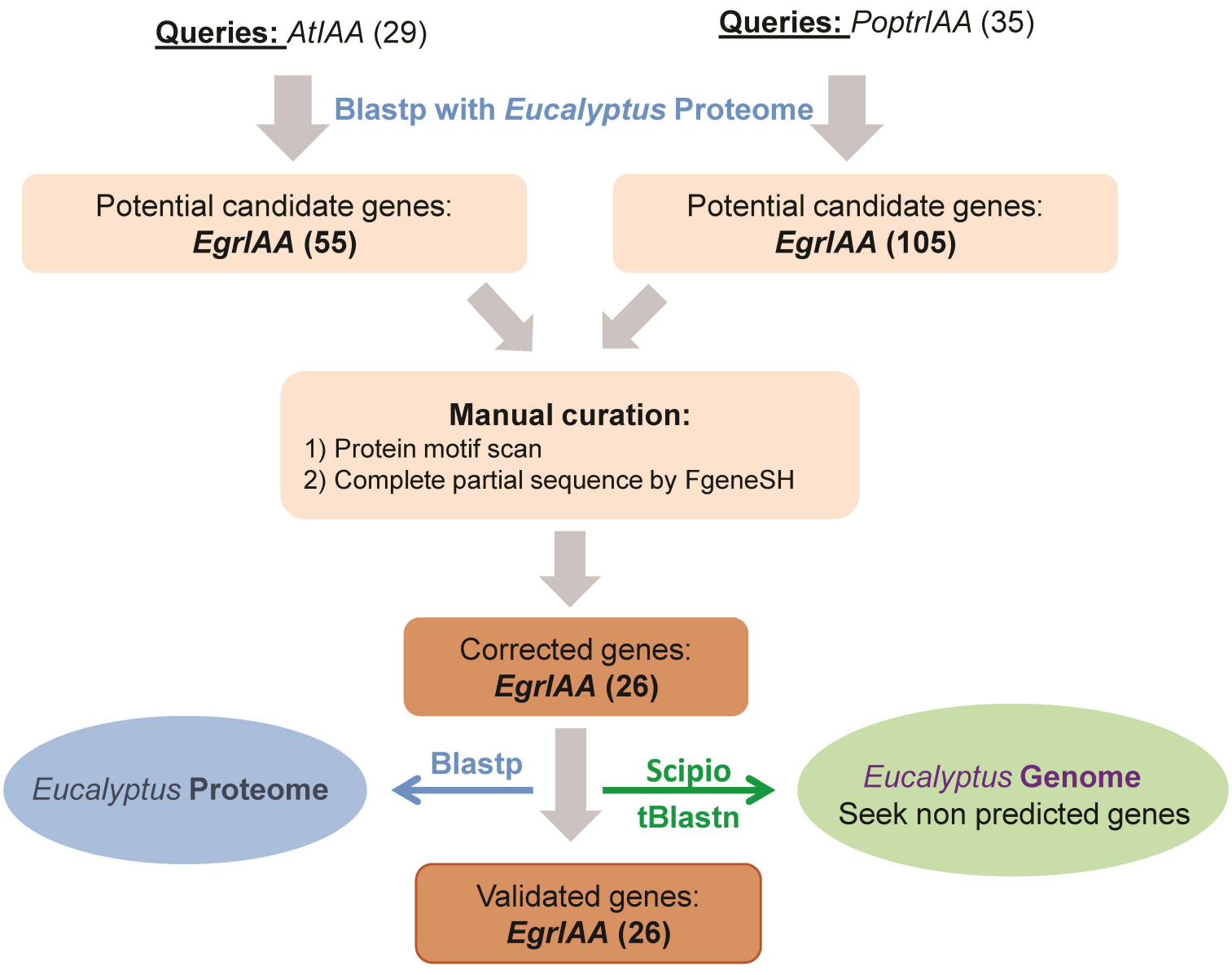
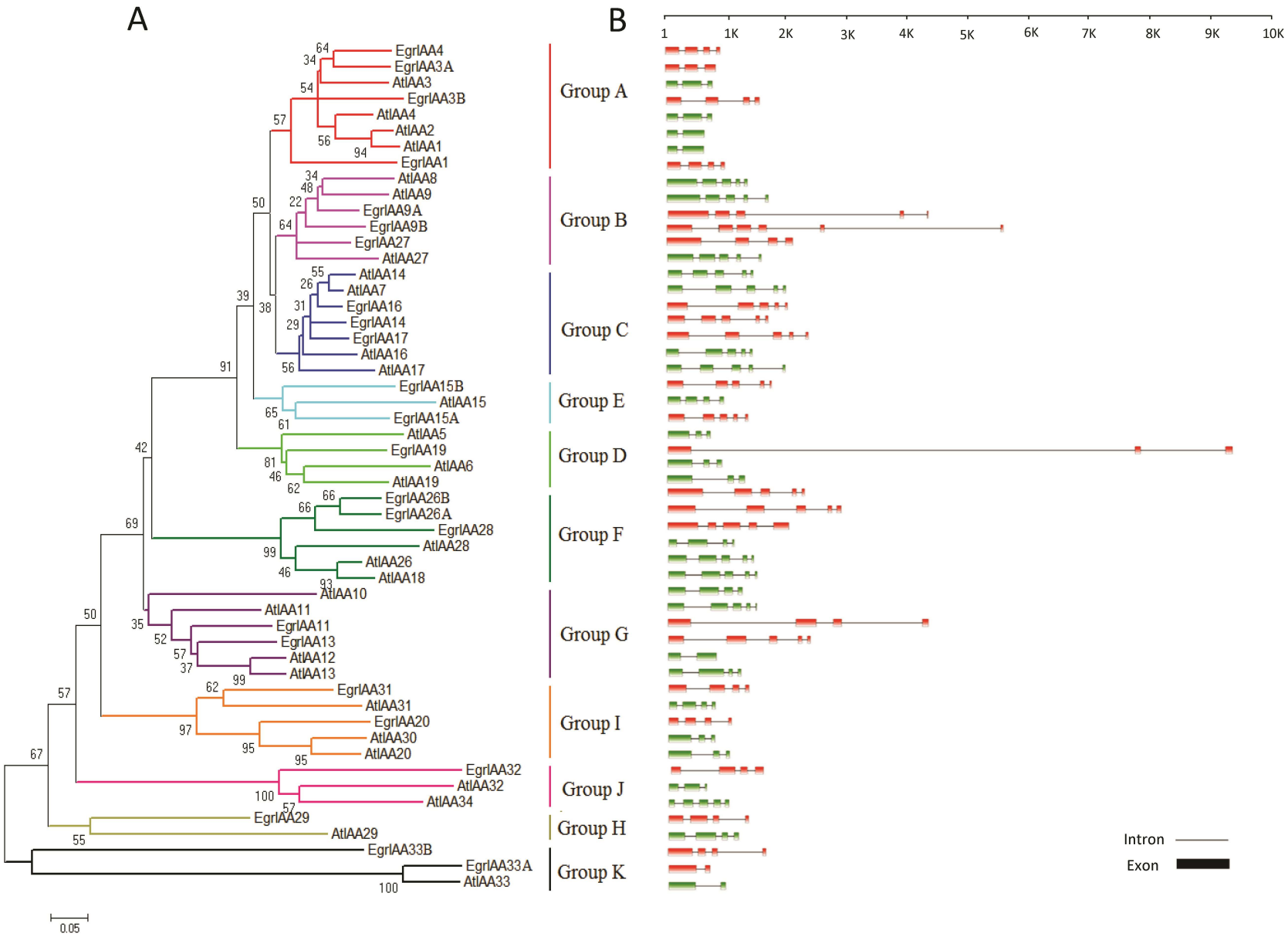
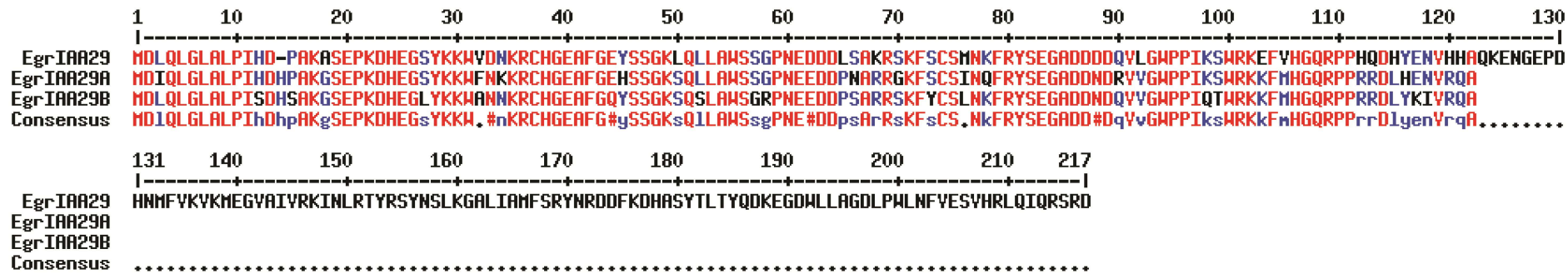


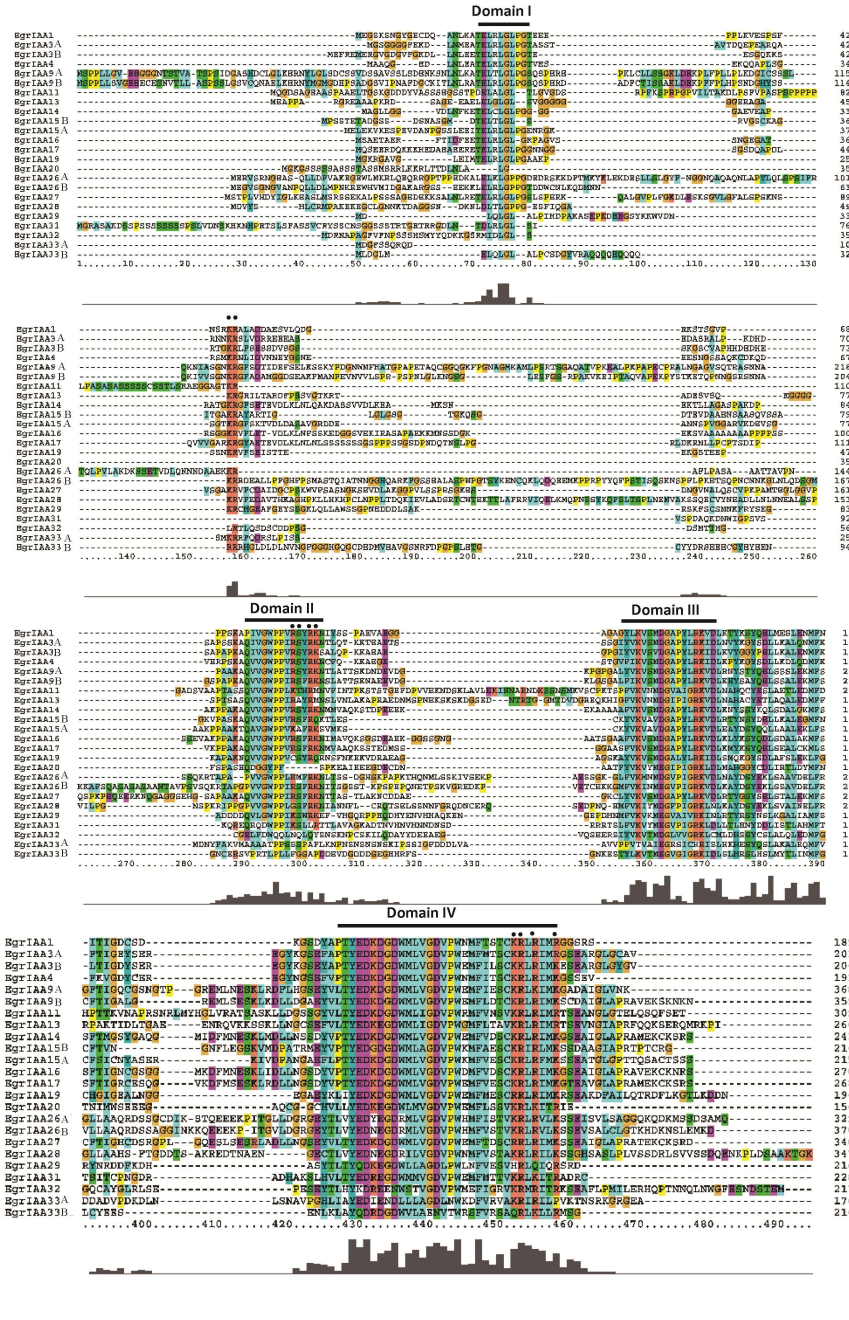
Supplementary Fig. S1 Procedure used for identifying *Aux/IAA* genes in *Eucalyptus grandis*. *Arabidopsis* Aux/IAA protein sequences were used to search for related proteins in the predicted *E. grandis* proteome by using BLASTP. Fifty-five *E. grandis* proteins identified in this initial search were further examined by manual curation using protein motif scanning and the FgeneSH (Solovyev 