**Suppl File S2**: **Multiple sequence alignment of *Dependoparvovirus* Rep78 proteins**

Note: the Rep78 protein of the bank vole dependoparvovirus MgAAV2(Genbank accession QHD57625) most probably contains a sequencing error in its C-terminus, resulting in an artefactual frameshift. Indeed:

1) its C-terminal sequence is highly dissimilar its sequence to that of all other dependoparvovirus Rep78;

2) instead, the frameshifted nucleotide sequence is highly similar to that other dependoparvovirus Rep78 and contains a DDx3EQ C-terminal motif.

The alignment below thus includes the last 50aa of Mg AAV2 Rep78 with the artefactual frameshift approximately corrected.

>AAV2|NC\_001401.2\_cds\_YP\_680423.1\_2/1-621

--------------M--------------------------------------------PGFYEIVIKVPSD

LDEHLPGISDSFVNWVAEKE--WELPP----DSDMDLNLI-----------EQAPLTVAEKLQRDFLTEWRR

VSKA-------PEALFFVQFEKG-ESYFHMHVLVETTGVKSMVLGRFLSQIREKL-IQRIYRGIEPT-LPNW

FAVTKTRNGA-GGGNKVVD---ECYIPNYLLPK-------TQPE---------LQWAWTNMEQY---LSACL

NLTERKRLVAQHL-THVSQTQE--------------QNKENQ-----NPNSDAPVI-RSKTSARYM------

ELVGWLVDKGITSEKQWIQEDQASYISFNAASNSRSQIKAALDNAGKIMSLTKTAPDYLVGQQPVED--IS-

SNRIYKILELNGYDPQYAASVFLGWATKKFGKRNTIW-LFGPATTGKTNIAEAIAHTV-PFYGCVNWTNENF

PFNDCVDKMVIWWEEGKMTAKVVESAKAILGGSKVRVDQKCKSSAQIDPTPVIVTSNTNMCAVIDGNSTTFE

HQQPLQDRMFKFELTRRLDHDFGKVTKQEVKDFFRWAK-DHVVEVEHEFYVK----------K-G-------

------------GAK--KRP-----------------------------------APSD-------------

--------------ADISE-PKR-VRE-SVAQPSTSDA--------------------------E-ASINYA

DRYQNKCSRHVG-MNLMLFPCRQC--ER-------------MNQNS---------NICFTHGQ---------

--------KDCLECFP---VSE----------------------SQ-----PVSVV----------------

-----------------------KKA------YQ-KLCYIHHIMGKVPD------------ACTACDLVNV-

-------------------------------D-LDDCIFEQ-------

>AAV4|NC\_001829.1\_cds\_NP\_044926.1\_1/1-623

--------------M--------------------------------------------PGFYEIVLKVPSD

LDEHLPGISDSFVSWVAEKE--WELPP----DSDMDLNLI-----------EQAPLTVAEKLQREFLVEWRR

VSKA-------PEALFFVQFEKG-DSYFHLHILVETVGVKSMVVGRYVSQIKEKL-VTRIYRGVEPQ-LPNW

FAVTKTRNGA-GGGNKVVD---DCYIPNYLLPK-------TQPE---------LQWAWTNMDQY---ISACL

NLAERKRLVAQHL-THVSQTQE--------------QNKENQ-----NPNSDAPVI-RSKTSARYM------

ELVGWLVDRGITSEKQWIQEDQASYISFNAASNSRSQIKAALDNASKIMSLTKTAPDYLVGQNPPED--IS-

SNRIYRILEMNGYDPQYAASVFLGWAQKKFGKRNTIW-LFGPATTGKTNIAEAIAHAV-PFYGCVNWTNENF

PFNDCVDKMVIWWEEGKMTAKVVESAKAILGGSKVRVDQKCKSSAQIDPTPVIVTSNTNMCAVIDGNSTTFE

HQQPLQDRMFKFELTKRLEHDFGKVTKQEVKDFFRWAS-DHVTEVTHEFYVR----------K-G-------

------------GAR--KRP-----------------------------------APND-------------

--------------ADISE-PKR-ACP-SVAQPSTSDA--------------------------E-APVDYA

DRYQNKCSRHVG-MNLMLFPCRQC--ER-------------MNQNV---------DICFTHGV---------

--------MDCAECFP---VSE----------------------SQ-----PVSVV----------------

----------------------RKRT------YQ-KLCPIHHIMGRAPEV-----------ACSACELANV-

-------------------------------D-LDDCDMEQ-------

>AAV3|NC\_001729\_1\_cds\_NP\_043940/1-624

--------------M--------------------------------------------PGFYEIVLKVPSD

LDERLPGISNSFVNWVAEKE--WDVPP----DSDMDPNLI-----------EQAPLTVAEKLQREFLVEWRR

VSKA-------PEALFFVQFEKG-ETYFHLHVLIETIGVKSMVVGRYVSQIKEKL-VTRIYRGVEPQ-LPNW

FAVTKTRNGA-GGGNKVVD---DCYIPNYLLPK-------TQPE---------LQWAWTNMDQY---LSACL

NLAERKRLVAQHL-THVSQTQE--------------QNKENQ-----NPNSDAPVI-RSKTSARYM------

ELVGWLVDRGITSEKQWIQEDQASYISFNAASNSRSQIKAALDNASKIMSLTKTAPDYLVGSNPPED--IT-

KNRIYQILELNGYDPQYAASVFLGWAQKKFGKRNTIW-LFGPATTGKTNIAEAIAHAV-PFYGCVNWTNENF

PFNDCVDKMVIWWEEGKMTAKVVESAKAILGGSKVRVDQKCKSSAQIEPTPVIVTSNTNMCAVIDGNSTTFE

HQQPLQDRMFEFELTRRLDHDFGKVTKQEVKDFFRWAS-DHVTDVAHEFYVR----------K-G-------

------------GAK--KRP-----------------------------------ASND-------------

--------------ADVSE-PKR-ECT-SLAQPTTSDA--------------------------E-APADYA

DRYQNKCSRHVG-MNLMLFPCKTC--ER-------------MNQIS---------NVCFTHGQ---------

--------RDCGECFPG--MSE----------------------SQ-----PVSVV----------------

----------------------KKKT------YQ-KLCPIHHILGRAPEI-----------ACSACDLANV-

-------------------------------D-LDDCVSEQ-------

>lcl|AY631966.1\_cds\_AAT46338.1\_1/1-622

--------------M--------------------------------------------PGFYEIVIKVPSD

LDEHLPGISDSFVNWVAEKE--WELPP----DSDMDRNLI-----------EQAPLTVAEKLQRDFLVHWRR

VSKA-------PEALFFVQFEKG-ESYFHLHVLVETTGVKSMVLGRFLSQIRDRL-VQTIYRGVEPT-LPNW

FAVTKTRNGA-GGGNKVVD---ECYIPNYLLPK-------TQPE---------LQWAWTNMEEY---ISACL

NLAERKRLVAQHL-THVSQTQE--------------QNKENL-----NPNSDAPVI-RSKTSARYM------

ELVGWLVDRGITSEKQWIQEDQASYISFNAASNSRSQIKAALDNAGKIMALTKSAPDYLVGPSLPAD--IK-

ANRIYRILELNGYDPAYAGSVFLGWAQKKFGKRNTIW-LFGPATTGKTNIAEAIAHAV-PFYGCVNWTNENF

PFNDCVDKMVIWWEEGKMTAKVVESAKAILGGSKVRVDQKCKSSAQIDPTPVIVTSNTNMCAVIDGNSTTFE

HQQPLQDRMFKFELTRRLEHDFGKVTKQEVKEFFRWAQ-DHVTEVAHEFYVR----------K-G-------

------------GAT--KRP-----------------------------------APSD-------------

--------------ADISE-PKR-ACP-SVPEPSTSDA--------------------------E-APVDFA

DRYQNKCSRHAG-MLQMLFPCKTC--ER-------------MNQNF---------NVCFTHGV---------

--------RDCSECFPG--ASE----------------------SQ-----P--VV----------------

----------------------RKKT------YQ-KLCAIHHLLGRAPEI-----------ACSACDLVNV-

-------------------------------D-LDDCVSEQ-------

>AAV1|NC\_002077.1\_cds\_NP\_049541.1\_1/1-623

--------------M--------------------------------------------PGFYEIVIKVPSD

LDEHLPGISDSFVSWVAEKE--WELPP----DSDMDLNLI-----------EQAPLTVAEKLQRDFLVQWRR

VSKA-------PEALFFVQFEKG-ESYFHLHILVETTGVKSMVLGRFLSQIRDKL-VQTIYRGIEPT-LPNW

FAVTKTRNGA-GGGNKVVD---ECYIPNYLLPK-------TQPE---------LQWAWTNMEEY---ISACL

NLAERKRLVAQHL-THVSQTQE--------------QNKENL-----NPNSDAPVI-RSKTSARYM------

ELVGWLVDRGITSEKQWIQEDQASYISFNAASNSRSQIKAALDNAGKIMALTKSAPDYLVGPAPPAD--IK-

TNRIYRILELNGYEPAYAGSVFLGWAQKRFGKRNTIW-LFGPATTGKTNIAEAIAHAV-PFYGCVNWTNENF

PFNDCVDKMVIWWEEGKMTAKVVESAKAILGGSKVRVDQKCKSSAQIDPTPVIVTSNTNMCAVIDGNSTTFE

HQQPLQDRMFKFELTRRLEHDFGKVTKQEVKEFFRWAQ-DHVTEVAHEFYVR----------K-G-------

------------GAN--KRP-----------------------------------APDD-------------

--------------ADKSE-PKR-ACP-SVADPSTSDA--------------------------EGAPVDFA

DRYQNKCSRHAG-MLQMLFPCKTC--ER-------------MNQNF---------NICFTHGT---------

--------RDCSECFPG--VSE----------------------SQ-----P--VV----------------

----------------------RKRT------YR-KLCAIHHLLGRAPEI-----------ACSACDLVNV-

-------------------------------D-LDDCVSEQ-------

>AAV8|NC\_006261.1\_cds\_YP\_077179.1\_1/1-625

--------------M--------------------------------------------PGFYEIVIKVPSD

LDEHLPGISDSFVNWVAEKE--WELPP----DSDMDRNLI-----------EQAPLTVAEKLQRDFLVQWRR

VSKA-------PEALFFVQFEKG-ESYFHLHVLVETTGVKSMVLGRFLSQIREKLGPDHLPAGSSPT-LPNW

FAVTKDAVMAPAGGNKVVD---ECYIPNYLLPK-------TQPE---------LQWAWTNMEEY---ISACL

NLAERKRLVAQHL-THVSQTQE--------------QNKENL-----NPNSDAPVI-RSKTSARYM------

ELVGWLVDRGITSEKQWIQEDQASYISFNAASNSRSQIKAALDNAGKIMALTKSAPDYLVGPSLPAD--IT-

QNRIYRILALNGYDPAYAGSVFLGWAQKKFGKRNTIW-LFGPATTGKTNIAEAIAHAV-PFYGCVNWTNENF

PFNDCVDKMVIWWEEGKMTAKVVESAKAILGGSKVRVDQKCKSSAQIDPTPVIVTSNTNMCAVIDGNSTTFE

HQQPLQDRMFKFELTRRLEHDFGKVTKQEVKEFFRWAS-DHVTEVAHEFYVR----------K-G-------

------------GAS--KRP-----------------------------------APDD-------------

--------------ADKSE-PKR-ACP-SVADPSTSDA--------------------------EGAPVDFA

DRYQNKCSRHAG-MLQMLFPCKTC--ER-------------MNQNF---------NICFTHGV---------

--------RDCSECFPG--VSE----------------------SQ-----P--VV----------------

----------------------RKRT------YR-KLCAIHHLLGRAPEI-----------ACSACDLVNV-

-------------------------------D-LDDCVSEQ-------

>AAV12|DQ813647/1-621

--------------M--------------------------------------------PGFYEVVIKVPSD

LDEHLPGISDSFVNWVAEKE--WELPP----DSDMDQNLI-----------EQAPLTVAEKLQREFLVEWRR

VSKF-------LEAKFFVQFEKG-DSYFHLHILIEITGVKSMVVGRYVSQIRDKL-IQRIYRGVEPQ-LPNW

FAVTKTRNGA-GGGNKVVD---ECYIPNYLLPK-------VQPE---------LQWAWTNMEEY---ISACL

NLAERKRLVAQHL-THVSQTQE--------------GDKENL-----NPNSDAPVI-RSKTSARYM------

ELVGWLVDKGITSEKQWIQEDQASYISFNAASNSRSQIKAALDNASKIMSLTKTAPDYLIGQQPVGD--IT-

TNRIYKILELNGYDPQYAASVFLGWAQKKFGKRNTIW-LFGPATTGKTNIAEAIAHAV-PFYGCVNWTNENF

PFNDCVDKMVIWWEEGKMTAKVVESAKAILGGSKVRVDQKCKASAQIDPTPVIVTSNTNMCAVIDGNSTTFE

HQQPLQDRMFKFELTRRLDHDFGKVTKQEVKDFFRWAA-DHVTDVAHEFYVT----------K-G-------

------------GAK--KRP-----------------------------------APSD-------------

--------------EDISE-PKR-PRV-SFAQPETSDA--------------------------E-APGDFA

DRYQNKCSRHAG-MLQMLFPCKTC--ER-------------MNQNS---------NVCFTHGQ---------

