# **Supporting information**

**Supporting information 01** –Sequence accession codes of FT and TFL1 of angiosperms and gymnosperms used to infer the phylogenetic trees. Each sequence is identified by its respective accession code retrieved from the GenBank database.

**Supporting information 02** – Fossil records used for calibration to the most recent common ancestor.

**Supporting information 03 -** Schematic overview of ancestral residue sequences alignment showing the conserved regions of FT (panel A) and TFL1 (B). Key residues are highlighted by an asterisk.

**Supporting information 04 -** Ramachandran plots of FT modeled structures exhibited > 90% of residues in favorable regions with the sum of residues in permitted regions (panels A to G). (A) angiosperms; (B) monocots; (C) eudicots; (D) brassicales (E) asterids, (F) *A. thaliana,* and (G) *C. fusiformis*.

**Supporting information 05** – Ramachandran plots of the modeled structures of TFL1 exhibited > 90% of residues in the favorable regions with the sum of residues in permitted regions (panels A to F). (A) angiosperms; (B) monocots; (C) eudicots; (D) brassicales; (E) non-brassicales, and (F) *A. thaliana*.

**Supporting information 06** –Local quality estimation exhibited by Qmean plot of the modeled ancestral structures of FT from angiosperms (panels A to E) and *A. thaliana* (F). (A) angiosperms; (B) monocots; (C) tricolpates; (D) brassicales (E) asterids, (F) *A. thaliana,* and (G) *C. fusiformis*.

**Supporting information 07** –Local quality estimation exhibited by Qmean plot of the modeled ancestral structures of TFL1 from angiosperms (panels A to E) and *A. thaliana* (F). (A) angiosperms; (B) monocots; (C) tricolpates; (D) brassicales; (E) non-brassicales, and (F) *A. thaliana*.

**Supporting information 08** – RMSD plots obtained over 20 ns of MD simulation for the modeled structures of FT (panel A) and TFL1 (B).

**Supporting information 08** – Alanine scanning plot of FT structures showing the effect of mutations on protein stability (panels A to C). (A) monocots; (B) eudicots and (C) asterids*.*

**Supporting information 09** – Alanine scanning plot of FT structures showing the effect of mutations on protein stability (panels A and B). (A) brassicales and (B) *C. fusiformis*.

**Supporting information 10** – Alanine scanning plot of TFL1 structures showing the effect of mutations on protein stability (panels A to C). (A) angiosperms; (B) monocots and (C) eudicots.

**Supporting information 11** – Alanine scanning plot of TFL1 structures showing the effect of mutations on protein stability (panels A to C). (A) brassicales (B) non-brassicales and (C) *A. thaliana.*