# Results

## Characterization of shared and species-specific chromatin states

We generated an universal chromatin states (CS) map annotation from ten common epigenomic marks using hiHMM software for the three widely-studied model plant species: *Arabidopsis thaliana*, *Oryza sativa* and *Zea mays*. We focused our analysis on a model with 16 states (**supplemental fig. S1**; see **Methods**). The states were divided into 5 functional groups (bivalent, active, divergent, repressive and quiescent/no signal), with different levels of genome coverage, TE enrichment and overlap with other genomic features (**fig. 1**).

Although the co-occurrence of pairs of epigenetic marks exists between these species, there are clearly specific patterns in both, CS and correlation analyses (**fig. 1**; **supplemental fig. S2**). Despite the diversity of the data, we found some conserved chromatin definitions such as Bivalent TSS/Promoter CS1, strongly linked to all active marks with very low enrichment in H3K27me3 and without clear presence of heavy repressive marks like 5mC and H3K9me2; and Active CS6, established in gene bodies and mainly constituted by H3K36me3, H3K4me2 and H3K4me3 in all the species. On the other hand, most of the states definitions strayed with some species-specific nuances at different levels, which could actually reflect our understanding of species-specific biology and how epigenomic complexity has evolved in plants.

De menos a mas divergente,. 1) Mismo estado de cromatina con diferente marcas de misma función y misma localización – heterocromatina. 2) estados de cromatina que con diferentes marcas misma función o parecida diferente localización – check. Para hacer el entendimiento de estas marcas mas fácil se ha añdido > al nombre de la definicion 3) Totalmente divergent CS10

Examples of conserved and species-specific.

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Futher analysis to confirm interpretation such as. RNapolII At active states etc. CMT3 heterochromatin etc. Guarantee our initial interpretation of the states

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Evolutionary information functional convergence and orthologous. CNEs PhastCons Bivalente active elements. TF motifs, functional convergence and orthologous.

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Again, Reflect different genomic architectures SNPs and TF motifs distribution.

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Estados de cromatina son capaces de llevar información evolutiva conservación mientras que manifiestan características que aluden a la diversidad tanto de la biología como de arquitectura genómica de cada especie.

## 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. LECIF approach diverse data conservation

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.

Under the initial hypothesis – integrative features needed for genomic elements and patterns discovery

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). AOX check in Ezoe tables.

DB and future of evolutionary epigenomics.