**Supplementary Material**

**Appendices.**

**Appendix I.** SPARE reads mapped to Arabidopsis *MIARNs* for wild-type, and *fiery1* plants.

**Appendix II.** SPARE reads mapped to Arabidopsis *MIRNAs* for *hyl1*, and *se* plants.

**Supplementary Figures**

**Supplementary Figure 1.** Original image of miR157 small RNA gel blot.

**Supplementary Figure 2.** Schematic illustrating the processing intermediates detected by the SPARE method.

**Supplementary Figure 3.** Alternative RNA folding structures of *MIR157c*.

**Supplementary Figure 4.** IsomiRs detected in wild-type plants due to variation in the first cleavage site.

**Supplementary Figure 5.** Processing intermediates of tandem *MIR169i-n* family members.

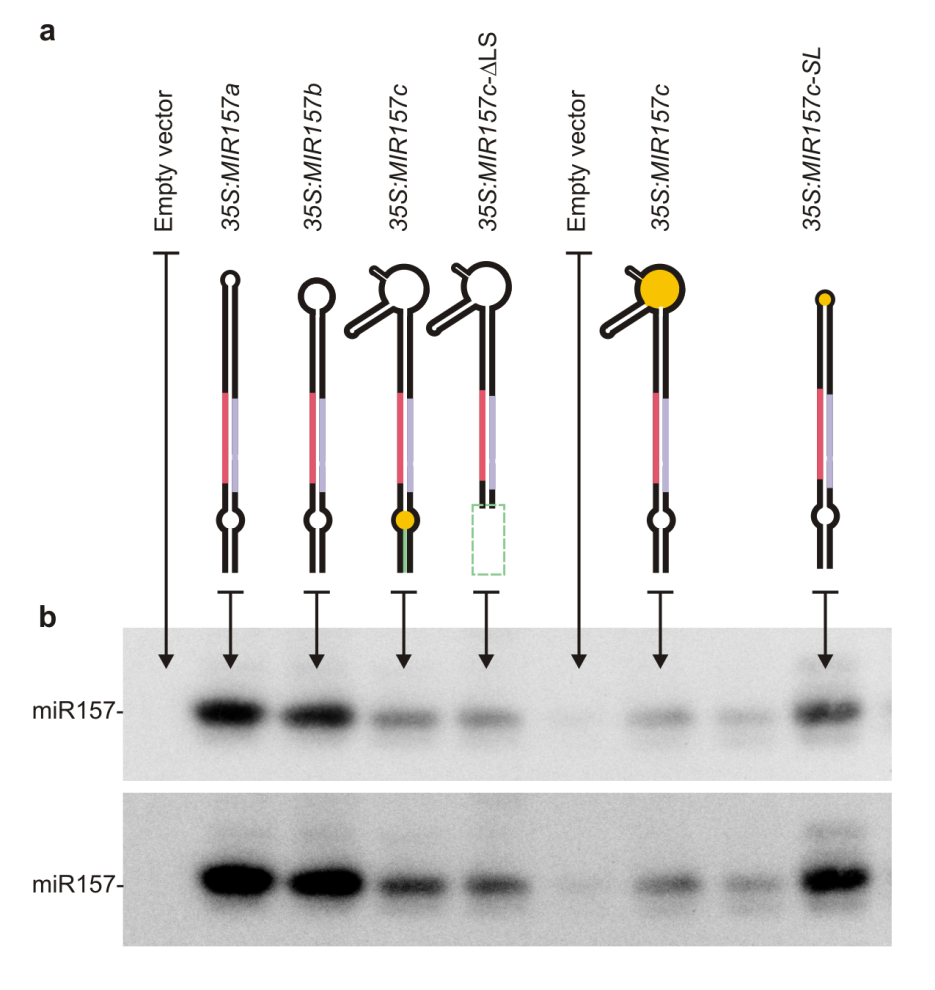
