Virus-derived small RNAs in the penaeid shrimp *Fenneropenaeus chinensis* during acute infection of the DNA virus WSSV

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Table S1 WSSV genes potentially regulated by WSSV miRNAs

Target genes	**WSSV miRNAs**	**Samples[a]**
ORF126	N1,m1	CEP+INT
ORF14	m11	CEP+INT
ORF61	N1,m1,m7	CEP+INT
putative DNA polymerase	m2,m6	CEP+INT
WSSV156	m11	CEP
WSSV507	m6	CEP+INT
wsv026	m1,m2	CEP+INT
wsv067	m6	CEP
wsv133	m1,m6	CEP+INT
wsv139	m12,m2	CEP+INT
wsv151	N1,m1,m2,m6,m9,m10	CEP+INT
wsv184	N1,m7	CEP+INT
wsv206	m1	CEP+INT
wsv269	miR-211	CEP
wsv277	m1,m11	CEP+INT
wsv282	m1,m6	CEP+INT
wsv303	m7,m9	CEP+INT
wsv340	N1,m6	CEP+INT
wsv387	m7	CEP+INT
wsv395	m1,m12,miR-211	CEP+INT
wsv415	m1,m7,m12	CEP+INT
wsv442	m1	CEP

[a]**CEP:** cephalothoraxes; **INT**: intestine

Table S2 Virus-derived sRNA profiles of animal viruses

Virus	Genome	Host	Genome covered[a]	Length (nt)	Strand polarity[b]	5’ bias[c]	Class	Reference[d]
ANV	+ssRNA	fruit fly	/	27~28	+	/	piRNA	(Wu et al., 2010)
DBV	dsRNA	fruit fly	/	~21	+	U	siRNA	(Wu et al., 2010)
DCV	+ssRNA	fruit fly	/	~21	+	/	siRNA	(Wu et al., 2010)
DCV	+ssRNA	fruit fly	/	27~28	+	/	piRNA	(Wu et al., 2010)
DCV	+ssRNA	fruit fly	/	~21	+87.4%	/	siRNA	(Sabin et al., 2013)
DENV2	+ssRNA	mosquito	/	20~23	+/-	/	siRNA	(Scott et al., 2010)
DENV2	+ssRNA	mosquito	/	24~30	+	/	piRNA	(Scott et al., 2010)
rDENV-4	+ssRNA	mosquito	/	~21	+59.3%	/	/	(Schirtzinger et al., 2015)
rDENV-4	+ssRNA	primate	/	~24	+99.0%	U	/	(Schirtzinger et al., 2015)
DNV	+ssDNA	insects	78.5%	~21	+87.5%	/	siRNA	(Ma et al., 2011)
DTrV	+ssRNA	fruit fly	/	~21	+	/	siRNA	(Wu et al., 2010)
DTV	dsRNA	fruit fly	/	/	/	/	siRNA	(Wu et al., 2010)
DXV	dsRNA	fruit fly	78~91%	~21	+	+U	siRNA	(Wu et al., 2010)
FHV	+ssRNA	fruit fly	/	~21	~50%	/	siRNA	(Aliyari et al., 2008; Flynt et al., 2009; Han et al., 2011)
FHV	+ssRNA	nematode	93%	23	~50%	U	siRNA	(Wu et al., 2010)
HaSNPV	dsDNA	cotton bollworm	/	~20	/	/	siRNA	(Jayachandran et al., 2012)
HiPV	+ssRNA	planthopper	72.9%	21~22	+67.4%	U	siRNA	(Xu et al., 2014)
HoCV-1	+ssRNA	leafhopper	100%	~21	+95%	/	siRNA	(Nandety et al., 2013)
HoVRV	dsRNA	leafhopper	100%	~21	-	/	siRNA	(Nandety et al., 2013)
IIV-6	dsDNA	insects	/	~21	+47%	/	siRNA	(Bronkhorst et al., 2012)
LGTV	+ssRNA	tick	/	~22	~50%	A	siRNA	(Schnettler et al., 2014)
MNV	+ssRNA	mosquito	/	/	/	/	/	(Wu et al., 2010)

RSV	-ssRNA	plant/insect	/	20-24	~50%	U	siRNA	(Xu et al., 2012)
RVFV	-ssRNA	insect/vertebrates	/	24~28	-90%	U	piRNA	(Leger et al., 2013)
RVFV	-ssRNA	insect/vertebrates	/	~21	~50%	/	siR/miR	(Leger et al., 2013; Sabin et al., 2013)
SFV	+ssRNA	mosquito	/	~21	+	/	siRNA	(Siu et al., 2011)
SINV	+ssRNA	mosquito	99%	~21	+	/	siRNA	(Myles et al., 2008; Wu et al., 2010)
TBEV	+ssRNA	tick	/	~22	~50%	/	siRNA	(Schnettler et al., 2014)
VACV	dsDNA	insect/mammal	most	~21	+68.8%	/	siRNA	(Sabin et al., 2013)
VSV	-ssRNA	insect/vertebrates	/	~21	+44/53%	/	siRNA	(Mueller et al., 2010)
VSV	-ssRNA	insect/vertebrates	/	~21	+54.5%	/	siR/miR	(Sabin et al., 2013)
WNV	+ssRNA	fruit fly	/	~25	/	/	siRNA	(Chotkowski et al., 2008)
WNV	+ssRNA	mosquito	82~92%	~21	vary	/	siRNA	(Brackney et al., 2009)
WSSV	dsDNA	crustacean	/	~22	/	/	miRNA/siRNA	(He and Zhang, 2012; Huang et al., 2014; Huang and Zhang, 2013)

[a] Proportion of viral genome length covered by sRNA reads.

[b] Polarity of viral sRNA: “+” and “–” stand for sRNAs matching the positive and negative strands of virus genome, respectively. Numbers in percentage represent proportion of sRNAs matching the corresponding strand of virus genome.

[c] Nucleotide preference at 5’ end of viral sRNA.

[d] Please find the references at the end of the Supplemental Materials.

