Electronic Supplementary Material

De novo transcriptome analysis of *Spodoptera exigua* multiple nucleopolyhedrovirus (SeMNPV) genes in latently infected Se301 cells

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Table S1. Names and sequences of the primers used for the RT-PCR and 5'/3' RACE-PCR

Primer	Sequence (5'-3')	Genome site (nt)	Product size (bp)
RT-PCR			
se5-F	GCCTCTGCTATCGTTGCT	6832–6849	858
se5-R	CTGATCGGTGGTTTCTCC	7689–7672	
se7-F	GAGGAGATACGAGGTGATG	9674–9692	753
se7-R	TTTCCAAACTTTAGTGCC	10426–10409	
se8-F	CGCCAAAGACATAGTCCA	12557–12574	1736
se8-R	GCGTCAACATTGCCATTA	14292–14275	
se12-F	TATAGCGTTCTGTTTAGCG	16124–16142	557
se12-R	ATTGGATTGGTGCCTTTG	16680–16663	
se43-F	TCAGCGTCAATAGACTCAT	43066–43084	651
se43-R	CGAAGCGATTCATAAAGTA	43716–43698	
se45-F	ACGACGACTTTACCCAGAA	44523–44541	656
se45-R	ATCGGCGACAAACTCAAT	45178–45161	
se89-F	ACCAACGCCGATTGTCTG	86155–86138	566
se89-R	GTGCGGTGGGCATCTTCA	85590–85607	
se90-F	AGGGACCGTGTCGAAGTA	86765–86748	301
se90-R	CTGCCACCGTCAATAGGA	86465–86482	
se124-F	GGTTGGGTGACGTGATAC	118937–118954	413
se124-R	GTCGCTACATTCGTAGTTGT	119349–119330	
se126-F	TGGGATACTCAAGCCTAAA	121203–121221	533
se126-R	TCTCGCTCACCTTCTTATT	121737–121756	

Primer	Sequence (5'-3')	Genome site (nt)	Product size (bp)
RACE-PCR		–	–
GSP-*se5*-F	CAAGAGGAGCCCTGGAAC	–	–
GSP-*se5*-R	GTGGAGGTAGAATACGGC	–	–
GSP-*se7*-F	GAGGAGATACGAGGTGATG	–	–
GSP-*se7*-R	CCGTGATTTCAAACCTTT	–	–
GSP-*se8*-F	CGCCAAAGACATAGTCCA	–	–
GSP-*se8*-R	ATTACCGTTACAACTGCG	–	–
GSP-*se12*-F	AGCGACATACCGTTGCAAGT	–	–
GSP-*se12*-R	GGCGATGTACGCGTTGAAAA	–	–
GSP-*se43*-F	CACCTTCGCCCTCAACAGAT	–	–
GSP-*se43*-R	AGCGCGTACAGAATGCTCTT	–	–
GSP-*se45*-F	TGTCTGCCGCACGAAAAGTA	–	–
GSP-*se45*-R	CTAAACGTCAGTCCGGGCAT	–	–
GSP-*se89*-F	CCGGCCAGTTTGCCAAATAC	–	–
GSP-*se89*-R	TCGTTTCCGCTAACGTCGAA	–	–
GSP-*se124*-F	CCAAAATCCCGACGACAACG	–	–
GSP-*se124*-R	GGTCGCGCATCATCATCAAC	–	–
GSP-*se126*-F	CGTTTCTGCGCGAATCTCTG	–	–
GSP-*se126*-R	TTGATCGCGAGCGAATACGA	–	–
NGSP-*se5*-F	TGATTTCGATGGCCTACCCG	–	–
NGSP-*se5*-R	TTTCCGGTCTGTCATCAGGC	–	–
NGSP-*se7*-F	AGCGCAGAACCGTATGTCAA	–	–
NGSP-*se7*-R	TCTCGTCTCGGTGACCGTAT	–	–
NGSP-*se8*-F	GTGCCGCATGAGCGATAAAG	–	–
NGSP-*se8*-R	TCGCTTTCGAACCTACCCAC	–	–
NGSP-*se12*-F	GAAGCGTTGACGCCGAAAAA	–	–
NGSP-*se12*-R	GCGCGGACGAACTTGAAAAT	–	–
NGSP-*se43*-F	GATTGCAGCCGTTCAAGAGC	–	–
NGSP-*se43*-R	CCCAAGGTGTACGTGTCGAT	–	–
NGSP-*se45*-F	CAGGCGTTGGATTGCATGTG	–	–
NGSP-*se45*-R	TTGACTATACTGTCGGCGGC	–	–
NGSP-*se89*-F	GGCGTCACCTTACGAGACAA	–	–
NGSP-*se89*-R	TGTCGAAGCAGCCGTACATT	–	–
NGSP-*se124*-F	CCGCCGTTAAACAACCATCG	–	–
NGSP-*se124*-R	TCTCCAAGACGACACTCCCA	–	–
NGSP-*se126*-F	GAGCATTCGTTGGTCGAAGC	–	–
NGSP-*se126*-R	AGAACTTGCGCACAAACGTC	–	–

Table S2. Statistical results of the stringent filtering processes

Cell line	Raw reads	Quality trimmed	Adaptor trimmed	rRNA trimmed	Clean ratio
P8-Se301-C1	54,569,296	54,292,372	53,666,292	52,784,058	96.7%
Se301	56,865,504	56,639,360	55,941,000	55,033,958	96.8%

Table S3. Statistical results concerning the primary unigenes from P8-Se301-C1 and Se301 cells

Cell line	Counts	Total length (nt)	N50 (nt)	Mean length	N%	GC%
P8-Se301-C1	116,048	136,121,302	2,137	1,173	0.0	37.5
Se301	104,600	122,303,958	2,145	1,169	0.0	37.6

