

Supplementary Data

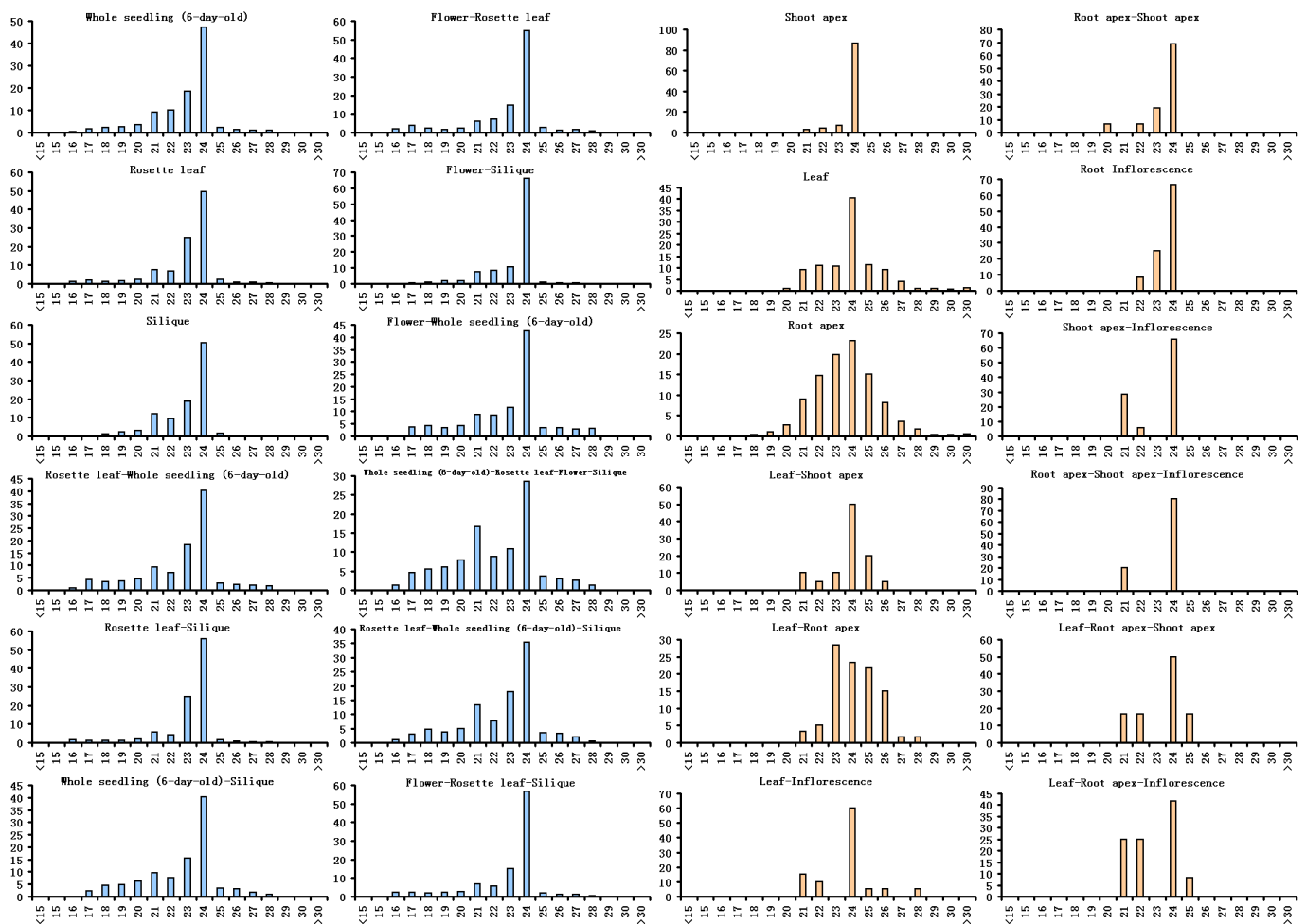
Characterization of expression patterns of small RNAs among various organs in *Arabidopsis* and rice based on 454 platform-generated high-throughput sequencing dataChaogang Shao¹, Xiaoxia Ma², Ming Chen^{3*}, Yijun Meng^{2*}

Fig. S1. Sequence length distribution of small RNAs (sRNAs) in *Arabidopsis* (the left twelve panels indicated by blue bars) and rice (the right twelve panels indicated by yellow bars). For multi-organ-expressed sRNAs, the panels “Rosette leaf—Silique” and “Leaf—Root apex—Shoot apex” for example, represent the sRNAs expressed in both rosette leaves and siliques in *Arabidopsis*, and the ones expressed in rice leaves, root and shoot apices, respectively. For all the panels, the sequence lengths (nt, nucleotide) are indicated by x axes, and the percentage of sRNAs in specific length in specific organ(s) is measured by y axes.

