davoudi H, de Barros Damgaard P, de Los Angeles de Chorro Y de Villa-Ceballos M, Deschler-Erb S, Detry C, Dill N, do Mar Oom M, Dohr A, Ellingvåg S, Erdenebaatar D, Fathi H, Felkel S, Fernández-Rodríguez C, García-Viñas E, Germonpré M, Granada JD, Hallsson JH, Hemmer H, Hofreiter M, Kasparov A, Khasanov M, Khazaali R, Kosintsev P, Kristiansen K, Kubatbek T, Kuderna L, Kuznetsov P, Laleh H, Leonard JA, Lhuillier J, Liesau von Lettow-Vorbeck C, Logvin A, Lõugas L, Ludwig A, Luis C, Arruda AM, Marques-Bonet T, Matoso Silva R, Merz V, Mijiddorj E, Miller BK, Mochlov O, Mohaseb FA, Morales A, Nieto-Espinet A, Nistelberger H, Onar V, Pálsdóttir AH, Pitulko V, Pitskhelauri K, Pruvost M, Rajic Sikanjic P, Rapan Papeša A, Roslyakova N, Sardari A, Sauer E, Schafberg R, Scheu A, Schibler J, Schlumbaum A, Serrand N, Serres-Armero A, Shapiro B, Sheikhi Seno S, Shevnina I, Shidrang S, Southon J, Star B, Sykes N, Taheri K, Taylor W, Teegen WR, Trbojević Vukičević T, Trixl S, Tumen D, Undrakhbold S, Usmanova E, Vahdati A, Valenzuela-Lamas S, Viegas C, Wallner B, Weinstock J, Zaibert V, Clavel B, Lepetz S, Mashkour M, Helgason A, Stefánsson K, Barrey E, Willerslev E, Outram AK, Librado P, **Orlando L**. 2019. Tracking Five Millennia of Horse Management with Extensive Ancient Genome Time Series. *Cell* 177:1419-1435.e31.
- 66) Zinger L, Bonin A, Alsos IG, Bálint M, Bik H, Boyer F, Chariton AA, Creer S, Coissac E, Deagle BE, De Barba M, Dickie IA, Dumbrell AJ, Ficaretola GF, Fierer N, Fumagalli L, Gilbert MTP, Jarman S, Jumpponen A, Kausrud H, **Orlando L**, Pansu J, Pawlowski J, Tedersoo L, Thomsen PF, Willerslev E, Taberlet P. 2019. DNA metabarcoding-Need for robust experimental designs to draw sound ecological conclusions. *Mol Ecol* 28:1857-1862.
- 67) Hanghøj K, Renaud G, Albrechtsen A, **Orlando L**. 2019. DamMet: ancient methylome mapping accounting for errors, true variants, and post-mortem DNA damage. *Gigascience* 8 pii:giz025.
- 68) Renaud G, Schubert M, Sawyer S, **Orlando L**. 2019. Authentication and Assessment of Contamination in Ancient DNA. *Methods Mol Biol* 1963:163-194.
- 69) Pont C, Wagner S, Kremer A, **Orlando L**, Plomion C, Salse J. 2019. Paleogenomics: reconstruction of plant evolutionary trajectories from modern and ancient DNA. *Genome Biol* 20:29.
- 70) Nistelberger HM, Pálsdóttir AH, Star B, Leifsson R, Gondek AT, **Orlando L**, Barrett JH, Hallson J, Boessenkool S. 2019. Sexing Viking Age horses from burial and non-burial sites in Iceland using ancient DNA. *J Arc Sci* 101:115-22.

2018– Peer-reviewed

- 71) Kalbfleisch TS, Rice ES, DePriest MS Jr, Walenz BP, Hestand MS, Vermeesch JR, O Connell BL, Fiddes IT, Vershinina AO, Saremi NF, Petersen JL, Finno CJ, Bellone RR, McCue ME, Brooks SA, Bailey E, **Orlando L**, Green RE, Miller DC, Antczak DF, MacLeod JN. 2018. Improved reference genome for the domestic horse increases assembly contiguity and composition. *Commun Biol* 1:197. Erratum in: *Commun Biol*. 2019 Sep 11;2:342.
- 72) **Orlando L**. 2018. Late Bronze Age cultural origins of dairy pastoralism in Mongolia. *PNAS* 115:12083-12085.
- 73) Taylor W, Schnaider S, Abdykanova A, Fages A, Welker F, Irmer F, Seguin-Orlando A, Khan N, Douka K, Kolobova K, **Orlando L**, Krivoshapkin A, Boivin N. 2018. Early pastoral economies along the Ancient Silk Road: biomolecular evidence from the Alay Valley Kyrgyzstan. *PLoS One* 13:ee0205646.
- 74) deBarros Damgaard PB, Marchi N, Rasmussen S, Peyrot M, Renaud G, Korneliusen T, Moreno-Mayar JV, Pedersen MW, Goldberg A, Usmanova E, Baimukhanov N, Loman V, Hedeager L, Pedersen AG, Nielsen K, Afanasiev G, Akmatov K, Aldashev A, Alpaslan A, Baimbetov G, Bazaliiskii VI, Beisenov A, Boldbaatar B, Boldgiv B, Dorzhu C, Ellingvåg S, Erdenebaatar D, Dajani R, Dmitriev E, Evdokimov V, Frei KM, Gromov A, Goryachev A, Hakonarson H, Hegay T, Khachatryan Z, Khaskhanov R, Kitov E, Kolbina A, Kubatbek T, Kukushkin A, Kukushkin I, Lau N, Margaryan A, Merkyte I, Mertz IV, Mertz VK, Mijiddorj E, Moiyesev V, Mukhtarova G, Nurmukhanbetov B, Orozbekova Z, Panyushkina I, Pieta K, Smrčka V, Shevnina I, Logvin A, Sjögren KG, Štolcová T, Tashbaeva K, Tkachev A, Tulegenov T, Voyakin D, Yepiskoposyan L, Undrakhbold S, Varfolomeev V, Weber A, Kradin N, Allentoft ME, **Orlando L**, Nielsen R, Sikora M, Heyer E, Kristiansen K, Willerslev E. 2018. 137 ancient human genomes from across the Eurasian steppes. *Nature* 557:369-374. Author correction in: 563:E16.
- 75) Mühlemann B, Jones TC, Damgaard PB, Allentoft ME, Shevnina I, Logvin A, Usmanova E, Panyushkina IP, Boldgiv B, Bazartseren T, Tashbaeva K, Merz V, Lau N, Smrčka V, Voyakin D, Kitov E, Epimakhov A, Pokutta D, Vicze M, Price TD, Moiseyev V, Hansen AJ, **Orlando L**, Rasmussen S, Sikora M, Vinner L, Osterhaus ADME, Smith DJ, Glebe D, Fouchier RAM, Drosten C, Sjögren KG, Kristiansen K, Willerslev E. 2018. Ancient hepatitis B viruses from the Bronze Age to the Medieval period. *Nature* 557:418-423. Author Correction in: 562:E4.
- 76) Janečka J, Davis B, Ghosh S, Paria N, Das P, **Orlando L**, Schubert M, Nielsen M, Stout T, Brashear W, Li G, Johnson C, Metz R, Al Zadjali A-M, Love C, Varner D, Bellott D, Murphy W, Chowdhary B, Raudsepp T. 2018. Horse Y chromosome assembly displays unique evolutionary features and putative stallion fertility genes. *Nat Comms* 9:2945.
- 77) Leonardi M, Boschin F, Giampoudakis K, Beyer RM, Krapp M, Bendrey R, Sommer R, Boscato P, Manica A, Nogues-Bravo D, **Orlando L**. 2018. Late Quaternary horses in Eurasia in the face of climate and vegetation change. *Sci Adv* 4:eaar5589.
- 78) McColl H, Racimo F, Vinner L, Demeter F, Gakuhari T, Moreno-Mayar JV, van Driem G, Gram Wilken U, Seguin-Orlando A, de la Fuente Castro C, Wasef S, Shoocongdej R, Souksavattay V, Sayavongkhamdy T, Saidin MM, Allentoft ME, Sato T, Malaspinas AS, Aghakhanian FA, Korneliusen T, Prohaska A, Margaryan A, de Barros

