Supplementary files

Table S1: The sequences of all oligonucleotides used.

| RNA	sequence
ath-miR156a	UGACAGAAGAGAGUGAGCAC
ath-miR158a	CUUUGUCUACAAUUUUGGAAA
ath-miR159a	UUUGGAUUGAAGGGAGCUCUA
ath-miR166a	GGACUGUUGUCUGGCUCGAGG
ath-miR168a	UCGCUUGGUGCAGGUCGGGAA
hsa-miR-16	UAGCAGCACGUAAAUAUUGGCG
hsa-miR-21	UAGCUUAUCAGACUGAUGUUGA
hsa-miR-122	UGGAGUGUGACAAUGGUGUUUG
hsa-miR-423	UGAGGGGCAGAGAGCGAGACUUU
hsa-let-7a	UGAGGUAGUAGGUUGUAUAGUU
piR-30198	AAGACTTAGAGATGGAAAGTAGTTCAATGG
piR-31068	AGCATTGGTGGTTCAGTGGTAGAATTCTCGC
piR-31925	ATTGGTGGTTCAGTGGTAGAATTCTCGCCTG
piR-43771	TCCCTGGTGGTCTAGTGGTTAGGATTCGGCA
piR-43773	TCCCTGGTTCGATCCCGGGTTTCGGCACC

**Table S2:** The primer sequences of the poly(A)-tailed RT-qPCR method.

| RNA	Primer sequence
ath-miR156a	GATGACAGAAGAGAGTGAG
ath-miR158a	GTCCCAAATGTAGACAAAG
ath-miR159a	TCTTTGGATTGAAGGGAG
ath-miR166a	TCGGACCAGGCTTCATTC
ath-miR168a	ATATCGCTTGGTGCAGGTC