**Supplementary Tables.**

**Supplementary Table 1.** SPARE primers and mix for cDNA synthesis.

**Supplementary Table 2.** Expressed sequences from binary vectors.

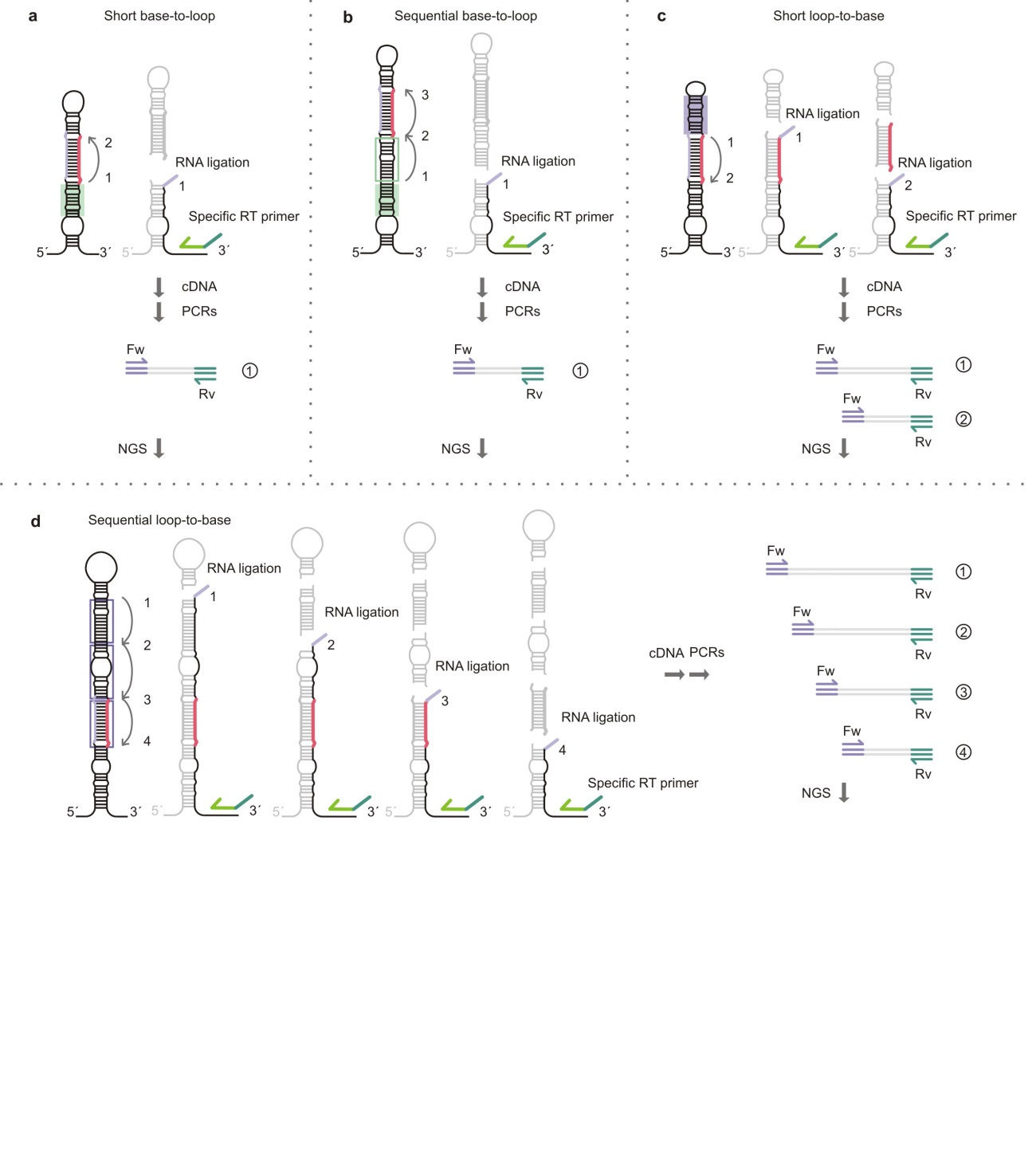
**Supplementary Table 3.** Normalized SPARE reads for wild-type and *fiery1* libraries.

**Supplementary Table 4.** Small RNA sequences used to calculate miRNA accuracy.



**Supplementary Figure 1. Original image of miR157 small RNA gel blot.**

(**a**) Schematic representation of wild-type and mutant versions of *MIR157a*, *MIR157b*, *MIR157c*, *MIR157c*-LS and *MIR157c*-SL. (**b**) Small RNA gel blots of transgenic lines expressing different precursors from the *35S* promoter.