- Damgaard P, Kaewsutthi S, Lertrit P, Nguyen TMH, Hung HC, Minh Tran T, Nghia Truong H, Nguyen GH, Shahidan S, Wiradnyana K, Matsumae H, Shigehara N, Yoneda M, Ishida H, Masuyama T, Yamada Y, Tajima A, Shibata H, Toyoda A, Hanihara T, Nakagome S, Deviese T, Bacon AM, Durringer P, Ponche JL, Shackelford L, Patole-Edoumba E, Nguyen AT, Bellina-Pryce B, Galipaud JC, Kinaston R, Buckley H, Pottier C, Rasmussen S, Higham T, Foley RA, Lahr MM, **Orlando L**, Sikora M, Phipps ME, Oota H, Higham C, Lambert DM, Willerslev E. 2018. The prehistoric peopling of Southeast Asia. **Science** 361:88-92.
- 79) Willmann C, Mata X, Hanghoej K, Tonasso L, Tisseyre L, Jeziorski C, Cabot E, Chevet P, Crubézy E, **Orlando L**, Esclassan R, Thèves C. 2018. Oral health status in historic population: Macroscopic and metagenomic evidence. **PLoS One** 13:e0196482.
- 80) de Barros Damgaard P, Martiniano R, Kamm J, Moreno-Mayar JV, Kroonen G, Peyrot M, Barjamovic G, Rasmussen S, Zacho C, Baimukhanov N, Zaibert V, Merz V, Biddanda A, Merz I, Loman V, Evdokimov V, Usmanova E, Hemphill B, Seguin-Orlando A, Yediay FE, Ullah I, Sjögren KG, Iversen KH, Choin J, de la Fuente C, Ilardo M, Schroeder H, Moiseyev V, Gromov A, Polyakov A, Omura S, Senyurt SY, Ahmad H, McKenzie C, Margaryan A, Hameed A, Samad A, Gul N, Khokhar MH, Goriunova OI, Bazaliiskii VI, Novembre J, Weber AW, **Orlando L**, Allentoft ME, Nielsen R, Kristiansen K, Sikora M, Outram AK, Durbin R, Willerslev E. 2018. The first horse herders and the impact of early Bronze Age steppe expansions into Asia. **Science** 360 pii: eaar7711.
- 81) Renaud G, Petersen B, Seguin-Orlando A, Bertelsen MF, Waller A, Newton R, Paillot R, Bryant N, Vaudin M, Librado P, **Orlando L**. 2018. Improved de novo genomic assembly for the domestic donkey. **Sci Adv** 4:eaag0392.
- 82) Wutke S, Sandoval-Castellanos E, Benecke N, Döhle HJ, Friederich S, Gonzalez J, Hofreiter M, Lõugas L, Magnell O, Malaspinas AS, Morales-Muñiz A, Orlando L, Reissmann M, Trinks A, Ludwig A. 2018. Decline of genetic diversity in ancient domestic stallions in Europe. **Sci Adv** 4:eaap9691.
- 83) Librado P, **Orlando L**. 2018. Detecting signatures of positive selection along defined branches of a population tree using LSD. **Mol Biol Evol** 35:1520-1535.
- 84) Dias GM, Bidault A, Le Chevalier P, Choquet G, Der Sarkissian C, **Orlando L**, Medigue C, Barbe V, Mangenot S, Thompson CC, Thompson FL, Jacq A, Pichereau V, Paillard C. 2018. *Vibrio tapetis* Displays an Original Type IV Secretion System in Strains Pathogenic for Bivalve Molluscs. **Front Microbiol** 9:227.
- 85) Alberto FJ, Boyer F, Orozco-terWengel P, Streeter I, Servin B, de Villemereuil P, Benjelloun B, Librado P, Biscarini F, Colli L, Barbato M, Zamani W, Alberti A, Engelen S, Stella A, Joost S, Ajmone-Marsan P, Negrini R, **Orlando L**, Rezaei HR, Naderi S, Clarke L, Flicek P, Wincker P, Coissac E, Kijas J, Tosser-Klopp G, Chikhi A, Bruford MW, Taberlet P, Pompanon F. 2018. Convergent genomic signatures of domestication in sheep and goats. **Nat Comms** 9:813.
- 86) Gaunitz C, Fages A, Hanghøj K, Albrechtsen A, Khan N, Schubert M, Seguin-Orlando A, Owens IJ, Felkel S, Bignon-Lau O, de Barros Damgaard P, Mittnik A, Mohaseb AF, Davoudi H, Alquraishi S, Alfarhan AH, Al-Rasheid KAS, Crubézy E, Benecke N, Olsen S, Brown D, Anthony D, Massy K, Pitulko V, Kasparov A, Brem G, Hofreiter M, Mukhtarova G, Baimukhanov N, Lõugas L, Onar V, Stockhammer PW, Krause J, Boldgiv B, Undrakhbold S, Erdenebaatar D, Lepetz S, Mashkour M, Ludwig A, Wallner B, Merz V, Merz I, Zaibert V, Willerslev E, Librado P, Outram AK, **Orlando L**. Ancient genomes revisit the ancestry of domestic and Przewalski's horses. 2018. **Science** 360:111-114.
- 87) Wagner S, Lagane F, Seguin-Orlando A, Schubert M, Leroy T, Guichoux E, Chancerel E, Bech-Hebelstrup I, Bernard V, Billard C, Billaud Y, Bolliger M, Crousch C, Ćufar K, Eynaud F, Heussner KU, Köninger J, Langenegger F, Leroy F, Lima C, Martinelli N, Momber G, Billamboz A, Nelle O, Palomo A, Piqué R, Ramstein M, Schweichel R, Stäuble H, Tegel W, Terradas X, Verdin F, Plomion C, Kremer A, **Orlando L**. 2018. High-Throughput DNA sequencing of ancient wood. **Mol Ecol** 27:1138-1154.
- 88) Pedersen CT, Albrechtsen A, Etter PD, Johnson EA, **Orlando L**, Chikhi L, Siegismund HR, Heller R. 2018. A southern African origin and cryptic structure in the highly mobile plains zebra. 2018. **Nat Ecol Evol** 2:491-498.
- 89) Moreno-Mayar JV, Potter BA, Vinner L, Steinrücken M, Rasmussen S, Terhorst J, Kamm JA, Albrechtsen A, Malaspinas AS, Sikora M, Reuther JD, Irish JD, Malhi RS, **Orlando L**, Song YS, Nielsen R, Meltzer DJ, Willerslev E. 2018. Terminal Pleistocene Alaskan genome reveals first founding population of Native Americans. **Nature** 553:203-207.

2017 – Peer-reviewed

- 90) Morard R, Lejzerowicz F, Darlin KF, Lecroq-Bennet B, Winther-Pedersen M, **Orlando L**, Pawlowski J, Mulitza S, de Vargas C, Kucera M. 2017. Planktonic foraminifera-derived environmental DNA extracted from abyssal sediments preserves patterns of plankton macroecology. **Biogeosciences** 14:2741-54. Heintzman PD, Zazula GD, MacPhee R, Scott E, Cahill JA, McHorse BK, Kapp JD, Stiller M, Wooller MJ, **Orlando L**, Southon J, Froese DG, Shapiro B. 2017. A new genus of horse from Pleistocene North America. *Elife*. 6. pii: e29944. Metcalf JL, Song SJ, Morton JT, Weiss S, Seguin-Orlando A, Joly F, Feh C, Taberlet P, Coissac E, Amir A, Willerslev E, Knight R, McKenzie V, **Orlando L**. 2017. Evaluating the impact of domestication and captivity on the horse gut microbiome. **Sci Rep** 7:15497.

