

THE GENOMIC DIVERSITY AND HISTORY OF DOMESTIC CHICKENS

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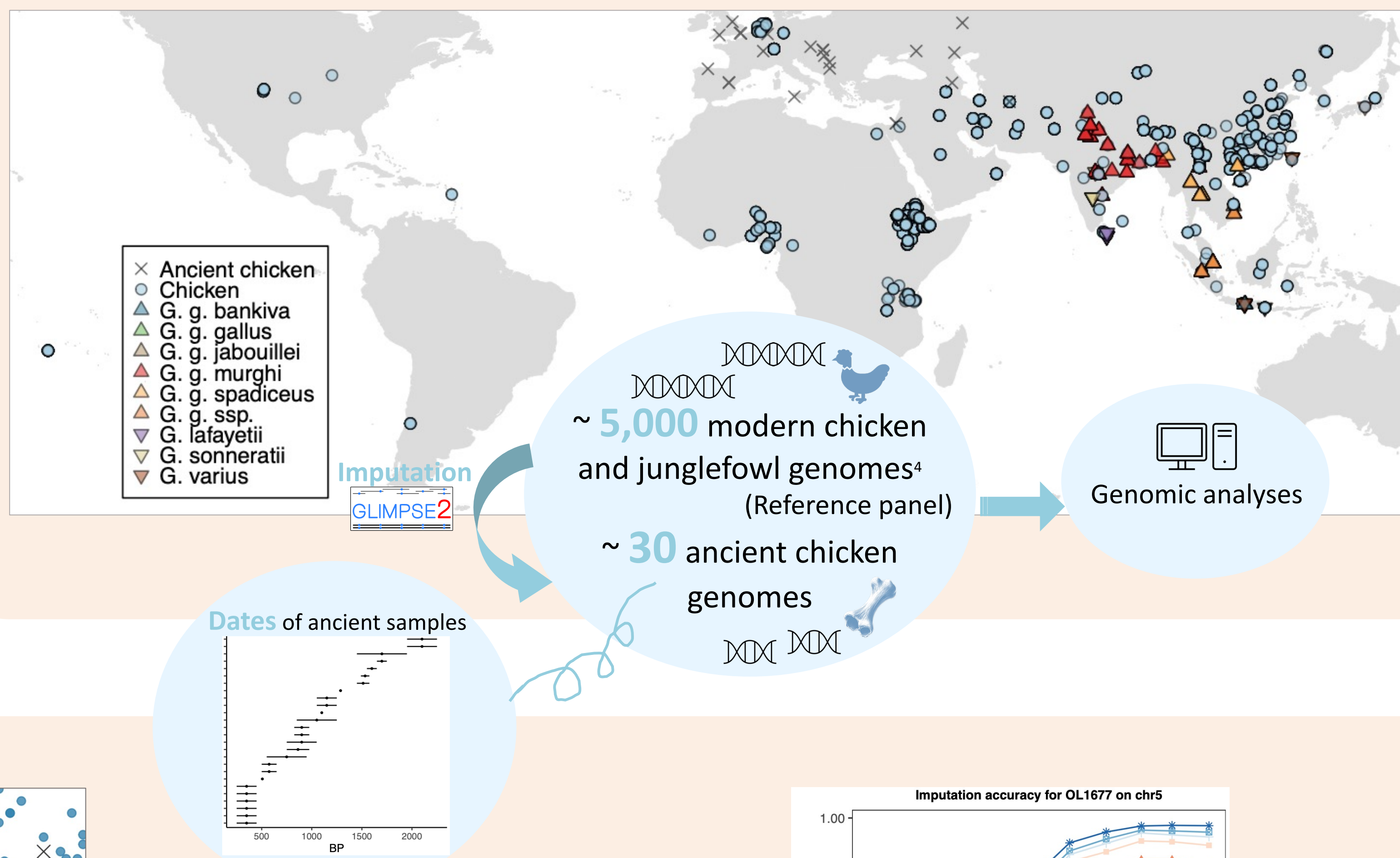
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