

Supplementary materials for this manuscript include the following:

Figure S1

Figure S2

Supplementary Text

Table S1

Table S2

Figure S1. Map representing the geographical regions considered for the analysis. Each color represents one area.

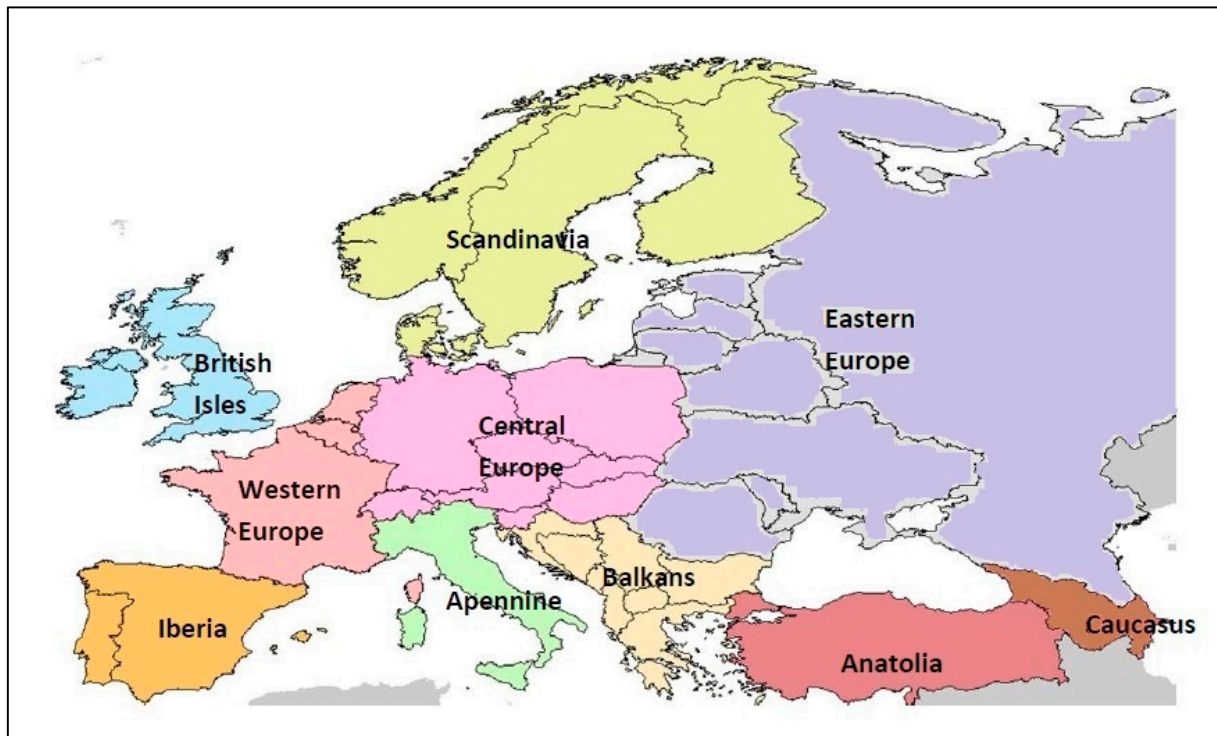
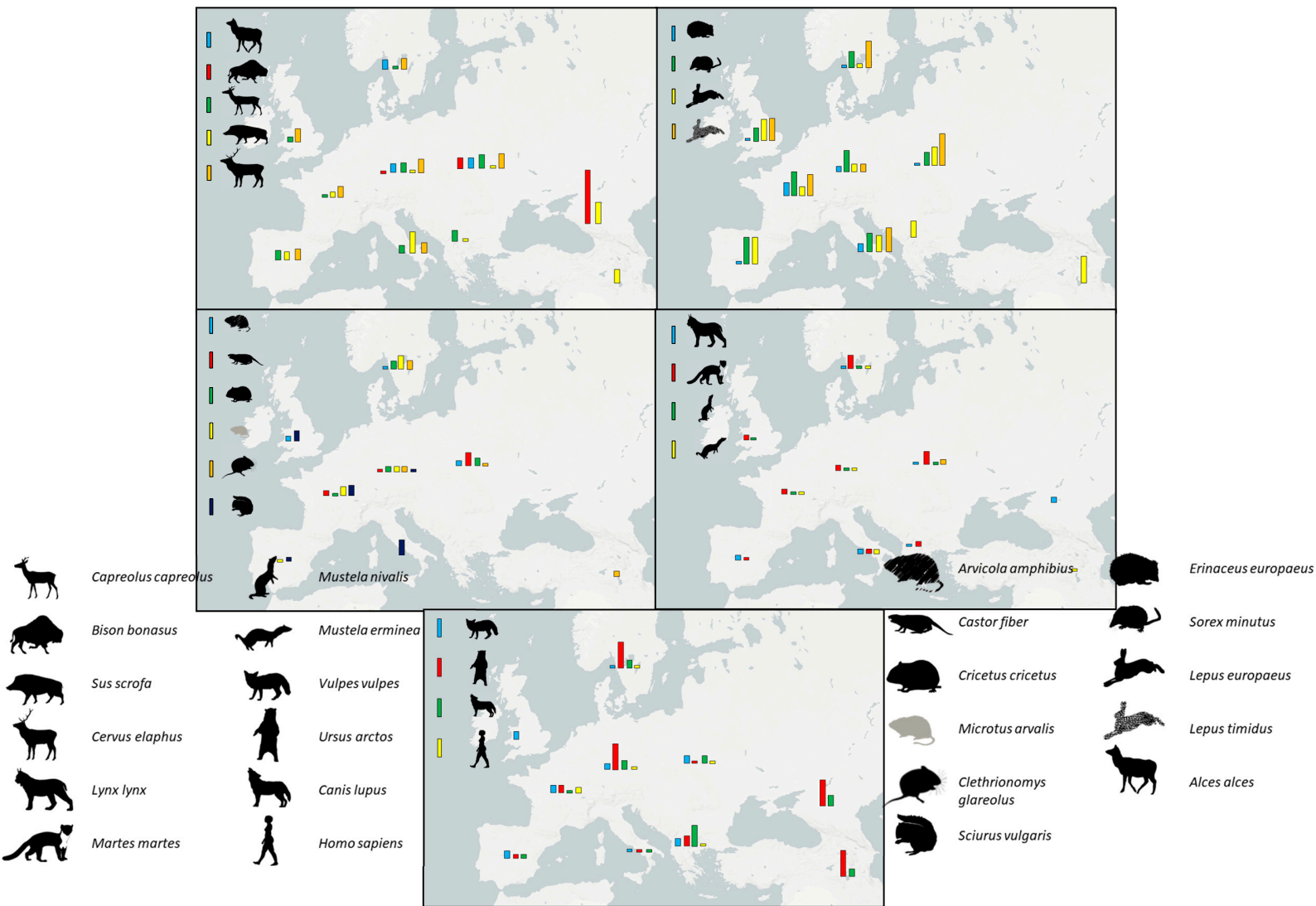


Figure S2. Maps displaying the nucleotide diversity values for each species per region analyzed. Bars represent nucleotide diversity values, and each color matches with the species that are classified by orders: Artiodactyla, Lagomorpha/Eulipotyphla, Rodentia, Carnivora, and Carnivora/Primates



Supplementary Text: Choice of samples.

An initial total of 225 species were considered in this study. This included all European terrestrial mammal species in the IUCN database (<http://www.iucnredlist.org/technical-documents/spatial-data>, downloaded 11/2015) and all European species considered in publications retrieved through Google Scholar and Web of Science using the keywords “phylogeography Europe” and “control region phylogeography” until December 2021. These 225 species are listed in the Supplementary Table S1.

All but 23 were excluded for the reasons indicated in Table S1. We only allowed terrestrial species to be included, and bats were excluded. Those in the arctic and commensal species were also excluded. The species had to have a sample range of 0.5 x 10⁶ km² or greater, larger than that would be too small for a general geographic pattern to be identified. Only those with 50 control region and/or D-loop sequences, excluding *CytB*, available on GenBank until December 2021 were included. Although there were species with good numbers of *CytB* sequences, it was decided to restrict the study to a single genetic marker to avoid conflicting signals between different markers.

Table S1. Two-hundred and twenty-five European mammal species considered for the analysis at the beginning of this project with an indication of the number of entries found on GenBank described as control region and D-loop, and for *CytB*. Species with more than 50 D-loop and control region sequences on GenBank are indicated, and the reasons for excluding the species with adequate data are also given. Inclusion for analysis in green, and exclusion with reason in pink.

Species	Common name	Terrestrial (excluding bats)	Control Region	D-loop	CytB	>50 sequences	Exclusion/ Inclusion
<i>Acomys minous</i>	Crete Spiny Mouse	✓	✗	✗	✗	✗	Insufficient data
<i>Alces alces</i>	Eurasian Elk	✓	308	112	32	✓	✓
<i>Apodemus agrarius</i>	Striped Field Mouse	✓	18	151	60	✓	Sample range restricted
<i>Apodemus alpicola</i>	Alpine Field Mouse	✓	1	1	0	✗	Insufficient data
<i>Apodemus epimelas</i>	Western Broad-toothed Field Mouse	✓	0	1	18	✗	Insufficient data
<i>Apodemus flavicollis</i>	Yellow-necked Field Mouse	✓	20	35	4	✓	Sample range restricted
<i>Apodemus mystacinus</i>	Eastern Broad-toothed Field Mouse	✓	41	57	16	✓	Sample range restricted
<i>Apodemus sylvaticus</i>	Long-tailed Field Mouse	✓	5	16	4	✗	Insufficient data
<i>Apodemus uralensis</i>	Herb Field Mouse	✓	3	2	144	✗	Insufficient data
<i>Apodemus witherbyi</i>	Steppe Field Mouse	✓	0	0	21	✗	Insufficient data
<i>Arvicola amphibius</i>	European Water Vole	✓	26	59	91	✓	✓
<i>Arvicola sapidus</i>	Southern Water Vole	✓	7	89	98	✓	Sample range restricted
<i>Arvicola scherman</i>	Montane Water Vole	✓	0	3	2	✗	Insufficient data
<i>Atelerix algirus</i>	North African Hedgehog	✓	0	15	59	✗	Insufficient data
<i>Balaena mysticetus</i>	Bowhead Whale	✗	✗	✗	✗	✗	Non-terrestrial
<i>Balaenoptera acutorostrata</i>	Common Minke Whale	✗	✗	✗	✗	✗	Non-terrestrial
<i>Balaenoptera borealis</i>	Sei Whale	✗	✗	✗	✗	✗	Non-terrestrial
<i>Balaenoptera edeni</i>	Bryde's Whale	✗	✗	✗	✗	✗	Non-terrestrial

<i>Balaenoptera musculus</i>	Blue Whale	X	X	X	X	X	Non-terrestrial
<i>Balaenoptera physalus</i>	Fin Whale	X	X	X	X	X	Non-terrestrial
<i>Barbastella barbastellus</i>	Western Barbastelle	X	0	29	54	X	Non-terrestrial
<i>Bison bonasus</i>	European Bison	✓	79	169	70	✓	✓
<i>Bos primigenius</i>	Aurochs	✓	21	93	0	✓	Extinct
<i>Canis aureus</i>	Golden Jackal	✓	14	37	77	✓	Sample range restricted
<i>Canis lupus</i>	Gray Wolf	✓	4968	4301	2815	✓	✓
<i>Capra ibex</i>	Alpine Ibex	✓	5	2	9	X	Insufficient data
<i>Capra pyrenaica</i>	Iberian Wild Goat	✓	32	7	37	X	Insufficient data
<i>Capreolus capreolus</i>	European Roe Deer	✓	122	734	168	✓	✓
<i>Castor fiber</i>	Eurasian Beaver	✓	34	61	19	✓	✓
<i>Cervus elaphus</i>	Red Deer	✓	846	870	575	✓	✓
<i>Chionomys nivalis</i>	European Snow Vole	✓	10	18	63	X	Insufficient data
<i>Clethrionomys glareolus</i>	Bank Vole	✓	92	129	1525	✓	✓
<i>Clethrionomys rufocanus</i>	Grey Red-backed Vole	✓	X	X	X	X	Insufficient data
<i>Clethrionomys rutilus</i>	Northern Red-backed Vole	✓	X	X	X	X	Insufficient data
<i>Cricetulus migratorius</i>	Gray Dwarf Hamster	✓	0	2	64	X	Insufficient data
<i>Cricetus cricetus</i>	Common Hamster	✓	0	180	126	✓	✓
<i>Crocidura canariensis</i>	Canarian Shrew	✓	X	X	X	X	Insufficient data
<i>Crocidura leucodon</i>	Bicolored Shrew	✓	3	3	84	X	Insufficient data
<i>Crocidura pachyura</i>	North African White-toothed Shrew	✓	X	X	X	X	Insufficient data
<i>Crocidura russula</i>	White-toothed Shrew	✓	41	45	117	✓	Sample range restricted
<i>Crocidura sicula</i>	Sicilian Shrew	✓	X	X	X	X	Insufficient data
<i>Crocidura suaveolens</i>	Lesser Shrew	✓	0	0	197	X	Insufficient data
<i>Crocidura whittakeri</i>	Whittaker's Shrew	✓	X	X	X	X	Insufficient data
<i>Crocidura zimmermanni</i>	Cretan White-toothed Shrew	✓	X	X	X	X	Insufficient data
<i>Cystophora cristata</i>	Hooded Seal	X	X	X	X	X	Non-terrestrial
<i>Delphinapterus leucas</i>	Beluga	X	X	X	X	X	Non-terrestrial

<i>Delphinus delphis</i>	Short-beaked Common Dolphin	X	X	X	X	X	Non-terrestrial
<i>Dicrostonyx groenlandicus</i>	Northern Collared Lemming	✓	0	19	350	X	Insufficient data
<i>Dinaromys bogdanovi</i>	Martino's Snow Vole	✓	0	0	53	X	Insufficient data
<i>Dryomys nitedula</i>	Forest Dormouse	✓	0	0	50	X	Insufficient data
<i>Eliomys melanurus</i>	Asian Garden Dormouse	✓	X	X	X	X	Insufficient data
<i>Eliomys quercinus</i>	Garden Dormouse	✓	0	0	53	X	Insufficient data
<i>Eptesicus bottae</i>	Botta's Serotine	X	0	0	39	X	Bat
<i>Eptesicus nilssonii</i>	Northern Bat	X	0	1	31	X	Bat
<i>Eptesicus serotinus</i>	Serotine	X	69	24	131	X	Bat
<i>Erignathus barbatus</i>	Bearded Seal	X	X	X	X	X	Non-terrestrial
<i>Erinaceus concolor</i>	Southern White-breasted Hedgehog	✓	45	5	23	✓	Taxonomical uncertainty * <i>E. concolor</i> and <i>E. roumanicus</i> are not well distinguished on Genbank
<i>Erinaceus europaeus</i>	Western European Hedgehog	✓	315	82	378	✓	✓
<i>Erinaceus roumanicus</i>	Northern White-breasted Hedgehog	✓	60	13	3	✓	Taxonomical uncertainty * <i>E. concolor</i> and <i>E. roumanicus</i> are not well distinguished on Genbank
<i>Eschrichtius robustus</i>	Gray Whale	X	X	X	X	X	Non-terrestrial
<i>Eubalaena glacialis</i>	North Atlantic Right Whale	X	X	X	X	X	Non-terrestrial
<i>Felis silvestris</i>	Wild Cat	✓	117	21	197	✓	Potential hybridization with <i>Felis domesticus</i>
<i>Feresa attenuata</i>	Pygmy Killer Whale	X	X	X	X	X	Non-terrestrial
<i>Galemys pyrenaicus</i>	Pyrenean Desman	✓	1	267	311	✓	Sample range restricted
<i>Glis glis</i>	Edible Dormouse	✓	0	2	52	X	Insufficient data
<i>Globicephala macrorhynchus</i>	Short-finned Pilot Whale	X	X	X	X	X	Non-terrestrial
<i>Globicephala melas</i>	Long-finned Pilot Whale	X	X	X	X	X	Non-terrestrial
<i>Grampus griseus</i>	Risso's Dolphin	X	X	X	X	X	Non-terrestrial
<i>Gulo gulo</i>	Wolverine	✓	271	5	53	X	Sample range restricted in European regions