hsa-miR-16	TAGCTAGCAGCACGTAAAT
hsa-miR-21	GTGTTAGCTTATCAGACTG
hsa-miR-122	TGGAGTGTGACAATGGTG
hsa-miR-423	GGGCAGAGAGCGAGACT
hsa-let-7a	GTGAGGTAGTAGGTTGTAT
piR-30198	AAGACTTAGAGATGGAAAG
piR-31068	GCATTGGTGGTTCAGTGG
piR-31925	ATTGGTGGTTCAGTGGTAG
piR-43771	TCCCTGGTGGTCTAGTGG
piR-43773	TCGATCCCGGGTTTCGG
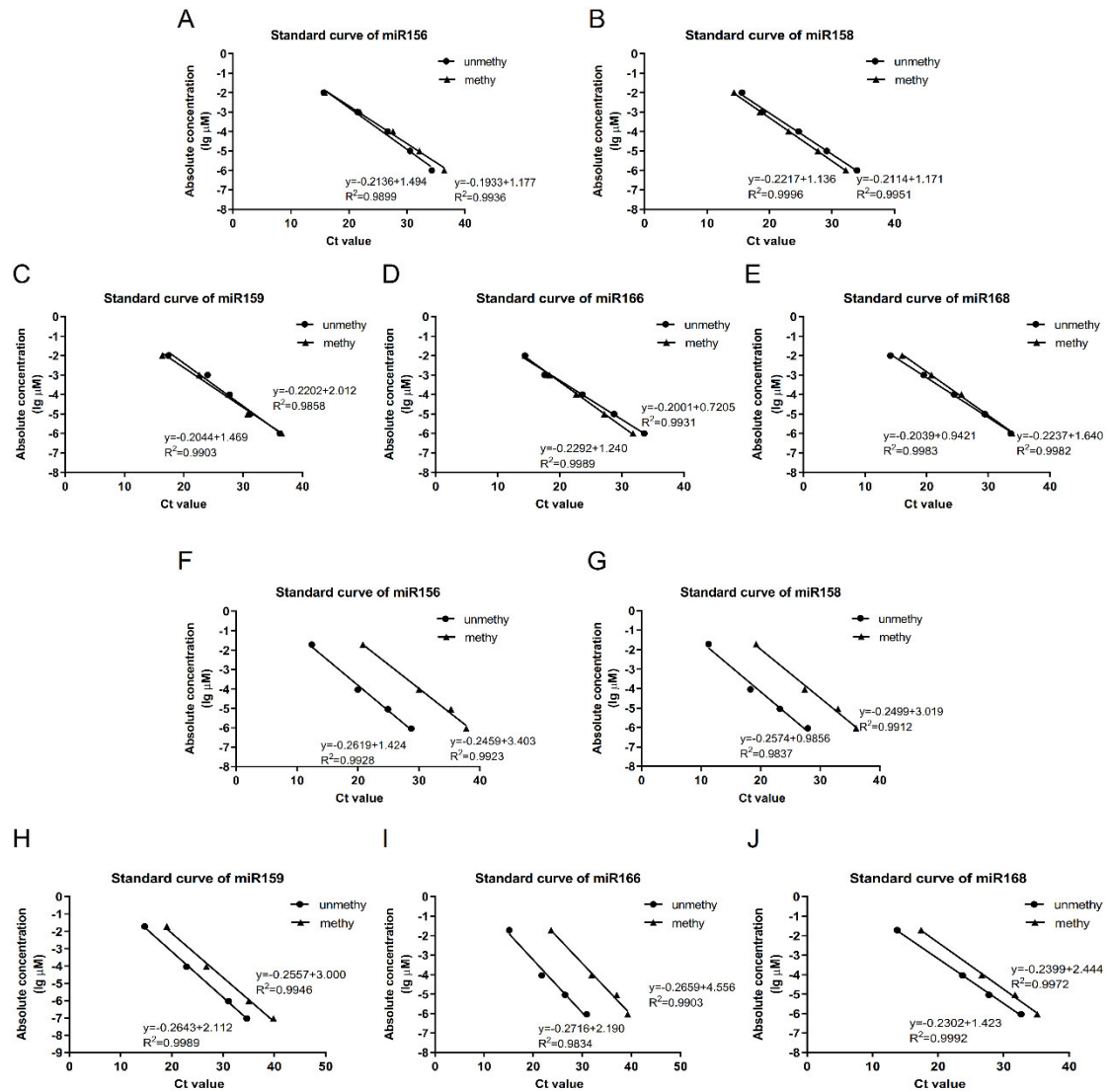
Fig S1: The standard curves of stem–loop RT-qPCR and poly(A)-tailed RT-qPCR for 5 synthetic plant miRNAs (miR156a, miR158a, miR159a, miR166a and miR168a). (A-E) The standard curves of 5 plant miRNAs determined by stem-loop RT-qPCR. (F-J) The standard curves of 5 plant miRNAs determined by poly(A)-tailed RT-qPCR. Below the regression equation is the goodness-of-fit.
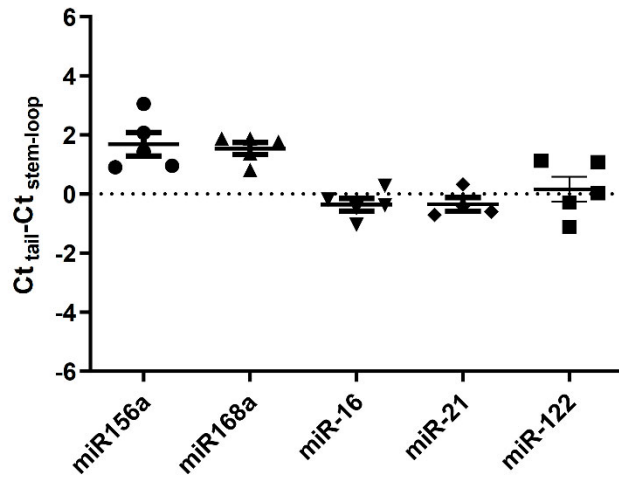
Fig S2: ΔCt values of plant miRNAs (miR156a and miR168a) and animal miRNAs (miR-16, miR-21 and miR-122) in rice-fed animals (n=5).
