Supplementary Information

For all species, the temporal frequency distribution of zooarchaeological records fluctuates over time, with record abundance increasing somewhat towards the present for most species (Fig. S). This follows expectations, as the likelihood of destruction of zooarchaeological samples is strongly associated with exposure to taphonomic pressures and, thus, archaeological time (Surovell & Brantingham 2007). This means that going back in time, the probability of encountering zooarchaeological records decreases (curvilinearly).

To assess how Holocene distributions of native European mammal species have changed over space and time, we built binomial regression models for site occupancy for each of the 15 species in the zooarchaeological database. Binomial regression models are one of the most widely-applied approaches for inferring species distributions (Hijmans & Elith 2017). Even in cases when only presence records exist, this method can be applied by substituting absence data with background or pseudo-absence data. The gold standard in species distribution modelling is to use background or pseudo-absence data restricted to and inclusive of all areas within the study region that are suitable and accessible to the species of interest (Araújo et al. 2019). In contrast to fossil assemblages which are deposited through natural processes, assemblages of zooarchaeological records reflect past human occupancy and their faunal exploitation across the landscape. Zooarchaeological sites can be prehistoric locations of refuse pits, or burial or killing sites. As such, the distribution of zooarchaeological sites is inherently biased towards sites of past human presence (for detailed site information see Sommer & Benecke 2004). Background data or random pseudo-absence points as suggested in the gold standard might in this case thus have different associations with human occupancy than species presence locations. We therefore instead selected pseudo-absence locations for each species from the database of presence records for the 14 other species, hence binding pseudo-absence locations to localities of past human occupancy in a similar manner as presence locations. In this way we prevent a discrepancy in human occupancy bias between presence and absence locations. This approach provides a suitably large number (>10 000) (Barbet-Massin et al. 2012) of pseudo-absence points for each species. This method also largely controls for biases in the temporal distribution of records, as the temporal distribution of pseudo-absence points is influenced by taphonomic pressures in a similar manner as presence points.

In regression-based species distribution models, it is advised to apply equal weighting to presence and (pseudo)absence records, to prevent unbalanced numbers of presence and (pseudo)absence records influencing model estimates (Barbet-Massin et al. 2012). Because weighting is not straightforward within the R “INLA” package, we derived a post-hoc sensitivity test to establish the robustness of posterior estimates against unbalanced presence/pseudo-absence samples. We implemented this by rerunning the optimal model structure for each species both with and without equal weighting within a frequentist modelling framework, where weighting of records can easily be included in the model function call (see

Table **S** and Fig. S for comparisons of model diagnostics and estimates, respectively).

After collating spatiotemporal covariate layers, variable estimates were extracted at all geospatial point locations in the zooarchaeological database of species occurrence records (Fig. S). After value extraction, variable distributions were assessed for collinearity. With the aim of reducing computational cost in subsequent model inference, variables with high correlation ($\rho > 0.8$) with other variables were removed from further analyses (Fig. S). After inspection of variable-pair correlations, annual mean temperature was removed from the dataset, resulting in a total of nine potential spatiotemporal covariates.

To overcome skewedness of covariate distributions, and to mitigate the impact of potentially high-leverage and -influence points, all remaining variables were transformed with the R "bestNormalize" package (Peterson 2017). Using the variables as transformed with this package (Fig. S) in generalized linear regression models, the assumption of a linear relationship between the response variable and covariates is relaxed, and instead a linear relationship is modelled between response and transformed covariate values (Peterson 2017). This pre-processing step thus removes the need for including quadratic or logarithmic variables to test non-linear relationships between response and covariates, which can be problematic in cases with zero or negative variable values. The modelling approach thus shows similarities to a Spearman's rank correlation, while retaining the full benefits of generalized linear regression model inference, such as testing multiple variables and model structures.