- 91) Fortes-Lima C, Gessain A, Ruiz-Linares A, Bortolini MC, Migot-Nabias F, Bellis G, Moreno-Mayar JV, Restrepo BN, Rojas W, Avendaño-Tamayo E, Bedoya G, **Orlando L**, Salas A, Helgason A, Gilbert MTP, Sikora M, Schroeder H, Dugoujon JM. 2017. Genome-wide Ancestry and Demographic History of African-Descendant Maroon Communities from French Guiana and Suriname. **Am J Hum Genet** 101:725-6.
- 92) Thompson LR, Sanders JG, McDonald D, Amir A, Ladau J, Locey KJ, Prill RJ, Tripathi A, Gibbons SM, Ackermann G, Navas-Molina JA, Janssen S, Kopylova E, Vázquez-Baeza Y, González A, Morton JT, Mirarab S, Zech Xu Z, Jiang L, Haroon MF, Kanbar J, Zhu Q, Jin Song S, Kosciolk T, Bokulich NA, Lefler J, Brislawn CJ, Humphrey G, Owens SM, Hampton-Marcell J, Berg-Lyons D, McKenzie V, Fierer N, Fuhrman JA, Clauser A, Stevens RL, Shade A, Pollard KS, Goodwin KD, Jansson JK, Gilbert JA, Knight R; Earth Microbiome Project Consortium. 2017. A communal catalogue reveals Earth's multiscale microbial diversity. **Nature** 551:457-463
- 93) Benazzo A, Trucchi E, Cahill JA, Maisano Delser P, Mona S, Fumagalli M, Bunnefeld L, Cornetti L, Ghirotto S, Girardi M, Ometto L, Panziera A, Rota-Stabelli O, Zanetti E, Karamanlidis A, Groff C, Paule L, Gentile L, Vilà C, Vicario S, Boitani L, **Orlando L**, Fuselli S, Vernesi C, Shapiro B, Ciucci P, Bertorelle G. 2017. Survival and divergence in a small group: the extraordinary genomic history of the endangered Apennine brown bear stragglers. **PNAS** 114:E9589-9597.
- 94) McKenzie VJ, Song SJ, Delsuc F, Prest TL, Oliverio AM, Korpita TM, Alexiev A, Amato KR, Metcalf JL, Kowalewski M, Avenant NL, Link A, Di Fiore A, Seguin-Orlando A, Feh C, **Orlando L**, Mendelson JR, Sanders J, Knight R. 2017. The Effects of Captivity on the Mammalian Gut Microbiome. **Integr Comp Biol** 57:690-704.
- 95) Sikora M, Seguin-Orlando A, Sousa VC, Albrechtsen A, Korneliusen T, Ko A, Rasmussen S, Dupanloup I, Nigst PR, Bosch MD, Renaud G, Allentoft ME, Margaryan A, Vasilyev SV, Veselovskaya EV, Borutskaya SB, Deviese T, Comeskey D, Higham T, Manica A, Foley R, Meltzer DJ, Nielsen R, Excoffier L, Lahr MM, **Orlando L**, Willerslev E. 2017. Ancient genomes show social and reproductive behavior of early Upper Paleolithic foragers. **Science** 358:659-62.
- 96) Schaefer RJ, Schubert M, Bailey E, Bannasch DL, Barrey E, Bar-Gal GK, Brem G, Brooks SA, Distl O, Fries R, Finno CJ, Gerber V, Haase B, Jagannathan V, Kalbfleisch T, Leeb T, Lindgren G, Lopes MS, Mach N, da Câmara Machado A, MacLeod JN, McCoy A, Metzger J, Penedo C, Polani S, Rieder S, Tammen I, Tetens J, Thaller G, Verini-Supplizi A, Wade CM, Wallner B, **Orlando L**, Mickelson JR, McCue ME. 2017. Developong a 670k genotyping array to tag ~2M SNPs across 24 horse breeds. **BMC Genomics** 18:565.
- 97) Gopalakrishnan S, Castruita JS, Sinding MH, Kuderna L, Raikkonen J, Petersen B, Sicheritz-Ponten T, Larson G, **Orlando L**, Marques-Bonet T, Hansen A, Dalen L, Gilbert MTP. 2017. The wolf reference genome sequence (*Canis lupus lupus*) and its implications for *Canis spp.* population genomics. **BMC Genomics** 18:495.
- 98) Warinner C, Herbig A, Mann A, Fellows Yates JA, Weiß CL, Burbano HA, **Orlando L**, Krause J. 2017. A robust framework for microbial archaeology. **Ann Rev Genomics Hum Genet** 18:321-356.
- 99) Librado P, Gamba C, Gaunitz C, Der Sarkissian C, Pruvost M, Albrechtsen A, Fages A, Khan N, Schubert M, Jagannathan V, Serres A, Kuderna LFK, Povolotskaya I, Seguin-Orlando A, Lepetz S, Neuditschko M, Theves C, Alquraishi S, Alfarhan AH, Al-Rasheid K, Rieder S, Samashev Z, Francfort HP, Benecke N, Hofreiter M, Ludwig A, Keyser C, Marques-Bonet T, Ludes B, Crubezy E, Leeb T, Willerslev E, **Orlando L**. 2017. Ancient genomic changes associated with domestication of the horse. **Science** 356:442-5.
- 100) Lefébure T, Morvan C, Malard F, Francois C, Konecky-Dupre L, Gueguen L, Weiss-Gayet M, Seguin-Orlando A, Ermini L, Der Sarkissian C, Charrier PN, Eme D, Mermillord-Blondin F, Duret L, Vieira C, **Orlando L**, Douady CJ. 2017. Less effective selection leads to larger genome. **Genome Res** 27:1016-1028.
- 101) Der Sarkissian C, Pichereau V, Dupont C, Ilsøe P, Perrigault M, Butler P, Chauvaud L, Eiriksson J, Scourse J, Paillard C, **Orlando L**. 2017. Ancient DNA analysis identifies marine mollusk shells as new metagenomic archives of the past. **Mol Ecol Resour** 17:835-53.
- 102) Leonardi M, Librado P, Der Sarkissian C, Schubert M, Alfarhan AH, Alquraishi SA, Al-Rasheid KAS, Gamba C, Willerslev E, **Orlando L**. 2017. Evolutionary patterns and processes: lessons from ancient DNA. **Syst Biol** 66:e1-e29.
- 103) Fabre PH, Upham NS, Emmons LH, Justy F, Leite YL, Loss AC, **Orlando L**, Tilak MK, Patterson BD, Douzery EJ. 2017. Mitogenomic phylogeny, diversification, and biogeography of South American spiny rats. **Mol Biol Evol** 34:613-633.
- 104) Llamas B, Willerslev E, **Orlando L**. 2017. Human evolution: a tale from ancient genomes. **Phil Trans Roy Soc B** 372. pii:20150484.
- 105) MacHugh D, Larson G, **Orlando L**. 2017. Taming the Past: Ancient DNA and the Study of Animal Domestication. **Ann Rev Anim Biosci** 5:329-51.
- 106) Renaud G, Hanghøj K, Willerslev E, **Orlando L**. 2017. gargammel: a sequence simulator for ancient DNA. **Bioinformatics** 33:577-579.
- 107) Boessenkool S, Hanghøj K, Nistelberger HM, Der Sarkissian C, Gondek A, **Orlando L**, Barrett JH, Star B. 2017. Combining bleach and mild pre-digestion improves ancient DNA recovery from bones. **Mol Ecol Resour** 17:742-751.
- 108) Cucchi T, Mohaseb A, Peigne S, Debue K, **Orlando L**, Mashkour M. 2017. Detecting taxonomic and phylogenetic signals in equid cheek teeth: towards new palaeontological and archaeological proxies. **R Soc Open Sci** 4:160997.

- 109) Schubert M, Mashkour M, Gaunitz C, Fages A, Seguin-Orlando S, Sheikhi S, Alfarhan AH, Alquraishi SA, Al-Rasheid KAS, Chuang R, Ermini L, Gamba C, Vila E, Weinstock J, Vedat O, **Orlando L**. 2017. Zonkey: a fast, simple, accurate and sensitive method to genetically identify F1-equid hybrids in archaeological assemblages. **J Arc Sci** 78:147-157.
- 110) Cruz-Davalos DI, Llamas B, Gaunitz C, Fages A, Gamba C, Soubrier J, Librado P, Seguin-Orlando A, Pruvost M, Alfarhan AH, Al Quraishi SA, Al-Rasheid KAS, Scheu A, Benecke N, Ludwig A, Cooper A, Willerslev E, **Orlando L**. 2017. Experimental conditions improving in solution target enrichment for ancient DNA. **Mol Ecol Resour** 17:508-522.

2016 – Peer-reviewed

- 111) Gamba C, Hanghøj K, Gaunitz C, Alfarhan AH, Alquraishi SA, Al-Rasheid KA, Bradley DG, **Orlando L**. 2016. Comparing the performance of three ancient DNA extraction methods for high-throughput sequencing. **Mol Ecol Resour** 16:459-69.
- 112) Wutke S, Benecke N, Sandoval-Castellanos E, Döhle HJ, Friederich S, Gonzalez J, Hallsson JH, Hofreiter M, Löugas L, Magnell O, Morales-Muniz A, **Orlando L**, Pálsdóttir AH, Reissmann M, Ruttikay M, Trinks A, Ludwig A. Spotted phenotypes in horses lost attractiveness in the Middle Ages. 2016. **Sci Rep** 6:38548.
- 113) Wutke S, Andersson L, Benecke N, Sandoval-Castellano E, Gonzalez J, Hallstein Hallson J, Hofreiter M, Lougas L, Magnell O, Morales-Muniz A, **Orlando L**, Pálsdóttir AH, Reissmann M, Ruttikay M, Speller C, Trinks A, Ludwig A. The origin of ambling horses. 2016. The origin of ambling horses. **Curr Biol** 26:R697-R699.
- 114) Metcalf JL, Turney C, Barnett R, Martin F, Bray SC, Vilstrup JT, **Orlando L**, Salas-Gismondi R, Loponte D, Medina M, De Nigris M, Civalero T, Fernández PM, Gasco A, Duran V, Seymour KL, Otaola C, Gil A, Paunero R, Prevosti FJ, Bradshaw CJ, Wheeler JC, Borrero L, Austin JJ, Cooper A. 2016. Synergistic roles of climate warming and human occupation in Patagonian megafaunal extinctions during the Last Deglaciation. **Sci Adv** 2:e1501682.
- 115) Louvel G, Der Sarkissian C, Hanghøj K, **Orlando L**. 2016. metaBIT, an integrative and automated metagenomic pipeline for analyzing microbial profiles from high-throughput sequencing shotgun data. **Mol Ecol Resour** 16:1415-1427.
- 116) Orlando L. 2016. Back to the roots and routes of dromedary domestication. **PNAS** 113:6588-90.
- 117) Schubert M, Lindgreen S, **Orlando L**. 2016. AdapterRemoval v2: rapid adapter trimming, identification, and read merging. **BMC Res Notes** 9:88.
- 118) Bayerova Z, Janova E, Matiasovic J, **Orlando L**, Horin P. 2016. Positive selection in the SLC11A1 gene in the family Equidae. **Immunogenetics** 68:353-64.
- 119) Imsland F, McGowan K, Rubin CJ, Henegar C, Sundstrom E, Berglund J, Schwochow D, Gustafson U, Imsland P, Lindblad-Toh K, Lindgren G, Mikko S, Millon L, Wade C, Schubert M, **Orlando L**, Penedo MCT, Barsh GS, Andersson L. 2016. Regulatory mutations in TBX3 disrupt asymmetric hair pigmentation that underlies Dun camouflage color in horses. **Nat Genet** 48:152-8.
- 120) Sigsgaard EE, Nielsen IB, Bach SS, Lorenzen ED, Robinson DP, Knudsen SW, Pedersen MW, Jaidah MA, **Orlando L**, Willerslev E, Møller PR, Thomsen PF. 2016. Population characteristics of a large whale shark aggregation inferred from seawater environmental DNA. **Nat Ecol Evol** 1:4.
- 121) Guillot G, Jónsson H, Hinge A, Mançhik N, **Orlando L**. 2016. Accurate continuous geographic assignment from low- to high-density SNP data. **Bioinformatics** 32:1106-8.
- 122) Soubrier J, Gower G, Chen K, Richards SM, Llamas B, Mitchell KJ, Ho SY, Kosintsev P, Lee MS, Baryshnikov G, Bollongino R, Bover P, Burger J, Chivall D, Crégut-Bonnouere E, Decker JE, Doronichev VB, Douka K, Fordham DA, Fontana F, Fritz C, Glimmerveen J, Golovanova LV, Groves C, Guerreschi A, Haak W, Higham T, Hofman-Kamińska E, Immel A, Julien MA, Krause J, Krotova O, Langbein F, Larson G, Rohrlach A, Scheu A, Schnabel RD, Taylor JF, Tokarska M, Tosello G, van der Plicht J, van Loenen A, Vigne JD, Wooley O, **Orlando L**, Kowalczyk R, Shapiro B, Cooper A. 2016. Early cave art and ancient DNA record the origin of European bison. **Nat Comms** 7:13158.
- 123) Librado P, Fages A, Gaunitz C, Leonardi M, Wagner S, Khan N, Hanghøj K, Alquraishi SA, Alfarhan AH, Al-Rasheid KA, Der Sarkissian C, Schubert M, **Orlando L**. 2016. The Evolutionary Origin and Genetic Makeup of Domestic Horses. **Genetics** 204:423-434.
- 124) Hanghøj K, Seguin-Orlando A, Schubert M, Madsen T, Pedersen JS, Willerslev E, **Orlando L**. 2016. Fast, accurate and automatic ancient nucleosome and methylation maps with epiPALEOMIX. **Mol Biol Evol** 33:3284-3298.
- 125) Pedersen MW, Ruter A, Schweger C, Friebe H, Staff RA, Kjeldsen KK, Mendoza ML, Beaudoin AB, Zutter C, Larsen NK, Potter BA, Nielsen R, Rainville RA, **Orlando L**, Meltzer DJ, Kjær KH, Willerslev E. 2016. Postglacial viability and colonization in North America's ice-free corridor. **Nature** 537:45-49.
- 126) Fernandez R, Schubert M, Vargas AM, Brownlow A, Vikingsson GA, Siebert U, Jensen LF, Øien N, Wall D, Rogan E, Mikkelsen B, Dabin W, Alfarhan AH, Alquraishi SA, Al-Rasheid KAS, Guillot G, **Orlando L**. 2016. A genome-wide catalogue of single nucleotide polymorphisms in white-beaked and atlantic white-sided dolphins. **Mol Ecol Resour** 16:266-76.