Table S4. Statistical results concerning the final unigenes from P8-Se301-C1 and Se301 cells

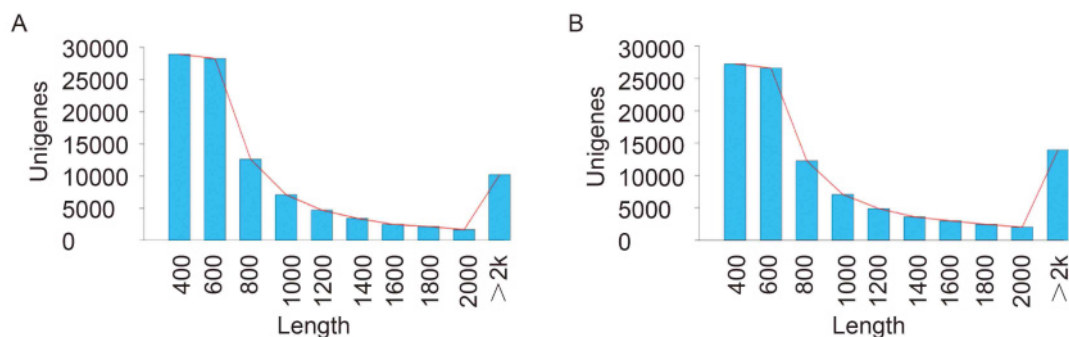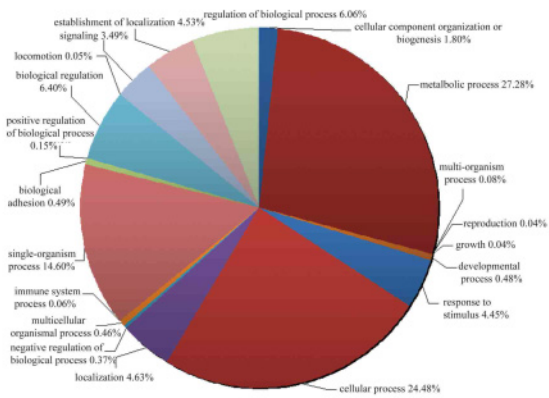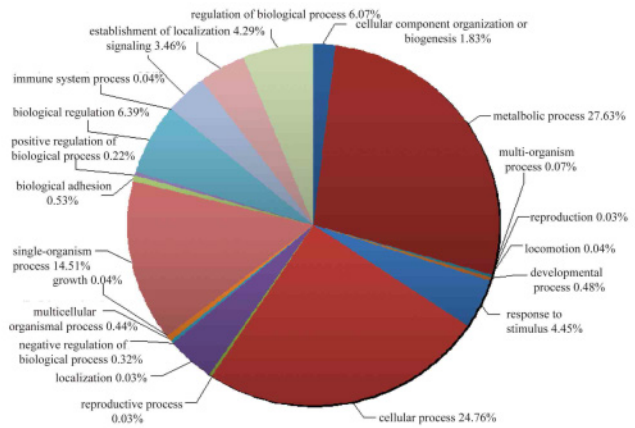| Cell line	Counts	Total length (nt)	N50 (nt)	Mean length	N%	GC%
P8-Se301-C1	112,565	121,964,401	1,824	1,093	0.0	37.3
Se301	102,996	109,124,144	1,803	1,082	0.0	37.4

Figure S1. (A) The distribution of the lengths of the final unigenes from P8-Se301-C1 cells. (B) The distribution of the lengths of the final unigenes from Se301 cells.
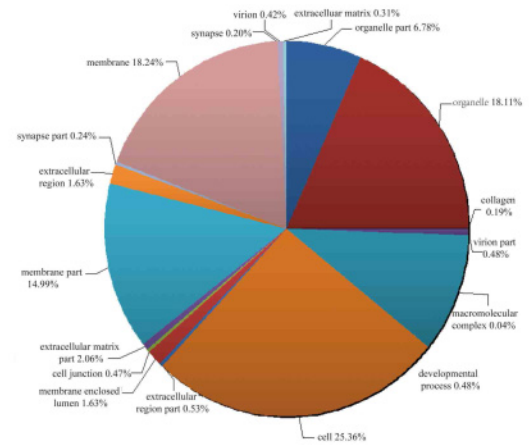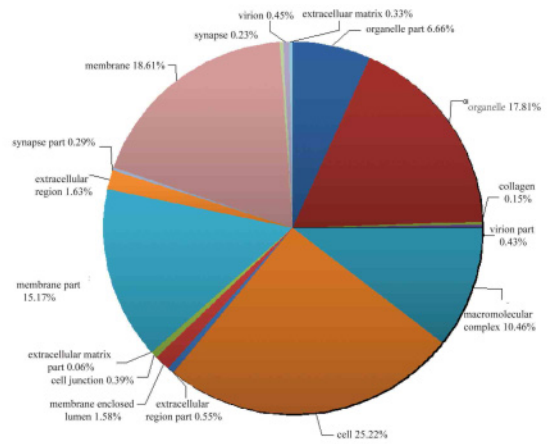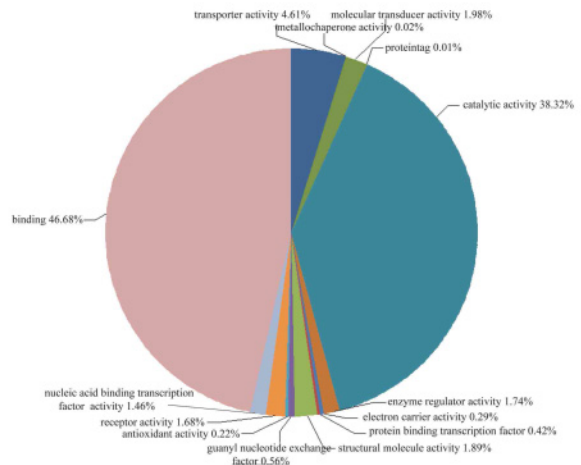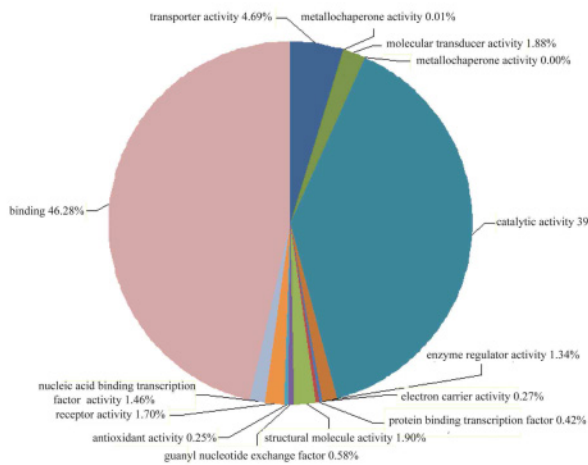
Figure S2. Gene ontology (GO) classification, including cellular components, biological processes, and molecular functions.

