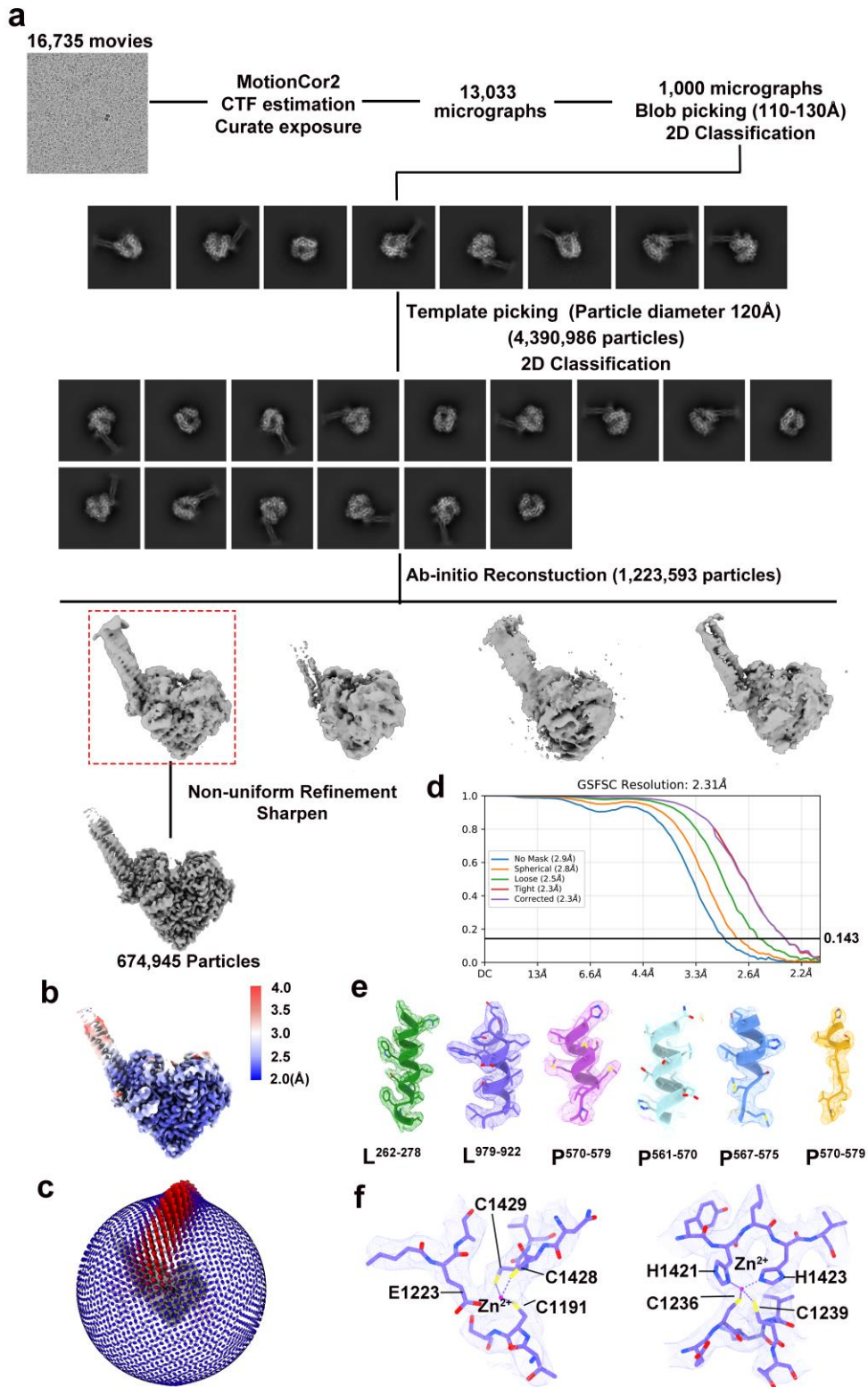


**Figure S1 | Purification of the truncated ( $L_{1-1451}$ -P) and full-length (L-P) NiV polymerase complexes.**

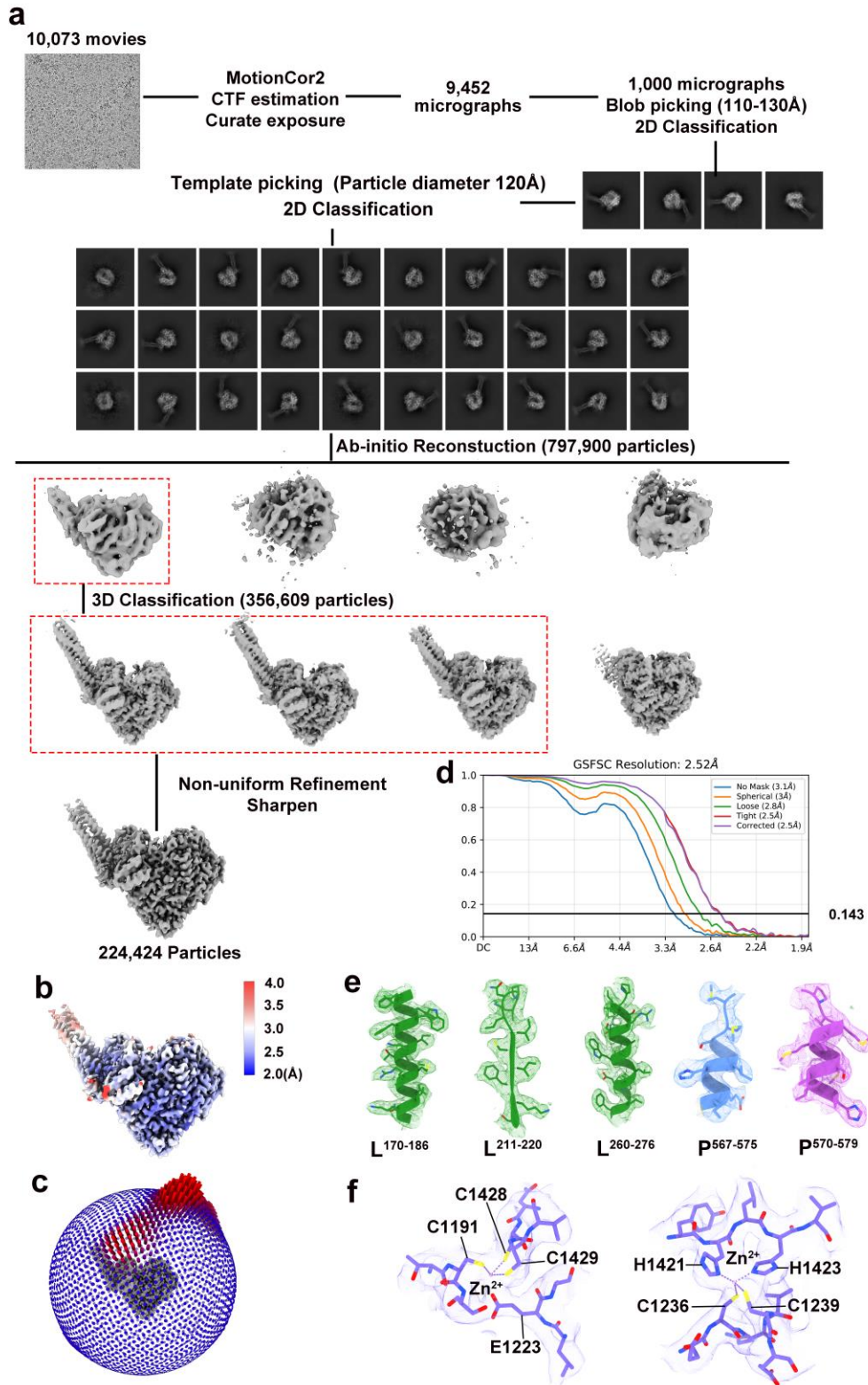
**a.** Size-exclusion chromatography and Coomassie-stained SDS-PAGE analysis of purified NiV  $L_{1-1451}$ -P complex. The molecular weights of the  $L_{1-1451}$  protein and P protein are about 170 kDa and 80 kDa, respectively. **b.** Size-exclusion chromatography and Coomassie-stained SDS-PAGE

analysis of purified NiV L-P complex. The molecular sizes of the L protein and P protein are about 250 kDa and 80 kDa, respectively.



