

A

Mouse kidney parvovirus NP

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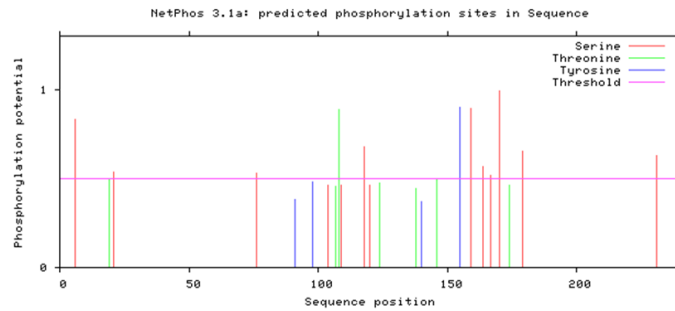
ChPV.2-Latroectus hesperus NP

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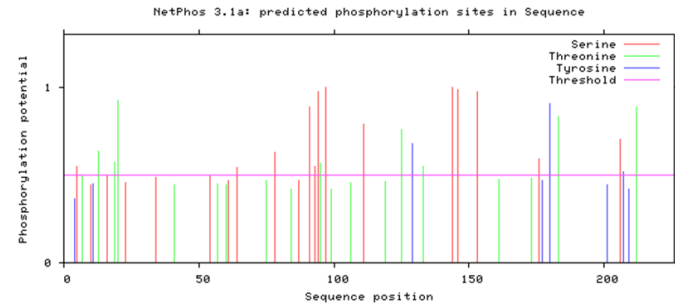
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201 Y G D P Q S Y P Y K L T L K K P A N H I N K L V N S
  
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KEY
 Annotations Helix Sheet Disordered Disordered protein binding

B



Mouse kidney parvovirus NP



ChPV.2-Latroectus hesperus NP

Figure S1

Predictions of secondary structure, disordered regions and potential phosphorylation sites in case of an amniote exogenous and an endogenous invertebrate chapparvovirus nucleoprotein (NP). (A) Secondary structure and disordered region predictions of NP from mouse kidney parvovirus and from the element ChPV.3-Latrodectus hesperus. (B) Predictions of potential phosphorylation sites in case of the same amniote chapparvovirus and an invertebrate endogenous chapparvoviral element NPs.