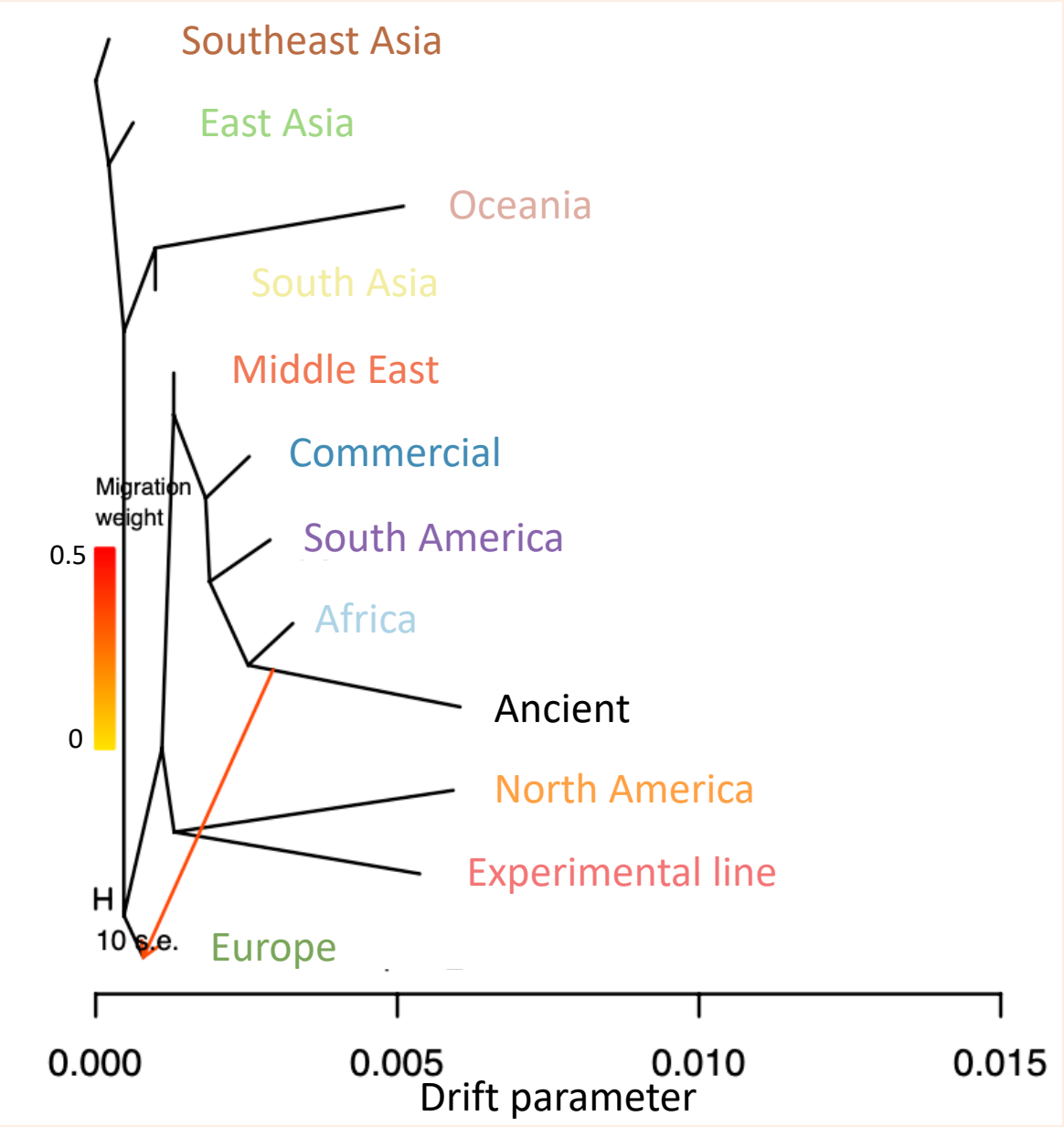
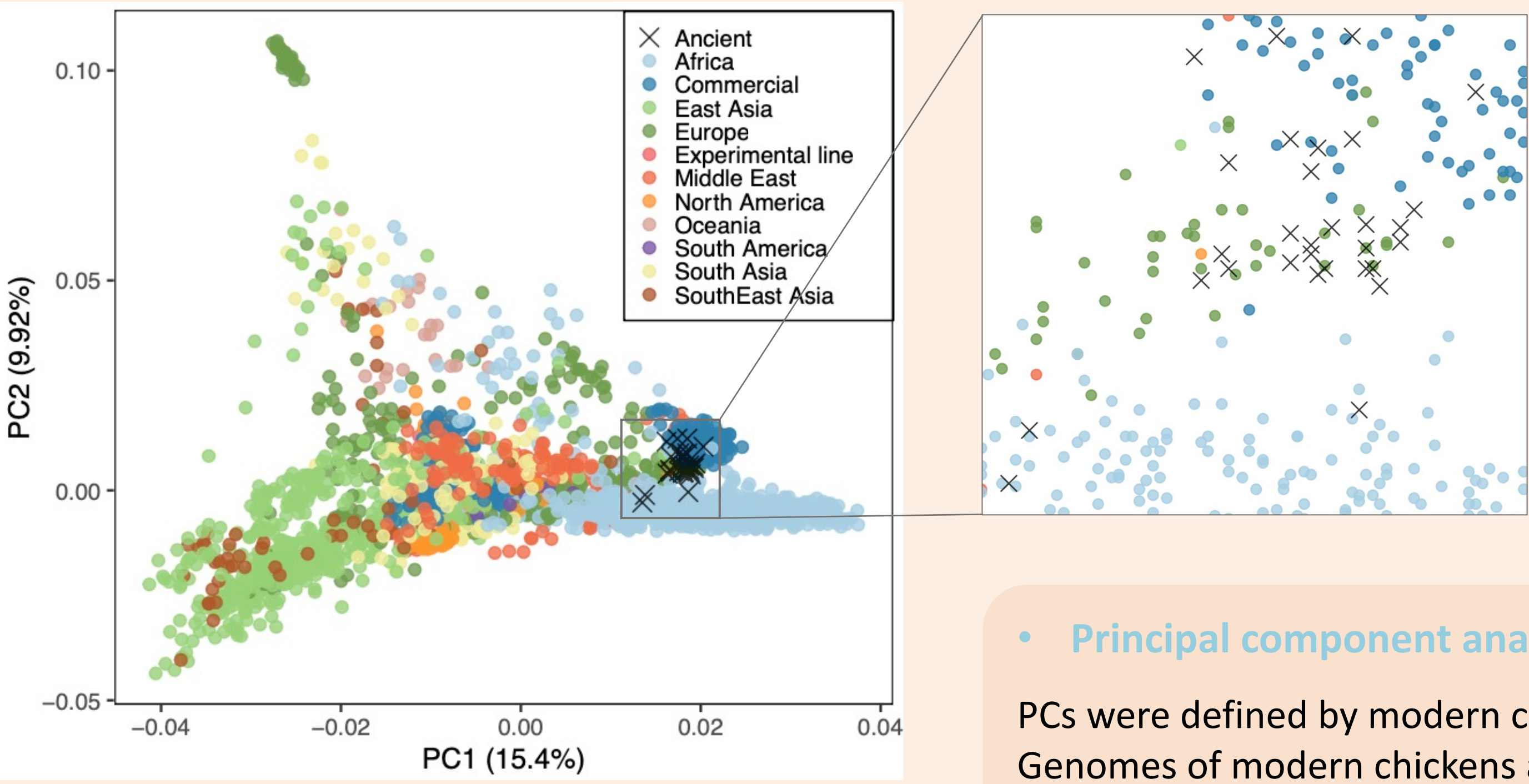
Background

