

Towards an integrative understanding of taxonomic diversity, climate adaptation, and introgression in Southeastern European white oak species

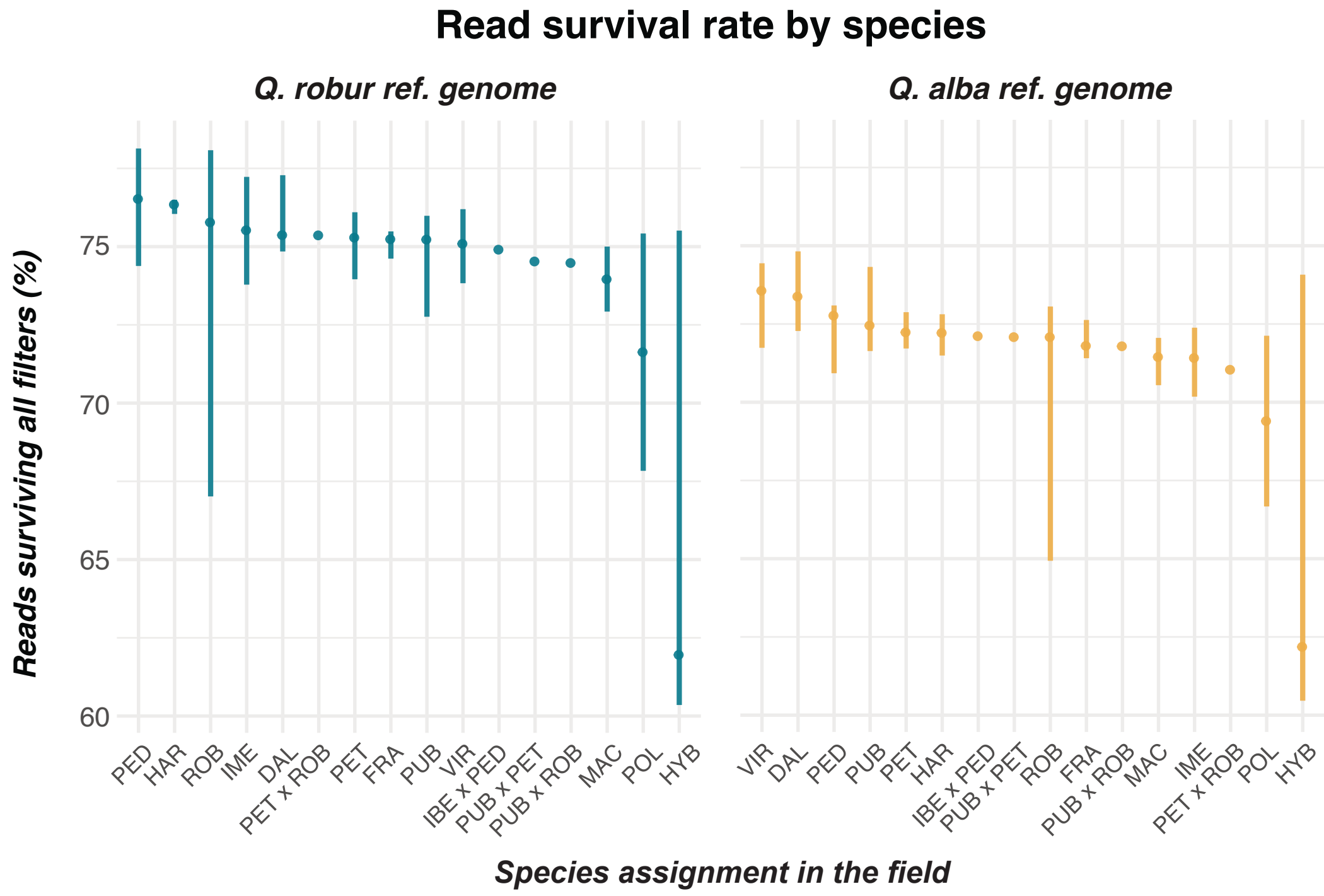
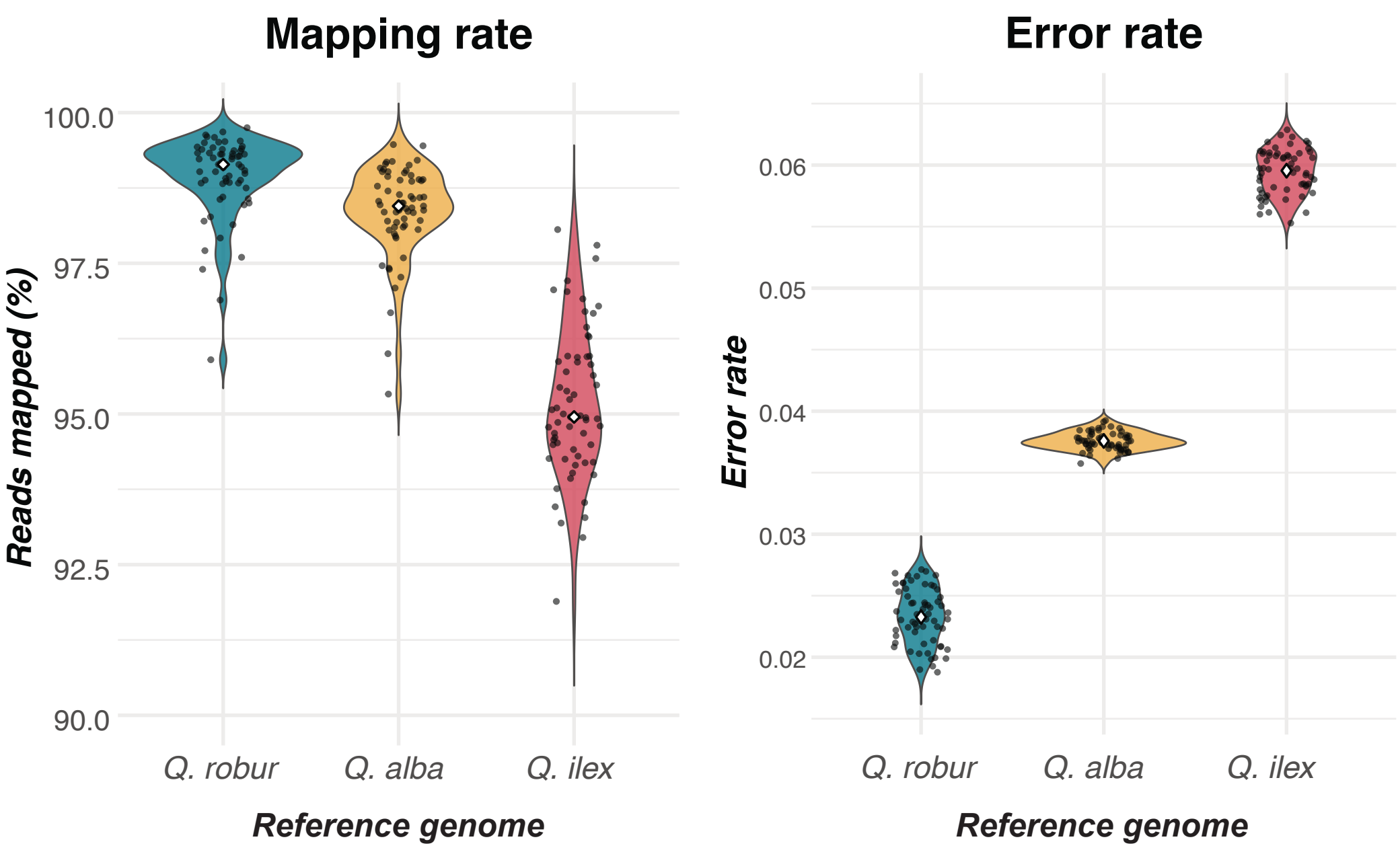
