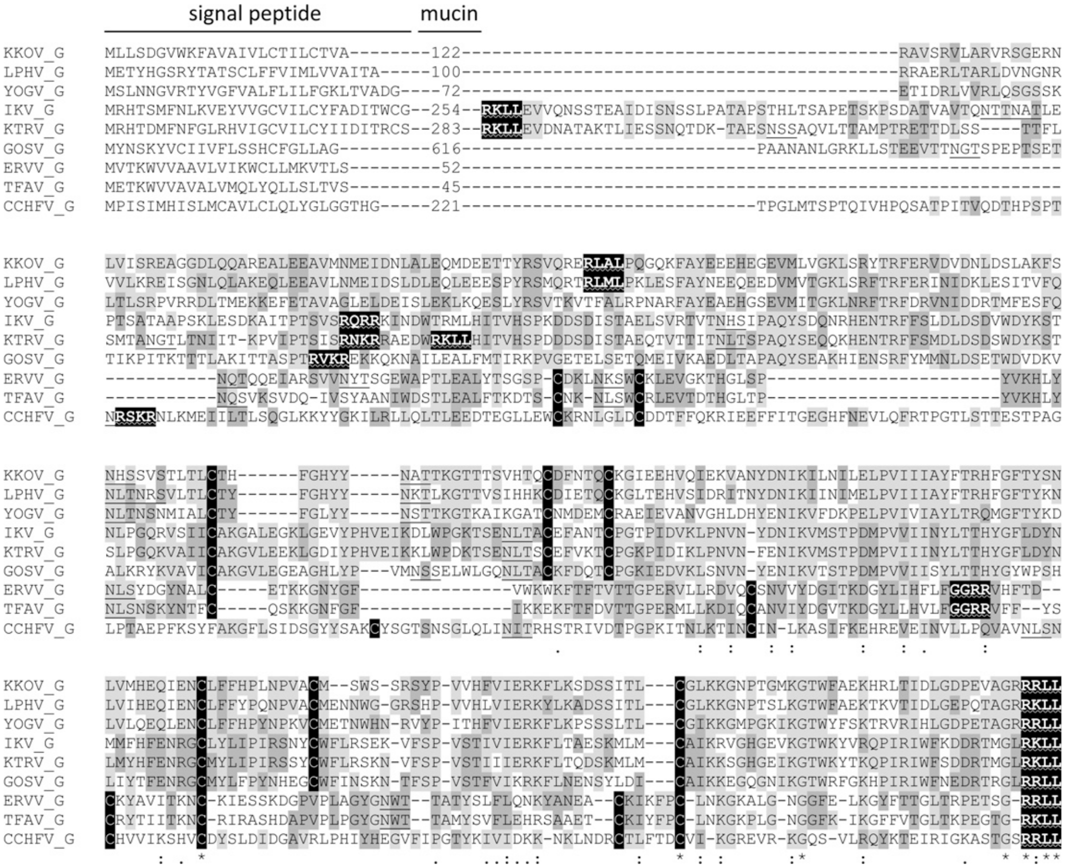

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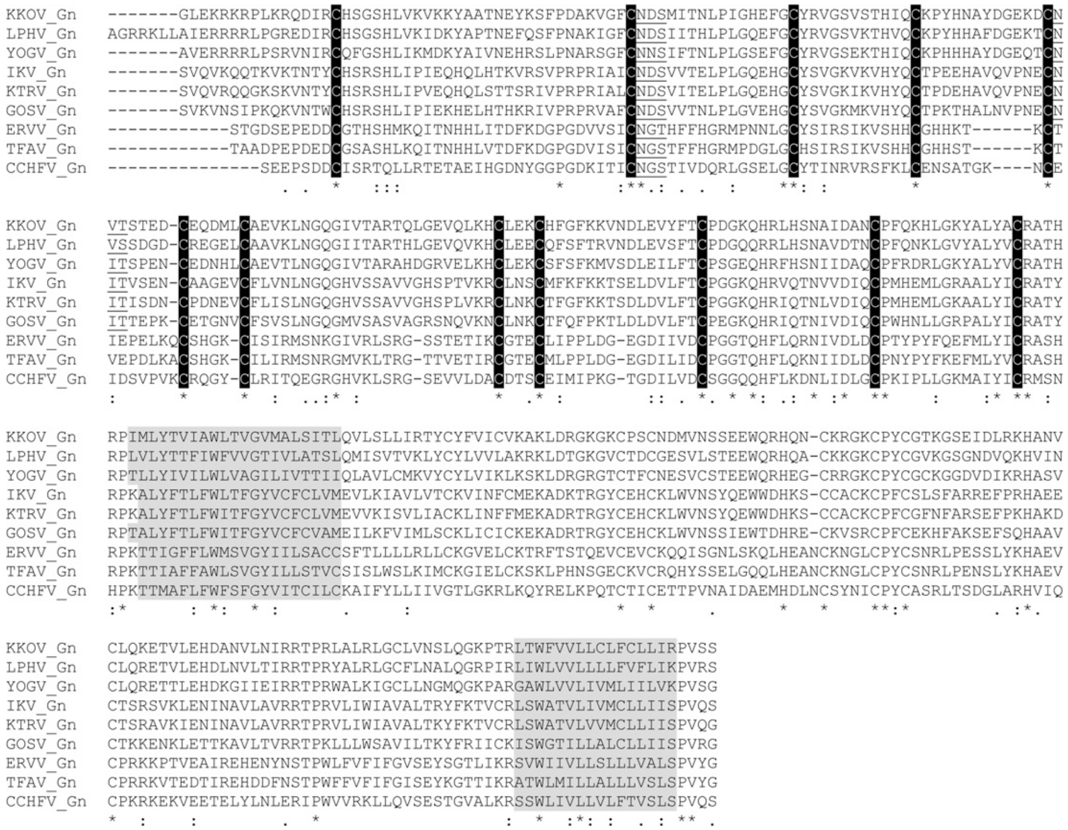
KKOV_G     MLLSDGVWKFAVAIVLCTILCTVA--------122-------------------------------------------RAVSRVLARVRSGERN
LPHV_G     METYHGSRYTATSCLFFVIMLVVAITA-----100-------------------------------------------RRAERLTARLDVNGNR
YOGV_G     MSLNNGVRTYVGFVALFLILFGKLTVADG----72-------------------------------------------ETIDRLVVRLQSGSSK
IKV_G      MRHTSMFNLKVEYVVGCVILCYFADITWCG--254--RKLLEVVQNSSTEAIDISNSSLPATAPSTHLTSAPETSKPSDATVAVTQNTTNATLE
KTRV_G     MRHTDMFNFGLRHVIGCVILCYIIDITRCS--283--RKLLEVDNATAKTLIESSNQTDK-TAESNSSAQVLTTAMPTRETTDLSS----TTFL
GOSV_G     MYNSKYVCIIVFLSSHCFGLLAG---------616-----------------------------PAANANLGRKLLSTEEVTTNGTSPEPTSET
ERVV_G     MVTKWVVAAVLVIKWCLLMKVTLS---------52-----------------------------------------------------------
TFAV_G     METKWVVAVALVMQLYQLLSLTVS---------45-----------------------------------------------------------
CCHFV_G    MPISIMHISLMCAVLCLQLYGLGGTHG-----221-----------------------------TPGLMTSPTQIVHPQSATPITVQDTHPSPT

KKOV_G     LVISREAGGDLQQAREALEEAVMNMEIDNLALEQMDEETTYRSVQRERLALPQGQKFAYEEEHEGEVMLVGKLSRYTRFERVDVDNLDSLAKFS
LPHV_G     VVLKREISGNLQLAKEQLEEAVLNMEIDSLDLEQLEEESPYRSMQRTRLMLPKLESFAYNEEQEEDVMVTGKLSRFTRFERINIDKLESITVFQ
YOGV_G     LTLSRPVRRDLTMEKKEFETAVAGLELDEISLEKLKQESLYRSVTKVTFALRPNARFAYEAEHGSEVMITGKLNRFTRFDRVNIDDRTMFESFQ
IKV_G      PTSATAAPSKLESDKAITPTSVSRQRRKINDWTRMLHITVHSPKDDSDISTAELSVRTVTNHSIPAQYSDQNRHENTRFFSLDLDSDVWDYKST
KTRV_G     SMTANGTLTNIIT-KPVIPTSISRNKRRAEDWRKLLHITVHSPDDDSDISTAEQTVTTITNLTSPAQYSEQQKHENTRFFSMDLDSDSWDYKST
GOSV_G     TIKPITKTTTLAKITTASPTRVKREKKQKNAILEALFMTIRKPVGETELSETQMEIVKAEDLTAPAQYSEAKHIENSRFYMMNLDSETWDVDKV
ERVV_G     -----------NQTQQEIARSVVNYTSGEWAPTLEALYTSGSP-CDKLNKSWCKLEVGKTHGLSP-----------------------YVKHLY
TFAV_G     -----------NQSVKSVDQ-IVSYAANIWDSTLEALFTKDTS-CNK-NLSWCRLEVTDTHGLTP-----------------------YVKHLY
CCHFV_G    NRSKRNLKMEIILTLSQGLKKYYGKILRLLQLTLEEDTEGLLEWCKRNLGLDCDDTFFQKRIEEFFITGEGHFNEVLQFRTPGTLSTTESTPAG

KKOV_G     NHSSVSTLTLCTH------FGHYY-----NATTKGTTTSVHTQCDFNTQCKGIEEHVQIEKVANYDNIKILNILELPVIIIAYFTRHFGFTYSN