A

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1     TTTAATACGACTCACTATAGGGCAAGCAGTGGTATCAACGCAGAGTACAT 50
      Bombyx mori akh2 mRNA for adipokinetic hormone-2 (nt 26-71)
51    GGGGAGTTCGACGTCGTTGAACATATTCCTTCAACACTTGTAGCTAATCA 100
101   TCAATATGGTTAACGATTCCAGAAACACTGATATCATCGACGCTGTCGTC 150
      se5 (SeMNPV nt 6190-7713 )
151   GCCGCCGCCGCCGAGCCTGAACCTCCTCAAAGCAGCGAGCCAATGCAGTA 200
201   CGACGATGATACACAAGTCATCAATCAACGCTCTGAAGACCGATTCCAAG 250
251   AGGAGCCCTGGAACGAGCGGTTGCAAGAAGATTTCGAGTACGAGCGTCAC 300
301   CAGCGGGAACGTCGTCAACAGCATCGAGATCGTCGTATGAGACAACAGAG 350
351   TGAGTTACGTGATCAAATTAGATTGATAAATAAACGACATGGTGAAATAT 400
401   GTGAGTTTTATCGTGTAATGTCGGGATTTATGCAGCATACACTAAAGAAA 450
451   AATGGGCGCATTATACAAAAACTCGCCATAGAACACTATATTCCAAATGA 500
501   TAATACATATTCACGAACACGACCATTACGGTCTCCTCCTAGATCACGAT 550
551   CTTCATCTAGGATCTTCGATTCTCCTAAATTTAATTATTCCGACGACGAC 600
601   GACCGACGACAACGTcCGATAATGATGTAATTGAAAATACTCCTGATGAA 650
651   ACTACTATTGCCGCCGACGTCGATGCCCCTGCCGACGTCGATGCTTCTGC 700
701   CCGACGTCGATGCCGATGTCGACATCGATGCCGATGCCGATGCATCTGCC 750
751   TCTGCTATCGTTGCTGAAATCAATGCTATTGCTGACGCCGCAGCCAATGC 800
801   GACGACGACAACAGTTGGTGAGGATTTGTTTGCCGCTGATTCTGATTTTA 850
851   ATTATTATTCTGATTCGGATGATGATTTTGATGTTGAAGAATTCAAGACA 900
901   AAAGTTGATAATGCTATTAGACGTTTAGCTATATTCTTTGAAAAACATCA 950
951   AAATGTTATTTTGAATCAGTACGCTATCAACAAAGATTTTTATGTGAATT 1000
1001  ACACTAATGAATTTGACGTTCGCTATTACAATCATTGCGTTGCGAACATG 1050
1051  CATTCCGATTGGATAGACATGTTTGATTTCGATGGCCTACCCGTCAACGT 1100
1101  GGATAATACAAATATGGCACACGAACAATGGAATGTGATATTTTATGAAA 1150
1151  TGTTGGAAATACATCCATGTAATCCTACCGACTCTTTGAAAAAGATATTC 1200
1201  GATTCAATTGTAAAGAATATTGTTACGCAGTTGGAGGAATTTTGCTATGT 1250
1251  TTACAATAATAAAATAATAAAAATTGTACGTGAAATTAACAAACCATTTA 1300
1301  ATATAGACGTGCTATTGAATGGCATTGAAATTTCCGCAGACAATGTTCGT 1350
1351  AAAACCGAAGAAGGTGTTAAAAATTTGTTTATGGATTCCATTTACTGTTC 1400
1401  ACGTTTTCAACAACAGCAGCAGGAGCATCAGCAGCAGCAGCAGGAGGAGG 1450
1451  TTGTGCCTGATGACAGACCGGAAACTCCACCTCCATCTTATGCCGCTGCA 1500
1501  ATGGCTGTCGCTGCTGATGCCACTGTTAGCATGAAATATATTCGTCGTCA 1550
1551  AATTAGATCATCTATGCGTCGTGAACGCAATCGCGACGGAGAAACCACCG 1600
1601  ATGACGAAGATCAAACAACAGCTGATGCATAATAATTTTTATTGTATTAT 1650
1651  CGATAGTATTAACAATTGTATTATGTTTTTGTATTAATAAATTTTTTTTT 1700
1701  ATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAATTCCCCCGTGTTATCCAC 1750
1751  CCGGCCTCACCAAAGAAGGGGGAACGAAGGGGGGGGGCCAAAAAAAAAA 1800
1801  CCTGCGAGGGGAAGACAAAAAGATCAATTTTGGTTTTAGCTAAAAGA     1847
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B

