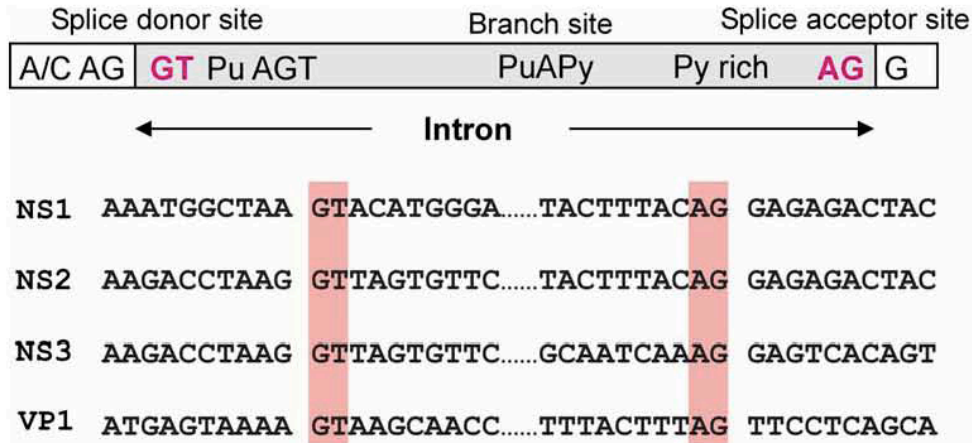


Novel Amdovirus in Gray Foxes

Technical Appendix



Technical Appendix Figure 1. Nucleotide sequence around the predicted RNA splicing sites in the gray fox amdovirus genome. Splice donor and receptor are shown in pink boxes. NS, nonstructural; VP, viral protein.

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GFADV 1 MAQAQIAEQKIQALFEQLKKEIADGEGLAWLFFQQAAYTDGDNKPKTEPPPLRTTSEDLRLVFDSEIEN-----IK
AMDV 1 MAQAQIDEQRRLQDLVYQLKKEINDGEGVAWLFFQQKTYTDKDNKPKTATPPPLRTTSEDLRLVFDSEIEN-----LT
MVM 1 MISGSGSLNQGAKRKNWAFKVKYKQLLKSVTYLFPHSVSRDAQKESNQLTMAGNAYSDEVLGATNWLKKEKSNQEVFVSFVFK
BPV 1 -MQPSRGLYSAHSPFKHLITITRQRLTHADPTVLSRDELNAWNWLQKIAQRVMDGMDHIVDILKCRKAN-----
AAV2 1 -----MPGFYEIVIKVPSDLDEHLPGISDFVNVAEKKEWELPFDSDMDLNLTEQAPLTVAEK-----

GFADV 72 SNTDCPSNNEI---NFCQLTLGKTIVSFDKHKHSRWNANNLQFIWQVEKGTKHLHHLCLVG---YSDSTADKKDISKS
AMDV 72 ASNEHPTNNEI---NFCQLTLGKTILLIDKHVKSRRWDSNKVNLIWQIEKGTQQPHHCCLG---YFDKNEPKDVQKS
MVM 81 NENVQINGKDI GWNSYKRELQEDLKSIFQRGAETTWQSEDMEWETTVDKTKQVFPDLSLVKCKLFEVLTNKNIFPGD
BPV 69 -----GWNYSYKRELQEDLKSIFQRGAETTWQSEDMEWETTVDKTKQVFPDLSLVKCKLFEVLTNKNIFPGD
AAV2 59 -----LQRDFLTEWRRVS-----KAP

