

**Supplementary Data S1.** The information of candidate EuGRFs identified in *E. ulmoides* through BLAST and HMM search.

**Supplementary Data S2.** The information of 38 candidate eul-miR396s identified in *E. ulmoides*.

**Supplementary Data S3.** The information of linked pairs of between *EuGRFs* with *GRFs* in *A. thaliana* and *E. ulmoides*.

**Supplementary Data S4.** The information of cis-elements on promoter regions of 8 *EuGRFs*.

**Supplementary Data S5.** Query Sequences of miRNA396s used for Local BLAST search.

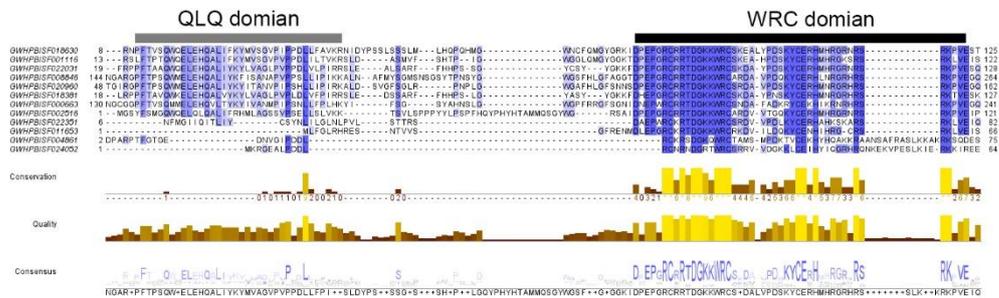
**Supplementary Data S6.** The list of primer sequences used in this paper.

**Supplementary Data S7.** The GRFs IDs and plant species used in the Maximum Likelihood tree.

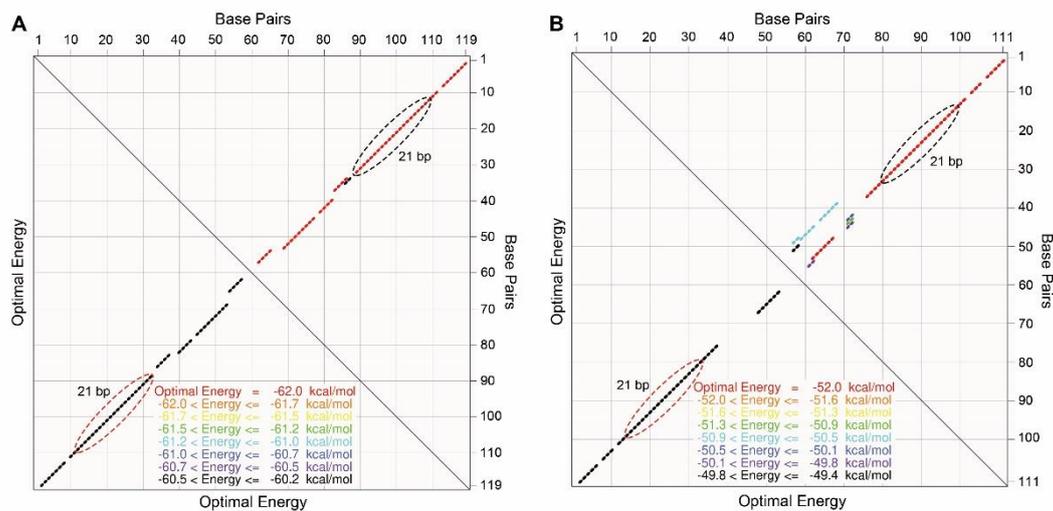
**Supplementary Data S8.** The amino acids sequences of EuGRFs identified in our unpublished genome.