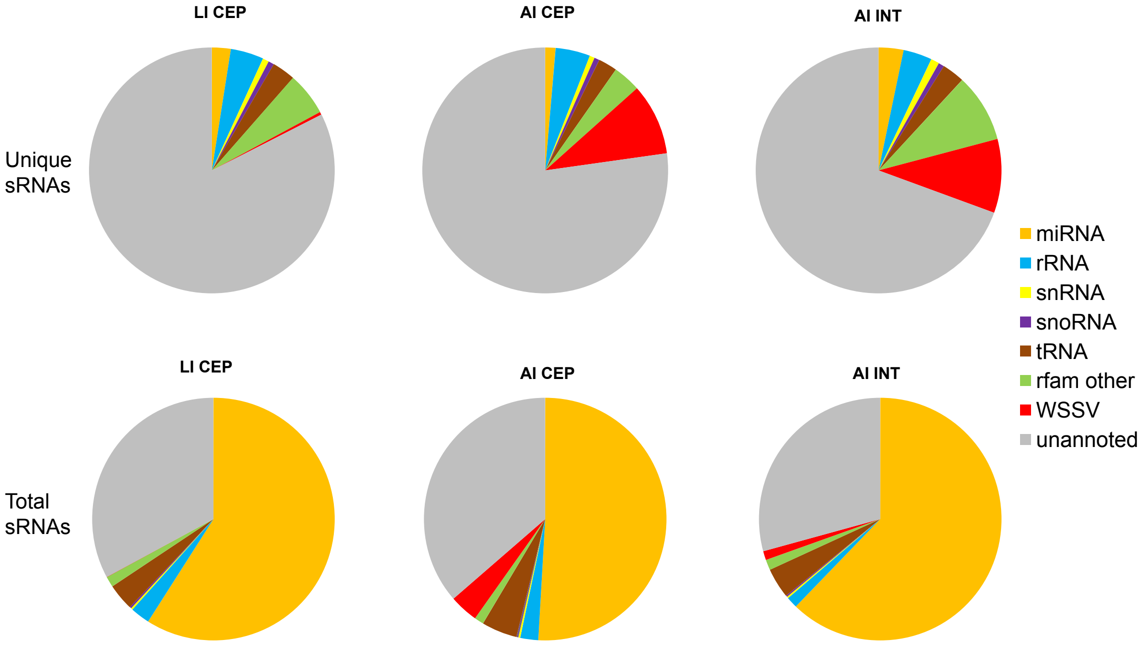

FIG S1 Classification of sRNA sequencing reads. The clean reads (17-35nt) were annotated in a preferential order by comparing to the WSSV genome, the Rfam non-coding RNA database and miRBase miRNA database. CEP and INT stand for cephalothoraxes and intestine of *F. chinensis*, respectively. LI and AI represent latent or acute stages of infection.

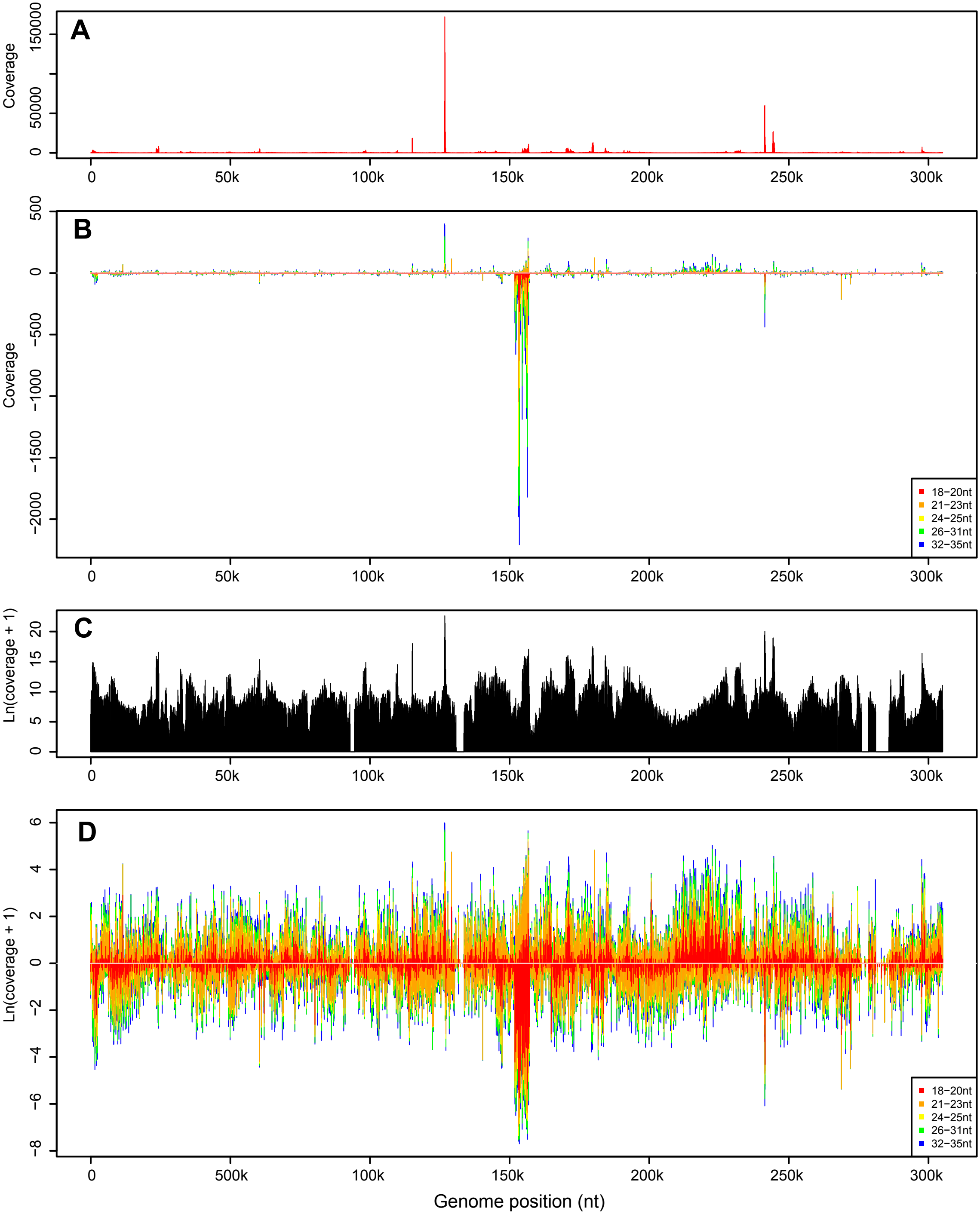

FIG S2 Expression of sRNAs and mRNAs along WSSV genome in intesine of *F. chinensis* during acute infection. **(A)** Sequencing coverage of mRNA reads (orientation unknown). **(B)** Sequencing coverage of sRNA reads. Bars beneath coverage 0 represent sRNAs in the reverse direction of genome. The lengths of sRNAs are indicated with different colors. **(C)** Coverage of mRNA reads in logarithmic scale. **(D)** Coverage of sRNA reads in logarithmic scale. Bars beneath coverage 0 represent sRNAs in the reverse direction.