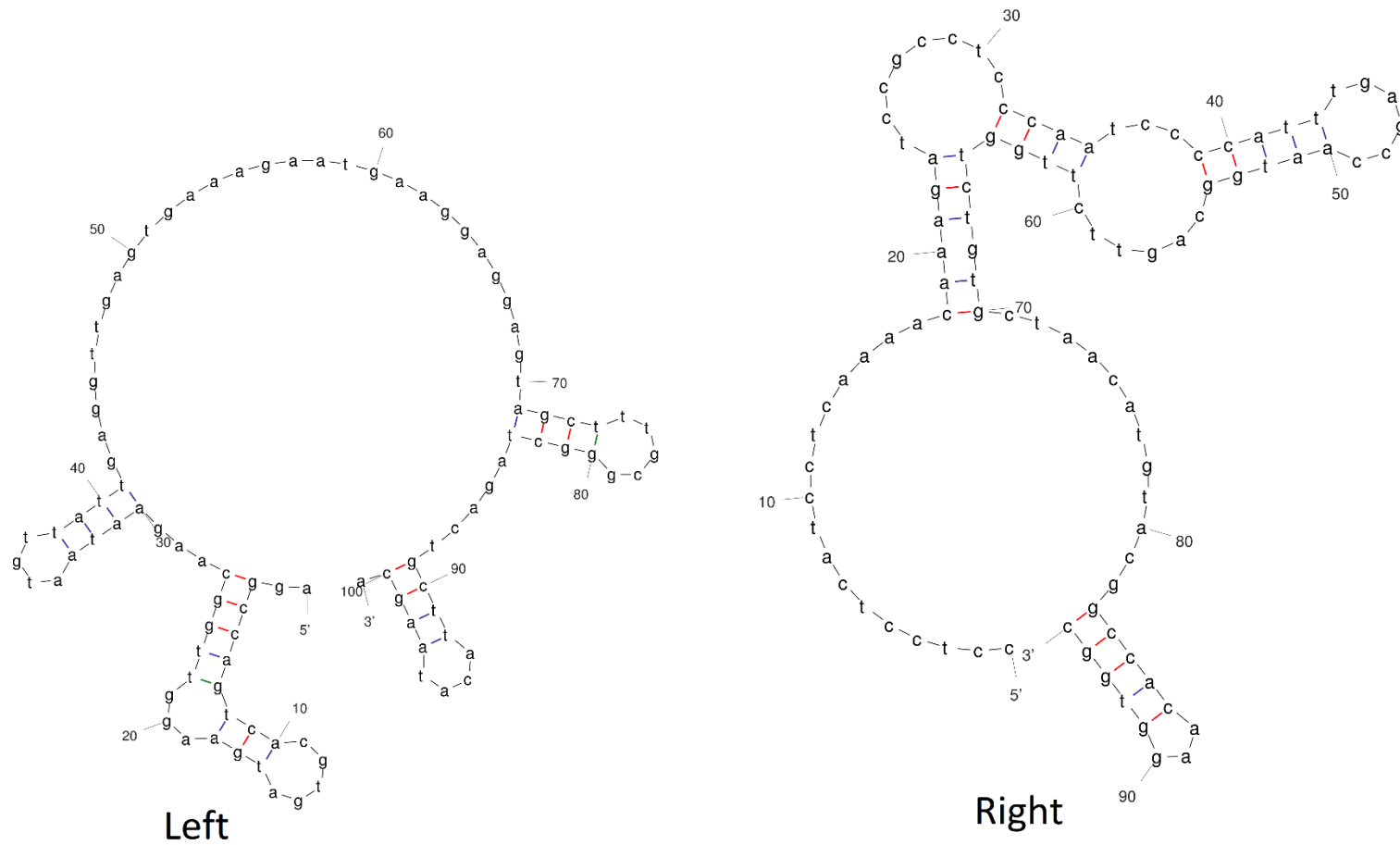


Figure S2

Secondary structure predictions of the *Syngnathus scovelli* chapparvovirus genome termini.