2007) program to complete partial sequences. Redundant and invalid genes were eliminated based on gene structure, the integrity of conserved motifs and EST support. Manual curation resulted in 26 *Egr*IAA protein sequences. We then used these 26 protein sequences in two subsequent additional searches: first, a BLASTP search against the *E. grandis* proteome to identify exhaustively all divergent *E. grandis Aux/IAA* gene family members and, second, tBLASTn searches against the *E. grandis* genome for any possible unpredicted genes. To confirm our findings, we also used poplar Aux/IAA proteins to repeat the complete search procedure described above with identical results obtained.



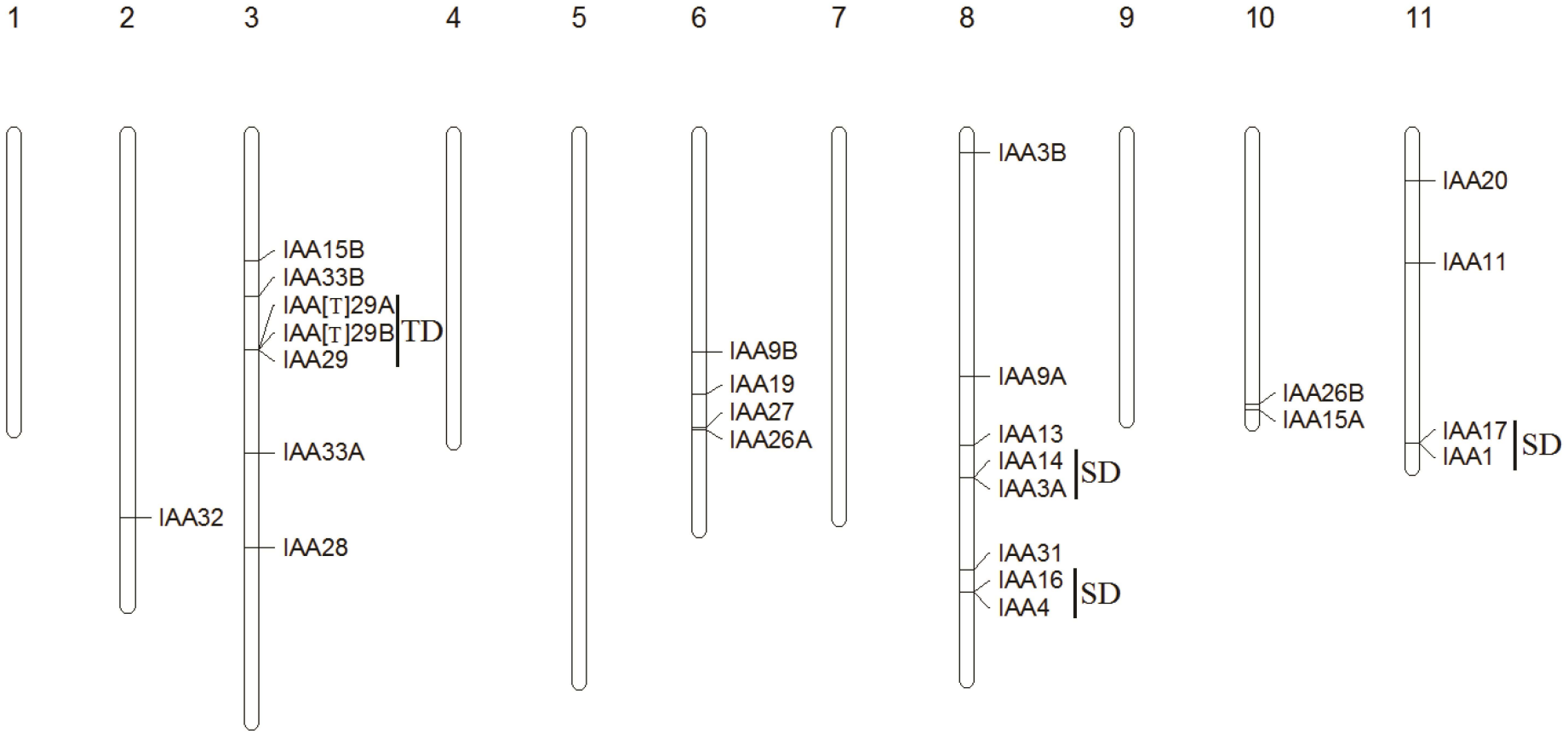
Supplementary Fig. S2 Phylogenetic analysis of *E. grandis* and *Arabidopsis* IAA proteins and the exon–intron organization of corresponding genes. (A) Neighbor-joining phylogenetic tree of *E. grandis* and *Arabidopsis* IAA proteins. Full-length predicted IAA protein sequences were aligned using Clustal_X2 program and phylogenetic tree was constructed by using the MEGA5 program and