## 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. thus highlighting plant kingdom epigenomic complexity. Deep and narrow vs shallow and broad - community. LECIF approach diverse data conservation. and exploiting that our approach could differ between constituvely active and repressive states. Previous works analyzing inter-species functional genomics were focused on comparing same assay matched experiments missing the power of diverse datasets for conservation inference .integrative features needed for genomic elements and patterns discovery. Comparisons with metazoans and mammals.

Functional translatation of the predictions and resource to explain complex biological mechanisms; diferencia de intensidad de estreses, con el estres AOX1C insensitive, lio con otras referencias, additional care; DFD values partial redundancy of aox1d con aox1a pero no al reves, aox1c almost stress insentitive. Stress promotes neofunctions

DB and future of evolutionary epigenomics.