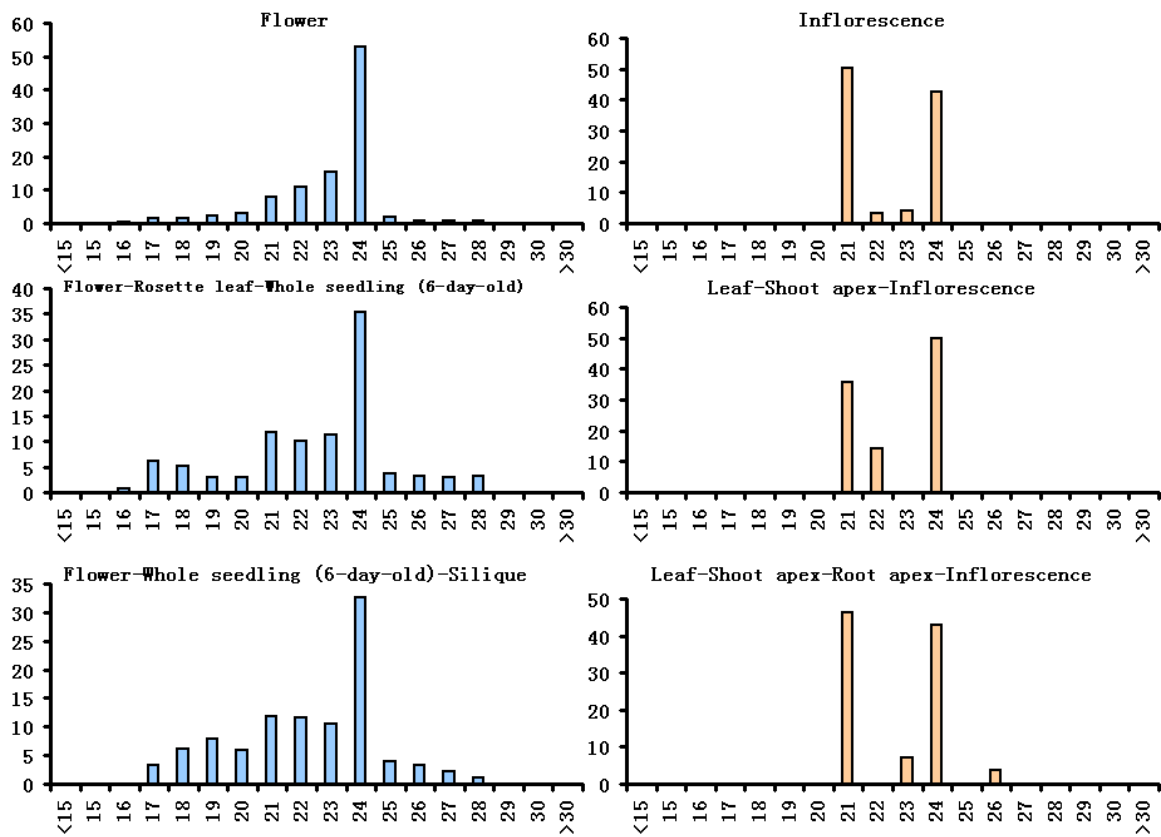


Fig. S2. Sequence length distribution of small RNAs (sRNAs) in Arabidopsis (the left three panels indicated by blue bars) and rice (the right three panels indicated by yellow bars). For multi-organ-expressed sRNAs, the panel “Leaf—Shoot apex—Inflorescence” for example, represents the sRNAs expressed in leaves, shoot apices, and inflorescences in rice. For all the panels, the sequence lengths (nt, nucleotide) are indicated by x axes, and the percentage of sRNAs in specific length in specific organ(s) is measured by y axes. Note that, for rice, the 21-nucleotide (nt) sRNAs occupy a dominant portion in all the three example provided here.