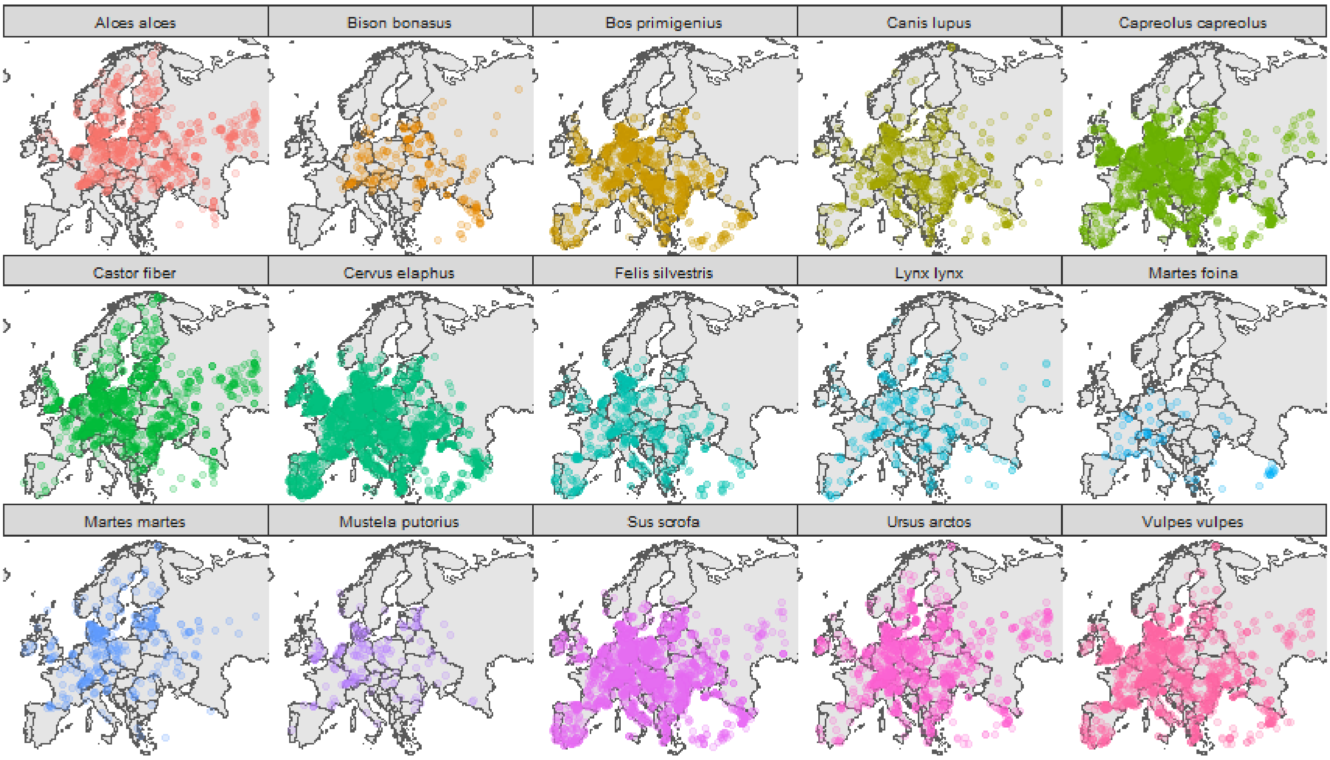

Fig. S1. Spatial distribution of Holocene zooarchaeological records across Europe for all 15 mammal species included in analyses.