<i>Halichoerus grypus</i>	Grey Seal	X	X	X	X	X	Non-terrestrial
<i>Homo sapiens</i>	Human	✓	80754	132238	66717	✓	✓
<i>Hyperoodon ampullatus</i>	North Atlantic Bottlenose Whale	X	X	X	X	X	Non-terrestrial
<i>Hystrix cristata</i>	Crested Porcupine	✓	29	47	23	✓	Sample range restricted
<i>Kogia breviceps</i>	Pygmy Sperm Whale	X	X	X	X	X	Non-terrestrial
<i>Kogia sima</i>	Dwarf Sperm Whale	X	X	X	X	X	Non-terrestrial
<i>Lagenodelphis hosei</i>	Fraser's Dolphin	X	X	X	X	X	Non-terrestrial
<i>Lagenorhynchus acutus</i>	Atlantic White-sided Dolphin	X	X	X	X	X	Non-terrestrial
<i>Lagenorhynchus albirostris</i>	White-beaked Dolphin	X	X	X	X	X	Non-terrestrial
<i>Lemmus lemmus</i>	Norway Lemming	✓	42	1	29	X	Insufficient data
<i>Lepus arcticus</i>	Arctic Hare	✓	3	63	8	✓	Sample range restricted in European regions
<i>Lepus capensis</i>	Cape Hare	✓	64	245	165	✓	Sample range restricted
<i>Lepus castroviejoi</i>	Broom Hare	✓	15	1	11	X	Insufficient data
<i>Lepus corsicanus</i>	Corsican Hare	✓	X	X	X	X	Insufficient data
<i>Lepus europaeus</i>	European Hare	✓	305	563	267	✓	✓
<i>Lepus granatensis</i>	Granada Hare	✓	15	226	239	✓	Sample range restricted
<i>Lepus timidus</i>	Mountain Hare	✓	151	188	258	✓	✓
<i>Lutra lutra</i>	Eurasian Otter	✓	86	14	53	✓	Sample range restricted
<i>Lynx lynx</i>	Eurasian Lynx	✓	74	17	47	✓	✓
<i>Lynx pardinus</i>	Iberian Lynx	✓	X	X	X	X	Insufficient data
<i>Marmota marmota</i>	Alpine Marmot	✓	1	0	18	X	Insufficient data
<i>Martes foina</i>	Beech Marten	✓	15	53	55	✓	Sample range restricted
<i>Martes martes</i>	Pine Marten	✓	55	153	160	✓	✓
<i>Martes zibellina</i>	Sable	✓	166	188	158	✓	Sample range restricted
<i>Megaptera novaeangliae</i>	Humpback Whale	X	X	X	X	X	Non-terrestrial
<i>Meles meles</i>	Eurasian Badger	✓	23	75	65	✓	Sample range restricted
<i>Mesocricetus newtoni</i>	Romanian Hamster	✓	X	X	X	X	Insufficient data
<i>Mesoplodon bidens</i>	Sowerby's Beaked Whale	X	X	X	X	X	Non-terrestrial
<i>Mesoplodon densirostris</i>	Blainville's Beaked Whale	X	X	X	X	X	Non-terrestrial
<i>Mesoplodon europaeus</i>	Gervais' Beaked Whale	X	X	X	X	X	Non-terrestrial

<i>Mesoplodon mirus</i>	True's Beaked Whale	✗	✗	✗	✗	✗	Non-terrestrial
<i>Micromys minutus</i>	Eurasian Harvest Mouse	✓	81	13	94	✓	Sample range restricted
<i>Microtus agrestis</i>	Field Vole	✓	2	2	431	✗	Insufficient data
<i>Microtus arvalis</i>	Common Vole	✓	287	138	1086	✓	✓
<i>Microtus bavaricus</i>	Bavarian Pine Vole	✓	✗	✗	✗	✗	Insufficient data
<i>Microtus brachycercus</i>	Calabria Pine Vole	✓	✗	✗	✗	✗	Insufficient data
<i>Microtus cabreræ</i>	Cabrera's Vole	✓	✗	✗	✗	✗	Insufficient data
<i>Microtus duodecimcostatus</i>	Mediterranean Pine Vole	✓	✗	✗	✗	✗	Insufficient data
<i>Microtus felteni</i>	Balkan Pine Vole	✓	✗	✗	✗	✗	Insufficient data
<i>Microtus gerbei</i>	Pyrenean Pine Vole	✓	✗	✗	✗	✗	Insufficient data
<i>Microtus guentheri</i>	Günther's Vole	✓	33	1	45	✗	Insufficient data
<i>Microtus levis</i>	East European Vole	✓	✗	✗	✗	✗	Insufficient data
<i>Microtus liechtensteini</i>	Liechtenstein's Pine Vole	✓	✗	✗	✗	✗	Insufficient data
<i>Microtus lusitanicus</i>	Lusitanian Pine Vole	✓	✗	✗	✗	✗	Insufficient data
<i>Microtus multiplex</i>	Alpine Pine Vole	✓	✗	✗	✗	✗	Insufficient data
<i>Microtus oeconomus</i>	Tundra Vole	✓	✗	✗	✗	✗	Insufficient data
<i>Microtus savii</i>	Savi's Pine Vole	✓	✗	✗	✗	✗	Insufficient data
<i>Microtus subterraneus</i>	European Pine Vole	✓	✗	✗	✗	✗	Insufficient data
<i>Microtus tatricus</i>	Tatra Vole	✓	✗	✗	✗	✗	Insufficient data
<i>Microtus thomasi</i>	Thomas's Pine Vole	✓	164	2	161	✓	Sample range restricted
<i>Miniopterus schreibersii</i>	Schreiber's Bent-winged Bat	✗	0	223	434	✓	Bat
<i>Monachus monachus</i>	Mediterranean Monk Seal	✗	✗	✗	✗	✗	Non-terrestrial
<i>Monodon monoceros</i>	Narwhal	✗	✗	✗	✗	✗	Non-terrestrial
<i>Mus macedonicus</i>	Macedonian Mouse	✓	7	120	2	✓	Sample range restricted
<i>Mus musculus</i>	House Mouse	✓	7523	2795	3321	✓	Non native commensal
<i>Mus spicilegus</i>	Mound-building Mouse	✓	32	4	5	✗	Insufficient data
<i>Mus spretus</i>	Western Mediterranean Mouse	✓	8	7	28	✗	Insufficient data
<i>Muscardinus avellanarius</i>	Hazel Dormouse	✓	0	12	42	✗	Insufficient data

<i>Mustela erminea</i>	Stoat	✓	119	220	330	✓	✓
<i>Mustela eversmanii</i>	Steppe Polecat	✓	5	7	5	✗	Insufficient data
<i>Mustela lutreola</i>	European Mink	✓	7	44	27	✓	Sample range restricted
<i>Mustela nivalis</i>	Least Weasel	✓	122	140	159	✓	✓
<i>Mustela putorius</i>	Western Polecat	✓	0	32	50	✗	Insufficient data
<i>Myomimus roachi</i>	Roach's Mouse-tailed Dormouse	✓	✗	✗	✗	✗	Insufficient data
<i>Myopus schisticolor</i>	Wood Lemming	✓	0	1	62	✗	Insufficient data
<i>Myotis alcathoe</i>	Alcathoe Myotis	✗	0	0	35	✗	Bat
<i>Myotis aurascens</i>	Steppe Whiskered Bat	✗	0	0	36	✗	Bat
<i>Myotis bechsteinii</i>	Bechstein's Myotis	✗	48	4	7	✗	Bat
<i>Myotis blythii</i>	Lesser Mouse-eared Myotis	✗	6	39	50	✓	Bat
<i>Myotis brandtii</i>	Brandt's Myotis	✗	515	144	43	✓	Bat
<i>Myotis capaccinii</i>	Long-fingered Bat	✗	0	0	1	✗	Bat
<i>Myotis dasycneme</i>	Pond Myotis	✗	0	0	1	✗	Bat
<i>Myotis daubentonii</i>	Daubenton's Myotis	✗	1	135	76	✓	Bat
<i>Myotis emarginatus</i>	Geoffroy's Bat	✗	0	0	51	✗	Bat
<i>Myotis myotis</i>	Greater Mouse-eared Bat	✗	61	143	99	✓	Bat
<i>Myotis mystacinus</i>	Whiskered Myotis	✗	0	0	22	✗	Bat
<i>Myotis nattereri</i>	Natterer's Bat	✗	38	0	89	✗	Bat
<i>Myotis punicus</i>	Maghreb Mouse-eared Bat	✗	27	0	1	✗	Bat
<i>Myotis schaubi</i>	Schaub's Myotis	✗	0	0	4	✗	Bat
<i>Neomys anomalus</i>	Southern Water Shrew	✓	0	0	32	✗	Insufficient data
<i>Neomys fodiens</i>	Eurasian Water Shrew	✓	2	2	39	✗	Insufficient data
<i>Nyctalus azoreum</i>	Azores Noctule	✗	✗	✗	✗	✗	Bat
<i>Nyctalus lasiopterus</i>	Giant Noctule	✗	0	427	219	✓	Bat
<i>Nyctalus leisleri</i>	Lesser Noctule	✗	15	30	31	✗	Bat
<i>Nyctalus noctula</i>	Noctule	✗	2	3	14	✗	Bat
<i>Odobenus rosmarus</i>	Walrus	✗	✗	✗	✗	✗	Non-terrestrial
<i>Orcinus orca</i>	Killer Whale	✗	✗	✗	✗	✗	Non-terrestrial

<i>Oryctolagus cuniculus</i>	European Rabbit	✓	474	343	103	✓	Commensal
<i>Ovibos moschatus</i>	Muskox	✓	240	19	32	✓	Sample range restricted in European regions
<i>Pagophilus groenlandicus</i>	Harp Seal	✗	✗	✗	✗	✗	Non-terrestrial
<i>Phoca vitulina</i>	Harbour Seal	✗	✗	✗	✗	✗	Non-terrestrial
<i>Phocoena phocoena</i>	Harbour Porpoise	✗	✗	✗	✗	✗	Non-terrestrial
<i>Physeter macrocephalus</i>	Sperm Whale	✗	✗	✗	✗	✗	Non-terrestrial
<i>Pipistrellus kuhlii</i>	Kuhl's Pipistrelle	✗	✗	✗	✗	✗	Bat
<i>Pipistrellus maderensis</i>	Madeira Pipistrelle	✗	✗	✗	✗	✗	Bat
<i>Pipistrellus nathusii</i>	Nathusius' Pipistrelle	✗	✗	✗	✗	✗	Bat
<i>Pipistrellus pipistrellus</i>	Common Pipistrelle	✗	160	103	122	✓	Bat
<i>Pipistrellus pygmaeus</i>	Pygmy Pipistrelle	✗	112	42	39	✓	Bat
<i>Pipistrellus savii</i>	Savi's Pipistrelle	✗	✗	✗	✗	✗	Bat
<i>Plecotus auritus</i>	Brown Big-eared Bat	✗	29	26	21	✗	Bat
<i>Plecotus austriacus</i>	Gray Big-eared Bat	✗	15	14	49	✗	Bat
<i>Plecotus kolombatovici</i>	Kolombatovic's Long-eared Bat	✗	18	3	2	✗	Bat
<i>Plecotus macrotis</i>	Mountain Long-eared Bat	✗	8	85	72	✓	Bat
<i>Plecotus sardus</i>	Sardinian Long-eared Bat	✗	✗	✗	✗	✗	Bat
<i>Plecotus teneriffae</i>	Tenerife Long-eared Bat	✗	✗	✗	✗	✗	Bat
<i>Prolagus sardus</i>	Sardinian Pika	✓	✗	✗	✗	✗	Insufficient data
<i>Pseudorca crassidens</i>	False Killer Whale	✗	✗	✗	✗	✗	Non-terrestrial
<i>Pteromys volans</i>	Siberian Flying Squirrel	✓	4	2	72	✗	Insufficient data
<i>Pusa hispida</i>	Ringed Seal	✗	✗	✗	✗	✗	Non-terrestrial
<i>Rangifer tarandus</i>	Reindeer	✓	918	1403	703	✓	Sample range restricted in European regions
<i>Rhinolophus blasii</i>	Blasius' Horseshoe Bat	✗	9	7	14	✗	Bat
<i>Rhinolophus euryale</i>	Mediterranean Horseshoe Bat	✗	3	23	16	✗	Bat
<i>Rhinolophus ferrumequinum</i>	Greater Horseshoe Bat	✗	121	174	89	✓	Bat

<i>Rhinolophus hipposideros</i>	Lesser Horseshoe Bat	✗	375	375	397	✓	Bat
<i>Rhinolophus mehelyi</i>	Mehely's Horseshoe Bat	✗	4	14	10	✗	Bat
<i>Rupicapra pyrenaica</i>	Pyrenean Chamois	✓	✗	✗	✗	✗	Insufficient data
<i>Rupicapra rupicapra</i>	Northern Chamois	✓	✗	✗	✗	✗	Insufficient data
<i>Saiga tatarica</i>	Mongolian Saiga	✓	✗	✗	✗	✗	Insufficient data
<i>Sciurus anomalus</i>	Caucasian Squirrel	✓	✗	✗	✗	✗	Insufficient data
<i>Sciurus vulgaris</i>	Eurasian Red Squirrel	✓	92	507	157	✓	✓
<i>Sicista betulina</i>	Northern Birch Mouse	✓	✗	✗	✗	✗	Insufficient data
<i>Sicista subtilis</i>	Southern Birch Mouse	✓	0	5	20	✗	Insufficient data
<i>Sorex alpinus</i>	Alpine Shrew	✓	✗	✗	✗	✗	Insufficient data
<i>Sorex antinorii</i>	Valais Shrew	✓	40	0	113	✗	Insufficient data
<i>Sorex araneus</i>	Eurasian Common Shrew	✓	266	97	56	✓	Sample range restricted
<i>Sorex arunchi</i>	Udine Shrew	✓	✗	✗	✗	✗	Insufficient data
<i>Sorex caecutiens</i>	Laxmann's Shrew	✓	2	1	115	✗	Insufficient data
<i>Sorex coronatus</i>	Crowned Shrew	✓	0	0	17	✗	Insufficient data
<i>Sorex granarius</i>	Lagranja Shrew	✓	0	0	7	✗	Insufficient data
<i>Sorex isodon</i>	Even-toothed Shrew	✓	1	0	9	✗	Insufficient data
<i>Sorex minutissimus</i>	Eurasian Least Shrew	✓	225	152	298	✓	Sample range restricted
<i>Sorex minutus</i>	Eurasian Pygmy Shrew	✓	158	0	344	✓	✓
<i>Sorex samniticus</i>	Apennine Shrew	✓	✗	✗	✗	✗	Insufficient data
<i>Spalax graecus</i>	Balkan Blind Mole Rat	✓	✗	✗	✗	✗	Insufficient data
<i>Spalax leucodon</i>	Lesser Mole Rat	✓	✗	✗	✗	✗	Insufficient data
<i>Spermophilus citellus</i>	European Ground Squirrel	✓	8	0	134	✗	Insufficient data
<i>Spermophilus suslicus</i>	Speckled Ground Squirrel	✓	108	12	3	✓	Sample range restricted
<i>Stenella coeruleoalba</i>	Striped Dolphin	✗	✗	✗	✗	✗	Non-terrestrial