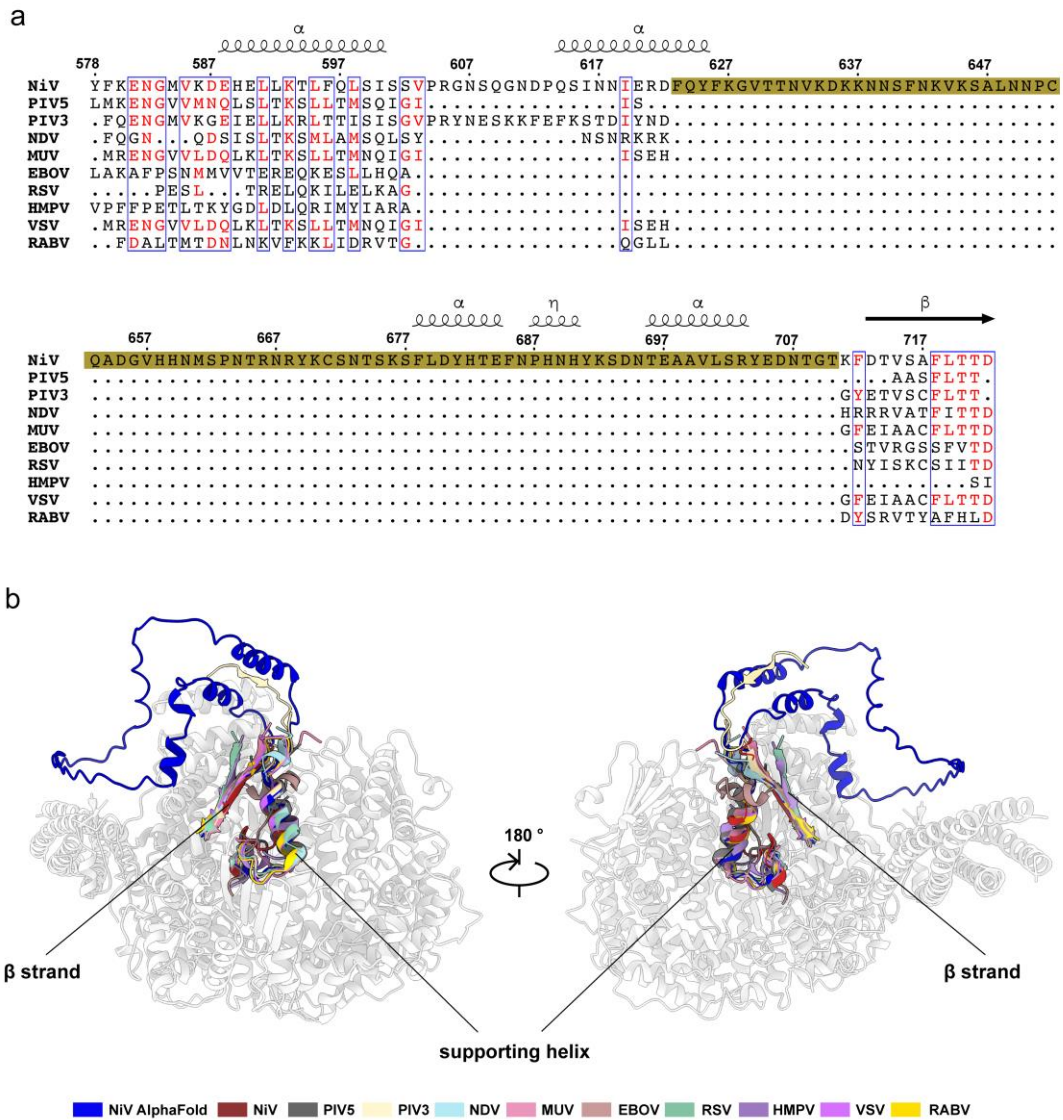
**Figure S2 | Cryo-EM data processing and analysis of the NiV L<sub>1-1451</sub>-P complex.**

**a.** Cryo-EM image processing flowchart for the NiV L<sub>1-1451</sub>-P complex sample. **b.** A local resolution map for the NiV L<sub>1-1451</sub>-P complex. **c.** Angular distribution of the particles used for the reconstruction of the NiV L<sub>1-1451</sub>-P complex structure. **d.** Fourier shell correlation curves of the reconstructed map for the NiV L<sub>1-1451</sub>-P complex. Overall resolution of the structure was assessed by the gold-standard FSC 0.143 cut-off criteria. **e.** Representative densities from the structure of the NiV L<sub>1-1451</sub>-P complex. **f.** Cryo-EM densities for the two zinc-binding sites within the PRNTase domain of NiV.



