# Supplementary Material

**Supplementary fig. S1. Overview of the methods workflow.**

**Supplementary fig. S2. Genome-wide intra and inter-species correlation and genome browser panels supporting the chromatin state calls. A)** Top left, pairwise correlations between chromatin modifications in each genome, average across all three species. Bottom right, pairwise correlations, averaged over tissues and conditions, within each species (pie chart) with inter-species variance (grey-scale background) of correlation coefficients for *A. thaliana (At)*, *O. sativa (Os)* and *Z. mays (Zm)*. **B-D)** Genome browser panels supporting the chromatin state calls for each species.

**Supplementary fig. S3. Inter-species chromatin states description based on KO dotplots highlighting convergent terms.** Each chromatin functional group is exemplified by a module with a single state (CS1 – bivalent; CS6 – active; CS10 – divergent; CS11 – heterochromatin). Each module is constituted by a dotplot showing significant KO enrichments for the genes covered by the CS for each species (*A. thaliana (At)*, *O. sativa (Os)* and *Z. mays (Zm)*). Colors denote species. Dot size indicates gene ratio. Bold KO terms highlight convergent terms for all the species.

**Supplementary fig. S4. Inter-species chromatin states description based on GO treemaps highlighting convergent terms.** Each chromatin functional group is exemplified by a module with a single state (CS1 – bivalent; CS6 – active; CS10 – divergent; CS11 – heterochromatin). Each module is constituted by three treemaps showing significant GO enrichments for the genes covered by the CS for each species (*A. thaliana (At)*, *O. sativa (Os)* and *Z. mays (Zm)*). Bold and dark GO terms highlight convergent terms for all the species.

**Supplementary fig. S5. LECIF score genome-wide distribution.** Circos to visualize gene density (first track), scores (second to fourth track) and chromatin states (inner track; colors indicate chromatin functional groups) across nuclear chromosomes and species. *A. thaliana (At)* and *O. sativa (Os)* chromosomes are zoomed in to reach *Z. mays (Zm)* scale.

**Supplementary table S1. Epigenomic data collection and chromatin states summary of protein-coding genes and orthologs percentage.**

**Supplementary table S2. Transcriptomic data collection.**

**Supplementary table S3. Degree of functional divergence genome-wide predictions and mutants information.**

**Supplementary table S4. LECIF training and tunning.**