<i>Stenella frontalis</i>	Atlantic Spotted Dolphin	X	X	X	X	X	Non-terrestrial
<i>Steno bredanensis</i>	Rough-toothed Dolphin	X	X	X	X	X	Non-terrestrial
<i>Suncus etruscus</i>	White-toothed Pygmy Shrew	✓	X	X	X	X	Insufficient data
<i>Sus scrofa</i>	Wild Boar	✓	5138	5601	1993	✓	✓
<i>Tadarida teniotis</i>	European Free-tailed Bat	X	X	X	X	X	Bat
<i>Talpa caeca</i>	Mediterranean Mole	✓	X	X	X	X	Insufficient data
<i>Talpa europaea</i>	European Mole	✓	0	2	367	X	Insufficient data
<i>Talpa levantis</i>	Levantine Mole	✓	0	0	18	X	Insufficient data
<i>Talpa occidentalis</i>	Iberian Mole	✓	2	0	31	X	Insufficient data
<i>Talpa romana</i>	Roman Mole	✓	0	0	120	X	Insufficient data
<i>Talpa stankovici</i>	Stankovic's Mole	✓	0	0	19	X	Insufficient data
<i>Tursiops truncatus</i>	Common Bottlenose Dolphin	X	X	X	X	X	Non-terrestrial
<i>Ursus arctos</i>	Brown Bear	✓	792	415	396	✓	✓
<i>Ursus maritimus</i>	Polar Bear	✓	509	143	398	✓	Sample range restricted in European regions
<i>Vespertilio murinus</i>	Particoloured Bat	X	0	53	29	✓	Bat
<i>Vormela peregusna</i>	Marbled Polecat	✓	0	21	20	X	Insufficient data
<i>Vulpes lagopus</i>	Arctic Fox	✓	80	100	57	✓	Sample range restricted in European regions
<i>Vulpes vulpes</i>	Red Fox	✓	137	708	328	✓	✓
<i>Ziphius cavirostris</i>	Cuvier's Beaked Whale	X	X	X	X	X	Non-terrestrial

Table S2. Mammal species chosen for the meta-analysis and the studies that provided the sequences included in the analysis. The sequences were retrieved from GenBank from the associated references. Unpublished means that the sequences were found in GenBank, but the paper was not published by the time this study was finished.

Species	References
<i>Arvicola amphibius</i>	Piertney et al. (2005), Brace et al. (2016)
<i>Microtus arvalis</i>	Haring et al. (2000), Fink et al. (2004), Heckel et al. (2005), Borkowska et al. (2010), Borkowska (2011)
<i>Clethrionomys glareolus</i>	Stacy et al. (1997), Matson et al. (2000), Matson and Baker (2001), Spitzenberger et al. (2000), Dekonenko et al. (2003), Dunina-Barkovskaya (2004), Yashina et al. (2005 <i>Unpublished</i>), Wickliffe et al. (2006), Meeks et al. (2007, 2009), Johansson et al. (2008), Razzauti et al. (2012), Çolak et al. (2016)
<i>Cricetus cricetus</i>	Neumann et al. (2004), Banaszek et al. (2009), Banaszek and Ziomek (2011), Schroder et al. (2014), Hegyeli et al. (2015), Feoktistova et al. (2016)
<i>Sciurus vulgaris</i>	Barratt et al. (1999), Reyes et al. (2000), Hale et al. (2004), Tamura and Hayashi (2007), Finnegan et al. (2008), Grill et al. (2009), Dozieres et al. (2012), Simpson et al. (2013), Liu et al. (2014), Rezouki et al. (2014), Madsen et al. (2015), Lucas et al. (2015)
<i>Castor fiber</i>	Durka et al. (2005), Horn et al. (2011, 2014), Kropf et al. (2013), Biedrzycka et al. (2014), Frosch et al. (2014a), Senn et al. (2014)
<i>Erinaceus europaeus</i>	Seddon et al. (2001), Bolfíková and Hulva (2012)
<i>Sorex minutus</i>	McDevitt et al. (2009, 2010, 2011)
<i>Lepus europaeus</i>	Thulin et al. (1997), Pierpaoli et al. (1999), Arnason et al. (2002), Kasapidis et al. (2005), Fickel et al. (2005, 2008), Schmidt and Fickel (2005 <i>Unpublished</i>), Fredsted et al. (2006), Melo-Ferreira et al. (2007, 2011), Sert et al. (2009), Stamatis et al. (2009), Menzies et al. (2010 <i>Unpublished</i>), Pietri et al. (2011), Antoniou et al. (2013), Canu et al. (2013), Sanz-Martín et al. (2014), Mengoni et al. (2015), Vernesi et al. (2016), Giannoulis et al. (2018)
<i>Lepus timidus</i>	Thulin et al. (1997), Pierpaoli et al. (1999), Wu and Zhang et al. (2000 <i>Unpublished</i>), Waltari et al. (2004), Waltari and Cook (2005), Fredsted et al. (2006), Melo-Ferreira et al. (2007, 2014), Stamatis et al. (2008), Prost et al. (2010), Vernesi et al. (2010 <i>Unpublished</i>), Zachos et al. (2010), Liu et al. (2011), Fu (2015 <i>Unpublished</i>), Mengoni et al. (2015)
<i>Canis lupus</i>	Tsuda et al. (1997), Vila et al. (1997, 1999), Randi et al. (2000), Valière et al. (2003), Verginelli et al. (2005), Björnerfeldt et al. (2006), Gomercic et al. (2010), Pilot et al. (2006, 2010, 2014), Baltrunaite et al. (2013), Boggiano et al. (2013), Druzhkova et al. (2013), Thalmann et al. (2013), Jansson et al. (2014), Ersmark et al. (2016), Koblmüller et al. (2016), Montana et al. (2017)
<i>Vulpes vulpes</i>	Okumura et al. (1996), Valiere et al. (2003), Statham et al. (2005, 2012, 2014), Arnason et al. (2006), Inoue et al. (2007), Kirschning et al. (2007), Zhong et al. (2010), Teacher et al. (2011), Edwards et al. (2012), Kutschera et al. (2013), Galov et al. (2014), Koepfli et al. (2015), Leite et al. (2015), Sun et al. (2015)
<i>Mustela erminea</i>	Kurose et al. (1999, 2005), Martinkova et al. (2007), Dawson et al. (2014), Emami Khoyi et al. (2016)
<i>Mustela nivalis</i>	Kurose et al. (1999, 2005), Lebarbenchon et al. (2006, 2010), Yu et al. (2011), Emami-Khoyi et al. (2016), Rodrigues et al. (2016)
<i>Martes martes</i>	Davison et al. (2001), Statham et al. (2005), Pertoldi et al. (2008, 2014), Ruiz-Gonzalez et al. (2008, 2013), Rozhnov et al. (2010), Hosoda et al. (2011), Nagai et al. (2012), Sindičić (2015 <i>Unpublished</i>), Korablev et al. (2017)
<i>Lynx lynx</i>	Hellborg et al. (2002), Gugolz et al. (2008), Sindičić et al. (2012), Ratkiewicz et al. (2014), Rueness et al. (2014), Rodríguez-Varela et al. (2015, 2016), Li et al. (2016), Paijmans et al. (2016)

<i>Ursus arctos</i>	Taberlet and Bouvet (1994), Leonard et al. (2000), Masuda et al. (2001), Barnes et al. (2002), Hofreiter et al. (2004), Valdiosera et al. (2007, 2008), Bon et al. (2008), Calvignac et al. (2008, 2009), García et al. (2009 <i>Unpublished</i>), Korsten et al. (2009), Murtshkvaladze et al. (2010), Edwards et al. (2011, 2014), Kocijan et al. (2011), Hailer et al. (2012), Bray et al. (2013), Frosch et al. (2014b), Salomashkina et al. (2014, 2017), Baca et al. (2014), Xenikoudakis et al. (2015), Ashrafzadeh et al. (2016), Çilingir et al. (2016), Fortes et al. (2016)
<i>Homo sapiens</i>	*Palaeolithic: Bramanti et al. (2009), Krause et al. (2010), Hervella et al. (2012), Brandt et al. (2013), Raghavan et al. (2014), Seguin-Orlando et al. (2014), Benazzi et al. (2015), Fu et al. (2015, 2016), Posth et al. (2016) *Mesolithic: Bramanti et al. (2009), Delsate et al. (2009), Malmström et al. (2009, 2015), Der Sarkissian et al. (2011, 2013, 2014), Sanchez-Quinto et al. (2012), Skoglund et al. (2012, 2014), Bollongino et al. (2013), Brandt et al. (2013), Lazaridis et al. (2014, 2016), Olalde et al. (2014), Haak et al. (2015), Hofmanová et al. (2015), Mathieson et al. (2015), Fu et al. (2016), Posth et al. (2016)
<i>Alces alces</i>	Polziehn and Strobeck (1997), Hundertmark et al. (2002), Swislocka et al. (2008, 2013), Moskvitina et al. (2011), Hassanin et al. (2012), Kholodova et al. (2014), Niedziałkowska et al. (2014), Kangas et al. (2015), Nemoikina et al. (2016), Wennerström et al. (2016)
<i>Capreolus capreolus</i>	Douzery and Randi (1997), Wiehler and Tiedemann (1998), Vernesi et al. (2002, 2016), Randi et al. (2004), Royo et al. (2007), Gentile et al. (2009), Hassanin et al. (2012), Zvychainaya et al. (2011), Fickel et al. (2012), Mucci et al. (2012), Baker and Hoezel (2013, 2014), Lorenzini et al. (2014), Matosiuk et al. (2014), Olano-Marin et al. (2014), Puraite et al. (2014), Biossa et al. (2015), Nemeth et al. (2015 <i>Unpublished</i>)
<i>Cervus elaphus</i>	Hmwe et al. (2006), Nussey et al. (2006), Egyed et al. (2008 <i>Unpublished</i>), Nielsen et al. (2008), Perez-Espona et al. (2009), Skog et al. (2009), Haanes et al. (2010), Niedziałkowska et al. (2011, 2012), Biedrzycka et al. (2012), Carden et al. (2012), Rosvold et al. (2012), Meiri et al. (2013), Krojerova-Prokesova et al. (2015), Borowski et al. (2016), Carranza et al. (2016), Frank et al. (2017)
<i>Bison bonasus</i>	Bork et al. (1991), Ward et al. (1999), Verkaar et al. (2004), Anderung et al. (2006), Wójcik et al. (2009), Zeyland et al. (2012), Yudin et al. (2012), Massilani et al. (2016), Soubrier et al. (2016), Wecek et al. (2016)
<i>Sus scrofa</i>	Okumura et al. (1996), Giuffra et al. (2000), Alves et al. (2003), Larson et al. (2005, 2007), Fang et al. (2006), Scandura et al. (2008), Hajji and Zachos (2011), Kim et al. (2011), Alexandri et al. (2012), van Asch et al. (2012), Ottoni et al. (2013), Kusza et al. (2014), Vilaça et al. (2014), Velickovic et al. (2015), Menendez et al. (2016)

References

- Alexandri, P., Triantafyllidis, A., Papakostas, S., Chatzinikos, E., Platis, P., Papageorgiou, N., Larson, G., Abatzopoulos, T. J. and Triantaphyllidis, C., 2012. The Balkans and the colonization of Europe: the post-glacial range expansion of the wild boar, *Sus scrofa*. *Journal of Biogeography*, 39 (4), 713-723.
- Alves, E., Ovilo, C., Rodriguez, M. C. and Silio, L., 2003. Mitochondrial DNA sequence variation and phylogenetic relationships among Iberian pigs and other domestic and wild pig populations. *Animal Genetics*, 34 (5), 319-324.
- Anderung, C., Baubliene, J., Daugnora, L., and Götherström, A., 2006. Medieval remains from Lithuania indicate loss of a mitochondrial haplotype in *Bison bonasus*. *Molecular Ecology*, 15(10), 3083-3083.
- Antoniou, A., Magoulas, A., Platis, P. and Kotoulas, G., 2013. Assessing the genetic landscape of a contact zone: the case of European hare in northeastern Greece. *Genetica*, 141 (1-3), 23-40.
- Arnason, U., Adegoke, J. A., Bodin, K., Born, E. W., Esa, Y. B., Gullberg, A., Nilsson, M., Short, R. V., Xu, X. and Janke, A., 2002. Mammalian mitogenomic relationships and the root of the eutherian tree. *Proceedings of the National Academy of Sciences USA*, 99 (12), 8151-8156.