LPHV_G     NLTNRSVLTLCTY------FGHYY-----NKTLKGTTVSIHHKCDIETQCKGLTEHVSIDRITNYDNIKIINIMELPVIIIAYFTRHFGFTYKN
YOGV_G     NLTNSNMIALCTY------FGLYY-----NSTTKGTKAIKGATCNMDEMCRAEIEVANVGHLDHYENIKVFDKPELPVIVIAYLTRQMGFTYKD
IKV_G      NLPGQRVSIICAKGALEGKLGEVYPHVEIKDLWPGKTSENLTACEFANTCPGTPIDVKLPNVN-YDNIKVMSTPDMPVVIINYLTTHYGFLDYN
KTRV_G     SLPGQKVAIICAKGVLEEKLGDIYPHVEIKKLWPDKTSENLTSCEFVKTCPGKPIDIKLPNVN-FENIKVMSTPDMPVIIINYLTTHYGFLDYN
GOSV_G     ALKRYKVAVICAKGVLEGEAGHLYP---VMNSSELWLGQNLTACKFDQTCPGKIEDVKLSNVN-YENIKVTSTPDMPVVIISYLTTHYGYWPSH
ERVV_G     NLSYDGYNALC-----ETKKGNYGF---------------VWKWKFTFTVTTGPERVLLRDVQCSNVVYDGITKDGYLIHFLFGGRRVHFTD--
TFAV_G     NLSNSKYNTFC-----QSKKGNFGF---------------IKKEKFTFDVTTGPERMLLKDIQCANVIYDGVTKDGYLLHVLFGGRRVFF--YS
CCHFV_G    LPTAEPFKSYFAKGFLSIDSGYYSAKCYSGTSNSGLQLINITRHSTRIVDTPGPKITNLKTINCIN-LKASIFKEHREVEINVLLPQVAVNLSN
                                                       .             :  :   : :      :   : .     :

KKOV_G     LVMHEQIENCLFFHPLNPVACM--SWS-SRSYP-VVHFVIERKFLKSDSSITL---CGLKKGNPTGMKGTWFAEKHRLTIDLGDPEVAGRRRLL
LPHV_G     LVIHEQIENCLFFYPQNPVACMENNWG-GRSHP-VVHLVIERKYLKADSSITL---CGLKKGNPTSLKGTWFAEKTKVTIDLGEPQTAGRRKLL
YOGV_G     LVLQEQLENCLFFHPYNPKVCMETNWHN-RVYP-ITHFVIERKFLKPSSSLTL---CGIKKGMPGKIKGTWYFSKTRVRIHLGDPETAGRRRLL
IKV_G      MMFHFENRGCLYLIPIRSNYCWFLRSEK-VFSP-VSTIVIERKFLTAESKMLM---CAIKRVGHGEVKGTWKYVRQPIRIWFKDDRTMGLRKLL
KTRV_G     LMYHFENRGCMYLIPIRSSYCWFLRSKN-VFSP-VSTIIIERKFLTQDSKMLM---CAIKKSGHGEIKGTWKYTKQPIRIWFSDDRTMGLRKLL
GOSV_G     LIYTFENRGCMYLFPYNHEGCWFINSKN-TFSP-VSTFVIKRKFLNENSYLDI---CAIKKEGQGNIKGTWRFGKHPIRIWFNEDRTRGLRRLL
ERVV_G     CKYAVITKNC-KIESSKDGPVPLAGYGNWT--TATYSLFLQNKYANEA--CKIKFPC-LNKGKALG-NGGFE-LKGYFTTGLTRPETSG-RRLL
TFAV_G     CRYTIITKNC-RIRASHDAPVPLPGYGNWT--TAMYSVFLEHRSAAET--CKIYFPC-LNKGKPLG-NGGFK-IKGFFVTGLTKPEGTG-RKLL
CCHFV_G    CHVVIKSHVCDYSLDIDGAVRLPHIYHEGVFIPGTYKIVIDKK-NKLNDRCTLFTDCVI-KGREVR-KGQS-VLRQYKTEIRIGKASTGSRRLL
                : . *                      .    ..:..:         :   * : :      :*     :         .   * *:**
```

