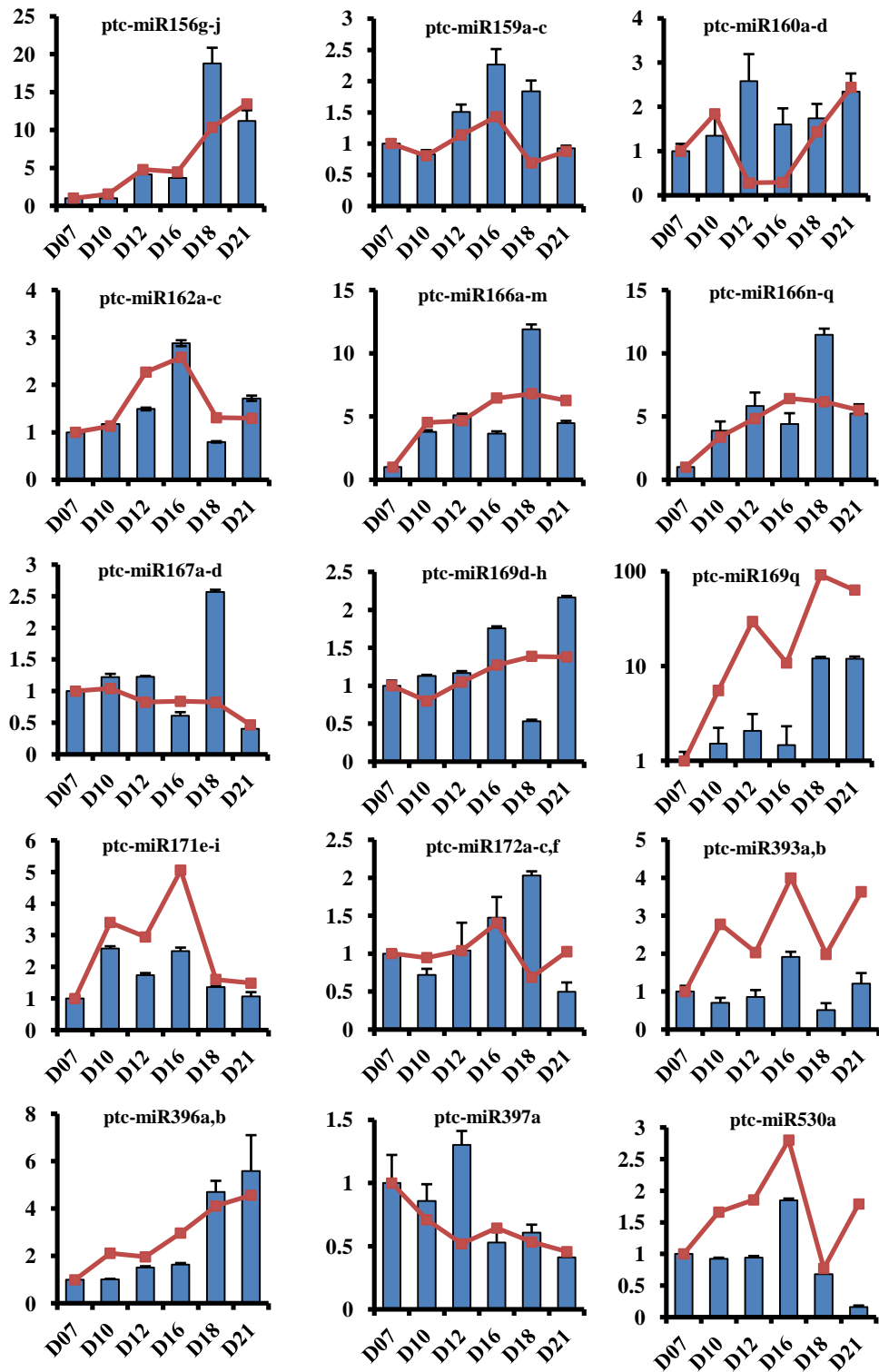


**Figure S1. Cross sections of SVS regenerated tissues upon debarking.** (A) the phloem, cambium zone and majority part of immature xylem were peeled off with the bark. (B) A few layers of immature xylem remained on the surface of the girdled trunk. (C) The callus covered the whole surface of the girdled trunk on the 7 DAG and discontinuous meristem cells were observed. (D) Continuous, flat meristem cells arranged irregularly between the callus and immature xylem on the 10 DAG. (E) The flat meristem cell layers had increased in size on the 12 DAG. (F) The flat meristem cell layers formed continuous and regular layers that are similar to a vascular cambium on the 16 DAG. (G) The newly cambium-like zone began to differentiate on the 18 DAG. (H) A large number of phloem cells outside the cambium and xylem cells inside the cambium were observed on the 21 DAG. The yellow arrows indicate the meristem cells and cambial region.



