# Methods

An overview of the methods workflow used in this study is shown in **supplementary fig. S1**.

## Data collection

We collected epigenomic (ChIP-, MeDIP-, ATAC- and DNase-seq) and transcriptomic (RNA-seq) data from three plant model species: *Arabidopsis thaliana*, *Oryza sativa* and *Zea mays*.

For the epigenomic data we used the previously published collection from the PCSD (Y. Liu et al., 2018) to ensure high-quality data. Then, we expanded the abovementioned list to include new common epigenetic marks published in the last years. The final epigenomic collection included 10 common marks represented by 130, 63 and 96 files for *A. thaliana*, *O. sativa* and *Z. mays*, respectively (**supplementary table S1**).

For the transcriptomic data we used the baseline collection of the manually curated database EBI-ATLAS (Papatheodorou et al., 2020). We filtered this list to only include studies that covered multiple tissues/organs. The transcriptomic final collection contained 118, 43 and 411 files for *A. thaliana*, *O. sativa* and *Z. mays*, respectively (**supplementary table S2**).

## Epigenomic data processing

Raw reads were trimmed and adapters were removed using trim\_galore v.0.6.6 as interface to CutAdapt (Martin, 2011). The remaining reads were aligned to the reference genome (*A. thaliana*: TAIR10, *O. sativa*: IRGSP-1.0, *Z. mays*: RefGen v4) using bowtie2 algorithm (Langmead & Salzberg, 2012). Mapped reads with MAPQ > 30 were used to secure optimal quality of the data. Aligned reads were sorted using SAMtools v.1.9 and duplicate reads were removed using Picard v.2.26 (<https://github.com/broadinstitute/picard>). For all the subsequent analysis we performed peak calling (narrow and broad), signal tracks building, correlation and formatting with MACS2 and deepTools (Ram et al., 2016; Zhang et al., 2008). Very briefly, the *–g* argument was changed for each species (*A. thaliana*: 91254070, *O. sativa*: 215463918, *Z. mays*: 1975365725), FDR < 0.1 was used for broad peaks calling and the arguments *--nomodel --shift 75 --extsize 150* were added for ATAC- and DNase-seq files processing. To guarantee the reproducibility of the analysis a docker was created and it is available at <https://hub.docker.com/r/rocesv/plantina-chiplike>.

## Inter-species chromatin states definition and annotation

We applied hiHMM (Sohn et al., 2015) to jointly infer multiple species chromatin states (CS) using commons marks signal tracks from several tissues as input. Signal tracks consisted in scaled log2 (fold change + 0.5) values averaged in 200 bp bins in all three species as described in the original application (Ho et al., 2014). The analysis was restricted to nuclear chromosomes. hiHMM can handle an unbounded number of hidden states so the number of states is learned from the training data instead of a pre-specified value by the user. The model inferred a total of 15 chromatin states with unmappable regions added a posteriori as the sixteenth state to avoid any bias in the segmentation. We defined the chromatin states based on the co-localization of marks and overlap enrichments of different genomic features using *OverlapEnrichment* in ChromHMM (Ernst & Kellis, 2017).

To further improve the interpretability of the states, additional annotation and description was performed. The annotation was based on significant overlap enrichments using the LOLA package (Sheffield & Bock, 2016) and was divided in: 1) Genetic variability represented by significant SNPs compiled in GWAS-ATLAS and AraGWAS (X. Liu et al., 2023; Togninalli et al., 2020). 2) Transcription factor binding motifs collected in PlantRegMap (Tian, Yang, Meng, Jin, & Gao, 2020). 3) Conservation covered by PhastCons elements in PlantRegMap and pairwise CNEs. 4) Other epigenomic features employing non-common liftovered information in PCSD. The description involved KEGG Orthology/Gene Ontology enrichments using clusterProfiler/REVIGO, respectively, and gene biotype-orthology correspondence using inParanoid information stored in Phytozome (Goodstein et al., 2012).

## Modelling paralogs degree of functional divergence

We reproduced two published models that predict genetic redundancy in *A. thaliana* paralogs (Cusack et al., 2021; Ezoe, Shirai, & Hanada, 2021) including our inter-species chromatin states distance metrics. To define state distance metrics, we first binned different genomic features (promoters and genes) into a fixed number of windows and computed both, presence (1 = present; 0 = absent) and frequency (% of bp covered in a window) vectors for each state and gene. Additionally, we also included a third type of vector being each element the frequency of a particular state over a non-binned genomic feature. Lastly, distinct distance metrics were calculated between genes of the same paralog pair comparing equivalent vectors using philentropy package (Drost, 2018).

