SUPPLEMENTARY TABLE 1. Primers used in this study.

Gene	Primer name	Sequence 5’-3’	Annealing temp.	Extension temp.
Viral segment qPCR primers				
	MdSegBRR	TTCTTAGCAGATGATGTCATCGC	55	65
	MdSegBLL	CGTGGATTGACAACGCGTTT	55	65
	MdSegBRL	AGCTTATGTCGACAAGCGCT	55	65
	MdSegBLR2	TGATTAATTTGTGATACTTCCATGTT	55	65
	PTP-J1F	CCAATTCGGAAGGGTCTCG	52	72
	PTP-J1R	GGGGTAGCACTTTTGTTTGTTATCT	52	72
Gene specific qPCR primers				
DNA pol δ (Locus 4754)	4754_F	ATCGTCTACCCGACGTTCAC	55	65
	4754_R	GTGGGCTATGAACTGGTCGT	55	65
DNA pol B2 (Locus 4897)	4897_F	TATACTGCTCCGGGACTTGC	55	65
	4897_R	CAGCCCCGTACAGATTGTTT	55	65
helicase	helicaseF	TCTTCCAACACACGATTCCA	55	65
	helicaseR	AAGAACGCGTACCACCAAAT	55	65
lef-4	lef4qPCRF	ACCCTTCACCAGGACAACTG	55	72
	lef4qPCRR	AAATAGTACGCGCCACCTTG	55	72
lef-9	lef9qPCRF	CATCTTGATCAGCGTGCAAT	55	72
	lef9qPCRR	ACGTCAGTATTCCCCAGCAC	55	72
p74	p74F	TCGGTAATTGATTGGGGAGA	55	72
	p74R	TGCAGCACCAAACAAACAAT	55	72
EF1-α	EF1aMdFqPCR	ATTGAAGGCCGAGCGTGAAC	52	72
	EF1aMdRqPCR	CCGAGGGTGAAAGCAAGGAG	52	72
Sequence correction primers				
lef-8	lef8span_F	CATGTGCTTTCCAATCATGC	55	65
	lef8span_R	TTGACATTTTTGCTTTTGAAGG	55	65
pif1	pif1span_F	TGTGACCCAGCAGATAACGA	55	65
	pif1span_R	TAATTGCCTTCTTGGGTTGG	55	65
p47	p47_F	TAAGAGCCGTGAATGGTGTG	55	65
	p47_R	ATTTACGCCGGTGCATTACT	55	65
19kda	19k_F	TCATATAATTTCCGACCGACA	55	65
	19k_R	TCGGCTTGCATTTAGACGTT	55	65
p74	p74span_F	TCAAAAGCAATCATGAGTATGACA	55	65
	p74span_R	TCAGTAACGCGATGTTCAGG	55	65
HzNVorf9-1-like	orf9-1F	AAAGCGGCGTTTGATAGAAA	55	65
	orf9-1R	TGCGATGCATTCTCCTGTTA	55	65
HzNVorf9-2-like	orf9-2F	TGTTACGAATGGCGACTGAA	55	65
	orf9-2R	TGGTGTATTCCGAATGTGTGA	55	65
HzNVorf64	orf64F	ATCGCGACAATACACCAACA	55	65
	orf64R	ACAAACCAATGTGGGAAAAA	55	65

SUPPLEMENTARY TABLE 2. *M. demolitor* encapsidated protein coding sequences matching assembled transcript loci