6. Arnason, U., Gullberg, A., Janke, A., Kullberg, M., Lehman, N., Petrov, E. A. and Väinölä, R., 2006. Pinniped phylogeny and a new hypothesis for their origin and dispersal. *Molecular Phylogenetics and Evolution*, 41 (2), 345-354.
7. Ashrafzadeh, M. R., Kaboli, M. and Naghavi, M. R., 2016. Mitochondrial DNA analysis of Iranian brown bears (*Ursus arctos*) reveals new phylogeographic lineage. *Mammalian Biology- Zeitschrift für Säugetierkunde*, 81 (1), 1-9.
8. Baca, M., Mackiewicz, P., Stankovic, A., Popovid, D., Stefaniak, K., Czarnogórska, K., Nadachowski, A., Gąsiorowski, M., Hercman, H. and Weglenski, P., 2014. Ancient DNA and dating of cave bear remains from Niedźwiedzia Cave suggest early appearance of *Ursus ingressus* in Sudetes. *Quaternary International*, 339, 217-223.
9. Baker, K. H. and Hoelzel, A.R., 2013. Evolution of population genetic structure of the British roe deer by natural and anthropogenic processes (*Capreolus capreolus*). *Ecology and Evolution*, 3 (1), 89-102.
10. Baker, K. H. and Hoelzel, A. R., 2014. Influence of Holocene environmental change and anthropogenic impact on the diversity and distribution of roe deer. *Heredity*, 112 (6), 607-615.
11. Baltrūnaitė, L., Balčiauskas, L. and Åkesson, M., 2013. The genetic structure of the Lithuanian wolf population. *Central European Journal of Biology*, 8 (5), 440-447.
12. Banaszek, A., Jadwiszczak, K. A., Ratkiewicz, M. and Ziomek, J., 2009. Low genetic diversity and significant structuring of the common hamster populations *Cricetus cricetus* in Poland revealed by the mtDNA control region sequence variation. *Acta Theriologica*, 54 (4), 289-295.
13. Banaszek, A. and Ziomek, J., 2011. The common hamster, *Cricetus cricetus* (L.) populations in the Lower San River Valley. *Zoologica Poloniae*, 56 (1-4), 49-58.
14. Barnes, I., Matheus, P., Shapiro, B., Jensen, D. and Cooper, A., 2002. Dynamics of Pleistocene population extinctions in Beringian brown bears. *Science*, 295 (5563), 2267-2270.
15. Barratt, E. M., Gurnell, J., Malarky, G., Deaville, R. and Bruford, M. W., 1999. Genetic structure of fragmented populations of red squirrel (*Sciurus vulgaris*) in the UK. *Molecular Ecology*, 8, S55-S63.
16. Benazzi, S., Slon, V., Talamo, S., Negrino, F., Peresani, M., Bailey, S. E., Sawyer, S., Panetta, D., Vicino, G., Starnini, E., Mannino, M. A., Salvadori, P. A., Meyer, M., Pääbo, S. and Hublin, J. J., 2015. The makers of the Protoaurignacian and implications for Neandertal extinction. *Science*, 348 (6236), 793-796.
17. Biedrzycka, A., Konior, M., Babik, W., Świsłocka, M. and Ratkiewicz, M., 2014. Admixture of two phylogeographic lineages of the Eurasian beaver in Poland. *Mammalian Biology- Zeitschrift für Säugetierkunde*, 79 (5), 287-296.
18. Biedrzycka, A., Solarz, W. and Okarma, H., 2012. Hybridization between native and introduced species of deer in Eastern Europe. *Journal of Mammalogy*, 93 (5), 1331-1341.
19. Biosa, D., Scandura, M., Tagliavini, J., Luccarini, S., Mattioli, L. and Apollonio, M., 2015. Patterns of genetic admixture between roe deer of different origin in central Italy. *Journal of Mammalogy*, 96 (4), 827-838.
20. Björnerfeldt, S., Webster, M. T. and Vilà, C., 2006. Relaxation of selective constraint on dog mitochondrial DNA following domestication. *Genome Research*, 16 (8), 990-994.
21. Boggiano, F., Ciofi, C., Boitani, L., Formia, A., Grottoli, L., Natali, C. and Ciucci, P., 2013. Detection of an East European wolf haplotype puzzles mitochondrial DNA monomorphism of the Italian wolf population. *Mammalian Biology-Zeitschrift für Säugetierkunde*, 78 (5), 374-378.
22. Bolfiková, B. and Hulva, P., 2012. Microevolution of sympatry: landscape genetics of hedgehogs *Erinaceus europaeus* and *E. roumanicus* in Central Europe. *Heredity*, 108 (3), 248-255.
23. Bollongino, R., Nehlich, O., Richards, M. P., Orschiedt, J., Thomas, M. G., Sell, C., ... and Burger, J., 2013. 2000 years of parallel societies in Stone Age Central Europe. *Science*, 342 (6157), 479-481.
24. Bon, C., Caudy, N., de Dieuleveult, M., Fosse, P., Philippe, M., Maksud, F., Beraud-Colomb, É., Bouzaid, E., Kefi, R. and Laugier, C., 2008. Deciphering the complete mitochondrial genome and phylogeny of the extinct cave bear

in the Paleolithic painted cave of Chauvet. *Proceedings of the National Academy of Sciences USA*, 105 (45), 17447-17452.

25. Bork, A. M., Strobeck, C. M., Yeh, F. C., Hudson, R. J. and Salmon, R. K., 1991. Genetic relationship of wood and plains bison based on restriction fragment length polymorphisms. *Canadian Journal of Zoology*, 69 (1), 43-48.
26. Borkowska, A., 2011. Seasonal variation of reproductive success under female philopatry and male-biased dispersal in a common vole population. *Behavioural Processes*, 86 (1), 39- 45.
27. Borkowska, A., Ratkiewicz, M. and Jaarola, M., 2010. Maintenance of genetic variation and moderate differentiation among populations under sex-biased dispersal in the common vole *Microtus arvalis* in patchy habitats. *Acta Theriologica*, 55 (4), 333-341.
28. Borowski, Z., Świśłocka, M., Matosiuk, M., Mirski, P., Krysiuk, K., Czajkowska, M., Borkowska, A. and Ratkiewicz, M., 2016. Purifying selection, density blocking and unnoticed mitochondrial DNA diversity in the red deer, *Cervus elaphus*. *PloS One*, 11 (9), e0163191.
29. Brace, S., Ruddy, M., Miller, R., Schreve, D. C., Stewart, J. R. and Barnes, I., 2016. The colonization history of British water vole (*Arvicola amphibius*; (Linnaeus, 1758)): origins and development of the Celtic fringe. *Proceedings of the Royal Society B: Biological Sciences*, 283 (1829), 20160130.
30. Bramanti, B., Thomas, M. G., Haak, W., Unterländer, M., Jores, P., Tambets, K., ... and Lueth, F., 2009. Genetic discontinuity between local hunter-gatherers and central Europe's first farmers. *Science*, 326 (5949), 137-140.
31. Brandt, G., Haak, W., Adler, C. J., Roth, C., Szécsényi-Nagy, A., Karimnia, S., ... and Dresely, V. , 2013. Ancient DNA reveals key stages in the formation of central European mitochondrial genetic diversity. *Science*, 342(6155), 257-261.
32. Bray, S. C. E., Austin, J. J., Metcalf, J. L., Østbye, K., Østbye, E., Lauritzen, S. E., Aaris-Sørensen, K., Valdiosera, C., Adler, C. J. and Cooper, A., 2013. Ancient DNA identifies post-glacial recolonisation, not recent bottlenecks, as the primary driver of contemporary mt DNA phylogeography and diversity in Scandinavian brown bears. *Diversity and Distributions*, 19 (3), 245-256.
33. Calvignac, S., Hughes, S., Tougard, C., Michaux, J., Thevenot, M., Philippe, M., Hamdine, W. and Hänni, C., 2008. Ancient DNA evidence for the loss of a highly divergent brown bear clade during historical times. *Molecular Ecology*, 17 (8), 1962-1970.
34. Calvignac, S., Hughes, S. and Hänni, C., 2009. Genetic diversity of endangered brown bear (*Ursus arctos*) populations at the crossroads of Europe, Asia and Africa. *Diversity and Distributions*, 15 (5), 742-750.
35. Canu, A., Scandura, M., Luchetti, S., Cossu, A., Iacolina, L., Bazzanti, M. and Apollonio, M., 2013. Influence of management regime and population history on genetic diversity and population structure of brown hares (*Lepus europaeus*) in an Italian province. *European Journal of Wildlife Research*, 59 (6), 783-793.
36. Carden, R. F., McDevitt, A. D., Zachos, F. E., Woodman, P. C., O'Toole, P., Rose, H., Monaghan, N. T., Campana, M. G., Bradley, D. G. and Edwards, C. J., 2012. Phylogeographic, ancient DNA, fossil and morphometric analyses reveal ancient and modern introductions of a large mammal: the complex case of red deer (*Cervus elaphus*) in Ireland. *Quaternary Science Reviews*, 42, 74-84.
37. Carranza, J., Salinas, M., de Andrés, D. and Pérez-González, J., 2016. Iberian red deer: paraphyletic nature at mtDNA but nuclear markers support its genetic identity. *Ecology and Evolution*, 6 (4), 905-922.
38. Çilingir, F. G., Akın Pekşen, Ç., Ambarlı, H., Beerli, P. and Bilgin, C. C., 2016. Exceptional maternal lineage diversity in brown bears (*Ursus arctos*) from Turkey. *Zoological Journal of the Linnean Society*, 176 (2), 463-477.
39. Çolak, R., Olgun Karacan, G., Kandemir, I., Çolak, E., Kankiliç, T., Yigit, N. and Michaux, J., 2016. Genetic variations of Turkish bank vole, *Myodes glareolus* (Mammalia: Rodentia) inferred from mtDNA. *Mitochondrial DNA Part A*, 27 (6), 4372-4379.
40. Davison, A., Birks, J. D. S., Brookes, R. C., Messenger, J. E. and Griffiths, H. I., 2001. Mitochondrial phylogeography and population history of pine martens *Martes martes* compared with polecats *Mustela putorius*. *Molecular Ecology*, 10 (10), 2479-2488.

41. Dawson, M. N., 2014. Natural experiments and meta-analyses in comparative phylogeography. *Journal of Biogeography*, 41 (1), 52-65.
42. Dekonenko, A., Yakimenko, V., Ivanov, A., Morozov, V., Nikitin, P., Khasanova, S., Dzagurova, T., Tkachenko, E. and Schmaljohn, C., 2003. Genetic similarity of Puumala viruses found in Finland and western Siberia and of the mitochondrial DNA of their rodent hosts suggests a common evolutionary origin. *Infection, Genetics and Evolution*, 3 (4), 245-257.
43. Delsate, D., Guinet, J. M., and Saverwyns, S., 2009. De l'ocre sur le crâne mésolithique (haplogroupe U5a) de Reuland-Loschbour (Grand-Duché de Luxembourg). *Bulletin de la Société Préhistorique Luxembourgeoise*, 31, 7-30.
44. Der Sarkissian, C., 2011. *Mitochondrial DNA in ancient human populations of Europe*. PhD thesis, University of Adelaide.
45. Der Sarkissian, C., Balanovsky, O., Brandt, G., Khartanovich, V., Buzhilova, A., Koshel, S., ... and Shumkin, V., 2013. Ancient DNA reveals prehistoric gene-flow from Siberia in the complex human population history of North East Europe. *PLoS Genetics*, 9(2), e1003296.
46. Der Sarkissian, C., Brotherton, P., Balanovsky, O., Templeton, J. E., Llamas, B., Soubrier, J., ... and Genographic Consortium., 2014. Mitochondrial genome sequencing in Mesolithic North East Europe unearths a new sub-clade within the broadly distributed human haplogroup C1. *PLoS One*, 9(2), e87612.
47. Douzery, E. and Randi, E., 1997. The mitochondrial control region of Cervidae: evolutionary patterns and phylogenetic content. *Molecular Biology and Evolution*, 14 (11), 1154-1166.
48. Dozières, A., Chapuis, J.-L., Thibault, S. and Baudry, E., 2012. Genetic structure of the French red squirrel populations: Implication for conservation. *PLoS One*, 7 (10), e47607.
49. Druzhkova, A. S., Thalmann, O., Trifonov, V. A., Leonard, J. A., Vorobieva, N. V., Ovodov, N. D., and Wayne, R. K., 2013. Ancient DNA analysis affirms the canid from Altai as a primitive dog. *PLoS One*, 8(3), e57754.
50. Dunina-Barkovskaya, Y. V., 2004. *Population genetics of rodents living in the Chornobyl environment based on mitochondrial and nuclear gene sequences*. MSc Thesis , Texas Tech University, Lubbock.
51. Durka, W., Babik, W., Ducroz, J. F., Heidecke, D., Rosell, F., Samjaa, R., P. Saveljev, A., Stubbe, A., Uleviclus, A. and Stubbe, M., 2005. Mitochondrial phylogeography of the Eurasian beaver *Castor fiber* L. *Molecular Ecology*, 14 (12), 3843-3856.
52. Edwards, C. J., Ho, S.Y.W., Barnett, R., Coxon, P., Bradley, D.G., Lord, T.C., O'Connor, T., 2014. Continuity of brown bear maternal lineages in northern England through the last-glacial period. *Quaternary Science Reviews* 96:131–139.
53. Edwards, C. J., Soulsbury, C. D., Statham, M. J., Ho, S. Y. W., Wall, D., Dolf, G., Iossa, G., Baker, P. J., Harris, S. and Sacks, B. N., 2012. Temporal genetic variation of the red fox, *Vulpes vulpes*, across western Europe and the British Isles. *Quaternary Science Reviews*, 57, 95-104.
54. Edwards, C. J., Suchard, M. A., Lemey, P., Welch, J. J., Barnes, I., Fulton, T. L., Barnett, R., O'Connell, T. C., Coxon, P. and Monaghan, N., 2011. Ancient hybridization and an Irish origin for the modern polar bear matriline. *Current Biology*, 21 (15), 1251-1258.
55. Egyed, B., Szabolcsi, Z., Zenke, P., Zoldag, L., Orosz, L. and Padar, Z., 2008. Molecular characterization of the red deer mitochondrial DNA control region. *Unpublished manuscript*.
56. Emami-Khoyi, A., Hartley, D. A., Ross, J. G., Murphy, E. C., Paterson, A. M., Cruickshank, R. H. and Else, T.-A., 2016. Complete mitochondrial genome of the stoat (*Mustela erminea*) and New Zealand fur seal (*Arctocephalus forsteri*) and their significance for mammalian phylogeny. *Mitochondrial DNA Part A*, 27 (6), 4597-4599.
57. Ersmark, E., Klütsch, C. F. C., Chan, Y. L., Sinding, M.-H. S., Fain, S. R., Illarionova, N. A., Oskarsson, M., Uhlén, M., Zhang, Y.-P. and Dalén, L., 2016. From the past to the present: wolf phylogeography and demographic history based on the mitochondrial control region. *Frontiers in Ecology and Evolution*, 4, 134.

