

Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: Ancient DNA and archaeological context data for all newly reported individuals. The table includes sample IDs, site information, archaeological dating, burial context, and basic genetic screening results.

File Name: Supplementary Data 2a

Description: Published modern-day groups and individuals used in this study for Western Eurasian PCA, information extracted from AADR v54.1.p1_HO_public.anno.

File Name: Supplementary Data 2b

Description: Published ancient groups and individuals used in this study for population genetics analyses, information extracted from AADR v54.1.p1_HO_public.anno. The table includes an additional column with the group labels assigned to individuals and groups for analysis.

File Name: Supplementary Data 3

Description: Results of f_4 -statistics in the form $f_4(\text{outgroup}, X; Y, Z)$. The outgroup is “OldAfrica” (as defined in Patterson et al. 2022 and listed in Supplementary Table 2b). X represents one of the three major ancestry sources, Early European Farmer (EEF)-related, Western Hunter-Gatherer (WHG), or Steppe-related ancestry, while Y and Z are the test populations.

File Name: Supplementary Data 4a

Description: Distal qpAdm modelling results for Late Bronze Age (LBA) individuals from Central Europe, using the parameter allSNPs: NO. The model uses the outgroups (OG) OldAfrica, Turkey_N, WHGB, and Afanasievo (as defined in Patterson et al. 2022).

File Name: Supplementary Data 4b

Description: Proximal qpAdm modelling results for early Late Bronze Age (LBA) individuals from Central Germany, using the parameter allSNPs: NO. Each row represents a two-way model using Germany_EBA_Unetice as the local source population, paired with a second geographically and/or chronologically proximate population. The model uses the outgroups (OG) OldAfrica, Turkey_N, WHGB, and Afanasievo (as defined in Patterson et al. 2022).

File Name: Supplementary Data 4c

Description: Proximal qpAdm modelling results for late Late Bronze Age (LBA) individuals from Central Germany, using the parameter allSNPs: NO. Each row represents a two-way model using Germany_EBA_Unetice as the local source population, paired with a second geographically and/or chronologically proximate population. The model uses the outgroups (OG) OldAfrica, Turkey_N, WHGB, and Afanasievo (as defined in Patterson et al. 2022).

File Name: Supplementary Data 4d

Description: Proximal qpAdm modelling results for early Late Bronze Age (LBA) individuals from South Germany, using the parameter allSNPs: NO. Each row represents a two-way model using, for example, Germany_Lech_EBA/Germany_Lech_MBA as the local source population, paired with a second geographically and/or chronologically proximate population. The model uses the outgroups (OG) OldAfrica, Turkey_N, WHGB, and Afanasievo (as defined in Patterson et al. 2022).

File Name: Supplementary Data 4e

Description: Proximal qpAdm modelling results for Late Bronze Age (LBA) individuals from Bohemia, Czechia, using the parameter allSNPs: NO. Each row represents a one-way or two-way model using, for example, Czech_EBA_Unetice/ Czech_MBA_Tumulus as the local source population, paired with a second geographically and/or chronologically proximate population. The model uses the outgroups (OG) OldAfrica, Turkey_N, WHGB, and Afanasievo (as defined in Patterson et al. 2022).

File Name: Supplementary Data 4f

Description: Proximal qpAdm modelling results for Late Bronze Age (LBA) and Iron Age (IA) individuals from SW_Central_Poland, using the parameter allSNPs: NO. Each row represents a one-way or two-way model using Poland_EBA/ Poland_MBA as the local source population, paired with a second geographically and/or chronologically proximate population. The model uses the outgroups (OG) OldAfrica, Turkey_N, WHGB, and Afanasievo (as defined in Patterson et al. 2022).

File Name: Supplementary Data 5a

Description: Results of biological relatedness analysis using BREADR. The table reports genetic relatedness inferred from genomic data among newly reported individuals, based on pairwise mismatch rates between individuals and associated confidence measures.

File Name: Supplementary Data 5b

Description: Results of biological relatedness analysis using READv2. The table reports genetic relatedness inferred from genomic data among newly reported individuals, based on pairwise mismatch rates between individuals and associated confidence measures.

File Name: Supplementary Data 5c

Description: Results of biological relatedness analysis using KIN. The table reports genetic relatedness inferred from genomic data among newly reported individuals, based on the detection of identical-by-descent (IBD) segments shared between individuals and associated confidence measures.

File Name: Supplementary Data 6

Description: Identity-by-descent (IBD) sharing results based on ancIBD analysis. For each pair of individuals, the table included the number and summed length of shared IBD segments longer than 8, 12, 16, and 20 centimorgans (cM), as well as the length of the

longest IBD segment. Genotype probabilities (frac_gp) for each imputed individual are also shown, along with the corresponding archaeological site information.

File Name: Supplementary Data 7

Description: Results of runs of homozygosity (ROH) analysis for individuals with >400,000 SNPs covered on the 1240k panel, estimated using the hapROH software. The table reports the maximum ROH length (max_roh), the number and total length of ROH segments exceeding 4, 8, 12, and 20 centimorgans (cM) per individual.

File Name: Supplementary Data 8

Description: Strontium and oxygen isotope values from the two archaeological sites (Kuckenburg and Esperstedt, Central Germany) in this study. Strontium values were obtained from both inhumations and cremations (total 51 individuals) and 20 animals.

File Name: Supplementary Data 9

Description: Mortuary practices data for individuals analysed in this study. The table includes burial type, genetic sex, estimated age-at-death, and special features from the burial context.

File Name: Supplementary Data 10

Description: Radiocarbon dates from six cremated individuals from Kuckenburg and Esperstedt, Central Germany. All dates were obtained directly from calcined human bone and are calibrated to a 95.4% probability range.

File Name: Supplementary Data 11

Description: Integrated dataset of individuals from Kuckenburg and Esperstedt, Central Germany used in statistical analyses. The table includes burial type, burial context, presence of trauma, genetic sex, age at death, presence of grave goods, isotopic data (strontium, oxygen, carbon, nitrogen), and EEF ancestry proportions. Variables presented here correspond to the categories used in the statistical tests described in the Methods section.

File Name: Supplementary Data 12

Description: Descriptive statistics and statistical tests comparing time periods, isotopic values ($^{87}\text{Sr}/^{86}\text{Sr}$, $\delta^{18}\text{O}$, $\delta^{13}\text{C}$), ancestry proportions, dietary markers, and burial variables. Methods include Shapiro–Wilk, Kruskal–Wallis, Welch’s t-test, Wilcoxon rank-sum test, and Fisher’s exact test. All statistical tests were two-sided unless otherwise stated. Results include test statistics, p-values, FDR-adjusted values, confidence intervals, and group sizes.

File Name: Supplementary Data 13

Description: Paleopathological and skeletal observations from Kuckenburg and Esperstedt, Central Germany. These observations include signs of trauma, infection, degenerative disease, and non-specific indicators of stress.

File Name: Supplementary Data 14

Description: HOPS pathogen screening summary statistics. Table indicated the number of assigned reads of each sample to the references or higher taxonomic level as indicated on the left. For species marked in green maltExtract of the HOPS pipeline authenticated potential candidates, marked in yellow, orange and red. Yellow: step 1 - samples with a declining edit distance. Orange: step 2 - candidates from step 1 with additional damage profile typical for aDNA. Red: step 3 - candidates from step 2 with additionally a declining edit distance of reads with potential aDNA damage.