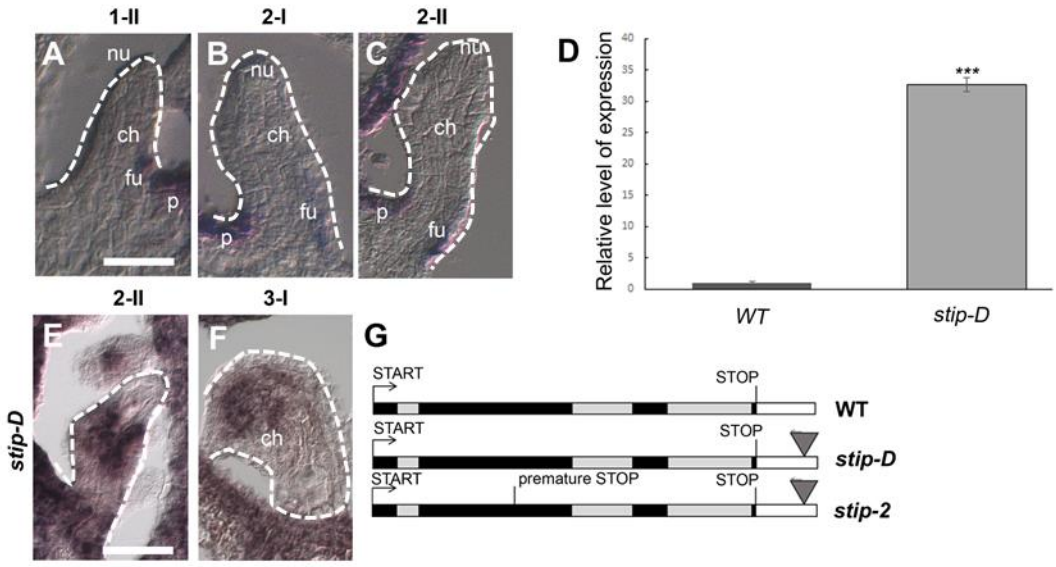

Fig. S1. (A-C) *In situ* hybridization on ovule tissue sections of *pSTIP:STIP-GFP*, using a *GFP* antisense probe. (D) Expression analysis of *STIP* by qRT-PCR in wild-type and *stip-D* inflorescences. Expression of *STIP* was normalized to that of *UBIQUITIN10* and the expression level in wild-type was set to 1. Asterisks indicate P<0.0001 in Student's t-test. (E-F) *In situ* hybridization on ovule tissue sections of *stip-D*, using a *STIP* antisense probe. (G) Schematic diagram of the *STIP* locus in wild-type, *stip-D*, and *stip-2.* As reported by Wu et al., (2005; 2007) *stip- 2* mutation has the same genetic background of *stip-D* (it harbors a T-DNA in the 3'UTR), but it presents a mis-match in the coding region, generating a premature stop codon, leading to a knock-out mutation. Black boxes, exons; grey boxes, introns; white box, 3'untranslated region; T-DNA insertion is represented with a grey triangle. Abbreviations: ch, chalaza; nu, nucellus; p, placenta; fu, funiculus. Scale bar, 20 µm.