**Figure S2. The expression profiles of known miRNAs during SVS regeneration based on sequencing and qRT-PCR analyses.** The line chart represents the relative expression fold changes of known miRNAs from solexa sequencing reads and the histogram indicates the relative expression fold changes of known miRNAs analyzed by real-time quantity PCR. Transcript levels on the 7 DAG are set to 1. The X-axis shows the regeneration stages on the 7, 10, 12, 16, 18 and 21 DAG. The Y-axis shows the relative expression fold changes of known miRNAs.

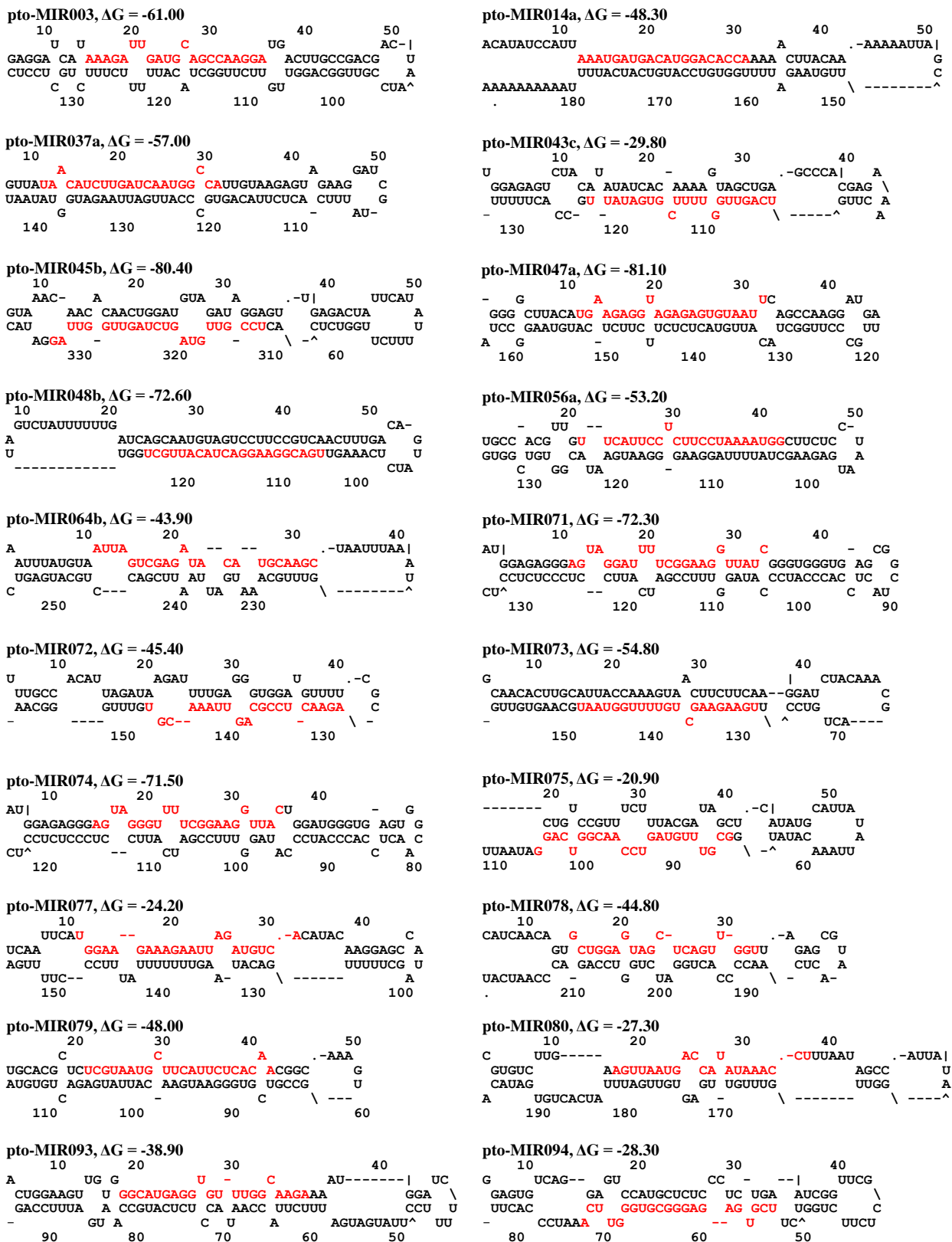
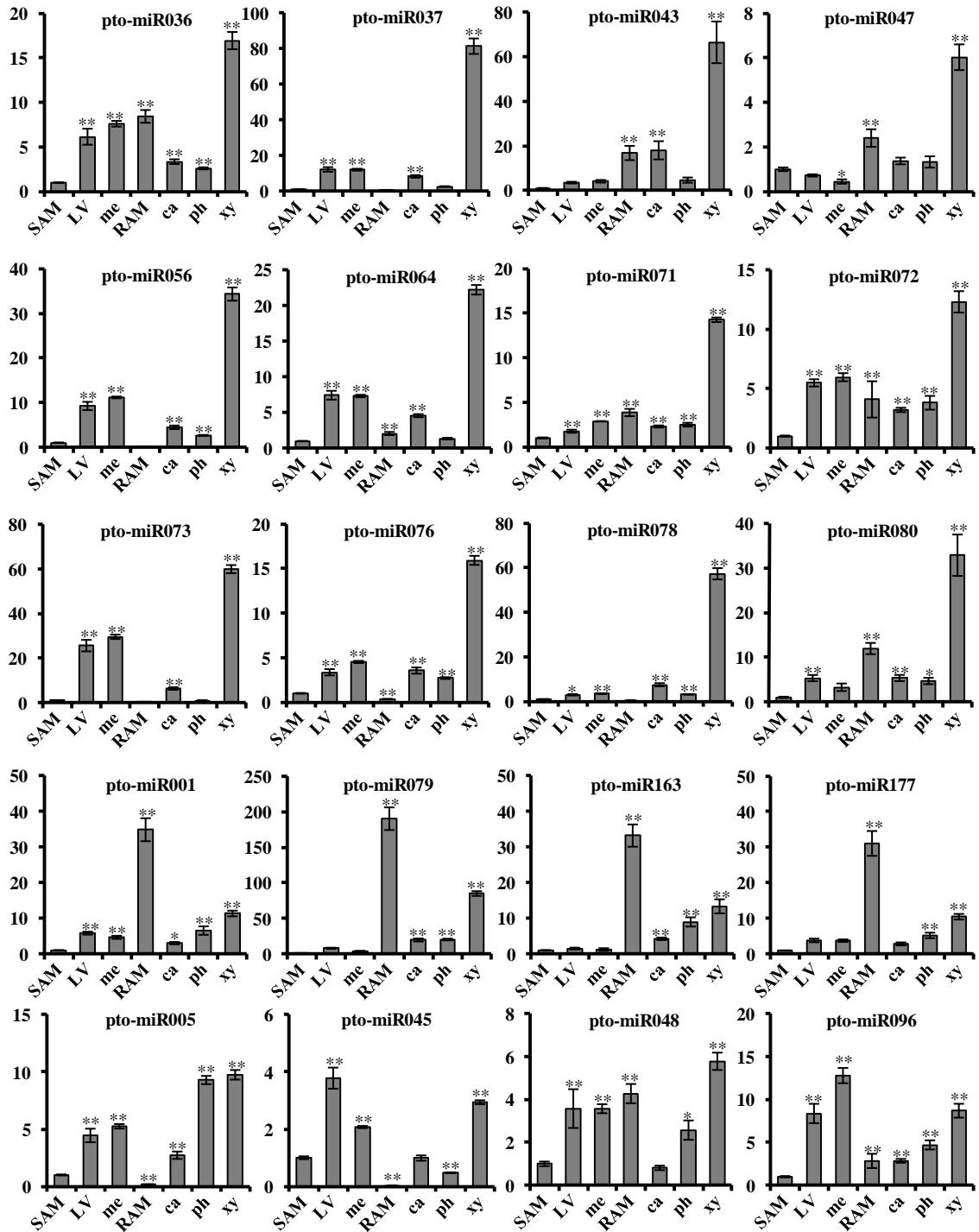