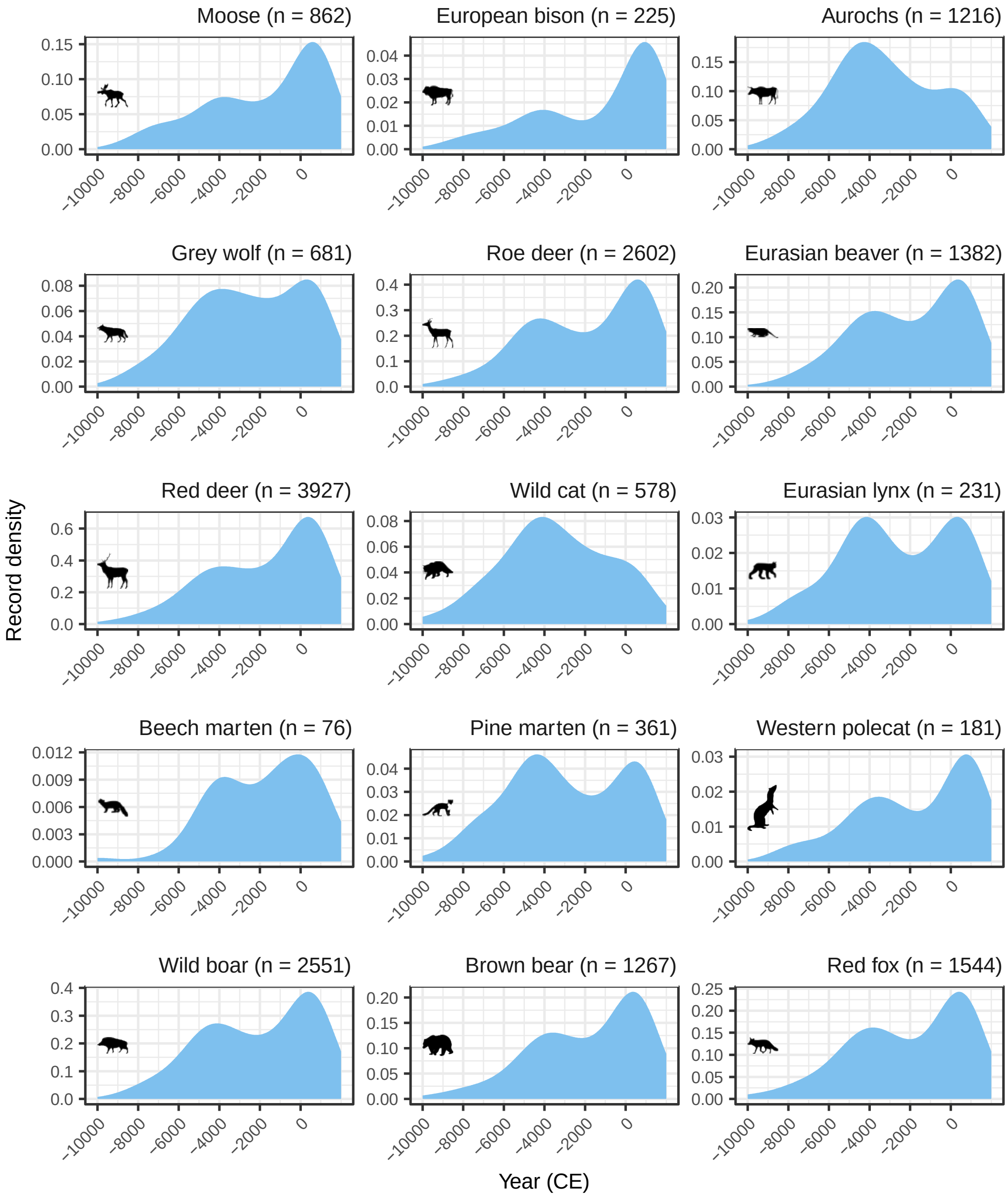

Fig. S2. Temporal frequency distribution of zooarchaeological occurrence records. For most species, the distribution has a bimodal shape, with greater record abundance towards the present. For *Bos primigenius* (aurochs) and *Felis silvestris* (wildcat) record abundance initially increases but declines after -5000 CE.