Supplemental Figure 1. The deduced amino acid sequences of the gp38 domain of nine nairoviruses aligned in ClustalX and adjusted visually. Cysteine residues are shaded in black and other conserved residues are shaded in gray. Predicted N-glycosylation sites are underlined. Predicted proteolytic cleavage sites that may define the N-terminus gp38 (furin-like or SKI-1) and N-terminus of Gn (R[R/K]LL) are shaded in black and underlined.



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KKOV_Gn    -------GLEKRKRPLKRQDIRCHSGSHLVKVKKYAATNEYKSFPDAKVGFCNDSMITNLPIGHEFGCYRVGSVSTHIQCKPYHNAYDGEKDCN
LPHV_Gn    AGRRKLLAIERRRRLPGREDIRCHSGSHLVKIDKYAPTNEFQSFPNAKIGFCNDSIITHLPLGQEFGCYRVGSVKTHVQCKPYHHAFDGEKTCN
YOGV_Gn    -------AVERRRRLPSRVNIRCQFGSHLIKMDKYAIVNEHRSLPNARSGFCNNSIFTNLPLGSEFGCYRVGSEKTHIQCKPHHHAYDGEQTCN
IKV_Gn     -------SVQVKQQTKVKTNTYCHSRSHLIPIEQHQLHTKVRSVPRPRIAICNDSVVTELPLGQEHGCYSVGKVKVHYQCTPEEHAVQVPNECN
KTRV_Gn    -------SVQVRQQGKSKVNTYCHSRSHLIPVEQHQLSTTSRIVPRPRIALCNDSVITELPLGQEHGCYSVGKIKVHYQCTPDEHAVQVPNECN
GOSV_Gn    -------SVKVNSIPKQKVNTWCHSRSHLIPIEKHELHTHKRIVPRPRVAFCNDSVVTNLPLGVEHGCYSVGKMKVHYQCTPKTHALNVPNECN
ERVV_Gn    ------------STGDSEPEDDCGTHSHMKQITNHHLITDFKDGPGDVVSICNGTHFFHGRMPNNLGCYSIRSIKVSHHCGHHKT------KCT
TFAV_Gn    ------------TAADPEPDEDCGSASHLKQITNHHLVTDFKDGPGDVISICNGSTFFHGRMPDGLGCHSIRSIKVSHHCGHHST------KCT
CCHFV_Gn   ---------------SEEPSDDCISRTQLLRTETAEIHGDNYGGPGDKITICNGSTIVDQRLGSELGCYTINRVRSFKLCENSATGK----NCE
                            . .  *   :::               *     :**.: . .  :    **: :        *            *

KKOV_Gn    VTSTED-CEQDMLCAEVKLNGQGIVTARTQLGEVQLKHCLEKCHFGFKKVNDLEVYFTCPDGKQHRLHSNAIDANCPFQKHLGKYALYACRATH
LPHV_Gn    VSSDGD-CREGELCAAVKLNGQGIITARTHLGEVQVKHCLEECQFSFTRVNDLEVSFTCPDGQQRRLHSNAVDTNCPFQNKLGVYALYVCRATH
YOGV_Gn    ITSPEN-CEDNHLCAEVTLNGQGIVTARAHDGRVELKHCLEKCSFSFKMVSDLEILFTCPSGEQHRFHSNIIDAQCPFRDRLGKYALYVCRATH
IKV_Gn     ITVSEN-CAAGEVCFLVNLNGQGHVSSAVVGHSPTVKRCLNSCMFKFKKTSELDVLFTCPGGKQHRVQTNVVDIQCPMHEMLGRAALYICRATY
KTRV_Gn    ITISDN-CPDNEVCFLISLNGQGHVSSAVVGHSPLVKRCLNKCTFGFKKTSDLDVLFTCPGGKQHRIQTNLVDIQCPMHEMLGKAALYICRATY
GOSV_Gn    ITTEPK-CETGNVCFSVSLNGQGMVSASVAGRSNQVKNCLNKCTFQFPKTLDLDVLFTCPEGKQHRIQTNIVDIQCPWHNLLGRPALYICRATY
ERVV_Gn    IEPELKQCSHGK-CISIRMSNKGIVRLSRG-SSTETIKCGTECLIPPLDG-EGDIIVDCPGGTQHFLQRNIVDLDCPTYPYFQEFMLYICRASH