GFADV 146 LSWFIKKINKELATLWSNHCTLODIKRPEDR--QQNLNVWLQDGITKPKYKYPNKQTRQYENKQVNLREYTLIYLFDKNK
AMDV 146 LGWFMKRLNKDLAVIYSNHCDIQDIKDPEDR--AKNLKVIWIEDGPTKPKYKYPNKQTKQDYNKPVHLRDYTFIYLFENKDK
MVM 161 VNWVQHEWQKDGQGWCHVLIIGKDFDSQAQGWRRQLNVYWSRWLVACNVQLTPAERIKLREIAEDNEVWTLTYKHK
BPV 69 -GTLVAQAINGTEFTITRYMLPKNR-----KQVADTVLTRHTTPEQ-----SYD
AAV2 75 EALFPVQFQKESYFHMHVLVETTGVKSMVLG-----RFLSQIREKLIQRIYRGIEPLPNWFAVTK

GFADV 224 IITEKGMDCYFAACNGGFIIDNMTEKERKIMRKMVLDDEQCSDMADDSDQWDDSQEPPKTEPPKVTETETISNVTYVDSAVVQP
AMDV 224 INTDSMDCYFAACNGGIVDNLTNERKTRKMYLDEQSSDIMDANIDWEDGQ---DAPKVTDTQ---DSATTKT
MVM 241 QTKKDYTKCVLFCN--MIAYYFLTKKKISTSPPRD--GGYFSSDSGKWNF-----LKEGE-----RHLVSKL
BPV 110 SHWGTYCFEAVCNGETVSEFTRKDLWRVINYIYTAHPAENMLNSN-----PSV
AAV2 137 TRNGAGGCKNKVDECYTPNYLLPKTQPELQAWATN--MEQVLSACLNLTERK-----RLVAQ

GFADV 304 GTSTIWAASCSTKATKPKTITETAKQPSKLLTTAKSFLDLSLFDIGCFPEDEMILKLSDTYIELSLEANGTNKTLTLLEHMNQ
AMDV 292 GTSLIWKSCATKVTSKKEVANPVQPPSKLLYSAQSTLDAIPNVGCFPEDEMILKQSDKYLELSLEPNPQKINTLLEHMNQ
MVM 301 YTDMMRPETVETVTTAQETKRGRIQTKREVSIKTLLKELVHKRVTSPEDEMIMMMPDSYHEMMAQPPGGENLKNTEICT
BPV 158 WGDLPVRSANRIDADDAEARSRIKLSRQKIMAEVQIRADGGLLTYNDLVVHLSLMLMLGEMPGGSKTAEQLTMIH
AAV2 192 HLTHVBSQTQEONKENQNPNSDAPVIRSKTSARYMELVGVVYDKGITSEKQWQEDQASVTSFNAASNSRSRQKKAADNAG

GFADV 384 VKTASILNAPFCIMKFNDE-----DEKPLININQMGLENEKVLKNIATVLTQSGKRGCIWFYGPGGTGKT
AMDV 372 VKTSTMITAFDCIIFKFNDE-----DDKPLLATIKDMGLNEQYLKVLCTTLTKQCGKRGCIWFYGPGGTGKT
MVM 381 LTLARTKTAFDLLEKAETSFLT-----NFSLPDTRTCRIFAFHGWNYVVKVCHAIACCVLNRQCGKRNITVLEHGPASTGKS
BPV 238 IKLCAKYNAYEFLMKTPATQNMNPGAPHYDCQGNLVFKLLNLQGNVNPQVGHVWVMMLSKKTGKRNITVLEHGPASTGKT
AAV2 272 KIMSLTKTAPDYLVGQQPVED-----ISSNRIYKILELNCYDPQYAAVFLGWATKKKGRNITVLEHGPASTGKT

GFADV 452 LLANLICTAVKNEGMVITSNQNFPTDCCGNRNMIVLEECGNLGNFIEDFKATFGGGDIKVDTKNKQPQAIGK-VTVITSN
AMDV 440 LLASLICTKATVNYGMVITSNPNFPPTDCCGNRNIIVWEECGNFGNWEEDFKATFGGGDVKVDTKNKQPQSIGK-CVIVITSN
MVM 456 LIAQATAQAVGNYGCVNAANVNFPEFNDCTNKNLIWVEEAGNFGQQVNOEKAICSGQTRIDQKGGSKQLEPTFVIMTIN
BPV 318 NLAKAICHAVGLYGCVNHNKQFPFNDAPNKMIWVEECIMTDTYVBAKCVLGGTHVRVDVKKHDSRELPQIPVLLSSN
AAV2 342 NIAEAIAHTVPIYGCVNWNTNENFPFNDQVDKMIWVEEGKMTAKVVEBAKATLGGSKVRVDQKCKSSAQIDPTFVITSN