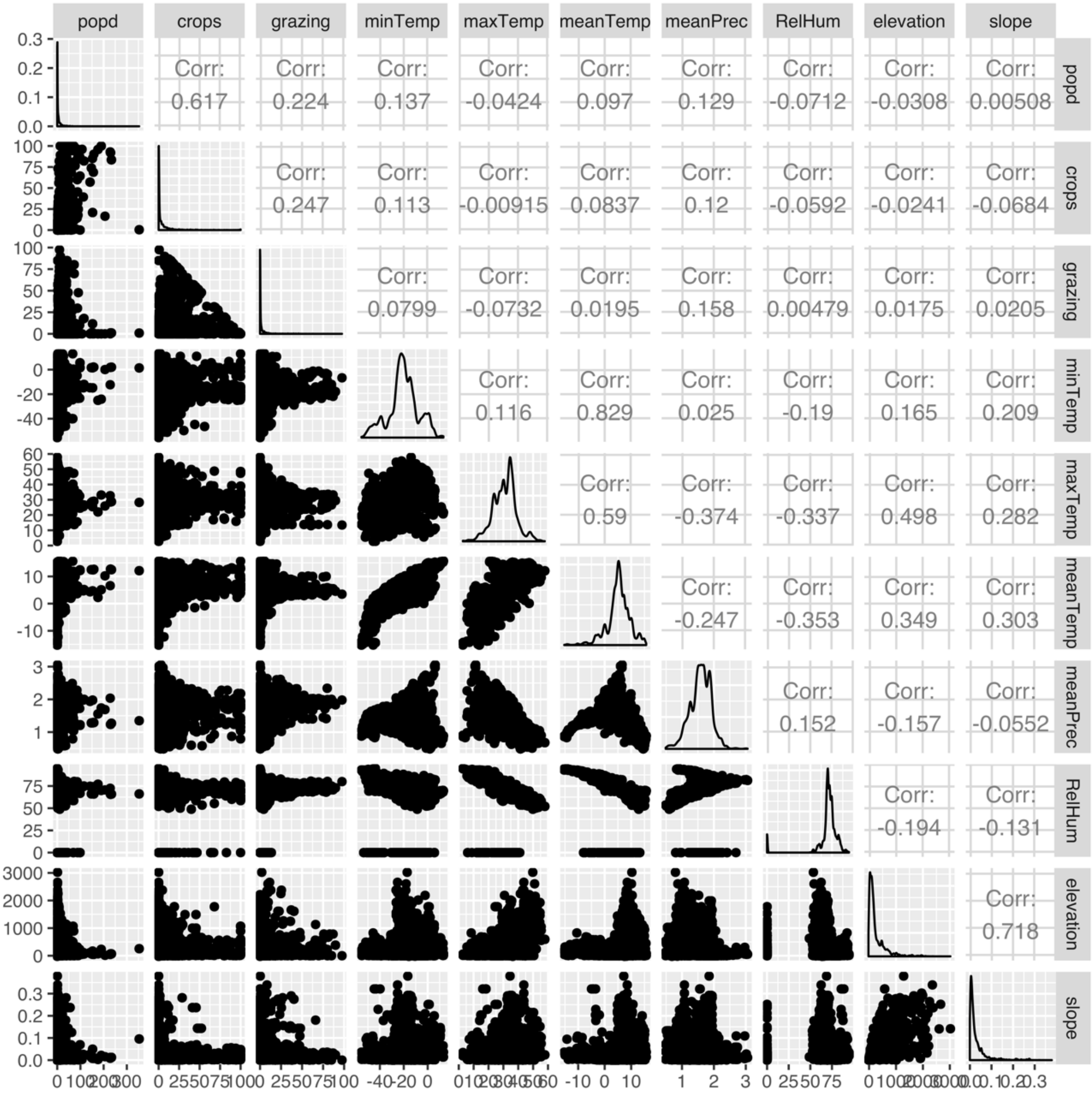

Fig. S3. Collinearity between untransformed spatiotemporal covariates. Annual mean temperature was removed for further analyses due to its high correlation with July maximum temperature and January minimum temperature.