A

		VR1																				
murine_ChPV_NY	1	MAEDVTFHNTYMVYWKNPFIYPNTNINPPN--AHTMSAG	INTGWHIIPTILWKHF	LTPKQWTEFTIN	FEAYTVKGY	SCTIYN	82															
MKDV	1	MAEDVTFHNTYMVYWKNPFIYPNTNINPPN--AHTMSAG	INTGWHIIPTILWKHF	LTPKQWTEFTIN	YEAYTVKGY	SCTIYN	82															
rat2	1	MATDVSFSNVFMAYWSNSPYNYKVSGAGRDH--T-RPTGTP	INTGWHILPLTLWKHF	TAKQWAE	LVINYEAY	TVKGF	SCTVYN	81														
Desmodus_rotond	1	MAEDVSYTNTYMAYWKNQPYIYPNNDTDPKSKTGOVMSTGE	INTGWHIIPTILWKHF	TTPKQWCNFM	IKYEAY	TVKGY	TVTVYN	84														
porcine7	1	MAEHITLSNTFMAYWENDPYQYPTYKPFQKN-----EIL	TSNTGWHILLN	LWRHF	LSPKQWYEL	CINYEAY	HVEGT	STTVFN	78													
turkey2	1	MADDISFSHSYMCYIKNQPYLYPTQKNPTMP-----QEST	LNTGWHIIPT	TLWKHF	CTPADW	VDLITHYEAY	SVTGYS	SVSIFN	78													
pit_viper	1	MATDHVFTNTYMCYWENKPYLYPANQPGVKR-----DGDV	YTTGWHII	PNML	LWRHV	TTPKQWAE	FQIQTEAY	HVKS	IKAI	IVYN	78											
cons	1	** . : :* * . * * : *			.*****: **:* . . : * : : *** * . . : : *		84															
		VR2 – DE loop		VR3		VR4																
murine_ChPV_NY	83	PIPMTQQ LAIQGT TAF	TAFNNTIYTLGAQDD	LYETAYHNWY	DDATG DYKAF	NLSFKEGQYK-----	NE --NGSWK KT M WP	156														
MKDV	83	PIPMTQQ LAIQGT TAF	TAFNNTIYTLGAQDD	LYETAYHNWY	DDSTG DYKAF	NLSFKEGQYK-----	NL --SGSWK KT I WP	156														
rat2	82	PVPMTQQ LAIQGT TFT	TAFNNTIYSLGVKDE	LYETSWYNW	ND PAGTGG FNNF	SLAYKEGYL-----	DS PR A A T Q K R T L L P	157														
Desmodus_rotond	85	PIPMTQQ LAIQGT TAF	TAFNNTIYTLGAQDD	IYETSYHNWY	LDT ---PFNHFN	LAYKEGQYK-----	DN --NNSW NK T V F P	155														
porcine7	79	PIPI TNNLPIQGT S	TFTAFNNTIYSLGAS	DDLYETGYQN	WY EDT ---L	WRSWYVAYKEGLV	PKPTTATKE GV --GNSW SRL T L L P	157														
turkey2	79	MT PM TT QIAIQGT N	TFTAFNNTIYALGY	TD EMCET GFFNWY	SS ---EY	DSPNLSLHEGLGK	-----	RH --DDT S Y R Y E L P	148													
pit_viper	79	PVPMTT QLAIQGS T	VFTAFNNTIYSLGY	TD TLYET DWFN	WN SPA - SD HI	DLN L AYKEGLAR	-----	TV --NG T T T RY I L P	151													
cons	85	*:* : : ** : . . ***** : ** * : ** : **					: : **			: : *	168											
		VR5		VR6																		
murine_ChPV_NY	157	IYSWR	TENARNASSSTYSY-LNG-----	IDS	YAVWPRTKD----	KELI	PTGVFWDPLNDANGILELRPGKNSMSFSWEQHPC	228														
MKDV	157	IYSWR	TENARNASSSTYSY-LNG-----	IDS	YAVWPRTKD----	KELI	PTGVFWDPLNDANGILELRPGKNSMSFSWEQHPC	228														
rat2	158	VYYW	KSPTELN	SVVTWTW-DQEYNSAAAGLIGN	VAVPITGT---NTIS	LPDGVFWDPLTSPDDIMELRPGKNSMTWSWERHDC	237															
Desmodus_rotond	156	VYSWR	TANPRNVSDTTYSY-IPT-----	VLS	YSTWPRVAN---	ESDI	PNGLFWDPLTDPDSIMELRPGKNSMSFSWNAHDC	227														
porcine7	158	TYLWS	APITAPETNWTWTW-NTNK-PY---	PTAG	TWAHTDA-GTEQ	VVAPARCFWDPFTNTDSIQELRPGKNAMSFHWKTHAA	235															
turkey2	149	IYLW	PKPHVRVTSQRTMGDWPYN-----	TEGY	TTWPKNQNNDDTNGIPTGLI	WDPFNMPKMLQELRPGKNAISFSWHPHDC	225															
pit_viper	152	TYLW	RQ N AR M AS F DS W AT-E P N-----	MSA	YPVYPIGGKVSASEGEQPSGV	FWDPFNRPNHITELRPGKNAIQYVWENHGC	227															
cons	169	* *		:	:			*	:***: . . : *****: : : * . *	252												
		VR7																				
murine_ChPV_NY	229	DENK	WFNIDQIAKWF	PYTVDTPYLN	PQ---T-YGPPG	SYKLY-GEDDPDQLTTPSSWT-A	YSAKN	DYTI	PNLLDMP	I	VP	MQ	WFW	306								
MKDV	229	DENK	WFNIDQIAKWF	PYTVDTPYLN	PQ---T-YGPPG	SYKLY-GEDDPDQLTTPSSWT-A	YSAKN	DYTI	PNLLDMP	I	VP	MQ	WFW	306								
rat2	238	DENK	WYNIDQLAR	WAPYTADMPV	WNLG---R-I	GGAGSYQPD-DIEDPKSLSGPRYGT-N-PATE	DYTI	PNLAN	M	I	VP	V	AW	WWW	314							
Desmodus_rotond	228	D	TNKWYNLD	CI	AKWTPYVHDN	PFQ HIG ---R-AGQAGSYKIT-TTDDPDPLSTYSSWATTE	L	KDD	F	T	I	PNLL	N	M	P	V	P	M	N	W	W	306