GFADV 531 KDITKVTIGAVETNVHSEPLKQRLVKIRCVKTIINPTTKITP-----NEWPMICAWLVKNGYQSTMAS
AMDV 519 TNITKVTIVGCVETNAHAEPKQRMKIRCMKTIINPKTKITP-----NEWPMICAWLVKNGYQSTMAS
MVM 536 ENITVVRIGCEERPEHTQPIIRDRLNIHLTHLPGDFGLVDK-----NEWPMICAWLVKNGYQSTMAS
BPV 398 HDVYTVVGCNATFGVHAAPLKERITQMNPFMKQLPNTFGEITPGMISNWLSHCAIHQEHLSLEGFAIKWDVQSVGNSFPL
AAV2 422 TNMCAVIDGNSITFEHQQLQDRMFKFELTRRLDHDFFGKVTK-----QEVKDFFRWAKDHVVEVEHEF

GFADV 572 -----CMLKKW-----LSTWEG---KPIQLNHENENLYRSK-----
AMDV 560 -----CMLKRW-----LNTWDR---QPIQLSHEMPELYLGKCRW-----
MVM 599 YCAKWGKVPDW-----SENVAEPKVPPIINLGSARSEPTTPKSTPLSQN-----
BPV 478 QTLCPGHSQNTFSENGVCWHCGGFIQPTPESDSDSDGDDPDGAVAGDSSTANSSESTVVSFSSNDSGLGSVTSSAPSPV
AAV2 485 YVKKGCAKKRP-----APSDADISEPKRVRESVAQPSSTDAEASINYADR-----

GFADV -----
AMDV -----
MVM 644 -----YALTPLASDLEDLAEFPWS-----TPNTPVAGTAETONTGEAGSKAC
BPV 558 DRAEETEEIPSECLEWMREVDRLSAHDINSLAQATGFIIEDPIEPEEGERDLAREDAEPEASTSHTPATKRARVEEG
AAV2 530 -----YQNKCSRHVGMNLMFPCR-----QGERMNQNSNICPTHGQKDCLEK

GFADV -----
AMDV -----
MVM 686 QDQGLSPTWSEIEEDLR-----ACFGAEPLKDKFSEPLNLD-----
BPV 638 EPWDGTQPIPEGDWIDFESRQKRRRLEREKGGEDMEDVEQSDPSAWGEKLGIVEKPGEEPVLVYCFETLPESEDEEGDS
AAV2 572 FPVSESQPVSVVKKAYQKLCYIHHIMGKVPDACTACDLVNVDLDDDCIFEQ-----

GFADV -----
AMDV -----
MVM -----
BPV 718 DKENKTHTV
AAV2 -----

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Technical Appendix Figure 2. Conservative domain in the left open reading frame of gray fox amdovirus and representative parvoviruses. GKRN region is marked in red.