1	CAGGCAATAGCAGAGTCTTGGCGACTCACTATAGGGCAGCAGTGGTATCA 50
51	ACGCAGAGTCTATGCCACTATCTTCTTGTTGTCGTTGTGCGCTCTTTTTC 100
101	AATCAAGCGATACGCAATATACGTGGGAGTGTAAAATGATGAAGAAAACG 150

se7 (SeMNPV nt 9261-10433)

151	ACGACAACTACAGTAATTTGGTCGTGGAAAAAAAAGGTGTCGGCAAGGGT 200
201	GAACCCCAATCGCGACGACAACAATTCAAAGTTTAAAGATTTGGGGGGGC 250
251	GTTTTCTCAGCAATCAAATTTTTCAGCTGAAAAAATACGTTCTTCGTTTT 300
301	CCCACCAACTATGGGCATAGGCACCTATTCTTCAACTTTCTGAAAGAGAT 350
351	GGAGTGTACCGTCCTCAAGTACGGCGAAGTCGAGCGCAGAACCGTATGTC 400
401	AAGGAGGATGCGGTAAAAAGTTTACCGGCGGTAATAAACTTTTGTTCTGT 450
451	GTCATAGACAACAATGGAACCGACGACGACGTCGACGATGGGCAATATGA 500
501	AAAATTCAAAGTCGTGTGTCACGTTTGTTCAAACGATTACGCTTACAAGA 550
551	GGAGATACGAGGTGATGCAATTGTTTCCCACCGTTTCGTTGAGCGTCGTC 600
601	GAACGTTTGTGTGAGGTCGGTTTCATTACTAAATACATTTTTCCCATCGA 650
651	TCTCGAGTATACGGTCACCGAGACGAGAACCGAGGTTTGCAACTAATCCA 700
701	CAATTTCTACAAGATGGTCAAGTCGATCATTCGCGAAAAGAAAACCAACG 750
751	AACACATTACTGAAATTAAATTGAGTACGTACGGCCGCGATCTCTTTATC 800
801	GAAACCGACGAGAATTGTGCCATGAGGAACGGCCAAAACGAGTACAATGA 850
851	GCACGTTTACGAACTCGAATTTCATCCGTCGCCTAGCACTATGATCCCGT 900
901	TTGTTCAGACGTACGCCGAGAAAAAACCCCTCACCTACTTCTACACGGTC 950
951	ACTAAACGTGTCTATCTCAGCTTTTTCGATTATGCCGTATGTTTTCCCAT 1000
1001	AAAATGTATAAACTATTGCAAAATGTGCAAACAGGACAAACTATACTTTA 1050
1051	AAATCAATCCCGTGCTCTACTGCAGCAAATGCGGATTTACCGATGCGAGC 1100
1101	TTCTTCAAAAACGCCCCCTTTCTCAAGAATACAGTGTTTTTGGCCAAATG 1150
1151	CGTCAAAGCTAAAACACTACCGCCAACTCGCATCTACTATTATGACATGA 1200
1201	ACCTATACAAATCGTACATGAACAAAGCATCTTTGTCATCGTCACCTACG 1250
1251	GCGTCTAAAAATAAGTTATTCGATTTCAAGCCAAAGGCACTAAAGTTTGG 1300
1301	AAAAATTTAATTGTCGTATATCTGTCAATGTTATATTGTATCTTGTAACT 1350
1351	GCACTCGAATTATATGAATATTAACAAAAAAAAAAAAAAAAAAAAAAAAA 1400

Bombyx mori dh40 mRNA for diuretic hormone 40 (nt 3116-3192)

1401	AAGTACTCTGCGTTGATCCACTGCTTGCCCTATAGTGAGTCGTATTAGGA 1450
1451	ATTCACTGGCCGTCGTTTTCAACGTCGTGACTGGGAAAACCTTGGCGTTA 1500
1501	CCCAATAAAAAAAAAAAAAAAAAAAAAAAAAA 1530

C

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1     GATAAAACGAGTCTAATACGGACTCACTATAGGGCAAGCAGTGGTATCAA 50
           Bombyx mori dh40 mRNA for diuretic hormone 40 (nt 1035-988)