--------KDCGECFP---GSE----------------------SQ-----PVSVV----------------

-----------------------RKT------YQ-KLCILHQLRG-APEI-----------ACSACDQLNP-

-------------------------------D-LDDCQFEQ-------

>RhinolophusPusillusBtAAV-CXC1|MK391482.1\_cds\_QDX47269.1\_1/1-636

-----------------------------------------------------------MSFYEVIIRVPHD

IEEHLPGISDHFVDWIANKE--WELPD----WADLDITLI-----------DMPQLTLAEKIQREFLTEWSK

ITKE-------KELVYFIQFEKG-EKFYHLHTLMSTEGMKSMVLGRYLNQIRQKL-VSQSYRGIEPQ-IPDW

LAVTKTKK---EGANRLRD---RDYIPAYLLPK-------VQSE---------LQWAWTSMDEY---KLATL

NLEERKRLVAAFQ-AELALKKS--------------AAEESQI---EKNGVGNPRW-RGKTTAKYM------

ELVNWLVERGITSEREWIKEDQESYLSFNSTGTARGQIKAALDNASRIMSTTKEAADYLIGQDVPED--IT-

SNRVYRIFEMNGYDPKYAGSILVGWCQKRFGKRNTVW-LFGPATTGKTNIAEAIAHAV-PFYGCVNWTNENF

PFNDCVDKMIIWWEEGKMTAKVVESAKAILGGSMVRVDQKCKSSSQIDQTPVIVTSNTNMCAVIDGNSTTFE

HQQPLEDRMFKFELTRRLDSDFGKITKAEIKDFMAWAR-ANEVPVTHEFRVK----------R-H-------

------------APIFSKRP-----------------------------------APEG-------------

----------EEP-EGIKD-CKR-FRS-SSFEEEQSSR--------------------------E-EPDNFA

LRYVNKCSRHLN-FVQMMFPCQIC--DR-------------MNQSV---------DVCFTHGA---------

--------KSCEICFP-----R----------------------GE-----PDG------------------

-------------IET-EVQEAQKEEQNFLAAYP-NRCNICKMRG-IYNP-----------ACGLCAEII--

-------------------------------DCIDDVNKEQ-------

>RhinolophusSinicusRs-BtAAV1|MF682927.1\_cds\_ATV81502.1\_1/1-654

--------------MAGYLSGSSQP----------------ASHSTSACR------GVKMSFYEVIIRVPHD

VEEHLPGISDHFVDWIANKE--WELPE----WSDMDITLI-----------DMPQLTLGEKLKREFLLEWHK

ITKL-------SNLDYFIQLEKG-EKFYHLHVLISVEGMKSMVLGRYLNQIRQKL-VSQIYRGIEPT-IPDW

LAVTKTKK---EGANRIRD---TGYIPAYLLPK-------VQSE---------LQWAWTSLEDY---KLATL

NLQERKRLADEFQ-AELALSRP--------------VIEETE--------AGNPRW-RGKSTAKYM------

ELVKWLVEKGITSEKEWIKEDQESYLTFNSTGTARGQIKAALDNAGRIMSTTKQAADYLIGPDVPPD--IK-

SNRVYRIFEMNGYDPRYAGSVLVGWCQKKFGKRNTVW-LFGPATTGKTNIAEAIAHAV-PFYGCVNWTNENF

PFNDCVDKMIIWWEEGKMTAKVVESAKAILGGSMVRVDQKCKSSSQIEQTPVIVTSNTNMCAVIDGNSTTFE

HQQPLEDRMFKFELTRRLDSDFGKISKTEIREFMAWAA-ANEVPVRHEFRVQ----------R-S-------

------------ITSLGKRP-----------------------------------APEG-------------

----------EEPGEGINA-AKR-PR--SSFDEPQPEG--------------------------E-DVENFA

LRYVNKCSRHLN-FVHMMFPCQIC--DR-------------MNQSV---------DVCFTHGV---------

--------KSCEICFP-----R----------------------GE-----PDG------------------

-------------VEE-QAKEAEKEEQNFIDAYP-NRCNICKMRG-HFNP-----------ACGLCAEIA--

-------------------------------DCIDDLNKEQ-------

>AAVbatCroatiaCull\_12|QHY93489.1/1-635 replicase [Adeno-associated virus Croatia cul1\_12]

-----------------------------------------------------------MSFYEVIIRVPHD

VEDQLPGVSDSFVDWIVRKE--WELPD----WSDMDITLI-----------DQPQLTLAEKIQREFLSEWQK

ITKE-------KETPHFVQLEKG-EKFYHLHTLVSTEGMKSMVLGRYLNQIRQKL-VSQIYRGVEPQ-IPDW

MAVTKVKK---EGANRIRD---TQYIPAYLLPK-------TQSE---------LQWAWTNLEEY---KLATL

NLEERKRLSEQYQ-TEFRRNQP--------------A-SDSQI---SETDSGNPRW-RGKSTARYM------

ELVKWLVERGITSEKQWIQEDQESYLSFNSTGTARGQIKAALDNAGRIMSTTKSASDYLIGPHPPED--VK-

NNRVYRIFELNGYDPKYAGSILVGWCRKEFGKRNTVW-LFGPATTGKTNIAEAIAHAV-PFYGCVNWTNENF

PFNDCVDKMIIWWEEGKMTAKVVESAKAILGGSMVRVDQKCKSSQQIEQTPVIVTSNTNMCAVIDGNSTTFE

HQQPLEDRMFKFELTRRLEPDFGKISKREIREFMNWAE-SNKVPVTHEFRVK----------K-F-------

------------APIF-KRH-----------------------------------APEG-------------

----------EES-EGINN-RKR-FRS-SSFEEESSER--------------------------A-DVENFA

LRYVNKCSRHLN-FVTMMFPCQIC--DR-------------MNQSV---------DVCFTHGA---------

--------KSCEICFP-----R----------------------SD-----PDGQVD---------------

------------CIEMGESEKAEKEE------MPENRCNTCKMRN-IFRP-----------NCGLCAELAL-

-------------------------------ECIDDVNKEQ-------

>AAV5|NC\_006152.1\_cds\_YP\_068408.1\_1/1-610

--------------M--------------------------------------------ATFYEVIVRVPFD

VEEHLPGISDSFVDWVTGQI--WELPP----ESDLNLTLV-----------EQPQLTVADRIRRVFLYEWNK

FSK--------QESKFFVQFEKG-SEYFHLHTLVETSGISSMVLGRYVSQIRAQL-VKVVFQGIEPQ-INDW

VAITKVKK---GGANKVVD---SGYIPAYLLPK-------VQPE---------LQWAWTNLDEY---KLAAL

NLEERKRLVAQFLAESSQRSQE--------------AASQRE-----FSA--DPVI-KSKTSQKYM------

ALVNWLVEHGITSEKQWIQENQESYLSFNSTGNSRSQIKAALDNATKIMSLTKSAVDYLVGSSVPED--IS-

KNRIWQIFEMNGYDPAYAGSILYGWCQRSFNKRNTVW-LYGPATTGKTNIAEAIAHTV-PFYGCVNWTNENF

PFNDCVDKMLIWWEEGKMTNKVVESAKAILGGSKVRVDQKCKSSVQIDSTPVIVTSNTNMCVVVDGNSTTFE

HQQPLEDRMFKFELTKRLPPDFGKITKQEVKDFFAWAK-VNQVPVTHEFKVPRELAG----TK-G-------

------------AEKSLKRP-----------------------------------LGDV-------------

----------TNT-SYKSL-EKR-ARL--SFVPETPRSS--DVTVDP----------------APLRPLNWN

SRYDCKCDYHAQ-FDNISNKCDEC--EY-------------LNRGK---------NGCICHNV---------

--------THCQICHG----------------------------IP-----PWE------------------

----------------------KENLSDF-------------------------------------------

-------------------------------GDFDDANKEQ-------

>BovineAAV|NC\_005889.1:368-2200/1-610

--------------M--------------------------------------------ATFYEVIVRVPFD

VEEHLPGISDNFVDWVTGQI--WELPP----ESDLNLTLI-----------EQPQLTVADRIRRVFLYEWNK

FSK--------QESKFFVQFEKG-SEYFHLHTLVETSGISSMVLGRYVSQIRAQL-VKVVFQNIEPR-INDW

VAITKVKK---GGANKVVD---SGYIPAYLLPK-------VQPE---------LQWAWTNLEEY---KLAAL

NLEERKRLVAQFQLESSQRSQE--------------ASSQRD-----VSA--DPVI-KSKTSQKYM------

ALVSWLVEHGITSEKQWIQENQESYLSFNSTGNSRSQIKAALDNASKIMSLTKSASDYLVGQTVPED--IS-

ENRIWQIFDLNGYDPAYAGSVLYGWCTRAFGKRNTVW-LYGPATTGKTNIAEAISHTV-PFYGCVNWTNENF

PFNDCVEKMLIWWEEGKMTSKVVEPAKAILGGSRVRVDQKCKSSVQVDSTPVIITSNTNMCVVVDGNSTTFE

HQQPLEDRMFRFELMRRLPPDFGKITKQEVKDFFAWAK-VNQVPVTHEFMVPKKVAG----TE-R-------

------------AETSRKRP-----------------------------------LDDV-------------

----------TNT-NYKSP-EKR-ARL--SVVPETPRSS--DVPVEP----------------APLRPLNWS

SRYECRCDYHAK-FDSVTGECDEC--EY-------------LNRGK---------NGCIFHNA---------

--------THCQICHA----------------------------VP-----PWE------------------

----------------------KENVSDF-------------------------------------------

-------------------------------NDFDDCNKEQ-------

>ParvoviridaeDogfe340C4|WDW25818.1/1-610 MAG: replication-associated protein [Canine parvovirus]

--------------M--------------------------------------------ATFYEVIVRVPFD

VEDHLPGISDSFVDWVTGQT--WELPP----ESDLNLTLI-----------EQPQLTVADRIRRVFLYEWNK

FSK--------QESKFFVQFEKG-SEYFHLHTLVETSGISSMVLGRYVSQIRAQL-VKVVFQNTEPR-INDW

VAITKVKK---GGANKVVD---SGYIPAYLLPK-------VQSE---------LQWAWTNIDEY---KLATL

NLEERKRLVAQFQLESLQHSQE--------------ASSQRD-----FSA--DPVI-KSKTSQKYM------

ALVSWLVEHGITSEKQWIQENQESYLSFNSTGNSRSQIKAALDNASKIMSLTKSASDYLVGQTVPED--IS-

ENRIWQIFDLNGYDPAYAGSVLYGWCTRAFGKRNTVW-LYGPATTGKTNIAEAISHTV-PFYGCVNWTNENF

PFNDCVDKMLIWWEEGKMTSKVVEPAKAILGGSRVRVDQKCKSSVQVDSTPVIITSNTNMCVVVDGNSTTFE

HQQPLEDRMFRFELMRRLPPDFGKITKQEVKDFFAWAM-ANQVPVTHEFMVPRKVAG----NK-K-------

------------AETSKKRQ-----------------------------------LVDV-------------

----------TST-SYKSP-EKR-ARL--SVAPETPRSS--DVPVEP----------------APLRPINWC

SRYECRCDYHAQ-FESVTGECADC--EY-------------LNRGK---------NGCMFHNA---------

--------THCQICHA----------------------------VP-----PWE------------------

----------------------KENVPDF-------------------------------------------

-------------------------------NDFDDCNKEQ-------

>CaliforniaSeaLion|NC\_038539.1:291-2093/1-600

--------------M--------------------------------------------ASFYEVVAKIPSD

LEEHLPGICDDFVSVIMSKE--WRLPE----SSDLVLDQI-----------DQPKLTIADAVRKVFYFEWLK

YCRD------VEEPLFFFQFEKG-KENFHVHMVIETSNVSSMVLGRYIGTIKKKL-VRKVFREVEPQ-MPDW

LAVTKTKQS--GGVNKTYD---KGYIPAYLLPK-------TQPE---------LQWAWTNIEEY---KSASL

NLAERKRLVDEFLA-SLRRDGP--------------SQSEPD-----DQQPHGPVI-RNRTSQKYM------

ALVSWLVENGITSEKQWIQEDQESYLSFNAAGSSRSQIKSALDNASRIMSLTKKASDYLVGQSVPED--IT-

ENKIYQLFKMNGYDPAYLGSILLGWCQGRFGKRNTVW-LYGPATTGKTNLAEAIAHSV-PFYGCVNWTNENF

PFNDCVDKMLIWWEEGKMTSKVVESAKAILGGSKVRVDQKCKSSVQIDSTPVIITSNTDMCCVIDGNSTTFE

HRQPLEDRMFRINLEQRLSHDFGKITKREVREFLAWAQ-EYEVDVEHTFEVT-KLA------K-P-------

------------KVTKRSAP-----------------------------------LSD--------------

--------------DYKSP-AKR-ARLIPDLVAEEATSS----ALAE----------------AEEWDLNWD

RRYDCRCEAHSM-SVRVEGLCRDC--EY-------------LNRGK---------NMCLVHGD---------

--------TGCHVCHA----------------------------VP-----PW-------------------

----------------------------V-------------------------------------------

-------------------------------SDPDDCTDEQ-------

>WXG22705.1/1-613 MAG: rep protein [Bat adeno-associated virus 2]