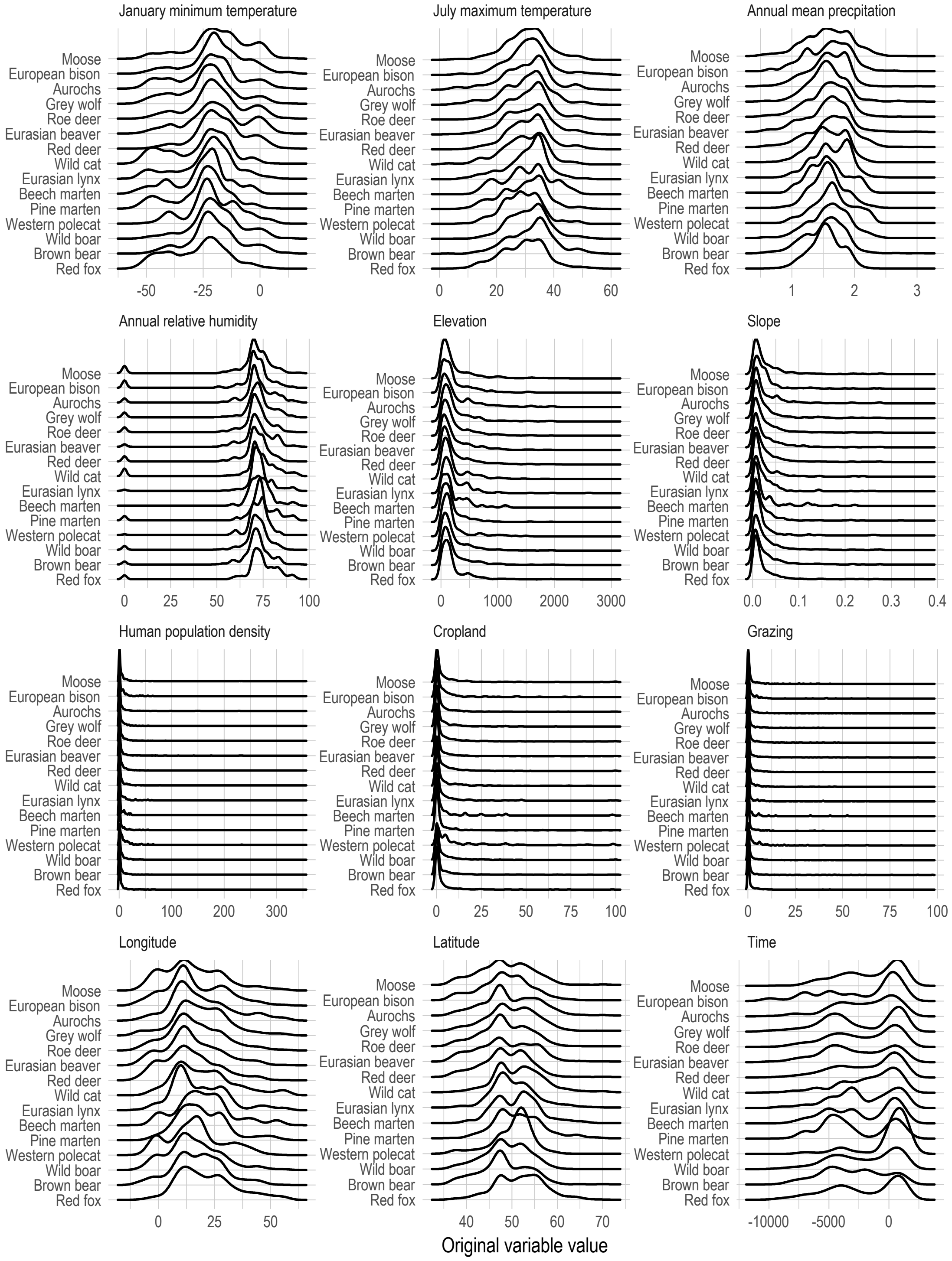

Fig. S4. Realized Holocene niche space for 15 European mammal species. Anthropogenic covariates (i.e. human population density, cropland and grazing) have distribution peaks around zero, as anthropogenic factors increased only moderately and locally between -10,000 CE and 1600 CE.