2015 – Peer-reviewed

- 127) Wales N, Carøe C, Sandoval-Velasco M, Gamba C, Barnett R, Samaniego JA, Madrigal JR, **Orlando L**, Gilbert MTP. 2015. New insights on single-stranded vs. double-stranded DNA library preparation for ancient DNA. **Biotechniques** 59:368-71.
- 128) Librado P, Der Sarkissian C, Ermini L, Schubert M, Jónsson H, Albrechtsen A, Fumagalli M, Yang MA, Gamba C, Seguin-Orlando A, Mortensen CD, Petersen B, Hoover CA, Lorente-Galdos B, Nedoluzhko A, Boulygina E, Tsygankova S, Neuditschko M, Jagannathan V, Thèves C, Alfarhan AH, Alquraishi SA, Al-Rasheid KAS, Sicheritz-Ponten T, Popov R, Grigoriev S, Alekseev AN, Rubin EM, McCue M, Rieder S, Leeb T, Tikhonov A, Crubézy E, Slatkin MW, Marques-Bonet T, Nielsen R, Willerslev E, Kantanen J, Prokhortchouk E, **Orlando L**. 2015. Tracking the origins of Yakutian horses and the genetic basis for their fast adaptation to subarctic environments. **PNAS** 112:E6889-97.
- 129) Madsen CL, Vilstrup JT, Fernandez R, Marchi N, Hakansson B, Krog M, Asferg T, Baagøe H, **Orlando L**. 2015. Mitochondrial Genetic Diversity of Eurasian Red Squirrels (*Sciurus vulgaris*) from Denmark. **J Hered** 106:719-27.
- 130) Rasmussen S, Allentoft ME, Nielsen K, **Orlando L**, Sikora M, Sjögren KG, Gorm Pedersen A, M Schubert, Van Dam A, Kapel CMO, Nielsen HB, Brunak S, Avetisyan P, Epimakhov A, Khalyapin MV, Gnuni A, Kriiska A, Lasak I, Metspalu M, Moiseyev V, Gromov A, Pokutta D, Saag L, Varul L, Yepiskoposyan L, Sicheritz-Pontén T, Foley RA, Lahr MM, Nielsen R, Kristiansen K, Willerslev E. 2015. Early Divergent Strains of *Yersinia pestis* in Eurasia 5,000 Years Ago. **Cell** 163:571-82.
- 131) **Orlando L**. 2015. The first aurochs genome revisits the breeding history of British and European cattle. **Genome Biol** 16:225.
- 132) **Orlando L**. 2015. Equids. **Curr Biol** 25:R973-8.
- 133) Der Sarkissian C, Ermini L, Schubert M, Yang MA, Librado P, Fumagalli M, Jonsson H, Bar-Gal GK, Albrechtsen A, Vieira FG, Petersen B, Ginolhac A, Seguin-Orlando A, Magnussen K, Fages A, Gamba C, Lorente-Galdos B, Polani S, Steiner C, Neuditschko M, Jagannathan V, Feh C, Greenblat CL, Ludwig A, Abramson NI, Zimmermann W, Schafberg R, Tikhonov A, Sicheritz-Ponten T, Willerslev E, Marques-Bonet T, Ryder OA, McCue M, Rieder S, Leeb T, Slatkin M, **Orlando L**. 2015. Evolutionary genomics and conservation of the endangered Przewalski's horse. **Curr Biol** 25:2577-83.
- 134) Rasmussen M, Sikora M, Albrechtsen A, Korneliusen TS, Moreno-Mayar JV, Poznick GD, Zollikofer CPE, Ponce de Leon M, Allentoft ME, Moltke I, Jonsson H, Valdiosera C, Malhi RS, Orlando L, Bustamante C, Stafford TW, Meltzer D, Nielsen R, Willerslev E. 2015. The ancestry and affiliations of Kennewick Man. **Nature** 523:455-8.
- 135) **Orlando L**, Gilbert MT, Willerslev E. 2015. Reconstructing ancient genomes and epigenomes. **Nat Rev Genet** 16:395-408.
- 136) Seguin-Orlando A*, Gamba C*, Der Sarkissian C, Ermini L, Louvel G, Boulygina E, Sokolov A, Nedoluzhko A, Lorenzen E, Lopez P, McDonald HG, Scott E, Tikhonov A, Stafford TW, Shapiro B, Willerslev E, Prokhortchouk E, **Orlando L**. 2015. Pros and cons of methylation-based enrichment methods for ancient DNA. **Sci Rep** 5:11826.
- 137) Damgaard PB, Margaryan A, Schroeder H, **Orlando L**, Willerslev E, Allentoft M. 2015. Improving access to endogenous DNA in ancient bones and teeth. **Sci Rep** 5:11184.
- 138) Wilting A, Courtiol A, Christiansen P, Niedballa J, Scharf AK, **Orlando L**, Balkenhol N, Hofer H, Kramer-Schadt S, Fickel J, Kitchener AC. 2015. Planning tiger recovery: Understanding intraspecific variation for effective conservation. **Sci Adv** 1:e1400175.
- 139) Hestand MS, Kalbfleisch TS, Coleman J, Zeng Z, Liu J, **Orlando L**, MacLeod JN. 2015. Annotation of the protein coding regions of the equine genome. **PLoS One** 10:e0124375.
- 140) Rebolledo-Mendez J, Hestand MS, Coleman SJ, Zeng Z, **Orlando L**, MacLeod JN, Kalbfleisch T. 2015. Comparison of the Equine Reference Sequence with its Sanger Source Data and new Illumina Reads. **PLoS One** 10:e0126852.
- 141) Allentoft ME, Sikora M, Sjögren KG, Rasmussen S, Rasmussen M, Stenderup J, Damgaard PB, Schroeder H, Ahlstrom T, Vinner L, Malaspinas AS, Margaryan A, Higham T, Chivall D, Lynnerup N, Harvig L, Baron J, Della Casa P, Dabrowski P, Duffy PR, Ebel AV, Epimakhov A, Frei K, Furmanek M, Gralak T, Gromov A, Gronkiewicz S, Grupe G, Hajdu T, Jarysz R, Khartanovich V, Khokhlov A, Kiss V, Kolar J, Kriiska A, Laak I, Longhi C, McGlynn G, Merkevicius A, Merkyte I, Metspalu M, Mkrtychyan R, Moiseyev V, Paja L, Plafi G, Polutta D, Pospieszny L, Price TD, Saag L, Sablin M, Shishlina N, Smrcka V, Soenov VI, Szeverenyi V, Toth G, Trifanova SV, Varul L, Vicze M, Yepiskoposyan L, Zhitenev V, **Orlando L**, Sicheritz-Ponten T, Brunak S, Nielsen R, Kristiansen K, Willerslev E. 2015. Population genomics of Bronze Age Eurasia. **Nature** 522:167-172.
- 142) Seguin-Orlando A, Hoover CA, Vasiliev SK, Ovodov ND, Shapiro B, Cooper A, Rubin EM, Willerslev E, **Orlando L**. 2015. Amplification of TruSeq ancient DNA libraries with Accuprime Pfx: consequences on nucleotide misincorporation and methylation patterns. **STAR** 1:STAR2015112054892315Y.0000000005.
- 143) Schroeder H, Avila-Arcos MC, Malaspinas AS, Poznick GD, Sandoval Velasco M, Carpenter ML, Moreno-Mayar JV, Siora M, Johnson PLF, Allentoft ME, Samaniego A, Havisser JB, Dee MW, Stafford TW, Salas A, **Orlando L**, Willerslev E, Bustamante CD, Gilbert MTP. 2015. Genome-wide ancestry of 17th-century enslaved Africans from the Caribbean. **PNAS** 112:3669-73.