TFAV_Gn    VEPDLKACSHGK-CILIRMSNRGMVKLTRG-TTVETIRCGTECMLPPLDG-EGDILIDCPGGTQHFLQKNIIDLDCPNYPYFKEFMLYVCRASH
CCHFV_Gn   IDSVPVKCRQGY-CLRITQEGRGHVKLSRG-SEVVLDACDTSCEIMIPKG-TGDILVDCSGGQQHFLKDNLIDLGCPKIPLLGKMAIYICRMSN
           :      *     *  :  ..:* :             *  .* :        :: . *. * *: .: * :*  **    :    :* ** :

KKOV_Gn    RPIMLYTVIAWLTVGVMALSITLQVLSLLIRTYCYFVICVKAKLDRGKGKCPSCNDMVNSSEEWQRHQN-CKRGKCPYCGTKGSEIDLRKHANV
LPHV_Gn    RPLVLYTTFIWFVVGTIVLATSLQMISVTVKLYCYLVVLAKRKLDTGKGVCTDCGESVLSTEEWQRHQA-CKKGKCPYCGVKGSGNDVQKHVIN
YOGV_Gn    RPTLLYIVILWLVAGILIVTTIIQLAVLCMKVYCYLVIKLKSKLDRGRGTCTFCNESVCSTEEWQRHEG-CRRGKCPYCGCKGGDVDIKRHASV
IKV_Gn     RPKALYFTLFWLTFGYVCFCLVMEVLKIAVLVTCKVINFCMEKADKTRGYCEHCKLWVNSYQEWWDHKS-CCACKCPFCSLSFARREFPRHAEE
KTRV_Gn    RPKALYFTLFWITFGYVCFCLVMEVVKISVLIACKLINFFMEKADRTRGYCEHCKLWVNSYQEWWDHKS-CCACKCPFCGFNFARSEFPKHAKD
GOSV_Gn    RPTALYFTLFWITFGYVCFCVAMEILKFVIMLSCKLICICKEKADRTRGYCEHCKLWVNSSIEWTDHRE-CKVSRCPFCEKHFAKSEFSQHAAV
ERVV_Gn    RPKTTIGFFLWMSVGYIILSACCSFTLLLLRLLCKGVELCKTRFTSTQEVCEVCKQQISGNLSKQLHEANCKNGLCPYCSNRLPESSLYKHAEV
TFAV_Gn    RPKTTIAFFAWLSVGYILLSTVCSISLWSLKIMCKGIELCKSKLPHNSGECKVCRQHYSSELGQQLHEANCKNGLCPYCSNRLPENSLYKHAEV
CCHFV_Gn   HPKTTMAFLFWFSFGYVITCILCKAIFYLLIIVGTLGKRLKQYRELKPQTCTICETTPVNAIDAEMHDLNCSYNICPYCASRLTSDGLARHVIQ
           :*      : *:  * :      .     :                    *  *     .      *   *    **:*        . :*.

KKOV_Gn    CLQKETVLEHDANVLNIRRTPRLALRLGCLVNSLQGKPTRLTWFVVLLCLFCLLIRPVSS
LPHV_Gn    CLQRETVLEHDLNVLTIRRTPRYALRLGCFLNALQGRPIRLIWLVVLLLLFVFLIKPVRS
YOGV_Gn    CLQRETTLEHDKGIIEIRRTPRWALKIGCLLNGMQGKPARGAWLVVLIVMLIILVKPVSG
IKV_Gn     CTSRSVKLENINAVLAVRRTPRVLIWIAVALTRYFKTVCRLSWATVLIVMCLLIISPVQS
KTRV_Gn    CTSRAVKIENINAVLAVRRTPRVLIWIAVALTKYFKTVCRLSWATVLVVMCLLIISPVQG
GOSV_Gn    CTKKENKLETTKAVLTVRRTPKLLLWSAVILTKYFRIICKISWGTILLALCLLIISPVRG
ERVV_Gn    CPRKKPTVEAIREHENYNSTPWLFVFIFGVSEYSGTLIKRSVWIIVLLSLLLVALSPVYG
TFAV_Gn    CPRRKVTEDTIREHDDFNSTPWFFVFIFGISEYKGTTIKRATWLMILLALLLVSLSPVYG
CCHFV_Gn   CPKRKEKVEETELYLNLERIPWVVRKLLQVSESTGVALKRSSWLIVLLVLFTVSLSPVQS
           *  :    :        .  *                  :  *  :*: :  . : ** .
