**Fig S6. Predicted targeting of a fern AGO1 mRNA by miR168.**

**(A)** Sequence of a transcript (Isotig\_21625) encoding AGO1 protein from the fern *L. japonicum*. The region predicted to be targeted by pmi-miR168 is indicated in yellow. The starting ATG and stop codon are highlighted in blue. **(B)** Alignment of part of the AGO1 transcripts from fern *L. japonicum* (Lja), the gymnosperm *Cunninghamia lanceolata* (Cla), the dicot *A. thaliana*, and the monocots *O. sativa* (Osa) and *Brachypodium distachyon* (Bdi). Residues displaying 100% identity are highlighted in blue. The region targeted by miR168 is indicated in red, and the Argonaute N-terminal domain domain (ArgoN) in green. Note that the miRNA-targeted region is conserved in all mRNAs and species. **(C)** Predicted pairing between pmi-miR168 and *L. japonicum* Isotig21625. The E-complementarity score between miRNA and target RNA as estimated by the psRNATarget program is shown.

**(A)**

>Isotig21625 (AGO1)

CGTGGTTAGCAGCAGCACGTCCTCTCGGCGCACAGCGTCCTTGTTCCGCTTCCTCAGGTGTTCCTTCAACTAAGAGAGCCTTTTCAGTATGCCGAGAAGACGCAAGACCCCAAAGGAAATCGAGGAGAGTTCTCAAGAAGCAACAGCTCAGTCTTCTCAAGGTGGAGCATCTTCTTCAAGTACTCCAGCTCAGGGCCGTgGGCAGCAGCCACCTGCACGCAGTCAGCAGGTTTCACAGCCCTCCGCAGGTAGAGGTCAGCAACCATCTGTACCAACTCCTGCAGGTAGAGGTCAGCTACCACCTGTACAAACTCCTGCAGGTAGAGGTCAGCAGGTGATACAACCTACTCCTGGTAGAGGTCAACAGGTTTCTCATGGTGCAAGTGGAACACAAAGTGTGCCCCCTGGTCAGGTTCCTGTGCAGGTGTTGCAACCTCCTTCAGGTAGAGGTCAGCAGGTCTCTCAGGTCACGGGACCACATAGTTTGCCTGCTGTCCAAGGTCCTCCGCAAGGAAGAGATGGACGAGGTAGAAGTCAAGGACGAGGAAGAGGTGGAGGCCCACCACATCCGAcCCCTCaAATGACTGTTGGTCAGCCTTACGTGCCGACCAACATAATACCTATTCCCGATCTGCCCCAAGCTCACACTACTCCAACTCCATACGGTCTGGAGCAGGCTGCCCACGCTCAATACATGCAGGCTGGCTATGGAGGGATGGCTCCTATTCCAACTATGCAACCACACCTTGTTGCTGTCCCTCAGCCAGCACCTTACCCTGGTATTCCACGTATGGGACAACCATCTCAGCCTCAAGCCAGTTACATGGGCACTTCACCAATCGGTCAGCCAGGCTTTGTTCAGGTTGGTATGTCAGCaTcAAGTTCAACTGTGGACTTGTCACAGCAAATGCAAAGAGTGgGAATACAAGGTCCTCCTCCAGCTATTCAGGAGCCTGGGCCATCAACTGCTCTAGCAGTTGCTCCGCCTGCATCCAGCAAGAAGTTGCGGTTCCCtGCaCGTCCTGGGATGGGAAGAGTAGGGATGCGCTGcACtGTGAAAGCTAACCACTTCTTTGCAGCAcTACCGGACAAAGATTTGCACCAATATGATGTTTCAATaACTCCCGAGGTAACCTCTCGGGGTGTCAACAGGGCTGTAATGCAGCAGCTTGTGCAGCACTATAGAATGAGTGCTCTGGGcTGCAGGCTACCAGCTTATGATGGACGCAAGAGCCTCTACACGGCaggTCCTCTTCCCTTTCAAAACAGGGAGTTTTCAATCACACTaGTGGATGATGATGATGGAAGTGGAGGGCCAAGACGAGAAAGACAGTTTAAAGTGGTAATCAAGTTTGCtGCTCGAGCTGATTTGCATCACCTGGGAGAGTTtCTTCAAGGCAGACAACTAGATGCACCTCAAGAGGCATTGCAGGTCTTAGATATTGTCTTGCGGGAGCTGCCAACACACAGGTTCTGTCCTGTTGGTAGATCATTCTACTCtCCTAATCTTGGTAGACGGCAACAACTTGGGGAAGGATTAGAGAGCTGGCGTGGATTTTATCAGAGCATTAGACCCACTCAGATGGGGCTATCTCTCAACATTGACATGTCTTCAACAGCGTTTATTGAGCCATTGCCGGTCATCGAGTTTGTTGCACAGTTGTTGGGAAAAGATGTTTCTAGGCATTTgTCGGATGCTGATAGAATAAAGATAAAAAAAGCCCTGCGAGGAGTCAAGGTAGAGGTCACTCATCGAGGGACAATGCGGAGAAAGTATCGGATATCTGGATTGACCTCaCAGCCAACCCAGGAaTTGACCTTTCCGGTcGAtGAACAAGGGACAATGAAGTCTGTGGTAGAGTATTTTCAAGAAACATATGGATACACTATCCGTAACACCACGCTTCCATGTCTTCAAGTGGGAAACCAACAGAGGCCAAATTACCTGCCAATGGAGGTGTGCAAGATTGTTGAAGGGCAGAGATACTCTAAGCGATTGAATGAGAAACAAATCACGGCACTGCTGAAGGTCACTTGcCAGcGACCTGTGGACAGAGAAAGAGACATTTTAGAGACAGTACATCATAACTCTTATGCtGAAGATCCTTATGCGAATGAGTTTGGTATACGTATCAGTGAGCAACTTGCTTCAGTTGAAGCCCGTGTATTGCCGGCCCCTAAGCTCAAGTACCATGATACggggaaaTTAAAGTATTGCCAGCCAGAGATTGGACAGTGGAACATGAGAGATAAGAAAATGGTGAATGGTGGAGTAGTCACaTATTGGGCATGTATCAATTTCTCCCGAAGtGTGCAaGATACTGCAGCTCATAGATTCTGTCACGAGCTGGCTtCAATGTGCCAAGTTTCtGGgATGTCTTTCAATGAACGCCCTGCAATTCCAATACACTCAGCACGACCTGATCAAGTTGAGCGAGCATTGAAAAATGTGTTTCGAGAATTTCAACAGAAAGAgAAAGGGCATGATCTTGAGCTTCTcGTTGCTATTTTACCTGATAATAATGGAACCCTCTACGGGGATCTCAAGAGAATATGTGAGACAGATCTtGGCCTGGTCTCTCAATGTTGTTTAACTAAGCACGTGTATAAGATGAGTAAGCAaTACCTGGCgAAtGTCGCGCTgAAAATCAATGTCAAGGTgGGTGGAAGGAATACtGTACTGGTGGATGCTCTCTCTCGCCAAATACCACTTGTCAGTGAcATCCCTACTATTATCTTTGGAGCTGATGTTACTCATCCCCATCCAGGAGAAGATTCTAGTCCGTCTATTGCTGCtGTGGTGGCCTCACAAGATTGGCCGGAAGTTACTAAATATGCAGGGCTGGTGTGTGCTCAAGAGCATCGTCAAGAATTGATACAAGATTTGTTCAAGAGTTGGGATGATCCTGCCCGTGGCCCACAAACGGGTGGcATGATAAAGGAGCTTCTgATATCTTTcCGACGAGCaACGGGTCAAAAGCCTCATCGAATTATCTTTTACAGGGATGGTGTTAGTGAGGGTCAGTTTTATCAAGTACTATTGTATGAGCTgGATGCAATTCGCAAGGCATGTGCTTCTCTGGAATCAAACTACCAACCTCCTGTCACATTTGTAGTGGTTCAGAAGCGCCACCATACACGaCTTTTTGCAAGCAATCATAATGATAGGCGAAGCATAGACAGCAGTGGAAACATTCTTCCAGGCACGGTGGTTGATTCAAAGATATGCCATCCTACAGAATTTGACTTCTATCTTTGCAGCCATGCTGGCATCCAGGGAACTAGCCGACCAGCTCATTACCATGTGTTGTGGGATGAAAACAAGTTCACAGCAGATGGGTTGCAGCTACTtACCAACAATCTTTGCTACACATATGCgCGCTGTACACGTTCTGTCTCAATTGTGCCCCCAGCATATTATGCgCACCTGGCAGCTTTTCGTGCACGGTTTTACATGGAACCTGAGTCgGATAGTGGTTCCCTTACTAGTGCAGCCCCACCACCCAGTAGGGGCACAGGTTCTGGTGCTTCGCGAGCTACtCGTGTGCCAGCTGGGGCTTCTGTCCGGCCTTTGCCAGCTGTGAAAGaAAATGTGAAGCGAGTGATGTTTTACTGCTAGGATCTTGGATTTGTAGCAGCTaACCTAAACTTGTACATGTGTAAAATGaGTTGTCTTTGAGTAAGGATGCCAGTAGTTATTGTCAAAGaAAACTAATGTGAACTCaGACTATGTGGTTTTGGCATTTTTTGTTGCCAGCTGTGTTATAGCCAATTTTGGGCTATTTGTATTGTAACATGTATATTCC

**(B)**



**(C)**

 **(E)**

**pmi-miR168v1** 21 AAGGGCUGGACGUGGUUCGCU 1

 :::::::.:::: :::::: 4.0

**Lja-Isotig21625** 624 UUCCCGAUCUGCCCCAAGCUC 644