**Supplementary Figure 2.** **Scheme illustrating the processing intermediates detected by the SPARE method.**

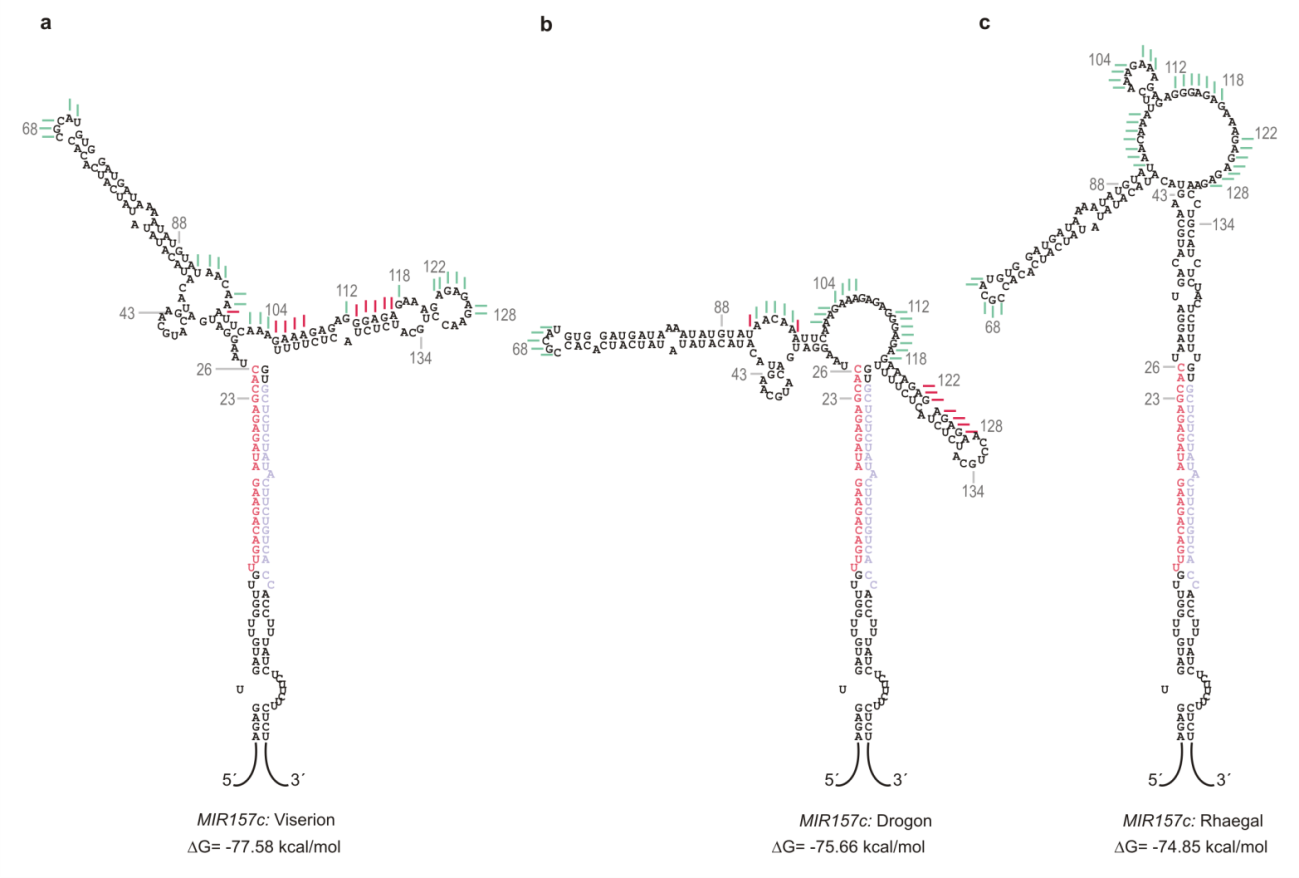
(**a**) Base-to-loop. After the proximal cut, the free 5´end is ligated with an RNA oligo (purple line) and retro-transcribed using specific primers (light and dark green). The PCR reactions render one fragment.

(**b**) Sequential base-to-loop. After the proximal cut, the free 5´end is ligated with an RNA oligo (purple line) and retro-transcribed using specific primers (light and dark green). The PCR reactions render one fragment.

(**c**) Loop-to-base. Both free 5´end are ligated with an RNA oligo (purple line) and retro-transcribed using specific primers (light and dark green). The PCR reactions render two distinct fragments, one for each cut.