To reproduce both studies we followed the workflow originally stablished for the best performing model. In brief, for the model described by Ezoe, Shirai & Hanada, 2021 feature selection was executed by two-tailed Wilcoxon rank sum test p-values between pairs labeled as redundant or divergent followed by logistic regression relative importance to examine the explanatory weights of the best variables. Due to the fact that this model is designed to perform genome-wide predictions and that only some of the distance state metrics could be informative, a small number of features is desirable. We combined the information of the best scored features into a single metric defined as custom chromatin state metric (CCSM) (**supplementary table S3**). To compare the performance of logistic regression models using different set of features we calculated the AUC-ROC and AU-PRC values. All the analysis were conducted in R software environment ([Team R Development Core 2013](javascript:;)).

On the other hand, in the model developed by Cusack et al., 2021 multiple transformations and interpretations of the same feature were included so all the distance state metrics and CCSM were considered. Only the available extreme (RD4) and inclusive (RD9) redundancy gene pair sets were analyzed deleting variables identified as mispredictors in the main article. Non-redundant gene pairs were randomly downsampled to generate balanced cross-validation sets. Feature selection was executed by random forest top 200 best transformed variables (determined by the feature importance in the trained models) for sets without (RD4-RD9) and with (RD4C-RD9C) chromatin information. The C value for SVM algorithm was set as hyperparamenter during the tunning. To measure SVM performance using different feature sets we calculated AUC-ROC and AU-PRC values. All the analyses were conducted using the pipeline implemented and developed by the authors (<https://github.com/ShiuLab/ML-Pipeline>).

## Redundancy genome-wide predictions

To generate genome-wide predictions we used the best performing model from the first pipeline described above. The stringent threshold for identifying high and low diversified pairs with the logistic regression formula (DFD = degree of functional divergence) was defined by 100 cross-validation test where the FDR was under 5 %. As a result, high/low divergent pairs have >0.5/<0.5 and >0.93/<0.46 DFD values with relaxed and stringent thresholds, respectively. *A. thaliana* genes (longest sequence) were used as queries to search for self-match homologous with DIAMOND v2 (E-value = 1e-04) (Buchfink, Reuter, & Drost, 2021). We only focused on pairs with the best hits, > 30 % identity and > 50 % coverage. We identified 7852 pairs of which 1444/6898 were predicted as high and 723/954 as low diversified duplicates with strict/relaxed thresholds, respectively. Ka (number of nonsynonymous substitutions per nonsynonymous site), Ks values (number of synonymous substitutions per synonymous site) and the similarity of expression patterns (Re) were calculated as described by Ezoe, Shirai & Hanada, 2021. An additional table is provided with filters such as same second closest paralog and expression in stress and seedling stages to assist experimental validation in future studies (**supplementary table S3**).

## Experimental validation of potential divergent paralogs

To illustrate that potential functional applications of the resources generated could reveal clues into complex biological problems, we focused in the experimental validation of mitochondrial alternative oxidases (AOX).

The *A. thaliana* T-DNA insertion line *aox1a* (SALK\_084897) was previously described as knockout and was validated by genotyping before using (Fuchs et al., 2022). We characterized *aox1c* (Sail\_420\_A04) and *aox1d* (SM\_3\_24421) insertion lines as homozygous and knockout by genotyping and RT-PCR analysis, respectively. Briefly, RNA was extracted as described by Valledor et al, 2014 and quantified by a Navi UV/Vis Nano Spectrophotometer, integrity was evaluated by agarose gel electrophoresis. cDNA was obtained from 500 ng of RNA using the RevertAid kit (ThermoFisher Scientific), where random hexamers were used as primers following the manufacturer's instructions. RT-PCR analysis reported these lines as knockouts because no amplification was detected in the mutants (all primers available in **supplementary table S3**).