```

SUPPLEMENTAL FIGURE 2. ClustalX alignment of the deduced amino acid sequences of the Gn proteins of nine nairoviruses. Conserved cysteine residues are shaded in black and two predicted transmembrane domains are shaded in gray. Predicted N-glycosylation sites are underlined. Identical (*), strongly conserved (:) and weakly conserved (.) residues as assigned in the Gronnet Pam250 matrix are indicated below the alignment.

```
KKOV_Gc     --------FRTNLQKEGAWEEGIEEVEYCKQDCWFENDICMCEKETG-KISRRILSVEPSKEP---HKHIAPG--TKKILRSIDVEAPWGTLHI
LPHV_Gc     --------LETNDQTEGLWEEGIEEVEKCGKGCWYNQDVCTCDKEEPLHTSRHILSVPAKDDT---EKATSKDRQGKKVMRSLDVEAPWGTLHI
YOGV_Gc     --------FATDDKIDGIWEEGIVEVTNCRQGCWYENDICQCEEKER-GGSRRLLSETPTQKPTA-AKSVKSHTSGRQIRRSLDVEAPWGTIHI
IKV_Gc      --------LKTGPLPDGIWDEYENEVLNCKENCIKALDSCICEDVDHSSKTEFS-TMRKLSSVVVQGPTPSQPEKIHRILKSIDVEAPWGTLHV
KTRV_Gc     --------LNTGPLPEGIWNEYENEVFNCKESCMKLPDSCVCNDQEQNLKTEFN-TMRKLNSIIMSGPTPGQAGKIHTVLKSIDVEAPWGTLHV
GOSV_Gc     --------FETGISSPGIWEEYEQEVHTCKEDCVKLDDGCICNEGELNALTAKGSNMRSLKSIVVQGPDNSPTFRPHKVLKSIDVEAPWGTLHV
ERVV_Gc     EQDFLFEGIGEEQLEKGLWEDEVELVEGCHQECFVVEAECLCP-SFQAGRQLLFYHLMN--------KQIR-TSNKLKLLSSVSLETPWGVVKI
TFAV_Gc     -NELFFDGIGDGQLEKGLWDEEIGLVENCHQECFITETECLCP-SFETGRKLLFFHLLN--------KQIR-SGRKMKLLSSISLDTPWGVVKI
CCHFV_Gc    --------VEMENLPAGTWEREEDLTNFCHQECQVTETECLCPYEALVLRKPLFLDSTA--------KGMKNLLNSTSLETSLSIEAPWGAINV
                    .       * *:     .  * : *      * *                                    :  *:.:::***.:::

KKOV_Gc     PETFSPAGSAKHISLSWESSKLVGNRVVLSGKSTAILKLNPRTSTSWEMSSPDANEKKVLTLSILDYTQIYSSRFEYITGDRKVSTWSEGSCTG
LPHV_Gc     PETFSPAGSVKHISLSWESSRVVGKRVILSGKSTAILKLNPKTSTSWEMTSPDANEKKILTLSILDYTQIYSSRFEYLTGDRKVTTWSEGSCTG
YOGV_Gc     PETYSPVGSVKHISLSWESSKVVGKKVILSGKSTALLKLNPRTSTSWEMSSEDSNEKKVLTLSILDYTQVYSSRFEYITGDRKVTTWAEGSCTG
IKV_Gc      PESYTPAQSAKHISLTWESSQAVGDKIVLSGRSSTVLKLEPKTSTVWTMENKEASEKKTLTISVLDFTQIYSAEFLYATGDRNIKTWSEGSCRG
KTRV_Gc     PESYTPAQSAKHISLTWESSQAVGDKIILSGRSSTVLKLEPKTSTVWTMETRDASEKKTLTVSILDFTQMYSAEFLYATGDRSIKTWSEGSCSG
GOSV_Gc     PESYSPAQSAKHISLSWESSQLIGDKVVLTGKSSAVLKLEPKTSTVWTMSNKDAKEKKTLTISILDYTQIYSAEFLYVTGDRLIKTWSEGSCSG
ERVV_Gc     EKGFKPTSSMANLQLSWSSEEEVGGKVILSGRSTSIIKLKERTGMVWELSSSRASEKKKLVVSIMDFSQEYKTQFQYLTGDRLVSEWPRATCTG
TFAV_Gc     EKSFKPVLSMSNLQLSWTSEEEVGGKIVVSGKSTAVLKLKEKTGMVWELSSSKATEKKTLIVSVMDYTQEYKTQLQYLTGDRLVSEWPRATCTG
CCHFV_Gc    QSTYKPTVSTANIALSWSSVEHRGNKILVSGRSESIMKLEERTGISWDLGVEDASESKLLTVSVMDLSQMYSPVFEYLSGDRQVGEWPKATCTG
             . :.*. *  :: *:* * .  * :::::*:* :::**: :*.  * :    :.*.* * :*::* :* *.. : * :*** :  *...:* *

KKOV_Gc     PCPKNCGCDDPSCHTREWLNSRNWRCNPTWCWGIGTGCSCCSAQVVDLYESWLVSIWQIEHIRTPVVACLEFDHENRVCEVVEAGIEIQLGPVT
