

<i>C. mitchellii</i>	eSCV1	contig_224958	Circoviridae	180bp of 5' flank similar to python (90 bp upstream of EVE); locus absent in cobra; present in <i>C. aquilus</i> , <i>C. triseriatus</i> , <i>C. atrox</i> and <i>C. tigris</i> ; negative PCR in <i>A. contortrix</i>	CmCc58-R54/CmCc5854=742**
<i>C. mitchellii</i>	eSCV2	contig_224959	Circoviridae	locus absent in python; clear empty site in cobra (both flanks present); absent in <i>A. contortrix</i> , <i>C. aquilus</i> and <i>C. triseriatus</i> ; present in <i>C. atrox</i> and <i>C. tigris</i>	CmCc59-F54/CmCc5954=823
<i>C. mitchellii</i>	eSCV3	contig_9220	Circoviridae	Likely empty site in cobra = 257 bp of 5' flank similar to cobra (726bp upstream of EVE); 528bp of 3' flank similar to cobra (450bp downstream of EVE); locus absent in python; negative PCR in <i>A. contortrix</i> ; present in <i>C. aquilus</i> , <i>C. triseriatus</i> , <i>C. atrox</i> and <i>C. tigris</i>	CmCr20-F55/CmCr20-55=920
<i>C. mitchellii</i>	eSCV4	contig_24347	Circoviridae	clear empty site in cobra; 210 bp of 3' flank similar to python (810 bp downstream of EVE); absent in <i>A. contortrix</i> , negative PCR in <i>C. aquilus</i> and <i>C. triseriatus</i> ; present in <i>C. atrox</i> and <i>C. tigris</i>	CmCr47-F55/CmCr47-R-5
<i>C. mitchellii</i>	eSCV5	contig_193549	Circoviridae	550 bp of 3' flank similar to cobra (120bp downstream of EVE); 180bp of 3' flank similar to python (810 downstream of EVE); absent in <i>A. contortrix</i> , <i>C. aquilus</i> and <i>C. triseriatus</i> ; present in <i>C. atrox</i> and <i>C. tigris</i>	CmCr49-F55/CmCr49-R-5
<i>C. mitchellii</i>	EBLN1	contig_173953	Bornaviridae	locus absent in cobra and python; negative PCR in <i>A. contortrix</i> ; present in <i>C. aquilus</i> , <i>C. triseriatus</i> , <i>C. atrox</i> and <i>C. tigris</i>	NA
<i>C. mitchellii</i>	EBLN2	contig_72541	Bornaviridae	locus absent in cobra and python; present in <i>A. contortrix</i> , <i>C. aquilus</i> ; <i>C. triseriatus</i> ; negative PCR in <i>C. atrox</i> and <i>C. tigris</i> .	CmB41-F153/CmB41-I54=1270
<i>C. mitchellii</i>	eSHBV1	contig_93260	Hepadnaviridae	Presence of orthologous EVE in Cobra ; 705 bp of 5' flank similar to python (10 bp upstream of EVE)	not tested
<i>C. mitchellii</i>	eSHBV2	contig_192207	Hepadnaviridae	250 bp of 3' flank similar to python and cobra (75 bp downstream of EVE); negative PCR in <i>A. contortrix</i> and <i>C. atrox</i> ; present in <i>C. aquilus</i> , <i>C. triseriatus</i> and <i>C. tigris</i>	NA
<i>P. molurus</i>	eSCV6	AEQU02103080	Circoviridae	locus absent in two other snake genomes	not tested
<i>P. molurus</i>	EBLN3	AEQU02058304	Bornaviridae	132 bp of 5' flank similar to rattle snake (1164 bp upstream of EVE)	not tested
<i>O. hannah</i>	eSHBV1	AZIM01000853	Hepadnaviridae	presence of EVE at orthologous locus in rattlesnake ; 500 bp of 5' flank similar to python	not tested
<i>O. hannah</i>	eSHBV3	AZIM01007891	Hepadnaviridae	locus absent in two other snake genomes	not tested

NA = not applicable, meaning that it was not possible to design primers because of the flanking region is absent in the current *C. mitchellii* genome as

* The sequence of the primers is provided in Supplementary Dataset 2.

** For each primer pair. the expected size of the PCR product if the EVE is present is indicated in base pairs.

Supplementary Table 2. Voucher numbers of the tissue samples used in this study.

Genus	Species	Subfamily	Voucher number
<i>Crotalus</i>	<i>aquilus</i>	Crotalinae	CA122
<i>Crotalus</i>	<i>tigris</i>	Crotalinae	KWS 252
<i>Crotalus</i>	<i>atrox</i>	Crotalinae	JMM 689
<i>Agkistrodon</i>	<i>contortrix</i>	Crotalinae	JMM 734
<i>Crotalus</i>	<i>triseriatus</i>	Crotalinae	CT2