# Results

## Characterization of shared and species-specific chromatin states

## Chromatin states features influence predictions of paralogs functional divergence

## Defining functional genomics conservation score

## Experimental validation of potential divergent duplicates

## Discussion

While this flexible framework provides a consistent definition of chromatin states across multiple genomes, thus making easier direct comparison between them, the “full-stack” approach allows the understanding of the potential epigenomic regulation over several tissues/conditions such as differentiating constitutively active regions (Vu & Ernst, 2022). Therefore, we adopted this holistic approach simplifying genome annotations across tissues and species through a single segmentation annotation to allow future evolutionary epigenomics applications.

Not replace and wide range of genomic prediction properties for the community. Diversity compared to mammals.

Despite these pairs do not pass the stringent threshold, they presented high enough DFD values to be considered high divergent paralogs. Furthermore, we decided to asses AOX redundancy in roots phenotypes (because 2/5 paralogs are not expressed simplying the system and it is easier to monitorize in seedling stages) under two different stresses considering previously described roles of these genes in response and retrograde-signalling (cita).