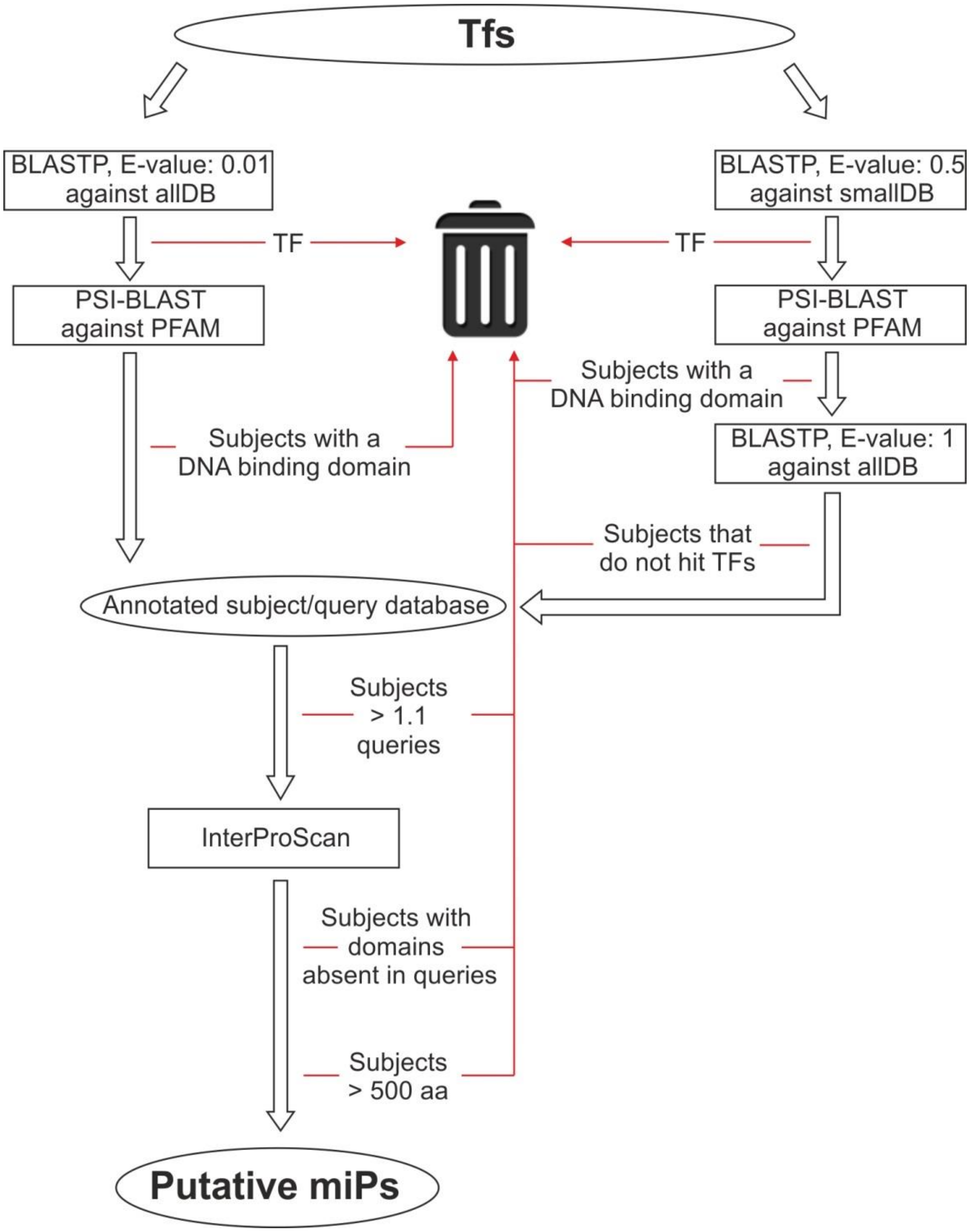
