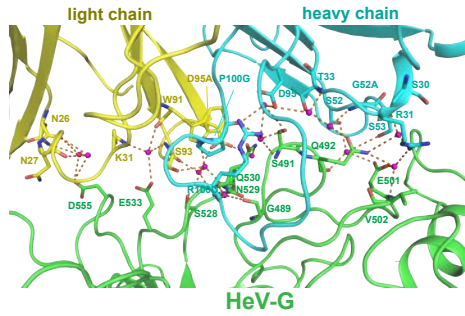
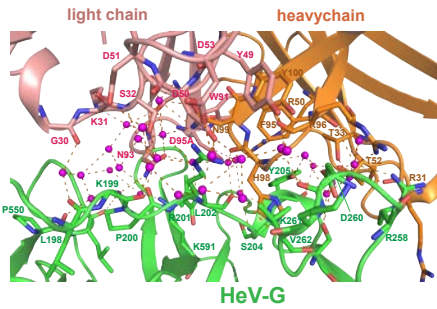


Supplemental Figure S4, Related to Figures 3 and 4

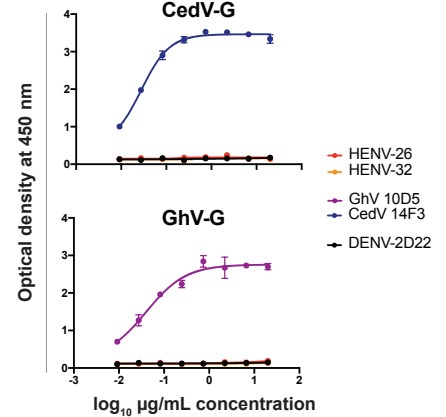
A. HENV-26 and HeV G complex



B. HENV-32 and HeV G complex



C. Binding to CedV or GhV



D. Sequence alignment of five henipavirus G proteins

Residues on HeV-G or NiV_M-G recognized by mAb HENV-26, HENV-32 or m102.3

HeV-G	VGLPNOICLOKTTSTILKPRLSYTLPIINTREGVCTDPLAVDNGFFAYSHLEKIGSGTRGIAKORIIIGV	252
NiV _M -G	VGLPNNICLOKTSNQILKPKLSYTLPLVVGQSGTCTDPLAMDEGYFAYSHLERIGSGSRGVSKORIIIGV	252
NiV _S -G	VGLPNNICLOKTSNQILKPKLSYTLPLVVGQSGTCTDPLAMDEGYFAYSHLERIGSGSRGVSKORIIIGV	252
CedV-G	AGPPKIFCKSVSKDPDFRLKQDVIYLVQDQRSICMNNPLDISDGFYIHYEGINSCKKSDSFKVLLSH	275
GhV-G	VAHGSPSCRFNFSSVPTIYYRIPGLYNRTALDERCLNPRITISSTKFAVYHSEYDKNCTRGFKYYELMTF	268
HeV-G	GEVLDRGGDKVPSMFMNTNVTWTPPNPSTIHHCSSYTHEDFYITLCAVSHVGDPIINSTSWTESLSLIRLAVRP	323
NiV _M -G	GEVLDRGGDEVPFLFMTNVTWTPPNPNTVYHCSAYYNNFEYVLCAYSTVGDPIINSTYWSGLMMTRLAVKP	323
NiV _S -G	GEVLDRGGDEVPFLFMTNVTWTPPNPNTVYHCSAYYNNFEYVLCAYSTVGDPIINSTYWSGLMMTRLAVKP	323
CedV-G	GEIVDRGGDVRPFLYLLSSHYHFSMQVINGVPTCNQSSFFVCHISNNTKTLDSYSSDEYYIYFNGID	346
GhV-G	GEILEGPEKERMFSRSFYSTNAVNYHSTPIVTVNEGFLCLECTSSDPLKANKLSNSTFFHLVIRHNK	339
HeV-G	KSDSGDYNQYIAITKVERGKDKVMPYGPSSGIKOGDTLYFPAVGFVLRTEFYQYDNSNCPIIHK...YS	390
NiV _M -G	KNSGGYVNHQALALRSIEKGRDKVMPYGPSSGIKOGDTLYFPAVGFVLRTEFYQYDNSNCPITK...YS	390
NiV _S -G	KNSGGYVNHQALALRSIEKGRDKVMPYGPSSGIKOGDTLYFPAVGFVLRTEFYQYDNSNCPITK...YS	390
