



The origin of social inequalities in Northern Italy: clues from ancient genomes

Maria Teresa Vizzari¹, Linda Pratesi², Margherita Vanni², Irene Dori², Francesco Savarino², Domenico Lo Vetro^{3,4}, Marco Baioni⁵, Jacopo Moggi Cecchi², Leonardo Lamanna⁶, Alessandra Sperduti⁷, David Caramelli², Stefania Vai², Silvia Ghirotto¹

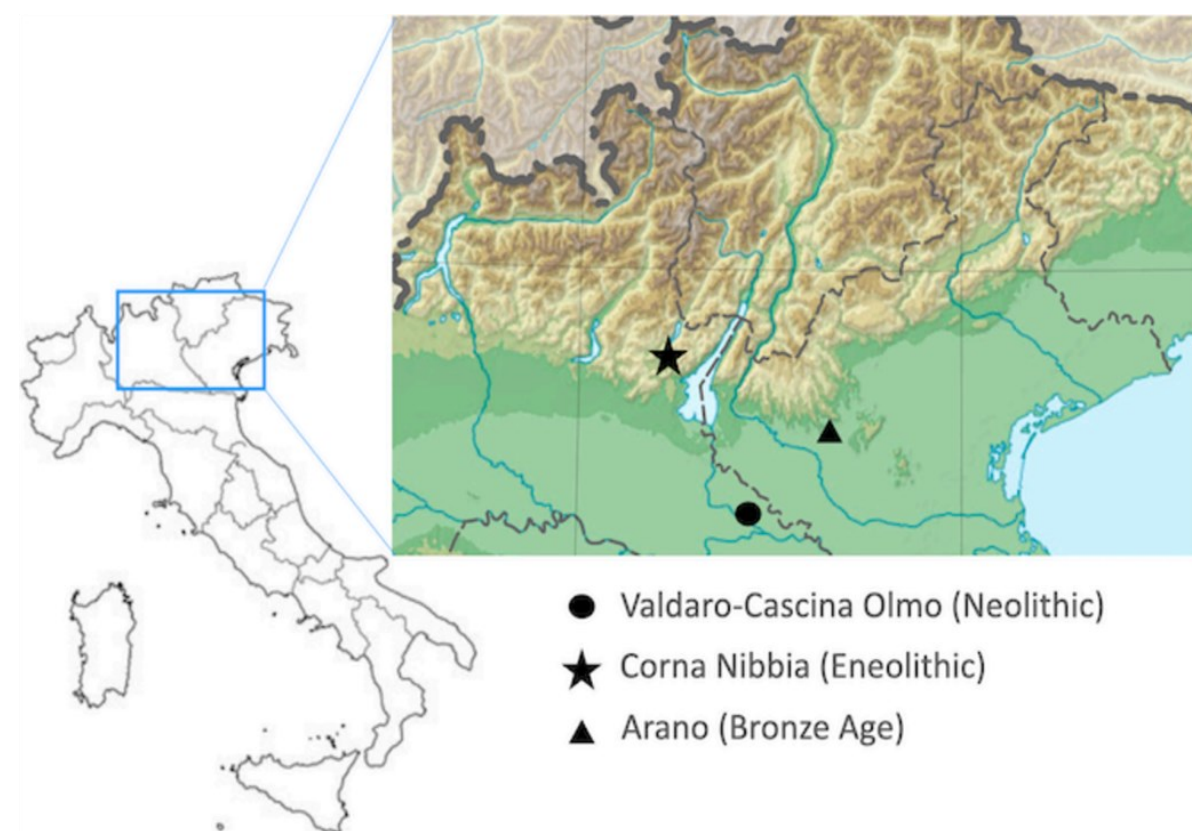
¹ Department of Life Science and Biotechnology, University of Ferrara, Ferrara, Italy, ² Department of Biology, University of Florence, Florence, Italy, ³ Department of Storia, Archeologia, Geografia, Arte e Spettacolo (SAGAS), University of Florence, Italy, ⁴ Florentine Museum and Institute of Prehistory, Florence, Italy, ⁵ MAVS, Museo Archeologico della Valle Sabbia, Gavardo, Brescia, Italy, ⁶ Soprintendenza Archeologia, Belle Arti e Paesaggio per le Province di Cremona, Mantova e Lodi, Italy, ⁷ Museo Nazionale Preistorico Etnografico Luigi Pigorini, Museo delle Civiltà, Rome, Italy.