neighbor-joining method with 1,000 bootstrap replicates. Bootstrap values are indicated at each node. (B) Exon–intron organization of the *EgrIAA* (in red) and *AtIAA* (in green) genes corresponding to the proteins in the phylogenetic tree. The sizes of exons and introns are indicated by the scale at the top. The information on exon–intron structure was extracted from the Phytozome database and visualized by using the FancyGene software (http://bio.ieo.eu/fancygene/).



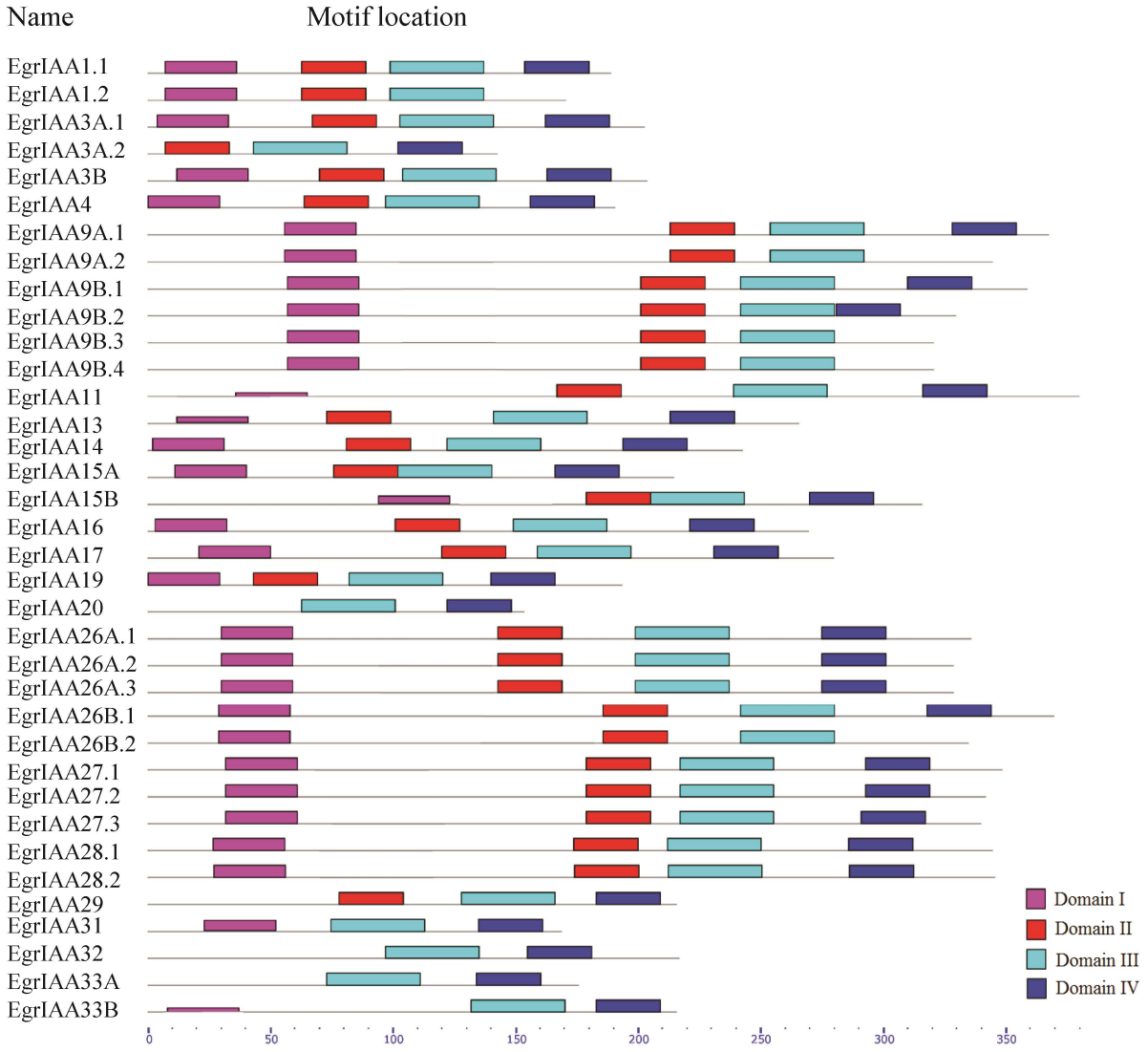