(**d**) Sequential loop-to-base. After each cut, the free 5´end is ligated with an RNA oligo (purple line) and retro-transcribed using specific primers (light and dark green). The PCR reactions therefore render several distinct fragments

See Supplementary Table 4 for detail description of the specific primers used for each *MIARN*.



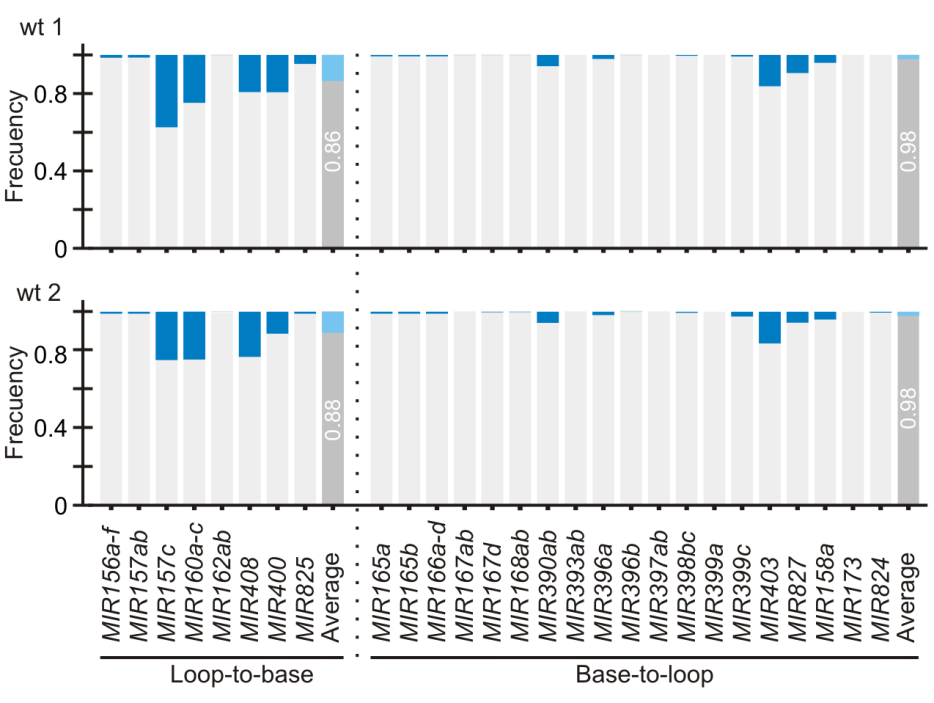
**Supplementary Figure 3. Alternative RNA folding structures of *MIR157c*.**

(**a**) Alternative secondary structure of *MIR157c* provided by the M fold program; G= -77.58 kcal/mol; named Viserion.

(**b**) Alternative secondary structure of *MIR157c* provided by the M fold program; G= -75.66 kcal/mol; named Drogon.

(**c**) Alternative secondary structure of *MIR157c* provided by the M fold program; G= -74.85 kcal/mol; named Rhaegal.

The miRNA is indicated in red and the miRNA\* in light purple. The grey lines and numbers show the corresponding bases to polyacrylamide gels presented in Figure 3. The green lines indicate the coincidence between experimentally determined and predicted secondary structure, while the red lines show an inconsistency, using nuclease S1. Note that only the Rhaegal structure has a coincidence between the computational prediction and the experimental data.



**Supplementary Figure 4. IsomiRs detected in wild-type plants due to variation in the first cleavage site.**

The most frequent miRNA sequence is indicated in gray, while additional variations due to changes in the first cut are indicated in blue.

Imagen que contiene objeto

Descripción generada con confianza alta

**Supplementary Figure 5. Processing intermediates of tandem *MIR169* family members.**

(**a**) Schematic representation of *MIR169n* and *MIR169m*, *MIR169l* and *MIR169k*, and *MIR169j* and *MIR169i*. The red line represents the miRNAs.

(**b**) Predicted secondary structure of *MIR169n*, *MIR169m*, *MIR169l*, *MIR169k*, *MIR169j* and *MIR169i*. The miRNA is indicated in red and the miRNA\* in light purple. Horizontal green lines indicate cleavage sites detected in wild-type plants while grey lines indicate processing intermediaries detected in *fiery1*. Part of the sequences are indicated with black line (see Data Set 1 for the complete sequence). Note the additional cuts in *MIR169k* and *MIR169i* that do not correspond withe processing of a productive miRNA.