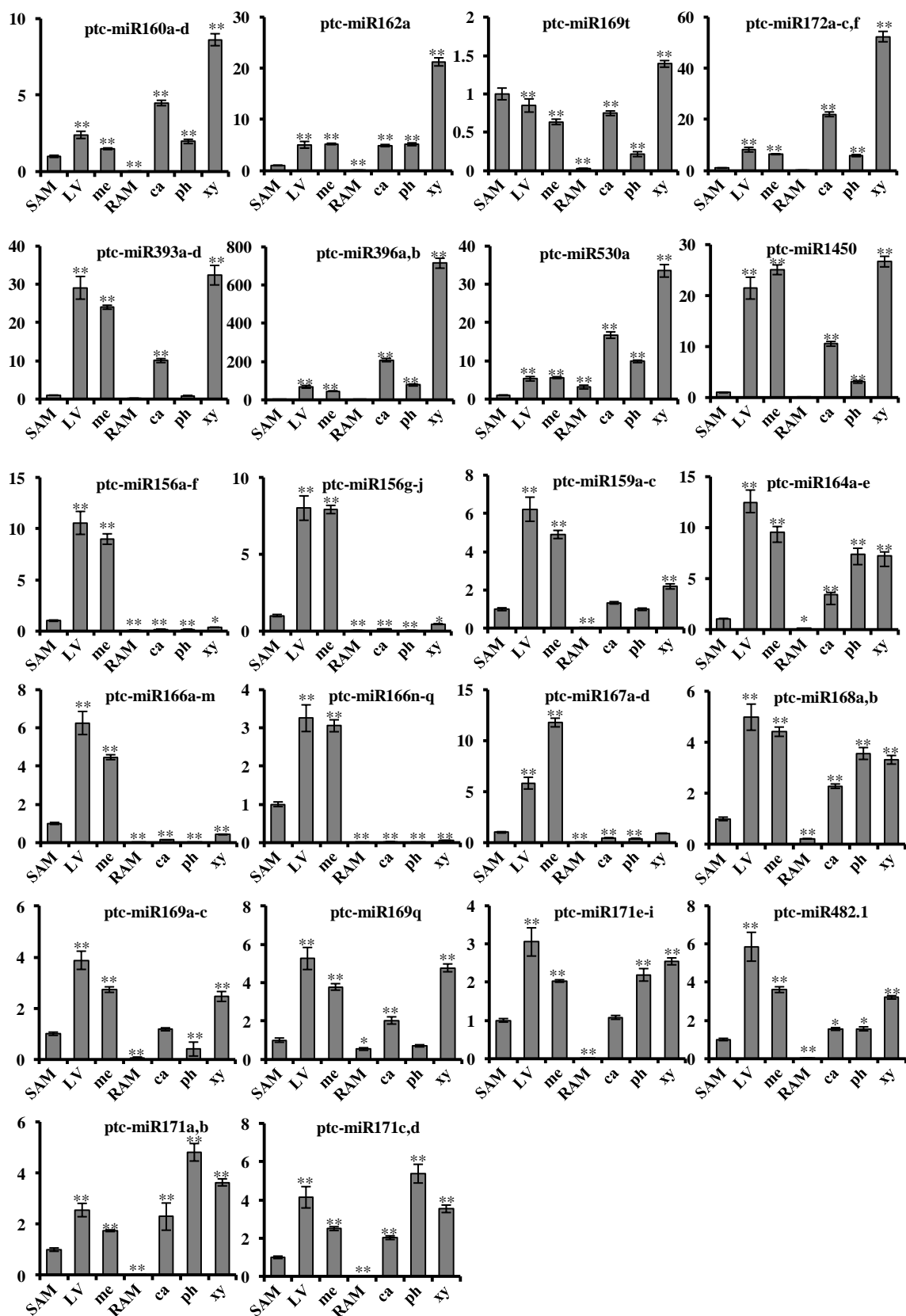


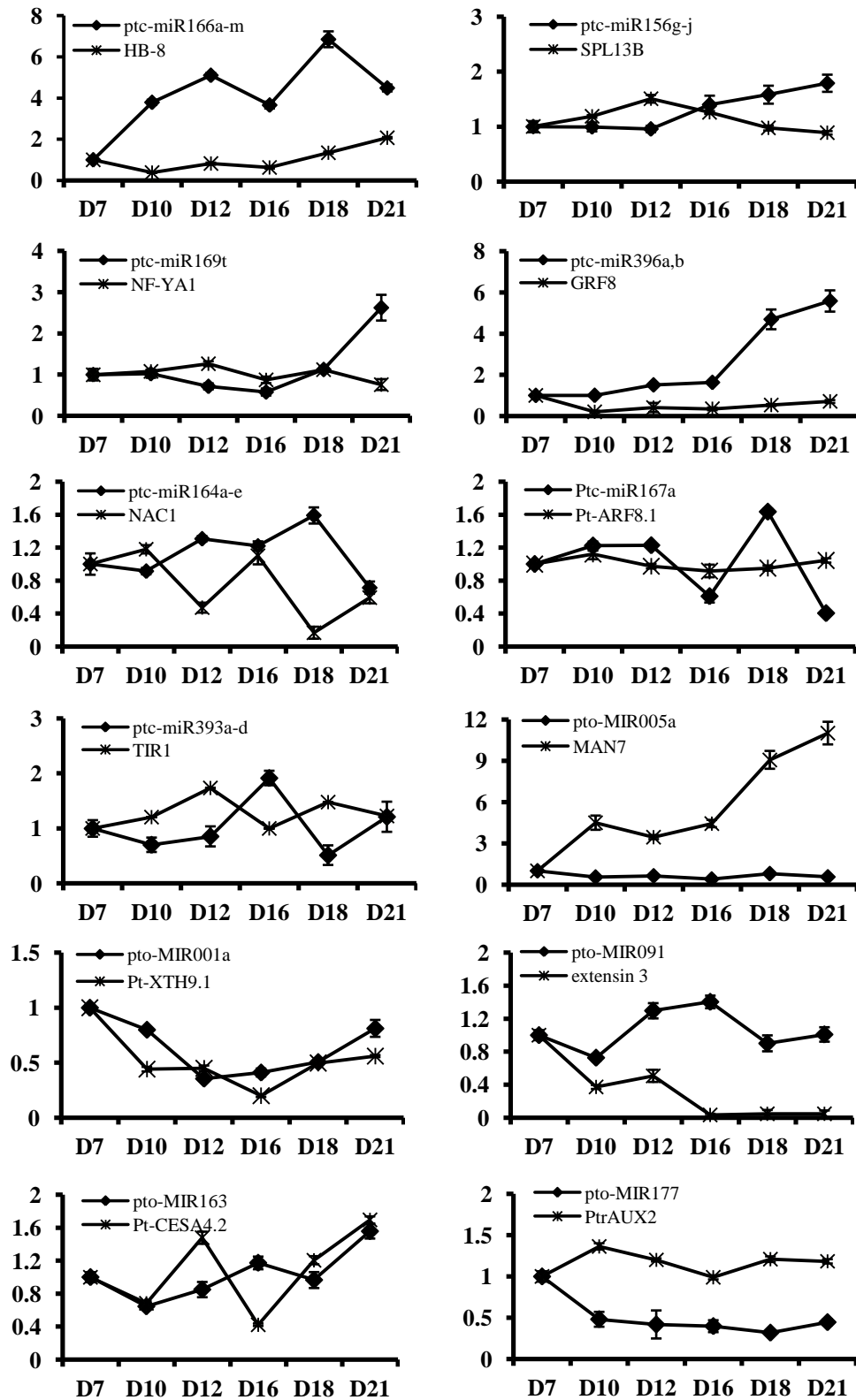
Figure S3. Predicted stem-loop structures of novel pre-miRNAs based on their cloned miRNA sequences.