Supplementary Fig. S3 Protein sequences alignment of *EgrIAA29* and two truncated genes, *EgrIAA29A* and *29B*.



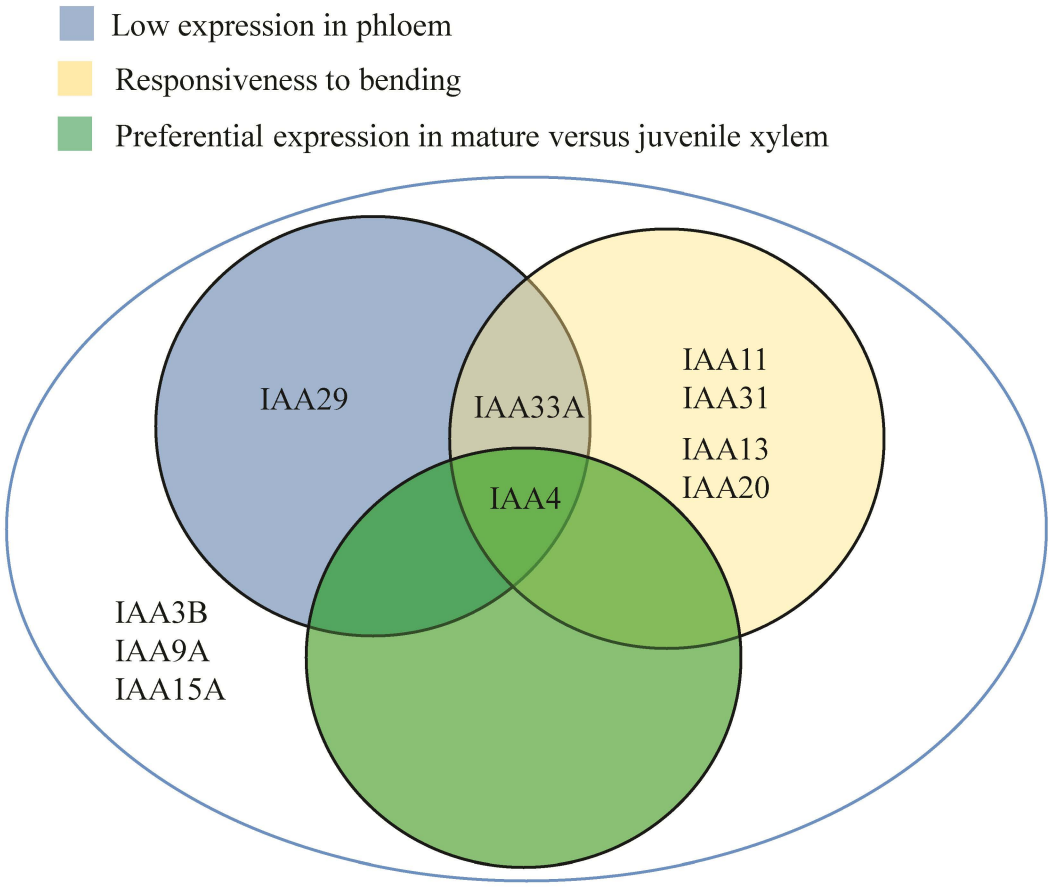
Supplementary Fig. S4 Multiple sequence alignment of predicted amino acid sequences of *Egr*IAA proteins. The multiple sequence alignment was obtained with Clustal_x2 and manual correction. The four highly conserved domains of Aux/IAA proteins were noted on the top of the alignment. Nuclear localization signals (NLSs) were indicated by dots. The amino acid position was given on the right of each sequence.