porcine7	236	DEHCWYNLDSLVLKLPYTPESGYSHNIREKTYQGPPGTRIVNENFQHPPTQTSISSDQ-S-KVFI EHDV PNIL TAPSVPIHWF	317
turkey2	226	DQNKWYNLDQIAWWWPYAAPSPYPNNN-----RPQTSQLS-TQCDPDLQSKYE---N-TNPGDYTMPDMSLMPITPTGWWW	297
pit_viper	228	DDGIWFNMDHIAFSFSPYFGDHPWDSF----S-AGFPGSYKLNQNAADDPEFLSPY-M-T-APTNRNWTIPNLANMPIVPTGWF	303
cons	253	* *:*:* :. ** : : * .*	336

VR8

HI loop

murine_ChPV_NY	307	QEIQKSIAEVPD----VKKPMLYWAGTEYEYKYGPTQC FLKGIPLFDD NDTHVATTTQGCFRISLHLAGKKRRSRIYAPTWG	385
MKDV	307	QEIQKSIAEVPD----VKKPMLYWAGTEYEYKYGPTQC FLKGIPLFDD NDTHVATTTQGCFRISLHLAGKKRRSRIYAPTWG	385
rat2	315	IEMQKSIVGTYD DNSSPQKEE ALYGPGEYEYKYPTQC FIKGLPLFDD DGNHISTTTQGCFKVTLHLAAKRRSRIYAPTWH	398
Desmodus_rotond	307	QEMQKSIAQTTT----LKKPALFWAGTEYEYKYPTQC FLKGVPLFDD NGTHVETLTQGCFRVTLHLAAKRRSRIYAPTWG	385
porcine7	318	IELERNLIEDKK----VEKPOLGWPGTEWATPKYPPMNN FIKGIPLTDE NETLVKTTITMGCFRNGIHLSCKRRSRMFAPTWG	396
turkey2	298	KEMQSSIILSPGEY--FSSRPDLFFAGTEYEFKYPTMQH FIKIIPLFDS QGNHIDISANISVRTTLHLKCKRRSAYFCPTYG	379
pit_viper	304	KEVKESIALTQDP----TTIPELMAAQTEYQYKYPTQW FIKGLPLFDA AGTHVETQTQGCVKITITHIQGKKRRSAIYAPTWG	383

cons	337	*: :. : * . ** : ** . : * : * : * * . : : .. : : * : * * * * : . * * :	420
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VR9