Accession	Gene name	Locus match	Segment	Adult RPKM	Pupal RPKM
YP_239362.1*	hypothetical protein 1	557	A	186	3
YP_239363.1*	hypothetical protein 2	557	A	186	3
YP_239364.1*	hypothetical protein	557	B	186	3
YP_239365.1	hypothetical protein 1		E		
YP_239366.1	hypothetical protein 2		E		
YP_239367.2	hypothetical protein 3		E		
YP_239368.1	viral ankyrin 1	7257	C	8	0
YP_239369.1	viral ankyrin 2	7257	C	8	0
YP_239370.1	hypothetical protein	10639	C	3	0
YP_239371.1	hypothetical protein	4559	F	6	0
YP_239372.1	viral ankyrin 2	2771	F	68	0
YP_239373.1*	viral ankyrin 1	2771	F	68	0
YP_239374.1	PTP		D		
YP_239375.1*	hypothetical protein 1	557	D	186	3
YP_239376.1*	hypothetical protein 2	557	D	186	3
YP_239377.1*	hypothetical protein 1	6724	G	5	0
YP_239378.1*	hypothetical protein 2	6724	G	5	0
YP_239379.1*	viral ankyrin 1	6005	G	11	0
YP_239380.1*	viral ankyrin 2	6005	G	11	0
YP_239381.1	PTP 1	7122	H	14	0
YP_239382.1	PTP 2	7122	H	14	0
YP_239383.1	PTP 3	7122	H	14	0
YP_239384.1*	viral ankyrin	7517	H	9	0
YP_239385.1	PTP 5	7122	H	14	0
YP_239386.1*	PTP 4	7473	H	5	0
YP_239387.1*	PTP 1	1720	J	105	0
YP_239388.1	viral ankyrin	1720	J	105	0
YP_239389.1	PTP 3	1720	J	105	0
YP_239390.1*	PTP 4	2822	J	44	0
YP_239391.1*	PTP 2	2822	J	44	0
YP_239392.1	hypothetical protein	2107	K	25	1
YP_239393.1	hypothetical protein 2	10566	M	6	0
YP_239394.1	hypothetical protein 4		M		
YP_239395.1	hypothetical protein 3		M		
YP_239396.1	hypothetical protein 1	7109	M	8	1
YP_239397.1	hypothetical protein 5	5413	M	15	0
YP_239398.1	hypothetical protein	726	N	25	0
YP_239399.1*	viral ankyrin 3	726	N	25	0
YP_239400.1*	PTP 2		N		
YP_239401.1	PTP 3	14728	N	very low	very low
YP_239402.1	viral ankyrin 1	6097	N	5	1
YP_239403.1*	viral ankyrin 2	835	N	1033	8
YP_239404.1	PTP 1	726	N	25	0
YP_239405.1	hypothetical protein	557	L	186	3
YP_239406.1*	viral ankyrin	2771	I	68	0
YP_239407.1	hypothetical protein MdBV_sIgp2	8271	I	14	0
YP_239418.1	Egf1.5		O		
YP_239420.1	Egf0.4		O		
YP_239421.1	Egf1.0		O		
YP_239422.1*	Glc1.8		O		

*Coding sequences correspond to ORFs in the encapsidated genome of MdBV whose expression was detected in adult female *M. demolitor* by Bitra et al. (11).

SUPPLEMENTARY TABLE 3. Similarity of MdBV transcripts to bracovirus, nudivirus and baculovirus genes