Supplementary Fig. S5 Chromosomal positions of the *EgrIAA* genes. The tandem duplications (TD) and segmental duplication (SD) are written on the right side of the corresponding genes. Chromosome scaffolds (1–11) are indicated at the top end of each chromosome.



Supplementary Fig. S6 Predicted proteins of all the transcripts of EgrIAA and their conserved domains. Conserved domains were predicted using the MEME web server (Bailey et al. 2009) with the following parameters: distribution of motif occurrences, zero or one per sequence; motif width ranges from 10 to 50 residues; maximum number of motifs to find, 4. The size and location of motifs can be estimated by the scale at bottom.

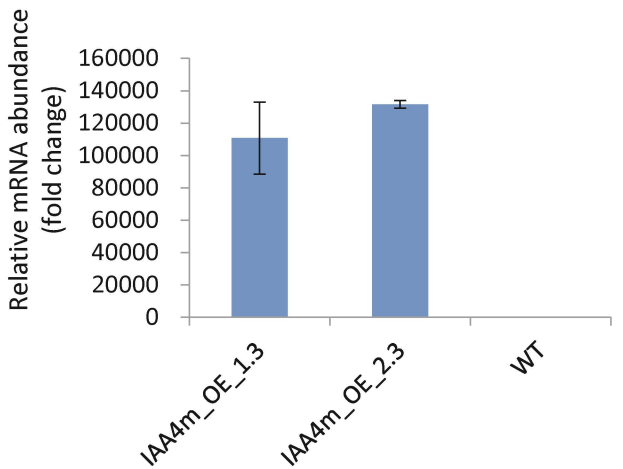


Supplementary Fig. S7 Venn diagram of overall strategy to identify the best potential candidate(s) involved in wood formation. Best potential candidate(s) should be i) highly expressed in vascular tissues; ii) preferentially expressed in xylem/cambium compare to phloem; iii) showing a response to bending; iv) preferential expression in mature versus juvenile xylem. Only *EgrIAA4* is fulfilling these conditions.