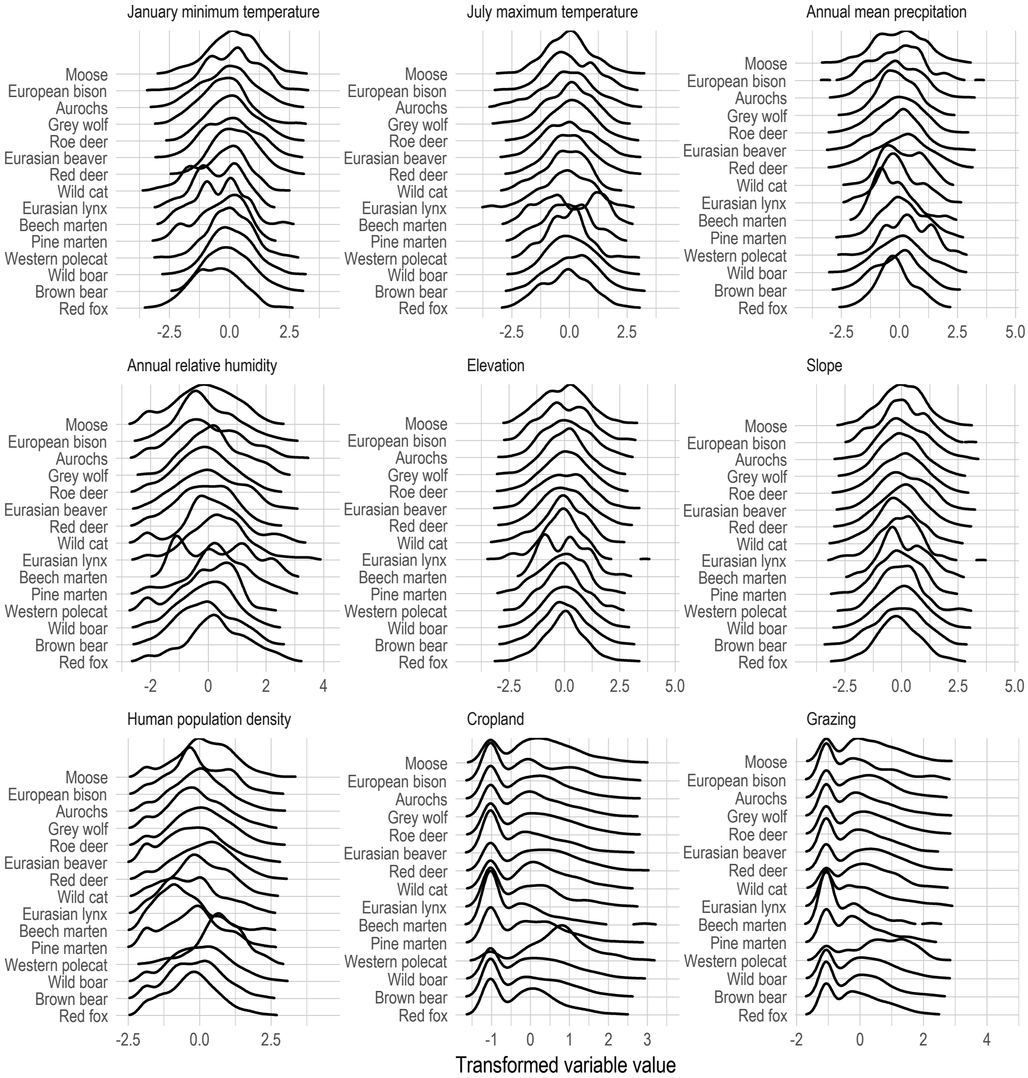

Fig. S5. Transformed distributions of spatiotemporal covariates. Variable distributions are centred on zero.