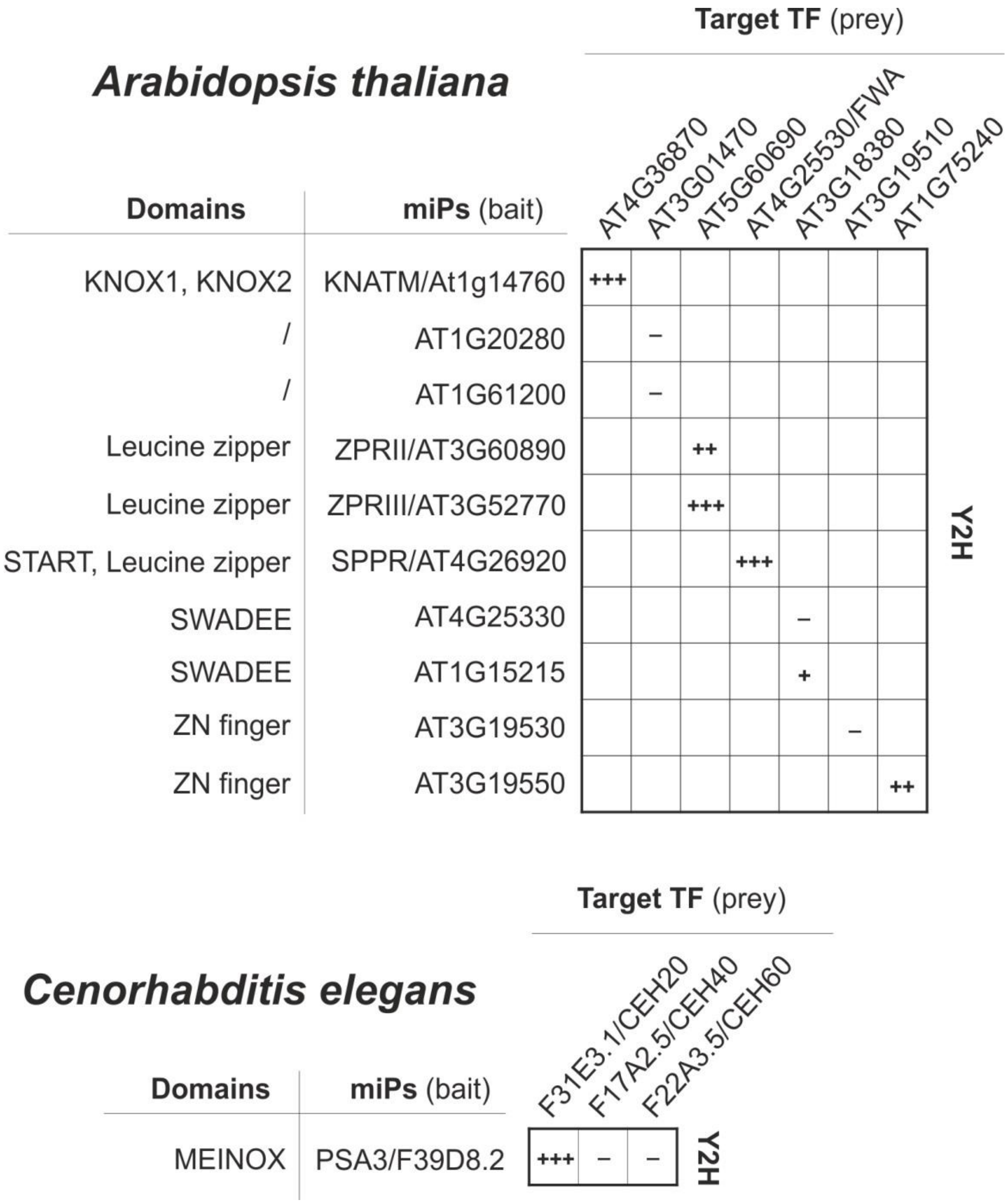
Supplemental figures:



Supplemental Figure 1. Flow chart of the algorithm used to predict miPs. Ovals, rectangles, and red lines represent protein databases, software processes, and filters. allDB, database comprising all proteins in a genome. smallDB, database comprising proteins shorter than 200 amino acids in a genome.



Arabidopsis thaliana

Target TF (prey) — Y2H

Domains	miPs (bait)	AT4G36870	AT3G01470	AT5G60690	AT4G25530/FWA	AT3G18380	AT3G19510	AT1G75240
KNOX1, KNOX2	KNATM/At1g14760	+++						
/	AT1G20280		–					
/	AT1G61200		–					
Leucine zipper	ZPRII/AT3G60890			++				
Leucine zipper	ZPRIII/AT3G52770			+++				
START, Leucine zipper	SPPR/AT4G26920				+++			
SWADEE	AT4G25330					–		
SWADEE	AT1G15215					+		
ZN finger	AT3G19530						–	
ZN finger	AT3G19550							++

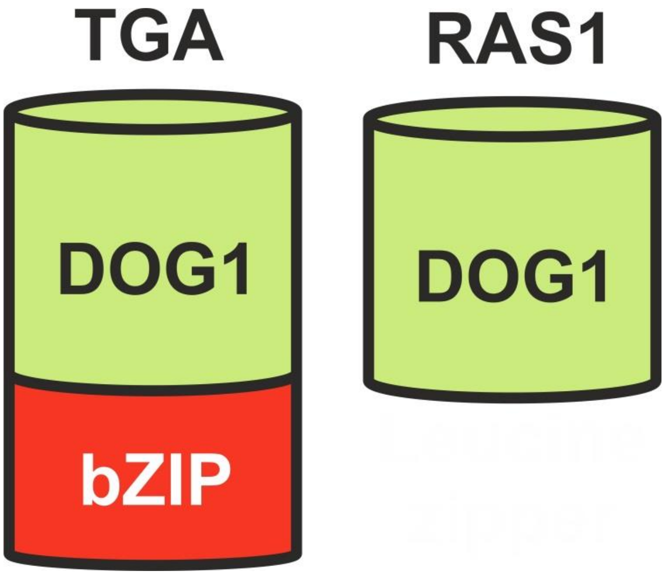
Cenorhabditis elegans

Target TF (prey) — Y2H

Domains	miPs (bait)	F31E3.1/CEH20	F17A2.5/CEH40	F22A3.5/CEH60
MEINOX	PSA3/F39D8.2	+++	–	–