51    CGCAGAGTACATGGGGAGTCTTGACTACGAAGAGAACCGAGTCGCAAGCA 100

101   AAATATGCTGCGTTTTAAAGTGATTGTGTGGCTGGTGGCGGCGTTGACGG 150
           se8 (SeMNPV nt 12498-14495)

151   TCGAGGCTAAATTCGCCAAAGACATAGTCCAAGTTACGCCGCTGCCTTCA 200

201   ACGTCGGGTCTATACTTTCAATACATAAACCGAATGCAGTTTGTACAAAA 250

251   CATTTGGCATTTTGTCATCGAAATGGACCACGGATCGGTGTTCTATCGCC 300

301   TTCAAAGTATTCATCAGCAGGCGCAAAAATTGCAGCAGAGTTTCATTTCG 350

351   CTGCGACAAAACCAGACCAGCGCCTTCGACGACTGCGCCAACGTCAAGTA 400

401   TCTCAAACTCGAGATCGATCACATGCTTAGCACGGTCATACCGAATCTAG 450

451   CGCAGCAGCACAATTTGCTCGATCAAAAAGTACCTCTGACTCCGTCGAAT 500

501   GCCACTTTGACGAAAGCTACGCTATCTCCGACGAAAAGACGCTCTAAACG 550

551   CGGCCTTTTTAATTTTATGGGACACGTCGACAAATATCTGTTTGGCATTA 600

601   TGGACAGCGACGACGCTCACGAACTGCACATGCTCGCCAACACCACAAAT 650

651   AGTTTAAACTCTCAAGTCAAACAGTTGAACGACGAACTTATTGTTCTAGC 700

701   CGATTATGTGGACCACGAGTTTCACGCCAGCCGTATGCGCGACGCGGACA 750

751   AGCAATGTAGGTACATCATCGAAAACTATAACATTCTATGCAAGCAACTG 800

801   GACGAGGTGGCCACGCTATACAATAAACTCGATTTGGCCGTCGATAATGC 850

851   TAAACTCAACCATCTCAATTCGTTTGTGGTCTCGCCCGAACGTCTCCTCA 900

901   ACGAAATGAACAATGTGAGCGGCCACCTGGCAGGCCTTTCGTGGCCCGTG 950

951   CCTCTCACCGAAAAAGCGATGCACGTTCTCATCGACAACGTCATCAATGT 1000

1001  GCATGTGTTTGTCACGGCGGAACGTAAATTGTTGTTCATCATCGAAGTGC 1050

1051  CTTTGGTCAGCAGCGAAGCGTTTGACGTGTTTCACAGCATACCGCTGCCG 1100

1101  TATTGCGACAAATCGCACAAATGCGCCATCATGTTGCCGGACAGCAAGTA 1150

1151  TCTCGGTGTGTCGGTGGATCGACGAAACTATGTGCGTTTGGACGACACGA 1200

1201  CTTCGTGCCGCATGAGCGATAAAGTCATGTTGTGTTTCAGACCTCAAATT 1250

1251  ATATACGACGTAAATCAGGCAAAGTTGTGCGACGTCCGCATCTTTATGAA 1300

1301  GAATGACAAGGACATTGATTATAAAAGAGACTGCGACGTCAGAGTGGGTA 1350

1351  GGTTCGAAAGCGAACTCTTTTACGCCACCTCCGACTATAACAATTGGCTC 1400

1401  TATGTCCTGCAGAATGACATTGATTTAAACATTCAGTGTATACCGTCGGC 1450

1451  GACGATTACGGATGGTTTTGGCATTGCGCCCGTCGTGTTGCGCGCCGGCG 1500

1501  TGGGCATAATTCACGCGACCGGCAATGACAACTGTAAACTTACCACCAAA 1550

1551  AAGTCGCGATTGACGGTGCACGATCTGTACAATAACCTCAACACTGTCAT 1600

1601  CGAAATACCCATGGGTCTATCGTACAACTTTACCGTGGCTCTACAGGATA 1650

1651  TCGATAAAATTTCCGTCGACGATATGAAAATTAACAACGATCTCGAACAT 1700

1701  ACAAATCTTCACGAACTGACCAGCCGCCTATACGATTTGCGGAGACGCAT 1750

1751  CAACAATAATACCGTCTTTTCGGGCAGTCAGGTTGTCGACGACAACGGCG 1800

1801  ACATATTCGCCGGCATGTCTTCGTGGTTTTCCAGCATCGGTATCGATTTT 1850

1851  CATTACGTAAAGATTGTAATGATCTGGATAGTAATGGCAATGTTGACGCT 1900

1901  GGCCACCGTTAAAATTTACCGCACTTGTTGTAGTGGCGCGTGCAGCACTT 1950

1951  TGTGTAATAATTTTAAAATTTGTAGAGGCAGCGAACACACGGTCGTGAGA 2000

2001  CGCGAAGACAGGGACATGTATTATCAGACCACGCTGCCAAAGTATAAACG 2050

2051  CGGCAAGAAACACGTCGACTCCATCTTTGACATGGAAATGGAACCCATGT 2100

2101  AACCGATTGATTGTAATAGTACTAGAGTAAAAGAAG                 2136
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D

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  1  TCTAAATACGACTCACTATAGGGCAAGCAGTGGTATCAACGCAGAGTACA  50
         Bombyx mori akh2 mRNA for adipokinetic hormone-2 (nt 27-71)
 51  TGGGGACAAACAATTGGTGTGACGACAGCGTCGTCGTGACCTCTAATGAG  100
              se11 (SeMNPV nt 15817- 15852)
101  GCTCCCGTTTTATATGGCTCACTTTAGGGCAAGCAGTGGTATCAACGCAG  150

151  AGTGCATGGGGAGTCGGCGATCGATCACAACCTGTGCGAACGCATCAGAT  200
              se11 (SeMNPV nt 15923-16101)
201  CTTCGATCGATACCAACGTCTATTACTCCACACCTCGATACAACATTGGC  250

251  AGTACTGTCACCAAAACTCTACTCAACAACAACAACAACAACAACAACAA  300

301  TGCCACCGTTGCTGTCGTGGACACCGTCAAATATTGACGATATTGACAAG  350
              se12 (SeMNPV nt 16064-16693)
351  AACGCGGAATATAGCGTTCTGTTTAGCGACATACCGTTGCAAGTGACATG  400

