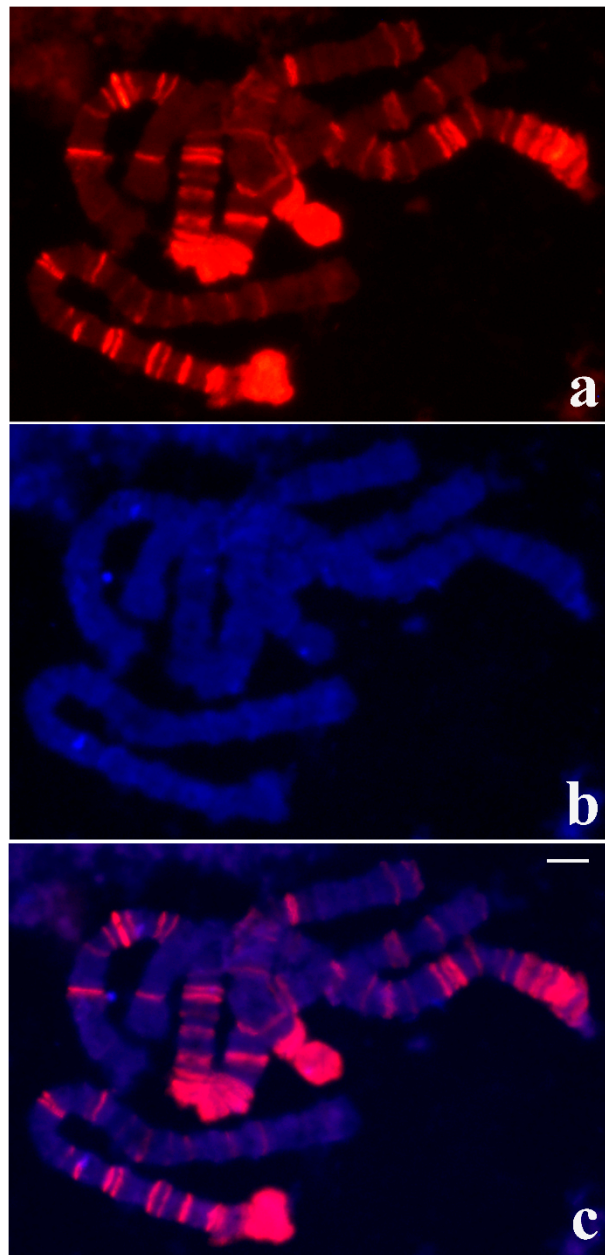


Supplementary Figure S3. Localization of phage 2 probe from the screening of the genomic library of *T. pubescens* in chromosomes of *R. americana*. Hybridization detection was made with alkaline

phosphatase and the chromosomes photographed under bright field. Heterochromatic ends identified in the figure correspond to the regions containing more intense hybridization signals.



Supplementary Figure S4. Localization of pTp-1 probe in *T. pubescens* chromosomes. (a) hybridization signals, (b) chromosomes stained with DAPI and (c) the merged hybridization and DAPI signals. Bar = 15 μ m.

a

>pTp-2.1R

TGTCCCCGTTTCGAACGAGAGCGGTCGGAGGTTTAATCGAAAACGGAGTAGTTCGTCATGCCGATAA

TG

TAGGGCGGAAATGTGCAGTGACGAGAAAGTGTGAAAGCGGTGGACAATGCAGTTGCCAAGATAATG

GGAA

GGCTGCAAAGTACATGGAGAGAGGAGCAGCGCAGCGAAGCAAATCGTCTGATGGTCTCTGATGGCGC

GTA

AGAGCGCAGCCCCTCCCCGAAGTAATGCTGTGAGGCGTTCCGGGGAGACGAGGGCGTGGTGGCCAA
 GGA
 GTGAGGGTTTAGTCGGTAAGAATCCGACACTCTGGGTGCTAATTCCAGATGTCTATGAAGATTCCCTC
 AA
 CCTTGTAAAAAAAAAAAAAAAAAAAAAAAAACACACACACACACACACGTAATTATTTCACTTA
 TTTG
 CTACTTTTTGTAGCAGTATTTACGGTCTTTGTTATCATGATTCGTGAAGTAAACACTGAAGCTCACTGTG
 TACGTAATTTATTCCGACTCCATAAAATCTGTCAATAAAGGAATAATTTTATAACAATGTACCATTCA
 A
 GACCTATTATGTTCTTCGACGTCCTGGAAATTGACAGATAATAAGGTAAACATTTGCTTACAGTTTCA
 A
 ACTGGTCTGAAATACACTTAGGAAGCTTCTCGTGAAGTATCGTTTTAGGAACTAGGGGAGACACTGG
 TT
 ACTCACCTTACAATGACTTTTAGTAAGCGATTATAAAACTACATCAAACACTTCATCTTAAATGTCACA
 A
 TAACTACACGTAAAAAGTACAATATGAATAAAATGATTTGCCTTCACGTTACTTCCTCACAATTAAT
 GG
 GTCCTGGTAATGAACTAGTTGGTGATGAACCTATAGCCAGTGATGATCGTATAGCTCAACAACATGAC
 AT
 AGCGTATGACAATGCAGTTGACGAAGGTGACATTTATGAAGCTGACGAGAGGGCGATTTTTGCATTCC
 TA
 CTAGATTGGATTAATAAAATAAAAATTGGCATTCTGCTATTGGAGTCATGGGTTTAGGCGTTAAACATT
 A
 TTAGATGTAATATGCTGTAGAGTTTTTTATTGAAGTAATTGGTCNANAGGACTGGTGAACACCACTGTC
 G
 ATAACCGTTTGCATTGGATGTACAGAGAAAAGATCCAATTCGATTTTACATTCATTTATGAGCTTTG
 T
 TTATGTACGCCATTTTAAATTTGTAAAAAAATCGTTATGTTTTTCTTGTGTTCTAGTAGTTGCCTTT
 TTAGTCGTTACTGTTTTACGTTTCTTGATGTTGCCCGTTGAGNGACTTTACTCGAATTGTGTTGCTCT
 ACTTTGAAAAGTTTTCTGCTGTTGGGTGANAAGTTTTTCTTAAAATTGNTTCTCAG