58. Fang, M., Berg, F., Ducos, A. and Andersson, L., 2006. Mitochondrial haplotypes of European wild boars with $2n=36$ are closely related to those of European domestic pigs with $2n=38$. *Animal Genetics*, 37 (5), 459-464.
59. Feoktistova, N. Y., Meschersky, I. G., Surov, A. V., Bogomolov, P. L., Tovpinetz, N. N. and Poplavskaya, N. S., 2016. Genetic structure of urban population of the Common hamster (*Cricetus cricetus*). *Russian Journal of Genetics*, 52 (2), 194-203.
60. Fickel, J., Bubliy, O. A., Brand, J., Mayer, K. and Heurich, M., 2012. Low genotyping error rates in non-invasively collected samples from roe deer of the Bavarian Forest National Park. *Mammalian Biology-Zeitschrift für Säugetierkunde*, 77 (1), 67-70.
61. Fickel, J., Hauffe, H. C., Pecchioli, E., Soriguer, R., Vapa, L. and Pitra, C., 2008. Cladogenesis of the European brown hare (*Lepus europaeus* Pallas, 1778). *European Journal of Wildlife Research*, 54 (3), 495-510.
62. Fickel, J., Schmidt, A., Putze, M., Spittler, H., Ludwig, A., Streich, W. J. and Pitra, C., 2005. Genetic structure of populations of European brown hare: implications for management. *Journal of Wildlife Management*, 69 (2), 760-770.
63. Fink, S., Excoffier, L. and Heckel, G., 2004. Mitochondrial gene diversity in the common vole *Microtus arvalis* shaped by historical divergence and local adaptations. *Molecular Ecology*, 13 (11), 3501-3514.
64. Finnegan, L. A., Edwards, C. J. and Rochford, J. M., 2008. Origin of, and conservation units in, the Irish red squirrel (*Sciurus vulgaris*) population. *Conservation Genetics*, 9 (5), 1099-1109.
65. Fortes, G. G., Grandal-d'Anglade, A., Kolbe, B., Fernandes, D., Meleg, I. N., García-Vázquez, A., Pinto-Llona, A. C., Constantin, S., de Torres, T. J. and Ortiz, J. E., 2016. Ancient DNA reveals differences in behaviour and sociality between brown bears and extinct cave bears. *Molecular Ecology*, 25 (19), 4907-4918.
66. Frank, K., Bleier, N., Tóth, B., Sugár, L., Horn, P., Barta, E., Orosz, L. and Stéger, V., 2017. The presence of Balkan and Iberian red deer (*Cervus elaphus*) mitochondrial DNA lineages in the Carpathian Basin. *Mammalian Biology-Zeitschrift für Säugetierkunde*, 86, 48-55.
67. Fredsted, T., Wincentz, T. and Villesen, P., 2006. Introgression of mountain hare (*Lepus timidus*) mitochondrial DNA into wild brown hares (*Lepus europaeus*) in Denmark. *BMC Ecology*, 6 (1), 17.
68. Frosch, C., Dutsov, A., Zlatanova, D., Valchev, K., Reiners, T. E., Steyer, K., Pfenninger, M. and Nowak, C., 2014b. Noninvasive genetic assessment of brown bear population structure in Bulgarian mountain regions. *Mammalian Biology-Zeitschrift für Säugetierkunde*, 79 (4), 268-276.
69. Frosch, C., Kraus, R. H. S., Angst, C., Allgöwer, R., Michaux, J., Teubner, J. and Nowak, C., 2014a. The genetic legacy of multiple beaver reintroductions in Central Europe. *PLoS One*, 9 (5), e97619.
70. Fu, Q., Hajdinjak, M., Moldovan, O. T., Constantin, S., Mallick, S., Skoglund, P., Patterson, N., Rohland, N., Lazaridis, I., Nickel, B., Viola, B., Prufer, K., Meyer, M., Kelso, J., Reich, D. and Pääbo, S., 2015. An early modern human from Romania with a recent Neanderthal ancestor. *Nature*, 524 (7564), 216-219.
71. Fu, Q., Posth, C., Hajdinjak, M., Petr, M., Mallick, S., Fernandes, and Reich, D., 2016. The genetic history of Ice Age Europe. *Nature*, 534 (7606), 200-205.
72. Fu, Y., 2015. The complete mitochondrial genome of *Lepus timidus*'s genetic structure, genetic diversity and phylogenetic evolution. *Unpublished manuscript*.
73. Galov, A., Sindičić, M., Andreanszky, T., Čurkovid, S., Deždek, D., Slavica, A., Hartl, G. B. and Krueger, B., 2014. High genetic diversity and low population structure in red foxes (*Vulpes vulpes*) from Croatia. *Mammalian Biology-Zeitschrift für Säugetierkunde*, 79 (1), 77-80.
74. García, C. B., Hartasánchez, A., Bonafonte, J. I., Pando, D., Galvez, A., Magadan, J. R. and Arruga, M. V., 2009. Genetic analysis of Cantabrian brown bear by noninvasive methods. *Unpublished manuscript*.
75. Gentile, G., Vernesi, C., Vicario, S., Pecchioli, E., Caccone, A., Bertorelle, G. and Sbordoni, V., 2009. Mitochondrial DNA variation in roe deer (*Capreolus capreolus*) from Italy: Evidence of admixture in one of the last *C. c. italicus* pure populations from central-southern Italy. *Italian Journal of Zoology*, 76 (1), 16-27.

76. Giannoulis, T., Stamatis, C., Tsiourlianos, A. and Mamuris, Z., 2018. Mitogenomic analysis in European brown hare (*Lepus europaeus*) proposes genetic and functional differentiation between the distinct lineages. *Mitochondrial DNA Part A*, 29 (3), 353-360.
77. Giuffra, E., Kijas, J. M. H., Amarger, V., Carlborg, Ö., Jeon, J. T. and Andersson, L., 2000. The origin of the domestic pig: independent domestication and subsequent introgression. *Genetics*, 154 (4), 1785-1791.
78. Gomerčid, T., Sindičid, M., Galov, A., Arbanasid, H., Kusak, J., Kocijan, I., Gomerčid, M. Đ. and Huber, Đ., 2010. High genetic variability of the grey wolf (*Canis lupus* L.) population from Croatia as revealed by mitochondrial DNA control region sequences. *Zoological Studies*, 49 (6), 816-823.
79. Grill, A., Amori, G., Aloise, G., Lisi, I., Tosi, G., Wauters, L. A. and Randi, E., 2009. Molecular phylogeography of European *Sciurus vulgaris*: refuge within refugia? *Molecular Ecology*, 18 (12), 2687-2699.
80. Gugolz, D., Bernasconi, M. V., Breitenmoser-Würsten, C. and Wandeler, P., 2008. Historical DNA reveals the phylogenetic position of the extinct Alpine lynx. *Journal of Zoology*, 275 (2), 201-208.
81. Haak, W., Lazaridis, I., Patterson, N., Rohland, N., Mallick, S., Llamas, B., ... and Fu, Q., 2015. Massive migration from the steppe was a source for Indo-European languages in Europe. *Nature*, 522(7555), 207-211.
82. Haanes, H., Røed, K. H., Flagstad, Ø. and Rosef, O., 2010. Genetic structure in an expanding cervid population after population reduction. *Conservation Genetics*, 11 (1), 11-20.
83. Hailer, F., Kutschera, V. E., Hallström, B. M., Klassert, D., Fain, S. R., Leonard, J. A., Arnason, U. and Janke, A., 2012. Nuclear genomic sequences reveal that polar bears are an old and distinct bear lineage. *Science*, 336 (6079), 344-347.
84. Hajji, G. E. M. and Zachos, F. E., 2011. Mitochondrial and nuclear DNA analyses reveal pronounced genetic structuring in Tunisian wild boar *Sus scrofa*. *European Journal of Wildlife Research*, 57 (3), 449-456.
85. Hale, M. L., Lurz, P. W. W. and Wolff, K., 2004. Patterns of genetic diversity in the red squirrel (*Sciurus vulgaris* L.): Footprints of biogeographic history and artificial introductions. *Conservation Genetics*, 5 (2), 167-179.
86. Haring, E., Herzig-Straschil, B. and Spitzenberger, F., 2000. Phylogenetic analysis of Alpine voles of the *Microtus* multiplex complex using the mitochondrial control region. *Journal of Zoological Systematics and Evolutionary Research*, 38 (4), 231-238.
87. Hassanin, A., Delsuc, F., Ropiquet, A., Hammer, C., van Vuuren, B. J., Matthee, C., Ruiz-Garcia, M., Catzeflis, F., Areskoug, V. and Nguyen, T. T., 2012. Pattern and timing of diversification of Cetartiodactyla (Mammalia, Laurasiatheria), as revealed by a comprehensive analysis of mitochondrial genomes. *Comptes Rendus Biologies*, 335 (1), 32-50.
88. Heckel, G., Burri, R., Fink, S., Desmet, J. F. and Excoffier, L., 2005. Genetic structure and colonization processes in European populations of the common vole, *Microtus arvalis*. *Evolution*, 59 (10), 2231-2242.
89. Hegyeli, Z., Kecskés, A., Korbut, Z. and Banaszek, A., 2015. The distribution and genetic diversity of the common hamster *Cricetus cricetus* in Central and Western Romania. *Folia Zoologica*, 64 (2), 173-182.
90. Hellborg, L., Walker, C. W., Rueness, E. K., Stacy, J. E., Kojola, I., Valdmann, H., Vilà, C., Zimmermann, B., Jakobsen, K. S. and Ellegren, H., 2002. Differentiation and levels of genetic variation in northern European lynx (*Lynx lynx*) populations revealed by microsatellites and mitochondrial DNA analysis. *Conservation Genetics*, 3 (2), 97-111.
91. Hervella, M., Izagirre, N., Alonso, S., Fregel, R., Alonso, A., Cabrera, V.M., and de la Rua, C., 2012. Ancient DNA from hunter-gatherer and farmer groups from Northern Spain supports a random dispersion model for the Neolithic expansion into Europe. *PLoS One*, 7, e34417.
92. Hmwe, S. S., Zachos, F. E., Sale, J. B., Rose, H. R. and Hartl, G. B., 2006. Genetic variability and differentiation in red deer (*Cervus elaphus*) from Scotland and England. *Journal of Zoology*, 270 (3), 479-487.
93. Hofmanová, Z., Kreutzer, S., Hellenthal, G., Sell, C., Diekmann, Y., Díez-del-Molino, D., ... and Kirsanow, K., 2016. Early farmers from across Europe directly descended from Neolithic Aegeans. *Proceedings of the National Academy of Sciences USA*, 113(25), 6886- 6891.

94. Hofreiter, M., Serre, D., Rohland, N., Rabeder, G., Nagel, D., Conard, N., Münzel, S. and Pääbo, S., 2004. Lack of phylogeography in European mammals before the last glaciation. *Proceedings of the National Academy of Sciences USA*, 101 (35), 12963-12968.
95. Horn, S., Durka, W., Wolf, R., Ermala, A., Stubbe, A., Stubbe, M. and Hofreiter, M., 2011. Mitochondrial genomes reveal slow rates of molecular evolution and the timing of speciation in beavers (*Castor*), one of the largest rodent species. *PLoS One*, 6 (1), e14622.
96. Horn, S., Prost, S., Stiller, M., Makowiecki, D., Kuznetsova, T., Benecke, N., Pucher, E., Hufthammer, A. K., Schouwenburg, C. and Shapiro, B., 2014. Ancient mitochondrial DNA and the genetic history of E urasian beaver (*Castor fiber*) in Europe. *Molecular Ecology*, 23 (7), 1717-1729.
97. Hosoda, T., Sato, J. J., Lin, L. K., Chen, Y. J., Harada, M. and Suzuki, H., 2011. Phylogenetic history of mustelid fauna in Taiwan inferred from mitochondrial genetic loci. *Canadian Journal of Zoology*, 89 (6), 559-569.
98. Hundertmark, K. J., Shields, G. F., Udina, I. G., Bowyer, R. T., Danilkin, A. A. and Schwartz, C. C., 2002. Mitochondrial phylogeography of moose (*Alces alces*): Late Pleistocene divergence and population expansion. *Molecular Phylogenetics and Evolution*, 22 (3), 375-387.
99. Inoue, T., Nonaka, N., Mizuno, A., Morishima, Y., Sato, H., Katakura, K. and Oku, Y., 2007. Mitochondrial DNA phylogeography of the red fox (*Vulpes vulpes*) in northern Japan. *Zoological Science*, 24 (12), 1178-1186.
100. Jansson, E., Harmoinen, J., Ruokonen, M. and Aspi, J., 2014. Living on the edge: reconstructing the genetic history of the Finnish wolf population. *BMC Evolutionary Biology*, 14 (1), 64.
101. Johansson, P., Olsson, G. E., Low, H.-T., Bucht, G., Ahlm, C., Juto, P. and Elgh, F., 2008. Puumala hantavirus genetic variability in an endemic region (Northern Sweden). *Infection, Genetics and Evolution*, 8 (3), 286-296.
102. Kangas, V. M., Kvist, L., Kholodova, M., Nygrén, T., Danilov, P., Panchenko, D., Fraimout, A. and Aspi, J., 2015. Evidence of post-glacial secondary contact and subsequent anthropogenic influence on the genetic composition of Fennoscandian moose (*Alces alces*). *Journal of Biogeography*, 42 (11), 2197-2208.
103. Kasapidis, P., Suchentrunk, F., Magoulas, A. and Kotoulas, G., 2005. The shaping of mitochondrial DNA phylogeographic patterns of the brown hare (*Lepus europaeus*) under the combined influence of Late Pleistocene climatic fluctuations and anthropogenic translocations. *Molecular Phylogenetics and Evolution*, 34 (1), 55-66.
104. Kholodova, M. V., Korytin, N. S. and Bolshakov, V. N., 2014. The role of the Urals in the genetic diversity of the European moose subspecies (*Alces alces alces*). *Biology Bulletin*, 41 (6), 522-528.
105. Kim, B. W., Cho, I. C., Park, M. S., Zhong, T., Lim, H. T., Lee, S. S., ... and Jeon, J. T., 2011. Characterization of the European type of maternal lineage evident in extant Jeju native pigs. *Genes & Genomics*, 33(2), 111-117.
106. Kirschning, J., Zachos, F. E., Cirovic, D., Radovic, I. T., San Hmwe, S. and Hartl, G. B., 2007. Population genetic analysis of Serbian red foxes (*Vulpes vulpes*) by means of mitochondrial control region sequences. *Biochemical Genetics*, 45 (5-6), 409-420.
107. Koblmüller, S., Vilà, C., Lorente-Galdos, B., Dabad, M., Ramirez, O., Marques-Bonet, T., Wayne, R. K. and Leonard, J. A., 2016. Whole mitochondrial genomes illuminate ancient intercontinental dispersals of grey wolves (*Canis lupus*). *Journal of Biogeography*, 43 (9), 1728-1738.
108. Kocijan, I., Galov, A., Detkovid, H., Kusak, J., Gomerčid, T. and Huber, Đ., 2011. Genetic diversity of Dinaric brown bears (*Ursus arctos*) in Croatia with implications for bear conservation in Europe. *Mammalian Biology-Zeitschrift für Säugetierkunde*, 76 (5), 615-621.
109. Koepfli, K.-P., Pollinger, J., Godinho, R., Robinson, J., Lea, A., Hendricks, S., Schweizer, R. M., Thalmann, O., Silva, P. and Fan, Z., 2015. Genome-wide evidence reveals that African and Eurasian golden jackals are distinct species. *Current Biology*, 25 (16), 2158-2165.
110. Korablev, M. P., Korablev, N. P., Korablev, P. N. and Tumanov, I. L., 2017. Intrapopulation polymorphism of the pine marten (*Martes martes*, Carnivora, Mustelidae) from Tver Oblast. *Biology Bulletin*, 44 (7), 794-806.