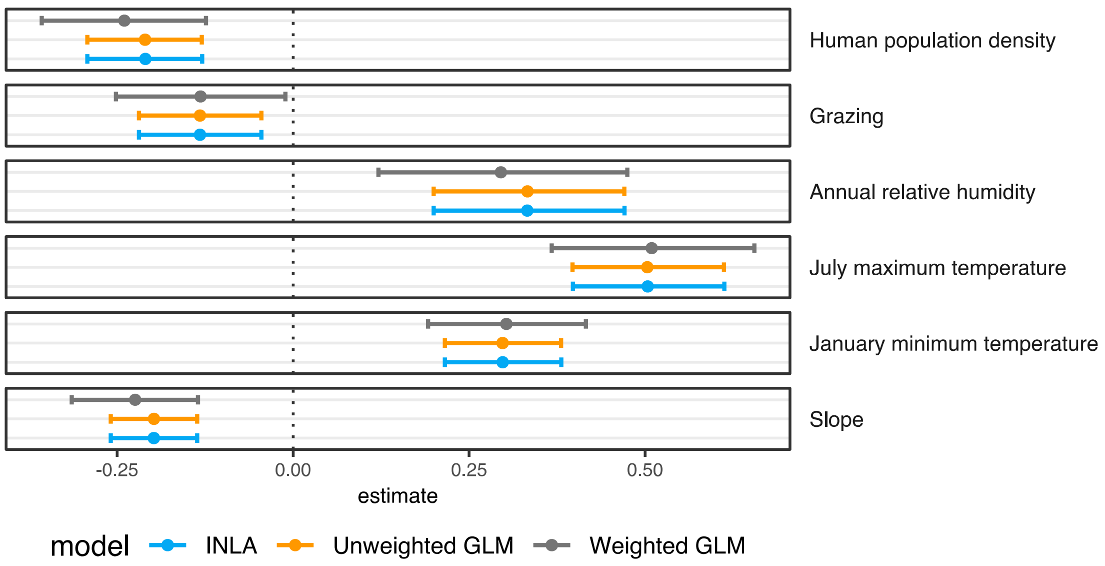

Fig. S6. Impact of model weighting on regression coefficient estimates. Showing regression coefficient estimates from a Bayesian hierarchical model (INLA), and unweighted and weighted frequentist generalized linear regression models (GLM) for *Bos primigenius* (aurochs). Results for other species are qualitatively comparable. In the weighted GLM, pseudo-absences were down-weighted so that the weighted sum of presence records equals the weighted sum of pseudo-absences.

Table S1. Detailed information on spatiotemporal covariates used for modelling. For analysis, all covariates were resampled to a 5 arcminute resolution using the R “raster” package (Hijmans 2019).

Covariate	Data source	Units	Native resolution	Approximate cell size at equator
Cropland land use	HYDE 3.2	% gridcell^{-1}	5 arcmin	10 km
Grazing land use	HYDE 3.2	% gridcell^{-1}	5 arcmin	10 km
Human population density	HYDE 3.2	capita km^{-2}	5 arcmin	10 km
July minimum temperature	PaleoView	°C	2.5 degree	300 km
January maximum temperature	PaleoView	°C	2.5 degree	300 km
Annual mean temperature	PaleoView	°C	2.5 degree	300 km
Annual mean precipitation	PaleoView	mm d^{-1}	2.5 degree	300 km
Annual relative humidity	PaleoView	%	2.5 degree	300 km
Elevation	GMTED2000	m	30 arcsec	1 km
Slope	GMTED2000	radians	30 arcsec	1 km

Table S2. Comparative model performance of frequentist generalized linear models. Showing McFadden pseudo-R^2 (McFadden 1974) area under receiver operating characteristic curve (AUC) and bootstrapped 95% confidence intervals of AUC from weighted and unweighted generalized linear models with optimal model structures derived in the Bayesian hierarchical model selection procedure.