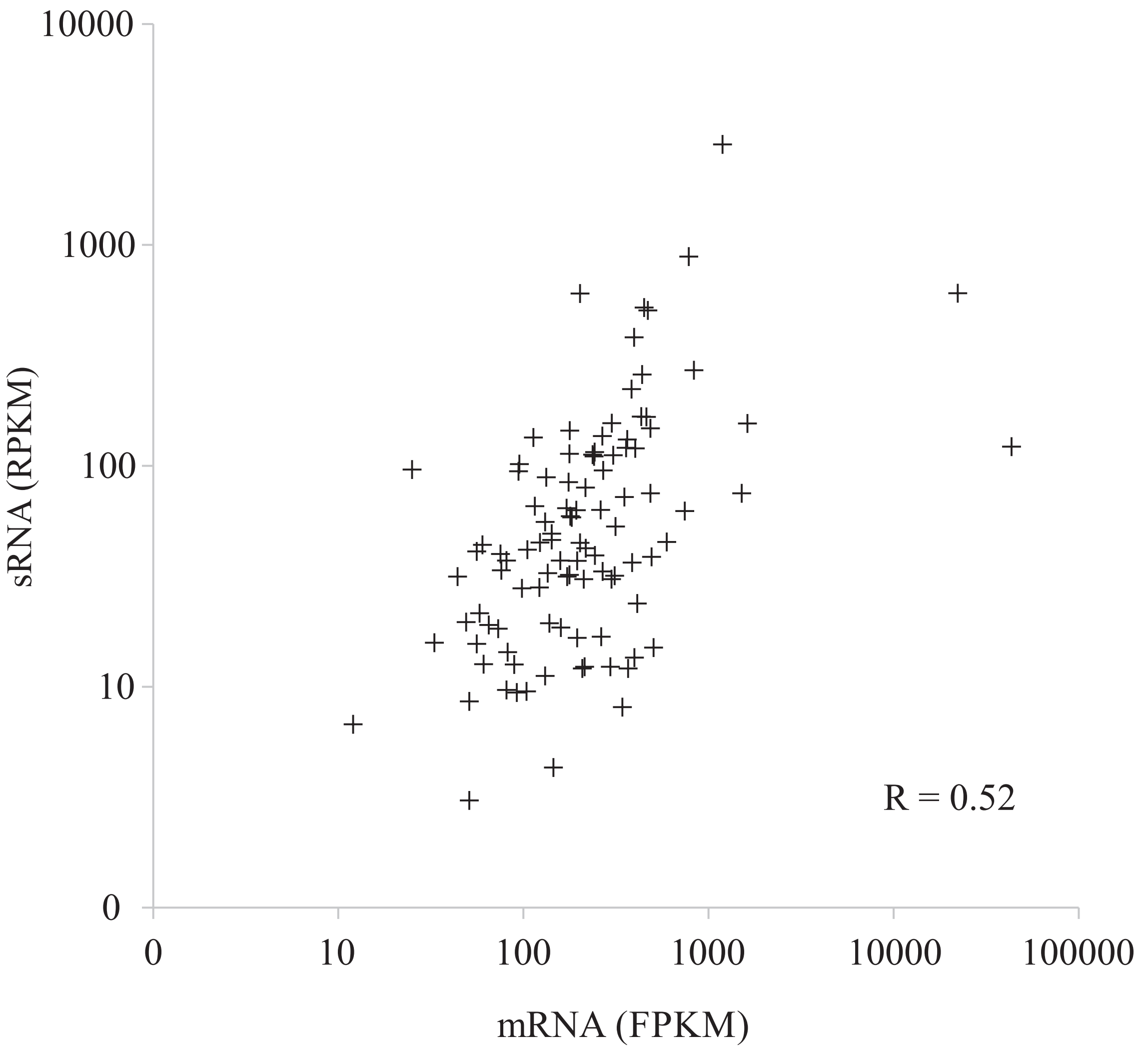

FIG S3 Relations between the expressions of sRNA and mRNA of WSSV in cephalothoraxes of *F. chinensis* during acute infection.

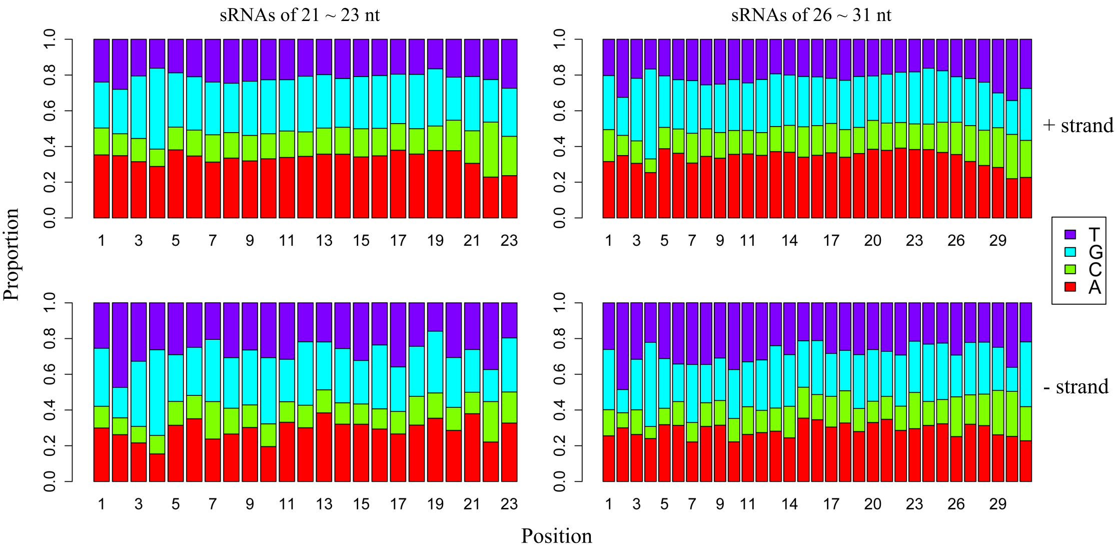

FIG S4 WSSV sRNAs did not show nucleotide preference of canonical piRNA in shrimp cephalothoraxes during acute infection. Nucleotide frequencies of total sRNAs at each position are shown with bars in different colors. Figures in the upper row show sRNAs mapped to the WSSV genome in the 5'-3' direction, the lower two figures show sRNAs matched to the reverse complement direction of the genome. Figures in the left column show sRNAs of length 21~23 nt, which is most aboundant in the AI sample. Figures in the right column show sRNAs of length 26-31 nt, which is in the range of canonical piRNA.