- The chicken (*Gallus gallus domesticus*), as the most numerous and ubiquitous domestic animal species, plays important roles in human societies for food, religion, entertainment and ornamentation¹.
- Fundamental questions regarding both the **geographical and temporal origins** and the subsequent **dispersal** of chickens remain contentious².
- Ancient DNA combines the **time-depth** of archaeology with the **resolution** of genetic data. However, aDNA is often characterized by post-mortem damage, such as **fragmentation and deamination** with low breadth and depth of coverage, hindering genotype calling.
- Imputation** using a large reference panel has the potential to improve genotyping accuracy for low-coverage genomes³.

Methods

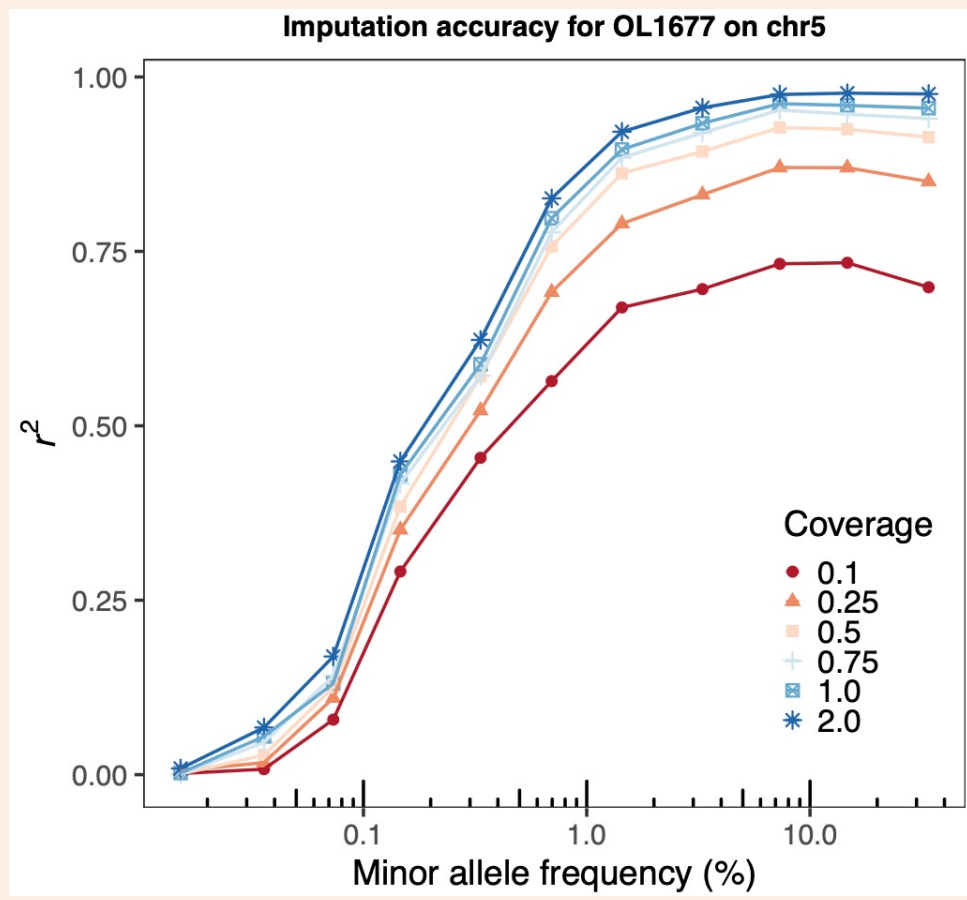


Results



• **TreeMix**
Colours indicates same main groups as in the PCA plot.
Admixture edge coloured by migration weight (TreeMix v1.13).

• **Imputation accuracy**
High coverage genomes downsampled to different depth of coverage.
For depths $\geq 0.75\times$ with $MAF > 2\%$, $r^2 > 0.9$.



Principal component analysis (PCA)

PCs were defined by modern chicken genomes, with the ancient genomes **projected** using smartpca from the EIGENSOFT (v7.2.1). Genomes of modern chickens are shown in filled circles.

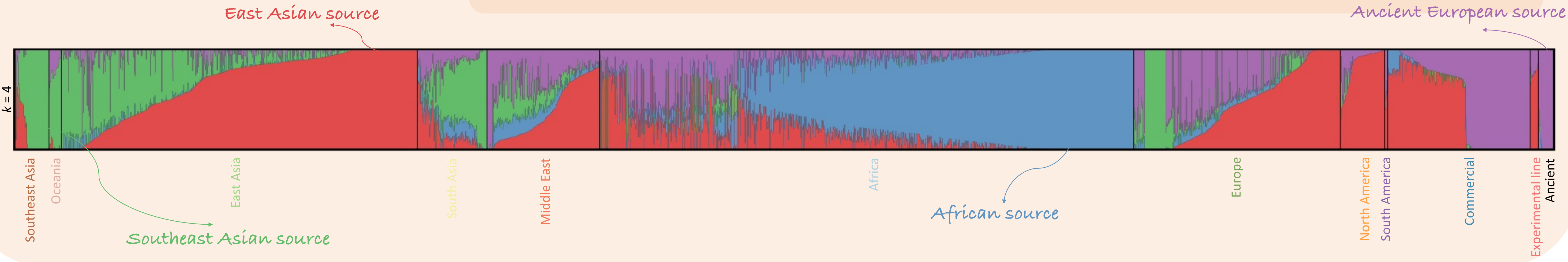
The results revealed geographical substructuring with chickens from different population groups forming **genetic clusters**, and a major **east-west axis** of chicken and junglefowl ancestry (PC1) in accordance with the geographical sampling locations. The western extreme of PC1 comprised chickens from East Asia and Southeast Asia. The east extreme is represented by chickens from Africa.

Ancient European chicken genomes **form a cluster** that overlaps with some of modern European, commercial and African chickens.

Supervised ADMIXTURE

We performed supervised admixture modelling using a set of **four possible source clusters** representing modern chickens from Southeast Asia, East Asia, Africa and ancient European chickens (AMIXTURE v1.3.0).

Ancient genomes show the **consistent ancestry source** with several individuals presenting some of African and Southeast Asia ancestry. Modern European fancy breeds possess divergent ancestry proportions as expected. Commercial chickens form two distinct groups.



Conclusions

- The genomic dataset of chickens and junglefowl has captured a large proportion of the extant **genetic variation** in the chicken genome.
- We demonstrated this large high-quality **reference panel** could be used to **impute low-coverage ancient chicken genomes** from Europe and Middle East dating to around 2000 years ago accurately.
- The **accuracy of the imputation** was evaluated by comparing the concordance between down-sampled imputed samples and original high-coverage ancient genomes.
- Principle component analyses and supervised admixture modelling analyses were performed to assess **population structures and global ancestry components**.

Next steps ...

Local ancestry inference
Demographic inference
Selection analysis