VR10

murine_ChPV_NY	386	PLSWRQCYATDT---PFAPSMVRYRTGGARRTWTNINRDAEG---VHKDFHYREDPYDITSTVPDTRGTATLTD SKATMHP --	460
MKDV	386	PLSWRQCYATDT---PFAPSMVRYRTGGARRTWTNINRDAEG---VHKDFHYREDPYDITSTVPDTRGTATLTD SKATMHP --	460
rat2	399	PHTWRFTHTIHA---PRVGSVRYRTGGARRTWTNLRAGP-G---LSGTIRVSRSTPYNTNSTYATTATTRTPTSTRMNY--	472
Desmodus_rotond	386	PLAWTQIYSIDA---PRAPNAVRYRTGGARRTWTNIEKES-G---E-SPYNIREDPYSTSTYDRSITSNTETISKQIR---	457
porcine7	397	PEM---THGINS---AFVLPPVRYRTGGARRSWQARTRDTRDK---EPQQTWYQWNPYMTG-TYSSTTTTSTYTTTTSRK----	466
turkey2	380	PLNWRMLYTNQPNRFNFRHSYVRYRTAGARLTWQNAQAGTEETNPASTIDVSHPRTSPIASSTN--TRMTTTFMTLEPRMSPVV	461
pit_viper	384	PFNWRHLYASDKQSRFTQNSYVRYRTGGARRTMTNYSLWP-T---PGSVDNPREPPYTTAKWTAATQTQGRVTPPTSVTK--	460

cons	421	* : . ***** . * * : : * * : .	504
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murine_ChPV_NY	461	-YEQAASGMV LNHKEMRQVRAAAEATR -----SQPAVA-MQTQ-----	496
MKDV	461	-YEQAASGMV LNHKEMRQVRAAAEATR -----SQPAVA-MQTQ-----	496
rat2	473	-----	472
Desmodus_rotond	458	-YRQMVN-----KRD-RT-----AETAVTMMDLQLPPNL-----	484
porcine7	467	-----	466
turkey2	462	TYDKES-----GEATIREPPIATHRKARRPPNIP-CSTEEAMLISLDQ	503
pit_viper	461	-LVQALA-----SR-----GKMATP-----	474

cons	505		563
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B

VR1

rat2	1	MATDVSFSNVFMAYWSNSPYNKVSGAG---RDHTRPTGTPINTGWHILPLTLWKHFHTAKQWAELVINYEAYTVKGFSCSTVYN	81
Desmodus_rotond	1	MAEDVSYTNTYMAYWKNQPYIYPNNDTDPKSKTGQVMSTGEINTGWHIIPITLWKHFHTPKQWCNFMIKYEAYTVKGYTVTVYN	84
porcine7	1	MAEHITLSNTFMAYWENDPYQYPTYKPF-----QKNEILTNTGWHILLNLRWFHFLSPKQWYELCINYEAYHVEGTSTTVFN	78
turkey2	1	MADDISFSHSYMCYIKNQPYLYPTQKNP-----TMPQESTLNTGWHIIPITLWKHFCTPADWVDLITHYEAYSVTGYSVSI FN	78
pit_viper	1	MATDHVFTNTYMCYWENKPYLYPANQPG-----VKRDGDVYVTGWHIIPNMLWRHVTTPKQWAEFQIQTEAYHVKSIIKAI VYN	78
Gulf_pipefish	1	M---KFSNSYAYIENQKNDYPDIGLE-----RNPSEYQTGYHRI PNQYWASFLT PKDWFNLIYNNKAFRVVGARCTVSN	72
ChPV.3L_hes	1	MT--LSFENISYAYIENAFYKYPTVNNT-----AMTYQITGWHVIPNQEYDDFLNLKQWTELIM-HKTFSPKSV EITVQN	72
ChPV.2L_hes	1	MS--ITFENINLYIENASYQYPKDNNI-----TMTYLNNGWHLIPNQEYDDYDLTHKQWTQLIM-HKTYAPKXVEITVQN	72

cons	1	* : * . * * : * : * : * : * : * : * : *	84
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VR2 - DE loop