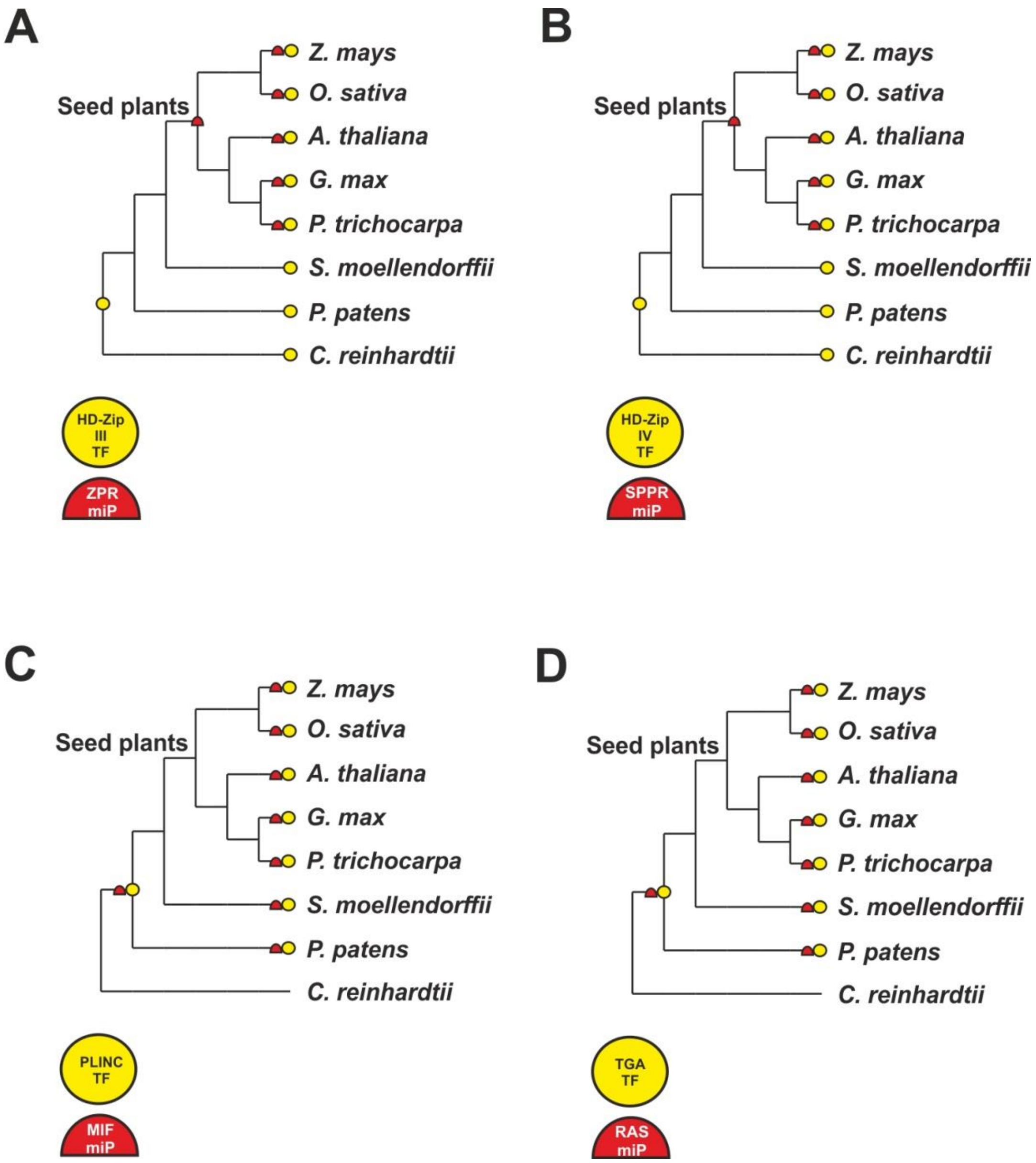
Supplemental Figure 2. Protein-protein interactions between putative miPs and their predicted target HD TFs from A. thaliana and C. elegans.

Interactions between miPs (bait) and target TFs (prey) were assessed by yeast two-hybrid (Y2H) using the lacZ reporter gene. Strong (+++), medium (++), mild (+), and no interactions (-) indicate strength of interaction. The predicted miP domains are listed on the left of each miP.