Gene name	Protein domains (PFAM)	MdBV locus	HzNV-1 ORF name	HzNV-1 Identity*	Cc ortholog	Cc Identity*	Ci ortholog	Ci Identity*	Role
dnapol		no hits	131						DNA replication, repair, recombination
helicase		3891	104	25%					
helicase 2		no hits	60						
integrase	Phage_integrase (PF00589.16)	3978	144	30%			CAR40240.1	53%	
		1667		no hits				33%	
ligase		no hits	36						
lef-3			-						
p47		703	75	25%	CAR31573.1	73%			Transcription
lef-4		2025	98	25%			CAR40187.1	55%	
lef-8	RNA_pol_Rbp2_6 (PF00562.22)		90	33%	CAR31572.1	87%	CAR40189.1	88%	
lef-9	RNA_pol_Rpb1_2 (PF00623.14), LEF-9 (PF05094.6)	3218	75	32%					
lef-5	Baculo_LEF5_C (PF11792.2), TFIIS_C (PF01096.12)	539: transcripts 2,7,8,9	101	no hits	CAT00573.1	41%			
vlf-1	Phage_integrase (PF00589.16)	539: transcripts 1,3,4,5,6,10	121	28%			CAR40190.1	50%	
p74	Baculo_p74 (PF04583.6), Baculo_p74_N (PF08404.4)		11	26%	CAR31575.1	48%	CAR40192.1	32%	Oral infectivity
pif-1	PIF (PF05092.6)		55	28%			CAR40193.1	36%	
pif-2		226	123	31%			CAR40194.1	39%	
pif-3	DUF666 (PF05006.6)	767	88	34%	CAR31576.1	54%			
19 kDa		1791	103	26%	CAR31579.1	51%	CAR40196.1	37%	Packaging, assembly, morphogenesis
ac68		no hits	74						
polh/gran		no hits	69						
38K	DUF705 (PF05152.6)	318	10	41%	CAR31574.1	69%	CAR40188.1	50%	
vp39			89	no hits	CAR31585.1	62%	CAR40200.1	44%	Unknown function
odv-e56-1		13843	76	no hits	CAR31577.1	37%	CAR40195.1	27%	
		1447		no hits		30%		23%	
odv-e56-2	Baculo_E56 (PF04639.6)	1083		28%	CAR31578.1	47%		30%	
vp91	CBM_14 (PF01607.18)	4098	46	no hits			CAR40191.1	32%	
ac81		no hits	33						
ac92	Evr1_Alr (PF04777.7)	5801	13	29%					
		2756							
odv-e66		175			CAR31580.1	32%	CAR40197.1	39%	
		1139						35%	
		2331						26%	

	4186						31%
	2730						36%
HzNVorf9-2		9	20%	CAR31583.1	83%	CAR40199.1	54%
HzNVorf9-1			no hits	CAR31582.1	92%	CAR40198.1	67%
HzNVorf64		64	21%	CAR31584.1	86%		
HzNVorf94	318	94		CAR82240.1	74%		
HzNVorf106	332	106	no hits	CAR31586.1	94%	CAR40201.1	61%
HzNVorf128	1167	128	no hits	CAR31587.1	74%	CAR40202.1	52%
HzNVorf140	3488	140	26%	CAR31588.1	55%	CAR40203.1	37%
	2966		no hits		25%		41%
	2965		no hits		32%		40%
PmV hypothetical protein	756	-		CAR31589.1	76%	CAR40204.1	42%
Cc50C22.5*	3938	-		CAR82243.1	66%		
	1624				68%		
	4428				63%		
	2935				57%		
Cc50C22.3	370	-		CAR82241.1	62%		
Cc50C22.6*	5905			CAR82244.1	36%		
	2485				44%		
27b (Cc50C22.7)	2287	-		CAR82245.1	72%	CBH32500.1	37%
AcMNPV p26	30882 (two copies)	YP_717557.1	30%				
AcMNPV p94	8308	NP_054164	35%				
	2884, transcript 4, 5		36%				

*genes were fragmented in assembly

SUPPLEMENTARY TABLE 4. Alignment of *M. demolitor* transcripts to orthologs shows that some genes have duplicated

Gene name	MdBV locus	Alignment ortholog species	Alignment ortholog name	Alignment ortholog length (amino acids)	Alignment positions
integrase	3978	*C. inanitus*	CAR40240.1	228	1-215
	1667				15-208
odv-e56	13843	*C. inanitus*	CAR40195.1	425	269-393
	1447				268-393
	1083				304-358
ac92	5801	*HzNV-1*	NP_690432.1	244	76-229
	2756				38-239
odv-e66	175	*C. inanitus*	CAR40197.1	637	100-636
	195				208-337
	337				388-579
	358				309-373
	431				114-231
	457				48-394
	645				-
	966				41-498
	1139				72-636
	1317				151-205
	1374				193-228
	1513				92-198
	1593				251-331
	1844				-
	2109				318-400
	2114				406-636
	2199				176-238
	2331				90-636
	2630				-
	2730				175-636
	2921				315-422
	3972				62-249
	4186				47-636
	4698				165-332
	5629				21-331
	5944				85-239
	5960				169-237
	11088				176-245
	16896				218-401
	23197				479-636
HzNVorf9-2		*C. congregata*	CAR31583.1	237	3-227
HzNVorf9-1			CAR31582.1	238	33-238
HzNVorf140	3488	*HzNV-1*	NP_690559.1	811	3-293
	2966				139-289
	2965				42-139
35a	417	*C. inanitus*	CBA62630.1	322	12-236
	420				141-233
	615				12-220

