



Fig. 1 Bioinformatic analysis of taе-miR399 and TaUBC24. (A) Base conservation analysis of miR399. (B) Sequence alignment analysis of miR399. (C) RNA secondary structure analysis of pre-taе-miR399, the straight line represented the mature sequence. (D) Cis-acting element analysis of upstream promoter sequence of taе-miR399 and its targets *TaUBC24*. The mature miR399 sequences were of monocots (*A. tauschii*, *B. distachyon*, *O. sativa*, *H. vulgare*, *S. bicolor*, *P. vulgaris*, *T. aestivum* and *Z. mays*) and eudicots (*A. thaliana*, *G. max*, *G. raimondii*, *N. tabacum*, *M. truncatula*, *P. trichocarpa*, *S. tuberosum*, *G. hirsutum*, *M. domestica*, *C. melo*, *M. esculenta*, *C. cardunculus*, *L. usitatissimum*, *P. persica*, *S. lycopersicum*, *F. vesca*, *P. abies*, *C. sativa*, *A. officinalis*, *B. napus*, *V. vinifera*, *A. caerulea*, *R. communis*, *A. lyrata*, *V. unguiculata*, *T. cacao* and *V. vinifera*) were obtained from the miRbase database.