**Supplementary Data S9.** The log file of the Maximum Likelihood tree constructed in this paper.

**Supplementary Data S10.** The collinearity file within the *E. ulmoides* genome.

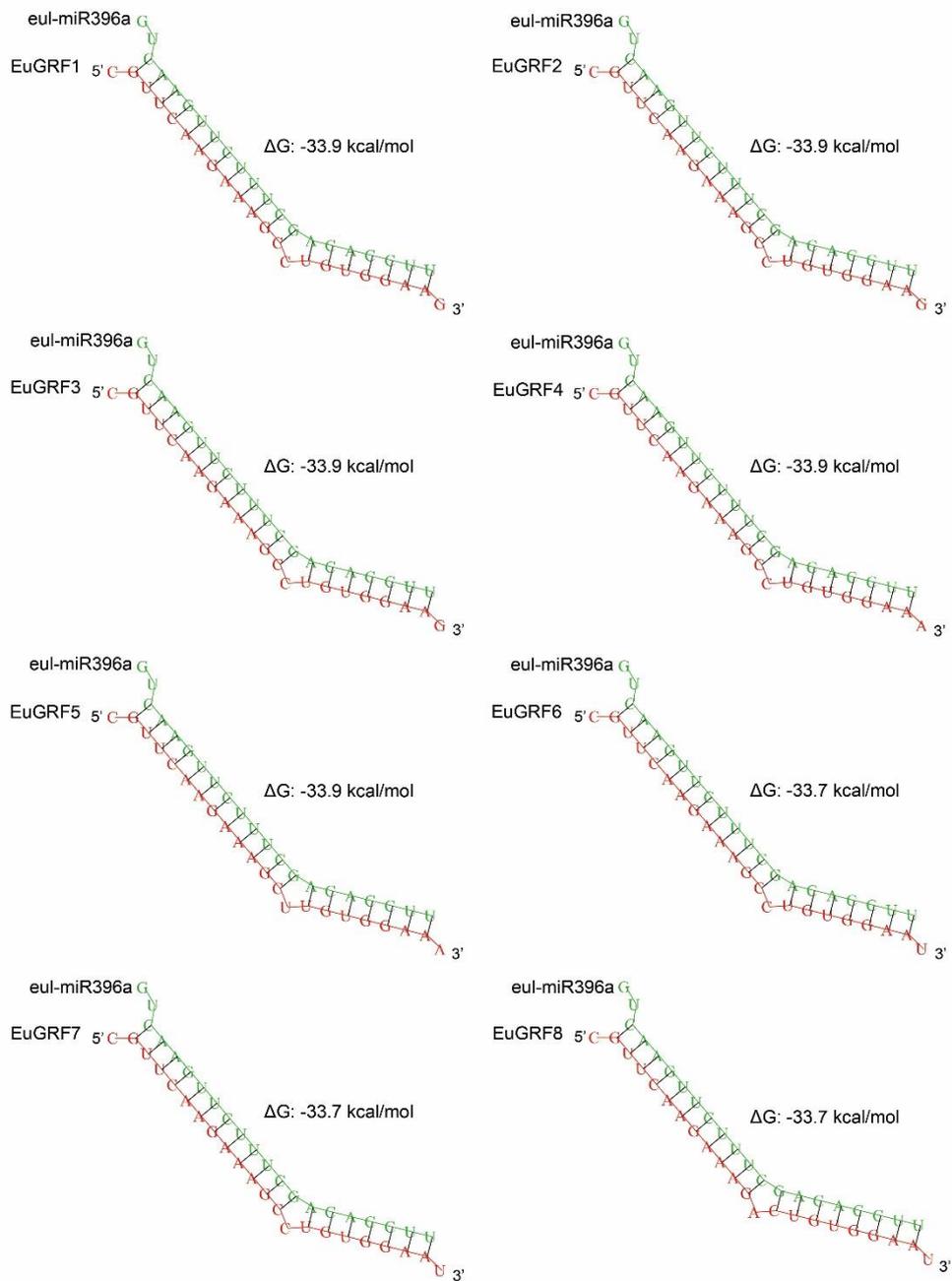


**Figure S1.** The amino acids sequence alignment of 12 GRF candidate proteins using MAFFT with default settings.

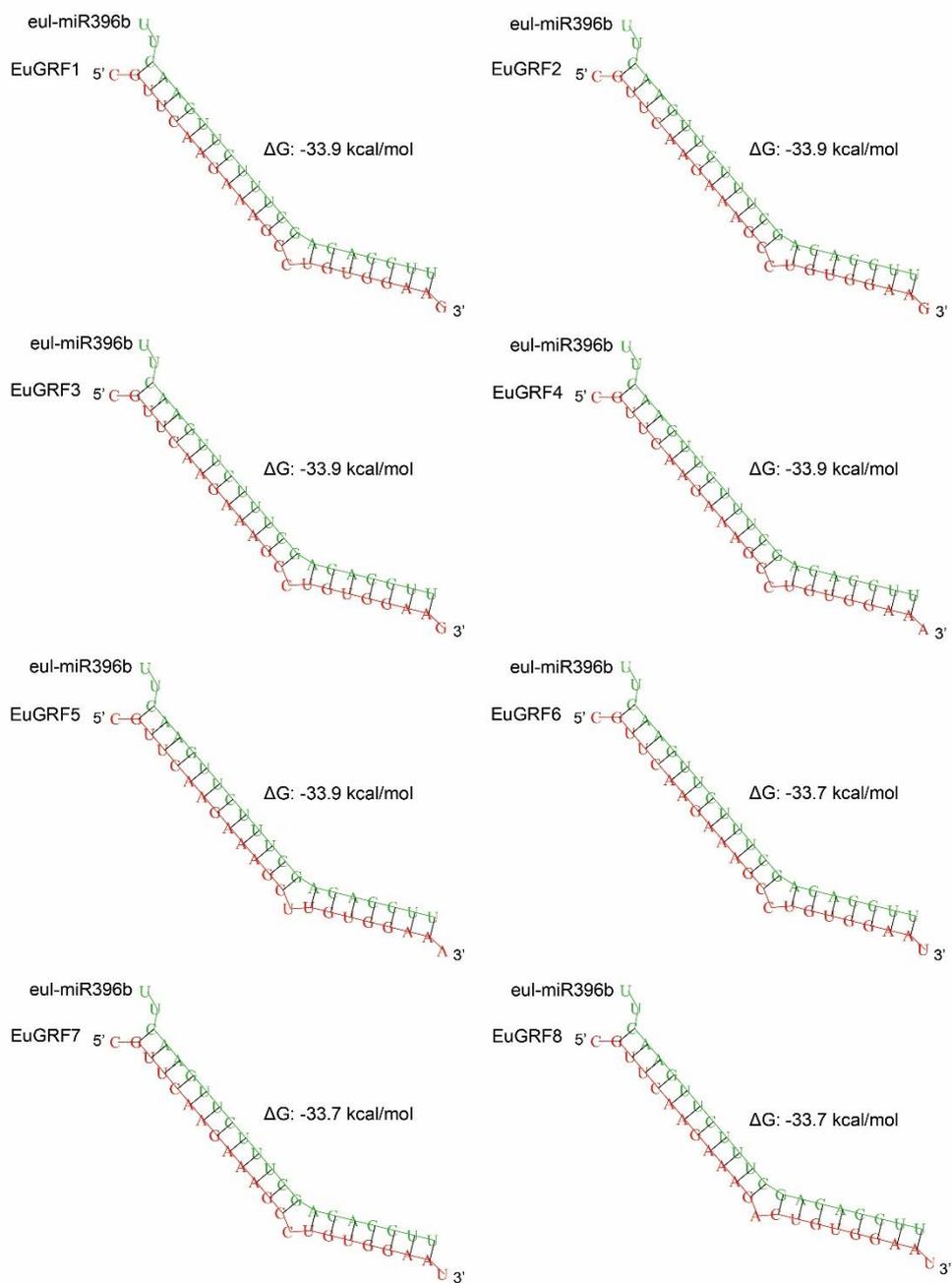


**Figure S2.** The energy dot plot for the hairpin structure formed by pre-miR396a (A) and pre-miR396b (B). The computed folding of pre-miR396a contains 51 base pairs out of 53 (96.2%) in the energy dot plot. The computed folding of pre-miR396b contain 50 base pairs out of 61 (82.0%) in the energy dot plot. The dashed lines represent the nucleotide bases of mature