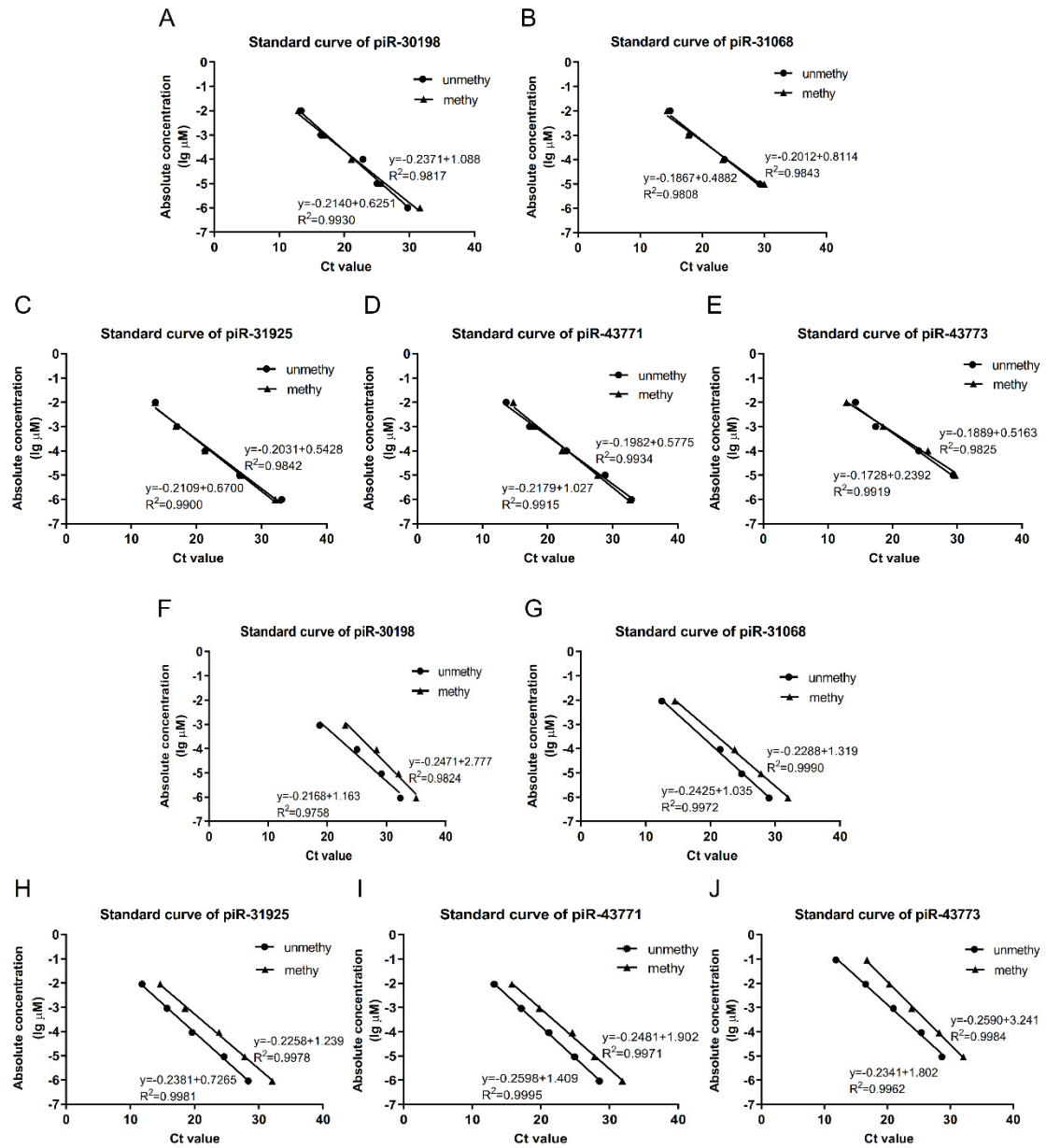
Fig S3: The standard curves of stem–loop RT-qPCR and poly(A)-tailed RT-qPCR for 5 synthetic piRNAs (piR-30198, piR-31068, piR-31925, piR-43771 and piR-43773). (A-E) The standard curves of 5 piRNAs determined by stem-loop RT-qPCR. (F-J) The standard curves of 5 piRNAs determined by poly(A)-tailed RT-qPCR. Below the regression equation is the goodness-of-fit.
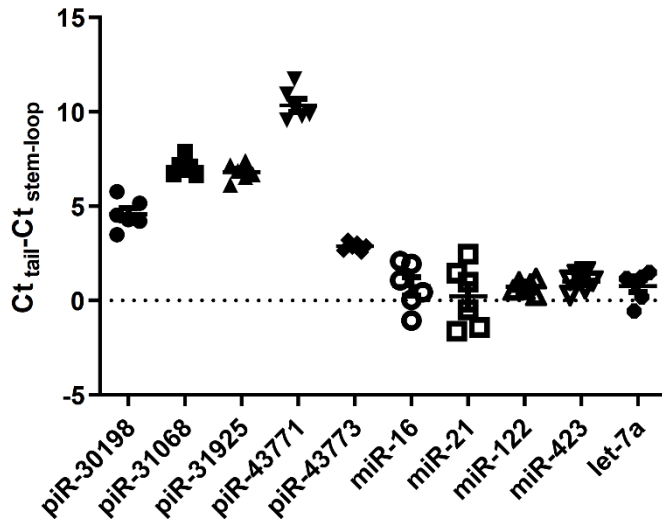
Fig S4: ΔCt values of piRNAs (piR-30198, piR-31068, piR-31925, piR-43771 and piR-43773) and animal miRNAs (miR-16, miR-21, miR-122 miR-423 and let-7a) in seminal plasma (n=6).