INTRODUCTION

Uncovering the dynamics promoting the onset and perpetration of social inequalities in prehistoric societies is a major challenge. We now have the opportunity to exploit archaeogenomic data to describe, with unprecedented resolution, past population structure and processes and to shed light on sociocultural dynamics (e.g., the lineage-based transmission of social status and wealth) which are the basis of the onset of inequalities. Two major population dynamics within the last 10,000 years impacted the genomic composition of Europeans: the Neolithic expansion and the Bronze Age migration from the Steppe; despite the importance of these events, our genetic understanding is mainly built upon pan-European sampling strategies, resulting in limited knowledge about the impact of these migrations at the level of single societies. **In this project, we propose a high-resolution multidisciplinary study of three burial sites in Northeast Italy from the Neolithic, Eneolithic, and Bronze Age periods to infer the social and genetic structure and their possible change in this time transect. The results of this study will help us to shed light on the onset of social inequality in Northern Italy, and on the cultural and biological mechanisms that promoted its development.**

AIMS OF THE PROJECT

- ✓ Sequencing of **approximately 110 individuals** showing in preliminary analysis > 60% of endogenous DNA.
- ✓ Average coverage level: 1x.
- ✓ Sex balance to investigate also uniparental markers.
- ✓ Radiocarbon dating.
- ✓ Isotopes analysis (Mobility pattern and Paleodiet).