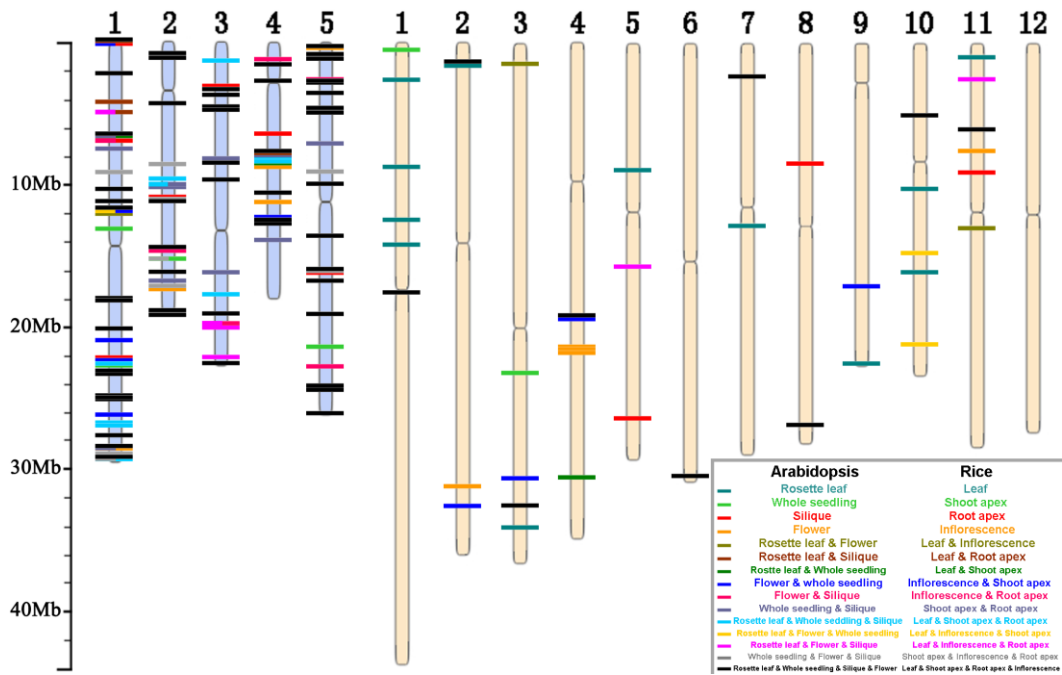


Fig. S3. Chromosome-wide distribution patterns of microRNAs (miRNAs) expressed in Arabidopsis (left five chromosomes in light blue color indicated by the numbers 1 to 5) and in rice (right twelve chromosomes in light yellow color indicated by the numbers 1 to 12) based on 454 sequencing data. The horizontal bars in different colors indicate miRNA genes with different expression patterns (see details in the bottom box on the right). The miRNAs were mapped to the corresponding chromosomes based on the genomic information retrieved from miRBase (release 15, <http://www.mirbase.org/index.shtml>). The bars with two different colors denote the miRNA genes that generate two mature miRNA coordinates with distinct expression patterns. The scale bar on the left measure the length of the chromosomes approximately.