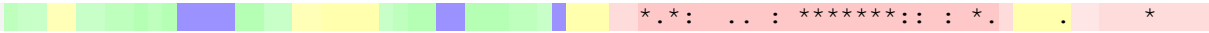
rat2	82	PVPMTQQLA-----I	91
Desmodus_rotond	85	PIPMTQQLA-----I	94
porcine7	79	PIPITNNLP-----I	88
turkey2	79	MTPMTTQIA-----I	88
pit_viper	79	PVPMTTQLA-----I	88
Gulf_pipefish	73	MIPLTEQAA-----I	82
ChPV.3L_hes	73	LIPITTQTA-----I	82
ChPV.2L_hes	73	LIPITTQIAINIXCYLLMFNRAXGPKLYFVTSYQFVSTIYLPCCKHDGGALTDLVEVWSILGVGETVN LKVVQSGLSPHSYVCI	156

cons	85	* : * : . : * : * : * : * : * : * : * : *	168
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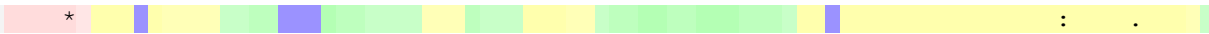
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rat2	92	QGTTTFTAFNNTIYSLGVKDELYETSWYNWNPAGTGGFNNSLAYKEGYLDS-----PRAATQKRTLLPVYWKSPTEPLN	169		
Desmodus_rotond	95	QGTTAFTAFNNTIYTLGAQDDIYETSYHNWYLD---TPFNHFNLAYKEGQYKDN-----NNSWNKTVFPVYSWRTANPRNV	167		
porcine7	89	QGTSTFTAFNNTIYSLGASDDLYETGYQNWYED---TLWRSWYVAYKEGLVPKPTTATKEGVGNSWSRLTLPYTLWSAPITAPE	169		
turkey2	89	QGTNTFTAFNNTIYALGYTDEMCEGTGFNWNYSSE---YDSPNLSLHEGLGKRH-----DDTSYRYELPIYLWPKPHVRVT	160		
pit_viper	89	QGSTVFTAFNNTIYSLGYTDTLYETDWFNWNWSPAS-DHIDLNLAYKEGLARTV-----NGTTTRYILPTYLWRAQNARMA	163		
Gulf_pipefish	83	QGNTTITTFNNTIYALCYTDNNYETEWEEPA-----RDLSEFMWREGLTN-----GARHMLPTYKHGIYRT---	143		
ChPV.3L_hes	83	QGTTTFSAFNNTIYALGYTDTKYETEFFEYSG-----TNTNIEQREGYNT-----ETNTRVSLPLYNHPTSN----	144		
ChPV.2L_hes	157	QGTTTFAAFNNTIYVLGYTDTKYETEFFXFKN-----TNINIENRESINT-----ETNTRVTLTVFQLPEVN----	218		

cons	169	** : : * * * * * * * * * * * : * : * : * : * : * : *	252
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		...VR5	VR6A	VR6B	
rat2	170	SVVTWTWDQ-EYNSAAAGLIGNVAWPITG---TNTISL-PDGVFWDPLTSPDDIMELRPGKNSMTWSWERHDCDENKWNIDQL	248		
Desmodus_rotond	168	SDTTYSYIP-T-----VLSYSTWPRVA---NESDI-PNGLFWDPLTDPDSIMELRPGKNSMSFSWNAHDCDTNKWYNLD CI	238		
porcine7	170	TNWTWTWNT-NK----PYPTAGTTWAHTDAG-TEQVVA-PARCFWDPFTNTDSIQELRPGKNAMSFHWKTHAADEHCWYNLDSL	246		

turkey2	161	SQRTMGDWPYN-----TEGYTTWPKNQNNDDTNGI-PTGLIWDPFNMPKMLQELRPGKNAISFSWHPHDCDQNKWYNLDQI	236
pit_viper	164	SFDSWATEP-N-----MSAYPVYPIGGKVSASEGEQ-PSGVFWDPFNRPNHITELRPGKNAIQYVWENHGCDGDIWFNMDHI	238
Gulf_pipefish	144	-----TTSQAHNVFYGWDPLCKAENILELRPGKNAVTFEWH-----KEE IWLNTHMM	191
ChPV.3L_hes	145	-----N-KTFLFWDPLLNPNDIMELRPGKNAIKYSWHRSSADDHIVYNTSGL	190
ChPV.2L_hes	219	-----N-KTMLYWGPLINPSEIMELRPGKNAIKYTWHRV-YDELDRHNL---	260
cons	253	 *. *: . . : ***** : : * . * . *	336