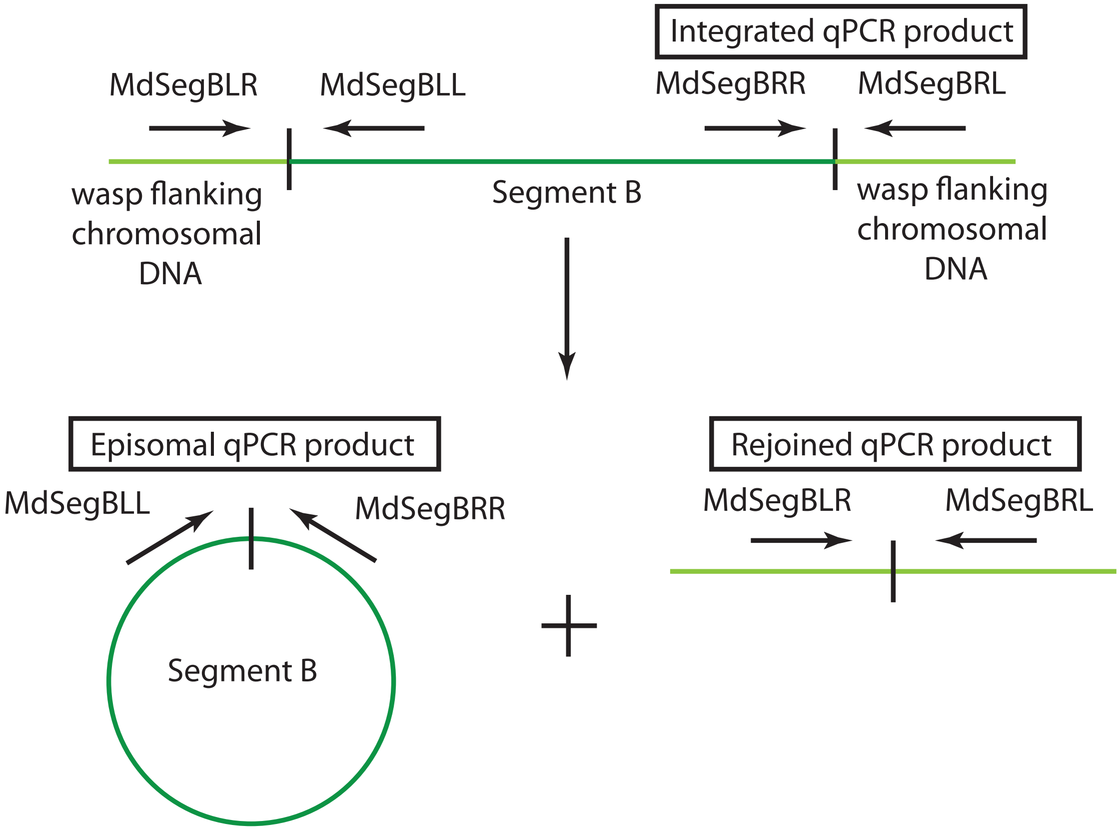
SUPPLEMENTARY TABLE 4. Matches to *Glyptapanteles flavicoxis* DNA polymerase B2 domain-containing protein (ACE75264.1, 1228 amino acids)*