-----------------------------------------------------------MSFYELVVKIPHD

LEENVPGAADSFVNWLLNKR--WELPE----GSDLDLDKI-----------DQPQLTLSDKIQRTILTDWRR

ITRS-------PGIKYFVQFEKG-SCYYHMHVLLEVGDVKSLVVGRYVSQMRKTI-VKVVYRDIEPR-LPDW

MALAKTKT---NGANRMRD---EGYIPAYLLPK-------RQPE---------LQWAWTNIQKF---ERAAL

NVSERRRVCEEEY-ADLALSQQ--------------SDASQN-----NYSESAPRR-VGRAAFDYM------

ALVKWLVEKGITSERAWMREDSDSYLSYNATGASRAQIKSSLDNACRIMANTKTAADYLIGDEVPED--IE-

DNRMFRIFKLNGYDPAYAASVLLGWCQRGFGKRNTVW-LFGPATTGKTNIAEAIAHSV-PFFGCVNWTNENF

PFNDCVDKMVIWWEEGKMTAKVVESAKAILGGSIVRVDQKCKSSAQIEQTPVIITSNTNMCEVIDGNSTSFE

HRQPLEDRMFKFELLHRLPPDFGKITKAEVRGFFAWAK-SVRVEVEPAFSVK----------K-I-------

------------PALFLKRP-----------------------------------RPEG-------------

----------AEPSEAINP-GKK-ARH-ESFAP----------ETLP-----------------EEEPANFA

LRYVHKCSRHLA-MNQMLFPCRNC--ER-------------MNLNC---------NICVPHGV---------

--------SDCTICFP-----RLEP------------------DGA-----PEPSV----------------

---------------VHDNHDLPVDNWDF---YV--------------------------------------

--------------------------------NLDDKNKEQ-------

>BatAAV\_YNM|NC\_014468/1-613

-----------------------------------------------------------MEFYSIVLRLPGD

FDSEVPGLQDSFYKWISGPR--RELPE----WSDLDPGQI-----------ESAYQILADKLVREFAQKWAA

FSED-------PRAPYFAQLEKG-RENFHVHVLASSKKVGSFVVGRYVRKMRQHL-VDVVFRKCEPV-DADW

LQVQKSGN---HKSNEIKD---EGFIPAYLLPK-------RQSE---------LQWAWTNIEKY---ERATL

SVAERARLVEEWK--RSLAAEE--------------SDPAE--------PERRPRK-STKSASEYM------

ALVRWLVDNGIATEREWMREDSDGYLSYNATGATRAQIKAALDNAARIMVNTKTAADYLVGRNPPLD--VE-

DNRIYRLFRMNGYDPAYAGSVLLGWCRTGFGKRNTVW-LFGPATTGKTNLAEAISHSV-PFYGCVNWTNENF

PFNDCVDKMIIWWEEGKMTSKVVESAKAILGGSKVRVDQKCKNSQQIEPTPVIITSNTNMCEVVDGNSTTFE

HRQPLEDRMFKFELTVRLQPTFGKITKQEVREFFKWAE-LNAVDVEYDFLVR----------K-I-------

------------NQSDTGGG-----------------------------------VKRG-------------

----------AEPTKDEPP-AKR-VFF-YGATSEGEDVR----EGAP----------------GESDSVNFA

ERYVSKCSKHLS-WSNMRYPCRAC--ER-------------MNADV---------NVCTPHGC---------

--------RDCPECFP-----R----------------------PA-----PVPIA----------------

---------------EHDLCLAPIEDSDF---YV--------------------------------------

-------------------------------GCIDDVNKEQ-------

>BatAAV2|WXG22610.1/1-611 MAG: rep protein [Bat adeno-associated virus 2]

-----------------------------------------------------------MEFYSVVIRLPND

FSDEVPGLQESFFAWIMSDR--NPLPE----WSDLDPGQI-----------DKPYQIVADKMVRECVAKWDG

LSRT-------ENQPYFAQLEKR-PENVHIHLLLSAKVIASFVAGRFFKHVVKHL-VDVVYRSCAPT-ADGW

FEVRKSST---RGANLIQT---EGFIPAYLLPK-------RQSE---------LQWAWTNIEKY---ARATL

NVAERARLVEEWKLERPSPKAE--------------SVSA------------VPVK-NAKSVTEYM------

ALVQWLVDNGIATERDWMRESTESYLSYNATGGSRAQIKAALDNAARIMINTKTASDYLIGASPPAN--VA-

DNRIYRLFALNGYDPAYAGSVLLGWCRNGFGKRNTVW-LFGPATTGKTNLAEAISHSV-PFYGCVNWTNENF

PFNDCVDKMIIWWEEGKMTSKVVESAKAILGGSKVRVDQKCKNSQQIEPTPVIITSNTNMCEVVDGNSTTFE

HRQPLEDRMFKFELAVRLQPSFGKITKQEVREFFKWAE-LNAVDVEYDFLVR----------K-I-------

------------GQSDTGGG-----------------------------------AKRG-------------

----------AEPSKDEPP-AKR-VFF-YGAPSEGEDVR----EGAP----------------GESDSVNFA

ERYVSKCSRHLS-WSNMRFPCRAC--ER-------------MNADA---------NVCTPHGC---------

--------GDCPDCFP-----R----------------------PA-----PVPIA----------------

---------------EHDLCLAPIEDSDF---YV--------------------------------------

-------------------------------GCVDDVNKEQ-------

>RhinolophusPusillus|MF682926\_\_Rp-BtAAV1\_34C\_MJ\_YN\_2012/1-666

-----------------------------------------------------------MSYYGIVVRIPWD

VIYQLPQVADSVLIQHETAQ--IFTPD----DSDLDIYEI-----------NNVEWSMAQEMHEHFINKWIE

ITKH-------EAVKYFAQLEKG-KEFFHIHYVIEMTGMKSMCLGRYLNVIEGHV-IRETFGIYHHK-IDNF

IQIDKTRT---NGPNRQYD---DDFILAYLIPK-------RQPE---------LQWAWTTIDKF---ARAAL

NIAERARLAEEFQLGLAARREE--------------ARLERI-----SNNNGNPKI-CGKSSRRYM------

ELVNWLVEKGVTSERDWIKEDQESYLSYNATGSSRGQIKAALENACRIMSTVKKASDYLVGTEFPED--IE-

KNRVYRIFQMNGYDPAYAGSIFLGWCRRQFGKRNTIW-LFGPATTGKTNIAEAVAHAV-PFYGCVNWTNENF

PFNDCVDKMIIWWEEGKMTAKIVESAKAILGGSTVRVDQKCKSSCQIEQTPVIVTSNTNMCAVIDGNSTTFE

HQQPLEDRMFKFELTTRLQSDFGKISKAEIKEFLAWAD-VNRVEVKHEFRVQ----------RVY-------

------------THVMMKRP-----------------------------------APAW-------------

----------EEPTEGINT-AKK-LKT-ESVAAVPSEG-------------------------EE----DFG

QRYVNRCTNHMN-LTVMRFPCKFC--AK-------------MNQTE---------DICFTHGA---------

--------KSCEICFPTNNVVKLSPVKIQYEEKKEQI------VEA-----PKEQILLC-------------

---------EKMADVEEEIKKKIQEERDFVEQYG-DRCNICKMRG-WFNP-----------KCGLCAEIK--

-------------------------------GLMDDLNKEQ-------

>ParvoviridaeDogfe340C1|WDW25820.1/1-602 MAG: Rep [Canine parvovirus]

--------------M--------------------------------------------ASFYQFVVKLPED

FASDLPNLSPALEESLTNFQ--VQIPD----WSDLNVNKI-----------DEIHVGIGERIQRCFNQEWRR

KSNN-------EEFKYFYQLEKA-SDKHHIHMMVETTGVKSMVLGRYVNQIKKTL-VDWVYGGAEPQFEEDW

FHVCKTSPV--GGTNRVYS---QSFIPTYLLPK-------KQEE---------LQWAWTNIKKY---IKAAL

SERVRDEIVEEHK-VELAAR-------------------EEA-----GEFQSTPKV-RNKTAETYM------

KLVQWLVENGITSERQWIQEHQESYLSYNASSSNRSQIKAAMDNASKIMSLTKKASDYLIGKCVPEN--IC-

NNRIYKILKLNNYHVEYVASILLGWSRGEFGKRNTIW-FFGPATTGKTNIAEAIAHAV-PFYGCVNWTNENF

PFNDCVDKMVIWWEEGKMTSKVVESAKAILGGSRVRVDQKCKSSVQIDPTPVVITSNTDMTVVVDGNSTTFE

HRQPLEDRIFKFFLEERLPDDFGKVTKEEVQQFFAWAE-QNRVKVEPCFTVP----------KSM-------

------------SGHALKRP-----------------------------------ASSC-------------

----------EG--EDIKR-AKS-AQP-SVADSLLIQADA-GARGSP---------------PTDWRPERWH

SRYFERCDFHGQREAIIEQFCKYC--EY-------------LNRGR---------AYCFPHEN---------

--------VRCQICHA----------------------------RA-----PWD------------------

---------------------------------------------------------------------NN-

-------------------------------VELEDVNKEQ-------

>UAJ21440.1/1-646 nonstructural protein 1 [Duck adeno-associated virus]

--------------MCA------------------------------------------ATYYEVIVELPSD

LETQLPLVSDSFVNWVTSKE--WEPPL----DSKWDMDQV-----------DQVQLTLGDKIQREILKHWRT

ITGN-------PEAKYFVQLEQG-ESYFHLHTLLECCKVKPLVLGRYINQIEKKL-VSTVYGGHNPQ-IDNW

MRITKTKSV--GGSNKIRA---ESYIPAYLIPK-------QQPE---------VQWAWTNIEEY---IKACL

NTDLRGSIAAEHF-EKQGLD----------------GPKKQSL---QFSSDGAPVI-ESKSSKRYM------

GLVGWLVEKGITTEKQWILENQESYLSFQASGNSARQIKTALDNAAKLMLLTKTAPDYLVGKDMVED--IT-

ENRIYKILEMNNYDPAYVGNIFLGWSKQQFGKRNTIW-LFGPATTGKTNIAEAIAHAV-PFYGCVNWTNENF

PFNDCTDKMIIWWEEGKMTAKVVETAKAILGGSKVRVDQKCKSSIQLDPTPVIITSNTNMCYVVDGNTTTFE

HAQPLQDRMFKLELTRRLPDNFGKVTKQEVRDFFKWAE-QNPVEIVPEFHVR----------K---------

-------------AESRKRP-----------------------------------APE--------------

-----------EREDKSLA-AKA-PRT---------------DEPLP---------------SPGEEGTSLS

RRYVFKCAKHLG-MVTMMWPCKDC--ER-------------ANSAV---------NQCILHKS---------

--------LACKECYP------------DY-D-----------ENP-----PLSDTQLSETDS-------FK

TSLLEAKSQDPPLV----------NDKKW------TACSYHQLTGVAKP------------TCSMCQLRNV-

--------------------------------DLDDCNSEQ-------

>QKN88764.1/1-636 MAG: replication protein [Dependoparvovirus sp.]

--------------MPS------------------------------------------PTFYEVIVELPSD

LDTQLPLVSDSFVNWITSKT--WEPPL----DSDWDMEQV-----------DQVQLTLGDKIQREILKQWRV

ITGD-------PDPKYYVQLEQG-ESYFHLHTLLECCNIKPLVLGRYIKQIEKKL-VSTVYGGHTPL-IDNW

MRITKTKAI--GGSNKIRA---QSYIPAYLIPK-------KQPE---------VQWAWTNIEEY---IKAVL

NASLRHSIGEEHV-QQQGLV----------------SRDSDNL---ARNSEGAPII-ASKCSKKYM------

ELVDWLVEKGITTEKQWLLENKESYRSFQASSNSARQIKAALQGAVQEMLLTKTASDYLVGKDPIGD--IT-

ENRIYQIMEMNGYDPLYVANLLVGWCQMKYGKRNTIW-LFGPATTGKTNIAEAIAHAV-PFYGCVNWTNENF

PFNDCLEKMIIWWEEGKMTAKIVETAKAILGGSKVRVDQKCKSSMQLEPTPVIITSNTNMCYVVDGNTTTFE

HAQPLQDRMFKLELLKRLPDDFGKVTKKEVKDFFAWGA-KNTLEVKSEFLVR----------K---------

-------------AESRKRH-----------------------------------APE--------------

----------VGSEDKSPP-AKA-PRA---------------DERQP---------------SSGEEGTSIS

SRYVLKCAKHLG-MVTMMWPCRDC--EK-------------ANCNI---------NQCILHKT---------

--------LSCKECFP------------DY-DVDS---------SP--------------------------

---------QPPLVKSEDELSKDKDSKIW------TPCSYHHLTGVANH------------KCSMCKLRNV-

--------------------------------DLDDCDDEQ-------

>QLF86431.1/1-650 MAG: replication protein [Dependoparvovirus sp.]