401  TCTCACTCCTTTCATCGACAACGGACTGCGCGTCAAGATCAACGGTCATC  450

451  GTTTGTATTATTTGATTAAAAATAAAGATCAATACGCCGAAGCGTTGACG  500

501  CCGAAAAACAACAAATGGTCATTGGAATTATATATACAAAAGTCACAAGA  550

551  ATGTGTGCTTTCAAAACGTTTCGAGCATAAATAACGTCGTTGACATTTTA  600

601  AAGACCAAGCTGAACATGCCCGACTGCATGCAAAGATTCTTGGCCGATTT  650

651  TCAAGTTCGTCCGCGCGGCAAACGTTTTCGCAAACGTTTCATTTTCAACG  700

701  CGTACATCGCCAACGTGATCACTTGCACCAAATGCAACAAACTGTGTCTC  750

751  GTAAAGGCCATGAGTTACATATACGGCTTCGATGAAAGTGTGTACAGGA  800

801  ATTCGACAGACTCTTGTTCCGAAACGACACTCTTTACAAGCCGCCCAACT  850

851  GCGAGAACATCAAGAACAAAGACAAGTTATGTTTTAAATCGGGCACATGC  900

901  AAAGGCACCAATCCAATTTGTAACTTTTAATAAAATACATTTTAAAAACA  950

951  AAAAAAAAAAAAAAAAAAAAAAAAAAAA                        978
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E

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  51  GCGTGTTGATGGTGCATTGTATGCTATCGCCGTCGCTGTTGTTCGCTAAA 100
          se42 (SeMNPV nt  42392-42606)
 101  TAAGACAGAACAAAGTCTAAAACACGTCGTCGATTGAACAGCATGCGTTC 150
 151  CAATTGTATAATTTTATCGAAAGCATATGCGACGGTGTTGAAAGCGGCGC 200
 201  TATCGTTGAAACTGCTCTTTATGATTCGAAATCATAGAGCCTGAAACATC 250
 251  TGCTGTGCATTGAACTTGGACGTATCCACTAGATTGTTGATATTTAAGAT 300
 301  CACGTTGAGTAATTGGTTTGGATTTTTCGGTTTGATAAAATTCATTATCA 350
 351  TGGAATCGCTGCAGCAACGTCTCTTCAAACACAAATCAATCCCTTACATT 400
          se43 (SeMNPV nt 42696-43856)
 401  TCTAAAAAATACATCAACGACCAACTCGGCGAGTACGTACTACGCAACAC 450
 451  CACCGACCATTTTCATCGGGCCATCCTGCCGCAAGCCGTGCTAGCGCTCG 500
 501  ACACGCTGTGCGTAGTCAAAGGCGGCGCCGCGATCGCTGTCCACATGAAA 550
 551  AACGGTCAACCTCGTCATCTCATCGACTTCGATCTTGAGGTGTACGCCGA 600
 601  CGACAAACGCATCACCGTCAACAATCTTCACTCGTTTATCGCTCTGCAAG 650
 651  CGCTCGAAGAGAAACTAAAAACTGTATGCGAAAAGTTTTACAATGATATC 700
 701  GACGAAACATTGGCCACCGTCAGCGTCAATAGACTCATGAACAACAACTA 750
 751  TGTGCGAAACAATATGATAATTTTTAAATCGTACGTCAACGAAGCCGTCG 800
 801  AAGTGATGCCCGACAACGTCACCTTCGCCCTCAACAGATTGCAGCCGTTT 850
 851  AAGAGCACCGTGTCGATGGTCAACGACGACTACTTTTTGGTCCGATATTC 900
 901  ATTTAACGTTCACATGAAGAGCGATTTGTCGCCGATGTGGCTGTACAAGG 1000
1001  AAAAAAATCGCGTATCGAGTCTACAATTCTTACCTTTGGACGTGTACTTT 1050
1051  TTGGATCTGAGCGTGAAACGTTCGCCCACGCCCCCCATCGACACGTACAC 1100
1101  CTTGGGCAACATTTACGGCATCGACGTGTACGTCGAGGACGTCAAGTATC 1150
1151  TCATAGCCGATCAGCTCGAGTGTATACTTTTCAATGTATTCAACTATTGT 1200
1201  TGGACCAAAGTCGACAGTAGAATCGATAGATTGTACAACCTAATCTCAAT 1250
1251   ACACAAAACGATTATTTCCAACCCACCGACAAGGAAACGGAGCGTTTCG 1300
1301  AAGAAATCATCAAACTCTCAAAGCAACGCTATACACTGCGCGACGTGAAG 1350
1351  AGCTTTTCTGTCGCGCTCGGGGCGCCTCGGGCCTAAACCGTCATCCAATT 1400
1401  TATCTTTATGAATCGCTTCGACAACCACGTCAAGTACGTGACCCATCAAA 1450
1451  TCAACTTTCCCCAACGTCCATGGGAGTGTGAATATTTTTCGAAATGTTGG 1500
1501  AAACAATTTTTGTACATCATTAACATTTATGTACAATCTGGATATAAAAT 1550
1551  TGAATTTTAAAAAAAAACCAAGATGTACTTGATAAAAAACGTCGGCGCTTT 1600
1601  CTGCTTGCCCTGTGCGCGCGGCCTATTGCACTTTTGATGGTTCACCCTTT 1650
1651  GGATTCATTATGTATATCGTCGTTGAACCATCGAACAACGA          1691
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F
1   ACCTAAATTTTAAATGGCTCCCTATTTGGGAAACACAGGGGTCTAAACCG 50