- 144) Der Sarkissian C, Vilstrup J, Schubert M, Seguin-Orlando A, Eme D, Weinstock J, Alberdi MT, Martin F, Lopez P, Prado J, Prieto A, Douady CJ, Stafford T, Willerslev E, **Orlando L**. 2015. Mitochondrial genomes reveal the extinct *Hippidion* as an outgroup to all living equids. **Biol Lett** 11:20141058.
- 145) Ersmark E, **Orlando L**, Sandoval-Castellanos E, Barnes I, Barnett R, Stuart A, Lister A, Dalen L. 2015. Population demography and genetic diversity in the Pleistocene Cave lion. **Open Quaternary** 1:1-15.
- 146) Welker F, Collins MF, Thomas JA, Wadsley M, Brace S, Cappellini E, Turvey ST, Reguero M, Gelfo JN, Kramarz A, Burger J, Thomas-Oates J, Ashford DA, Ashton P, Rowsell K, Porter DM, Kessler B, Fisher R, Baessmann C, Kaspar S, Olsen J, Kiley P, Elliott JA, Kelstrup C, Mullin V, Hofreiter M, Willerslev E, Hublin JJ, **Orlando L**, Barnes I, MacPhee RDE. 2015. Ancient proteins resolve the evolutionary history of Darwin's South American Ungulates. **Nature** 522:81-4.
- 147) Perry GH, **Orlando L**. 2015. Ancient DNA and human evolution. **J Hum Evol** 79:1-3.
- 148) Ermini L, Der Sarkissian C, Willerslev E, **Orlando L**. 2015. Major transitions in human evolution revisited: a tribute to ancient DNA. **J Hum Evol** 79:4-20.
- 149) Der Sarkissian C, Allentoft M, Avila-Arcos M, Barnett R, Campos PF, Cappellini E, Ermini L, Fernandez R, da Fonseca R, Ginolhac A, Hansen AJ, Jonsson H, Korneliusson T, Margaryan A, Martin MD, Moreno-Mayar JV, Raghavan M, Rasmussen M, Sandoval Velasco M, Schroeder H, Schubert M, Seguin-Orlando A, Wales NA, Gilbert MTP, Willerslev E, **Orlando L**. 2015. Ancient Genomics. **Philos Trans R Soc Lond B Biol Sci** 370:20130387.
- 150) Pedersen MW, Overballe-Petersen S, Ermini L, Sarkissian CD, Haile J, Hellstrom M, Spens J, Thomsen PF, Bohmann K, Cappellini E, Schnell IB, Wales NA, Carøe C, Campos PF, Schmidt AM, Gilbert MT, Hansen AJ, **Orlando L**, Willerslev E. 2015. Ancient and modern Environmental DNA. **Philos Trans R Soc Lond B Biol Sci** 370:20130383.

2014 – Peer-reviewed

- 151) Schubert M, Jónsson H, Chang D, Der Sarkissian C, Ermini L, Ginolhac A, Albrechtsen, Dupanloup I, Foucal A, Petersen B, Fumagalli M, Raghavan M, Seguin-Orlando A, Korneliusson T, Velazquez AMV, Stenderup J, Hoover CA, Rubin CJ, Alfarhan AH, Alqurqishi SA, Al-Rasheid KAS, MacHugh DE, Kalbfleisch T, MacLeod JN, Rubin EM, Sicheritz-Ponten T, Andersson L, Hofreiter M, Marques-Bonet T, Gilbert MTP, Nielsen R, Excoffier L, Willerslev L, Shapiro B, **Orlando L**. 2014. Prehistoric genomes reveal the genetic foundation and cost of horse domestication. **PNAS** 111:E5661-9.
- 152) Jónsson H, Schubert M, Seguin-Orlando A, Ginolhac A, Petersen L, Fumagalli M, Albrechtsen A, Petersen B, Korneliusson TS, Vilstrup JT, Lear T, Myka JL, Lundquist J, Miller DC, Alfarhan AH, Alqurqishi SA, Al-Rasheid KA, Stagegaard J, Strauss G, Bertelsen MF, Sicheritz-Ponten T, Antczak DF, Bailey E, Nielsen R, Willerslev E, **Orlando L**. 2014. Speciation with gene flow in equids despite extensive chromosomal plasticity. **PNAS** 111:18655-60.
- 153) Zhang G, Li C, Li Q, Li B, Larkin DM, Lee C, Storz JF, Antunes A, Greenwold MJ, Meredith RW, Ödeen A, Cui J, Zhou Q, Xu L, Pan H, Wang Z, Jin L, Zhang P, Hu H, Yang W, Hu J, Xiao J, Yang Z, Liu Y, Xie Q, Yu H, Lian J, Wen P, Zhang F, Li H, Zeng Y, Xiong Z, Liu S, Zhou L, Huang Z, An N, Wang J, Zheng Q, Xiong Y, Wang G, Wang B, Wang J, Fan Y, da Fonseca RR, Alfaro-Núñez A, Schubert M, **Orlando L**, Mourier T, Howard JT, Ganapathy G, Pfenning A, Whitney O, Rivas MV, Hara E, Smith J, Farré M, Narayan J, Slavov G, Romanov MN, Borges R, Machado JP, Khan I, Springer MS, Gates J, Hoffmann FG, Opazo JC, Håstad O, Sawyer RH, Kim H, Kim KW, Kim HJ, Cho S, Li N, Huang Y, Bruford MW, Zhan X, Dixon A, Bertelsen MF, Derryberry E, Warren W, Wilson RK, Li S, Ray DA, Green RE, O'Brien SJ, Griffin D, Johnson WE, Haussler D, Ryder OA, Willerslev E, Graves GR, Alström P, Fjeldså J, Mindell DP, Edwards SV, Braun EL, Rahbek C, Burt DW, Houde P, Zhang Y, Yang H, Wang J, Avian Genome Consortium, Jarvis ED, Gilbert MTP, Wang J. Comparative genomics reveals insights into avian genome evolution and adaptation. 2014. **Science** 346:1311-1320.
- 154) Jarvis ED, Mirarab S, Aberer AJ, Li B, Houde P, Li C, Ho SYW, Faircloth BC, Nabholz B, Howard JT, Suh A, CC Weber, RR da Fonseca, Li J, Zhang F, Li H, Zhou L, Narula N, Liu L, Ganapathy G, Boussau B, Bayzid MM, Zavidovych V, Subramanian S, Gabaldón T, Capella-Gutiérrez S, Huerta-Cepas J, Rekepalli B, Munch K, Schierup M, Lindow B, WC Warren, Ray D, Green RE, Bruford MW, Zhan X, Dixon A, Li S, Li N, Huang Y, Derryberry EP, Bertelsen MF, Sheldon FH, Brumfield RT, Mello CV, Lovell PV, Wirthlin M, Schneider MPC, Prosdociami F, Samaniego JA, Velazquez AMV, Alfaro-Núñez A, Campos PF, Petersen B, Sicheritz-Ponten T, Pas A, Bailey T, Scofield P, Bunce M, Lambert DM, Zhou Q, Perelman P, Driskell AC, Shapiro B, Xiong Z, Zeng Y, Liu S, Li Z, Liu B, Wu K, Xiao J, Yinqi X, Zheng Q, Zhang Y, Yang H, Wang J, Smeds L, Rheindt FE, Braun M, Fjeldsa J, **Orlando L**, Barker FK, Jónsson KA, Johnson W, Koepfli KP, O'Brien S, Haussler D, Ryder OA, Rahbek C, Willerslev E, Graves GR, Glenn TC, McCormack J, Burt D, Ellegren H, Alström P, Edwards SV, Stamatakis A, Mindell DP, Cracraft J, Braun EL, Warnow T, Jun W, Gilbert MTP, Zhang G. 2014. Whole-genome analyses resolve early branches in the tree of life of modern birds. **Science** 346:1320-1331.
- 155) Malaspinas AS, Lao O, Schroeder H, Rasmussen M, Raghavan M, Moltke I, Campos PF, Santana Sagredo D, Rasmussen S, Goncalves VF, Albrechtsen A, Allentoft ME, Johnson PLF, Li M, Reis S, Bernardo DV, DeGiorgio M, Duggan AT, Bastos M, Wang Y, Stenderup J, Moreno-Mayar VJ, Brunak S, Sicheritz-Ponten T, Hodges E, Hannon GJ, **Orlando L**, Price DT, Jensen JD, Nielsen R, Heinemeier J, Olsen J, Rodrigues-Carvalho C, Mirazon Lahr M,