111. Korsten, M., Ho, S. Y. W., Davison, J., Pähni, B., Vulla, E., Roht, M., Tumanov, I. L., Kojola, I., Andersone-Lilley, Z. and Ozolins, J., 2009. Sudden expansion of a single brown bear maternal lineage across northern continental Eurasia after the last ice age: a general demographic model for mammals? *Molecular Ecology*, 18 (9), 1963-1979.
112. Krause, J., Briggs, A. W., Kircher, M., Maricic, T., Zwyns, N., Derevianko, A., and Pääbo, S., 2010. A complete mtDNA genome of an early modern human from Kostenki, Russia. *Current Biology*, 20(3), 231-236.
113. Krojerová-Prokešová, J., Barančková, M. and Koubek, P., 2015. Admixture of eastern and western European red deer lineages as a result of postglacial recolonization of the Czech Republic (Central Europe). *Journal of Heredity*, 106 (4), 375-385.
114. Kropf, M., Hölzler, G. and Parz-Gollner, R., 2013. Genetički dokazi o porijeklu današnje populacije europskog dabra (*Castor fiber*) u donjoj austriji. *Šumarski list*, 137 (11-12), 591-596.
115. Kurose, N., Abramov, A. V. and Masuda, R., 2005. Comparative phylogeography between the ermine *Mustela erminea* and the least weasel *M. nivalis* of Palaearctic and Nearctic regions, based on analysis of mitochondrial DNA control region sequences. *Zoological Science*, 22 (10), 1069-1078.
116. Kurose, N., Masuda, R. and Yoshida, M. C., 1999. Phylogeographic variation in two mustelines, the least weasel *Mustela nivalis* and the ermine *M. erminea* of Japan, based on mitochondrial DNA control region sequences. *Zoological Science*, 16 (6), 971-977.
117. Kusza, S., Podgorski, T., Scandura, M., Borowik, T., Jávora, A., Sidorovich, V. E., Bunevich, A. N., Kolesnikov, M. and Jędrzejewska, B., 2014. Contemporary genetic structure, phylogeography and past demographic processes of wild boar *Sus scrofa* population in Central and Eastern Europe. *PLoS One*, 9 (3), e91401.
118. Kutschera, V. E., Lecomte, N., Janke, A., Selva, N., Sokolov, A. A., Haun, T., Steyer, K., Nowak, C. and Hailer, F., 2013. A range-wide synthesis and timeline for phylogeographic events in the red fox (*Vulpes vulpes*). *BMC Evolutionary Biology*, 13 (1), 114.
119. Larson, G., Albarella, U., Dobney, K., Rowley-Conwy, P., Schibler, J., Tresset, A., Vigne, J. D., Edwards, C. J., Schlumbaum, A., Dinu, A., Balacescu, A., Dolman, G., Tagliacozzo, A., Manaseryan, N., Miracle, P., Van Wijngaarden-Bakker, L., Masseti, M., Bradley, D. G. and Cooper, A., 2007. Ancient DNA, pig domestication, and the spread of the Neolithic into Europe. *Proceedings of the National Academy of Sciences USA*, 104 (39), 15276-15281.
120. Larson, G., Dobney, K., Albarella, U., Fang, M., Matisoo-Smith, E., Robins, J., Lowden, S., Finlayson, H., Brand, T., Willerslev, E., Rowley-Conwy, P., Anderson, L. and Cooper, A. 2005. Worldwide phylogeography of wild boar reveals multiple centers of pig domestication. *Science*, 307 (5715), 1618-1621.
121. Lazaridis, I., Nadel, D., Rollefson, G., Merrett, D. C., Rohland, N., Mallick, S., ... and Connell, S., 2016. Genomic insights into the origin of farming in the ancient Near East. *Nature*, 536(7617), 419-424.
122. Lazaridis, I., Patterson, N., Mittnik, A., Renaud, G., Mallick, S., Kirsanow, K., Sudmant, P. H., Schraiber, J. G., Castellano, S. and Lipson, M., 2014. Ancient human genomes suggest three ancestral populations for present-day Europeans. *Nature*, 513 (7518), 409-413.
123. Lebarbenchon, C., Poitevin, F., Arnal, V. and Montgelard, C., 2010. Phylogeography of the weasel (*Mustela nivalis*) in the western-Palaearctic region: combined effects of glacial events and human movements. *Heredity*, 105 (5), 449-462.
124. Lebarbenchon, C., Poitevin, F. and Montgelard, C., 2006. Genetic variation of the weasel (*Mustela nivalis*) in Corsica based on mitochondrial control region sequences. *Mammalian Biology-Zeitschrift für Saugetierkunde*, 71 (3), 164-171.
125. Leite, J. V., Álvares, F., Velo-Antón, G., Brito, J. C. and Godinho, R., 2015. Differentiation of North African foxes and population genetic dynamics in the desert—insights into the evolutionary history of two sister taxa, *Vulpes rueppellii* and *Vulpes vulpes*. *Organisms Diversity & Evolution*, 15 (4), 731-745.

126. Leonard, J. A., Wayne, R. K. and Cooper, A., 2000. Population genetics of Ice Age brown bears. *Proceedings of the National Academy of Sciences USA*, 97 (4), 1651-1654.
127. Li, G., Davis, B. W., Eizirik, E. and Murphy, W. J., 2016. Phylogenomic evidence for ancient hybridization in the genomes of living cats (Felidae). *Genome Research*, 26 (1), 1-11.
128. Liu, Z., Li, B., Ma, J., Zheng, D. and Xu, Y., 2014. Phylogeography and genetic diversity of the red squirrel (*Sciurus vulgaris*) in China: Implications for the species' postglacial expansion history. *Mammalian Biology-Zeitschrift für Säugetierkunde*, 79 (4), 247-253.
129. Liu, J., Yu, L., Arnold, M. L., Wu, C.-H., Wu, S.-F., Lu, X. and Zhang, Y.-P., 2011. Reticulate evolution: frequent introgressive hybridization among Chinese hares (genus *Lepus*) revealed by analyses of multiple mitochondrial and nuclear DNA loci. *BMC Evolutionary Biology*, 11 (1), 223.
130. Lorenzini, R., Garofalo, L., Qin, X., Voloshina, I. and Lovari, S., 2014. Global phylogeography of the genus *Capreolus* (Artiodactyla: Cervidae), a Palearctic meso-mammal. *Zoological Journal of the Linnean Society*, 170 (1), 209-221.
131. Lucas, J. M., Prieto, P. and Galián, J., 2015. Red squirrels from south-east Iberia: low genetic diversity at the southernmost species distribution limit. *Animal Biodiversity and Conservation*, 38 (1), 129-138.
132. Madsen, C. L., Vilstrup, J. T., Fernández, R., Marchi, N., Håkansson, B., Krog, M., Asferg, T., Baagøe, H. and Orlando, L., 2015. Mitochondrial genetic diversity of Eurasian red squirrels (*Sciurus vulgaris*) from Denmark. *Journal of Heredity*, 106 (6), 719-727.
133. Malmström, H., Gilbert, M. T. P., Thomas, M. G., Brandström, M., Storå, J., Molnar, P., ... and Willerslev, E., 2009. Ancient DNA reveals lack of continuity between Neolithic hunter-gatherers and contemporary Scandinavians. *Current Biology*, 19(20), 1758-1762.
134. Malmström, H., Linderholm, A., Skoglund, P., Storå, J., Sjödin, P., Gilbert, M.T.P., ... Götherström, A., 2015. Ancient mitochondrial DNA from the northern fringe of the Neolithic farming expansion in Europe sheds light on the dispersion process. *Philosophical Transaction of the Royal Society B*, 370, 20130373.
135. Martínková, N., McDonald, R. A. and Searle, J. B., 2007. Stoats (*Mustela erminea*) provide evidence of natural overland colonization of Ireland. *Proceedings of the Royal Society of London B: Biological Sciences*, 274 (1616), 1387-1393.
136. Massilani, D., Guimaraes, S., Brugal, J.-P., Bennett, E. A., Tokarska, M., Arbogast, R.-M., Baryshnikov, G., Boeskorov, G., Castel, J.-C. and Davydov, S., 2016. Past climate changes, population dynamics and the origin of Bison in Europe. *BMC Biology*, 14 (1), 93.
137. Masuda, R., Amano, T. and Ono, H., 2001. Ancient DNA analysis of brown bear (*Ursus arctos*) remains from the archeological site of Rebun Island, Hokkaido, Japan. *Zoological Science*, 18 (5), 741-751.
138. Mathieson, I., Lazaridis, I., Rohland, N., Mallick, S., Patterson, N., Roodenberg, S. A., ... and Sirak, K., 2015. Genome-wide patterns of selection in 230 ancient Eurasians. *Nature*, 528(7583), 499-503.
139. Matosiuk, M., Borkowska, A., Świsłocka, M., Mirski, P., Borowski, Z., Krysiuk, K., Danilkin, A. A., Zvyachaynaya, E. Y., Saveljev, A. P. and Ratkiewicz, M., 2014. Unexpected population genetic structure of European roe deer in Poland: an invasion of the mtDNA genome from Siberian roe deer. *Molecular Ecology*, 23 (10), 2559-2572.
140. Matson, C. W. and Baker, R. J., 2001. DNA sequence variation in the mitochondrial control region of red-backed voles (*Clethrionomys*). *Molecular Biology and Evolution*, 18 (8), 1494-1501.
141. Matson, C. W., Rodgers, B. E., Chessier, R. K. and Baker, R. J., 2000. Genetic diversity of *Clethrionomys glareolus* populations from highly contaminated sites in the Chornobyl region, Ukraine. *Environmental Toxicology and Chemistry*, 19 (8), 2130-2135.
142. McDevitt, A. D., Rambau, R. V., O'Brien, J., McDevitt, C. D., Hayden, T. J. and Searle, J. B., 2009. Genetic variation in Irish pygmy shrews *Sorex minutus* (Soricomorpha: Soricidae): implications for colonization history. *Biological Journal of the Linnean Society*, 97 (4), 918-927.

143. McDevitt, A. D., Vega, R., Rambau, R. V., Yannic, G., Herman, J. S., Hayden, T. J. and Searle, J. B., 2011. Colonization of Ireland: revisiting 'the pygmy shrew syndrome' using mitochondrial, Y chromosomal and microsatellite markers. *Heredity*, 107 (6), 548-557.
144. McDevitt, A. D., Yannic, G., Rambau, R. V., Hayden, T. J. and Searle, J. B., 2010. Postglacial recolonization of continental Europe by the pygmy shrew (*Sorex minutus*) inferred from mitochondrial and Y chromosomal DNA sequences. *Relict species*. Springer, 217-236.
145. Meeks, H. N., Chessser, R. K., Rodgers, B. E., Gaschak, S. and Baker, R. J., 2009. Understanding the genetic consequences of environmental toxicant exposure: Chernobyl as a model system. *Environmental Toxicology and Chemistry*, 28 (9), 1982-1994.
146. Meeks, H. N., Wickliffe, J. K., Hoofer, S. R., Chessser, R. K., Rodgers, B. E. and Baker, R. J., 2007. Mitochondrial control region variation in bank voles (*Clethrionomys glareolus*) is not related to Chernobyl radiation exposure. *Environmental Toxicology and Chemistry*, 26 (2), 361-369.
147. Meiri, M., Lister, A. M., Higham, T. F. G., Stewart, J. R., Straus, L. G., Obermaier, H., Gonzalez Morales, M. R., Marín-Arroyo, A. B. and Barnes, I., 2013. Late-glacial recolonization and phylogeography of European red deer (*Cervus elaphus* L.). *Molecular Ecology*, 22 (18), 4711-4722.
148. Menéndez, J., Goyache, F., Beja-Pereira, A., Fernández, I., Menéndez-Arias, N. A., Godinho, R., and Álvarez, I., 2016. Genetic characterisation of the endangered Gochu Asturcelta pig breed using microsatellite and mitochondrial markers: Insights for the composition of the Iberian native pig stock. *Livestock Science*, 187, 162-167.
149. Melo-Ferreira, J., Boursot, P., Carneiro, M., Esteves, P. J., Farelo, L. and Alves, P. C., 2011. Recurrent introgression of mitochondrial DNA among hares (*Lepus spp.*) revealed by species-tree inference and coalescent simulations. *Systematic Biology*, 61 (3), 367-381.
150. Melo-Ferreira, J., Boursot, P., Randi, E., Kryukov, A., Suchentrunk, F., Ferrand, N. and Alves, P. C., 2007. The rise and fall of the mountain hare (*Lepus timidus*) during Pleistocene glaciations: expansion and retreat with hybridization in the Iberian Peninsula. *Molecular Ecology*, 16 (3), 605-618.
151. Melo-Ferreira, J., Vilela, J., Fonseca, M. M., da Fonseca, R. R., Boursot, P. and Alves, P. C., 2014. The elusive nature of adaptive mitochondrial DNA evolution of an arctic lineage prone to frequent introgression. *Genome Biology and Evolution*, 6 (4), 886-896.
152. Mengoni, C., Mucci, N. and Randi, E., 2015. Genetic diversity and no evidences of recent hybridization in the endemic Italian hare (*Lepus corsicanus*). *Conservation Genetics*, 16 (2), 477-489.
153. Menzies, B. R., Barbara, D., Kathleen, R., Robert, H., Frank, G. and Thomas, H., 2010. British hares are derived from very recent translocations of the central European clade of brown hare, *Lepus europaeus*. *Unpublished manuscript*.
154. Montana, L., Caniglia, R., Galaverni, M., Fabbri, E. and Randi, E., 2017. A new mitochondrial haplotype confirms the distinctiveness of the Italian wolf (*Canis lupus*) population. *Mammalian Biology-Zeitschrift für Säugetierkunde*, 84, 30-34.
155. Moskvitina, N. S., Nemoikina, O. V., Tyuten'kov, O. Y. and Kholodova, M. V., 2011. Retrospective evaluation and modern state of the moose (*Alces alces* L.) population in West Siberia: Ecological and molecular-genetic aspects. *Contemporary Problems of Ecology*, 4 (4), 444.
156. Mucci, N., Mattucci, F. and Randi, E., 2012. Conservation of threatened local gene pools: landscape genetics of the Italian roe deer (*Capreolus c. italicus*) populations. *Evolutionary Ecology Research*, 14 (7), 897-920.
157. Murtskhvaladze, M., Gavashelishvili, A. and Tarkhnishvili, D., 2010. Geographic and genetic boundaries of brown bear (*Ursus arctos*) population in the Caucasus. *Molecular Ecology*, 19 (9), 1829-1841.