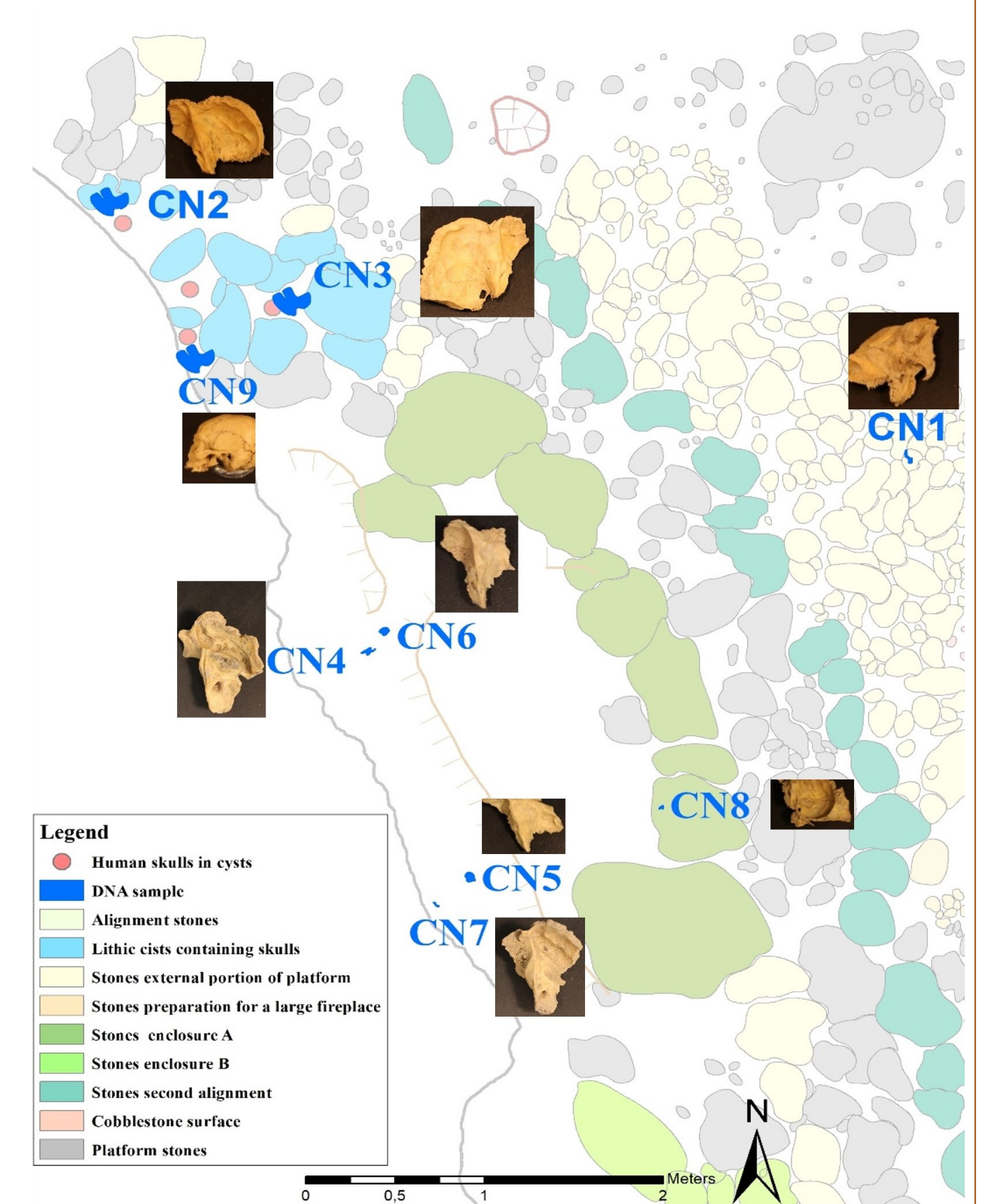
CORNA NIBBIA – BURIAL SITE

This necropolis is characterized by complex funerary rituals with fragmented and mixed skeletal remains belonging to at least 29 individuals.