CedV-G	RPKTKKIPINMTADN...RIHFHTFSGGVCLGEEFIIVTTVINTDVFTHD...YCESFNSVQTGKS	411
GhV-G	DEKIVSMPSFNLSLTDQ...EIVQIIAEGGGTAESGNLYFPCIGRLHKKRVTHP...LCKKSN...RT	400
HeV-G	KAENCRLSMGLRPNNSHYILRSGLLKYNLSDGENPKVVFIEISDQRLSIGSPSKIYDSLGPVVFYQASFSWD	461
NiV _M -G	KPENCRLSMGLRPNNSHYILRSGLLKYNLSDGENPKVVFIEISDQRLSIGSPSKIYDSLGPVVFYQASFSWD	461
NiV _S -G	KPENCRLSMGLRPNNSHYILRSGLLKYNLSDGENPKVVFIEISDQRLSIGSPSKIYDSLGPVVFYQASFSWD	461
CedV-G	LKEICSELSRPTNSSRYNLNGLIMISQNMDFKIQLNGTYNKLSPSGRSLKTLGGVLYVGSMSWD	482
GhV-G	DDSECLSKSYVYVQGGSPQHGVNCLIRIRNAQRDPTWVITVDLNTYPSRSRIFGFSKFMMLYVSSVSWH	471
HeV-G	TMIKLGDVDTVDPRLVQRNNSVTSRPGGSCQPRFNVCPEVCEWETVYNDVAFILDRLNWVSAGVYINSNOTA	532
NiV _M -G	TMIKFGDVLTVNPLVNNWRDNTVTSRPGGSCQPRFNVCPEVCEWETVYNDVAFILDRINWISAGVYINSNOTA	532
NiV _S -G	TMIKFGDVLTVNPLVNNWRDNTVTSRPGGSCQPRFNVCPEVCEWETVYNDVAFILDRINWISAGVYINSNOTA	532
CedV-G	TYLKAQFVFKWKPFTPNMNNVTISRPNGNCPHYHCKPEICVYGGTYNDIAPLDLGMVYVYVILDSDLA	553
GhV-G	TLLQVAEITDLKDYQLDLDTPTYISRPGGSECFGNVYCTVCEWETVYNDVYVSLTPNNDLTVYVYKSEVA	542
HeV-G	ENPVFAVFKDNEILYQVPLAEDDTNAQKTIITDCFLLENVIWICISLVEYDTGDSVIRPKLFAVKIPEQDSE	603
NiV _M -G	ENPVFTVFKDNEILYRAQLASEDTNAQKTIITNCFLLNKIWICISLVEYDTGDNVIRPKLFAVKIPEQDSE	602
NiV _S -G	ENPVFTVFKDNEILYRAQLASEDTNAQKTIITNCFLLNKIWICISLVEYDTGDNVIRPKLFAVKIPEQDSE	602
CedV-G	ENPFIYVNSTTILYKERVSKDELNTRSTITSCFLFLDEPWCISVLETNRFNGKSIIRPEIYSYKLPKY...	622
GhV-G	ENPVFAIISRDQILKEFFLDAWISSARTTISCFMNFNIWICIAALEITRLNNDIIRPIYYSFWLTDQRT	613

Contact residues on G for indicated mAb

- m102.3 (purple line)
- HENV-32 (orange box)
- HENV-26 (red box)