51   AGTACACGGGGGTACAGTATTAAAGTGTAATCAATCTAGAATACAACACT 100
       se44 (SeMNPV nt 44305-44312)

101   ATCATCAATACAAATATGTCTGCCGCACGAAAAGTACTGTTTCCCATCCA 150

151   ACACATTGATCTGTGGGCTTCTTATAAACAGGCGTTGGATTGCATGTGGA 200
       se45 (SeMNPV nt 44408-45394)

201   AAGTGGAAGAGGTGGATCTATCCAAAGACTACGACGACTTTACCCAGAAG 250

251   CTCACCGACAACGAGCGCAACTTTATCGAGAAAATTTTGGCCTTTTTCGC 300

301   CGCCGCCGACAGTATAGTCAACATCAACATCATAGAGCATATGCAACGCA 350

351   CCGTGCCCGAACTGGAGGCGCAATACTTTTACAATCAACAGGTGCTCATC 400

401   GAATGTATTCACACGGAAATGTACAATCTTCTCATACACGCTTTGATTAA 450

451   AGACGAAAGAAACAAGAGATGCTTTTGAATGGTTTCGAGAATATGCCCT 500

501   GCGTGCGCAGAAAGGCCGAATGGGCGATGAAGTATATTGACGATGAAAAG 550

551   ATAACTTTGGCCGAACGATTGGTCGCATTCGCCATTGTCGAAGGAGTGTT 600

601   CTTTTCGGGGAGTTTTGCGGCGATATTTTACATGAAAACCAAGGGAGTGA 650

651   TGCCCGGACTGACGTTTAGCAACGAATTGATTTCGAGAGACGAAGGTCTG 700

701   CACACCAACTTTGCCTGCCTCTACTATAATACGAGAGTCGATCAAAAGTT 750

751   GGACGCGCCCACCGTCAACGACATGTTCTCCGAAGCCGTGGCCATCGAGA 800

801   TGGAATTTTTTGCTGAGGCTCTGCCCGAATCGTTGGTGGGAATGAACGCG 850

851   AATATGATGAGAAAGTACATTGAGTTTGTCGCCGATCGTCTTCTCGTCCA 900

901   GTTAAAGTATCCCAAGATGTACTATACTGAGAACCCATTCGAGTTTATGA 950

951   ACAATATTTCGTTGGAGGGCAAAACTAATTTTTTTTGAGAAACGCGTCGGC 1000

1001   GAATACAAGCGTTTCGGCGCCGGCGAAGACAAATTTCAATTGTTGGAAGA 1050

1051   CTTTTAATAGAAATGAAGAAAGGATTATTGTATATTTTGTATTTGAGTAA 1100

1101   TAAAGAAATTTACATGTA   1118

G

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1     CGAGTTCAGGTTAGACATAGTTCGTTCCCCAAATTTTAGAAGCGGAAAGG 50

51    ATTGCGTTTGAGTGACCAGTTTGGAGCGAGCTAATGAAGCCGTGTATAAT 100
            se88 (SeMNPV nt 85088-85799 )
101   ACCCGTACGATCTTCGATCGGCCTTCCAGTTGGACGATGACCAAATATGA 150

151   CACGATGAGCAGCCGAATTTCAAATGTTTTACCATAATAGTAGAAACCGT 200

201   TCTTGGCGAGCGTCTCGCGATTGTCCCTGTAGTGTGTACGTGAAGTTTTA 250

251   AATATGAGAAAGGATTGTTTGCGTAGCGCTTCGTTTACGAAATAGCCGCT 300

301   CGGTGGCCATGGGACACGTCGAGAACGTATGATACTTGAGGCGACGTGCG 350

351   TCGAGCTTTTTGATGTATAGCGAACAATATGCGCATTTGTAATTGCATAA 400

401   CGCGTCTCGGTAGATACCCCCGGCGACGAGATCGTCGATGTATTCTCGAG 450

451   TCAGGCAACTGTTTTCAAAGGTTTCGAGGCGATCGCGCGGATCCTGATAG 500
            se89 (SeMNPV nt 85499-86398 )
501   AATCCCGGCGGGGCCAAGTCGTACGTTTTCCAATTTCTCACGGCGAGCAT 550

551   CGGCGGTGCGGTGGGCATCTTCAAGAATGCAAAGCAATTGTTCGAGCGCT 600

601   CGTATTTGTTTGTGGGCAAAGTGTCGAGTGCGCGCGTCGAATTTGCGCCC 650

651   CTTTTCGACGACGATGCCATCGGCCAATTTTCCTTTGCAAACTAAATACT 700

701   TTTCAGAGTTTGCGGCTCGAGAATGCGCCGGTTTGTATATGGCGAATTCG 750

751   TTAAAGTGCGAAACGAAATCTTGGAGAAGACTTATTGTTGAGCGTTCGAA 800

801   CGTATCGAAAATTTTCAAGACACAATTGCCGCCGGCGCGCAAGGCATCCA 850

851   CGTAATATACGAACACTCTTTGCGTATTAGATTGTACGAACAGACGATTC 900

901   CTGATCGTTTTCGTTTCCGCTAACGTCGAATGCGCCGTCGGCGACGACCA 950

951   GATCACACTTGTTCCTGCAAAAGTACATCAATTCGAATAGCACGTTGGCG 1000

1001  TCGAAAATGTTGCCCGTGTCGAAGCAGCCGTACATTTTTCTAAAATTGGG 1050

1051  ATGGTCAAAGTTGTAATCGCAATCGTTGTCTCGTAAGGTGACGCCGTAGC 1100

1101  CCAGACAATCGGCGTTGGTGTCAAATATGTATTTGGCAAACTGGCCGGGG 1150

1151  CCTCCGCACAGATCGAGGAACACGTTCACGTTGCGACACAATTGAAACTT 1200

1201  GTCGTCAATGTCTCGCATCTTGAAATAGCATCGATTACGTACGTGCTGTC 1250

1251  CCCGTTCTAAAGTTTGTCGAGCGCGTCGTATGTCGCGTACGTCATACTCG 1300

1301  TTCAATTTATCCTTTAACGCGTTCAATTGTTTTTTTCAAATCCGTCAATCC 1350

1351  TTTATCTTCCATTGTTTATG                                 1370
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   1   CATCTAATACGACTCACTATAGGGCAAGCAGTGGTATCAACGCAGAGTAC 50
               Bombyx mori akh2 mRNA for adipokinetic hormone-2 (nt 2-71)