b

VP [Haematobia irritans densovirus]

Sequence ID: [QCH41363.1](#) Length: 687 Number of Matches: 1

Range 1: 4 to 64 [GenPeptGraphics](#) Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
61.2 bits(147)	6e-06	Compositional matrix adjust.	31/61(51%)	40/61(65%)	0/61(0%)

+3

Query 813 FTLLPHN*MGPGNELVGDEPIASDDRIAQQHDIAYDNAVDEGDIYADERAIFAFVLDWI 992
 FTL++ +GPGN L EPI D IA++HDIAYD A +DIY+AD AI F D++
 Sbjct 4 FTLIGYKYLGPNSLDKGEPINKADSIAREHDIAYDRAKTKEDIYKADREAIQFKDDFL 63

Query 993 K 995

K

Sbjct 64 K 64

Structural protein [Periplaneta fuliginosa densovirus]**Sequence ID: [NP_051016.1](#) Length: 242 Number of Matches: 1****Range 1: 154 to 223 [GenPeptGraphics](#) Alignment statistics for match #1**

Score	Expect	Method	Identities	Positives	GapsFrame
48.5 bits(114)	0.019	Compositional matrix adjust.	28/70(40%)	39/70(55%)	0/70(0%)

+3

Query 828 HN*MGPGNELVGDEPIASDDRIAQQHDIAYDNAVDEGDIYEADERAIFAFVLDWIKK*KL
1007

H+ +GPGN L +EP+ DD IA++HD AY NA D+ AD++AI F D+ K L

Sbjct 154 HHYLGPGNPLDNNPVDRDDAIAEEHDKAYANAKSSIDVINADKKAIDHFSDFEKNGNL
213

Query 1008 AFCYWSHGFR 1037

G +

Sbjct 214 HSLIGKTGLQ 223

Viral protein, partial [Helicoverpa armigera densovirus]**Sequence ID: [AEI26261.1](#) Length: 448 Number of Matches: 1****Range 1: 8 to 63 [GenPeptGraphics](#) Alignment statistics for match #1**

Score	Expect	Method	Identities	Positives	GapsFrame
50.8 bits(120)	0.007	Compositional matrix adjust.	27/57(47%)	35/57(61%)	1/57(1%)

+3

Query 828 HN*MGPGNELVGDEPIASDDRIAQQHDIAYDNAVDEGDIYEADERAIFAFVLDWIKK 998
HN+GPG + EP+ DD IA++HD+AY NA DIY+AD+ A F D KK

Sbjct 8

HNLYLPGTKDFTKEPVDEDEIARRHDLAYANATSHQDIYKADKEASKEF-FDSFKK 63

Structural protein VP [Human CSF-associated densovirus]**Sequence ID: [ANG55948.1](#) Length: 840 Number of Matches: 1****Range 1: 243 to 302 [GenPeptGraphics](#) Alignment statistics for match #1**

Score	Expect	Method	Identities	Positives	GapsFrame
50.4 bits(119)	0.015	Compositional matrix adjust.	26/60(43%)	37/60(61%)	0/60(0%)

+3

Query 810 AFTLLPHN*MGPGNELVGDEPIASDDRIAQQHDIAYDNAVDEGDIYEADERAIFAFVLDW
989

+TL H +GPGN + +P+ DD IA++HD AY A ++DI ADE+A F+ DW

Sbjct 243 GYTLPGHKFIGPGNPVDTEVPVDEDDAIAKEHDEAYATAKNQKDIAIADEQAADKFLSDW
302

Supplementary Figure S5. (a) Partial sequence of pTp-2.1 plasmid. (b) Protein alignment results obtained by BLASTx.