VR7

rat2	249	ARWAPYTAD-MPWWNLGRI----GGAGSYQPD-DIEDPKLSLGP-RYG-TNPATEDY-TIPNLANMPIVPAVWWWIEMQKSIVG	323
Desmodus_rotond	239	AKWTPYVHD-NPFQHIGRA----GQAGSYKIT-TTDDPDLSTYSSWATTELTKDDF-TIPNLLNMPVPMNWWWQEMQKSIAQ	315
porcine7	247	VKLFPPYTP-E-SGYSHNIREKTYQGPPGTRIVNENFQHPPTQTSISSDQ--SKVFIEH-DVPNILTAPSVPIHWFWIELEARNLIE	326
turkey2	237	AWWWPYAAP-SPYPNNN-----RPQTSQLSTQC-DPDRLOSK--YE--NTNPGDY-TMPDMSLMPITPTGWWWKEMQSS IIL	306
pit_viper	239	ASFSPYFGD-HPWDSFS-A----GFPGSYKLNQNADDPEFLS-P--YMTAPTNRNWTIPNLANMPIVPTGWFWEKVESIAL	312
Gulf_pipefish	192	QQFDPTHTP-GI-ANTA-----TVY-----SQEIHNQTHSNVTPHSHLNRWISQTD TAPAT	240
ChPV.3L_hes	191	FTLDPTFNSENM-----LMDF-DRRNTNVTPYQQHQHWLKSNTHTGFGQ	233
ChPV.2L_hes	261	-NITP-----YLHHQHWIHRNQTEFGR	281
cons	337	 * : .	420

VR8

HI-loop

VR9...

rat2	324	TYDDNSSPQKEEALYGPTEYEYQYKYPPTQC FIKGLPLFD DDGNHISTTTQGC FKVTLHLAALKRRSRIYAPTWHPHTWR-FTH	406
Desmodus_rotond	316	TTT-----LKKPALFWAGTEYEYQYKYPPTQC FLKGVPLFD DNTHVETLTQGC FRVTLHLAALKRRSRIFAPTWGPLAWT-QIY	393
porcine7	327	DKK-----VEKQQLGWPGTEWATPKYPPMNN FIKGIPLTDE NETLVKTI TMGCFRNGIHLSCKKRRSRMFAPTWGPEM----TH	401
turkey2	307	SPGE--YFSSRPDLFFAGTEYEFKYPTMQH FIKI IPLFDS QGNHIDISANISVRTTLHLKCKKRRSAYFCPTYGPLNWR-MLY	387
pit_viper	313	TQD----PTTIPELMAAQTEYQYKYPPTQW FIKGLPLFDA AAGTHVETQTQGCVKIT IHIQKKRRSAIYAPTWGPFNWR-HLY	391
Gulf_pipefish	241	ARH-----WSKQAIQRPGIMEQQFRYPIPNW FIKMIPLFDS QNNLIKTTAQVLTIMELTVDTI PQSLAINMPI IDDI I-----	314
ChPV.3L_hes	234	-----HFQYQMSGLYQNNFTKPIPN FIKMIPLFDE NNALINTTAQIC IHKKITFDVTPLDASLNRP I I PSMLYDNEFY	307
ChPV.2L_hes	282	-----QFN YQMSGMPENNFFKSI PN FIKMIPLFDE NNALINTTAQVC IHRKITFDIEPLFSSINRPLAPENMYNTPLY	355
cons	421	 . . . : * : * : * * . . : . : . *	504