LPHV_Gc     PCPKDCGCNDPSCHTKQWLNTRNWRCNPTWCWGIGTGCSCCSAKVVDLYKNWLVSIWQIEHLRTPVVACLEFDHENRVCDVVEAGIEIQLGPVT
YOGV_Gc     PCPKECGCSDPTCHTKEWPNSRNWRCNPTWCWGIGTGCSCCAAKVVDLYERWLVSLWQIEYLKTPVVACLEFDHDNRVCDVVEAGIEMQLGPVT
IKV_Gc      DCPLNCGCNTQTCHIQNWMNVRNWRCNPTWCWRVGTGCSCCASDITELYADWLATIWKIEHKKTAVIACVEFDHEQRVCESVEAGVEVQLGPVK
KTRV_Gc     DCPKNCGCNTQTCHIQSWLNVRNWRCNPTWCWRVGTGCSCCASDVTELYTNWLTTVWRVEHKKTAVVACVEFDHEQRICESVEAGVEIQLGPVK
GOSV_Gc     NCPDNCGCLRQTCHVQNWLNVRNWRCNPTWCWRIGTGCSCCASDISELFQDWLVSIWKIEHQKTAVIACVEFDHDQRICESVEAGVEIQLGPVK
ERVV_Gc     PCPDRCACHTSTCTWKTWPNSRKWTCNPTWCWGVGTGCTCCGMDVEKPFQNYLVAKWSTEYIKTDVIVCVEVSEEERHCDLIQAGSRFHLGPIT
TFAV_Gc     PCPDRCACHTSTCTWKAWPNSRKWTCNPTWCWGVGTGCTCCGMDIEKPYQNYLAAKWSTEYIKTDVVVCVETSDEERHCDIIQAGSRFHLGPIT
CCHFV_Gc    DCPERCGCTSSTCLHKEWPHSRNWRCNPTWCWGVGTGCTCCGLDVKDLFTDYMFVKWKVEYIKTEAIVCVELTSQERQCSLIEAGTRFNLGPVT
             **  *.*   :*  : * : *:* ******* :****:**. .: . :  ::   *  *: :* .:.*:*   ::* *. ::** ..:***:.

KKOV_Gc     VAFSDPFGEQKLLPKRIAVYHKRDSDHEHVDLLHNHGIGGAEQYCKLQSCTHGTAGDYQILNPDALVFDDITSINYFKKIDAA---NKVWMSWE
LPHV_Gc     VAFSDPFGEQKILPQRIAVYHKRDVDHEHVDLLHNHGIGGAEQYCKLQSCTHGTAGDYQIINPDALVFDDITSMNYFKKLDVY---NKLWMSWE
YOGV_Gc     VAFSDPFGEQRILPRRIAVYHKRDTDHEHVDLLHNHGIGGADQYCKLESCTHGTAGDYQITDPDALVYDDVTSMNYFKKIDTH---NKEWMSWE
IKV_Gc      VEFSDPFGENQILNQRIALFHKIPKMSTHVDLFHNFGVTSATSFCNIESCTHGTVGDYQIYDPDVFVLDDVTSANYFKKLNNKT---KVWMSWE
KTRV_Gc     VGFSDPFGETQILNQRIALFHKIPEVTTHIDLFHNFGVTSATSFCNIQSCTHGTVGDYQIFDPDVFVLDDVTSTNYFKKLNNKT---KVWMSWE
GOSV_Gc     VSFSDPFGETKVLSHRIAIYHKVPGTANHIDFYHNYGLSSATSFCNIQSCTHGTVGDYQVFDPDAFVLDDVTSPNYFKRMDNST---KVWMSWE
ERVV_Gc     VLVSDPQSVAKKLPSEVITLH--KVQGGEVDLMHVNKILTANSLCKPQSCTHGSPGDIQIFKPDYLVKYS--ISKRINAIEDHSWANDTWMSWQ
TFAV_Gc     VLISDPQNVVKKLPSEVATIH--KVQSSEVDVMHVDRILTANGLCKLQSCTHGSPGDIQIFKPDYLVKHS--ISKRINAIEDHWWANDTWMSWQ
CCHFV_Gc    ITLSEPRNIQQKLPPEIITLHP-RIEEGFFDLMHVQKVLSASTVCKLQSCTHGVPGDLQVYHIGNLLKGDKVNGHLIHKIEPH--FNTSWMSWD
            : .*:* .  : *  .:   *        .*. *   :  *   *: :*****  ** *: . . ::  .    : :: ::     .  ****:

KKOV_Gc     GVNLGYYCNPGDWTTCTAENVVVRNSEAFQNRNNLERNYSVSHFFHSSRIYGAGKTLSMDLKGRPVQSGGNINVYITVNNLELNSKKVNLQGIK
LPHV_Gc     GVNLGYYCNPGDWTTCTAENIVVRNSEAFSNRNNLERNYSVSHFFHSSRVYGSGKSLVMDLKGRPIQSGGNINVYVTVNNLELNSKKVVITGLK
YOGV_Gc     GVNLGYYCNPGDWTTCTAENIVERNSESFKNRNDMERNFTKSHFFHSSRVYGAGNSLAMDLKARPIQSGGSINVYITVNNLELSSKKVALEGLR
IKV_Gc      GISVSYYCNPGDWTTCVTDGVVERNSEAFANVFKSETNYSTTHFFHSSRVVSEGKTLSLDLKARPLSSGGDITAYITVDGLELYSKEIHLEGLK
KTRV_Gc     GVSVSYYCNPGDWTTCVSDGVVEKNSEAFANVFKSETNYSTTHFFHSSRVVSQGKTLSLDLKARPISAGGDLTAFITVDGLELFSKEIHLEGLK