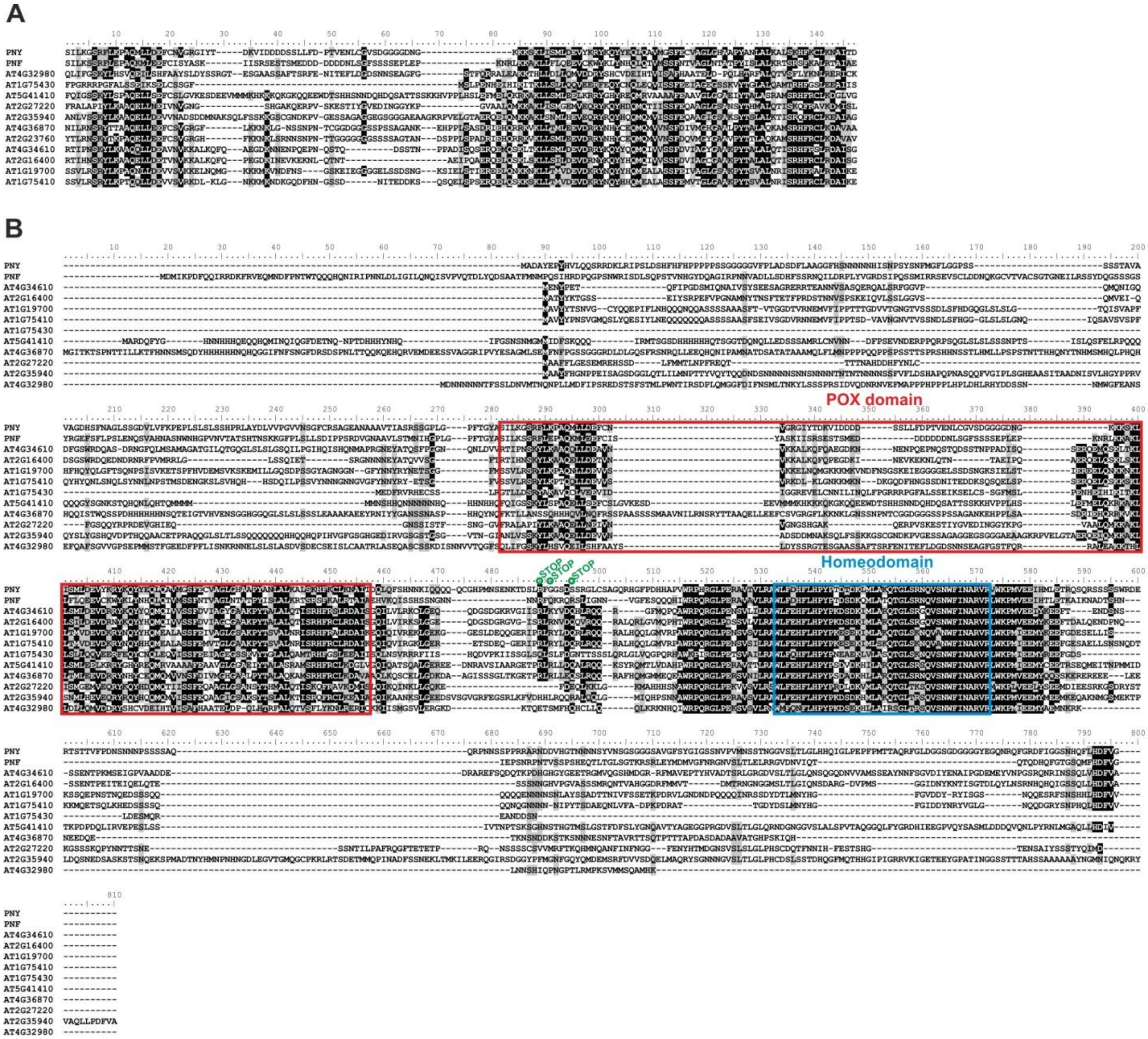
Supplemental Figure 3. Scheme of TGA and RAS1.

DOG1, DELAYED IN GERMINATION 1 domain; bZIP, basic domain leucine zipper.



Supplemental Figure 4. Phylogenetic analyses of miPs in plants.

Phylogenetic distribution of miPs (red semi-circles) and their TF targets (yellow circles). (A) ZPR and HD-Zip III. (B) SPPR and HD-ZipIV. (C) MIF and PLINC HD-Zinc finger. (D) RAS and TGA.



Supplemental Figure 5. KNATM selectivity for BELL paralog TFs.
(A) Multiple sequence alignment of the POX domain of all A. thaliana BELL TFs. (B) Multiple sequence alignment of all A. thaliana BELL TFs in full-length. The POX PPID and the HD DBD are highlighted in red and blue rectangles, respectively. Premature stop codons obtained from the reverse Y2H experiment, which enabled PNF to interact with KNATM, are highlighted in green rectangles.