Locus	Transcript length	Subject match coordinates	% similarity	% subject coverage	Adult mean RPKM	Pupal mean RPKM	*p*-value
10019	522	445-617	56	14	4	0	4.4e-06
10180	717	669-883	53	17	very low	very low	
10361	573	134-313	47	15	very low	very low	
10553	866	625-789	68	13	very low	very low	
10756	2659	257-1140	60	72	2	2	n.s.
11498	816	472-664	57	16	very low	very low	
12184	857	467-648	51	15	3	0	3.3e-06
12231	317	871-975	78	8	10	0	9.7e-10
12242	835	271-486	57	18	2	0	0.0001
12338	328	410-518	55	9	very low	very low	
12633	416	1114-1220	71	9	7	0	6.2e-06
12728	630	859-1067	74	17	3	0	2.5e-05
12920	556	374-558	54	15	very low	very low	
12987	220	768-835	82	5	4	0	0.0001
13718	554	699-881	69	15	5	1	2.4e-06
13723	1191	483-881	67	32	5	0	2.4e-06
14648	287	813-905	65	7	4	0	2.3e-08
14805	395	949-1020	72	6	2	0	0.0008
15304	543	803-852	55	4	4	0	3.7e-05
15419	798	567-796	59	19	2	0	3.5e-05
15463	380	364-481	59	10	2	0	6.2e-07
15469	845	38-288	50	20	very low	very low	
15652	227	394-469	53	6	very low	very low	
16000	276	40-132	48	7	5	0	3.2e-06
17404	1131	866-1215	65	28	very low	very low	
17698	229	429-502	54	6	very low	very low	
17737	489	185-297	46	9	very low	very low	
18235	312	739-840	73	8	3	0	3.3e-06
18411	395	1056-1180	60	10	very low	very low	
21801	259	823-905	64	7	3	0	0.001
22047	278	780-872	63	7	very low	very low	
22230	429	167-297	52	11	2	0	1.3e-05
23289	225	768-840	64	6	very low	very low	
23368	651	636-812	65	14	very low	very low	
23714	467	910-998	73	7	very low	very low	
27221	447	29-126	46	8	very low	very low	
28411	336	1038-1148	71	9	2	0	0.0008
29048	227	690-764	78	6	very low	very low	
29170	265	424-511	50	7	very low	very low	

33517	265	51-139	47	7	very low	very low	
40086	328	898-1005	75	9	2	0	0.0002
4358	2787	310-1215	68	74	16	5	2.0e-08
4897	1364	704-1152	73	36	94	0	1.5e-09
6255	1302	3-268	40	22	1	1	n.s.
7467	2645	296-673	57	31	14	3	3.3e-06
7500	548	1056-1215	70	13	14	1	2.4e-06
8326	280	362-543	55	15	12	0	3.2e-05
8541	1049	38-327	46	24	11	2	1.4e-07
8689	634	602-812	69	17	10	1	9.4e-07
8921	537	175-343	51	14	5	0	2.7e-05
9130	1833	622-1215	68	48	7	0	7.8e-08
9136	462	625-777	68	12	4	0	1.6e-05

*Loci with DNA_pol_B_2 HMM hits are underlined.

SUPPLEMENTARY FIG. 1. Diagram showing the qPCR primers and products used to differentiate between integrated, episomal, and rejoined DNAs from the *M. demolitor* encapsidated Segment B. Primer names correspond to the sequences listed in Supplementary Table 1. The upper part of the panel shows Segment B integrated into the wasp chromosome. When excision occurs, Segment B circularizes, creating the episomal form of the segment. The DNA previously flanking the integrated form of Segment B is rejoined at the sites of Segment B excision.



SUPPLEMENTARY FIG. 2. Maximum likelihood tree based upon the *vlf-1, integrase (HzNVorf144),* and *HzNVorf140* genes in other BVs and nudiviruses. Genes within yellow boxes have intact phage_integrase (PF00589.16) domains. Numbers at nodes represent bootstrap replicates (nodes without bootstrap support > 75 are not shown). The loci identified from the *M. demolitor* transcriptome are from this study and indicated in red while orthologs from other BV-carrying wasps or nudiviruses are indicated in black. Nudivirus taxa are *Heliothis zea* Nudivirus 1 (*HzNV*-1), *Gryllus bimaculatus* Nudivirus (*GbNV), Oryctes rhinocerus* Nudivirus (*OrNV*), *Penaeus monodon* Nudivirus (*PmNV*) and *Autographa californica* Multiple Nucleopolyhedrosis Virus (*AcMNPV*). *Vlf-1* from the baculovirus AcMNPV served as the outgroup.