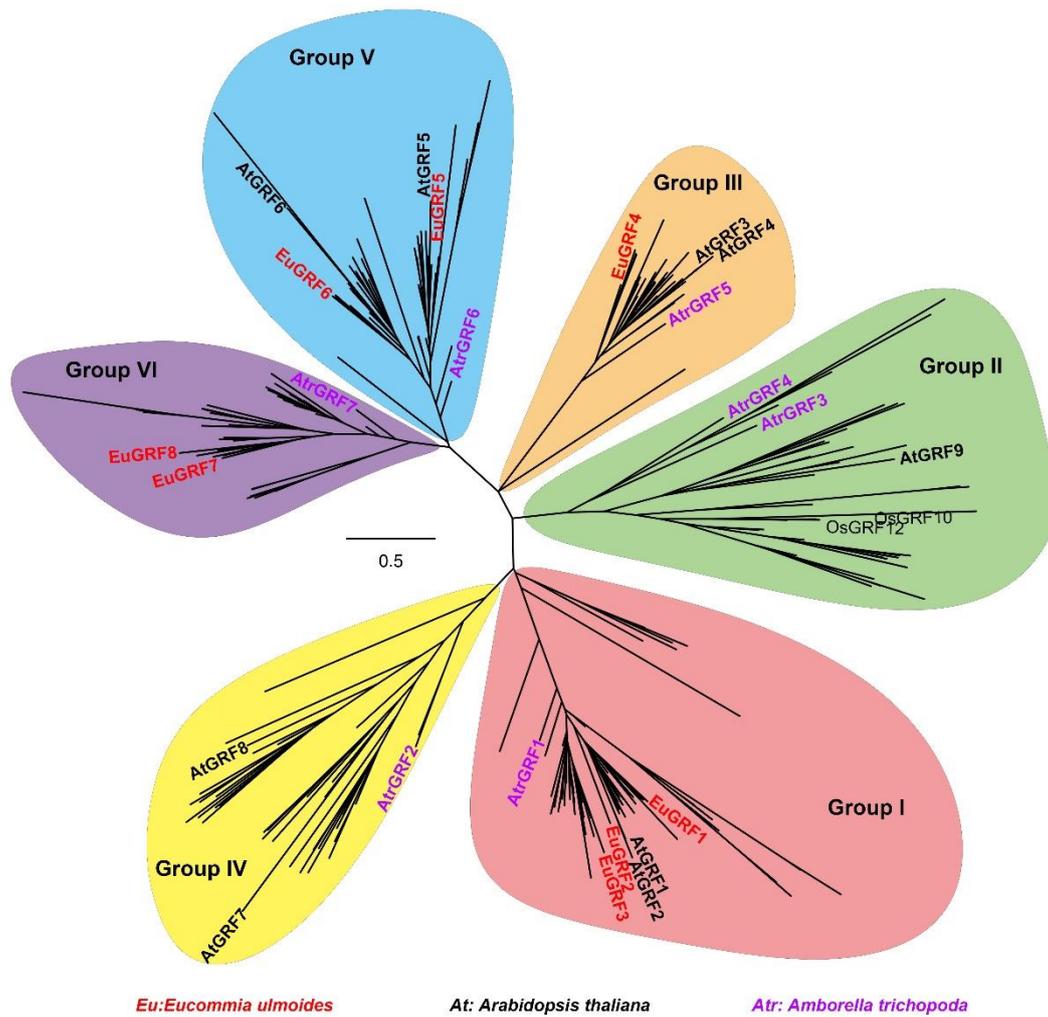
eul-miR396s.



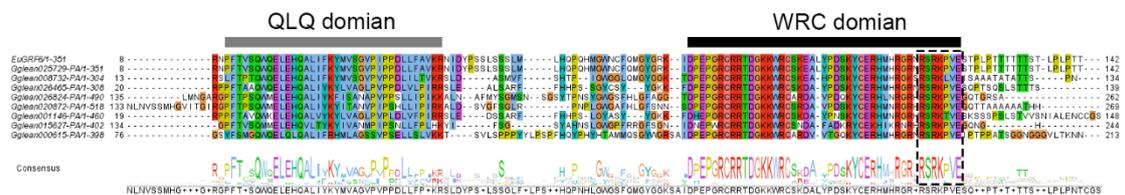
**Figure S3.** The degree of complementarity between eul-miR396a and all EuGRFs. The free energies of duplex structures were displayed on the right.



**Figure S4.** The degree of complementarity between eul-miR396b and all EuGRFs. The free energies of duplex structures were displayed on the right.



**Figure S5.** The Maximum Likelihood tree constructed using protein sequences of 290 GRFs derived from 27 terrestrial species. The scale bar indicates the branch length.



**Figure S6.** The amino acids sequence alignment of EuGRFs identified in our unpublished genome. The sequence alignment was performed using MAFFT with default settings. The conserved "RSRK-VE" motif is depicted within the dashed enclosure.