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GFADV 1  -----
AMDV 1  -----
MVM 1  -----
BPV 1  -----
AAV2 1  MAADGYLPDWLEDTLSEGITRQWVKLPGPPFPKPAERHKDDSRGLVLPYGYKYLGFPGNSLDQGEPTNPSSDAAAKEHDEAYD
GFADV 1  -----MSKIPQHYP-----GKRSAPRHRVFTIQAK-
AMDV 1  HHNTLLSLYLCTYFTLVLPQHYP-----GKRSAPRHRVFTIQAK-
MVM 48  QYIKSGKNPYLYPSAADQRFIDQTKDAKDWGCKVGHYFFRTKRAFAPKLTATDSEPGTSGVSRAGKTRTPDAYTFINQAR-
BPV 49  DLLKEGKNPYLYENTHDQNLIDELKDDTSFGCKLARGVFQIKKALAPALPG-----TSKGGDRALKRKLKLYFARBNKG
AAV2 81  RQLDSGKNPYLYKYNHADAERFQERLKEEDTSFGCNLGRAVFOAKKRVLEPLGLVEEP--VKTAPGKTRPVEHSPVVEPDDSSG
GFADV 26  KKKQHSNPAVSHQEDTIEEMDSNETEQMDISEQQ-QVAEHGG-----VCKSTGGFNNTTEFKVTNN-EVIT
AMDV 38  KKKQ-TNPAVYHGEDTIEEMDS TEAEQMDTEQATNQTAEEAGCGGGCGGGCGGGCGVGNSTGGFNNTTEFKVINN-EVYI
MVM 127  AKKLLTSSAAQSSQTMSDG-TSQDPSGNAVHSAARVERAADCPGSSGGGSGGGCGVGVSTGSDYDQTHYRFLGDGWVEI
BPV 121  AKKANREAPASTSNQNMVSNDFNDEAGNQPIELATRSVVGSGSVGGGGRGSGVGVSTGGTGGTIFG-----ENI
AAV2 159  TGKAGQQPARKRLNFGQTDGADSVEDDPPQLGQPPAAPSGLTNTMATGSGAPMADNNEGADGVGNSSSGNWHCDSTWMDGR
GFADV 91  TCNATRVVHINQASTDEYLIFNAGREID-KTPKGSNLNLEFFMDFDHFQOVMTWFLVDSNAGVWMSPKDFQOMKVLCSSE
AMDV 116  TCHATRMVHINQADTDEYLIFNAGRITDTRKTHQKLNLEFPVYDDDFHQQVMTWFLVDSNAGVWMSPKDFQOMKTLCSSE
MVM 206  TALA TRVHLNMPKSENCRIRVHNTDTSVKGN-----MAKDDAHEQIWTWPSLVDANAGVWVLPQSDWQYICNPMQSG
BPV 195  VVTKNTRQFTCDIKNGHLYKSEVLNTGDTAHRQY-----AITPWSYFNPQYSSHPSNDWQHLVNDYER
AAV2 239  VITSTRTRWALPTYNNHLYKQISSQSGASNDNHY-----FGYSTPWGYFDNRFHCHFSPRDWQRLINNNWG
GFADV 170  IELVSLBOEIDNVVVIKVTETTQGGTSVIYNNDLTASLOVALDNNILPYTPAAPLOETLGFVWPRATKPTQYRYVHPS
AMDV 196  ISLVTLBOEIDNVVVIKVTETTQGGTSVIYNNDLTASLOVALDNNILPYTPAAPLGETLGFVWPRATKPTQYRYVHPC
MVM 280  LNLVSLBOEIDNVVVIKVTETTQDLGQAIKLYNNDLTACMMVAVDNNILPYTPAANSMETLGFVWPKPTIASPYRYV--
BPV 261  FRPKAMIVRVVNLQTKQIMTD--GAMGTVYNNDLTAGMHIIFCDGDRHYPYVQHPWDDQCMPELNSIWELPQYAVTPAP
AAV2 306  FRPKRPNFKLNIQVKEVITQON---DGTTTIANNLTSTVQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMVFPQYGLTLN
GFADV 250  YIYNRYPNIQKKSQEQSSTYTAIQDDYFSVDQDYFNFTIENNIPTEILRTGDNPHETGRVFEKSKPKCLTMSVQSTRCLGL
AMDV 276  YIYNRYPNIQKVATELTDWAVQDDYLSVDEQYFNFTIENNIPINILRTCDNPHETCLVEFNKPKCLTLTMSVQSTRCLGL