- Neves W, Kayser M, Higham T, Stoneking M, Pena SDJ, Willerslev E. 2014. Two ancient human genomes reveal Polynesian ancestry among the indigenous Botocudos of Brazil. **Curr Biol** 24:20-22.
- 156) Seguin-Orlando A, Korneliussen TS, Sikora M, Malaspinas AS, Manica A, Moltke I, Albrechtsen A, Ko A, Margaryan A, Moiseyev V, Goebel T, Westaway M, Lambert D, Khartanovich V, Wall JD, Nigst PR, Foley RA, Lahr MM, Nielsen R, Orlando L, Willerslev E. 2014. Paleogenomics. Genomic structure in Europeans dating back at least 36,200 years. **Science** 346:1113-1118.
- 157) Orlando L, Willerslev E. 2014. An epigenetic window into the past? **Science** 345:511-512.
- 158) 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, Malaspinas 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, Villemis R, Crawford MH, Nielsen FC, Dissing J, Heinemeier J, Meldgaard M, Bustamante C, O'Rourke DH, Jakobsson M, Gilbert MT, Nielsen R, Willerslev E. 2014. The genetic prehistory of the New World Arctic. **Science** 345:1255-1259.
- 159) Orlando L, Cooper A. 2014. Using ancient DNA to understand evolutionary and ecological process. **Annu Rev Ecol Evol Syst** 45:573-98.
- 160) Fabre PH, Vilstrup JT, Raghavan M, Der Sarkissian C, Willerslev E, Douzery EJP, Orlando L. 2014. Rodents of the Caribbean: origin and diversification of hutias unraveled by next-generation museomics. **Biol Lett** 10:20140266.
- 161) Schubert M, Ermini L, Sarkissian CD, Jónsson H, Ginolhac A, Schaefer R, Martin MD, Fernández R, Kircher M, McCue M, Willerslev E, Orlando L. 2014. Characterization of ancient and modern genomes by SNP detection and phylogenomic and metagenomic analysis using PALEOMIX. **Nat Protoc** 9:1056-82.
- 162) Orlando L. 2014. A 400,000-year-old mitochondrial genome questions phylogenetic relationships amongst archaic hominins. **Bioessays** 36:598-605.
- 163) Liu S*, Lorenzen ED*, Fumagalli M*, Li B, Harris K, Xiong Z, Zhou L, Korneliussen TS, Somel M, Babbitt C, Wray G, Li J, He W, Wang Z, Fu W, Xiang X, Morgan CC, Dherty A, O'Connell MJ, McInerney JO, Born EW, Dalen L, Dietz R, Orlando L, Sonne C, Zhang G, Nielsen R, Willerslev E, Wang J. 2014. Population genomics reveal recent speciation and rapid evolutionary adaptation in polar bears. **Cell** 157:785-94.
- 164) Der Sarkissian C*, Ermini L*, Jonsson H, Alekseev A, Crubezy E, Shapiro B, Orlando L. 2014. Shotgun Microbial Profiling of Fossil Remains. **Mol Ecol** 23:1780-98.
- 165) Rasmussen M, Anzick SL, Waters MR, Skoglund P, DeGiorgio M, Stafford TW Jr, Rasmussen S, Moltke I, Albrechtsen A, Doyle SM, Poznick GD, Gudmundsdottir V, Yadav R, Malaspinas AS, Stockton White SV, Allentoft ME, Cornejo OE, Tambets K, Eriksson A, Heintzman PD, Karmin M, Korneliussen 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. 2014. The genome of a Late Pleistocene human from a Clovis burial site in western Montana. **Nature** 506:225-9.
- 166) Willerslev E, Davidson J, Moora M, Zobel M, Coissac E, Edwards ME, Lorenzen ED, Vestergaard M, Gussarova G, Haile J, Craine J, Bergmann G, Gielly L, Boessenkool S, Epp LS, Pearman PB, Cheddadi R, Murray D, Brathen KA, Yoccoz N, Binney H, Cruaud C, Winckler P, Goslar T, Aslos IG, Bellemain E, Brysting AK, Elven R, Sonstebo JH, Murton J, Sher A, Rasmussen M, Ronn R, Mourier T, Cooper A, Austin J, Moller P, Froese D, Zazula G, Pompanon F, Rioux D, Niderkorn V, Tikhonov A, Savvinov G, Roberts RG, MacPhee RDE, Gilbert MTP, Kjaer KH, Orlando L, Brochmann C, Taberlet P. 2014. Fifty thousand years of arctic vegetation and megafaunal diet. **Nature** 506:47-51.
- 167) Pedersen JS, Valen E, Vargas Velazques 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. 2014. Genome-wide nucleosome map and cytosine methylation levels of an ancient human genome. **Genome Res** 24:454-66.
- 168) 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, Magi R, Campos PF, Balanovska E, Balanovsky O, Khusnutdinova E, Litvinov S, Osipova LP, Fedorova SA, Voevoda MI, DeGiorgio M, Sicheritz-Ponten T, Brunak S, Bemeshchenko S, Kivisild T, Villemis R, Nielsen R, Jakobsson M, Willerslev E. 2014. Upper Palaeolithic Siberian genome reveals dual ancestry of Native Americans. **Nature** 505:87-91.

2013 – Peer-reviewed

- 169) 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, Korneliussen T, Malaspinas 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 C, 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. 2013. Recalibrating *Equus* evolution using the genome sequence of an early Middle Pleistocene horse. **Nature** 499:74-8.

- 170) Overballe-Petersen S*, Harms K*, **Orlando L**, Moreno Mayar JV, Rasmussen S, Dahl TW, Rosing MT, Poole AM, Sicheritz-Ponten T, Brunak S, Inselmann S, de Vries J, Wackernagel W, Pybus OG, Nielsen R, Johnsen PJ, Nielsen KM, Willerslev E. 2013. Bacterial natural transformation by highly fragmented and damaged DNA. **PNAS** 110:19860-5.
*Equal contributors
- 171) Martin MD, Cappellini E, Samaniego JA, Zepeda ML, Campos PF, Seguin-Orlando A, Wales N, **Orlando L**, Ho SY, Dietrich FS, Mieczkowski PA, Heitman J, Willerslev E, Krogh A, Ristaino JB, Gilbert MT. 2013. Reconstructing genome evolution in historic samples of the Irish potato famine pathogen. **Nat Comms** 4:2172.
- 172) Zhang H, Pajimans J, Chang F, Wu X, Chen G, Lei C, Yang X, Wei Z, Bradley DG, **Orlando L**, O'Connor T, Hofreiter M. 2013. Morphological and genetic evidence for early Holocene cattle management in North-Eastern China. **Nat Comms** 4:2755.
- 173) Jónsson H, Ginolhac A, Schubert M, Johnson PL, **Orlando L**. 2013. mapDamage 2.0: fast approximate Bayesian estimates of ancient DNA damage parameters. **Bioinformatics**. 29:1682-4.
- 174) Vilstrup JT, Seguin-Orlando A, Stiller M, Ginolhac A, Raghavan M, Nielsen SCA, Weinstock J, Froese D, Vasiliev SK, Ovodov ND, Clary J, Helgen KM, Fleischer RC, Cooper A, Shapiro B, **Orlando L**. 2013. Mitochondrial phylogenomics of modern and ancient equids. **PLoS ONE** 8:e55950.
- 175) Seguin-Orlando A, Schubert M, Clary J, Stagegaard J, Alberdi JT, Prado JL, Prieto A, Willerslev E, **Orlando L**. 2013. Ligation bias in Illumina next-generation DNA libraries: implications for sequencing ancient genomes. **PLoS ONE** 8:e78575.
- 176) Pedersen MW, Ginolhac A, **Orlando L**, Olsen J, Andersen K, Holm J, Funder S, Willerslev E, Kjaer KH. 2013. A comparative study of ancient environmental DNA to pollen and macrofossils from lake sediments reveals taxonomic overlap and additional plant taxa. **Quat Sci Rev** 75:161-8.
- 177) Cardoso JL, Vilstrup JT, Eisenmann V, **Orlando L**. 2013. First evidence of *Equus asinus* in the Chalcolithic disputes the Phoenicians as the first to introduce donkeys into the Iberian Peninsula. **J Arc Sci** 40:4483-90.