GOSV_Gc     GVSVSYYCNPGDWTTCVSDNIVERNGDAFSNVFKSETNFSTTHFFHSTRITGAGKTMALDLKGRPLSSGGDMTAYVTVEGLELFSKEIHLEGLK
ERVV_Gc     GSDLDYYCTTGSWPTCTFSGVVKQNSDAFKNLETLEFNLMEEFFFHSSRVEVKGSTLGFPVKSRPKEGGGELSVLVEVNGLELHSKLIDPLGLS
TFAV_Gc     GTDLDYYCTTGSWPTCTYSGVVRQNTDSFKNLETTEFDLLEEYFFHSSRVEVHGRTLNFPVKSRPKEGGGELTVLVEVNGLELHSKLIVPVGLM
CCHFV_Gc    GCDLDYYCNMGDWPSCTYTGVTQHNHASFVNLLNIETDYTKNFHFHSKRVTAHGDTPQLDLKARPTYGAGEITVLVEVADMELHTKKIEISGLK
            * .:.***. *.*.:*.  .:. :*  :* *    * :    ..***.*:   * :  : :*.**  ..*.:.. : * .:** :* :   *:

KKOV_Gc     VALKTCSGCFGCNLGAECQVSLAISEPEEFHLHLRSRTPGVTVPDTSFLVISGEE-KVFRIRVFSIQKTGNFCVEILESKHCPDCKGEDLVSCV
LPHV_Gc     VNLRACTGCFGCNLGAECQISLSLTEPDEFHLHLKSVTPGVTVPDTSFLVTSSEE-KMFNIRVFSILKDVNFCIEVLESKHCPECDKKDLQSCL
YOGV_Gc     LQLRSCSGCFGCNIGAECQISMSITEPEQFHLHLKSLTPGITVPDTSFLVTSEEE-RNFKVRIFSIEKSGNFCLELFESKLCKTCRREDVSACT
IKV_Gc      ISMGSCTGCFACNLGATCSFTLAIRRPERFNLHITSDTAGVVVPDTSFLVEADRF-NTYNIKIFSVEKDTNVCIKILEGKFCKTCPKENLVACK
KTRV_Gc     VSMGSCTGCFACNLGATCSFTLSIRKPEKFNLHLISKTAGVVVPDTSFLVESDKF-NTYTIKVFSVDKKTDICVEILEGKFCKTCPKENLVSCK
GOSV_Gc     LTLGLCKGCFACNLGATCEITLSIRKPDSFNLHIRSKSPGVVVPDTSFLVESDKH-NSFTIKVFSVEKEPKVCLEIVERKFCQHCPESNVVSCQ
ERVV_Gc     LKITSCKGCYSCSSGFYCDVVLNIEEPSEMTVHVECNNPNIVLTESSLIAKSGAL-SASKVKGFSALRETRLCLILQE----SKVTKKEVKDCI
TFAV_Gc     FKITSCKGCYSCSSGFICDVVLGVDSPPELTVHAECTNPNIVLTEGSLIARQGQT-STAKIKGFSVLKTTRLCIVLQE----SKVLEKLIEDCT
CCHFV_Gc    FASLACTGCYACSSGISCKVRIHVDEPDELTVHVKSDDPDVVAASSSLMARKLEFGTDSTFKAFSAMPKTSLCFYIVEREHCKSCSEEDTKKCV
            .    *.**:.*. *  *.. : :  *  : :*  .  ..:. .. *::.          .: **      .*. : *         .    *

KKOV_Gc     GLELEDPKPVLLEHRSVLFSKSNQTCEGGVISCWAGSAGNLFKGIGSFLSSHFGSIFKGLLMAVLPVLLIAGGIFFSPQIISFL---RLFKRGR
LPHV_Gc     QLTFEDPKPVLLEHRSVLFSKSNQTCGDSTISCWSSSAGILFKGIGNFLSTHFGSIFRGILLSVLPILLIVGLIFFSPQIISLM---RLCKRGR
YOGV_Gc     SLNLEDPKPVLLEHRSTLFSKSNKTCGGGLLSCWSESAGGLLKGVGSFLVGQFGSIFKGILSFLIPIALVAGLIFFSPQIFGLL---RMCKKGR
IKV_Gc      RFSFENPKEVALEHRSTIFAKSTQSCGNSTLSCMLSGTKNFFSGIGGFFNGYFGSILKGILSTVLPIALIVLTIFFGPKLSFVL---RLCKKGR
KTRV_Gc     NFILDDPKEVALEHRSTIFAKSTQSCGNSTLSCMLSGAKSFFSGIGSFFSGYFGSILKGVLFTVLPIILVVLAVFYGPKMLFIL---RFCKKGR
GOSV_Gc     NVKFEDPKEIALEHRSTIFSKSTQKCGNSTMSCLFSGASSFFKGIGGFFSGYFGSIIKGVLMTILPIALIVLTVFYGPKLAFVL---KFCKKGR
ERVV_Gc     DIKLEEPKDVIIERGSTLLSHQNDTCT-SGFGCWLGNAKSFSLGLGMMFQNYFGSIIIGLIIFVLPVIALLVFFCLGKRILIC-RRLKHCFRSN
TFAV_Gc     ELKLDDPKDVIIERGSTLLSHQNDSCS-YGLGCWLANVGTFGSGLSMIFQNYFGSVILGFLFFVLPVVLLLVFFCLGDKIFFC-RKFKWCFKSN
CCHFV_Gc    NTKLEQPQSILIEHKGTIIGKQNSTCT-AKASCWLESVKSFFYGLKNMLSGIFGNVFMGIFLFLAPFILLILFFMFGWRILFC---FKCCRRTR
               :::*: : :*: ..::.:....*     .*   ..  :  *:  ::   **.:: *.:   : *.  :   .  .::      ::   : .