158. Nagai, T., Raichev, E. G., Tsunoda, H., Kaneko, Y. and Masuda, R., 2012. Preliminary study on microsatellite and mitochondrial DNA variation of the stone marten *Martes foina* in Bulgaria. *Mammal Study*, 37 (4), 353-358.
159. Nemoikina, O. V., Kholodova, M. V., Tyutenkov, O. Y. and Moskvitina, N. S., 2016. Mitotypical peculiarities of the population of moose *Alces alces* of southeastern West Siberia. *Biology Bulletin*, 43 (4), 335-343.
160. Neumann, K., Jansman, H., Kayser, A., Maak, S. and Gattermann, R., 2004. Multiple bottlenecks in threatened western European populations of the common hamster *Cricetus cricetus* (L.). *Conservation Genetics*, 5 (2), 181-193.
161. Niedziałkowska, M., Fontaine, M. C. and Jędrzejewska, B., 2012. Factors shaping gene flow in red deer (*Cervus elaphus*) in seminatural landscapes of central Europe. *Canadian Journal of Zoology*, 90 (2), 150-162.
162. Niedziałkowska, M., Hundertmark, K. J., Jędrzejewska, B., Niedziałkowski, K., Sidorovich, V. E., Górny, M., Veeroja, R., Solberg, E. J., Laaksonen, S. and Sand, H., 2014. Spatial structure in European moose (*Alces alces*): genetic data reveal a complex population history. *Journal of Biogeography*, 41 (11), 2173-2184.
163. Niedziałkowska, M., Jędrzejewska, B., Honnen, A.-C., Otto, T., Sidorovich, V. E., Perzanowski, K., Skog, A., Hartl, G. B., Borowik, T. and Bunevich, A. N., 2011. Molecular biogeography of red deer *Cervus elaphus* from eastern Europe: insights from mitochondrial DNA sequences. *Acta Theriologica*, 56 (1), 1-12.
164. Nielsen, E. K., Olesen, C. R., Pertoldi, C., Gravlund, P., Barker, J. S. F., Mucci, N., Randi, E. and Loeschcke, V., 2008. Genetic structure of the Danish red deer (*Cervus elaphus*). *Biological Journal of the Linnean Society*, 95 (4), 688-701.
165. Nussey, D. H., Pemberton, J., Donald, A. and Kruuk, L. E. B., 2006. Genetic consequences of human management in an introduced island population of red deer (*Cervus elaphus*). *Heredity*, 97 (1), 56-65.
166. Okumura, N., Ishiguro, N., Nakano, M., Hirai, K., Matsui, A., and Sahara, M., 1996. Geographic population structure and sequence divergence in the mitochondrial DNA control region of the Japanese wild boar (*Sus scrofa leucomystax*), with reference to those of domestic pigs. *Biochemical Genetics*, 34(5-6), 179-189.
167. Olalde, I., Allentoft, M. E., Sánchez-Quinto, F., Santpere, G., Chiang, C. W., DeGiorgio, M., ... and Ramírez, O., 2014. Derived immune and ancestral pigmentation alleles in a 7,000- year-old Mesolithic European. *Nature*, 507(7491), 225-228.
168. Olano-Marin, J., Plis, K., Sönnichsen, L., Borowik, T., Niedziałkowska, M. and Jędrzejewska, B., 2014. Weak population structure in European roe deer (*Capreolus capreolus*) and evidence of introgressive hybridization with Siberian roe deer (*C. pygargus*) in northeastern Poland. *PLoS One*, 9 (10), e109147.
169. Ottoni, C., Girdland Flink, L., Evin, A., Geörg, C., De Cupere, B., Van Neer, W., ... and Decorte, R., 2012. Pig domestication and human-mediated dispersal in western Eurasia revealed through ancient DNA and geometric morphometrics. *Molecular Biology and Evolution*, 30(4), 824-832.
170. Paijmans, J. L. A., Fickel, J., Courtiol, A., Hofreiter, M. and Förster, D. W., 2016. Impact of enrichment conditions on cross-species capture of fresh and degraded DNA. *Molecular Ecology Resources*, 16 (1), 42-55.
171. Pérez-Espona, S., Pérez-Barbería, F. J., Goodall-Copestake, W. P., Jiggins, C. D., Gordon, I. J. and Pemberton, J. M., 2009. Genetic diversity and population structure of Scottish Highland red deer (*Cervus elaphus*) populations: a mitochondrial survey. *Heredity*, 102 (2), 199-210.
172. Pertoldi, C., Barker, S. F., Madsen, A. B., Jørgensen, H., Randi, E., Muñoz, J., Baagoe, H. J. and Loeschcke, V., 2008. Spatio-temporal population genetics of the Danish pine marten (*Martes martes*). *Biological Journal of the Linnean Society*, 93 (3), 457-464.
173. Pertoldi, C., Elschot, K., Ruiz-Gonzalez, A., van de Zande, L., Zalewski, A., Muñoz, J., Madsen, A. B., Loeschcke, V., de Groot, A. and Bijlsma, R., 2014. Genetic variability of central– western European pine marten (*Martes martes*) populations. *Acta Theriologica*, 59 (4), 503-510.

174. Pierpaoli, M., Riga, F., Trocchi, V. and Randi, E., 1999. Species distinction and evolutionary relationships of the Italian hare (*Lepus corsicanus*) as described by mitochondrial DNA sequencing. *Molecular Ecology*, 8 (11), 1805-1817.
175. Pierny, S. B., Stewart, W. A., Lambin, X., Telfer, S., Aars, J. and Dallas, J. F., 2005. Phylogeographic structure and postglacial evolutionary history of water voles (*Arvicola terrestris*) in the United Kingdom. *Molecular Ecology*, 14 (5), 1435-1444.
176. Pietri, C., Alves, P. C. and Melo-Ferreira, J., 2011. Hares in Corsica: high prevalence of *Lepus corsicanus* and hybridization with introduced *L. europaeus* and *L. granatensis*. *European Journal of Wildlife Research*, 57 (2), 313-321.
177. Pilot, M., Branicki, W., Jędrzejewski, W., Goszczyński, J., Jędrzejewska, B., Dykyy, I., Shkvrya, M. and Tsingarska, E., 2010. Phylogeographic history of grey wolves in Europe. *BMC Evolutionary Biology*, 10 (1), 104.
178. Pilot, M., Greco, C., Jędrzejewska, B., Randi, E., Jędrzejewski, W., Sidorovich, V. E., Ostrander, E. A. and Wayne, R. K., 2014. Genome-wide signatures of population bottlenecks and diversifying selection in European wolves. *Heredity*, 112 (4), 428-442.
179. Pilot, M., Jędrzejewski, W., Branicki, W., Sidorovich, V. E., Jędrzejewska, B., Stachura, K. and Funk, S. M., 2006. Ecological factors influence population genetic structure of European grey wolves. *Molecular Ecology*, 15 (14), 4533-4553.
180. Polziehn, R. O. and Strobeck, C., 1998. Phylogeny of wapiti, red deer, sika deer, and other North American cervids as determined from mitochondrial DNA. *Molecular Phylogenetics and Evolution*, 10 (2), 249-258.
181. Posth, C., Wißing, C., Kitagawa, K., Pagani, L., van Holstein, L., Racimo, F., Wehrberger, K., Conard, N. J., Kind, C. J. and Bocherens, H., 2017. Deeply divergent archaic mitochondrial genome provides lower time boundary for African gene flow into Neanderthals. *Nature Communications*, 8, 16046.
182. Prost, S., Knapp, M., Flemmig, J., Hufthammer, A. K., Kosintsev, P., Stiller, M. and Hofreiter, M., 2010. A phantom extinction? New insights into extinction dynamics of the Don-hare *Lepus tanaiticus*. *Journal of Evolutionary Biology*, 23 (9), 2022-2029.
183. Pūraitė, I., Paulauskas, A., Sruoga, A. and Prakas, P., 2014. Mitochondrial DNA variation in roe deer population from Lithuania. *Balkan Journal of Wildlife Research*, 1 (1), 13-19.
184. Randi, E., Alves, P. C., Carranza, J., Milošević-Zlatanović, S., Sfougaris, A. and Mucci, N., 2004. Phylogeography of roe deer (*Capreolus capreolus*) populations: the effects of historical genetic subdivisions and recent nonequilibrium dynamics. *Molecular Ecology*, 13 (10), 3071-3083.
185. Randi, E., Lucchini, V., Christensen, M. F., Mucci, N., Funk, S. M., Dolf, G. and Loeschcke, V., 2000. Mitochondrial DNA variability in Italian and East European wolves: detecting the consequences of small population size and hybridization. *Conservation Biology*, 14 (2), 464-473.
186. Raghavan, M., Skoglund, P., Graf, K. E., Metspalu, M., Albrechtsen, A., Moltke, I., and Karmin, M., 2014. Upper Palaeolithic Siberian genome reveals dual ancestry of Native Americans. *Nature*, 505(7481), 87-91.
187. Ratkiewicz, M., Matosiuk, M., Saveljev, A. P., Sidorovich, V., Ozolins, J., Männil, P., Balčiauskas, L., Kojola, I., Okarma, H. and Kowalczyk, R., 2014. Long-range gene flow and the effects of climatic and ecological factors on genetic structuring in a large, solitary carnivore: the Eurasian lynx. *PLoS One*, 9 (12), e115160.
188. Razzauti, M., Plyusnina, A., Niemimaa, J., Henttonen, H. and Plyusnin, A., 2012. Co-circulation of two Puumala hantavirus lineages in Latvia: A Russian lineage described previously and a novel Latvian lineage. *Journal of Medical Virology*, 84 (2), 314-318.
189. Reyes, A., Gissi, C., Pesole, G., Catzeflis, F. M. and Saccone, C., 2000. Where do rodents fit? Evidence from the complete mitochondrial genome of *Sciurus vulgaris*. *Molecular Biology and Evolution*, 17 (6), 979-983.
190. Rézouki, C., Dozières, A., Le Coeur, C., Thibault, S., Pisanu, B., Chapuis, J.-L. and Baudry, E., 2014. A viable population of the European red squirrel in an urban park. *PLoS One*, 9 (8), e105111.

191. Rodrigues, M., Bos, A. R., Hoath, R., Schembri, P. J., Lymberakis, P., Cento, M., Ghawar, W., Ozkurt, S. O., Santos-Reis, M. and Merilä, J., 2016. Taxonomic status and origin of the Egyptian weasel (*Mustela subpalmata*) inferred from mitochondrial DNA. *Genetica*, 144 (2), 191-202.
192. Rodríguez-Varela, R., García, N., Nores, C., Álvarez-Lao, D., Barnett, R., Arsuaga, J. L. and Valdiosera, C., 2016. Ancient DNA reveals past existence of Eurasian lynx in Spain. *Journal of Zoology*, 298 (2), 94-102.
193. Rodríguez-Varela, R., Tagliacozzo, A., Ureña, I., García, N., Crégut-Bonnoure, E., Mannino, M. A., Arsuaga, J. L. and Valdiosera, C., 2015. Ancient DNA evidence of Iberian lynx palaeoendemism. *Quaternary Science Reviews*, 112, 172-180.
194. Rosvold, J., Røed, K. H., Hufthammer, A. K., Andersen, R. and Stenøien, H. K., 2012. Reconstructing the history of a fragmented and heavily exploited red deer population using ancient and contemporary DNA. *BMC Evolutionary Biology*, 12 (1), 191.
195. Royo, L. J., Pajares, G., Alvarez, I., Fernández, I. and Goyache, F., 2007. Genetic variability and differentiation in Spanish roe deer (*Capreolus capreolus*): a phylogeographic reassessment within the European framework. *Molecular Phylogenetics and Evolution*, 42 (1), 47-61.
196. Rozhnov, V. V., Meschersky, I. G., Pishchulina, S. L. and Simakin, L. V., 2010. Genetic analysis of sable (*Martes zibellina*) and pine marten (*M. martes*) populations in sympatric part of distribution area in the northern Urals. *Russian Journal of Genetics*, 46 (4), 488-492.
197. Rueness, E. K., Naidenko, S., Trosvik, P. and Stenseth, N. C., 2014. Large-scale genetic structuring of a widely distributed carnivore-the Eurasian lynx (*Lynx lynx*). *PLoS One*, 9 (4), e93675.
198. Ruiz-González, A., Madeira, M. J., Randi, E., Abramov, A. V., Davoli, F. and Gómez-Moliner, B. J., 2013. Phylogeography of the forest-dwelling European pine marten (*Martes martes*): new insights into cryptic northern glacial refugia. *Biological Journal of the Linnean Society*, 109 (1), 1-18.
199. Ruiz-González, A., Rubines, J., Berdión, O. and Gómez-Moliner, B. J., 2008. A non-invasive genetic method to identify the sympatric mustelids pine marten (*Martes martes*) and stone marten (*Martes foina*): preliminary distribution survey on the northern Iberian Peninsula. *European Journal of Wildlife Research*, 54 (2), 253-261.
200. Salomashkina, V. V., Kholodova, M. V., Semenov, U. A., Muradov, A. S. and Malkhasyan, A., 2017. Genetic variability of brown bear (*Ursus arctos* L., 1758). *Russian Journal of Genetics*, 53 (1), 108-117.
201. Salomashkina, V. V., Kholodova, M. V., Tuten'kov, O. Y., Moskvitina, N. S. and Erokhin, N. G., 2014. New data on the phylogeography and genetic diversity of the brown bear *Ursus arctos* Linnaeus, 1758 of Northeastern Eurasia (mtDNA control region polymorphism analysis). *Biology Bulletin*, 41 (1), 38-46.
202. Sánchez-Quinto, F., Schroeder, H., Ramirez, O., Ávila-Arcos, M. C., Pybus, M., Olalde, I., Velazquez, A. M. V., Marcos, M. E. P., Encinas, J. M. V. and Bertranpetit, J., 2012. Genomic affinities of two 7,000-year-old Iberian hunter-gatherers. *Current Biology*, 22 (16), 1494-1499.
203. Sanz-Martín, M. J., Estonba, A., Manzano, C., Iriondo, M., Pérez-Suárez, G., Fernández, A. and Palacios, F., 2014. Genetic structure of brown and Iberian hare populations in northern Iberia: Implications for conservation of genetic diversity. *Journal of Wildlife Management*, 78 (4), 632-644.
204. Scandura, M., Iacolina, L., Crestanello, B., Pecchioli, E., Di Benedetto, M. F., Russo, V., Davoli, R., Apollonio, M. and Bertorelle, G., 2008. Ancient vs. recent processes as factors shaping the genetic variation of the European wild boar: are the effects of the last glaciation still detectable? *Molecular Ecology*, 17 (7), 1745-1762.
205. Schmidt, A. and Fickel, J., 2005. Periglacial survival and postglacial re-colonization of central Europe - Origin of today's genetic structure in European brown hare (*Lepus europaeus* Pallas, 1778). *Unpublished manuscript*.
206. Schröder, O., Astrin, J. and Hutterer, R., 2014. White chest in the west: pelage colour and mitochondrial variation in the common hamster (*Cricetus cricetus*) across Europe. *Acta Theriologica*, 59 (2), 211-221.