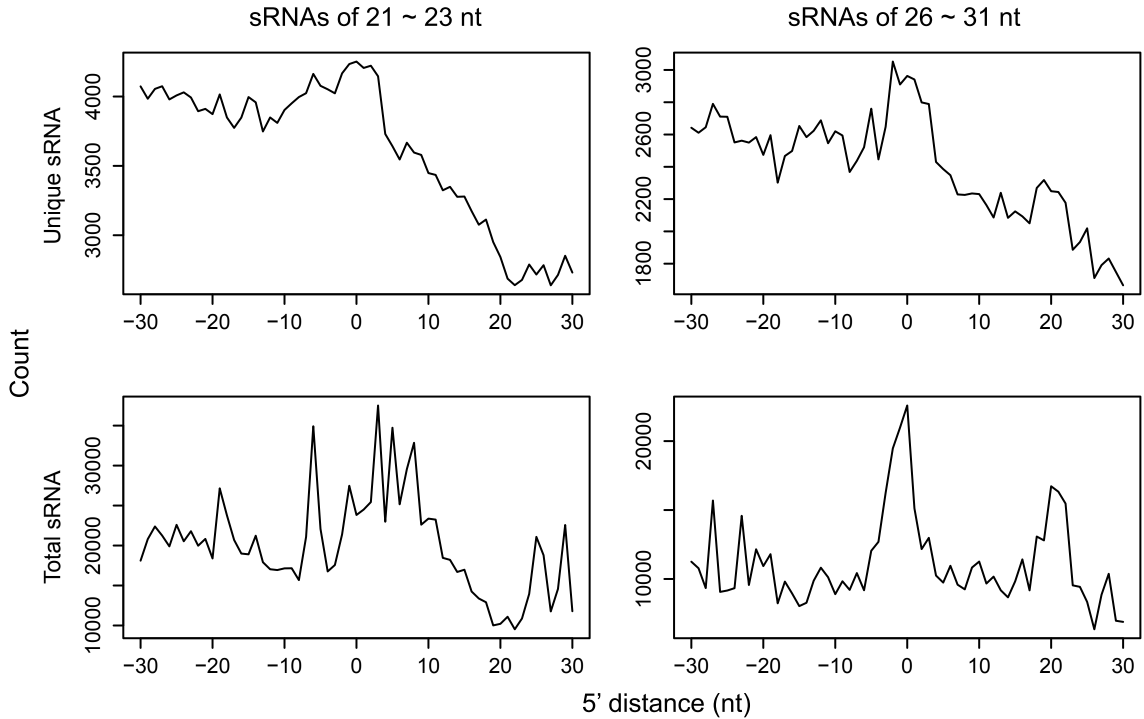

FIG S5 WSSV sRNAs did not show typical 5' distances (10nt) of canonical piRNA in shrimp cephalothoraxes during acute infection. Frequency map of the distance between sRNAs that mapped to opposite strands of the WSSV genome.

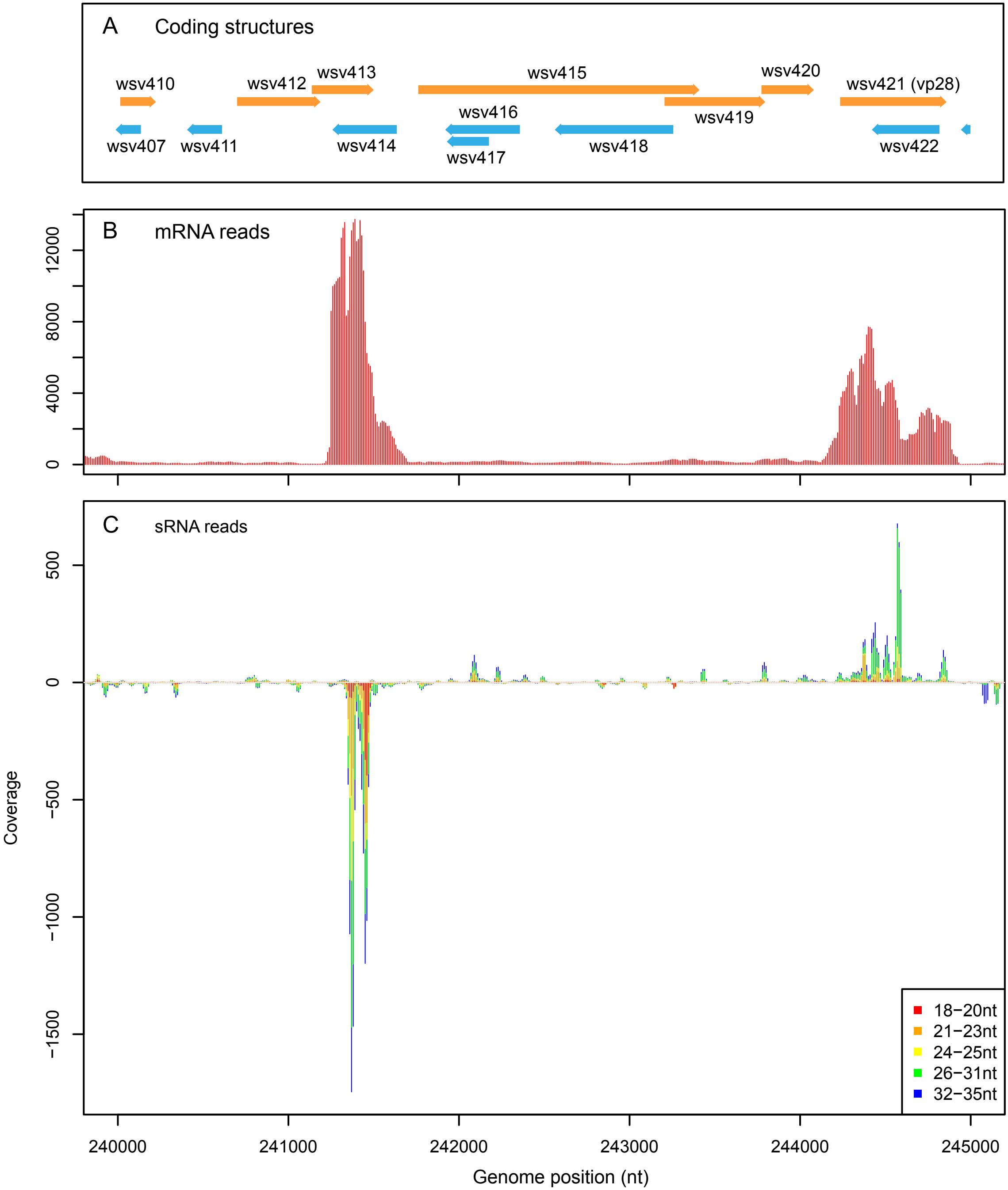

FIG S6 Expression of sRNAs and mRNAs around vp28 gene in WSSV genome during acute infection in shrimp cephalothoraxes. (**A**) Coding structures. Arrows represent coding sequences annotation from NCBI. Orange arrows indicateCDS in plus strand, while cyan arrows indicate CDS in minus strand. (**B**) Sequencing coverageof mRNA reads (orientation unknown). (**C**) Sequencing coverage of sRNA reads. Bars beneath coverage 0 represent sRNAs in the reverse direction. The lengths of sRNAs are indicated with different colors.