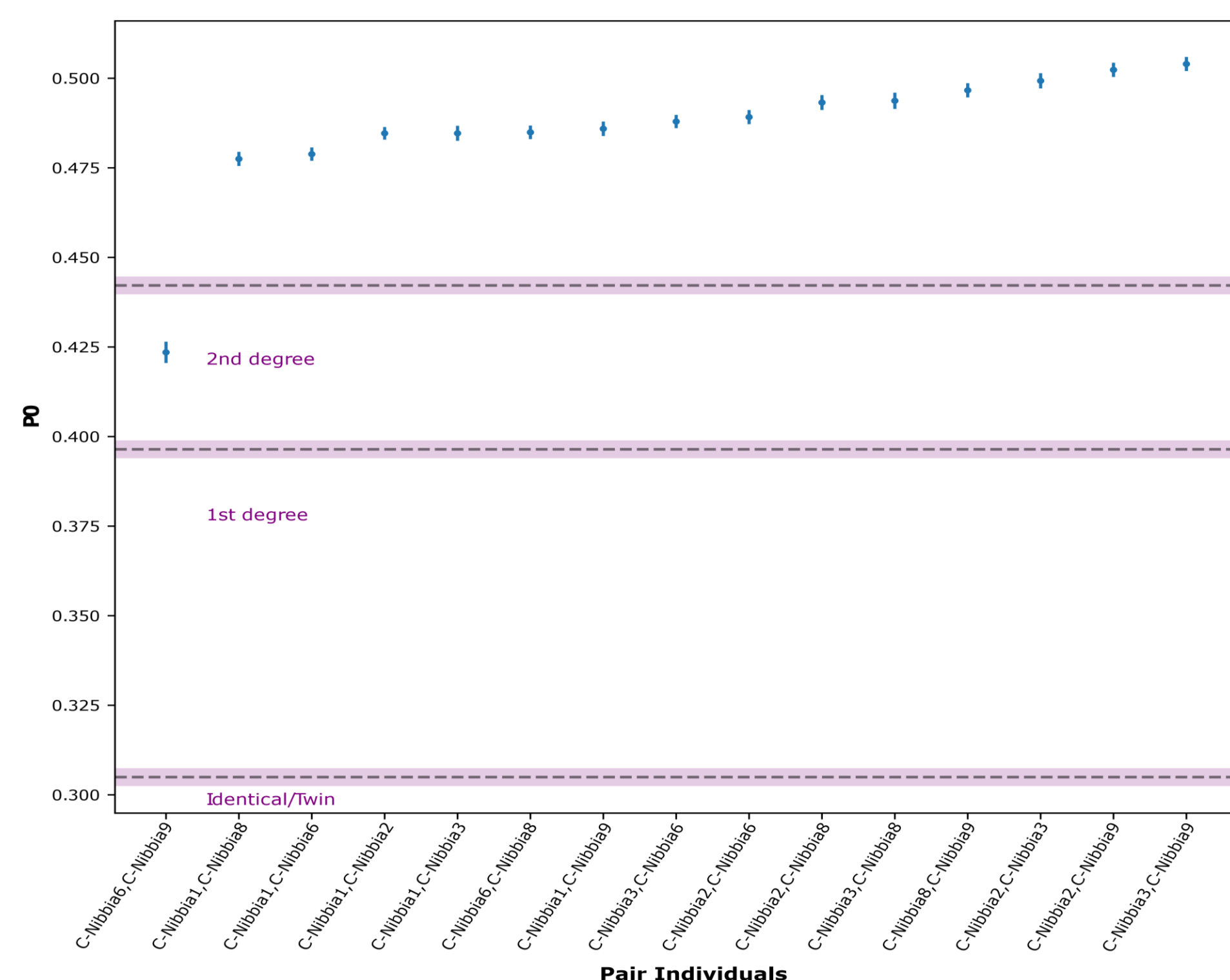
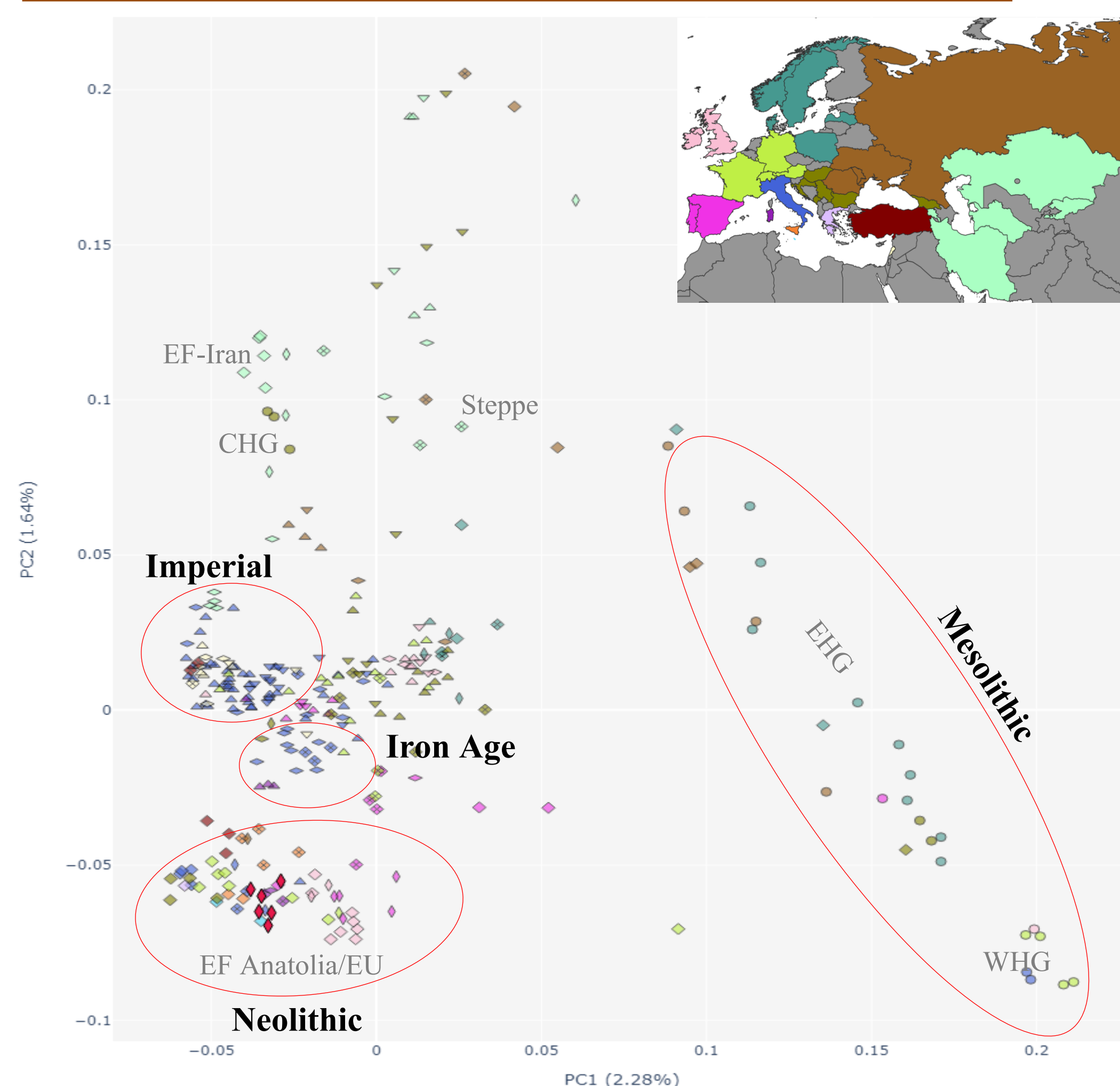
The skeletal remains of approximately 22 individuals were already collected and consist in **9 petrous bones ascribable to different individuals**, and another set of post-cranial specimens ascribable to 13 individuals.