--------------MPS------------------------------------------PTFYEVIVELPSD

LDTQLPLVSDSFVNWITSKT--WEPPL----DSDWDMEQV-----------DQVQLTLGDKIQREILKQWRV

ITGD-------PDPKYYVQLEQG-ESYFHLHTLLECCNIKPLVLGRYIKQIEKKL-VSTVYGGHTPL-IDNW

MRITKTKAI--GGSNKIRA---QSYIPAYLIPK-------KQPE---------VQWAWTNIEEY---IKAVL

NASLRHSIGEEHV-QQQGLV----------------SRDSDNL---VRNSEGAPII-ASKCSKKYM------

ELVDWLVEKGITTEKQWLLENKESYRSFQASSNSARQIKAALQGAVQEMLLTKTASDYLVGKDPIGD--IT-

ENRIYQIMEMNGYDPLYVANLLVGWCQMKYGKRNTIW-LFGPATTGKTNIAEAIAHAV-PFYGCVNWTNENF

PFNDCLEKMIIWWEEGKMTAKIVETAKAILGGSKVRVDQKCKSSMQLEPTPVIITSNTNMCYVVDGNTTTFE

HAQPLQDRMFKLELLKRLPDDFGKVTKKEVKDFFAWGA-KNTLEVKSEFLVR----------K---------

-------------AESRKRH-----------------------------------APE--------------

----------VGSEDKSPP-AKA-PRA---------------DERQP---------------SSGEEGTSVS

ARYVLKCAKHLG-MVTMMWPCRDC--EK-------------ANCNI---------NQCILHKT---------

--------LSCKECFP------------DY-EQESV-------TTP-----PLS------------------

ESDEEVTSHQPPLVNLRDELLRSEKQKTW------TPCSYHHLTGVANH------------KCSMCKLRNV-

--------------------------------DLDDCDDEQ-------

>DependoparvoBird|QKN88762.1/1-647 MAG: replication protein [Dependoparvovirus sp.] Isolate hftbif18par1

--------------MPS------------------------------------------PTFYEVIVELPSD

LDTQLPLVSDSFVNWITSKT--WEPPL----DSDWDMEQV-----------DQVQLTLGDKIQREILKQWRV

ITGD-------PDPKYYVQLEQG-ENYFHLHTLLECCNIKPLVLGRYIKQIEKKL-VSTVYGGHTPL-IENW

MRITKTKAI--GGSNKIRA---QSYIPAYLIPK-------KQPE---------VQWAWTNIEEY---IKAVL

NAALRHSIGEEHF-QQQGLA----------------LRDSTNL---ARNSEGAPII-ASKCSKKYM------

ELVDWLVEKGITTEKQWLLENKESYRSFQASSNSARQIKAALQGAVQEMLLTKTASDYLVGKDPIGD--IT-

DNRIYKILEMNGYDPLYVANLFVGWCQMKFGKRNTIW-LFGPATTGKTNIAEAIAHAV-PFYGCVNWTNENF

PFNDCTEKMIIWWEEGKMTAKIVETAKAILGGSKVRVDQKCKSSIQLEPTPVIITSNTNMCYVVDGNTTTFE

HAQPLQDRMFKLELLKRLPDDFGKVTKKEVKDFFAWGA-KHTLKVNSEFLVQ----------K---------

-------------AESRKRH-----------------------------------APE--------------

----------VGSEDKSPP-AKA-ARA---------------DELQP---------------SSGEEGTSVS

VRYVLKCAKHLG-MVTMMWPCRDC--EK-------------ANCNI---------NQCILHKT---------

--------LSCKECFP------------DY-D-DT---------NP-----PSS------------------

SSDEDIPSHQPPLVSIRDEPSRGEKSNIW------VPCSYHHLTGVANH------------KCSMCKLRNV-

--------------------------------DLDDCDNEQ-------

>QKN88760.1/1-658 MAG: replication protein [Dependoparvovirus sp.]

--------------MPS------------------------------------------PTFYEVIVELPSD

LDTQLPLVSDSFVNWITSKT--WEPPL----DSDWDMEQV-----------DQVQLTLGDKIQREILKQWRV

ITGA-------PDPKYYVQLEQG-ESYFHLHTLLECCNIKPLVLGRYIKQIEKKL-VSTVYGGHTPL-IENW

MRITKTKAT--GGSNKIRA---QSYIPAYLIPK-------KQPE---------VQWAWTNIEEY---IKAVL

NASLRHSIGEEHV-QQQGLVSRDSQEDVQRQS--LFSRDSDNL---ARNSEGAPII-ASKCSKKYM------

ELVDWLVEKGITTEKQWLLENKESYRSFQASSNSARQIKAALQGATQEMLLTKTASDYLIGKDTVGD--IT-

ENRIYQIMEMNGYDPLYVANLLVGWCQMKYGKRNTIW-LFGPATTGKTNIAEAIAHAV-PFYGCVNWTNENF

PFNDCLEKMIIWWEEGKMTAKIVETAKAILGGSKVRVDQKCKSSMQLEPTPVIITSNTNMCYVVDGNTTTFE

HAQPLQDRMFKLELLKRLPDDFGKVTKKEVKDFFAWGA-KNTLEVKSEFLVR----------K---------

-------------AESRKRH-----------------------------------APE--------------

----------VGSEDKSPP-AKA-PRA---------------DERQP---------------SSGEEGTSVS

SRYVLKCAKHLG-MVTMMWPCRDC--EK-------------ANCNI---------NQCILHKT---------

--------LSCKECFP------------DY-DLDF---------SPR-EGSPL-------------------

-------KSQPPLVKSEDELSKDKDSKIW------TPCSYHHLTGVANH------------KCSMCKLRNV-

--------------------------------DLDDCDNEQ-------

>AAV\_MHH-05-2015|NC\_040671.1:431-2377/1-648

--------------MTT------------------------------------------PTYYELIVELPSD

IDTQLPLVSDSFVRWVTSKT--WEPPL----DSKWDMDQV-----------DQVQLTLGDKIQREILKQWRT

ITGD-------PDPKYYVQLEQG-ETYFHLHTLLQCCNIKPLVLGRYVKQIEKKL-VSTVYGGHNPL-IDNW

LRITKTKSI--GGSNKIRA---QSYIPAYLIPK-------KQPE---------VQWAWTNIEEY---IKAVL

NSELRHQIGEAHF-QEQGLA----------------LRDSTNL---SRNSEGAPII-VSKCTKKYM------

ELVEWLVEKGITTEKQWLLENKESFRSFQASSNSARQIKAALQGATQEMLLTKTASDYLIGKDPIGD--MT-

DNRIYKILEMNGYDPLYVANLFVGWCQMKFGKRNTIW-LFGPATTGKTNIAEAIAHAV-PFYGCVNWTNENF

PFNDCLEKMIIWWEEGKMTAKIVETAKAILGGSKVRVDQKCKSSMQLEPTPVIITSNTNMCYVVDGNTTTFE

HAQPLQDRMFKLELLKRLPDDFGKVTKKEVRDFFAWGA-KHTVEVDSCFLVR----------K---------

-------------AESRKRH-----------------------------------APE--------------

----------VASEDKSPP-AKA-ART---------------DELQH---------------LSGEEGTSVS

ARYVLKCAKHLG-MVTMMWPCRDC--EK-------------ANCNI---------NQCILHKS---------

--------LSCKECFP------------DY-DSDVSVQEGEPSGNP-----PLS------------------

SSDEDIPSHQPPLV---------KDCKPW------TPCSYHHLTGVANR------------NCSMCKLRNV-

--------------------------------DLDDCDSEQ-------

>AvianAAV|NC\_006263.1:244-2235/1-663

----------------M------------------------------------------RSYYEVIVQLPND

VESQVPGISDSFVNWITSRE--WTLPE----DADWDLDQV-----------DQVQLTLGDKIQREIRNHWGT

MAKE-------PDFHYFIQLEQG-EVFFHLHVLLETCSVKPMVLGRYIRHIQQKI-VSKVYCGHEPA-MEGW

MRVTKTKNF--GGANKVRA---ESYIPAYLIPK-------QQPE---------VQWAWTNVPEY---IKACL

HRELRASLARLHF-EEAGLS-----------------QSKENL---ARTADGAPVI-ATRVSKRYM------

ELVDWLVEKGITTEKEWLLENRESFRSFQASSNSARQIKTALQGAIQEMLLTKTAEDYLVGKEPVSDDEIR-

QNRIYKILELNHYDPAYVGSILVGWCQKKWGKRNTLW-LFGPATTGKTNIAEAIAHAV-PFYGCVNWTNENF

PFNDCVEKMIIWWEEGKMTAKVVETAKAILGGSRVRVDQKCKASVPIEPTPVIITSNTNMCYVIDGNTTTFE

HKQPLEDRMFKLELLTRLPDDFGKVTKQEVRQFFRWSQ-DHLTPVIPEFLVR----------K---------

-------------AESRKRP-----------------------------------AP---------------

-----------SGEGYISP-TKR-PAL---------------AEQQQ---------------AS-ESAEPVP

TRYRIKCSKHCG-MDKMLFPCQIC--ES-------------MNRNI---------NICAIHKT---------

--------TECKECFP------------EYGDKDTV-----P-ELP-----PCTEHNVSRCYQCHSGELYRV

TSD----SDEKPAP-ESDE----GTEPSY------APCTIHHLMGKSRGL----------VSCAACRLKNST

L-----------------------------HDDLDDGDLEQ-------

>WBY51256.1/1-654 replication protein [Psittacidae dependoparvovirus]

-----------MAAGRD------------------------------------------TQFFELIVQLPSD

IETQLPNISESFVNWITGKQ--WRLPE----GSDWNLDKV-----------DQVQLTLGDKIQREIYRYWVS

ITHN-------ENAEFFVQLEES-PNYFHLHVLLECCGIKPLVLGRYVKHLQQKL-ISTVYSGHAPQ-IENW

LRITKTKAV--GGSNKMRG---KSYIPAYLIPK-------VQPE---------VHWAWTNIPEY---APACL

NARLRAEIAETHF-LEAGYTQR--------------TPPEGGL---AKNGDGAPVI-LSKASRRYM------

ELVDWLVDKGITTEKQWLTENKESYRSFQASGNSARQIKVALQNAIQEMLLTKTAPDYLIGRDPPDEEQIRT

SNRIYDIFQRNGYDPAYAANVLVGWCKGAFNKRNTVW-LFGPATTGKTNIAEAIAHAV-PFYGCVNWTNENF

PFNDCLNKMIIWWEEGKMTAKIVESAKAILGGSRVRVDQKCKSSEEIQPTPVIITSNTNMCHVIDGNSTTFE

HQKPLEDRMFLFELVKPLPPNYGKVTKQEVLDFFRWGL-DHPIEVTHEFRVP----------K---------

-------------AAASKRKRTNEN--------------------------EFSSTPEAIKEAFGTA-----

-------SPPIRREDVFAV-TA------------------------------------------SGDSSADL

DRYERKCTKHLH-LDKVRFYCSAC--EG-------------INRRL---------DVCFSHGT---------

--------LNCEECFP-------------------------------------Q------------------

-----------------------ENKAVF------EACASCHLMGKKPDP----------VKCPACKLKNVA

LLMGEDSSDE---------SSLVRP-----EQEWDDTLNEQ-------

>Psittacidae|QTE03943.1/1-676 MAG replication-associated protein [Psittacidae dependoparvovirus]

--------------MDS------------------------------------------NKFYEIIVQLPND

IEAELPNISDSFVNWISNRE--WTLPE----GSDWDLDQV-----------DQVQLTLGDKIQREMYRHWVG

ITHD-------ENAYFFTQLEQS-PNYFHLHVLFQCCGIKPMVLGRYVKQIQQRV-VSTVYSGHNPQ-IENW

MRITKTKNV--GGCNKIRD---KSYIPAYLIPK-------QQPE---------VHWAWTNIQEY---VNACL

NARLRQEIAEAHL-QEAGF-EN--------------LSQEGGL---ARNSDGAPVI-PGKASRRYM------

ELVDWLVDRGITTEKQWLTENKESYRSFQASSNSARQIKAALQNAIQEMLLTKSAPDYLIGKTIPSEEDIR-

KNKIYDIFQRNGYDPAYAANVLVGWCKGAFNKRNTIW-LFGPATTGKTNIAEAIAHAV-PFYGCVNWTNENF

PFNDCLNKMIIWWEEGKMTAKVVESAKAILGGSRVRVDQKCKSSEEIQPTPVIITSNTNMCHVIDGNSTTFE

HQKPLEDRMFLFELVKVLPPDFGKVTKQEVRDFFRWGI-ENPIEVTHEFRVP----------K---------

-------------AAASKRKSTNQN-----------------------PDDEFQFTPETIKRATTSA-----

-------FQSVSRENTFDS-TSR-FEE---------------TRTQK---------------ETSGSSTPEL

DRYERKCAKHLH-LDKVRFYCSGC--ET-------------INRRL---------DVCFSHGV---------

--------LNCEECFP------------S--D-------------------PVQ------------------

-----------------------KIKLCY------QPCAICHLLGKSPDV----------KKCAACRLKNVT

MQIIEESSSESEGRASNEASSLIRP-----EQEWDDTLNEQ-------

>Dependo\_wpk049par01|QKE60686.1/1-675 MAG: replication protein [Dependoparvovirus sp.]