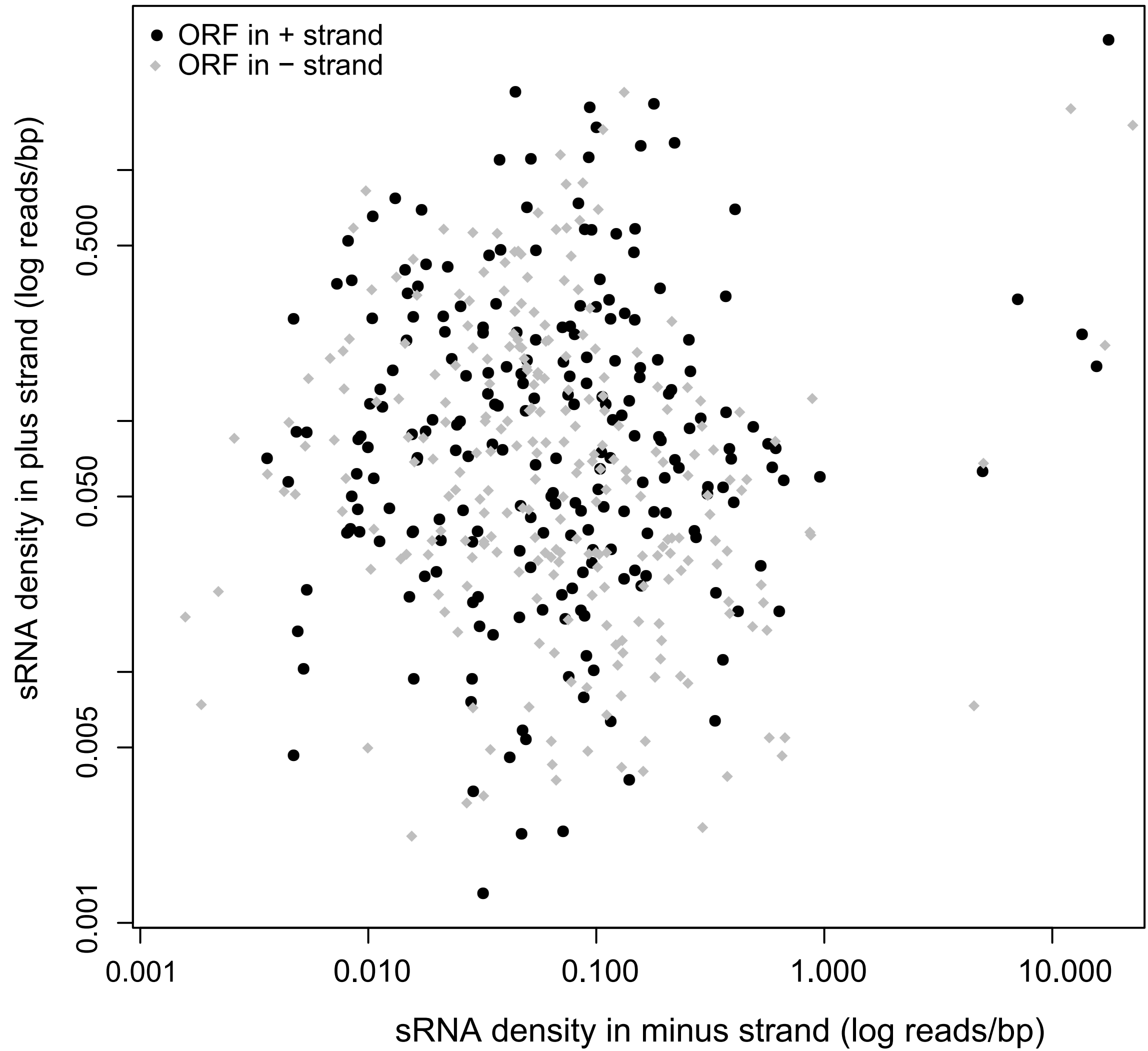

FIG S7 Scatter plot of sRNAs from individual ORFs that map to the WSSV plus and minus strands in shrimp cephalothoraxes during acute infection. For each ORF, the total number of sRNAs derived from each strand was divided by the length of the ORF. The data were log-transformed. Black circles and grey diamonds indicate ORFs on the plus and minus strands of the WSSV genome, respectively.

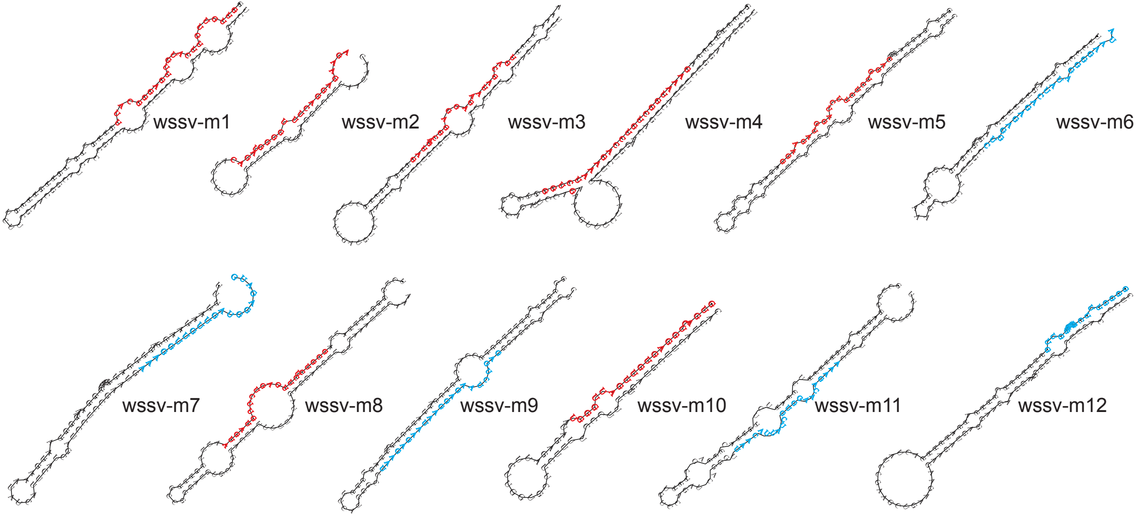

FIG S8 Structures of candidate WSSV miRNA precursors. Pre-miRNA structures were predicted using RNAfold (MFE < -25 kcal/mole). Red color indicates mature miRNAs located at the 5'-arm (5p) of the precursor, and blue indicates mature miRNAs located at the 3' arm (3p).