KKOV_Gc     S-------VVGYRKKGYRPLTEEKDLD----LTAEEKAFLSGIIGKKKE------
LPHV_Gc     S-------VVGFRKRFYKPLTDGADMG----LSAEEKAFLTGIFGKKKE------
YOGV_Gc     S-------VVGYKRRFYRPLTEDKEVN----LTAEEKAFLGGVIGKKKE------
IKV_Gc      A-------LKSLSYEPMKQITDIDEFLKKETSSDEGKNFLRSVLGPKLKPA----
KTRV_Gc     A-------LTSMNYEPIKQITNIDDFLKTEASSDEGGNFLKSVLGPKLKPA----
GOSV_Gc     A-------LKNITYKPIEPVRSVDDYLGKELHTDEARAVMKSLIN-KLK------
ERVV_Gc     --------LEDKQK-FKQLLTELKHSNLLKIMKEDAKSSWRGLANKALGKTPKMD
TFAV_Gc     --------KEDKEK-FKQMVTELKQTNLIKKMKEEAKTSWRGLANKALGKSTKEE
CCHFV_Gc    GLFKYRHLKDDEETGYRRIIEKLNNKKGKNKLLDGERLADRRIAELFSTKTHIG-
                      .      . : .  .                 :
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Supplemental Figure 3. ClustalX alignment of the deduced amino acid sequences of the Gc proteins of nine nairoviruses. Conserved cysteine residues are shaded in black and one predicted transmembrane domain is shaded in gray. Identical (*), strongly conserved (:) and weakly conserved (.) residues as assigned in the Gronnet Pam250 matrix are indicated below the alignment. Potential SKI-1 proteolytic cleavage sites near the N-terminus that may generate the fully processed glycoprotein are shaded in black and underlined. Predicted N-glycosylation sites are underlined. Identical (*), strongly conserved (:) and weakly conserved (.) residues as assigned in the Gronnet Pam250 matrix are indicated below the alignment.

```
KKOV_L    PGDGTCFFSSVSKYIFN--TTEMWKTVKSTCANYARAHWQEVMEMDRRYQSPETYIEDLMNDQYWGGSVEAEILSKALNMTIH
LPHV_L    PGDGTCFFSSVSKYIFN--TTELWQTVKSTCANYARAHWKEVMEMDRQYAEADAYISDLMRDQYWGGSIEAEILSKALNMTIY
YOGV_L    PGDGTCFFSSVSKYIFN--TTEQWRAVKTTCANYARANWDTVMEIDRHYQNADHYVNDLMRDQYWGGSVEAEILNKALNMTVH
IKV_L     LPDGRCFFRAMAKFMFN--SSDEWLIVKRACIEYSRQHWNRFLVYTRLYPSSADYERDIMRDDYWGGSLEAEVLSDLYNLTIH
KTRV_L    QPDGRCFFRAMAKFMFN--SSDEWLIVKRACIEYARQHWNKFLVFTRLYQTPADYERDIMRDDYWGGSLEAEVLSDLYNLTIH
GOSV_L    VPDGKCFFRAMAKFMFN--SDEEWLLVKRACVEFARQHWDRFLEFTRNYQRANDYERDIMRDDYWGGSLESDILSELYNVTIH
ERVV_L    VGDGNCFYRALSRLHSESRTSNEHLYYRLLIPDAVDKYFDIEPEAIGLGLNKQEYVSKAILDGEWAGSLEASMLSKFLDITII
TFAV_L    VGDGNCFYRALSRLHSKDKTSDEHLYYRLLIPDAAQRYFDTEQEAVGLGLTKEEYASRAILDGEWAGSLEASMLSKFLDITII
CCHFV_L   PGDGNCFYHSIAELTMPNKTDHSYHYIKRLTESAARKYYQEEPEARLVGLSLEDYLKRMLSDNEWGSTLEASMLAKEMGITII
            ** **: :::.      : .     :    .     :.              *    : *  *..::*:.:* .  .:*:

KKOV_L    IWVSGDGVWVNNARRWGADQIHASLNLIHVHGGHFNLL
LPHV_L    IWVSGDGVWVSNARRWGGEPIQTSLNLIHVHGGHFNLL
YOGV_L    IWVSDDGVWVQNARRWGREAVAASLNLVHVHGGHFNLL
IKV_L     FWVTDDHQWIHHVQRWKNNAPHMSINLLFNQN-HFDLL
KTRV_L    FWVTNDHQWIHHVQRWKNNAPHMSINLLFNQN-HFDLL
GOSV_L    FWVTDDHLWIHHVQRWGLEAPHISINLLFNQN-HFDLL
ERVV_L    IWIVDDSGTIISANRYGEGRPSQAYNLCMVGNAHFDSL
TFAV_L    IWIIDGSGTITSAQRYGNNKPSKAYNLCLIGNTHFDSL
CCHFV_L   IWTVAASDEVEAGIKFGDGDVFTAVNLLHSGQTHFDAL
          :*       :    ::      : **      **: *
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Supplemental Figure 4. ClustalX alignment of the deduced amino acid sequences of the OTU-like protease domain in the L proteins of nine nairoviruses. Identical (*), strongly conserved (:) and weakly conserved (.) residues as assigned in the Gronnet Pam250 matrix are indicated below the alignment. Fully conserved residues that may be critical in the active site fold are shaded in gray.