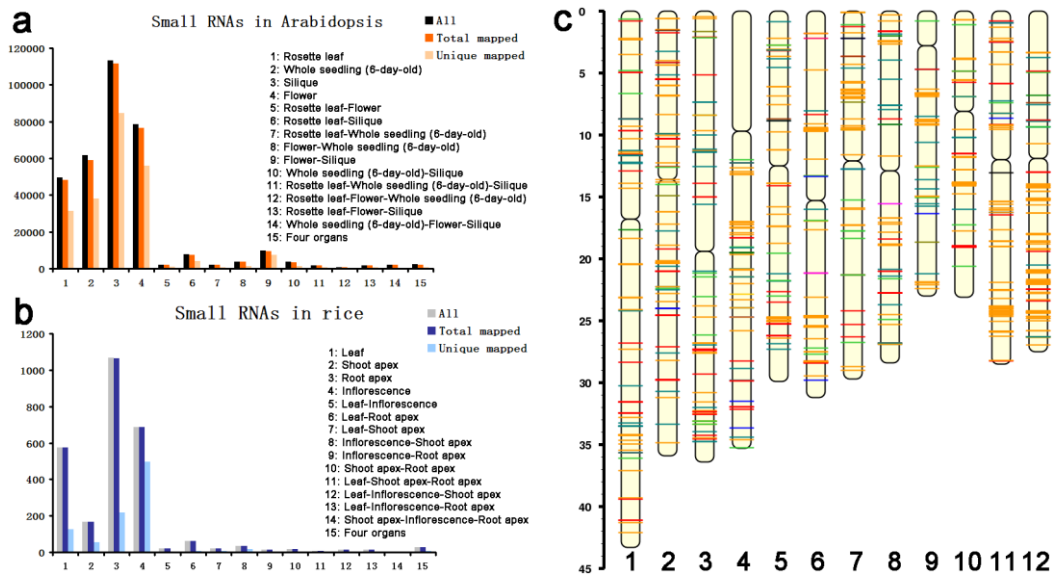


Fig. S4. Small RNAs (sRNAs) expressed in Arabidopsis and rice. **(A)** Statistical result of sRNAs after mapping them to the genome in Arabidopsis. **(B)** Statistical result of sRNAs after mapping them to the genome in rice. For both **(A)** and **(B)**, "All" represents all the 454 short reads employed for this analysis. "Total mapped" represents all the sRNAs that could be mapped to the corresponding genomes. "Unique mapped" represents the sRNAs with unique genomic loci based on our BLAST results. The y axes indicate the number of sRNAs with a specific expression pattern. The x axes indicate 15 different expression patterns (details listed on the right of each diagram) in Arabidopsis and rice. **(C)** Chromosome-wide distribution patterns of sRNAs in rice (the twelve chromosomes in light yellow color indicated by the numbers 1 to 12). Based on our BLAST result, only the sRNAs with unique genomic loci were drawn on the chromosomes. The horizontal bars in different colors indicate sRNAs with different expression patterns (the color code is the same as the one used in Fig. S3). The scale bar on the left measure the length (MB, megabase pairs) of the chromosomes approximately.

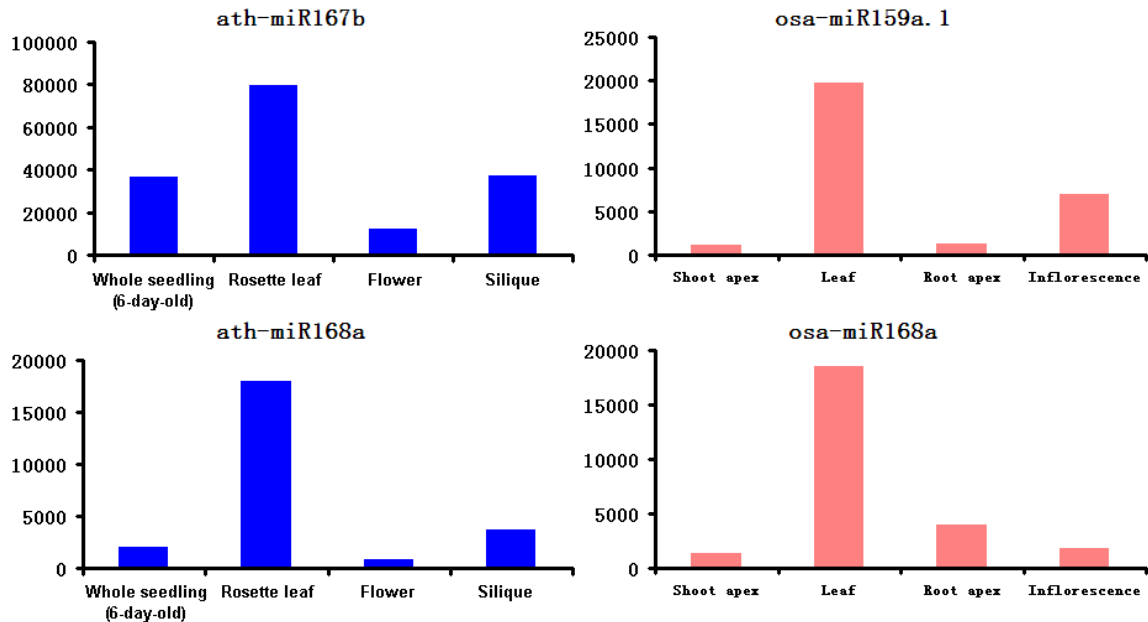


Fig. S5. Expression levels of *ath-miR167b* and *ath-miR168a* in Arabidopsis (blue bars), and *osa-miR159a.1* and *osa-miR168a* in rice (pink bars). For all the four panels, the y axes measure the expression levels of the corresponding miRNAs.