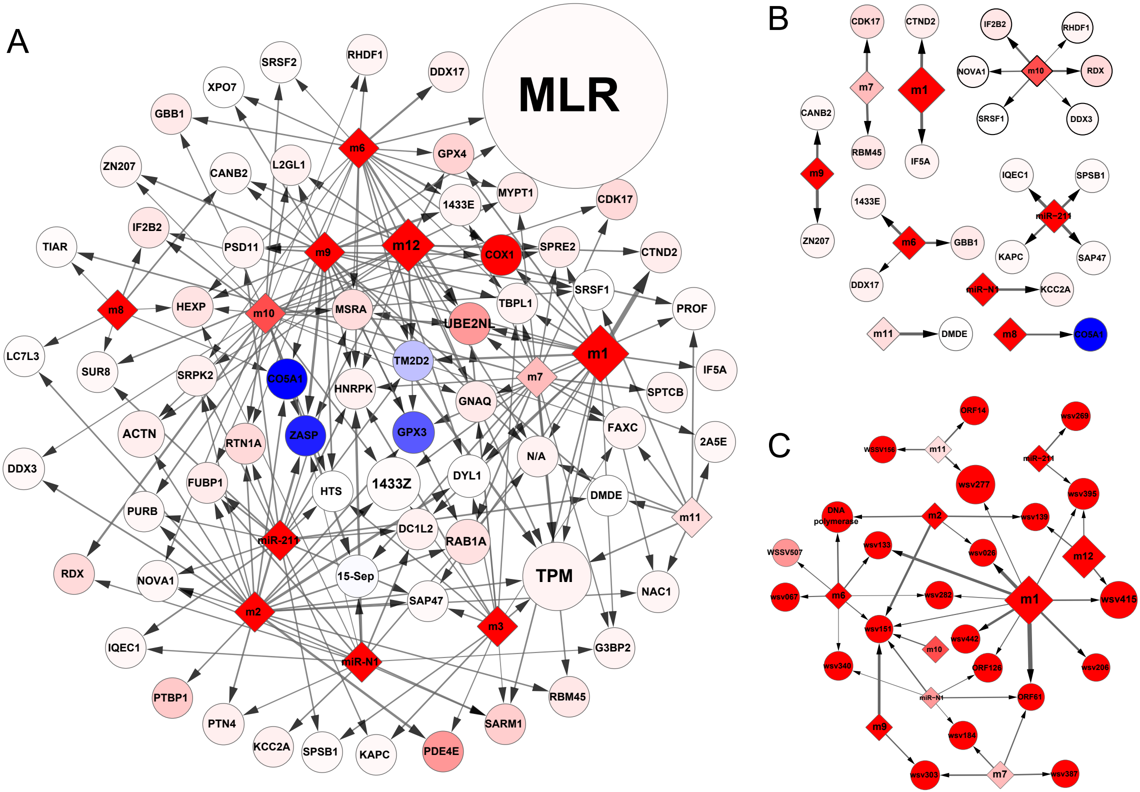

FIG S9 Visualization of viral miRNA regulation network. Diamonds represent miRNAs, while circles represent target genes. Red or blue colors indicate up-regulation or down-regulation during acute infection, respectively. Size of a symbol indicates expression level of a miRNA or target gene. **(A)** Target genes that are shared in three hosts (*F. chinensis, L. vannamei and E. carincauda*). **(B)** Target genes with binding sites that are evolutionally conserved. **(C)** Predicted regulation of WSSV miRNAs on its own mRNAs.

Text S1

Small RNA reads from acute WSSV-infected cephalothorax of *F. chinensis* which overlapped with the vp28 siRNA probes of Huang et al. (2013).

```
>inf_0160452_x3
ACAACACTGTGACCAAGACCATCGAAACCCACA
>inf_0210481_x2
CACAACACTGTGACCAAGACCATCGAAACCCACA
>inf_0317586_x2
CAACACTGTGACCAAGACCATCGAAACCCAC
>inf_0362208_x1
AACACTGTGACCAAGACCATCGAAACCCA
>inf_0364443_x1
AACACTGTGACCAAGACCATCGAAACCCACA
>inf_0747546_x1
CACAACACTGTGACCAAGACCATCGAAACCCA
>inf_0857103_x1
CAACACTGTGACCAAGACCATCGAAACCCACA
>inf_0873829_x1
TGTGACCAAGACCATCGAAACCCACACAGGCA
>inf_1053362_x1
AACACTGTGACCAAGACCATCGAAACCCACACA
>inf_1174596_x1
ACTGTGACCAAGACCATCGAAACCCACA
>inf_1186243_x1
ACAACACTGTGACCAAGACCATCGAAACCCA
>inf_1207632_x1
TGACCAAGACCATCGAAACCCACACAGGC
>inf_1271115_x1
CAACACTGTGACCAAGACCATCGAAACCCACAC
>inf_1576499_x1
AACACTGTGACCAAGACCATCGAAACCCAC
```

Text S2

Sequences of the 12 WSSV pre-miRNAs were conserved in 4 WSSV strains (gi58866698, gi426202315, gi721172032 and gi19481591).

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MUSCLE (3.8) multiple sequence alignment
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wssv-m1->gi426202315:152245-152334
GGTTGTTGTTCATGTTGAGGGCATTGTTGTTGTTGTTGTTCGTCTTCGAACGGCATCACC
wssv-m1->gi58866698:91297-91386
GGTTGTTGTTCATGTTGAGGGCATTGTTGTTGTTGTTGTTCGTCTTCGAACGGCATCACC
wssv-m1->gi721172032:147629-147718
GGTTGTTGTTCATGTTGAGGGCATTGTTGTTGTTGTTGTTCGTCTTCGAACGGCATCACC
wssv-m1->gi19481591:120829-120918
GGTTGTTGTTCATGTTGAGGGCATTGTTGTTGTTGTTGTTCGTCTTCGAACGGCATCACC