Preliminary genetic screenings conducted on the post-cranial remains revealed poor genetic preservation, making them unsuitable for whole genome sequencing.

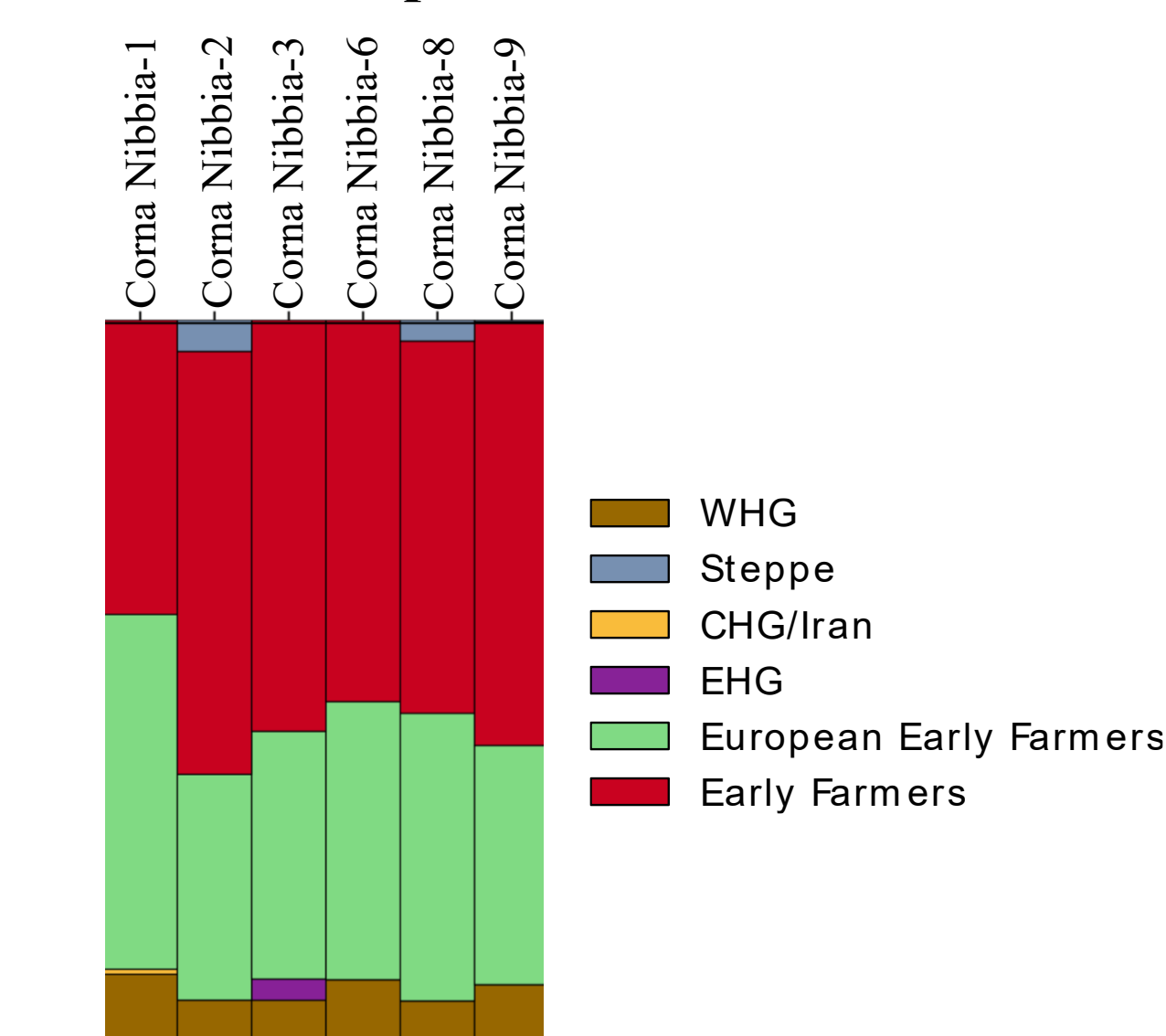
Screenings performed on the petrous bones, instead, highlighted a **good endogenous DNA preservation in 6 out of 9 available samples**, which were subsequently sequenced using the whole-genome shotgun strategy, **reaching the target coverage of 1x**.