**Figure S3 | Cryo-EM data processing and analysis of the NiV L-P complex.**

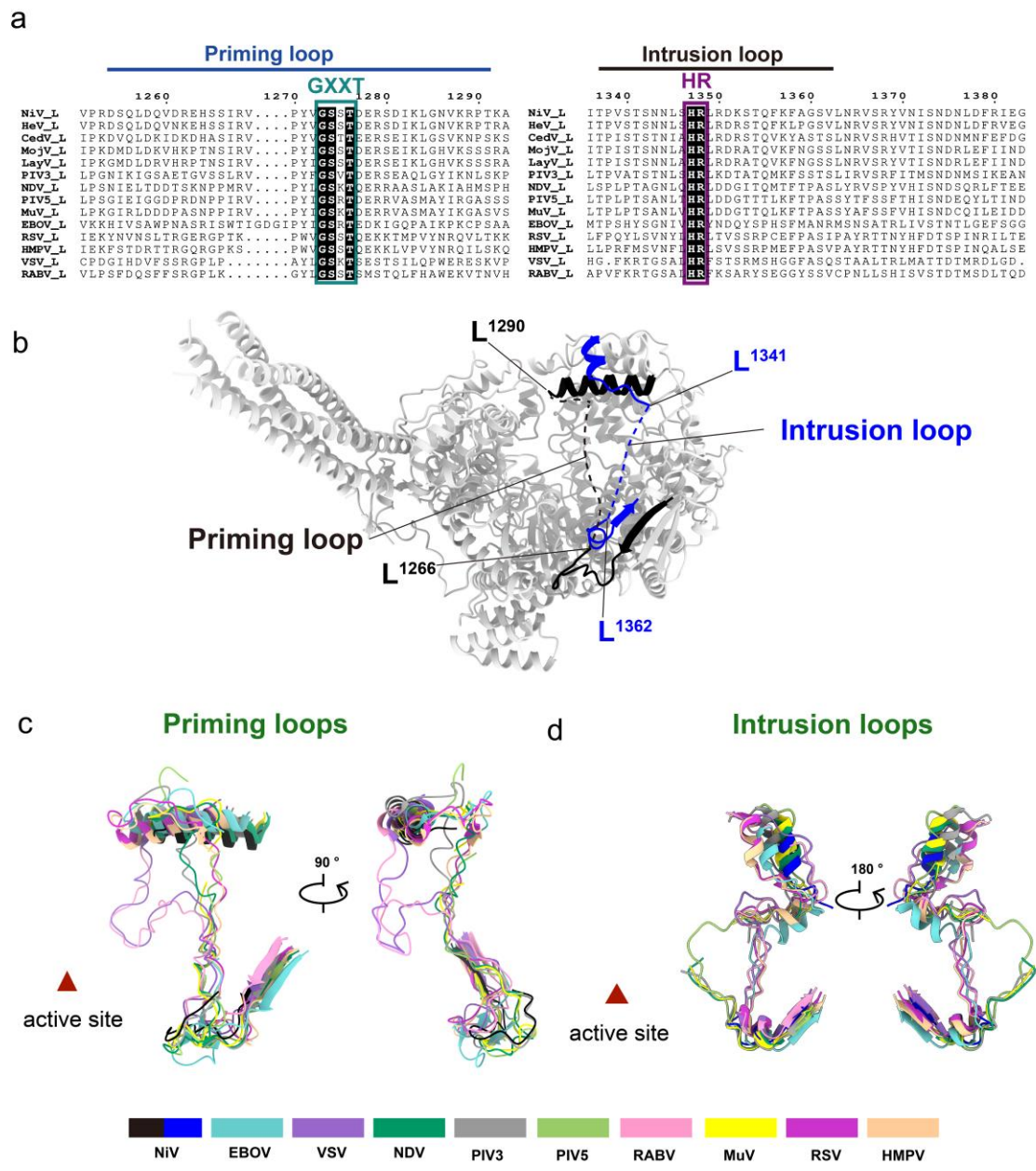
**a.** Cryo-EM image processing flowchart for the NiV L-P complex sample. **b.** A local resolution map for the NiV L-P complex. **c.** Angular distribution of the particles used for the reconstruction of the NiV L-P complex structure. **d.** Fourier shell correlation curves of the reconstructed map for the NiV L-P complex. Overall resolution of the structure was assessed by the gold-standard FSC 0.143 cut-off criteria. **e.** Representative densities from the structure of the NiV L-P complex. **f.** Cryo-EM densities for the two zinc-binding sites within the PRNTase domain of NiV.



**Figure S4 | The RdRp domain of NiV L protein contains a long insertion sequence compared to other NNS RNA virus polymerases.**

**a.** Multiple sequence alignment of polymerase L protein sequences, the long insertion sequence is highlighted in brown. L protein sequences used are NiV (nipah virus), PIV5 (Parainfluenza virus 5), PIV3 (Parainfluenza virus type 3), NDV (Newcastle disease virus), MuV (Mumps virus), EBOV (Ebola virus), RSV (respiratory syncytial virus), HMPV (Human

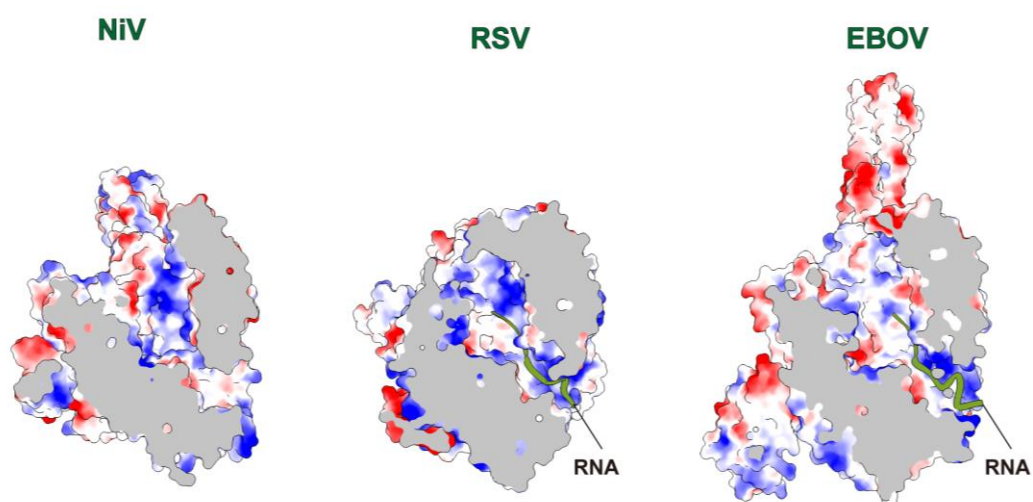
metapneumovirus), VSV (Vesicular stomatitis virus) and RABV (Rabies virus). **b.** Structural superposition of NiV polymerase complex structure (grey) with an AlphaFold2 predicted long insertion sequence structure (blue) and experimental polymerase structures of *Mononegavirales* (colored) indicates that the long insertion sequence (highlighted in brown) form a large loop. This loop is potentially flexible, situated between the supporting helix and a  $\beta$ -sheet in the NiV polymerase.



**Figure S5 | Structural features of the priming and intrusion loops in NiV polymerase compared to those of other NNS RNA viruses.**

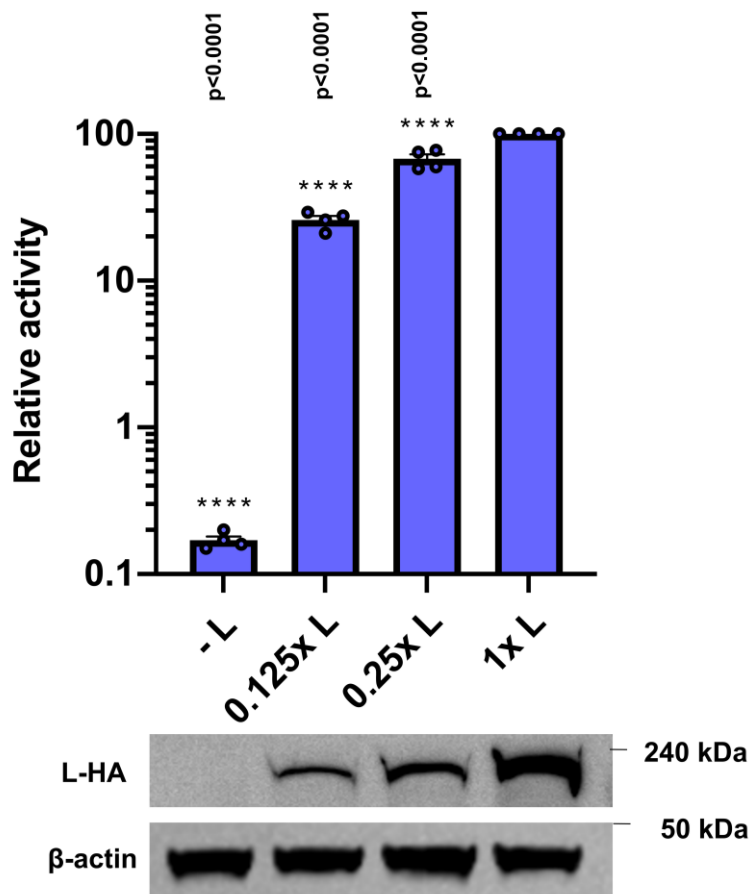
**a.** Multiple sequence alignment of the GXXT and HR motifs in different *Mononegavirales*. The highly conserved GXXT and HR motifs among *Mononegavirales* are highlighted in colored boxes. **b.** The locations of the priming loop and the intrusion loop in the structure of the NiV L-P complex