207. Seddon, J. M., Santucci, F., Reeve, N. J. and Hewitt, G. M., 2001. DNA footprints of European hedgehogs, *Erinaceus europaeus* and *E. concolor*: Pleistocene refugia, postglacial expansion and colonization routes. *Molecular Ecology*, 10 (9), 2187-2198.
208. Seguin-Orlando, A., Korneliusson, T. S., Sikora, M., Malaspinas, A. S., Manica, A., Moltke, I., and Goebel, T., 2014. Genomic structure in Europeans dating back at least 36,200 years. *Science*, 346(6213), 1113-1118.
209. Senn, H., Ogden, R., Frosch, C., Syrůčková, A., Campbell-Palmer, R., Munclinger, P., Durka, W., Kraus, R. H. S., Saveljev, A. P. and Nowak, C., 2014. Nuclear and mitochondrial genetic structure in the Eurasian beaver (*Castor fiber*)—implications for future reintroductions. *Evolutionary Applications*, 7 (6), 645-662.
210. Sert, H., Slimen, H. B., Erdoğan, A. and Suchentrunk, F., 2009. Mitochondrial HVI sequence variation in Anatolian hares (*Lepus europaeus* Pallas, 1778). *Mammalian Biology- Zeitschrift für Säugetierkunde*, 74 (4), 286-297.
211. Simpson, S., Blampied, N., Peniche, G., Dozières, A., Blackett, T., Coleman, S., Cornish, N. and Groombridge, J. J., 2013. Genetic structure of introduced populations: 120-year-old DNA footprint of historic introduction in an insular small mammal population. *Ecology and Evolution*, 3 (3), 614-628.
212. Sindičid, M., 2015. Direct submission to Genbank. *Unpublished manuscript*.
213. Sindičid, M., Gomerčid, T., Galov, A., Polanc, P., Huber, Đ. and Slavica, A., 2012. Repetitive sequences in Eurasian lynx (*Lynx lynx* L.) mitochondrial DNA control region. *Mitochondrial DNA*, 23 (3), 201-207.
214. Skog, A., Zachos, F. E., Rueness, E. K., Feulner, P. G. D., Mysterud, A., Langvatn, R., Lorenzini, R., Hmwe, S. S., Lehoczky, I. and Hartl, G. B., 2009. Phylogeography of red deer (*Cervus elaphus*) in Europe. *Journal of Biogeography*, 36 (1), 66-77.
215. Skoglund, P., Malmström, H., Omrak, A., Raghavan, M., Valdiosera, C., Günther, T., ... and Apel, J., 2014. Genomic diversity and admixture differs for Stone-Age Scandinavian foragers and farmers. *Science*, 344(6185), 747-750.
216. Skoglund, P., Malmström, H., Raghavan, M., Storå, J., Hall, P., Willerslev, E., ... and Jakobsson, M., 2012. Origins and genetic legacy of Neolithic farmers and hunter-gatherers in Europe. *Science*, 336(6080), 466-469.
217. Soubrier, J., Gower, G., Chen, K., Richards, S. M., Llamas, B., Mitchell, K. J., Ho, S. Y. W., Kosintsev, P., Lee, M. S. Y. and Baryshnikov, G., 2016. Early cave art and ancient DNA record the origin of European bison. *Nature Communications*, 7, 13158.
218. Spitzenberger, F., Englisch, H., Hammer, S.E., Hartl, G.B. and Suchentrunk, F., 2000. Relationships between *Clethrionomys glareolus* populations of the Eastern Alps based on different genetic marker systems. *Folia Zool.* 48, 69-94.
219. Stacy, J. E., Jorde, P. E., Steen, H., Ims, R. A., Purvis, A. and Jakobsen, K. S., 1997. Lack of concordance between mtDNA gene flow and population density fluctuations in the bank vole. *Molecular Ecology*, 6 (8), 751-759.
220. Stamatis, C., Giannouli, S., Suchentrunk, F., Sert, H., Stathopoulos, C. and Mamuris, Z., 2008. Recruitment of mitochondrial tRNA genes as auxiliary variability markers for both intra-and inter-species analysis: The paradigm of brown hare (*Lepus europaeus*). *Gene*, 410 (1), 154-164.
221. Stamatis, C., Suchentrunk, F., Moutou, K. A., Giacometti, M., Haerer, G., Djan, M., Vapa, L., Vukovic, M., Tvrtkovid, N. and Sert, H., 2009. Phylogeography of the brown hare (*Lepus europaeus*) in Europe: a legacy of south-eastern Mediterranean refugia? *Journal of Biogeography*, 36 (3), 515-528.
222. Statham, M. J., Murdoch, J., Janecka, J., Aubry, K. B., Edwards, C. J., Soulsbury, C. D., Berry, O., Wang, Z., Harrison, D. and Pearch, M., 2014. Range-wide multilocus phylogeography of the red fox reveals ancient continental divergence, minimal genomic exchange and distinct demographic histories. *Molecular Ecology*, 23 (19), 4813-4830.

223. Statham, M. J., Sacks, B. N., Aubry, K. B., Perrine, J. D. and Wisely, S. M., 2012. The origin of recently established red fox populations in the United States: translocations or natural range expansions? *Journal of Mammalogy*, 93 (1), 52-65.
224. Statham, M. J., Turner, P. D., and O'Reilly, C., 2005. Use of PCR amplification and restriction enzyme digestion of mitochondrial D-loop for identification of mustelids in Ireland. *Irish Naturalists' Journal*, 28 (1), 1-6.
225. Sun, W.-I., Zhong, W., Bao, K., Liu, H.-I., Ya-Han, Y., Wang, Z. and Li, G.-Y., 2016. The complete mitochondrial genome of silver fox (Caniformia: Canidae). *Mitochondrial DNA Part A*, 27 (5), 3348-3350.
226. Świsłocka, M., Czajkowska, M., Duda, N., Danyłow, J., Owadowska-Cornil, E. and Ratkiewicz, M., 2013. Complex patterns of population genetic structure of moose, *Alces alces*, after recent spatial expansion in Poland revealed by sex-linked markers. *Acta Theriologica*, 58 (4), 367-378.
227. Świsłocka, M., Ratkiewicz, M., Borkowska, A., Komenda, E. and Raczyski, J., 2008. Mitochondrial DNA diversity in the moose, *Alces alces*, from northeastern Poland: evidence for admixture in a bottlenecked relic population in the Biebrza valley. *Annales Zoologici Fennici*, 45, 360-365.
228. Taberlet, P. and Bouvet, J., 1994. Mitochondrial DNA polymorphism, phylogeography, and conservation genetics of the brown bear *Ursus arctos* in Europe. *Proc. R. Soc. Lond. B*, 255 (1344), 195-200.
229. Tamura, N. and Hayashi, F., 2006. Five-year study of the genetic structure and demography of two subpopulations of the Japanese squirrel (*Sciurus lis*) in a continuous forest and an isolated woodlot. *Ecological Research*, 22 (2), 261.
230. Teacher, A. G. F., Thomas, J. A. and Barnes, I., 2011. Modern and ancient red fox (*Vulpes vulpes*) in Europe show an unusual lack of geographical and temporal structuring, and differing responses within the carnivores to historical climatic change. *BMC Evolutionary Biology*, 11 (1), 214.
231. Thalmann, O., Shapiro, B., Cui, P., Schuenemann, V. J., Sawyer, S. K., Greenfield, D. L., Germonpré, M. B., Sablin, M. V., López-Giráldez, F. and Domingo-Roura, X., 2013. Complete mitochondrial genomes of ancient canids suggest a European origin of domestic dogs. *Science*, 342 (6160), 871-874.
232. Thulin, C. G., Jaarola, M. and Tegelström, H., 1997. The occurrence of mountain hare mitochondrial DNA in wild brown hares. *Molecular Ecology*, 6 (5), 463-467.
233. Tsuda, K., Kikkawa, Y., Yonekawa, H. and Tanabe, Y., 1997. Extensive interbreeding occurred among multiple matriarchal ancestors during the domestication of dogs: evidence from inter-and intraspecies polymorphisms in the D-loop region of mitochondrial DNA between dogs and wolves. *Genes & Genetic Systems*, 72 (4), 229-238.
234. Valdiosera, C. E., García, N., Anderung, C., Dalén, L., Crégut-Bonnouere, E., Kahlke, R. D., Stiller, M., Brandström, M., Thomas, M. G. and Arsuaga, J. L., 2007. Staying out in the cold: glacial refugia and mitochondrial DNA phylogeography in ancient European brown bears. *Molecular Ecology*, 16 (24), 5140-5148.
235. Valdiosera, C. E., García-Garitaigotia, J. L., Garcia, N., Doadrio, I., Thomas, M. G., Hänni, C., Arsuaga, J.-L., Barnes, I., Hofreiter, M. and Orlando, L., 2008. Surprising migration and population size dynamics in ancient Iberian brown bears (*Ursus arctos*). *Proceedings of the National Academy of Sciences USA*, 105 (13), 5123-5128.
236. Valière, N., Fumagalli, L., Gielly, L., Miquel, C., Lequette, B., Poulle, M.-L., Weber, J.-M., Arlettaz, R. and Taberlet, P., 2003. Long-distance wolf recolonization of France and Switzerland inferred from non-invasive genetic sampling over a period of 10 years. *Animal Conservation*, 6 (1), 83-92.
237. Van Asch, B., Pereira, F., Santos, L. S., Carneiro, J., Santos, N. and Amorim, A., 2012. Mitochondrial lineages reveal intense gene flow between Iberian wild boars and South Iberian pig breeds. *Animal Genetics*, 43 (1), 35-41.
238. Veličkovic, N., Djan, M., Ferreira, E., Stergar, M., Obreht, D., Maletid, V. and Fonseca, C., 2015. From north to south and back: the role of the Balkans and other southern peninsulas in the recolonization of Europe by wild boar. *Journal of Biogeography*, 42 (4), 716-728.

239. Verginelli, F., Capelli, C., Coia, V., Musiani, M., Falchetti, M., Ottini, L., Palmirotta, R., Tagliacozzo, A., De Grossi Mazzorin, I. and Mariani-Costantini, R., 2005. Mitochondrial DNA from prehistoric canids highlights relationships between dogs and South-East European wolves. *Molecular Biology and Evolution*, 22 (12), 2541-2551.
240. Verkaar, E. L. C., Nijman, I. C. J., Beeke, M., Hanekamp, E. and Lenstra, J. A., 2004. Maternal and paternal lineages in cross-breeding bovine species. Has wisent a hybrid origin? *Molecular Biology and Evolution*, 21 (7), 1165-1170.
241. Vernesi, C., Hoban, S. M., Pecchioli, E., Crestanello, B., Bertorelle, G., Rosà, R. and Hauffe, H. C., 2016. Ecology, environment and evolutionary history influence genetic structure in five mammal species from the Italian Alps. *Biological Journal of the Linnean Society*, 117 (3), 428-446.
242. Vernesi, C., Pecchioli, E., Caramelli, D., Tiedemann, R., Randi, E. and Bertorelle, G., 2002. The genetic structure of natural and reintroduced roe deer (*Capreolus capreolus*) populations in the Alps and central Italy, with reference to the mitochondrial DNA phylogeography of Europe. *Molecular Ecology*, 11 (8), 1285-1297.
243. Vernesi, C., Pecchioli, E., Crestanello, B., Bertorelle, G., Tonolli, S., Rosa, R., Gaggiotti, O. and Hauffe, H. C., 2010. A multi-species, multi-locus landscape genetics approach shows that ecology, environment and evolutionary history affect diversity and differentiation in five mammal species from the eastern Italian Alps. *Unpublished manuscript*.
244. Vilà, C., Amorim, I. R., Leonard, J. A., Posada, D., Castroviejo, J., Petrucci-Fonseca, F., Crandall, K. A., Ellegren, H. and Wayne, R. K., 1999. Mitochondrial DNA phylogeography and population history of the grey wolf *Canis lupus*. *Molecular Ecology*, 8 (12), 2089-2103.
245. Vilà, C., Savolainen, P., Maldonado, J. E., Amorim, I. R., Rice, J. E., Honeycutt, R. L., Crandall, K. A., Lundeberg, J. and Wayne, R. K., 1997. Multiple and ancient origins of the domestic dog. *Science*, 276 (5319), 1687-1689.
246. Vilaça, S. T., Biosa, D., Zachos, F., Iacolina, L., Kirschning, J., Alves, P. C., Paule, L., Gortazar, C., Mamuris, Z. and Jędrzejewska, B., 2014. Mitochondrial phylogeography of the European wild boar: the effect of climate on genetic diversity and spatial lineage sorting across Europe. *Journal of Biogeography*, 41 (5), 987-998.
247. Waltari, E. and Cook, J. A., 2005. Hares on ice: phylogeography and historical demographics of *Lepus arcticus*, *L. othus*, and *L. timidus* (Mammalia: Lagomorpha). *Molecular Ecology*, 14 (10), 3005-3016.
248. Waltari, E., Demboski, J. R., Klein, D. R. and Cook, J. A., 2004. A molecular perspective on the historical biogeography of the northern high latitudes. *Journal of Mammalogy*, 85 (4), 591-600.
249. Ward, T. J., Bielawski, J. P., Davis, S. K., Templeton, J. W. and Derr, J. N., 1999. Identification of domestic cattle hybrids in wild cattle and bison species: a general approach using mtDNA markers and the parametric bootstrap. *Animal Conservation*, 2 (1), 51-57.
250. Węcek, K., Hartmann, S., Pajmans, J. L. A., Taron, U., Xenikoudakis, G., Cahill, J. A., Heintzman, P. D., Shapiro, B., Baryshnikov, G. and Bunevich, A. N., 2016. Complex admixture preceded and followed the extinction of wisent in the wild. *Molecular Biology and Evolution*, 34 (3), 598-612.
251. Wennerström, L., Ryman, N., Tison, J.-L., Hasslow, A., Dalén, L. and Laikre, L., 2016. Genetic landscape with sharp discontinuities shaped by complex demographic history in moose (*Alces alces*). *Journal of Mammalogy*, 97 (1), 1-13.
252. Wickliffe, J. K., Dunina-Barkovskaya, Y. V., Gaschak, S. P., Rodgers, B. E., Chessser, R. K., Bondarkov, M. and Baker, R. J., 2006. Variation in mitochondrial DNA control region haplotypes in populations of the bank vole, *Clethrionomys glareolus*, living in the Chernobyl environment, Ukraine. *Environmental Toxicology and Chemistry*, 25 (2), 503-508.
253. Wiehler, J. and Tiedemann, R., 1998. Phylogeography of the European roe deer *Capreolus capreolus* as revealed by sequence analysis of the mitochondrial control region. *Acta Theriologica*, 43 (Suppl. 5), 187-197.

254. Wójcik, J. M., Kawałko, A., Tokarska, M., Jaarola, M., Vallenback, P. and Pertoldi, C., 2009. Post-bottleneck mtDNA diversity in a free-living population of European bison: implications for conservation. *Journal of Zoology*, 277 (1), 81-87.
255. Wu, C. and Zhang, Y., 2000. Molecular phylogeny of Chinese hare (*Lepus*) inferred from mitochondrial cytochrome b gene and control region sequences. *Unpublished manuscript*.
256. Xenikoudakis, G., Ersmark, E., Tison, J. L., Waits, L., Kindberg, J., Swenson, J. E. and Dalén, L., 2015. Consequences of a demographic bottleneck on genetic structure and variation in the Scandinavian brown bear. *Molecular Ecology*, 24 (13), 3441-3454.
257. Yashina, L.N., Oleinik, O.V. and Kovaleva, V.I. Comparative analysis of morphological and molecular genetic diversity of mouse-like rodents. *Unpublished Manuscript*.
258. Yu, L., Peng, D., Liu, J., Luan, P., Liang, L., Lee, H., Lee, M., Ryder, O. A. and Zhang, Y., 2011. On the phylogeny of Mustelidae subfamilies: analysis of seventeen nuclear non-coding loci and mitochondrial complete genomes. *BMC Evolutionary Biology*, 11 (1), 92.
259. Yudin, N. S., Kulikov, I. V., Gunbin, K. V., Aitnazarov, R. B., Kushnir, A. V., Sipko, T. P. and Moshkin, M. P., 2012. Detection of mitochondrial DNA from domestic cattle in European bison (*Bison bonasus*) from the Altai Republic in Russia. *Animal Genetics*, 43 (3), 362.
260. Zachos, F. E., Ben Slimen, H., Hackländer, K., Giacometti, M. and Suchentrunk, F., 2010. Regional genetic in situ differentiation despite phylogenetic heterogeneity in Alpine mountain hares. *Journal of Zoology*, 282 (1), 47-53.
261. Zeyland, J., Wolko, Ł., Lipioski, D., Woźniak, A., Nowak, A., Szalata, M., Bocianowski, J. and Słomski, R., 2012. Tracking of wisent–bison–yak mitochondrial evolution. *Journal of Applied Genetics*, 53 (3), 317-322.
262. Zhong, H.-M., Zhang, H.-H., Sha, W.-L., Zhang, C.-D. and Chen, Y.-C., 2010. Complete mitochondrial genome of the red fox (*Vulpes vulpes*) and phylogenetic analysis with other canid species. *Zoological Research*, 31 (2), 122-130.
263. Zvychainaya, E. Y., Danilkin, A. A., Kholodova, M. V., Sipko, T. P. and Berber, A. P., 2011. Analysis of the variability of the control region and cytochrome b gene of mtDNA of *Capreolus pygargus* Pall. *Biology Bulletin*, 38 (5), 434-439.