Table S1. Detailed information of the small RNA high-throughput sequencing datasets (generated by 454 sequencing technology) retrieved from Gene Expression Omnibus (GEO, <http://www.ncbi.nlm.nih.gov/geo/>) for this study.

Arabidopsis (<i>Arabidopsis thaliana</i>)	
GEO series number	Description
GSE5228	High-throughput sequencing of small RNAs from <i>Arabidopsis thaliana</i>
The GEO series GSE5228 contains the following four data sets.	
GEO accession number	Library description
GSM118373	Small RNAs from rosette leaves
GSM118374	Small RNAs from whole seedlings (6-day-old)
GSM118372	Small RNAs from whole flowers
GSM118375	Small RNAs from whole siliques
Rice (<i>Oryza sativa</i>)	
GEO series number	Description
GSE16350	Endogenous small RNAs of meristematic and a terminally differentiated tissue of rice
The GEO series GSE16350 contains the following 12 data sets.	
GEO accession number	Library description
GSM409316	Endogenous small RNAs from shoot apex of rice - replicate 1
GSM409317	Endogenous small RNAs from shoot apex of rice - replicate 2
GSM409318	Endogenous small RNAs from shoot apex of rice - replicate 3
GSM409322	Endogenous small RNAs from mature leaf of rice - replicate 1
GSM409323	Endogenous small RNAs from mature leaf of rice - replicate 2
GSM409324	Endogenous small RNAs from mature leaf of rice - replicate 3
GSM409313	Endogenous small RNAs from root apex of rice - replicate 1
GSM409314	Endogenous small RNAs from root apex of rice - replicate 2
GSM409315	Endogenous small RNAs from root apex of rice - replicate 3
GSM409319	Endogenous small RNAs from developing inflorescence of rice - replicate 1
GSM409320	Endogenous small RNAs from developing inflorescence of rice - replicate 2
GSM409321	Endogenous small RNAs from developing inflorescence of rice - replicate 3

Table S2. MicroRNAs expressed in multiple organs in Arabidopsis and rice.

Arabidopsis (<i>Arabidopsis thaliana</i>)	
Rosette leaf & Flower	ath-miR856
Rosette leaf & Silique	ath-miR472, ath-miR830*, ath-miR838, and ath-miR857
Flower & Silique	ath-miR156h, ath-miR399d, ath-miR826, ath-miR834, ath-miR851-3p, and ath-miR864-3p
Whole seedling* & Silique	ath-miR393a, ath-miR781, ath-miR828, ath-miR831, ath-miR835-3p, ath-miR837-3p, ath-miR844, ath-miR849, ath-miR853, ath-miR863-3p, and ath-miR1888
Whole seedling* & Flower	ath-miR158b, ath-miR395f, ath-miR774, ath-miR829.2, ath-miR845b, and ath-miR2112-5p
Whole seedling* & Rosette leaf	ath-miR837-5p, and ath-miR852
Rosette leaf & Silique & Whole seedling*	ath-miR167c, ath-miR777, ath-miR779.2, ath-miR833-5p, ath-miR841, ath-miR843, ath-miR844*, ath-miR846, ath-miR850, and ath-miR858
Rosette leaf & Flower & Whole seedling*	ath-miR829.1
Whole seedling* & Flower & Silique	ath-miR156g, ath-miR319c, ath-miR395a, ath-miR402, ath-miR833-3p, ath-miR860, ath-miR862-5p, ath-miR869.2, and ath-miR1886.2
Rosette leaf & Flower & Silique	ath-miR771, ath-miR827, ath-miR830, and ath-miR851-5p
Rice (<i>Oryza sativa</i>)	
Leaf & Inflorescence	osa-miR396e, osa-miR528, and osa-miR1883a
Leaf & Root apex	-
Inflorescence & Root apex	-
Shoot apex & Root apex	-
Inflorescence & Shoot apex	osa-miR166h, osa-miR167b, osa-miR166l, and osa-miR1868
Leaf & Shoot apex	osa-miR169c
Leaf & Root apex & Shoot apex	-
Leaf & Inflorescence & Shoot apex	osa-miR167f, osa-miR171d, and osa-miR444c.1
Shoot apex & Inflorescence & Root apex	-
Leaf & Inflorescence & Root apex	osa-miR164b, and osa-miR1862e

*Arabidopsis 6-day-old whole seedlings