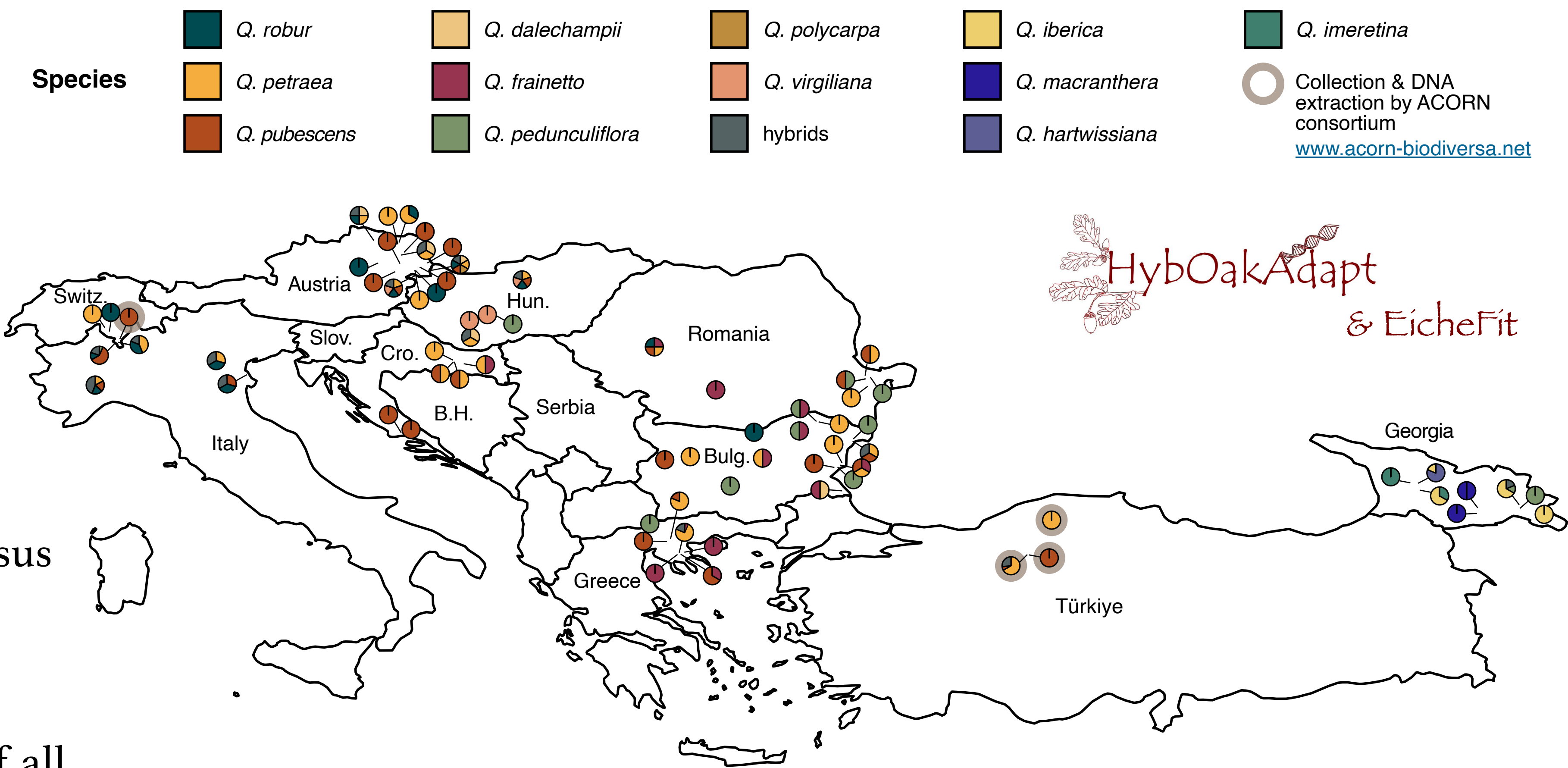
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Introduction & hypothesis