structure. **c-d.** Comparison of priming (**c**) and intrusion (**d**) loops in the NiV polymerase with those of other *Mononegavirales* shows that the backbone trajectories of residues at both ends of the NiV priming and intrusion loops align well with the conformations observed for HMPV, NDV, and PIV5 polymerases. Polymerase structures used are EBOV (PDB: 8JSM), VSV (PDB: 5A22), NDV (PDB: 7YOU), PIV3 (PDB: 8KDC), PIV5 (PDB: 6V85), RABV (PDB: 6UEB), MuV (PDB: 8IZL), RSV (PDB: 8SNX) and HMPV (PDB: 6U5O). The location of the polymerase catalytic site is indicated by a red triangle.



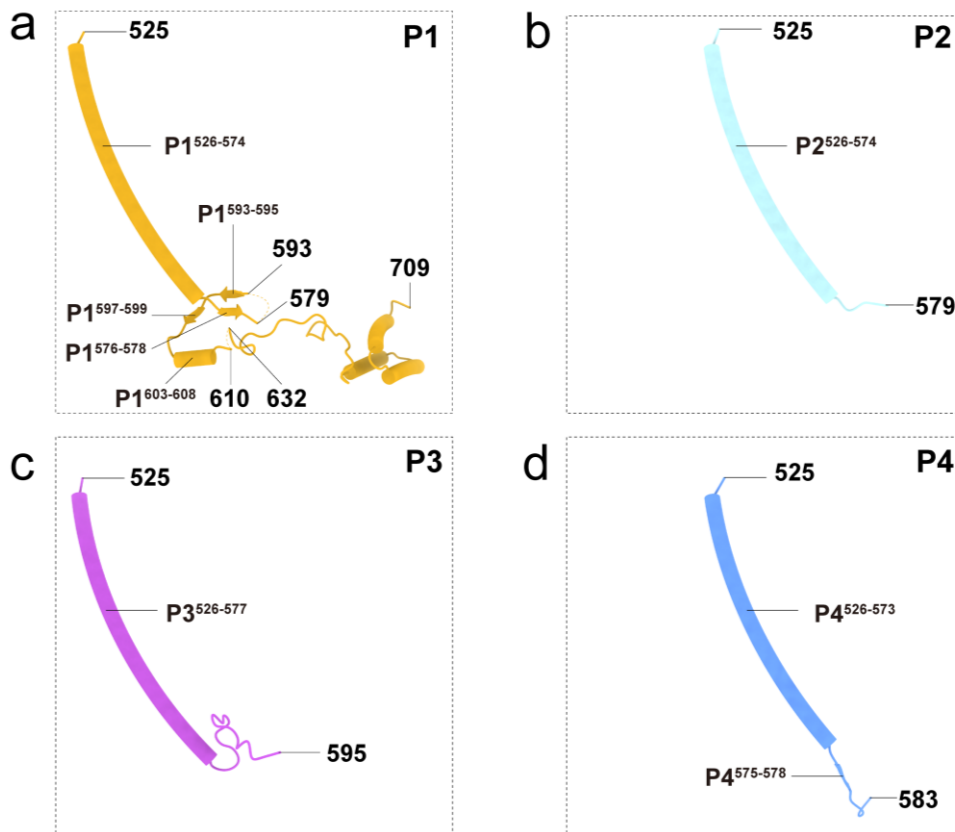
**Figure S6 | Polymerase cavity electrostatic potentials compared among NiV, RSV and EBOV.**

Cut views to show the electrostatic potentials of NiV, RSV and EBOV polymerase cavities. Bound template RNAs (green) are included for the RSV (PDB: 8SNX) and EBOV (PDB: 8JSM) structures. Blue and red colors indicate positive and negative surface charges.



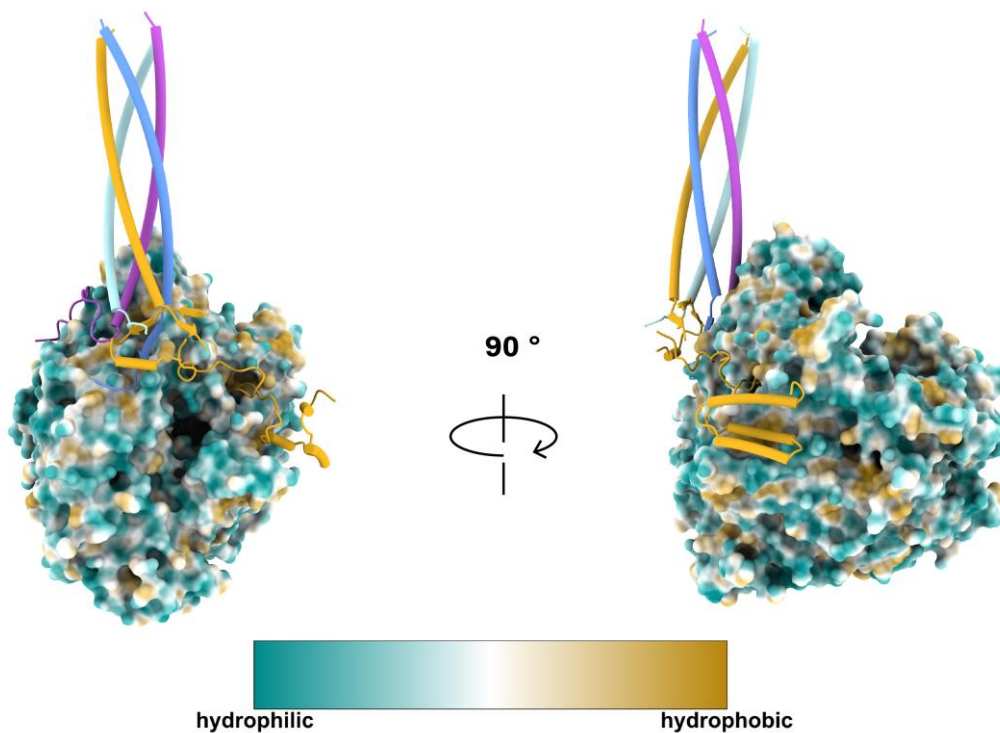
**Figure S7 | L protein expression titration experiment.**

1×L, 0.25×L, 0.125×L and -L lanes represent protein expression levels in mini-replicon experiments, where 1µg, 0.25 µg, 0.125 µg and 0 µg of L protein expression plasmid were transfected. Corresponding mini-replicon activities are reported as mean ± SEM from four independent experiments (n=4). All statistics used one-way ANOVA Dunnett's multiple comparisons test. (ns,  $p > 0.05$ ; \*,  $p < 0.05$ ; \*\*,  $p < 0.01$ ; \*\*\*,  $p < 0.001$ ; \*\*\*\*,  $p < 0.0001$ ).