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wssv-m1->gi426202315:152245-152334
GACATCATTTCTTCATTCGAGGTAGAGACT
wssv-m1->gi58866698:91297-91386
GACATCATTTCTTCATTCGAGGTAGAGACT
wssv-m1->gi721172032:147629-147718
GACATCATTTCTTCATTCGAGGTAGAGACT
wssv-m1->gi19481591:120829-120918
GACATCATTTCTTCATTCGAGGTAGAGACT
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MUSCLE (3.8) multiple sequence alignment

wssv-m2->gi58866698:164455-164511
AGAAGAGGACTTTGGGGTAGACATTTTCTTCCTCTCCCCTTCCAGGTCCTTAATAAC
wssv-m2->gi721172032:221267-221323
AGAAGAGGACTTTGGGGTAGACATTTTCTTCCTCTCCCCTTCCAGGTCCTTAATAAC
wssv-m2->gi426202315:225865-225921
AGAAGAGGACTTTGGGGTAGACATTTTCTTCCTCTCCCCTTCCAGGTCCTTAATAAC
wssv-m2->gi19481591:194131-194187
AGAAGAGGACTTTGGGGTAGACATTTTCTTCCTCTCCCCTTCCAGGTCCTTAATAAC

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MUSCLE (3.8) multiple sequence alignment

wssv-m3->gi58866698:285122-285215
AAAATTTCTTGACGATAAGAGGAGGCAGTAGGTGAGGCTGCTTGTTTGATGTGTCAGCCA
wssv-m3->gi426202315:236397-236490
AAAATTTCTTGACGATAAGAGGAGGCAGTAGGTGAGGCTGCTTGTTTGATGTGTCAGCCA
wssv-m3->gi721172032:241024-241117
AAAATTTCTTGACGATAAGAGGAGGCAGTAGGTGAGGCTGCTTGTTTGATGTGTCAGCCA

wssv-m3->gi19481591:271018-271111
AAAATTTCTTGACGATAAGAGGAGGCAGTAGGTGAGGCTGCTTGTTTGATGTGTCAGCCA

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wssv-m3->gi58866698:285122-285215
CATCTGCGTCATACATTATATTTCCAAGAATTTT
wssv-m3->gi426202315:236397-236490
CATCTGCGTCATACATTATATTTCCAAGAATTTT
wssv-m3->gi721172032:241024-241117
CATCTGCGTCATACATTATATTTCCAAGAATTTT
wssv-m3->gi19481591:271018-271111
CATCTGCGTCATACATTATATTTCCAAGAATTTT

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MUSCLE (3.8) multiple sequence alignment

wssv-miR-211-a->gi426202315:272850-27294
GCCCTGTTCCAGAAATGGCTGTCCAGAAATCTGGGTCGGACAGATTCCAGAAACGTTTCT
wssv-miR-211-a->gi58866698:28422-28515
GCCCTGTTCCAGAAATGGCTGTCCAGAAATCTGGGTCGGACAGATTCCAGAAACGTTTCT
wssv-miR-211-a->gi721172032:277471-27756
GCCCTGTTCCAGAAATGGCTGTCCAGAAATCTGGGTCGGACAGATTCCAGAAACGTTTCT
wssv-miR-211-a->gi19481591:173-266
GCCCTGTTCCAGAAATGGCTGTCCAGAAATCTGGGTCGGACAGATTCCAGAAACGTTTCT

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wssv-miR-211-a->gi426202315:272850-27294
AACCATTTCTGGAACAGTCATTTCTGGAAAGGGT
wssv-miR-211-a->gi58866698:28422-28515
AACCATTTCTGGAACAGTCATTTCTGGAAAGGGT
wssv-miR-211-a->gi721172032:277471-27756
AACCATTTCTGGAACAGTCATTTCTGGAAAGGGT
wssv-miR-211-a->gi19481591:173-266
AACCATTTCTGGAACAGTCATTTCTGGAAAGGGT

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MUSCLE (3.8) multiple sequence alignment

wssv-miR-211-b->gi426202315:273818-27390
CTGTTCCAGAAATGGCTGTCCAGAAATCTGGGTCGGCCAGATTCCAGAAACGTTTCTAAC
wssv-miR-211-b->gi58866698:29716-29803
CTGTTCCAGAAATGGCTGTCCAGAAATCTGGGTCGGCCAGATTCCAGAAACGTTTCTAAC
wssv-miR-211-b->gi19481591:1141-1228
CTGTTCCAGAAATGGCTGTCCAGAAATCTGGGTCGGCCAGATTCCAGAAACGTTTCTAAC
wssv-miR-211-b->gi721172032:278439-27852
CTGTTCCAGAAATGGCTGTCCAGAAATCTGGGTCGGCCAGATTCCAGAAACGTTTCTAAC

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wssv-miR-211-b->gi426202315:273818-27390
CATTTCTGGAACAGTCATTTCTGGAAAG
wssv-miR-211-b->gi58866698:29716-29803
CATTTCTGGAACAGTCATTTCTGGAAAG
wssv-miR-211-b->gi19481591:1141-1228
CATTTCTGGAACAGTCATTTCTGGAAAG
wssv-miR-211-b->gi721172032:278439-27852
CATTTCTGGAACAGTCATTTCTGGAAAG

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MUSCLE (3.8) multiple sequence alignment

wssv-miR-211-c->gi19481591:820-903
TCCAGAAATGGCTGTCCAGAAATCTGGGTCGGCCAGATTCCAGAAACGATTCTAACCATT
wssv-miR-211-c->gi426202315:273497-27358
TCCAGAAATGGCTGTCCAGAAATCTGGGTCGGCCAGATTCCAGAAACGATTCTAACCATT
wssv-miR-211-c->gi721172032:278118-27820
TCCAGAAATGGCTGTCCAGAAATCTGGGTCGGCCAGATTCCAGAAACGATTCTAACCATT
wssv-miR-211-c->gi58866698:29395-29478
TCCAGAAATGGCTGTCCAGAAATCTGGGTCGGCCAGATTCCAGAAACGATTCTAACCATT

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wssv-miR-211-c->gi19481591:820-903
TCTGGAACAGTCATTTCTGGAAAG
wssv-miR-211-c->gi426202315:273497-27358
TCTGGAACAGTCATTTCTGGAAAG
wssv-miR-211-c->gi721172032:278118-27820
TCTGGAACAGTCATTTCTGGAAAG
wssv-miR-211-c->gi58866698:29395-29478
TCTGGAACAGTCATTTCTGGAAAG

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MUSCLE (3.8) multiple sequence alignment


wssv-miR-N1->gi19481591:231993-232086
GCTTGAGTATTGGCAGGTCTCTTCTAGGTAGAAGGAGAGAGAGTGCTTGTTGTGTTGCTC
wssv-miR-N1->gi721172032:258800-258893
GCTTGAGTATTGGCAGGTCTCTTCTAGGTAGAAGGAGAGAGAGTGCTTGTTGTGTTGCTC
wssv-miR-N1->gi426202315:263397-263490
GCTTGAGTATTGGCAGGTCTCTTCTAGGTAGAAGGAGAGAGAGTGCTTGTTGTGTTGCTC
wssv-miR-N1->gi58866698:202307-202400
GCTTGAGTATTGGCAGGTCTCTTCTAGGTAGAAGGAGAGAGAGTGCTTGTTGTGTTGCTC