Residues on HeV-G or NiV_M-G contacting ephrinB2 or ephrinB3 receptor

HeV-G	VGLPNOICLOKTTSTILKPRLSYTLPIINTREGVCTDPLAVDNGFFAYSHLEKIGSGTRGIAKORIIIGV	252
NiV _M -G	VGLPNNICLOKTSNQILKPKLSYTLPLVVGQSGTCTDPLAMDEGYFAYSHLERIGSGSRGVSKORIIIGV	252
NiV _S -G	VGLPNNICLOKTSNQILKPKLSYTLPLVVGQSGTCTDPLAMDEGYFAYSHLERIGSGSRGVSKORIIIGV	252
CedV-G	AGPPKIFCKSVSKDPDFRLKQDVIYLVQDQRSICMNNPLDISDGFYIHYEGINSCKKSDSFKVLLSH	275
GhV-G	VAHGSPSCRFNFSSVPTIYYRIPGLYNRTALDERCLNPRITISSTKFAVYHSEYDKNCTRGFKYYELMTF	268
HeV-G	GEVLDRGGDKVPSMFMNTNVTWTPPNPSTIHHCSSYTHEDFYITLCAVSHVGDPIINSTSWTESLSLIRLAVRP	323
NiV _M -G	GEVLDRGGDEVPFLFMTNVTWTPPNPNTVYHCSAYYNNFEYVLCAYSTVGDPIINSTYWSGLMMTRLAVKP	323
NiV _S -G	GEVLDRGGDEVPFLFMTNVTWTPPNPNTVYHCSAYYNNFEYVLCAYSTVGDPIINSTYWSGLMMTRLAVKP	323
CedV-G	GEIVDRGGDVRPFLYLLSSHYHFSMQVINGVPTCNQSSFFVCHISNNTKTLDSYSSDEYYIYFNGID	346
GhV-G	GEILEGPEKERMFSRSFYSTNAVNYHSTPIVTVNEGFLCLECTSSDPLKANKLSNSTFFHLVIRHNK	339
HeV-G	KSDSGDYNQYIAITKVERGKDKVMPYGPSSGIKOGDTLYFPAVGFVLRTEFYQYDNSNCPIIHK...YS	390
NiV _M -G	KNSGGYVNHQALALRSIEKGRDKVMPYGPSSGIKOGDTLYFPAVGFVLRTEFYQYDNSNCPITK...YS	390
NiV _S -G	KNSGGYVNHQALALRSIEKGRDKVMPYGPSSGIKOGDTLYFPAVGFVLRTEFYQYDNSNCPITK...YS	390
CedV-G	RPKTKKIPINMTADN...RIHFHTFSGGVCLGEEFIIVTTVINTDVFTHD...YCESFNSVQTGKS	411
GhV-G	DEKIVSMPSFNLSLTDQ...EIVQIIAEGGGTAESGNLYFPCIGRLHKKRVTHP...LCKKSN...RT	400
HeV-G	KAENCRLSMGLRPNNSHYILRSGLLKYNLSDGENPKVVFIEISDQRLSIGSPSKIYDSLGPVVFYQASFSWD	461
NiV _M -G	KPENCRLSMGLRPNNSHYILRSGLLKYNLSDGENPKVVFIEISDQRLSIGSPSKIYDSLGPVVFYQASFSWD	461
NiV _S -G	KPENCRLSMGLRPNNSHYILRSGLLKYNLSDGENPKVVFIEISDQRLSIGSPSKIYDSLGPVVFYQASFSWD	461
CedV-G	LKEICSELSRPTNSSRYNLNGLIMISQNMDFKIQLNGTYNKLSPSGRSLKTLGGVLYVGSMSWD	482
GhV-G	DDSECLSKSYVYVQGGSPQHGVNCLIRIRNAQRDPTWVITVDLNTYPSRSRIFGFSKFMMLYVSSVSWH	471
HeV-G	TMIKLGDVDTVDPRLVQRNNSVTSRPGGSCQPRFNVCPEVCEWETVYNDVAFILDRLNWVSAGVYINSNOTA	532
NiV _M -G	TMIKFGDVLTVNPLVNNWRDNTVTSRPGGSCQPRFNVCPEVCEWETVYNDVAFILDRINWISAGVYINSNOTA	532
NiV _S -G	TMIKFGDVLTVNPLVNNWRDNTVTSRPGGSCQPRFNVCPEVCEWETVYNDVAFILDRINWISAGVYINSNOTA	532
CedV-G	TYLKAQFVFKWKPFTPNMNNVTISRPNGNCPHYHCKPEICVYGGTYNDIAPLDLGMVYVYVILDSDLA	553
GhV-G	TLLQVAEITDLKDYQLDLDTPTYISRPGGSECFGNVYCTVCEWETVYNDVYVSLTPNNDLTVYVYKSEVA	542
HeV-G	ENPVFAVFKDNEILYQVPLAEDDTNAQKTIITDCFLLENVIWICISLVEYDTGDSVIRPKLFAVKIPEQDSE	603
NiV _M -G	ENPVFTVFKDNEILYRAQLASEDTNAQKTIITNCFLLNKIWICISLVEYDTGDNVIRPKLFAVKIPEQDSE	602
NiV _S -G	ENPVFTVFKDNEILYRAQLASEDTNAQKTIITNCFLLNKIWICISLVEYDTGDNVIRPKLFAVKIPEQDSE	602
CedV-G	ENPFIYVNSTTILYKERVSKDELNTRSTITSCFLFLDEPWCISVLETNRFNGKSIIRPEIYSYKLPKY...	622
GhV-G	ENPVFAIISRDQILKEFFLDAWISSARTTISCFMNFNIWICIAALEITRLNNDIIRPIYYSFWLTDQRT	613

HeV-G contacts on indicated receptor

- ephrinB2 (red box)
- ephrinB3 (yellow box)