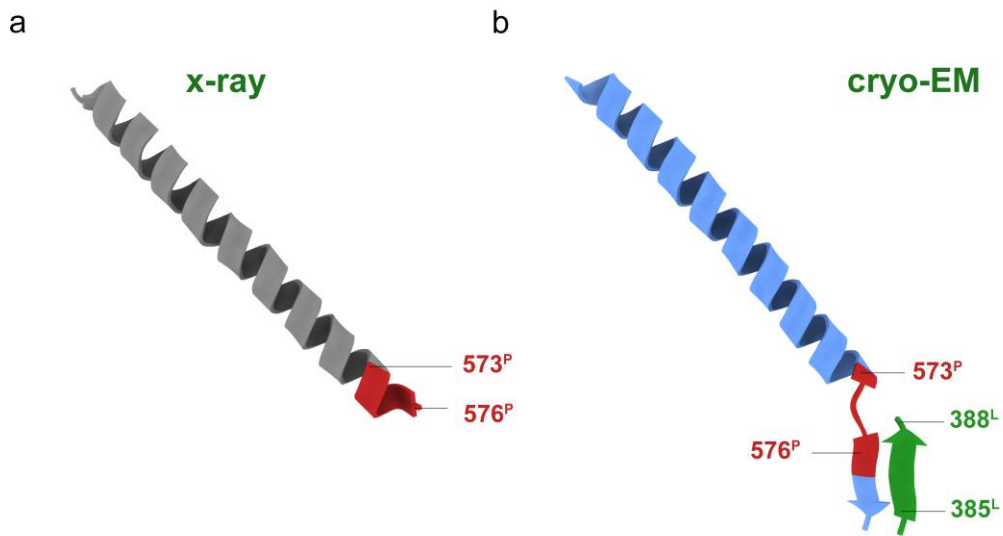
**Figure S8 | Structures of P protein monomers within the P protein bundle within the NiV L<sub>1-1451</sub>-P complex.**

**a-d.** Structures of the four P protein monomer – P1 (a), P2 (b), P3 (c) and P4 (d) within the L protein bound P protein bundle. Secondary structural elements and their starting and end residues are shown.



**Figure S9 | Binding of the P protein bundle on the L protein surface.**

The surface of the L protein is coloured according to the hydrophobicity of its surface residues. The P1, P2, P3 and P4 monomers of the P protein bundle are colored yellow, cyan, magenta and blue, respectively.



**Figure S10 | Conformational change of the NiV P protein upon L protein binding.**

**a.** An  $\alpha$ -helix extracted from the X-ray structure of the NiV P protein tetramer. Residues 573-576 at the C-terminal end of the helix is shown in red. **b.** The structure of P4 within the P protein tetramer in the cryo-EM structure. Upon L binding, the residues (P<sup>573-576</sup>, red) refold to transform into a loop and part of a  $\beta$ -strand to bind L<sup>385-388</sup>, forming an antiparallel sheet.

NiV_L	-----MADELSISDIYYPECHLDSPIVSGKLISAIEYAQL-----RHNQPSDDKRL	46
NDV_L	----MAGSGSERAEHQIILPESHLSSPLVKHKLLYYWKLTLGL-----PLPDECFDHL	49
RSV_L	MDPIIINGNSA-----NVYLTDSYLKGVISFS-----ECNALGYSYIFNGPYLKNDYFNL	48
EBOV_L	-----MATQHTQYPDARLSSPIVLDQCDLVTRACGLYSSYSLNPLQRNCKLPKH	49
	:          *          :	
NiV_L	--SENIRLNLHGKRKSLYLRSKQGDYIRNN-IKN-LKEFMHIAYPECNNILF-----	96
NDV_L	ILSRQWKKILES--STPDIERMIKLGRSVHQT-LSH-SSKLTGILHPRCLEDLV-----	99
RSV_L	ISRQ-----NPLIEHMLNKLKLNITQSLISKYHKGEEKLEEPTYFQSLLMTYKSM	97
EBOV_L	IYRLKYDVTVTKFLS--DVPVATLPIDFIVPILLKALSGNGFCVPEPRCQQFLD-----	101
	:          :          :          *          :	
NiV_L	-----SITSQGMTSKLDNIMKKSFKAYNIIISKVIGMLQNI	133
NDV_L	-----GLDIPDSTNKFRRIEKKIQIHNTRYGEPFTRLCSSVE	136
RSV_L	TSSEQIATTNLLKKIIRRAIEISDVKYAAILNKLGLKEKDKIKSNNGQDE-----D	148
EBOV_L	-----EIIKYTMQDA-----LFLKYYL--KN-VGA----Q	124
	:          :	
NiV_L	RNLITQDRRDEIINI-----HEC-----RRLGDLGKNM-SQSKWYECFL	171
NDV_L	KKLLGSSWTHKIRRS-----EEF-----DSLRTDPAFW-FHSSWSTAKF	174
RSV_L	NSVITTI IKDDILSAVKDNQSHLKADKNHSTKQKDTIKTLLKLMCSMQHPPSWL---I	205
EBOV_L	EDCVDDHFQEKILSS-----I-QGNEFLHQMF	150
	.. :          ..*          :          :	
NiV_L	FWFTIKTEMRAVIKNS---QKPK-FRSDSCI IHMRDKSTEIILNPNL-----	214
NDV_L	AWLHVQIQRHLLIVAA---RTRS---ASNKLVTLSHRSGQVFTPEL-----	215
RSV_L	HWFNLYTKLNNILTQY---RSNEVKNHGFTLIDNQTLSGFQFILNQ-----	248
EBOV_L	FWYDLAILTRRGRLNRGNSRSTW-FVH-DDLIDLGYGDYVFWKIPISLLPLNTQGI PHA	208
	* :          :          :          :	
NiV_L	-----ICIFKSDKTGK--KCYLTPEMVLMYCDVLEGRMMMETTVKSDIKYQPL-----	261
NDV_L	-----VIVTHTNEN---KFTCLSQLVLMYADMMEGRDMVNIISSTAVHLRCL-----	260
RSV_L	-----YGCIVYHKELK---RITVTTYNQFLTWKDISLRLNVCLITWISNCLNLTNKS LG	300
EBOV_L	AMDWYQTSVFKAEAVQGHITHIVSVSTADVLIMCKDLITCRFNTTILSKIAEVEDPVCSDY-	267
	: :          : : :          * : *          :	
NiV_L	-----ISRSNALWGLIDPLFPVMGNRIYIVSMIEPLVLA LQ LKDEARILRGAFLHHC	315
NDV_L	-----AEKIDDLRLVDALARDLGNQVYDVVALMEGFAYGA VOLLIEP SGTFAGDFEFSEN	314
RSV_L	LRCGFNVILTQLFLYGDGILKLFHNEGFIYI KEVEGFI MSLIILNITEEDQFRKRFVNSM	360
EBOV_L	-----PNFKIVSMLYQSGDYLLSILGSDGYKIKFLEPLCLAKIQ LCKY TERKGRFLTQM	323
	:          * :          : : :          * : :          :	
NiV_L	LKEMHQELSECG---FTD---Q---KIRSMF-----IDDLLSILNIDNIHL	352
NDV_L	LQELRDTLI-CL---L-P---Q---RIADSV-----THAIAINFSGLEQNN	349
RSV_L	LNNITDAANKAQKN--LLSRVCHTLTLLDRTVSDNIINGR WILLSKFLKLIKLAGDNNLNN	418
EBOV_L	LAVNITLEEITEIRALKPSQA L KIREF L-----R--TLRLEMTPOQ	364
	: . :          : :          : :          :	
NiV_L	LAEFFSFRTFPGHPILEAKVAAEKVREHMLADKVLVEMAFIMKAHAIFCGTIINGYRDRHG	412
NDV_L	AAEMLCLLRLWGHPLLESRAAAKAVR AQMCAP RVDMDITQVLSFFFGTIINGYRKKNA	409
RSV_L	LSELYFLFRIFGHMPVDERQAMDAVK LNCNETREYLLSLSMLRGAFYRIIKGFVNYYN	478
EBOV_L	LCELFSTQKHWGHPVLHSETAIQKVKKHATV KALRPVITFETY CVFKYSIAKHYFDSQG	424
	. * : : : * * * : . * : : : * : * : : .	
NiV_L	GAWPPLVLAHASKHIIRLKNSGESLTIDDCVK-NWESFCGIQDFMELKLDSDLSMYM	471
NDV_L	GVWPRVKAHTIYGNVIAQLHADSAEISHDIMLR-EYKNLSAIEFEACIEYDPVTNLSMFL	468
RSV_L	-RWPTLRNALVLRWLTYYKLNTPSLELTERDLVLSGLRFYREFRIPKKVDLEMI I	537
EBOV_L	-SWYSVTSDRNITPGLNSYIKRNQ-FPPLPMIKELLEWIFYLDHPPLFSTKIIISDLSIFI	482
	* :          :          :          :          :          * : : : :	
NiV_L	KDKALSPIKDEWDSVYPREVLSTYTPP-----K---STEPRLVDVFNVDENFDPMNM	520
NDV_L	KDKAIAHPRNNWLASFRNLLSEEQY-----KNVQDSTSTNRLLIEFLESNDFDPYKE	521
RSV_L	NDKAISPPKNLIWTSFPRNYMPSHIQYIEHEKLFSESDKSRVLEYLRDNKFNEDCL	597
EBOV_L	KDRATAVERTCWDVAFEPNVLGYNPP-----H---KFSTKRVPQFLEQENFSIENV	531
	: * : * : : : : : :          . . . * : : : : . * . .	
NiV_L	LEYVLSGAYLEDEQFNVSYSLKEKETKQAGRLFAMTYKMRACQVIAEALIASGVGKYFK	580
NDV_L	MEYLTTLEYRDDSVAVSYSLKEEVEKVGRIFAKLTKKLRNCQVMAEGLADQIAPFFQ	581
RSV_L	YNCVVNQSYLNNPNHVSLTGKERELS-VGRMFAMQPQGMFRQVILAEKMAENILQFFP	656
EBOV_L	LSYAQKLEYLTPQYRNFSFSLKEKELN-VGRTFGKLPYPTRNVQTLCEALLADGLAKAFP	590
	. . * * . * : * * * . * * * . * * : * : * : . *	
NiV_L	ENGMVKDEHELLKTLFQLS ISSVPRGNSQGNDPQSINNIERDFQYFKGVTTNVKDKKNS	640
NDV_L	GNGVIQDSISLTKSMLAMSQLSYNSNRK-----	609
RSV_L	ESLTRYGDLELQKILELKAGISNK-----	680
EBOV_L	SNMMVVTEREQKESLLHQAS-----	610
	. . . : : : :	
NiV_L	FNKVKSAALNNPCQADGVHNNMSPNTRNRYKCSNTSKSFLDYHTEFNPHNHYSKDNTAAAV	700
NDV_L	-----R-----ITDCKERVS	619
RSV_L	-----	680
EBOV_L	-----	610