2012 – Peer-reviewed

- 178) Biagini P, Thèves C, Balaesque P, Géraud A, Cannet C, Keyser C, Nikolaeva D, Gérard P, Duchesne S, **Orlando L**, Willerslev E, Alekseev AN, de Micco P, Ludes B, Crubézy E. 2012. Variola virus in a 300-year-old Siberian mummy. **N Engl J Med** 367:2057-9.
- 179) Parducci L, Jorgensen T, Tollesfrud MM, Elverland E, Alm T, Fontana SL, Bennett KD, Haile J, Matetovici I, Suyama Y, Edwards ME, Andersen K, Rasmussen M, Boessenkool S, Coissac E, Brochmann C, Taberlet P, Houmark-Nielsen M, Larsen NK, **Orlando L**, Gilbert MT, Kjaer KH, Alsos IG, Willerslev E. 2012. Glacial survival of boreal trees in northern Scandinavia. **Science** 335:1083-6.
- 180) Sánchez-Quinto F, Schroeder H, Ramirez O, Avila-Arcos MC, Pybus M, Olalde I, Velazquez AM, Marcos ME, Encinas JM, Bertranpetit J, **Orlando L**, Gilbert MT, Lalueza-Fox C. 2012. Genomic affinities of two 7,000-year-old Iberian hunter-gatherers. **Curr Biol** 22:1494-9.
- 181) Schubert M, Ginolhac A, Lindgreen S, Thompson JF, Al-Rasheid KA, Willerslev E, Krogh A, **Orlando L**. 2012. Improving ancient DNA read mapping against modern reference genomes. **BMC Genomics** 13:178.
- 182) Ginolhac A, Vilstrup J, Stenderup J, Rasmussen M, Stiller M, Shapiro B, Zazula G, Froese D, Steinmann KE, Thompson JF, Al-Rasheid K, Gilbert TMP, Willerslev E, **Orlando L**. 2012. Improving the performance of true-Single Molecule Sequencing for ancient DNA. **BMC Genomics** 13:177.
- 183) Overballe-Petersen S, **Orlando L**, Willerslev E. 2012. Next-generation sequencing offers new insights into DNA degradation. **Trends Biotechnol** 30:364-8.
- 184) Mourier T, Ho SY, Gilbert MT, Willerslev E, **Orlando L**. 2012. Statistical guidelines for detecting past population shifts using ancient DNA. **Mol Biol Evol** 29:2241-51.
- 185) Dalen L, **Orlando L**, Shapiro B, Brandstrom-Durling M, Quam R, Gilbert MT, Diez Fernandez-Lomana JC, Willerslev E, Arsuaga JL, Gotherstrom A. 2012. Partial genetic turnover in Neandertals: continuity in the East and population replacement in the West. **Mol Biol Evol** 29:1893-7.
- 186) Cappellini E, Jensen LJ, Szklarczyk D, Ginolhac A, da Fonseca RA, Stafford TW, Holen SR, Collins MJ, **Orlando L**, Willerslev E, Gilbert MT, Olsen JV. 2012. Proteomic analysis of a pleistocene mammoth femur reveals more than one hundred ancient bone proteins. **J Proteome Res** 11:917-26.
- 187) Foote AD, Thomsen PF, Sveegaard S, Wahlberg M, Kielgast J, Kyhn LA, Salling AB, Galatius A, **Orlando L**, Gilbert MT. 2012. Investigating the potential use of environmental DNA (eDNA) for genetic monitoring of marine mammals. **PLoS One** 7:e41781.
- 188) Jacobsen MW, Hansen MM, **Orlando L**, Bekkevold D, Bernatchez L, Willerslev E, Gilbert MT. 2012. Mitogenome sequencing reveals shallow evolutionary histories and recent divergence time between morphologically and ecologically distinct European whitefish (*Coregonus spp.*). **Mol Ecol** 21:2727-42.
- 189) Thomsen PF, Kielgast J, Iversen LL, Wiuf C, Rasmussen M, Gilbert MT, **Orlando L**, Willerslev E. 2012. Monitoring endangered freshwater biodiversity using environmental DNA. **Mol Ecol** 21:2565-73.

- 190) Jørgensen T, Kjaer KH, Haile J, Rasmussen M, Boessenkool S, Andersen K, Coissac E, Taberlet P, Brochmann C, **Orlando L**, Gilbert MT, Willerslev E. 2012. Islands in the ice: detecting past vegetation on Greenlandic nunataks using historical records and sedimentary ancient DNA meta-barcoding. **Mol Ecol** 21:1980-8.
- 191) Jørgensen T, Haile J, Möller P, Andreev A, Boessenkool S, Rasmussen M, Kienast F, Coissac E, Taberlet P, Brochmann C, Bigelow NH, Andersen K, **Orlando L**, Gilbert MT, Willerslev E. 2012. A comparative study of ancient sedimentary DNA, pollen and microfossils from permafrost sediments of northern Siberia reveals long-term vegetational stability. **Mol Ecol** 21:1989-2003.
- 192) Andersen K, Bird KL, Rasmussen M, Haile J, Breuning-Madsen H, Kjaer KH, **Orlando L**, Gilbert MT, Willerslev E. 2012. Meta-barcoding of 'dirt' DNA from soil reflects vertebrate biodiversity. **Mol Ecol** 21:1966-79.
- 193) Yoccoz NG, Brathen KA, Gielly L, Haile J, Edwards ME, Goslar T, von Stedingk H, Brysting AK, Coissac E, Pompanon F, Thuiller W, Winckler C, Cruaud F, Gavory M, Rasmussen M, Gilbert MTP, **Orlando L**, Brochmann C, Willerslev E, Taberlet P. 2012. DNA from soil mirrors plant taxonomic and growth form diversity. **Mol Ecol** 21:3647-55.

2011 – Peer-reviewed

- 194) Lorenzen ED*, Nogués-Bravo D*, **Orlando L***, Weinstock J*, Binladen J*, Marske KA*, Ugan A, Borregaard MK, Gilbert MTP, Nielsen R, Ho SYW, Goebel T, Graf KE, Byers D, Stenderup JT, Rasmussen M, Campos PF, Leonard JA, Koepfli K-P, Froese D, Zazula G, Stafford Jr. TW, Aaris-Sørensen K, Batra P, Haywood AM, Singarayer JS, Valdes PJ, Boeskorov G, Burns JA, Davydov SP, Haile J, Jenkins DL, Kosintsev P, Kuznetsova T, Lai X, Martin LD, McDonald HG, Mol D, Meldgaard M, Munch K, Stephan E, Sablin M, Sommer RS, Sipko T, Scott E, Suchard MA, Tikhonov A, Willerslev R, Wayne RK, Cooper A, Hofreiter M, Sher A, Shapiro B, Rahbeck C, Willerslev E. 2011. Species-specific responses of Late Quaternary megafauna to climate and humans. **Nature** 479:359-64. * Equal Contributors
- 195) 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 F, Tridico S, Metspalu E, Nielsen K, Ávila- Arcos MC, Moreno-Mayar JV, Muller C, Dortch J, Gilbert MTP, Lund O, Wesolowska A, Karmin M, Weiner LA, Wang B, Li J, Tai S, Xiao F, Hanihara T, van Driem G, Jha AR, Ricaut F-X, de Knijff P, Migliano AB, Gallego-Romero I, Kristiansen K, Lambert DM, Brunak S, Forster P, Brinkmann B, Nehlich O, Bunce M, Richards M, Gupta R, Bustamante C, Krogh A, Foley RA, Lahr MM, Balloux F, Sicheritz-Pontén T, Vilems R, Nielsen R, Jun W, Willerslev E. 2011. An Aboriginal Australian genome reveals separate human dispersals into Asia. **Science** 334:94-8.
- 196) **Orlando L**, Ginolhac A, Raghavan M, Vilstrup J, Rasmussen M, Magnussen K, Steinmann K, Kapranov P, Thompson JF, Zazula G, Froese D, Moltke I, Shapiro B, Hofreiter M, Al-Rasheid KA, Gilbert MT, Willerslev E. 2011. True Single Molecule DNA Sequencing of a Pleistocene horse bone. **Genome Res** 21:1705-19.
- 197) Ginolhac A, Rasmussen M, Gilbert MT, Willerslev E, **Orlando L**. 2011. mapDamage: testing for damage patterns in ancient DNA sequences. **Bioinformatics** 27:2153-5.
- 198) Foote AD, Morin PA, Durban JW, Willerslev E, **Orlando L**, Gilbert MT. 2011. Out of the Pacific and back again: insights into the matrilineal history of Pacific killer whale ecotypes. **PLoS One** 6:e24980.
- 199) Vilstrup JT, Ho SY, Foote AD, Morin PA, Krieb D, Krützen M, Parra GJ, Robertson KM, de Stephanis R, Verborgh P, Willerslev E, **Orlando L**, Gilbert MT. 2011. Mitogenomic phylogenetic analyses of the Delphinidae with an emphasis on the Globicephalinae. **BMC Evol Biol** 11:65.

<2011 – Peer-reviewed

- 200) Campos PF, Kristensen T, **Orlando L**, Sher A, Kholodova MV, Gotherstrom A, Hofreiter M, Drucker DG, Kosintsev P, Tikhonov A, Baryshnikov GF, Willerslev E, Gilbert MT. 2010. Ancient DNA sequences point to a large loss of mitochondrial genetic diversity in the saiga antelope (*Saiga tatarica*) since the Pleistocene. **Mol Ecol** 19:4863-75.
- 201) Lari M, Rizzi E, Milani L, Corti G, Balsamo C, Vai S, Catalano G, Pilli E, Longo L, Condemi S, Giunti P, Hanni C, De Bellis G, **Orlando L**, Barbujani G, Caramelli D. 2010. The microcephalin ancestral allele in a Neanderthal individual. **PLoS One** 5:e10648.
- 202) Campos PF, Willerslev E, Sher A, **Orlando L**, Axelsson E, Tikhonov A, Aaris-Sorensen K, Greenwood AD, Kahlke RD, Kosintsev P, Krakhmalnaya T, Kuznetsova T, Lemey P, MacPhee R, Norris CA, Shepherd K, Suchard MA, Zazula GD, Shapiro B, Gilbert MT. 2010. Ancient DNA analyses exclude humans as the driving force behind late Pleistocene musk ox (*Ovibos moschatus*) population dynamics. **PNAS** 107:5675-80.
- 203) 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, Grunnow B, Meldgaard M, Andreasen C, Fedorova SA, Osipova LP, Higham TF, Ramsey CB, Hansen TV, Nielsen FC, Crawford MH, Brunak S, Sicheritz-Ponten T, Vilems R, Nielsen R, Krogh A, Wang J, Willerslev E. 2010. Ancient human genome sequence of an extinct Palaeo-Eskimo. **Nature** 463:757-62.