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wssv-miR-N1->gi19481591:231993-232086
TTCTGCTGGCTTGCAGAGAACTGATGCTTCTGGC
wssv-miR-N1->gi721172032:258800-258893
TTCTGCTGGCTTGCAGAGAACTGATGCTTCTGGC
wssv-miR-N1->gi426202315:263397-263490
TTCTGCTGGCTTGCAGAGAACTGATGCTTCTGGC
wssv-miR-N1->gi58866698:202307-202400
TTCTGCTGGCTTGCAGAGAACTGATGCTTCTGGC

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MUSCLE (3.8) multiple sequence alignment


wssv-m6->gi426202315:173896-173966
TTCCCCGGTATGTTTTTCAAGCTGCGAGTGCCCGCAAAGCCTCTCTTGCCTGGAGAGACT
wssv-m6->gi19481591:207488-207558
TTCCCCGGTATGTTTTTCAAGCTGCGAGTGCCCGCAAAGCCTCTCTTGCCTGGAGAGACT
wssv-m6->gi721172032:178523-178593
TTCCCCGGTATGTTTTTCAAGCTGCGAGTGCCCGCAAAGCCTCTCTTGCCTGGAGAGACT
wssv-m6->gi58866698:222694-222764
TTCCCCGGTATGTTTTTCAAGCTGCGAGTGCCCGCAAAGCCTCTCTTGCCTGGAGAGACT

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wssv-m6->gi426202315:173896-173966     ATAGGGGAATA
wssv-m6->gi19481591:207488-207558      ATAGGGGAATA
wssv-m6->gi721172032:178523-178593     ATAGGGGAATA
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wssv-m6->gi58866698:222694-222764      ATAGGGGAATA
                                       ***********

MUSCLE (3.8) multiple sequence alignment


wssv-m7->gi58866698:259013-259097
TTTTAATAACCATTTCATTGCATCCGGAAAGGGTAATGAAATATCATTCATCGATCCTCC
wssv-m7->gi426202315:15003-15087
TTTTAATAACCATTTCATTGCATCCGGAAAGGGTAATGAAATATCATTCATCGATCCTCC
wssv-m7->gi721172032:10394-10478
TTTTAATAACCATTTCATTGCATCCGGAAAGGGTAATGAAATATCATTCATCGATCCTCC
wssv-m7->gi19481591:288700-288784
TTTTAATAACCATTTCATTGCATCCGGAAAGGGTAATGAAATATCATTCATCGATCCTCC

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wssv-m7->gi58866698:259013-259097     GAATGAAAGGTTGTTGATGGAGATG
wssv-m7->gi426202315:15003-15087      GAATGAAAGGTTGTTGATGGAGATG
wssv-m7->gi721172032:10394-10478      GAATGAAAGGTTGTTGATGGAGATG
wssv-m7->gi19481591:288700-288784     GAATGAAAGGTTGTTGATGGAGATG
                                      *************************

MUSCLE (3.8) multiple sequence alignment


wssv-m8->gi426202315:54512-54606
TCTGGGGATTTATTAGCGTCTCTTGAGTCTTGTAGTAATTTCGTTTGCCGGGATGTGCGG
wssv-m8->gi721172032:49896-49990
TCTGGGGATTTATTAGCGTCTCTTGAGTCTTGTAGTAATTTCGTTTGCCGGGATGTGCGG
wssv-m8->gi19481591:22069-22163
TCTGGGGATTTATTAGCGTCTCTTGAGTCTTGTAGTAATTTCGTTTGCCGGGATGTGCGG
wssv-m8->gi58866698:286613-286707
TCTGGGGATTTATTAGCGTCTCTTGAGTCTTGTAGTAATTTCGTTTGCCGGGATGTGCGG

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wssv-m8->gi426202315:54512-54606
TACTATTTTTATAGAGGACGTTTTTAAATTTCAAA
wssv-m8->gi721172032:49896-49990
TACTATTTTTATAGAGGACGTTTTTAAATTTCAAA
wssv-m8->gi19481591:22069-22163
TACTATTTTTATAGAGGACGTTTTTAAATTTCAAA
wssv-m8->gi58866698:286613-286707
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TACTATTTTTATAGAGGACGTTTTTAAATTTCAAA

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MUSCLE (3.8) multiple sequence alignment

wssv-m9->gi721172032:251521-251611
GGCGGTGCTTTTCCTCCCACCTCTCCATTATTCTTCTTTAGTCTCTTCATGGGCCTAAGA
wssv-m9->gi426202315:246894-246984
GGCGGTGCTTTTCCTCCCACCTCTCCATTATTCTTCTTTAGTCTCTTCATGGGCCTAAGA
wssv-m9->gi58866698:2652-2742
GGCGGTGCTTTTCCTCCCACCTCTCCATTATTCTTCTTTAGTCTCTTCATGGGCCTAAGA
wssv-m9->gi19481591:281516-281606
GGCGGTGCTTTTCCTCCCACCTCTCCATTATTCTTCTTTAGTCTCTTCATGGGCCTAAGA

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wssv-m9->gi721172032:251521-251611
GAATAAGGAGAATCTGAGGGAGGGGATCGGC
wssv-m9->gi426202315:246894-246984
GAATAAGGAGAATCTGAGGGAGGGGATCGGC
wssv-m9->gi58866698:2652-2742
GAATAAGGAGAATCTGAGGGAGGGGATCGGC
wssv-m9->gi19481591:281516-281606
GAATAAGGAGAATCTGAGGGAGGGGATCGGC
****
MUSCLE (3.8) multiple sequence alignment

wssv-m10->gi721172032:252819-252885
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wssv-m10->gi58866698:3950-4016
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wssv-m10->gi721172032:252819-252885 TCATCAC
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wssv-m10->gi426202315:248192-248258     TCATCAC
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MUSCLE (3.8) multiple sequence alignment

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GCTGGGAGTCTAGGTTTCTTCCCATTCTTGTTACCCCAGCTCTTGTCCAGATCAGGGTTA
wssv-m11->gi721172032:257200-257294
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MUSCLE (3.8) multiple sequence alignment

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wssv-m12->gi426202315:150367-150466
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wssv-m12->gi19481591:118951-119050
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Text S3

WSSV primary miRNA (pri-miRNA) sequences.

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