For stress evaluation, *aox1a*, *aox1c* and *aox1d* seeds were surface-sterilized in a 2.8 % hypochlorite solution and washed several times with sterile water; they were stratified for 3 days at 4 ºC in darkness. The in vitro culture of seeds was carried out in 12x12 plates (Greiner) containing 50 ml of MS medium (cita), 5.8 pH, 1 % (w/v) sucrose and 0.8 % (w/v) agar and they were vertically placed under long-day photoperiod (16 h light 21 ºC, 8 h dark 18 ºC) for control conditions. To avoid a position effect, the four genotypes (Col-0 as wildtype, *aox1a*, *aox1c* and *aox1d*) were located in every plate position by rotating sectors in different plates. For the combined heat and drought stress, 2.5 % PEG8000 (ThermoFisher Scientific) was added to the initial plates and seedlings were subjected to 1 h 37 ºC stress every day at the same hour, gradually increasing and decreasing temperature. For the antimycin A (AA) treatment, 50 μM AA (Sigma-Aldrich) was added to the initial plates; control conditions were setted as a mock due to AA being dissolved in ethanol solution. Phenotypic monitoring was conducted 5 days after germination by scanning culture plates with high-resolution scans (Epson Perfection V600); hypocotyl and root lengths were measured with ImageJ software (Schneider, Rasband, & Eliceiri, 2012)for at least twelve biological replicates. Furthermore 3,3-Diaminobenzidine (DAB) staining (Sigma-Aldrich) was performed 5 days after germination for at least 3 biological replicates per treatment, following the protocol described by Daudi & A. O’Brien, 2012; DAB quantification was carried out by ImageJ.

## RNA-seq data processing

Sequence quality of RNA-seq libraries was evaluated by FastQC and multiQC (Andrews, 2013; Ewels, Lundin, & Max, 2016). Raw reads were trimmed and adapters were removed using trim\_galore v.0.6.6. Cleaned reads were mapped using STAR v.2.7.10 (Dobin et al., 2013) changing reference genome and minimum/maximum intron size accordingly to species. Bigwig files were obtained using *bamCoverage* command from deepTools (Ram et al., 2016).

## Whole genome alignments and identification of conserved non-coding elements

Whole genome alignments (WGA) were computed for each pairwise comparison of these three species. In summary, *lastz* alignments with far(vs *A. thaliana*; > 100 MYA according to TimeTree (Kumar et al., 2022)) and medium(*O. sativa* vs *Z. mays*; > 15 & < 100 MYA) *distance* arguments were performed using CNEr package interface (Tan, Polychronopoulos, & Lenhard, 2019). This was followed by format conversion, chains building and processing using lavToPsl, maf-convert, axtChain and chainMergeSort. RepeatFiller (Osipova, Hecker, & Hiller, 2019) was applied to the chains in order to improve the identification of conserved non-coding elements (CNEs). After RepeatFiller, we executed ChainCleaner (Suarez, Langer, Ladde, & Hiller, 2017) to improve alignment specificity and chains were then converted into aligments nets using chainNet (modified version that computes real score of partial nets) and netToAxt. Finally, Axt files were used as input to the pairwise identification of CNEs using the CNEr package with 45 identities over 50 length windows while taking into account the difference in whole genome duplications history between these species as decribed in Ren et al., 2018.

In order to take advantage of previously processed epigenetic tracks in PCSD that are not included in our initial collection (not common for all the species), we executed another WGA pipeline to liftover these files to the new reference assemblies. In summary, we used near as *distance* argument, skipped the RepeatFiller and ChainCleaner step because we aligned the same species, and the liftover was carried out using CrossMap v.0.6.2 (Hao Zhao et al., 2014). To guarantee the reproducibility of the analysis a docker was created and it is available at <https://hub.docker.com/r/rocesv/compcnes>.

## Functional genomics conservation score

LECIF algorithm (Kwon & Ernst, 2021) was applied to obtain functional genomics conservation score between all the possible pairwise comparisons integrating whole genome alignments, epigenomic, chromatin states, and transcriptomic information. The negative to positive sample weight ratio was setted to 10 because species under study are distantly related, with lower number of samples aligning but more likely to be functional conserved. For the training and evalutation we adopted the same approach as the authors based in odd and even chromosomes (**supplementary table S4**). LECIF downstream analyses were performed in R software environment ([Team R Development Core 2013](javascript:;)).

## Database resource

We developed PlantFUN(ctional)CO(nservation) database to provide public availability of the functional integrative tracks generated in this work and to facilitate future research in evolutionary functional genomics. PlantFUNCO contains three main tools: 1) Search section with interactive tables to retrieve gene- or superenhancer-level (Hainan Zhao et al., 2022) functional and comparative genomics information. 2) Shiny application to compute LOLA genomic overlap enrichments of user query bed files over chromatin states and LECIF/PhyloP binned scores. 3) JBrowse2 genome browser (Diesh et al., 2023). PlantFUNCO is available at <https://rocesv.github.io/PlantFUNCO>.

# Data availability

All the data generated in this study is available at PlantFUNCO database <https://rocesv.github.io/PlantFUNCO> and <https://zenodo.org/record/7852329>. All the code used in this work is available at <https://github.com/RocesV/PlantFUNCO_manuscript>.

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