

Table S1. Major primer sequences in this study

Primer name	Primer sequence (5'-3')
RNA5' Adapter	GTTCAGAGTTCTACAGTCCGACGATC
RNA3' Adapter	AGATCGGAAGAGCACACGTCT
bmo-miR-6497-3p-F for OE	<u>CCACTAGTCCAGTGTGGTGGCCAAAAAGGTAATTCCATTCC</u>
bmo-miR-6497-3p-R for OE	<u>ACTGTGCTGGATATCTGCAGTTTCCCAAGTCCCTCGCTC</u>
bmo-miR-6497-3p-SL primer	<u>CTCAACTGGTGTCTGCTGGAGTCCGGCAATTCAGTTGAGAGACCCGG</u>
bmo-miR-6497-3p-F	<u>ACACTCCAGCTGGGGATGCGGCCCGTGCC</u>
bmo-miR-6497-3p-R	TGGTGTCTGCTGGAGTCG
U6-F	<u>CTCGCTTCGGCAGCACA</u>
U6-R	<u>AACGCTTCACGAATTTGCGT</u>
Cycle-F	GCCAGTCAAGGAGGAGGT
Cycle-R	AGAGTTCGTGGTGGGAGC
Pdp-F	GAAGGAGAATATGGGCTTACGG
Pdp-R	GTGTTGTGCTATGCGGGTG
SW22934-F	<u>TTCGTACTGCTCTTCTCGT</u>
SW22934-R	<u>CAAAGTTGATAGCAATTCCT</u>
Cycle 3'UTR-F	GTCATGTGAAAACCTAGCCTTAGTG
Cycle 3'UTR-R	CATATCATCAGATGCTTTACCAGTTAG

†: the solid line indicates the sequence of homology arm primer for constructing overexpression vector, and the dotted line indicates the regular part in primer.

Table S2. Information statistics on mapping with reference genome

Sample	Total sRNA	Mapped sRNA	" + "Mapped sRNA	" - "Mapped sRNA
BK25	13172384 (100.00%)	11290246 (85.71%)	6815481 (51.74%)	4474765 (33.97%)
BK15	12211015 (100.00%)	10778240 (88.27%)	6660938 (54.55%)	4117302 (33.72%)
HP25	8595053 (100.00%)	7410664 (86.22%)	5103721 (59.38%)	2306943 (26.84%)
HP15	7543817 (100.00%)	6299620 (83.51%)	3800764 (50.38%)	2498856 (33.12%)