--------------MAN------------------------------------------PSYFEFVIRLPAD

VEEDLPGIPDSFIDWLCRES--PELPE----GSDLDPEQI-----------EMPMVVLGQRIIKIILNAWRS

ITKQ-------QDVKYYVQLEKV-DSAFHLHVLVETCKVPSFTLGRHVNRIKEDI-VRQVYQKVAPR-IDDW

FSIAKTRGG--HKSNKIHS---ESYIDAYLLGK-------VQPE---------LQWAWTNIPAY---VSACL

SLAERQELVKNHR-IELGHRFS--R-----------SASISS-----STGSTAPVI-QTKSADRYM------

ALVDWLVENGITTAKQWLQEDKDSYLSFHATGSSSRQVKSALENACEVMSLTKTAADYLIGKQVPED--IT-

QNRIYKLFELNGYDPHYAGKILLGWCKREHGKRNTVW-LFGPATTGKTILAEAIAHAV-PFFGCVNWTNENF

PFNDCVNKMLIWWEEGKMTTKIVESAKAILGGSQVRVDQKCKSSSPIEQTPVIITSNTPMYRVYDGNSTTFE

HEKPLKDRMFCFEFLRPLDKTFGKVTKQEVKEFFAWAQAQDDVIVEDSFHVL----------K---------

-------------SRGVKRSHDCDP---------------------------LPICPEG-------------

----------AEPKEATPT-TEV-INISAAAPPSSVDDGT-ASSADP--------------PPPPPPDSAEV

SLYKNKCSRHLA-LSIVKYVCRDC--EL-------------LNKKG--------GDVCIMHNQ---------

--------EGCSQCFP------------GYEES----------IEP-----PVHKKSK--------------

-----------------------------------TVCGQCHLLGNNFCTHYEPMVIGKLMRCTSCVIKYR-

-------------------NGVTLPPWGDCQMCMDLDELEQ-------

>BirdAAV|QKE54950.1/1-601 replication protein [Parvoviridae sp.] METAGENOME

-------MCDLANALQSALQ-------------------------------------EGTKFYELIIRLPGD

VDSHLPGISETFIRWLTTTT--PTLPN----DHEWNLTLC-----------NQPLVVLATAVTNSITQKWRS

FQQ--------RTLRTFYQLEEG-TEYFHLHCLLETGDLRSFVLGRYVRQISLHL-TTTIFENTTPQ-LENW

ITITKSRR---GGQNKQQD---LQYILGYLIPK-------KQPE---------CHWAWSNIPLL---KKACL

NTTERDRLHALYA----------------DL----LGDKENQDPD-P-TINRAPII-SNRAARKYA------

EVVDWLVQQGITTEKQWLIEDKDSYRSFQSTANSSRQVRAALENARAEMLLTKSAQDYLIGRSASPD--MD-

TNRIYQIFLKNGYDPLLCSNILVRWATRAFNKRNTIW-LFGPATTGKTNIAEAIAHTV-PFYGCVNWTNENF

PFNDCVDKMIIWWEEGKMTNKVVEAAKAILGGSRVRVDQKCKGSVQIEPTPVIVTSNTDMTIVADGNSYTME

HKDPLEERMFKFLLTHKLPPSFGKITKQEVRAFLKWGQ-DNPVNVEPTFLVP----------K---------

-----------------------------------------------------AQEP---------------

------------------P-PT------DNIDSATNE------QPGP------------S----APRKRPAD

ELDAQPCSDHQDQNTLAVLACTKCHPETAG--KSPRFSNKYFRETF----------QCMFHKT---------

--------FNCLECYP---------------------------DTP--------------------------

-----------------------------------DSTDIE-------------------------------

----------------------------------DDVFDEQ-------

>Bird\_cfw059par1QKN88755.1/1-599 capsid protein [Dependoparvovirus sp.]

-----------MNSVEELLH-------------------------------------HNKQYFELIIRLPGD

VDNHLPGISDHFVQWLTTTI--PDLPD----DHDWDVAKV-----------NQPLVVLAGAITHTISSKWRS

FQQ--------QTLKTFYQLEEG-TEYFHLHCLLEMGSIKSFVLGRYIRQIAQTL-TTNLFENRTPN-LENW

FSITKSRR---GGQNKIQD---HHYLLAYLIPK-------LQPE---------CQWAWTNIPLL---QKATL

NASERARLHNLYL----------------CN----ISEKENHTPT-PDSLTKAPII-SNRTARKYC------

EVVDWLVAQGITTEKQWLIEDKDSYRSFQSTANSSRQVRAALDNARAEMLLTKSAPDYLLGPSTSTD--MD-

TNRIYQIFLKNGYDPLLCANILVRWASRDFNKRNTIW-LYGPATTGKTNIAEAIAHAV-PFYGCVNWTNENF

PFNDCVDKMIIWWEEGKMTNKVVEAAKAILGGSKVRVDQKCKGSVQIEPTPVIITSNTDMTVVADGNSITME

HKEPLEERMFKFQLNIKLPIDFGKITKQEVRNFFRWGA-DNKVNIVPQFNVP----------Q-N-------

----------------------------------------------------INNAT---------------

------------------P-PD------SSLPCA---------QPGP------------ST-STTPTKRKAL

EPLATRCEEHADCNNLSVLCCSAC---TSGKPKSPKFSNKYFRENF----------HCMIHGT---------

--------FNCLECYP---------------------------LSS--------------------------

-----------------------------------DDTDID-------------------------------

----------------------------------DDVFAEQ-------

>MuscovyDuck|NC\_006147.2:548-2431/1-627

------------MAFSRPLQI------------------------------------SSDKFYEVIIRLPSD

IDQDVPGLSLNFVEWLSTGVWEPT--------GIWNMEHV-----------NLPMVTLADKIKNIFIQRWNQ

FNQ--------DETDFFFQLEEG-SEYIHLHCCIAQGNVRSFVLGRYMSQIKDSI-LRDVYEGKQVK-IPDW

FSITKTKR---GGQNKTVT---AAYILHYLIPK-------KQPE---------LQWAFTNMPLF---TAAAL

CLQKRQELLDAFQ----------------E------SEMNAVVQE-DQASTAAPLI-SNRAAKNYS------

NLVDWLIEMGITSEKQWLTENKESYRSFQATSSNNRQVKAALENARAEMLLTKTATDYLIGKDPVLD--IT-

KNRIYQILKLNNYNPQYVGSVLCGWVKREFNKRNAIW-LYGPATTGKTNIAEAIAHAV-PFYGCVNWTNENF

PFNDCVDKMLIWWEEGKMTNKVVESAKAILGGSAVRVDQKCKGSVCIEPTPVIITSNTDMCMIVDGNSTTME

HRIPLEERMFQIVLSHKLEGNFGKISKKEVKEFFKWAN-DNLVPVVSEFKVP----------T-N-------

------------EQTKLTEP-----------------------------VPERANEPSE-------------

------------PPKIWAP-PTR-EEL-EEILRASPELFA-SVAPLP------------SSPDTSPKRKKTR

GEYQVRCAMHSLDNSMNVFECLEC--ERA---NFPEFQS--LGENF-----------CNQHGW---------

--------YDCAFCNE---------------------------LKD--------------------------

-----------------------------------DMNEIEHV-----------------------------

-------------------------------FAIDDMENEQ-------

>GooseParvovirus|NC\_001701.1\_cds\_NP\_043514.1\_1/1-627

------------MALSRPLQI------------------------------------SSDKFYEVIIRLSSD

IDQDVPGLSLNFVEWLSTGVWEPT--------GIWNMEHV-----------NLPMVTLAEKIKNIFIQRWNQ

FNQ--------DETDFFFQLEEG-SEYIHLHCCIAQGNVRSFVLGRYMSQIKDSI-IRDVYEGKQIK-IPDW

FAITKTKR---GGQNKTVT---AAYILHYLIPK-------KQPE---------LQWAFTNMPLF---TAAAL

CLQKRQELLDAFQ----------------E------SDLAAPLPD-PQASTVAPLI-SNRAAKNYS------

NLVDWLIEMGITSEKQWLTENRESYRSFQATSSNNRQVKAALENARAEMLLTKTATDYLIGKDPVLD--IT-

KNRVYQILKMNNYNPQYIGSILCGWVKREFNKRNAIW-LYGPATTGKTNIAEAIAHAV-PFYGCVNWTNENF

PFNDCVDKMLIWWEEGKMTNKVVESAKAILGGSAVRVDQKCKGSVCIEPTPVIITSNTDMCMIVDGNSTTME

HRIPLEERMFQIVLSHKLEPSFGKISKKEVREFFKWAN-DNLVPVVSEFKVR----------T-N-------

------------EQTNLPEP-----------------------------VPERANEPEE-------------

------------PPKIWAP-PTR-EEL-EELLRASPELFS-SVAPIP------------VTPQNSPEPKRSR

NNYQVRCALHTYDNSMDVFECMEC--EKA---NFPEFQP--LGENY-----------CDEHGW---------

--------YDCAICKE---------------------------LKN--------------------------

-----------------------------------ELAEIEHV-----------------------------

-------------------------------FELDDAENEQ-------

>WGJ63685.1/1-628 REP [Goose parvovirus]

------------MALSRPLQI------------------------------------SSDKFYEVIIRLSSD

IDHDVPGLSLNFVEWLSTGVWEPT--------GIWNMEHV-----------NLPMVTLAEKIKNIFIQRWNQ

FNQ--------DETDFFFQLEEG-SEYIHLHCCIAQGNVRSFVLGRYMSQIKDSI-IRDVYEGKQIK-IPDW

FAITKTKR---GGQNKTVT---AAYILHYLIPK-------KQPE---------LQWAFTNMPLF---TAAAL

CLQKRQELLDAFQ----------------E------SDLAAPLPD-PQASTVAPLI-SNSATKNYS------

NLVDWLIEMGITSEKQWLTENRESYRSFQATSSNNRQVKAALENARAEMLLTKTATDYLIGKDPVLD--IT-

KNRVYQILKMNNYNPQYIGSILCGWVKREFNKRNAIMALTGPATTGKTNIAEAIAHAV-PFYGCVNWTNENF

PFNDCVDKMLIWWEEGKMTNKVVESAKAILGGSAVRVDQKCKGSVCIEPTPVIITSNTDMCMIVDGNSTTME

HRIPLEERMFQIVLSHKLEPSFGKISKKEVREFFKWAN-DNLVPVVSEFKVR----------T-N-------

------------EQTNLPEP-----------------------------VPERANEPEE-------------

------------PPKIWAP-PTR-EEL-EELLRASPELFS-SVAPIP------------VTPQNSPEPKRSR

NNYQVRCALHTYDNSMDVFECMEC--EKA---NFPEFQP--LGENY-----------CDEHGW---------

--------YDCAICKE---------------------------LKN--------------------------

-----------------------------------ELAEIEHV-----------------------------

-------------------------------FELDDAENEQ-------

>QKN88756.1/1-570 MAG: replication protein [Dependoparvovirus sp.]

----------------------------------------------------------MTSFFEIVVRLPND

FYAELPGISDAWVDNICEEN--LHPPD----TCDFNLDLV-----------EPPYVALAERIRQEINLEWSY

RAG---------PHKFFIQLEKG-EENYHIHVLLEPVEVKSFVFGRYLPGFKERI-KDRVYAGIEPQ-TADW

FEAAKVKK---GGANALRH---VSYITNYLLPK-------KQPE---------LQWAWTNLEEF---RLAAL

NLHERARLVEEQRL-ALEERHK-------EA-----TAPTNV----------TPRV-GGKSAERYM------

ALVNWLVTNGITSEKEWIQADQESYLTHNANSNSRAQIKTALDNASRIMQLTKTACDYLIGPEPPAD--VT-

TNRVYRIFEMNGYDPQLAGSILLGWANRRFGKRNAIW-LFGPATTGKTNIAEAIAHAV-PFYGCVNWTNENF

PFNDCVNKMLIWWEEGKMTAKIVESAKSILGGSRVRVDQKCKSSQQIDSTPVIITSNTDMTMVVDGNTTTFE

HREALEDRMFQFYLGKRLDNDFGKITKTEVREFFKWAE-LNPTTPPHVFRVP----------RVN-------

------------DAG-YKRPDSPAA------------------------SSYATERPS--------------

------------GEE---PAAKR-PRY-E-HKPVDNGRV--EKSTLDLWLE----------GNPTPAALVVH

DLMEAS----------------GS--V--------------FDMTV---------R----------------

---------EC----------------------------------------P--------------------

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-----------------------------------DSNKEQ-------

>MurineAAV1|MF416383.1\_cds\_AWB14637.1\_1/1-572

----------------------------------------------------------MTSFYEVVVKLPSD

FYDDLPGIDHVWIDNLCEEN--LHPPD----TCDFDLSLV-----------EPAYVNLAERIKQEIILEWSY

RAG---------KHRYFIQLEKG-EQFFHLHVLLDTVDVKGFVFARYASGFKQRI-RERVYCGIEPL-IPDW

FEITKTKKV--GGANAVRG---EAYIYNYLLPK-------KQSE---------LQWAWTNIPTF---ELAAL

NLNERQRLLEERRAEELAAREE-------RQ-----QSDSNS----------QNRV-YGKAAERYM------

ALVNWLVSNGITSEKEWIQADQVSYLTQNATSNGRAQIKTALDNASRIMQLTKTATDYLIGPSPPAD--VT-

TNRVYRIFEMNGYDPQLAGSILLGWANRRFGKRNAIW-LYGPATTGKTNIAEAIAHAV-PFYGCVNWTNENF

PFNDCVNKMLIWWEEGKMTAKIVESAKSILGGSRVRVDQKCKASQQIDSTPVIITSNTDMTMVVDGNTTTFE

HREALEDRMFQFYLGKRLDNDFGKIDKKEVREFFKWAE-LNQVPPPHVFRVP----------RVH-------

------------DAG-YKRPDSPAA------------------------SSYATERPS--------------

------------GEE---PAAKR-PRY-E-HKPVDNGRE--EKSTLDLWFH----------GNPTPAPMVVH

DLMDSS----------------GS--V--------------FNMTI---------R----------------

---------EC----------------------------------------P--------------------

------------------------------------------------------------------------

-----------------------------------DSNKEQ-------

>QKN88758.1/1-565 MAG: replication protein [Dependoparvovirus sp.]