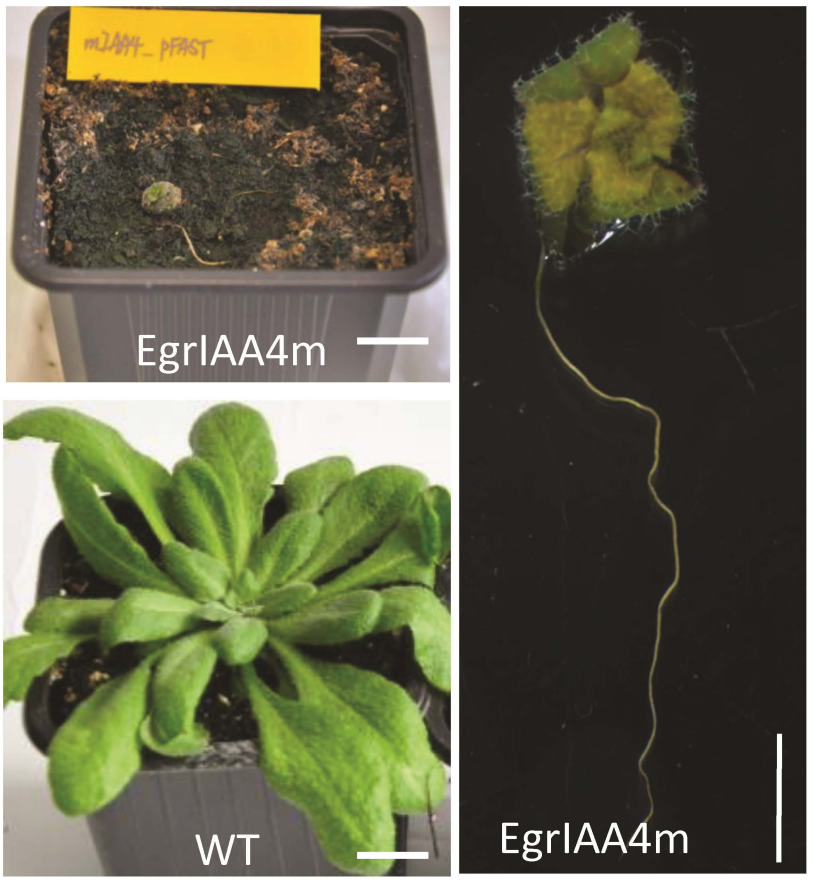
A

MAAQGEDLNLEATELRLGLPGTVEPEKQQAPLSGRSMKRNLIDVNNEYGSNEEESNGSSA
QKCDKQDVHRPSKAQVVGWPPVRSYRKNCFQKKAEGESTGVFIKVSMDGAPYLRKIDLKP
YKGYSDLLKDLQGMFKFKVGEYCEREGYNGSEFVPTYEDKDGDWMLVGDVPWNMFITSCK
RLRIMKGSSEV

B



C



Supplementary Fig. S8 Protein sequence of *EgrIAA4* and the phenotype of *EgrIAA4m* transgenic *Arabidopsis*. (A) Amino acid sequence of mutated EgrIAA4m protein. In the mutated EgrIAA4m cDNA, the 80th codon encoding the conserved Pro residue (highlighted in red) was changed to a codon encoding a Ser residue. (B) Transcript levels of *EgrIAA4m* in transgenic *Arabidopsis* under the control of the 35SCaMV promoter. Three technical replicates were used for each qRT-PCR experiment. Bars shows averages ratio of the *EgrIAA4m* relative to that of *AtUBQ10*. Error bars represent SE. (C) *EgrIAA4m* transgenic and wild type *Arabidopsis* plants grown for 40 days. Scale bar: 1 cm.