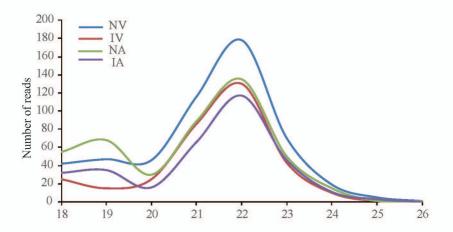
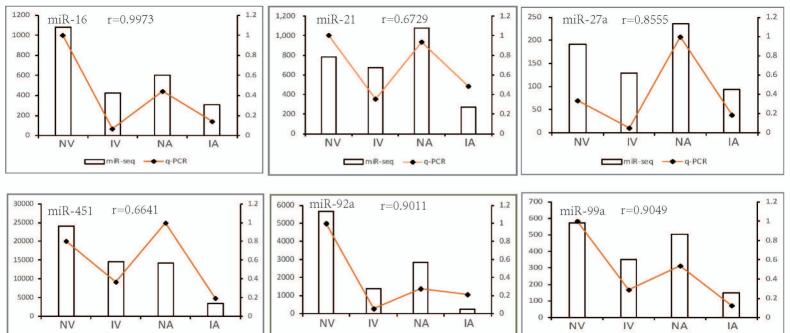
- 1 Fig S1.The length distribution of small RNA sequences.
- 2 Fig.S2. Validation miRNA-seq results by qRT-PCR technology.
- 3
- 4





miR-seq

	NV		IV		NA		IA	
lib	Total	% of Total						
Raw reads	12,749,883	100.00	13,292,222	100.00	11,423,982	100.00	13,002,222	100.00
3ADT&length filter	2,112,083	16.57	2,456,086	18.48	3,645,906	31.91	4,771,832	36.70
Junk reads	932	0.01	179	0.00	422	0.00	2,958	0.02
Rfam	19,185	0.15	19,838	0.15	24,763	0.22	26,316	0.20
mRNA	36,649	0.29	43,273	0.33	38,640	0.34	51,511	0.40
Repeats	556	0.00	42	0.00	263	0.00	329	0.00
valid reads	10,585,695	83.03	10,779,036	81.09	7,719,070	67.57	8,156,987	62.74

Table S1. Statistics of the distribution for small RNAs during a series of filters