----------------------------------------------------------MALFFEIVVKLPND

FYADLPGIADAWVEAICEEE--LHPPD----TCDFDLSLV-----------EAPYVTLAERVRQEINLEWSY

RAG---------THKYFIQLEKG-EQFFHLHVLIDRVDVKSFIFGRYVPGFKERI-RDRVYGGIEPQ-LPDW

FTVSKTKK---GGSNAQRD---EGYIYAYLLPK-------KQSE---------LQWAWTNIPKF---ELAAL

NLHERQRLLDEKRAEDLAAEQE-------NP-----RTEHN------------PRS-FGKAAERYM------

ALVNWLVENGITSEKEWIRADQVSYLTQNATSNGRAQIRSALDNASRIMQLTKTAIDYLIGPTPPED--VT-

TNRVYKIFSLNGYDPRLAGSILLGWAARRFGKRNTVW-LYGPATTGKTIIARAIAHAV-PFYGNVNWNNENF

PFNDSVNKMLIWWEEGKITAKTVEAAKAILGGSDVRVDQKCKASQQIDTTPVIITSNTDMTLVVDGNTTTFD

HKEALEDRMFQFYLFKKLDHDFGRVTKEEIRGFFKWAE-LNPVDVPHVFRVP----------RTL-------

------------DIS----SSSPSA------------------------STFAASTSE--------------

------------SEE---PVAKR-PRY-E--QPVDKGRV--EKSTLDFWLE----------GRPTPKPTFVA

DLSDST----------------ES--V--------------FDMKV---------R----------------

---------EC----------------------------------------P--------------------

------------------------------------------------------------------------

-----------------------------------DSNKEQ-------

>MurineAAV2|MF416384.1\_cds\_AWB14639.1\_1/1-565

----------------------------------------------------------MASFFEVVVKLPND

FFADLPGISDLWVETICNEE--LHPPD----TCDFDLSLV-----------ESPYVALAERVKQEIILEWSY

RAG---------THKYFIQLEKG-EHFFHLHVLLDCVNVKSFIFGRYVAGFRERI-RDRVYSGIEPQ-LPDW

LTSSKTKK---GGSNAQRD---EGYIYAYLLPK-------KQSE---------LQWAWTNIPKF---ELAAL

NLNERQRLLDEKRAEDLAAEAE-------NP-----KPEHN------------PRS-FGKAAERYM------

ALVNWLVENGITSEKEWIRADQVSYLTQNATSNGRAQIKSALDNASRIMQLTKTAIDYLIGPTPPED--VT-

TNRVYKIFSLNGYDPRLAGSILLGWAARRFGKRNTVW-LYGPATTGKTIIARAIAHAV-PFYGNVNWNNENF

PFNDSVNKMLIWWEEGKITAKTVEAAKAILGGSDVRVDQKCKASQQIDTTPVIITSNTDMTLVVDGNTTTFD

HKEALEDRMFQFYLFRKLDHTFGRVTKEEIRGFFKWAE-LNQVEVPHVFRVP----------RTL-------

------------DIS----SSSPSA------------------------STVAASTSE--------------

------------SEE---PADKR-PRY-E--QPVDNGRE--EKSTLDLWLE----------GRPTPKPMFVA

DLSAAK----------------SS--V--------------FDMKV---------R----------------

---------DC----------------------------------------P--------------------

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-----------------------------------DSNKEQ-------

>QTE04020.1/1-574 MAG: replication protein [Anser anser dependoparvovirus]

-----------------------------------------------------------MYFYEIIVKLPND

FDTELPGICDAWIDALCAEN--LTLPD----TSDLDASQI-----------EEAYVALGQRIVNEILLEWKY

RTG--------VRYEYFVQLEKG-EHGYHLHVLLEQSNVKSFVFGRYAPGIKRRI-VDKVYSGVEPV-IDLW

FKLSKTREQ--GGANALRH---ESYLYNYLLPK-------TQPE---------LQYAWTNIDKF---LLAAV

NLNERKRLVDEYRA-QFQKPSE-------DE-----ESAHSDG--------PVPKV-RNKTSERYM------

ALVKWLVENGITSEQEWVKTDMESFLTHNASSSSRAQIKTALDNASRIMQLTKTASDYLIGQKPPED--VS-

TNRVYRIFEMNGYDPRLAGSILYGWARRQFGKRNTIW-LYGPATTGKTIIAEAIAHAV-PFYGCVNWNNENF

PFNDSVNKMLIWWEEGKMTAKVVEAAKCILGGSRVRVDQKCKSSQQIESTPVIITSNTDLTVVVDGNTTTME

HRQPLEDRMFQFNLVHRLTPDFGKVTKQEIREFFKWAE-LNKTEVPDAFRVP----------RVQ-------

------------EDGEYISESSSAQ------------------------PSDETATSS--------------

------------GEE-HRP-SKR-PRY-E--DSVDDGGR--VKSTLEKWLL----------DNPMPTPASVS

DNSDSE----------------NP--V--------------FDMRV---------R----------------

---------EC----------------------------------------P--------------------

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-----------------------------------DSNKEQ-------

>WDW25764.1/1-605 MAG: replication-associated protein [Canine parvovirus]

--------------MCEQASSSFHF----------------RTPSSTH---------LAMEFFSLTAKLPTD

LDNDVPGISQSMRDNYYAAD--VQLPH----TSDMNPADI-----------DGPSVLVGGMVVDSMVRFWRE

KMM--------DDFQYFAQLELS-EHSFHVHCLLETKGTKGFVLGRYMPQLKERI-ESDVFGGNEIQ-LPYW

LKARKTKQQ--GGANVTVN---EGYILNYLLPK-------RQTE---------LQWAWSNIERY---ERALL

NIEERKRIEDEFKAEAQRRKAE-------GL-----EPEF-P-----------QRS-SSSASDRYM------

ALVNWLVEHGITSEKEWIQEDQESYIRHHTHSNGRAQIKAALDNAAKIMSLTKSAKDYLIGPSPPSS--PE-

ENRIYRIFETNGYDPKLAGSILLGWARRGFGKRNAIW-LYGPATTGKTNIAEAIAHAV-PFYGCVNWTNENF

PFNDCVDKMLIWWEEGKMTAKIVESAKAILGGSKVRVDQKCKSSQQIDSTPVIITSNTDMTVVVDGNITTME

HRQPLEDRMFMFYLGKRLPDDFGKISKREVREFFKWAE-LNKMEVVPEFNVP----------SE--------

--------------SDYKRKRETGI------------------------EPFVTRTPDSADA----------

-----------SSEA-PAP-KKP--RY-----------E--TKSKEQILYEHLLAENLGEISNET-----VN

DQHDVSCKHGKH------LFCAEC--D--------------FNKNV---------KT--YNKY---------

--------LEC----------------------------------------P--------------------

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-----------------------------------DSNKEQ-------

>BankVoleMgAAV1|QHD57622.1/1-593 replication protein [Adeno-associated virus]

-----------------------------------------------------------MEFFSVVIKLPTD

IDSDVPGVSENLRDEFYSAD--VPPPA----SSDMNPAEV-----------DSPSVEMASRIVRSVRNFWRE

KVM--------EDFCDFFQLELS-DDKFHIHCLFETKGTKGFVLGRYVPQFKERI-ESDVFGGNEIS-IPNW

FKPRKTKQQ--GGANQTVN---EGFILNYLLPK-------RQSE---------LQWAWSNIERY---ERALL

NLEERKRIEDEFKAENQRRKEQ-------GL-----EPEFKP-----------PRT-GGSASDRYM------

ELVNWLVEHGITNEKEWIQEDQESYIRHHTNSNGRAQIKSALDNAAKIMSLTKSAKDYLIGPCPPSS--PE-

ENRIYKIFQKNGYDPALAGSILVGWAKRQFGKRNAIW-LYGPATTGKTNIAEAIAHAV-PFYGCVNWTNENF

PFNDCVDKMLIWWEEGKMTAKIVESAKAILGGSKVRVDQKCKSSQQIDSTPVIITSNTDMRLVVDGNQTTYE

HKQPLEDRIFRFYLGKRLPDDFGKISKREVREFFKWAE-TNKVEVTPTFMVP----------VL--------

--------------GDHKRKRETDC------------------------EPFVARSSNETDALPDS------

----------LTEEE-SAP-KKT--RY-E---------E--QKTPAQIAYEQILK----AIADDTPKPDLVH

DYHDVTCKHGKH------LFCADC--D--------------FNKNV---------KS--YNKY---------

--------LEC----------------------------------------P--------------------

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-----------------------------------DSNKEQ-------

>WDW25800.1/1-602 MAG: replication-associated protein [Canine parvovirus]

--------------MEDQ----------------------------------------KTTFFSITVDLPGD

FTTDVDNLPEAWLDNLFSAQ--LNLPP----ESDLNPEQI-----------EAVYVRLAEQIIEQIRLEWAF

RVG--------KSYADFYQLELA-DRGYHIHVLLETKDVKGFVFARFLPSFKQRI-RDRVYAGREIL-LSDW

FKTRKTKNV--GGANQTVN---EGYILNYLLPK-------RQSE---------LQYAWSNIEKY---VPALL

NISERERLVSEHLELVKQRQAE-------RA-----ANGEAN-----------PRV-SGKTSERYM------

ALVNWLVEHGITSEKEWIREDQESYLTHNASSSSRSQIKAALDNASKIMMLTKSAEDYLIGQSPPIC--PE-

ENRVYRIFEMNGYDPVVAGSILLGWAKRRFGKRNAIW-LYGPATTGKTNIAEAIAHAV-PFYGCVNWTNENF

PFNDCVDKMLIWWEEGKMSAKIVESAKAILGGSKVRVDQKCKASQQIDSTPVIITSNTDMTIVVDGNQTTRE

HRQPLEDRMFQFYLGRRLPDDFGKISKKEIREFFKWAE-LNRVDVISQFEVP----------AYR-------

--------------GDYKRKREPEP------------------------DSFPAQTLERTD-----------

------------ARE-SSP-AKT-PRY-ETVAETETKTE--TKSQAQILYEQILVENCGGITG----NVTIS

DHHDVECKHGKS------LFCTDC--E--------------FNKNV---------KT--HDKY---------

--------LEC----------------------------------------P--------------------

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-----------------------------------DSNKEQ-------

>ParvoviridaeDogfe352C3|WDW25804.1/1-601 MAG: replication-associated protein [Canine parvovirus]

--------------MQN-----------------------------------------NTSFFEIRVKLPAD

FTCDVKSLPDAWMDELFGSS--IQLPD----TSDMNADQI-----------EPTYVNLSQRIVEQIRLEWNY

RVG--------KSYADFYQLEQT-ENGFHIHVLIETKDVKGFVLARFIPSFKQRI-TERVYAGCEIL-LDDW

FSPRKTKNV--GGANRTVD---KGYILTYLMPK-------KQSE---------LQWAWSNIDEY---SLALL

NLRERERLHTEYLAECAELRAQ-------RT-----ANGEAD-----------PEI-TGKTSEKYM------

SLVNWLVEHGITSEKEWIRENQKSYLTYNASSTNRAQIKSALDNAGKIMMLTKSAEDYLIGQSPPSY--VE-

GNRIYKIFKMNGYDPLLAGSILLGWAQRRFGKRNAVW-LYGPATTGKTNIAEAIAHAV-PFYGCVNWTNENF

PFNDCVDKMLIWWEEGKMTAKIVESAKAILGGSKVRVDQKCKSSQQIDSTPVIITSNIDMTIVVDGNQTTME

HRQPLEDRIFQFYLGRRLPDNFGKISKKEVREFFKWAE-LNRIDVTPCFHVP----------TV--------

--------------CQYKRKRESAP------------------------ESVRENTSEKTDVLPDA------

----------LPTEE-SSP-KKA--RY-E-----DKKTD--AKTPEQILYEQMLAENLGETKE----QPIVH

ENTDVACKHGKH------LFCSDC--D--------------FNKNV---------NT--YNKY---------

--------LEC----------------------------------------P--------------------

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-----------------------------------DSNKEQ-------

>BIRD2|QKE54991.1/1-612 replication protein [Parvoviridae sp.]

--------------MVP-----------------------------------------ETFFFEIRVLLPND

FNEDIERFPEDCIDEIFSAP--VYLPD----SSDMNPTLI-----------DNPYVTVAGRIVTAIRLEWAY

RVG--------KDFLDFYQLERT-ENGHHLHVLLETKDVKGFVLGRFLPSFRERI-QNRVYSGCHVL-IPDW

FKPRKNKNV--GGANRTVN---RGYIYNYLLPK-------RQSE---------LQWAWSNIEAL---QSALL

NISERERLVKEYLAQLKPVLDE-------RE-----ASGENH-----------PRI-GGKNSERYM------

ALVQWLVEQGITSEKQWIQENQDSYVSYNTSSTSRSQIKAALDNASKIMMLTKSAKDYLIGPSPPTC--LE-

ENRLYKIFKMNGYDPALAGSILIGWFQKKFGKRNAVW-LYGPATTGKTNIAEAIAHAV-PYYGCVNWTNENF

PFNDCVDKMLIWWEEGKMTAKIVESAKAILGGSKVRVDQKCKASQQIDSTPVIITSNTDMTVVVDGNITTME

HREPLEDRMFQFYLGRRLPDDFGKITKQEVREFFKWAE-LNQVEVTPCFRVP----------VR--------

---------------DLKRKRQPEV------------------------ESVAAETPEETD-APHAAAGTVS

DQEPDRGTVFLPAENYEEP-AKK-VRA-E---PRETHGG--PKQSLMEAYLQTLEANTPPSVG----PIEVH

DHSDVRCGHGKA------LFCDEC--D--------------FIKKV--------------------------

---------EC----------------------------------------P--------------------

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-----------------------------------DSNKEQ-------

>WRQ19904.1/1-508 MAG: rep protein [Adeno-associated virus]

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-----------------------------MHLLFDTKGVKSIVLGRYVAQLLDRI-VNYVFGGAKPT-NPDW

LVICKTKPV--GGSNKIFS---ESYIPAYFLPK-------VQSE---------LQWAWTNIKKY---EPAAL

NLAERARIIEEHK-ASIAHKLV--------------FSDEEP--------EGTPVI-KNRASAKYM------

SLVNWLVENGITTEKQWIMENQESYISFNATGNSRSQIKSALDNAIKVMSLTKTAEDYLIGKDCPED--IS-

QNRIYKILRLNGYDPAYVGSIFLGWCRRSFGKRNTIW-LYGPATTGKTNIAEAISHTV-PFYGCVNWTNENF

PFNDCIDKMVVWWEEGKMTNKVVESAKAILGGSKVRVDQKCKASQQIDPTPVIITSNTDMCVVVDGNMNTYE

HKQPLEDRMFKIVLEERLDPEFGKITKQEVKDFFKWAE-DNKMKVEFDFLVK----------KAG-------

------------SVPA-KRE-----------------------------------APP--------------

--------------SDRVP-AKK-PRI-SVAD-FLIQ----NVTQND---------------DESYKKVDWN

SRYECRCDDHSN-DVIVKSVCLNC--EY-------------LNRNK---------NCCMKHNL---------

--------NKCEMCFR----------------------------YP-----PWQ------------------

-----------------------------------------------------------------CDVIDN-

-------------------------------VDLDDINKEQ-------

>Dependoparvovirus\_zftwig05par3|QKN88780.1/1-613 MAG: replication protein [Dependoparvovirus sp.]