  51   ATGGGGATATTCAAAGCGGACAGCGTACCAGTAGGTCGATTCATCGCTTT 100
                    se90 (SeMNPV nt 86521-86789)

 101   GTTCAAATTATCGTTGGTGATCAATAGAGTTTTATCTTTGATTTCGTATA 150

 151   TCAAAGGTCGATTGTAGTCAAAGTTTTGAAAATTGGCATTGTTAATCAAT 200

 201   GTACGAAACGTGTTACTTGTCGGCGAATTAAGTAGAATATCGATCATCAA 250

 251   ATCCTTCCAAGCGTGTTCCCTGCTCTCGGGTGATACTTCGACACGGTCCC 300

 301   TGTTCAAAAGACGCCATCGAACCATGTCTTTTTCAAAATCTCTAATGAAG 350
                    se91 (SeMNPV nt 86788-86860)

 351   AATATGGCCGAGATTGAGTATGAGTCGTCGTCGTCGTCGTCGTCGTA 400

 401   TCGTCTATTAAGACGCTAGCGCAAAAATGTCAGCACAACAATTCACGGCC 450
                    se124 (SeMNPV nt 118809-119391)

 451   GATCTACAGGCTCTCATCGATCGGGTCAAGCGGCGCCAAAATCCCGACGA 500

 501   CAACGACGACGCCGCCGCCGTTAAACAACCATCGCGGTTGGGTGACGTGA 550

 551   TACAGCACCTCGGTCGCAACGGTCTGCTTTTGCAACGCAAAAAGGATGAA 600

 601   AATTTCGACATCAACGAAACCATAGACATTTCGGACGTGGCACGCGACTA 650

 651   TCTCAATCTTTTGCAAACGGAAAAGTTGAGTTCGTGCCGATTGTGCTATC 700

 701   ACAACGACGAAACGCTACGCTGCGAGTTTCACAAAAAGTACATTTTCAAC 750

 751   AAAAACCCTAAAGATCACTACGACGAATATGTGAATTTTCTCAACAGCGA 800

 801   GATGGGAGTAATCAGTTTCGTCGAACTCTATTACACGTATCTGGGAGTTG 850

 851   TCGTCTTGGAGAATTGTTTCGTTGATGATGATGCGCGACCTCACCGGATT 900

 901   CTCGTCCATTCGCGAACTATTGACGTACTACAACTACGAATGTAGCGACG 950

 951   ACGTCGACACCGTACCTTACGAAACTATGGATTGTGAATAAATCATATGA 1000

1001   TGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA              1035
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   I         1    GTATGAGAGAGAGGAGAAAGTCTGGGCGATTTCATCACCCTGAATGTGTC 50

            51    AGGAACGGGGTGTTGGGTGGGTGAGTAGCGGTACAGTTTACCGGAAAAAA 100

           101    TATGTCCGTTTTGCGGTGATACGGGGCATTTAACAAACTATTCGAATGTC 150
                      se126 (SeMNPV nt 120802-121788)
           151    TGTCGTTTCTGCGGGAATCTCTGCCCCTCGACAATTACCTCGACAGCTTT 200

           201    TTGCCCGAAGTAGCGGCCGACATTGGGATACTCAAGCCTAAAGCTCCGGC 250

           251    GGTCGTGTATCTGGTGGGCATGTTGGTGAAGGGCGGCGTCGAGCCGTTTT 300

           301    ACGTATTCGACATGGCAAAAGTTAGGAGATGCTATGAGCACACTTCGGCG 350

           351    AGTTTTTGAGCATTCGTTGGTCGAAGCAGTACATCCACAACGACGCCTAT 400

           401    GCCAATGTCATCATCAAGTACAAGGGTTTCGATTGCGATAAAATGAAGCT 450

           451    GCAAAATTCGGCGTGCGTCAATCTACCCAGCGACGATGCCGTAGgAAGAA 500

           501    AGACGACGTTTGTGCGCAAGTTCTTCGATATTAAGCATCATAACAACGAA 550

           551    AAGAACTATATGACGGGCCGCCTCATCAAGTCGGTAAAATGCGAGCCGTT 600

           601    CACTGTGAAGAGATTCAACGAATTGTTTCAGTTCGAGCAGGACAGCAAGA 650

           651    GTTCCGACGAAGTTGACATGTTGGTGGGGATACAAATTGATGGATTCAAG 700

           701    CAGGGCAAAAACGACATTGAATTCGATACATTAGTAAACAATAAGAAGGT 750

           751    GAGCGAGAAATCGTATTCGCTCGCGATCAAACCCATGGTGTTTTTCCACA 800

           801    TTGAAGAATAATATAATAAATTTAATTATTTAAATATCATGTATGTGTTT 850

           851    TATATTAACGGTAGTCATGTGGAGAAGAGATTTGGTCGGGAGTTTATTAA 900

           901    TTTCATTTGCGGTGGCAAGATCAAGCACGACATAGAGCCCGAACAATGCA 950

           951    CGAGGAAGCGTGTGGTGGTTAGATCTAGTTATGCCGCAAAAAAGTTGCTC 1000

          1001    GCCGCCAACGGCCGAGCGTTTTGGCCGGACGGCACAAAGTTTCGATGCAA 1050

          1051    ACAACTCAATAATCATCACCAACACCACCACCACCTTTATCGCCGACGAC 1100

          1101    GCGACGGCATCAAAACATCATCTTCTTTACATCATCGTGGCGGCGACGGC 1150

          1151    AATAGCGTCAACGACGACGAATTATGTTGTGACCGACGTCAAAGCAGTCC 1200
                             se127 (SeMNPV nt 121816-122307)
          1201    CGCGTTCAGCGAGGATTGGTACGATAGCACCGGCCTTCATAGACATAAACT 1250

          1251    TTGATGATGATATTAACAACGACAACGACAAGTCATATTATAACAATGAC 1300

          1301    ACCGTACAAAATTTAAACATGCGTATATAGTATAAATAAAAAATTTAAAT 1350

          1351    GTGACAAAAAAAAAAAAAAAAAAAAAAAAAAAGTACTCTGCGTTGATACC 1400
                      Bombyx mori sifa mRNA for SIFamide (nt 462-524)
          1401    ACTGCTTGCCCTAAAGGGAGC                               1421
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Figure S3. The full-length transcripts containing (A) *se5*, (B) *se7*, (C) *se8*, (D) *se12*, (E) *se43*, (F) *se45*, (G) *se89*, (H) *se124* and (I) *se126*. The sequences that align to the SeMNPV genome are presented in blue and the sequences that align with the host genome are presented in black.