

Supplementary Materials: Over-Expression of GmGla-Regulated Soybean *miR172a* Confers Early Flowering in Transgenic *Arabidopsis thaliana*

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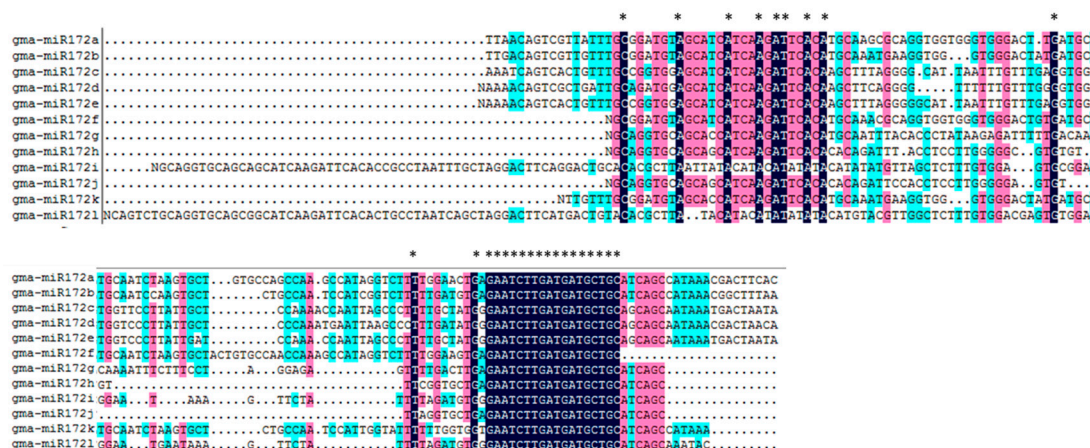


Figure S1. Pre-miRNA sequence alignment of *miR172* family members in soybean. Blue, homology 100%; pink, homology $\geq 75\%$; light blue, homology $\geq 50\%$. * represent conserved nucleotides in all pre-miRNAs.

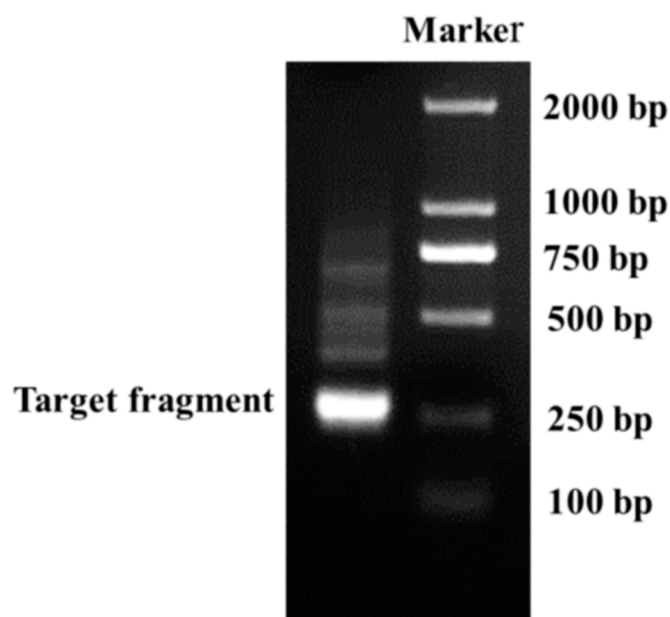


Figure S2. 5'RACE nested PCR product (*Glyma03g33470*), spanning between the primer and cleavage sites, was used for cloning into a vector for DNA sequencing. Lane Marker represents 2000 bp DNA marker.

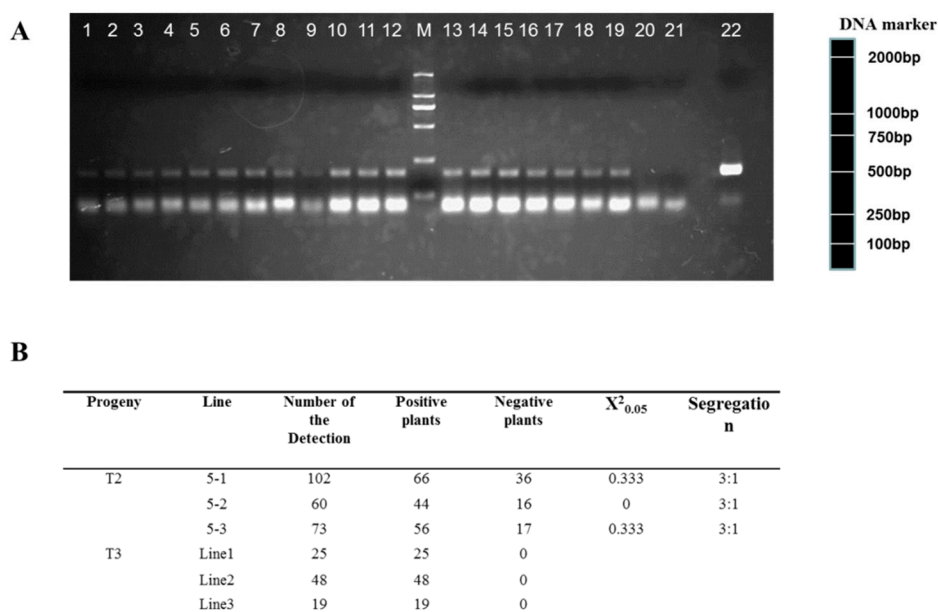


Figure S3. Identification of transgenic Arabidopsis by PCR amplification. (A) Identification of T3 transgenic Arabidopsis by PCR amplification. Lane M: DNA marker; lane 20: Water control; lane 21: Negative control; lane 22: Positive control plasmid; lane 1–19: Transgenic plants. The PCR target fragment is 159 bp; (B) Segregation of the *gma-miR172c* in the progeny of self fertilized transgenic Arabidopsis and chi-square test X^2 analysis.

Table S1. Potential AP2-Like target genes of *gma-miR172a* from PMRD (Available at: <http://bioinformatics.cau.edu.cn/PMRD/>).

Target Gene	Target Description
<i>Glyma17g18640</i>	Q9AXI4 APETAL2-like protein Blast E-value: 5E-165
<i>Glyma11g05720</i>	Q9AXI4 APETAL2-like protein Blast E-value: 4E-138
<i>Glyma02g09600</i>	B9HLZ7 AP2 domain-containing transcription factor Blast E-value: 1E-61
<i>Glyma01g39520</i>	A7PLE5 Transcription factor APETALA2 (Chromosome chr7 scaffold_20, whole genome shotgun sequence) Blast E-value: 5E-152
<i>Glyma19g36200</i>	B9SGS1 Floral homeotic protein APETALA2, putative (EC 1.3.1.74) Blast E-value: 2E-131
<i>Glyma15g04930</i>	B9SW78 Protein AINTEGUMENTA, putative (EC 1.3.1.74) Blast E-value: 8E-133
<i>Glyma03g33470</i>	B9SGS1 Floral homeotic protein APETALA2, putative (EC 1.3.1.74) Blast E-value: 4E-129
<i>Glyma05g18170</i>	Q9AXI4 APETAL2-like protein Blast E-value: 6E-131