-----------------------------------------------------------MEFYELIIQLPND

YSA----LSDGFIDSFSAVE----VPSV---SGDWNCSLV-----------DPLSWAVADSFVEAIR-NWSA

EISK------STAPSYFIQQEQG-EDYIHLHCCVETCIANSNVLGRYVNRLKGVL--AGLLEGHVHK--EDW

ISITKTGGS--SGKNKVCQ---ESYIIYYLLGK-------TQPD---------AIWAWSDIEKF---QDALL

DNTLRRELLEKYTAENPPKPKE----------------------------LKNPVV-ETLTAQKYM------

DLIDWLVEKGITTEKQWLLEDRTSFRSHQAGQGTARHIKEALKAAAQEILLTKCAKDYLVTKENDFEN-IK-

QNRIYKIMELNGYDPHLVACIFAKWSNREFGKRNTIW-LHGPATTGKTNIAEAIAHSV-PFYGCVNWTNDTF

PFNDCVNKLIIWWEEGKMTAKTVETAKAILGGSKVRVDQKCRGSEELEPTPVIITSNTNMCWVIDGNTTTYE

HKTPLQERMFKLELTVQLKPDFGKVTKQEVKQFFTWGA-TYPGIPPSVFAVE----------KKGGAATS--

----TAHAPLPTAPTGEKRKAEEEV-KSPTKKLLQTDIRSLTQ-----KKHWTDSIQEDVH-----------

----------LQTYKKWKS-ERE-TEMTENSVKKTIENF--N--------------------QGDGEG---A

YYYKMKCSKHLH-LDVLKYPCVEC--GR-------------ANWEI---------NCCRPHQL---------

--------KDCKECFP---------------------------IN---------------------------

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------------------------------------------------

>AvianAAV\_BR\_DF12|YP\_010802670.1/1-600 Rep78 [Avian adeno-associated virus]

-----------------------------------------------------------MEFYEIVVQLPND

YSV----LSDGFIDAFTSTE----VPPV---AGHWDTTVI-----------DRLTWKVGDVFAEQIV-AWAT

ATAK------GKTPAFFIQEEQG-EEYVHLHCCIETVVSASHVLGRYVNKLKNVL--SGVLEGYVHK--DDW

ITINKSGGA--YTKNKVCD---LNYITFYLVGK-------TQPD---------VLWAWSNIDRY---QAALL

DNEERKRLLEEYIRENPPKKKE----------------------------LKTPVV-DTANAQKYM------

DLIDWLVEKGITTEKQWLLEDRTSFRSHQAGQGTARHIKEALKAAAQEILLTKCAKDYLVVKDQTYDD-IE-

DNRIYRIMKMNGYDPHVVAAIFSRWCNREYGKRNTVW-LHGPATTGKTNIAEAIAHAV-PFYGCVNWTNETF

PFNDCVNKLIIWWEEGKMTAKTVETAKAILGGSKVRVDQKCRGSEELEPTPVIITSNTNMCWVIDGNTTTYE

HKTPLQERMFKLELTTPLSPDFGKITKREVRQFFSWGA-AYEGVPEPVFQVP----------KTTSQAI---

-----------------KRAMTSTE-QSPPLKVQKVASHSLTQ-----KPHWTERLPEDVH-----------

----------LHAYRKWKA-ERD--QIQKGGVGTT--------TAEE---------------SSEGEG---P

FYYKQKCSKHLH-LEALKYQCLEC--SR-------------ANWEI---------NNCRPHGV---------

--------ANCKECFP---------------------------INE--------------------------

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-----------------------------------NA-----------

>Dependoparvovirus\_ltt164par2|QLF86430.1/1-623 MAG: replication protein [Dependoparvovirus sp.]

--------------MSSRDSERP--------RDDQSPSLLRECYSLTHSLDSLRAIPYRMSFYELIIQLPND

YSH----LSDGFFDTFNE-P----VPEV---QSDWDCSLV-----------DTLTWNVAYHFKEKIL-EWAD

GTSK------SKSPDHFIQLEKG-EEYDHLHCCIETCVAESHVLGRYVNKLKVRL--AGLLEGYVHK--EDW

ISISKTSSS--NSKNRVND---KNYILYYLLGK-------TQPD---------AVWAWSDIEEF---QEALL

DNTVRKSLLDKYLKENPPAPKV----------------------------KKTPVV-DTAAAQRYM------

DLVDWLVEKGITTEKQWLLEDRQSFRSHQAGQGTARHIKEALKAAAQEILLTKCAKDYLVIKDVDFAT-IE-

ENRIYRIMKLNGYDPHMIAAIFYRWCNREYGKRNTIW-LHGPATTGKTNIAEAVAHAV-PFYGCVNWTNDTF

PFNDCINKLIIWWEEGKMTAKTVETAKAILGGSKVRVDQKCKGSEELEPTPVIITSNTNMCWVVDGNTTTYE

HKEPLQERMFKLELTTQLDPSFGKITKEEVRQFFSWGA-LYEGTPTSEFMVS----------KAT-------

---------------GTKRKAEEAP-PTGLKKLLT-------------EKHWTDKMSEDVH-----------

----------LQTYRKWKE-SRE-KDLMENSVQKTIESF--K---------------------------EQE

YIYKMKCSKHLH-LDVMKYPCVEC--MK-------------ANYEI---------NCCNPHKL---------

--------KDCKECFP---------------------------INS--------------------------

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>CanaryDependo1|WOP79071.1/1-688 replication protein [Canary dependoparvovirus 1]

MHDIRSLSSNHTAALTSSDLSPPIRDYLQDYKDSESST---HSHSLARRRGETDGTEKTMEFYEIVIQLPND

FSS----LSEDFIEAFSSAE----VPSL---ETDWDVSLV-----------DPLTWKVADAFVEHVI-AWAR

STSK------GKTPSYFIQQEQG-EEYVHLHCCIETVVSPSNVLGRYVNKLKTVL--AGLLEGYVHK--EDW

ISVTKAGGV--CSKNRTTN---TGYIVYYLLGK-------TQPD---------AIWAWSDLEEF---QAALL

DNAARKALLEKYVQDHPTQQKP----------------------------KKTPVI-DTANAQRYM------

DLIDWLVEKGITTEKQWLLEDRISFRSHQAGQGTARHIKEALKAAAQEILLTKCAKDYLVMKDGDFED-IK-

ENRIYKIMKINGYDPHMVACIFAKWCNREYGKRNTVW-LHGPATTGKTNIAEAIAHSV-PFYGCVNWTNDTF

PFNDCVNKLIIWWEEGKMTAKTVETAKAILGGSKVRVDQKCKGSEELEPTPVIITSNTNMCWVVDGNTTTYE

HKTPLQERMFKLELTVQLKPDFGKITKQEVRQFFTWGA-TYPGVPSSEFAVR----------KSAPVAVV--

----VEEKRQMAPPVGEKRKMESSSDQSPLRKMLVEGSGSLAQTT--NKTHWTEKLGEDVH-----------

----------LQTYRKWKA-TRE-AEMMKNSVRTTIENF--NNSEGT---------------EGGGEEEEKT

YIYKLKCSKHMH-LDVMKYPCLEC--SR-------------ANWEI---------NCCRPHKV---------

--------KDCIECFP---------------------------YPR--------------------------

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-----------------------------------EGEMKQ-------

>Dependoparvovirus\_sis142par1|QKE54964.1/1-672 MAG: replication protein [Parvoviridae sp.]

---------------MSSDLSPPITVRRLEYKESESRT---HSHSLTHRRRETDGAEERMEFYEIVIQLPND

FSS----LSEDFIETFSSAE----VPAV---DTDWDVSLV-----------DPLTWKVADVFVEHVI-SWSR

TTSK------GKTPSYFIQQEQG-EEYVHLHCCIETVVSPSNVLGRYVNKLKTVL--AGLLEGYVHK--EDW

ISVTKAGGV--CSKNRTTN---TGYIVYYLLGK-------TQPD---------AIWAWSDLEEF---QPALL

DNAARKALLEKYVQEHPIQQKP----------------------------KKTPVI-DTANAQRYM------

DLIDWLVEKGITTEKQWLLEDRISFRSHQAGQGTARHIKEALKAAAQEILLTKCARDYLVMKEGEFGD-IQ-

ENRIYKIMKINGYDPHMVACIFAKWSNREYGKRNTIW-LHGPATTGKTNIAEAIAHSV-PFYGCVNWTNDTF

PFNDCVNKLIIWWEEGKMTAKTVETAKAILGGSKVRVDQKCKGSEELEPTPVIITSNTNMCWVVDGNTTTYE

HKTPLQERMFKLELTVQLKPDFGKITKQEVRQFFTWGA-TYPGVPSSEFAVR----------KSAPVAVV--

----VEEKRQTMPPVGEKRKMEDASEQSPLRKLLVEGSGSLAQTT--KKPHWTEKLGEDVH-----------

----------LQTYRKWKA-TRE-AEMMKNSVKTTIESF--KSPGET---------------EGGGEGEE-T

YMYKMKCSKHMH-LDVMKYPCLEC--SR-------------ANWEI---------NCCRPHRV---------

--------KDCIECFP---------------------------YPR--------------------------

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-----------------------------------DGEMKQ-------

>FelineDependoparvo|QJQ50419.1/1-624 non-structural replication protein [Feline dependoparvovirus]

----------------------------------------------------------MAQYYEIVMKLPND

ISTQVPGILESSVDVLTSQK--CELPS----LSYWDLTLV-----------PKAVVSLASCLVRVIIAFWQC

INPI-------AACPYFIQLEKG-KEWHHLHILLSDAACDSLVLGRYTNKLRHRL-VDAVYDGIEPD-IPDW

FCVHKTRL---GGKNKKVG---EDYIFRYLLSK-------VQPD---------VLWCWTDLHHL---QPLVL

DNRCRQELMVKAD----------------------RAAAESESTDQSEAADRAPVI-SGIGAANYS------

RLVEWLVEQGITSEKQWLETDKNSYRSFHANANSSRQIRAALENARVEMLLLKSAGDYLIGDSWPSD--IE-

SNKVYKLFTLNRYDPALVGGILLRWCQKLWGKRNTIW-LTGPASTGKTNLAEAIAHAV-PIYGCVNWTNENF

PFNDCTDKMIIWWEEGKMTAKLVEPAKAILGGSKVRVDQKCKQSVQIEPTPVIITSNIDMTLVIDGNSITRE

HEEPLQHRMWKIVLDSVLPPTWGKITSAEVKSFLAWAS-DQNEIVQPVFEVP----------RV--------

-----------------QTPIH-------------------------EQVMVDLTLPELDS-----------

-------VPCNR--GSSTPPSEE-PVIVPCATPPA------VRPSTP-----------------LPSPRYVR

SVT-YVCLEHDR------GDCDQC-SEE---------------------------EICFT------------

----QTDWLQCDERMS--TISEESG------------------IEPLLTPTPSPPSF---------------

-----------------------------------------EMYGWSPIT----------------------

-----------------------------LHEAF-DVDFPDPEE----

>DesmodusRotundus|MG745677.1\_cds\_AVR53758.1\_1/1-717

--------------MGDLYWTAAER---------------WESDSSTHGYREGVILGKMLFFYELIIRLPND

LARDCPGMSETCMDALLHSS--VELPP----KAVWDMSKV-----------NLGMVSMAQCIVRILVCFWQM

LNPL-------VDTPYFIQLEEG-KQYYHLHCLLSWKACDSLVLGRYIKKVKERI-IEAAFGGIEPG-TTEW

FAVHKTRT---GGKNKVVD---ALYIERYLLPK-------KQSE---------VQWAWTDIPEY---KDAVL

DASRRAMFQLQMP----------------------VACLEDMPGD--PGAVPGPSI-SGSSAENYC------

RLVDWLVSEGITSERQWLQKDKLSYRSFHANSNSSRQIKAALENAKAEMLLTRTAGDYLVGGTLHNP--ID-

TNKIFLLFCLNNYDPQVAATILLKWCRCEWGKRNTVW-FTGPASTGKTNLAEAIAHAV-PLYGCVNWTNENF

PFNDCVGKMLIWWEEGKMTAKIVESAKAILGGSKVRVDQKCKNSIQVDPTPVIITSNVDMTLVIDGNTITAE

HREPLEHRMWKFTFEHQLEPTWGKICKEEVLDFFCWAA-ERPVEVAPTYCVP----------KVAGGGVLPP

PEVDLTEDMDDEDIPAAQQPIEVDF--------------ALSTEIDGQQVVVSGPPPSPE------------

--------PGTRSVGTST---EE-PAPLLSTTPPAESATLKSPPRSPDPQE------GPSSLIAPPAPKKSR

YGTRLVCLEHNQ------EECEIC-GEE---------------------------LCLFTAGFPTPETEDSS

SSTSSVD-LQCHETLS--DMSGLSD------------------VSPPSPPTPDPPV----------------

---------------------------------------------GSPVP----------------------

-----------------------------LIDLFDDMDYMPPFRYQPE

>SnakeParvo1|NC\_006148.1\_cds\_YP\_068093.1\_1/1-562

-----------------------------------------------------------MAFYEVVFRLPRD

NNNLL--DEDRY---------QPELKE----EDDWPEEYLT--------SEDASFIGLAYAVLSEIRRFFG-

-----------KELQWFAQVEWCPTAGYHMHVLLNHPKLSNQTYGRKVNELACRI--VDTFGLINPE---EV

ISTHYVKSN--YGHKKVRVIHLESYLKNYFFRK-TLAPPNYTEEGDYKREEEVVLWAFTNIVAW---KPFVR

NLIKRSELA--------------------------TVPKQPEN---PAGDGPAPRV--TAGTRHFM------

ETIDWLVKHGITTEREFCHANRPLYLSMLASTSGAGQIKRALDQAKHMMTSTMSAEDYLTTEEDVIEP-PT-

ENRIYKIMKLNRYDPELAAALFYGWTCKNFGKRNTIW-LYGPATTGKTIIAQAIAHAV-KLFAGVNWTNENF

PFCNCPGKLLIWWEEGKMTNKMVETAKCILGGSAVPVDIKGKPAEMCPQTPCIITSNTNMCQVYDGNSSSFE

HQEPLEERMFMFRLNTKLPSTFGKITEEEVKQFITWGR-SLKVQVPHQFRVP----------TTGEY-----

-----------------KRP-----------------------------------APEA-------------

----------KAHSSDEPP-KEK-VAR----------------------------------------IDDSL

TRY-----------------VNN--IDE-------------SATSREMFLEIANTNQCMLHHC---------

--------FSCTECYP--------------------------------------------------------

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----------------------------EL---LDDMDKEQ-------