The white oak species complex includes widespread European oak species and is **strikingly diverse in Southeastern Europe**. The evolutionary processes underlying this taxonomic richness remain unclear. We hypothesize that **climate adaptation and adaptive introgression** during the divergence of white oak lineages played a major role.

Study design

- **1,200** trees collected in SE Europe, Türkiye & the Caucasus
- **12 taxonomic groups** (species / subspecies)
- Combination of **pure & mixed stands**
- Putative hybrids included
- Whole-genome sequencing & herbarium specimens of all trees

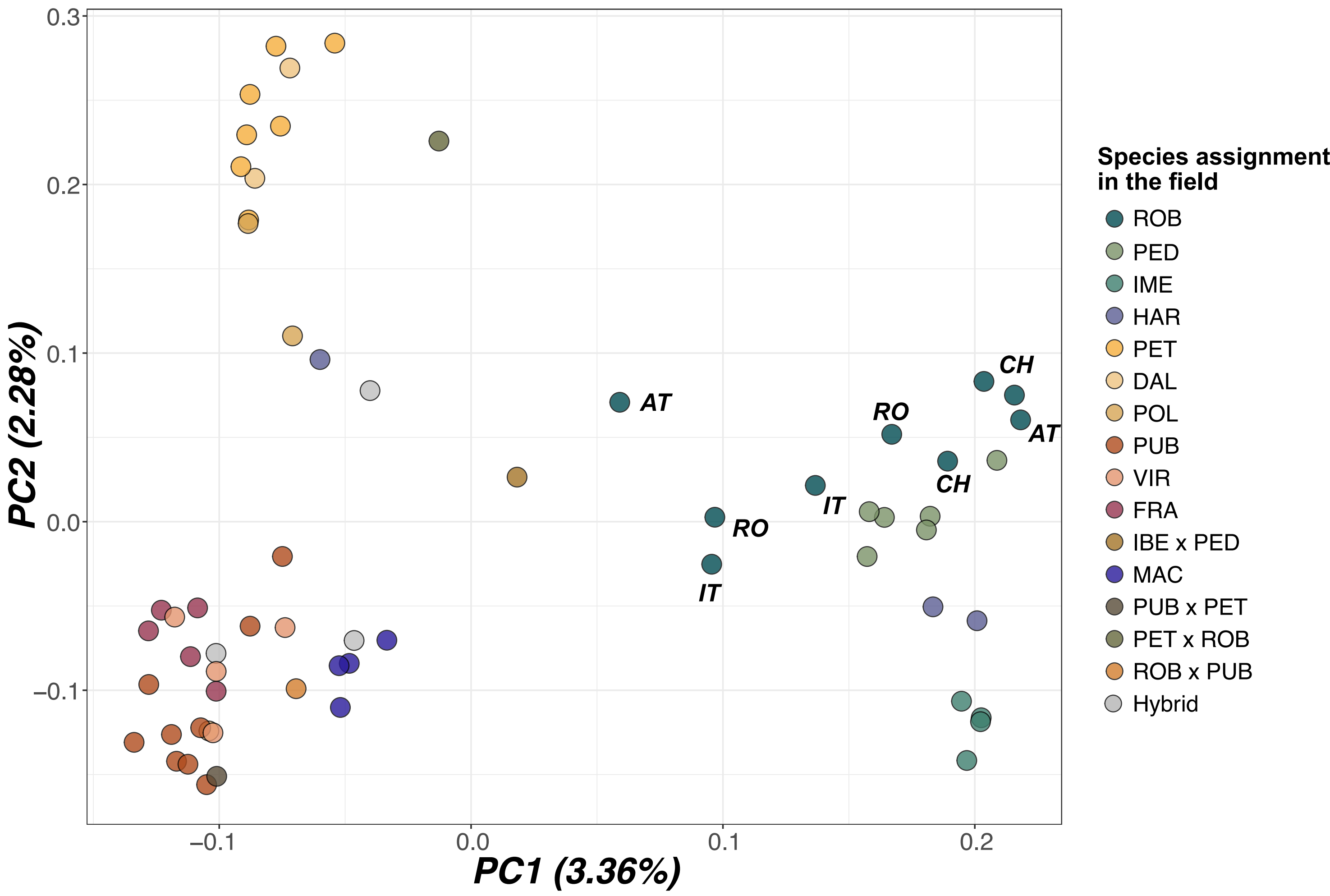


Comparing reference genomes

We compared mapping performance of 63 samples representing the diversity of our full sampling to three publicly available reference genomes: *Q. robur* (DToL), *Q. alba* and *Q. ilex*. Mapping and error rates worsen with increased divergence. *Q. robur* is the best performing reference and shows minimal species bias.