- 204) Orlando L, Metcalf JL, Alberdi MT, Telles-Antunes M, Bonjean D, Otte M, Martin F, Eisenmann V, Mashkour M, Morello F, Prado JL, Salas-Gismondi R, Shockey BJ, Wrinn PJ, Vasil'ev SK, Ovodov ND, Cherry MI, Hopwood B, Male D, Austin JJ, Hanni C, Cooper A. 2009. Revising the recent evolutionary history of equids using ancient DNA. **PNAS** 106:21754-21759.
- 205) Depaulis F, Orlando L, Hanni C. 2009. Using classical population genetics tools with heterochronous data: time matters! **PLoS One** 4:e5541.
- 206) Orlando L, Calvignac S, Schnebelen C, Douady CJ, Godfrey LR, Hanni C. 2008. DNA from extinct giant lemurs links archaeolemurids to extant indriids. **BMC Evol Biol** 8:121.
- 207) Orlando L, Male D, Alberdi MT, Prado JL, Prieto A, Cooper A, Hanni C. 2008. Ancient DNA clarifies the evolutionary history of American Late Pleistocene equids. **J Mol Evol** 66:533-8.
- 208) Valdiosera CE, Garcia-Garitagotia JL, Garcia N, Doadrio I, Thomas MG, Hanni C, Arsuaga JL, Barnes I, Hofreiter M, Orlando L, Gotherstrom A. 2008. Surprising migration and population size dynamics in ancient Iberian brown bears (*Ursus arctos*). **PNAS** 105:5123-8.
- 209) Krause J, Lalueza-Fox C, Orlando L, Enard W, Green RE, Burbano HA, Hublin JJ, Hanni C, Fordea J, de la Rasilla M, Bertranpetit J, Rosas A, Paabo S. 2007. The derived FOXP2 variant of modern humans was shared with Neandertals. **Curr Biol** 17:1908-2.
- 210) Levasseur A, Orlando L, Bailly X, Milinkovitch MC, Danchin EG, Pontarotti P. 2007. Conceptual bases for quantifying the role of the environment on gene evolution: the participation of positive selection and neutral evolution. **Biol Rev Camb Philos Soc** 82:551-72.
- 211) Krause J, Orlando L, Serre D, Viola B, Prufer K, Richards MP, Hublin JJ, Hanni C, Derevianko AP, Paabo S. 2007. Neanderthals in central Asia and Siberia. **Nature** 449:902-4.
- 212) Orlando L, Pages M, Calvignac S, Hughes S, Hanni C. 2007. Does the 43 bp sequence from an 800,000 year-old cretan dwarf elephantid really rewrite the textbook on mammoths? **Biol Lett** 3:57-9; discussion 60-3.
- 213) Orlando L, Hanni C, Douady CJ. 2007. Mammoth and elephant phylogenetic relationships: *Mammot americanum*, the missing outgroup. **Evol Bioinform Online** 3:45-51.
- 214) Orlando L, Mashkour M, Burke A, Douady CJ, Eisenmann V, Hanni C. 2006. Geographic distribution of an extinct equid (*Equus hydruntinus*: Mammalia, Equidae) revealed by morphological and genetical analyses of fossils. **Mol Ecol** 15:2083-93.
- 215) Orlando L, Darlu P, Toussaint M, Bonjean D, Otte M, Hanni C. 2006. Revisiting Neandertal diversity with a 100,000 year old mtDNA sequence. **Curr Biol** 16:R400-2.
- 216) Orlando L, Eisenmann V, Reynier F, Sondaar P, Hanni C. 2003. Morphological convergence in *Hippidion* and *Equus* (*Amerhippus*) South American equids elucidated by ancient DNA analysis. **J Mol Evol** 57:S29-40.
- 217) Orlando L, Leonard JA, Thenot A, Laudet V, Guerin C, Hanni C. 2003. Ancient DNA analysis reveals woolly rhino evolutionary relationships. **Mol Phylogenet Evol** 28:485-99.
- 218) Orlando L, Mauffrey JF, Cuisin J, Patton JL, Hanni C, Catzeflis F. 2003. Napoleon Bonaparte and the fate of an Amazonian rat: new data on the taxonomy of *Mesomys hispidus* (Rodentia: Echimyidae). **Mol Phylogenet Evol** 27:113-20.
- 219) Orlando L, Bonjean D, Bocherens H, Thenot A, Argant A, Otte M, Hanni C. 2001. Ancient DNA and the population genetics of cave bears (*Ursus spelaeus*) through space and time. 2002. **Mol Biol Evol** 19:1920-33.
- 220) Loreille O, Orlando L, Patou-Mathis M, Philippe M, Taberlet P, Hanni C. 2001. Ancient DNA analysis reveals divergence of the cave bear, *Ursus spelaeus*, and brown bear, *Ursus arctos*, lineages. **Curr Biol** 11:200-3.

Non-peer reviewed (7)

- 1) Orlando L. 2024. Aux origines de la plus belle conquête de l'humanité. *Archéologia* 632:32-35.
- 2) Orlando L. 2013. Decoding genomes of the past. *Biofutur* 349:28-30.
- 3) Orlando L. 2006. La Dame de Vix: prince ou princesse? In: *Les Maux de nos ancêtres*. Pour la Science HS 50, January-March 2006.
- 4) Orlando L. 2006. Les tests ADN face aux énigmes de l'Histoire. In: *Les Maux de nos ancêtres*. Pour la Science HS 50, January-March 2006.
- 5) Orlando L, Hanni C. 2001. La génétique Néandertalienne et l'origine de l'Homme. *Medecine Sciences* 17:273-277.
- 6) Orlando L, Hanni C. 2000. De l'ADN fossile à l'ARN ancien: le cas de la grippe espagnole. *Medecine Sciences* 16:1269-70.
- 7) Orlando L, Hanni C. 2000. Du nouveau pour l'ADN ancien. *Médecine Sciences* 8-9:I-XVI.

Books, Chapters (12)

- 1) MONTPELLIER
- 2) Orlando L. 2023. *La Conquête du Cheval. Une histoire génétique*. Odile Jacob (EAN13:9782415004361).

- 3) **Orlando L.** 2021. L'ADN fossile, une machine à remonter le temps. Odile Jacob (EAN13:9782738154231).
- 4) Clément J, Spruyt M, Davoudi H, Fages A, Mashkour M, Mosaheb A, **Orlando L.** 2020. Les chevaux antiques du plateau iranien: entre étude philologique, examen iconographique, recherche archéozoologique et analyse paléogénétique. In: Croiser les sciences pour lire les animaux. Baratay E eds, Editions Sorbonne (ISBN-13: 979-1035105884).
- 5) Fémélat A, Macé M, **Orlando L.** 2020. Les chevaux de Léonard de Vinci. Regards croisés entre histoire de l'art, mathématiques et biologie. In: Croiser les sciences pour lire les animaux. Baratay E eds, Editions Sorbonne (ISBN-13:979-1035105884).
- 6) **Orlando L.** 2019. L'ADN ancien comme nouvelle source historique. In: Aux sources de l'histoire animale. Baratay E eds, Editions Sorbonne (ISBN-13 : 979-1035103446).
- 7) **Orlando L.** 2018. An ancient DNA perspective on horse evolution. In: Paleogenomics. Linqvist C, Rajora OP eds. Springer, pp 325-351.
- 8) Hanghøj K, **Orlando L.** 2018. Ancient epigenetics. Springer. In: Paleogenomics. Linqvist C, Rajora OP eds. Springer, pp 75-111.
- 9) **Orlando L,** Hanni C. 2014. Neandertal evolution and human origins: a tale from the Scladina child. In: The juvenile Neandertal facial remains from Scladina Cave. Etudes et Recherches Archéologiques de l'Université de Liège, pp 379-394.
- 10) **Orlando L,** Hanni C. 2011. Twelve years of Neandertal genetic discoveries: state-of-the-art and future challenges. In: Continuity and Discontinuity in the peopling of Europe. Vertebrate Paleobiology and Paleanthropology, Condemi S, Weinger GC eds, Springer, Netherlands. pp 223-238
- 11) **Orlando L.** 2005. L'origine de l'humanité et l'homme de Néandertal. In: Sur les chemins de la découverte, Farouki N eds, Presses Universitaires de France. 256 pp., ISBN: 978-2130547587
- 12) **Orlando L.** 2005. L'anti-Jurassic Park. Faire parler l'ADN fossile. Belin/Pour la Science, collection Regards. 271 pp., ISBN: 978-2701141367
- 13) Ginolhac A, **Orlando L,** Hanni C. 2003. Determination du sexe de la "Dame" de Vix. In: La tombe princière de Vix, C. Rolley eds, Editions Picard, 383 pp. ISBN: 978-2708406971