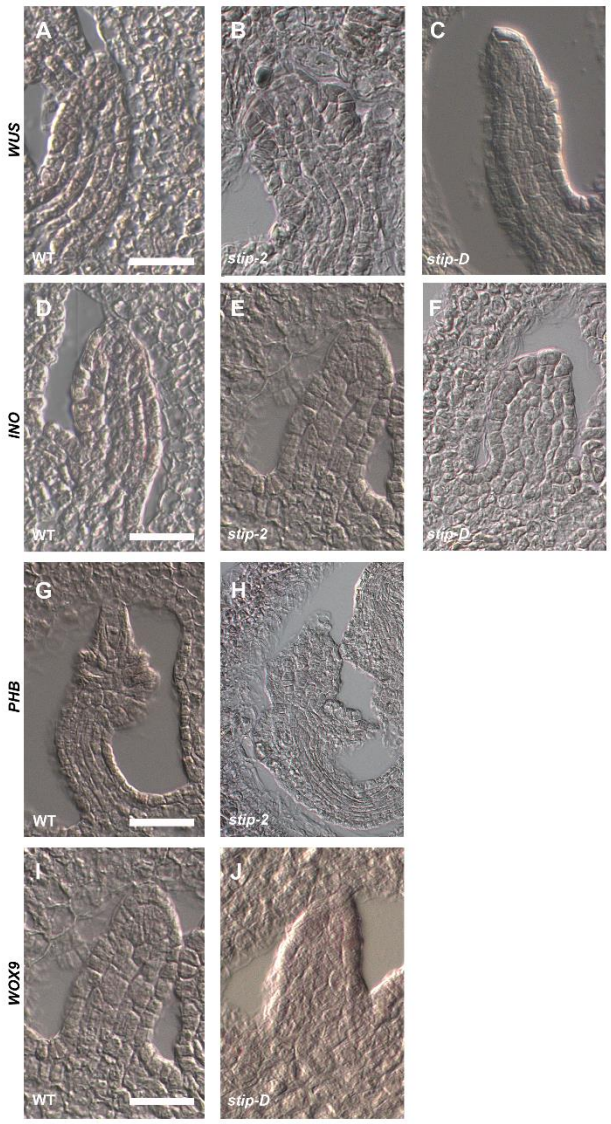

Fig. S2. (A-J) Sense probe controls for the all the *in situ* hybridization assays performed: *WUS* (A-C), *INO* (D-F), *PHB* (G-H) and *WOX9* (I,J). Scale bars, 20 µm.

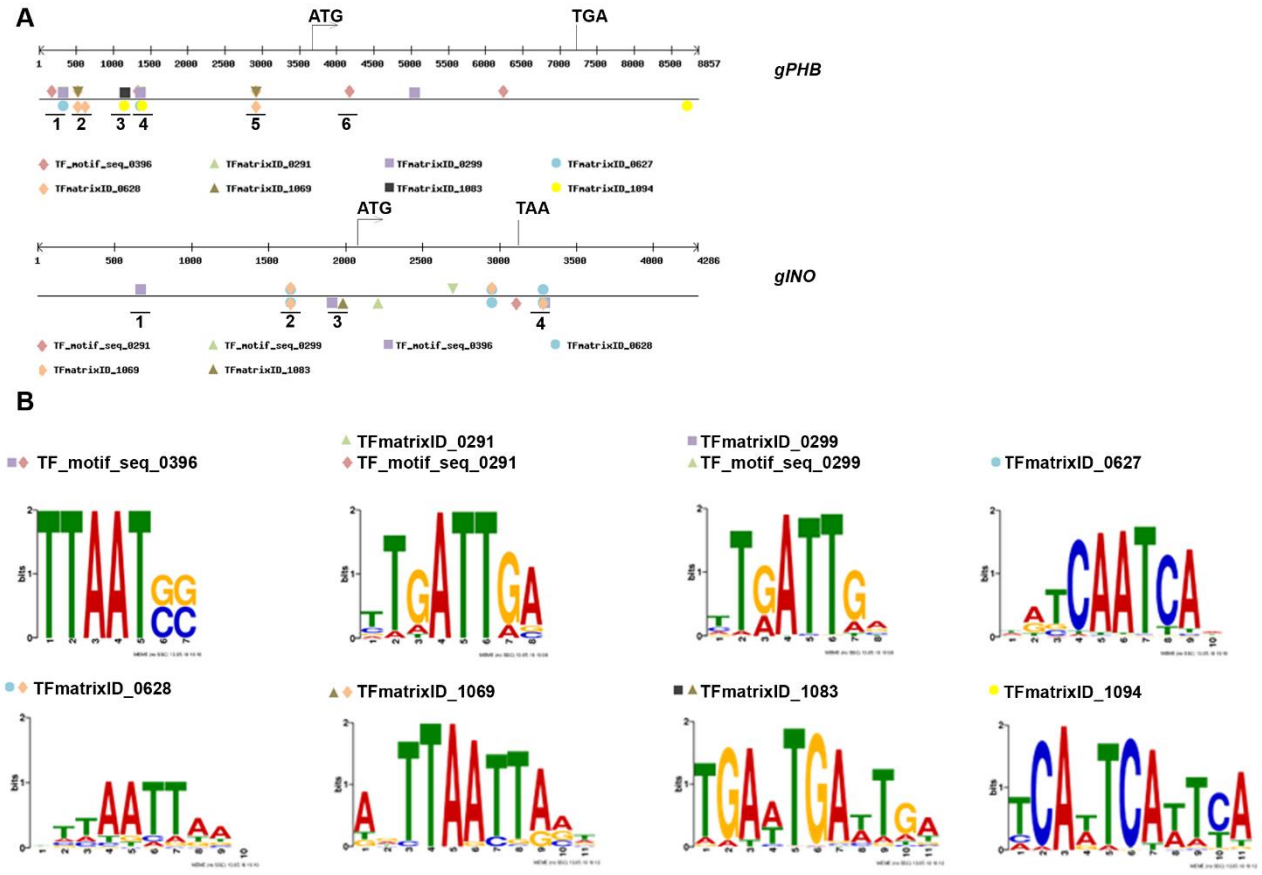

Fig. S3. (A) Schematic representation of WOX homeodomain binding site in *PHB* and *INO* loci. The regions tested in STIP-GFP ChIP-PCR assays are marked with black lines and numbered. (B) Consensus logo of binding sequences of WOX homeodomain transcription factors detected on *PHB* and *INO* loci. Analysis was performed using PlantPan 3.0 ((http://plantpan.itps.ncku.edu.tw).

Table S1. List of primers used in this study.

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