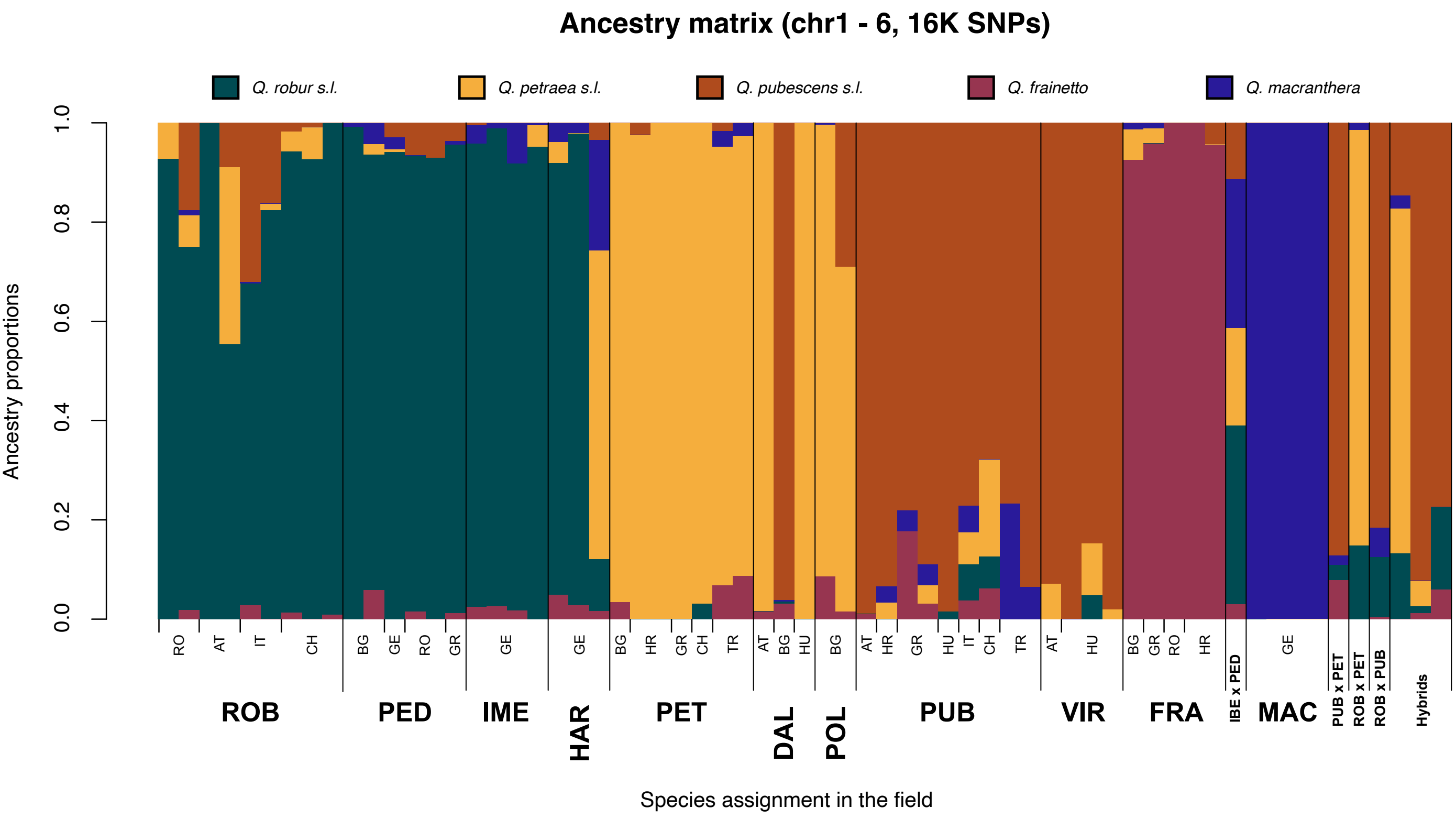
Genetic clustering

The first two components of a PCA (right) reveal **three main genetic clusters** corresponding to *Q. petraea*, *Q. robur* and *Q. pubescens*. Subspecies and regional varieties show close relatedness to the corresponding main lineages. *Q. frainetto* and *Q. macranthera* cluster with *Q. pubescens*, while samples field-assigned as *Q. hartwissiana* cluster both with *Q. robur* and *Q. petraea*. A genetic gradient in *Q. robur* does not match a broad geographic pattern.



Hybridization patterns

Admixture analyses reveal a complex introgression structure. At K = 5, five main lineages are clearly distinguished, including the previously understudied *Q. frainetto* and *Q. macranthera*. Despite this, most samples carry ancestry from more than two species. Our next step is to investigate whether this introgression facilitated climate adaptation in southeastern European white oaks.



Future aims

- PCA & Admixture analyses on full dataset
- Phylogenomics and demographic modelling to uncover the evolutionary history of SE European white oaks
- Identify genomic regions associated with local adaptation using Genome-Environment Association analyses
- Study introgression along the genome, test association with local adaptation

Check out Aglaia Szukala's poster **Pro** (session 2) on leaf morphometrics !