MVM 357  FCVDRLSVTYENQEGTVEHNVMGTPKGMNSQFF---TIENIQITLRTGDEEATGTVEYEDTNSVKLTLHWQTNROLGQ
BPV 338  ISVVDN-NTTNTVBEHLKGVPLYMLENSDHEVLNNGRIYR-TYIQWLRLMRDRKQ--HHIQHASDDVQSTGQKQKQLLI
AAV2 382  NGSQAVGRSSFYCLEYFPFQMLRTGNNTFSTYTFEDVPPHSSYAHSQSLDRMLNPLIDQYLYLRTNTPGTTTQSRRLQ
GFADV 330  PPLCKPKTDT-KLVTSI--ENGEMDCYVEGQOHTRKCHFWGEKAEKNTENRVRPYNIGYQFPEWIVPAGLQGSYFTG
AMDV 356  PPLCKPKTDTTHKVTSK--ENGADL-IYIQGDNTRLGHFWGEERGKNAEMNRIRPYNIGYQFPEWIIIPAGLQGSYFAG
MVM 434  PPLLSFPPEADTDAGTFTAQGSR-----HGTTQMCGVNVVS-----EATRTRPAQVFCQNDHDFASRAGPFAAP
BPV 414  QRTKQNKQRFQNAALR-----HGTNWMSSGPGIARGTINATLQTQSAGALVTM
AAV2 462  FSAQAGASDIRDQSRNWLTP-----GPCYRQQRVSKTSADNNNSQYSWTGATKYHLNGR
GFADV 407  GPRQWSDTTKAGAGTHSQTVQONFSTRYVFDNRHGGDNQVDTIDSIPIQERKGYVSEQELQQAATTLTATNKAQ--TGKKWE
AMDV 433  GPRQWSDTTKAGAGTHSQHLQONFSTRYVFDNRHGGDNEVDLLDGIPHERSNYVSDNEIEQHTAKQPKLRTPPIHHSKID
MVM 499  -----KVPADITQGVKDEANGSVRYSYCKOHGEN---WASHGPAPER---YTWDETSFGSGRD-----
BPV 461  V-----TNGADVSGVRAVRVGYSTDPYICGQPPESDGLLRLRYSASAAEG-----
AAV2 514  DSLVNPGPAMASHKDDDEKFFPQSGVLIKCKQGSSEKTNVDIEKVMITDEE-----
GFADV 485  SWEEEGWPAASGTHFEDEWLYFDYFNFSGETTKNFPQEVLSIDGLQMKKMLNAYQETVQGDDVGPVYPWQIQWDDKPDMDH
AMDV 513  SWEEEGWPAASGTHFEDEWLYLDYFNFSGEQELNFPHEVLDAAQMKKLLNSYQPTVAQDNVGPVYPWQIQWDDKPEHMDH
MVM 551  -----TKDGFIQSAPLVVPPPLNGLITNANPIGKTND-IHFSNVFNSYGLTAFSHPSPVYPQGIWDDKELDLEH
BPV 505  -----QQNPILENAARHTFTREARTKLITGNSGADGYKEWMLPN-----QMWDSAPHSRYNPIWVKVPRVNR
AAV2 564  -----EIRTTNPVATEQVGSVSTNLQRGNRQAATAADVNTQGVLP-----MVWQDRDVLVQGPWAKIPIHTDG
GFADV 565  KPSMNYNAPFVCKNPPGQLLVKLTENLTDKFN-YDEDP--DRIKTYCYFTWRCKLTLRGLQTSQWNPVKRERIGEPG
AMDV 593  KPSMNNNAPFVCKNPPGQLFVKLTENLTDTFN-YDENP--DRIKTYCYFTWRCKLVLRGKLSQVTCWNPVKRELIGEPG
MVM 620  KPRLHITAPFVCKNNAQCMLVRLGPNLTDQYDNPNGATL--SRIVTYGTFWRCKLTMRAKLRANTWNPVYQVSAEDNG
BPV 569  KTLLEDTDGDSIPMSHPPCTIFIKLAR---IPVPNGD--SFLNIYVTGQVSCVWVEVEKRGTKNWRPEYMHSAENMS
AAV2 627  HFHPSPLMGGFGLKHPPQIILIKNTPVPANPSTTFSAAKFAEFTIQVSTGQVSVIEWELQKENSQRWNPETIQYTSN---
GFADV 642  VFSKSNYHKQIPNNRGNFPIGICYGRSTVRYLY
AMDV 670  VPTKDYHKQIPNNKGNFPIGLQYGRSTIYIY
MVM 698  NSYMS-VTKWLPATGNMQSVPLITRPPVARTY
BPV 642  VDAYTINNAGVYAGAVQNADVMQTRFNHRYL-
AAV2 704  YNKSVDNFTVDTNGVSEPRPIGTRYLTRNL-

