**SUPPLEMENTARY MATERIAL 2.** A brief transposable elements annotation steps used in this work.

**Dataset**: Fifty-seven genomes used in this analysis were downloaded from Ensembl Plants, version 41. Plus, ten new genomes were added from version 45.

**Identification**: A set of methodologies performed into steps were used to identify TEs.

**Step 1**:To identify transposable elements four tools were used: **A)** TEs identification with RepeatScout (version 1.0.5) resulted in a library. The output was before classified using PASTEClassifier. **B)** RepeatModeler (version 10.0.10) was used to create a TEs consensus to use as library to RepeatMasker.

**Step 2**: Genome-wide identification of TEs using RepeatMasker (version 4.0.7) with a Repbase library (version 20181026) and with libraries from RepeatModeler and RepeatScout. We filtered score less than 250 (recommended by RepeatMasker to avoid increase of false positive numbers) and coverage sequence of over 60%. Sequences that did not reach these requirements were discarded.

**Step 3**: For Class II - Subclass 2 TEs, we used HelitronScanner (version 1.1) and MITE-Hunter (release 11-2011).

**Step 4**: For the identification of LTR retrotransposons, we used LTR\_retriever, version 1.8. To identify Non-LTR retrotransposons, we used MGEScan-non-LTR, version 3.0, both in default parameters.

**Filter**: Removing undesired (low complexity, simple repeat and other nomenclature that is not Transposable Elements) repeats record.

**Annotation**: GFF3 file available to be downloaded.