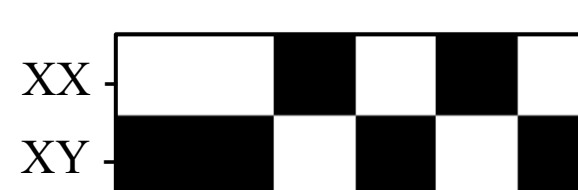
GENETIC STRUCTURE AND KINSHIP ANALYSIS



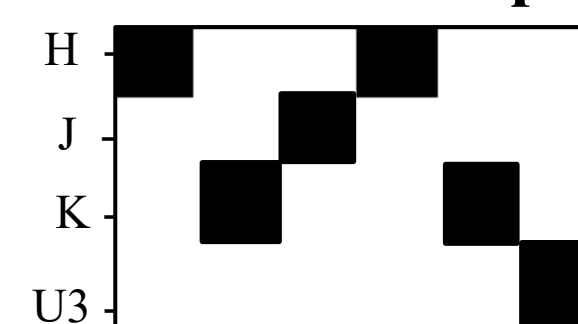
Genomic components



Molecular Sex



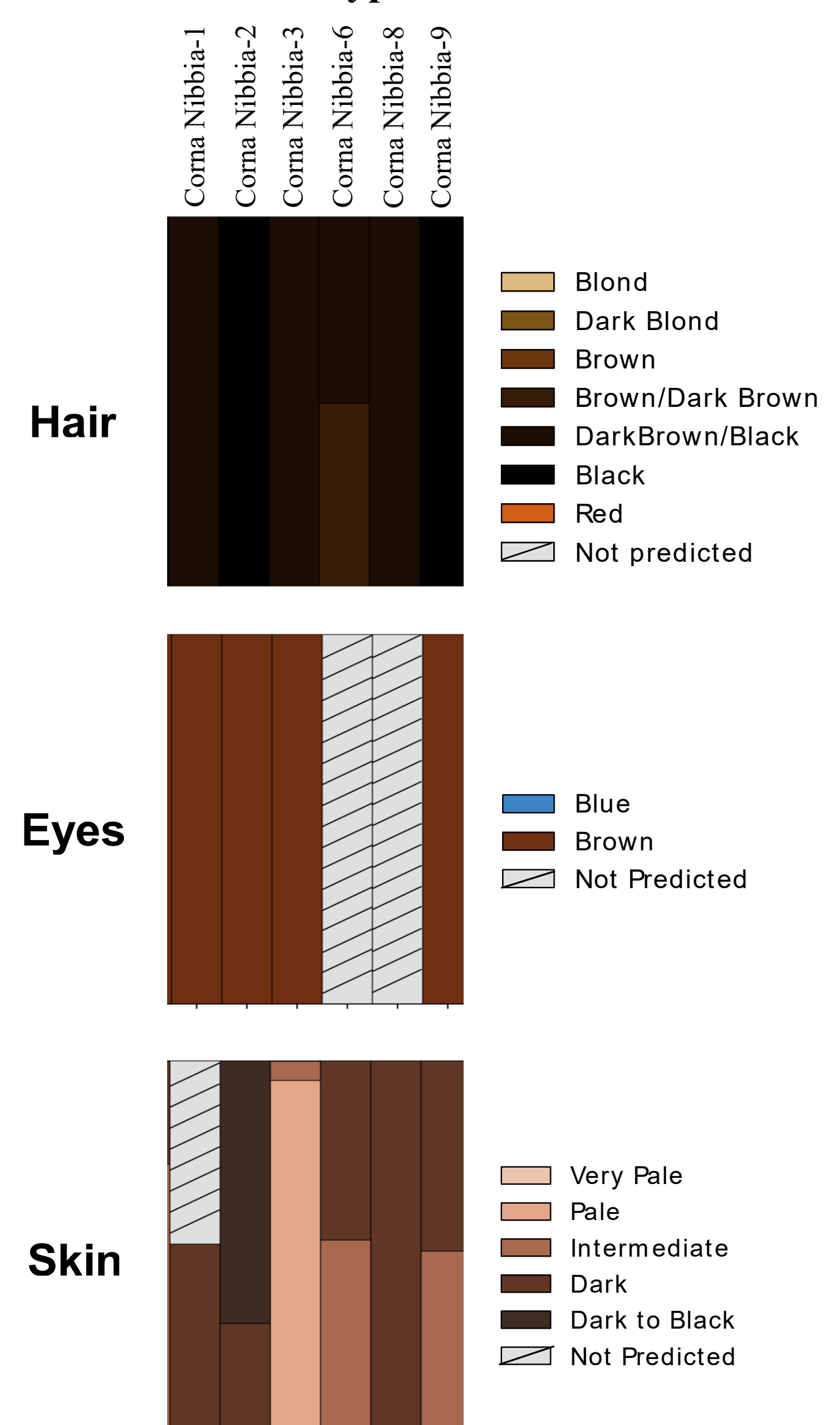
Mitochondrial haplotypes



Y chromosome haplotypes



Phenotypes



PRELIMINARY RESULTS

Preliminary results indicate that the Corna Nibbia samples exhibit patterns of genetic variability compatible with those observed in coeval Italian and European groups.

Employing the HirisPlex System integrated with Genotype Likelihoods/Imputation we estimated phenotype probabilities for each sample. Interesting CN-3 is the only individual showing pale skin color.

Regarding kinship analyses, among the six individuals, we identified only one pair (CN-6 and CN-9) showing a second-degree relationship (i.e. half siblings, avunculate or grandparent/grandchild).



Finanziato dall'Unione europea
NextGenerationEU



Ministero dell'Università e della Ricerca



Italiadomani
PIANO NAZIONALE DI RIPRESA E RESILIENZA



Università degli Studi di Ferrara

Funded by the European Union - NextGenerationEU - mission 4, component C2, investment 1.1. - project PRIN 2022 PNRR P20228M8ZN - CUP F53D23008180001

CONTACT ME!