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Technical Appendix Figure 3. Conservative domains in the right open reading frame of gray fox amdovirus and representative parvoviruses. PGY region (putative phospholipases A2 domain) is marked in blue and TPW, YNN, and PIW region are marked in red.


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GFADV      1  MDSNETEQMDISEQQ-QVAEHGG-----GVGKSTGGFNNTTEFKVTNNEVIITCNATRVHINQASTDEYLI
M20036    1  MDSTEAEQMDTEQATNQTAEAGGGGGGGGGGGGGGGGGVNSTGGFNNTTEFKVTNNEVITCHATRVMHINQADTDEYLI
GU183265  1  MDSTEAEQMDTEQATNQTAEAGGGGGGGGGGGGGGGGGVNSTGGFNNTTEFKVTNNEVITCHATRVMHINQADTDEYLI
DQ371395  1  MDSTEAEQMDTEQATNQTAEAGGGGGGGGGGGGGGGGGVNSTGGFNNTTEFKVTNNEVITCHATRVMHINQADTDEYLI

GFADV      67  FNAGREID-KTPKGSLNLEFFMFDDPHQVMTPPFLVDSNAGVWMSPKDFQQMKVLCSEISLVSLEQEIDNVTIKTVTE
M20036    81  FNAGRTTDTKTAQKLDLEFFVYDDFHQQVMTPPFLVDSNAGVWMSPKDFQQMKTLCSEISLVSLEQEIDNVTIKTVTE
GU183265  80  FNAGRTTDTKTAQKLDLEFFVYDDFHQQVMTPPFLVDSNAGVWMSPKDFQQMKTLCSEISLVSLEQEIDNVTIKTVTE
DQ371395  81  FNAGRTTDTKTAQKLNLEFFVYDDFHQQVMTPPFLVDSNAGVWMSPKDFQQMKTLCSDISLISLEQEIDNVTIKTVTE

GFADV      146  TTQGGTSVIQMNNDLTASLQVALDTNNILPYTPAAPLGETLGFVPWRATKPTQYRYYHPSYINRYPNIQKSQEQSTYT
M20036    161  TNQGNASTKQFNNDLTASLQVALDTNNILPYTPAAPLGETLGFVPWRATKPTQYRYYHPCYINRYPNIQKVATETLTWD
GU183265  160  TNQGNASTKQFNNDLTASLQVALDTNNILPYTPAAPLGETLGFVPWRATKPTQYRYYHPCYINRYPNIQKTQQOLEWT
DQ371395  161  TNQGNASTKQFNNDLTASLQVALDTNNILPYTPAAPLGETLGFVPWRATKPTQYRYYHPCYINRYPNIQKTG-QELEWT

GFADV      226  AIQDDYFSVDQDYFNFITIENNIPINLRTGDNFHTGRYEFKSKPCKLTMSYQSTRCLGLPLCKPKTD-TKLVTSLENG
M20036    241  AVQDDYLSVDEQYFNFITIENNIPINLRTGDNFHTGLYEFNSKPCKLTLSYQSTRCLGLPLCKPKTD-THKVTSKENG
GU183265  240  GTQDDYLSVDEQYFNFITIENNIPINLRTGDNFHTGLYEFKSKPCKLTLSYQSTRCLGLPLCKPKTDVTHKVTSLENG
DQ371395  240  GTQDDYLSVDEQYFNFITIENNIPINLRTGDNFHTGLYEFKSKPCKLTFSYQSTRCLGLPLCKPKTDKTHKATSKENG