NiV_L	V-----LAKTVAQ-TVLE-IITKADKDVLKQHLAIDSDDNINSLITEFLIVDPELF	1542
NDV_L	I-----LSISSGK-LIGQ-SVVSYDEETS IKNDAIIVYDNTRNWISEAQNSDVVRL	1463
RSV_L	ISDYFHNTYILSTNLAGHWILIQLMKDSK-----GIFEKDWGEGYITDHMFINLKV-	1533
EBOV_L	L-----SGWELAK-TIMQ-SIISDSNNSST---DPISSGETRSFTTHFLTYPKIGL	1464
:	:	:
NiV_L	ALYLGQISISIKWAFEIHRRRPRGRHTMVDLL--SDLVSN---TSKHTYKVLSNALSHPRV	1597
NDV_L	FEYAALEVLLDCSYQLYLRVRLNNVVLYM--SDLYKN---MPGILLSNIAATISHPII	1518
RSV_L	--FFNAYKTYL---LCFHKGYGKAKLECDMNTSDLLCVLELIDSSYWKSMKVFLEQKV	1587
EBOV_L	LYSFGAFVSYLGNITILRTKKTLDNFLYYL--TTQIHN---LPHRSRLRILKPTFKHASV	1519
:	:	:
NiV_L	FKRFVNCGLLLP-----TQGPYLHQQDFEKLSQLNLLVTSYMIYLMNWCDFKK--SPFLI	1649
NDV_L	HSRLHTVGLISH-----DGSHQLADTDFIELSAKLLVSCTRRVVSGLYAGNK--YDLLF	1570
RSV_L	IKYILSQDASLH-----RVKGC-----HSFKLWF	1611
EBOV_L	MSRLMSIDPHFSIYIGGAAGDRGL--SDAARLFLRTSISSEFLTFVKEWIINRGTIIVPLWI	1577
:	:	:
NiV_L	AEQDE---TVISLREDII-----TSKHLCVIIDLYANHHKPPWIIDLNPQ--EKICV	1696
NDV_L	PSVLD---DNLNEKMLQL-----ISRLCLYTVLFATTREIPKIRGLPAE--EKCAM	1617
RSV_L	LKRLN-----VAEFTVCPWVNIIDYHPTHMKAI	1639
EBOV_L	VYPLEGQNPTPVNNFLHQIVELLVHDSRRHQAFKTTIND--H-----VHPH-----	1621
:	:	:
NiV_L	LRDFISKSRHVD--TSS--RSWNTSDLDFVIFYASLTYLRRGIKQLR-----	1740
NDV_L	LTEYLLSDAVRPLLSPE--QVDSITSPSIVTFPANLYMRSKSLNLIR-----	1663
RSV_L	LT-YIDLVRM-GLINI DRIHIKNKHKFNDFYTSNLFYINYNFSDNTH--LLTKHIRIANS	1696
EBOV_L	-----DN--LVYTCKSTASNFFHASLAYWRSRHRNSNRKDLTRNSSTG-S	1663
:	:	:
NiV_L	-----IRQVTEVIDT-----T-----TMLRDNIIVENPPIK-	1766
NDV_L	-----EREDRDSILA-----L-----MFPQEPLFEFPLVQD	1689
RSV_L	ELENNYKLYHPTPETLENILANPIKSNDKKTLNDYCIKKNVDSIMLPLS--NKKLIK-	1753
EBOV_L	STNNSDGHIK---RSQEQTTRDPHDGTERSIVL--QMSHEIKRTTIPQENTHQGSPFQ-	1716
:	:	:
NiV_L	-----TGVLDIRGCI IYNLEE-----ILSMNTKSASK-----	1793
NDV_L	IGARVKDQLTMKPAAFHLHDLAPARYDAYT-----LE---QAR-SD-----	1728
RSV_L	-----SSAM--IRTNYSKQDLYNLFPMVVIDR--IIDHSGNTAKS---NQ----	1791
EBOV_L	-----SFLSDSACGTANPKLNFDRSRHNKVSQDHNSASKREGHQIISH	1759
:	:	:
NiV_L	-----KIFNL---NSRPSVEN-----HKYRRIGLNSSS	1818
NDV_L	-----CALAD---MGEDQLVR-----YLFRGVGTASSS	1753
RSV_L	-----LYTT---TSHQISLVHNSTSLYCMLPWHHINRNFVFSSTGCKISI	1834
EBOV_L	RLVLPFFFTLSQGTRQLTSSNESQTQDEISKYLRQLRSVI-----DTTVYCRFTGIVSSM	1813
:	:	:
NiV_L	CYKALNLSPLIQRYLPSGAQRLFIEGSGSMMLLYQSTLQGISFYFN-SGIDGDYIPGQR	1877
NDV_L	WYKASHLLSVPEIRCARHGNSLYLAEGSGAIMSLELHIPHETIYYN-TLFSNEMNPPQR	1812
RSV_L	EYILKDL-----KIKDPNCIAFIEGAGNLLRRTVVELHPDIRYIYRSLKDCNDH---	1884
EBOV_L	HYKLDEVLWEIEN--FKSAVTLAE GEGAGALL--IQKYQVKTFFFN-TLATESSIESEI	1868
:	:	:
NiV_L	ELK-----LFPSEYSIAEEDPSLTGKLGVLVPLFNGRPETTWIGNLD-----	1920
NDV_L	HFG-----PTPTQFLNSVYRNLQAEVPP--CKDGFVQEFRTLWRENTTEE--SDLTS	1860
RSV_L	-----SLPIEFN-----RLYNGHINIDYGENLTI PATDATNN	1916
EBOV_L	VSGMTTPRMLLPVMSKFHNDQIEIILNNSA-----SQITDITNPTWFKDQRA-----	1915
:	:	:
NiV_L	-SYEYIINRTAGRSIGLVHSDMESGIDKNVEEILVEHSHLISI-AINVMMEDGLLVSKIA	1978
NDV_L	KAVGYITSVVPPYRSVSLHCDIEIPPGSNQSLDQLATNLSLI-AMHSVREGGVVIVKIL	1919
RSV_L	IHWSYL-HIKFAEPI SLFVCDAE LSVTVNWSKII EWSKHVRCKYCSSVNKCLMIVKYH	1975
EBOV_L	-----RLPRQVEVITMDAETTENINRSKLYEAVHKLILH-HVDPVSVLK-AVVLVKVF	1964
:	:	:
NiV_L	YTPGFPI SR LFNMYRSYFGLVLVCFPVYSNPDPSTEVYLLCLQKTV-----KTIVPPQK-	2031
NDV_L	YSMYYFHLLVNLFTPCSVKGYVLSNGYACRGDMECYVVFVMGYLGGPTFVNEVVRMAKT	1979
RSV_L	AQDDID--FKLDNIT--ILKTYVCLG--SKLKGSEVYLVLTIGPANIFPV-FNVVQNAKL	2028
EBOV_L	LSDTEGMLWLNDNLAPFFATGYLIKPI TSSARSSEWYL-CLTNFLSTTRK---MPHQNH	2019
:	:	:
NiV_L	-VLEHSNLHDEVNDQGITSVIFKIKNSQSKQFHDDLK-----KYYQIDQFFV-PT	2080
NDV_L	LIQRHGTL LAKSDETALMA-LF---TSQKQRVDNLS-----SPLPRLA-KL	2021
RSV_L	ILSRTKNFI-----MP-----KKADKESIDANIK-----SLIPFLCYPI	2062
EBOV_L	LS-----CKQVILTALQLQIQR--SPYWLSHLTQYADCDLHLSYIRLGFPSLE-KV	2067
:	:	:
NiV_L	KITSDEQVLLQAGLKLNGPEILKS-----EISYDIGSDINTLRDTI IIMLNEAMNY	2131
NDV_L	LRRNIDTALIEAGGQVPRPFCAESLVNLTSDITQTTQVIASHIDTVIRSVIYMEAE---	2077
RSV_L	TKKGINTALS KLSVVS GDILSYSIAGR N-EVFS-----NKLINHKHMNI LKWFNHV LNF	2116
EBOV_L	LYHRYNLVDSK-----RGPLVS-----V-----TQHLAHLRAEIRELTND-YNQ	2105
:	:	:

NiV_L	FDDNRSPSHHLEFPVLERTRIKTIMNCVTKKVIVYSLIKFKDT-----KSS	2178
NDV_L	-GDLADTVFLFTPYNLSIDGKKRTSLKQCTRQILEVTILGLGPE-----DLN	2123
RSV_L	RS----TELNY-----	2123
EBOV_L	QRQSRTQTYHF---IRTAKGRITKLVNDYLKFFLIVQALKHNGTWQAEFKKLPELISVCN	2162
NiV_L	ELYHIKNNIRRKVL----ILDFRSKLMTKTLPKGMQERRE----KNGFKEVWIVDLSNRE	2230
NDV_L	RVGDIISLILRGTISLEDLIPLRITYLKMSTCPKYLKSVLGLTKLREMFSDGSMLYLTRAQ	2183
RSV_L	-----NHLYMVESTYPYLSELLNSLTNELKKLIKITGS-----LLYNFHNE	2165
EBOV_L	RFYHIRDCNCEERFLVQTL-----YLH-RMQDSEVKLIERLTGLLSLFPDGLYRFD----	2212
	. * . ::	
NiV_L	VKIWWKIIGY-----ISII--	2244
NDV_L	QKFYMKTVGNNAVKGYNSSKN	2204
RSV_L	-----	2165
EBOV_L	-----	2212

### Figure S11 | Aligment of NiV, NDV, RSV, and EBOV L protein sequences.

Hydrophobic or aromatic residues contacted by P1 (yellow), P2 (cyan), P3 (magenta) and P4 (blue) monomers of the P tetramer are shade according to the P monomer they contacted with. Residues contacted by two P monomers are indicated by both shades and colored letters. Residues contacted by three P monomers are indicated by shades, colored letters, and underlines.

Total BSA = 3537 Å<sup>2</sup>

>NiV P1 (BSA = 1743 Å<sup>2</sup>)

MDKLELVNDGLNIIDFIQKNQKEIQKTYGRSSIQQPSIKDQTKAWEDFLQCTSGESEQVEGG  
MSKDDGDVERRNLEDLSSTSPDGTIGKRVSNTRDWAEAGSDDIQLDPVVTDVVYHDHGECT  
GYGFTSSPERGWSYDTSGANNGNVCLVSDAKMLSYAPEIAVSKEDRETDLVHLENKLSTTGL  
NPTAVPFTRLNRLSDPAKDSPVIAEHYYGLGVKEQNVGPQTSRNVNLDSEIKLYTSDDEEADQL  
EFEDEFAGSSSEVIVGISPEDEEPSSVGGKPNESIGRTIEGQSIRDNLQAKDNKSTDVPGAG  
PKDSAVKEEPPQKRLPMLAEFEFCGSEDPIIRELLKENSLINCQQKDAQPPYHWSIERSI  
SPDKTEIVNGAVQTADRQRPGTTPMPKSRGPIPKKGTDAKYPSAGTENVPVGSKSGATRHRVRS  
PPYQEGKSVNAENVQLNASTAVKETDKSEVNPVDDNDSLDDKYIMPSDDFSNTFFPHDTRDL  
NYHADHLGDYDLETLCESVLMGVINSIKLINLDMRLNHIEEQVKEIPKIINKLESIDRVLA  
KTNTALSTIEGHLVSMIMIPGKGGKERKGNKNNPELKPVIIGRDILEQQSLFSFDNVKNFRDG  
SLTNEPYGAAVQLREDLILPELNFEETNASQFVPMADDSSRDVIKTLIRTHIKDRELRLSELI  
GYLNKAENDEEIQEIANTVNDIIDGNI