	Unweighted GLM				Weighted GLM			
Species	pseudo-R^2	AUC	2.5% CI_{AUC}	97.5% CI_{AUC}	pseudo-R^2	AUC	2.5% CI_{AUC}	97.5% CI_{AUC}
Moose	0.13	0.77	0.75	0.79	0.18	0.77	0.76	0.79
European bison	0.06	0.71	0.68	0.75	0.14	0.72	0.69	0.75
Aurochs	0.03	0.63	0.62	0.65	0.04	0.63	0.62	0.65
Grey wolf	0.01	0.56	0.54	0.58	0.01	0.56	0.54	0.58
Roe deer	0.01	0.55	0.54	0.56	0.01	0.55	0.54	0.56
Eurasian beaver	0.03	0.62	0.60	0.63	0.05	0.62	0.60	0.63
Red deer	0.03	0.61	0.60	0.62	0.04	0.61	0.60	0.62
Wild cat	0.04	0.67	0.65	0.69	0.08	0.67	0.65	0.69
Eurasian lynx	0.01	0.57	0.54	0.61	0.02	0.57	0.54	0.61
Beech marten	0.07	0.75	0.70	0.80	0.18	0.76	0.71	0.80
Pine marten	0.07	0.74	0.72	0.76	0.14	0.74	0.72	0.76
Western polecat	0.02	0.64	0.60	0.68	0.06	0.64	0.60	0.68
Wild boar	0.01	0.57	0.55	0.58	0.01	0.57	0.55	0.58
Brown bear	0.03	0.62	0.61	0.64	0.03	0.62	0.61	0.64
Red fox	0.00	0.56	0.54	0.57	0.01	0.55	0.54	0.57

Table S3. Bayesian hierarchical model performance. Showing area under receiver operating curve (AUC) values and bootstrapped 95% confidence intervals of models with environmental and anthropogenic covariates for 15 European mammal species.

Species	AUC	2.5% CI	97.5% CI
Moose	0.77	0.76	0.79
European bison	0.71	0.68	0.74
Aurochs	0.63	0.62	0.65
Grey wolf	0.55	0.53	0.57
Roe deer	0.55	0.54	0.56
Eurasian beaver	0.62	0.61	0.64
Red deer	0.61	0.6	0.62
Wild cat	0.67	0.65	0.69
Eurasian lynx	0.56	0.53	0.6
Beech marten	0.73	0.68	0.78
Pine marten	0.74	0.72	0.76
Western polecat	0.64	0.61	0.68
Wild boar	0.56	0.55	0.58
Brown bear	0.62	0.61	0.64
Red fox	0.55	0.54	0.57

References

Araújo, M.B., Anderson, R.P., Barbosa, A.M., Beale, C.M., Dormann, C.F., Early, R., Garcia, R.A., Guisan, A., Maiorano, L., Naimi, B., O'Hara, R.B., Zimmermann, N.E. & Rahbek, C. (2019). Standards for distribution models in biodiversity assessments. *Science Advances*, 5, eaat4858.

Barbet-Massin, M., Jiguet, F., Albert, C.H. & Thuiller, W. (2012). Selecting pseudo-absences for species distribution models: how, where and how many? *Methods in Ecology and Evolution*, 3, 327–338.

Hijmans, R.J. (2019). raster: Geographic Data Analysis and Modeling.

Hijmans, R.J. & Elith, J. (2017). Species distribution modeling with R, 1–79.

McFadden, D. (1974). Conditional logit analysis of qualitative choice behavior. In: *Front. Econom.* (ed. Zarembka, P.). Cambridge, MA, pp. 105–142.

Peterson, R.A. (2017). bestNormalize: A suite of normalizing transformations.

Sommer, R. & Benecke, N. (2004). Late- and Post-Glacial history of the Mustelidae in Europe. *Mammal Review*, 34, 249–284.

Surovell, T.A. & Brantingham, P.J. (2007). A note on the use of temporal frequency distributions in studies of prehistoric demography. *Journal of Archaeological Science*, 34, 1868–1877.