GFADV      305  GEMDCVVEGQOHTRKGHFWGEEKAEKNTELNRVRPYNIGVQPEWIPAGLOGSYFTGGPROSDTTKGAGTHSQTVQON
M20036    321  ADL-TYIQGDNTRLGHFWGERGKKNAEMNRIRPYNIGVQYPEWIPAGLOGSYFAGGPROSDTTKGAGTHSQHLQON
GU183265  320  ADL-TYIEGDNTRLGHFWGERGKKNAEMNRVRPYNIGVQYPEWIPAGLOGSYFAGGPROSDTTKGAGTHSQOLQON
DQ371395  320  ADL-IDVQRQRNTRLGHFWGEQRGKKNAEMNRIRPYNIGVQYPEWIPAGLOGSYFAGGQROSDTTKGAGTHSQNLQON

GFADV      385  FSTRYVFDRNHGGDNQVDTLDSIPTQERGKYYSEQELQQATLTATNKAQ--TGKKWESWEEGWPAASGTHFEDEVLYF
M20036    400  FSTRYIYDRNHGGDNEVDLDGIPIHERSNYSDNETEQHTAKOPKLRTPPIHHSKIDSWEEGWPAASGTHFEDEVIYL
GU183265  399  FSTRYIYDRNHGGDNEVDLDGIPIHERSNYSDNETEQHTAKOPKLRVPPIHHSKIDSWEEGWPAASGTHFEDEVIYL
DQ371395  399  FSTRYIYDRNHGGDREVNLDGIPIHERSKYSDNETEQHTAKOPKLRTPPIHHSKIDSWEEGWPAASGTHFEDEVIYL

GFADV      463  DYFNFSGETTKNFPQEVLSDGLQMKKLLNAYQPTVQDDVGPVYPWQIWDKKPDMDHKPSMNYNAPPVCKNNPPGOLLV
M20036    480  DYFNFSGEQELNFPHEVLDDAAQMKKLLNSYOPTVAODNVGPVYPWQIWDKKPHMDHKPSMNNAPPVCKNNPPGOLFV
GU183265  479  DYFNFSGEQTELFPHEVLDDAAQMKKLLNSYOPTVAODNVGPVYPWQIWDKKPDMDHKPSMNNAPPVCKNNPPGOLFV
DQ371395  479  DYFNFSGETELFPHEVLDDAAQMKKLLNSYOPTVADNVGPVYPWQIWDKKPDMDHKPSMNSASFVCKNNPPGOLFV

GFADV      543  KLTENLTDTFNYDEDPDRIKTYGYFTWRGKLTLRGKLCOTSCWNPVKRERIGEPGVFSKSNYHKQIPNNRGNFEIGLQYG
M20036    560  KLTENLTDTFNYDENPDRIKTYGYFTWRGKLVLKGKLSQVTCWNPVKRELIGEPGVFTKDKYHKQIPNNKGNFEIGLQYG
GU183265  559  KLTENLTDTFNYDENPDRIKTYGYFTWRGKLVLKGKLSQVTCWNPVKRELIGEPGVFTKDNYHKQIPNNKGNFEIGLQYG
DQ371395  559  KLTENLTDTFNYDENPDRIKTYGYFTWRGKLVLKGKLSQVTCWSPVKRELIGEPGVFTKDNYHKQIPNNKGNFEIGLQYG

GFADV      623  RSTVKYLY
M20036    640  RSTIKYIY
GU183265  639  RSTIKYIY
DQ371395  639  RSTIKYIY

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Technical Appendix Figure 5. Viral protein 2 alignment of gray fox amdovirus and representative amdoviruses. Black highlights 70%–100% similarity, gray highlights 50–70% similarity.