>BeardedDragon|NC\_027429.1\_cds\_YP\_009154712.1\_1/1-565

------------------------------------------------------------MPYEMIFRVPKE

DEDAWCEDNDRY---------EARLAE----GDDWPQERLE--------EDDRWFVNLCYAARGIFKKYFG-

-----------KSLTYFMQVEWSPADGHHMHCVLDDPKLKANNYNYHLDQLSMKM--KTEFKW-KSA---NM

LQKSVQRAA--NRHLKLRYCQFESYIKNYFYKKEVISPEEEQPNGDFERVRDCVLWAFTNLDNW---KPSVR

NIILRNQL---------------------------KAPDQVTT---VPG-GPKPRQ--GANVEAFM------

ETIDWLVKNGITTERQFCQANRTLYLSMLATNSGAGQIKRALEQAKHMMQSTMTAADYLTREERVETC-SE-

TNRIRVIMEKNGYDPLLAANIFNGWLNKEYGKRNTIW-LYGPATTGKTIIAQAIAHGA-VLFGGVNWTNENF

PFCNCPGKLLIWWEEGKMTQKMVETAKCILGGAVVPVDIKGKMAELCETTPVIITSNTNMCQVFDGNSSSFE

HTEPLEERMFMFRLNKKLEPDFGKVTLDEVKEFITWGR-DNPVQVPYQFRVP----------SVATPP-QKS

I-----------NEVLGKRR-----------------------------------AISD-------------

----------GA--GEETR-STK-LVL----------------------------------------LNDSL

TRY-----------------CNNI-TER-------------VNTR-----EIAQNNQCMLHHV---------

--------FNCSECYP--------------------------------------------------------

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----------------------------EL---LDDCDMEQ-------

>SlowLoris|AIZ50117.1/1-582 NS1 [Slow loris parvovirus 1]

--------------MTE-------------DRPDLSPL-------------------NGKGFWELVIKLVNS

PWTENSTLFSKY-DWIEFCD--LEGSD--DPWYDWPEDEI-----------DIYMAILGIKAIKAITRVLRE

RSKN-------KTCNYFGQIEQG-GEFFHIHLLFEVDGFVSFLLGRMFETLRQTL-RNSVYFGYPFE-VSSE

IAITKVKT---GGRNKVQD---GSYIVNYLLKK-------IPPGE--------VQYAISNIECL---RPYCN

SVRNRRALLESVP-------------V-------------------SVERFSEPIIMKGKTVDKFM------

QTLQWCVDEGVTSETIWYKKNPASFRSYQVSAQSRAQAKSILTQAKMEIQISKRLSDYLCREPKENEL-FS-

ENYVSLLFEANGYSASKAAATLARWAAHQSGKRNTIW-LWGPPTTGKTLLASAIANCS-PMFGNVNWNNANF

PFNDCHKQLLIWWEEGSMLQKFVECAKALLGGTSVRVDRKGTDSALVLRTPVIITSNTDMTCVVDGPVKSWE

HKEALEDRMIKYNFERRLPMNLRSITEEEIRQFF-WFG-SCLQCPPLEFLVP-------------------P

DGCD--------SETAYQKLSSLFA---------------------APLGDSTIKTPDL-------------

----N---------------SSR----------------------------------YIDDGDEGPSERSVK

RRRLSLCSVSTE--------------EA------------------------ASAASCLL------------

--------DLCSGSFS--DGSE-----------------G--------------------------------

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---------------------------GSFREALGN------------

>BatTadarida|UJO02142.1/1-400 Rep [Tadarida brasiliensis associated dependoparvovirus]

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ALVKWLVDAGIATERQWMQEDADSYLSYNATGASRGQIKSSLENACRIMLSTKRAADYLVGASPPED--VT-

QNRIYRLFALNGYDPAYAGSVLLGWCRSGFGKRNTVW-LFGPATTGKTNLAEAISHAV-PFYGCVNWTNENF

PFNDCVDKMIIWWEEGKMTAKVVEAAKAILGGSKVRVDQKCKSSQPIEPTPVIITSNTNMCEVVDGNSTTFE

HRQPLEDRMFRFELTVRLQPTFGKITKTEVKEFLKWAE-INSVEVEPDFVVK----------KNF-------

------------VQSDSGGG-----------------------------------VKRA-------------

----------GEPLKGAPS-PKR-VFF-YGSSPTETDA-----AAAPC-----------QPIGTEFDCVNFA

ERYVSKCSKHLS-WSNMRFPCKAC--ER-------------MNADV---------NICQAHGT---------

--------HDCVDCFP-----Q----------------------PL-----PEPCV----------------

---------------VHDMCDASIRDADF---YV--------------------------------------

--------------------------------CTDDLNKEQ-------

>MarsupialAAV1|AZP54391.1/1-428 rep protein, partial [Marsupial adeno-associated virus 1]

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--------------------------------------------------------AWTNLEEY---EEILL

NIPARLQLAATAA-ASLPLPSSGRR-----------QAAETQ----SSSGRTAPLY-YGKHTQKYM------

DLVAWLVEEGITSEKQWIVENQESYLSFQATSNGARQIKAALDNASKIMNLTKTAADYLITKHESNFDNIE-

ENRIYKIFDMNGYDPLYAGNILTGWCKREFGKRNTIW-LYGKATTGKTNIAEVISHSV-PFWGCVNWTNENF

PFNDCVDKMIIWWEEGKMTSKVVETAKAILGGAKVRVDQKCKSSVQLDSTPVIITSNTDMCYVVDGNTTTFE

HKQPSQDRMFQFLLMKRLPDDFGKVTREEVRQFFKWAN-ENKVDVTREFTVK-KRAPSESPAK---------

------------TDDDRKRK------------------------------WNFLKAPPT-------------

---------AEPPHKKRAT-APK-ASF-PFRDRTNEEII---ERDAP----------------TQESDLEFL

KRFGLDLKQSEN------------------------------------------------------------

----------SESNFK-----------------------------------PDEIE----------------

-------------------------------------------------------------NC---------

--------------------------------DLDDIQDEQ-------

>CanaryDependo2PROBABLYMISSESCTERM|WOP79082/1-501 replication protein [Canary dependoparvovirus 2]

-----------------------------------------------------------------MNSSPVP

VSPRTPGASPS-----------SFFPDVSLSSLDSDEDDVDGPLDRATSGSDEPDSGVMSGYEFEFVSRFLS

VCRSVCGSMFRRPFVYFAQLEYGAECGAHVHLMVPVSMCGSQVIARWMKNVSRSM---------QTG-KSNW

GFTWTMAHLR-NGKVRMVD---VHYLFRYLLKK-------VAPE---------CGGRWTSFKVFEPDQEGKV

ADETVKRVMEVYE-------------MWMRECEMIRGEFESK----TKKLASSPTS-IKTTKRQRMCVDVMQ

DLVRWFVNKKVTSMQKWMKVDMDHYIKYQSYSTYRPMIKPAMEMATSILLNNGTLIDFLTGVELGR---LQ-

YNRIEDVFRRNGYDPMLAAALFFKWAKRELGKRNTIL-LYGPPTTGKTVIASAICHVVDPFYGNVNWNNENF

PFNDCVEKMLIWWEEGRITAKNVEAAKCILGGVSCRVDRKGKESIEIRATPVIITSNLDMTAVYEGNTVNFD

HKTALEDRMTCFNLRCRLEHDFGRVTSEEVYDWFAKGDLHSGRDIPDTFNFP--------------------

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**>BankVoleMgAAV2**\_FRAME3\_CORRECT\_Cterm\_Startnotsure|QHD57625.1/1-50 start of frameshift not sure

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--------------------------------------------------------------CTPS------

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-------------------------------------------------------------------PDVVH

DNHDVTCKHGKH------LFCADC--E--------------FVKQK---------RV--DNKY---------

--------LEC----------------------------------------P--------------------

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-----------------------------------DSNKEQ-------

>PygmyChameleon|A0A0G3ZB75|A0A0G3ZB75\_9VIRU/1-111 Nonstructural protein (Fragment) OS=Pygmy chameleon parvovirus OX=1670664 PE=4 SV=1

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---------------------FGKVTEQEVKEFITWGR-SLDIEVPHQFRVP----------VSGAY-----

-----------------KRP-----------------------------------APEA-------------

----------EAHSSDEQP-KEK-VAR----------------------------------------LDDSL

TRY-----------------ANN--IDK-------------SATGREAFLEIATTNQCMLHHT---------

--------FSCTECYP--------------------------------------------------------

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----------------------------EL---VDDLMKEQ-------

>RatAAV1|Q2VJ49|Q2VJ49\_9VIRU/1-104 Rep (Fragment) OS=Rat adeno-associated virus 1 OX=341227 PE=4 SV=1

-------------------------------------------------------------------QVPVP

HVFSVPTCSAAAV---------QKRPT---------------------------------------------

----------SPSPPFHGETARD-------------------------------------------------

-ADRKTRKK-----------------PRYDRPK---------PE----------------------------

-----------------------------------------------------PAK------------D---

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QN----------------------------------------------------------------------

----CLDK---WLEESP------------------------------PPRPSVVHD------LQDSGDTVFD

------------------------------------------------FRVV----------R---------

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--------------------------E---------------------------------------------

--------VEC----------------------------------------P--------------------

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-----------------------------------DSNKEQ-------

>AAVp01|FJ688147.1\_cds\_ACN42943.1\_1/1-253

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---------------------------------------------------------------CVNWTNENF

PFNDCVDKMLIWWEEGKMTNKVVESAKAILGGSRVRVDQKCKSSAQIDATPVIVTSNTNMCIVVDGNSTTFE

HQQPLEDRMFKFELTKRLPPDFGKITKREVKDFFAWAE-ANLVPVTHEFRVP----------K-G-------

------------AEKSLKRP-----------------------------------LSDV-------------

----------TDT-SYKSP-EKR-ARV--SFAPETPDCS--DETADP----------------APPRPIDWT

SRYDCRCDSHAR-VETVDEMCEEC--EY-------------LNRGK---------NGCIPHKM---------

--------NYCQICHD----------------------------VP-----PWL------------------

----------------------KEKVSDV-------------------------------------------

-------------------------------VDLDDANKEQ-------

>Serpentine2|ACJ66590.1/1-213 non-structural protein 1, partial [Serpentine adeno-associated virus 2]

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PFCNCPGKMLIWWEEGKMTQKIVETAKCILGGTRVPVDVKCKMAEICEGTPVIITSNTNMCQVFDGNSSSFE

HTEPLQERMFKIRLNIKLPSDFGRVTKQEVQDFIRWGS-DHPMEISHVFETP----------KEAPPLIQTP

I----------------KNR-----------------------------------EKEA-------------

----------ETSFEEQPP-SKR-VCL----------------------------------------DSEKQ

VRHTTE-------------ICNNI-VPR-------------ANLL-----ELANTTQCMLHGT---------

--------FTCMECYP--------------------------------------------------------

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----------------------------ELTECVDDVDVEQ-------

>CornSnake|AKM49966.1/1-218 nonstructural protein, partial [Corn snake parvovirus]

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------------------------------------------------------AYTV-KLFAGVNWTNENF

PFCNCPGKFLIWWEEGKMTNKMVETAKCILGGAAVPVDIKGKPAEMCMQTPVIITSNTDMCQVYDGNSSSFE

HTEPLEERIFMFRLNYKLAPNFGKVTEQEVKEFITWGR-GLNIDIPYQFRVP----------TSGSY-----

-----------------KRR-----------------------------------GSED-------------

----------AASFSLEPP-SKKDVNP----------------------------------------QISAA

TKY-----------------VCNL-VDK-------------ASVS-----ELAKTNQCMLHHA---------

--------FECTECYP--------------------------------------------------------

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----------------------------EL---LDDMDKEQ-------