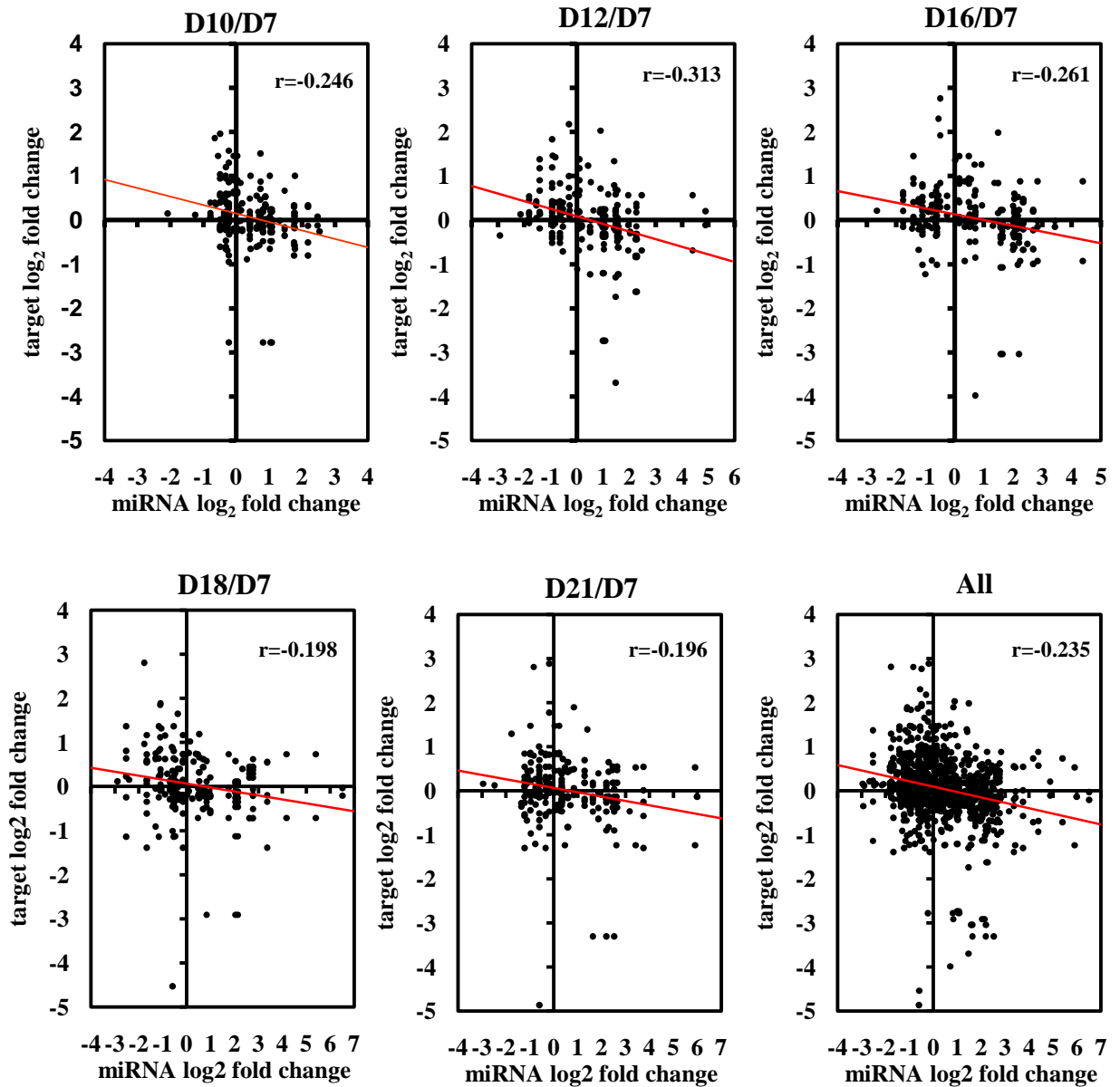
**Figure S4. The expression of novel miRNAs in different tissues of *P. tomentosa* by universal qPCR.** SAM, shoot apical meristem; LV, leaf vein; me, mesophyll; RAM, root apical meristem; ca, cambium; ph, phloem; xy, xylem. \*\*  $P$ -value $\leq 0.01$ ; \*  $0.01 < P$ -value $\leq 0.05$ .



**Figure S5.** The expression of known miRNAs in different tissues of *P. tomentosa* by universal qPCR. SAM, shoot apical meristem; LV, leaf vein; me, mesophyll; RAM, root apical meristem; ca, cambium; ph, phloem; xy, xylem. \*\*  $P$ -value $\leq 0.01$ ; \*  $0.01 < P$ -value $\leq 0.05$ .



**Figure S7. The expression profiles of miRNAs and their target genes during SVS regeneration as validated by universal qRT-PCR.**



**Figure S8. Pearson Correlation Coefficient between the expression of miRNAs and their target genes during SVS regeneration.**