...VR9

VR10

rat2	407	TIHAP---RVGSYVR-----YRTGGARRTWTNLRAGP--GLSG---TIRVSRTPYNTNSTYATTATTRTT--	463
Desmodus_rotond	394	SIDAP---RAPNAV-----YRTGGARRTWTNIEKES--G-ES---PYNIREDPYSTSTTYDRSITSNTE--	449
porcine7	402	GINSA---FVLPVVR-----YRTGGARRSWQARTRDT--RDKEPQ-QTWYQWNPYMTGT-YSTTTTSTY--	459
turkey2	388	TNQPNRFNFRHSYVR-----YRTAGARLTWQONQAGTEETNPASTIDVSHPRTPSPYIASSTNTRMTTTFMTLE	454
pit_viper	392	ASDKQSRTFQNSYVR-----YRTGGARRTMTNYS LW--PTPGS---VDNPREPPYTTAKWTAATQTQGRVTQ	453
Gulf_pipefish	315	-----A--PNH-----TPNSVPYCMFRY-QPIIPINVG--	338
ChPV.3L_hes	308	TTNYKGITFH-AHAAYQHNIQKLDQMTAKQEKKINGKILTWP IYYEAP---KD---KIKNDFFPWVTQTERNNELI-HLG--	380
ChPV.2L_hes	356	TQKY-----NLYQSLSIYA-----	369

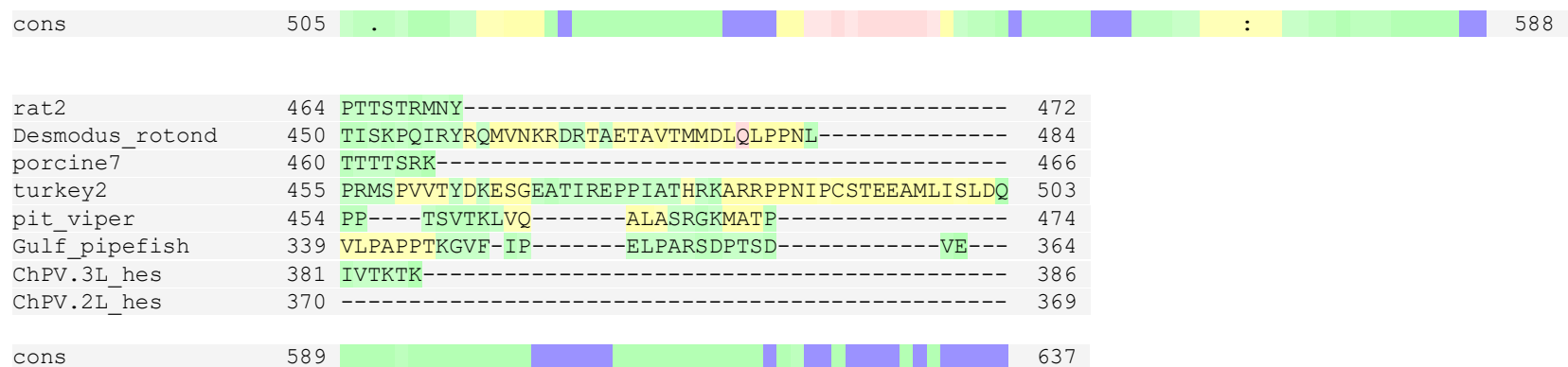


Figure S3

Variable regions at the derived amino acid sequence level identified among chapparvovirus capsid proteins. (A) Alignment of amniote chapparvovirus capsid protein ORF (VP) derived amino acid sequences, containing both isolates of murine origin. Variable regions (VRs) are marked by the black bars and coloring is based on sequence similarity (red = highly similar, blue = not similar). The conserved loops making up the fivefold symmetry axes of the capsid are highlighted in bold. (B) The same alignment incorporating the complete VP protein sequences of all novel chapparvovirus sequences reported in this study.