>NiV P2

MDKLELVNDGLNIIDFIQKNQKEIQKTYGRSSIQQPSIKDQTKAWEDFLQCTSGESEQVEGG  
MSKDDGDVERRNLEDLSSTSPDGTIGKRVSNTRDWAEAGSDDIQLDPVVTDVVYHDHGECT  
GYGFTSSPERGWSYDTSGANNGNVCLVSDAKMLSYAPEIAVSKEDRETDLVHLENKLSTTGL  
NPTAVPFTRLNRLSDPAKDSPVIAEHYYGLGVKEQNVGPQTSRNVNLDSEIKLYTSDDEEADQL  
EFEDEFAGSSSEVIVGISPEDEEPSSVGGKPNESIGRTIEGQSIRDNLQAKDNKSTDVPGAG  
PKDSAVKEEPPQKRLPMLAEFEFCGSEDPIIRELLKENSLINCQQKDAQPPYHWSIERSI  
SPDKTEIVNGAVQTADRQRPGTTPMPKSRGPIPKKGTDAKYPSAGTENVPVGSKSGATRHRVRS  
PPYQEGKSVNAENVQLNASTAVKETDKSEVNPVDDNDSLDDKYIMPSDDFSNTFFPHDTRDL  
NYHADHLGDYDLETLCESVLMGVINSIKLINLDMRLNHIEEQVKEIPKIINKLESIDRVLA  
KTNTALSTIEGHLVSMIMIPGKGGKERKGNKNNPELKPVIIGRDILEQQSLFSFDNVKNFRDG  
SLTNEPYGAAVQLREDLILPELNFEETNASQFVPMADDSSRDVIKTLIRTHIKDRELRLSELI  
GYLNKAENDEEIQEIANTVNDIIDGNI

>NiV P3 (BSA = 1176 Å<sup>2</sup>)

MDKLELVNDGLNIIDFIQKNQKEIQKTYGRSSIQQPSIKDQTKAWEDFLQCTSGESEQVEGG  
MSKDDGDVERRNLEDLSSTSPDGTIGKRVSNTRDWAEAGSDDIQLDPVVTDVVYHDHGECT  
GYGFTSSPERGWSYDTSGANNGNVCLVSDAKMLSYAPEIAVSKEDRETDLVHLENKLSTTGL  
NPTAVPFTRLNRLSDPAKDSPVIAEHYYGLGVKEQNVGPQTSRNVNLDSEIKLYTSDDEEADQL  
EFEDEFAGSSSEVIVGISPEDEEPSSVGGKPNESIGRTIEGQSIRDNLQAKDNKSTDVPGAG  
PKDSAVKEEPPQKRLPMLAEFEFCGSEDPIIRELLKENSLINCQQKDAQPPYHWSIERSI  
SPDKTEIVNGAVQTADRQRPGTTPMPKSRGPIPKKGTDAKYPSAGTENVPVGSKSGATRHRVRS  
PPYQEGKSVNAENVQLNASTAVKETDKSEVNPVDDNDSLDDKYIMPSDDFSNTFFPHDTRDL  
NYHADHLGDYDLETLCESVLMGVINSIKLINLDMRLNHIEEQVKEIPKIINKLESIDRVLA  
KTNTALSTIEGHLVSMIMIPGKGGKERKGNKNNPELKPVIIGRDILEQQSLFSFDNVKNFRDG  
SLTNEPYGAAVQLREDLILPELNFEETNASQFVPMADDSSRDVIKTLIRTHIKDRELRLSELI  
GYLNKAENDEEIQEIANTVNDIIDGNI

>NiV P4 (BSA = 617 Å<sup>2</sup>)

MDKLELVNDGLNIIDFIQKNQKEIQKTYGRSSIQQPSIKDQTKAWEDFLQCTSGESEQVEGG  
MSKDDGDVERRNLEDLSSTSPDGTIGKRVSNTRDWAEAGSDDIQLDPVVTDVVYHDHGECT  
GYGFTSSPERGWSYDTSGANNGNVCLVSDAKMLSYAPEIAVSKEDRETDLVHLENKLSTTGL  
NPTAVPFTRLNRLSDPAKDSPVIAEHYYGLGVKEQNVGPQTSRNVNLDSEIKLYTSDDEEADQL  
EFEDEFAGSSSEVIVGISPEDEEPSSVGGKPNESIGRTIEGQSIRDNLQAKDNKSTDVPGAG  
PKDSAVKEEPPQKRLPMLAEFEFCGSEDPIIRELLKENSLINCQQKDAQPPYHWSIERSI  
SPDKTEIVNGAVQTADRQRPGTTPMPKSRGPIPKKGTDAKYPSAGTENVPVGSKSGATRHRVRS  
PPYQEGKSVNAENVQLNASTAVKETDKSEVNPVDDNDSLDDKYIMPSDDFSNTFFPHDTRDL  
NYHADHLGDYDLETLCESVLMGVINSIKLINLDMRLNHIEEQVKEIPKIINKLESIDRVLA  
KTNTALSTIEGHLVSMIMIPGKGGKERKGNKNNPELKPVIIGRDILEQQSLFSFDNVKNFRDG  
SLTNEPYGAAVQLREDLILPELNFEETNASQFVPMADDSSRDVIKTLIRTHIKDRELRLSELI  
GYLNKAENDEEIQEIANTVNDIIDGNI

Total BSA = 3575 Å<sup>2</sup>

>NDV\_P1 (BSA = 1303 Å<sup>2</sup>)

MATF<sup>T</sup>DAEIDELFETSGTVIDSIIITAQGKPVETVGRSAIPQGKTKALSLAWEKHGNTNTPAA  
QESAGEQDQHGQNQASNSNRATPEEGPHSSQAQAATQPQEDANESQLKTGASSLLSMLDKL  
SNKSSNAKKGPPQSPPPQALHSGKSPAVEQTQHGANQGRAQQETGHQAAPSPGPPGTGVNIA  
FPGQRGVSPQSVGATQPAPQSGQNQGSTPASADHVQPPVDFVQAMMSMMEAISQRVSKIDYQ  
LDLVLKQTSSIPTMRSEIQQLKTSVAVMEANLGMMKI**ILD**PGCANVSSLSDLRAVAKSH**PV**LI  
**AGP**GDPSPYVTQGGE**I**ALNKLSQ**P**VPHPSDLIKHATSGG**P**DIG**I**ERD**T**VR**A**L**I**LSR**P**MHPSS  
SSKLLSKLDSAGSVVEEIRKIKRLAL**NG**

>NDV\_P2 (BSA = 366 Å<sup>2</sup>)

MATF<sup>T</sup>DAEIDELFETSGTVIDSIIITAQGKPVETVGRSAIPQGKTKALSLAWEKHGNTNTPAA  
QESAGEQDQHGQNQASNSNRATPEEGPHSSQAQAATQPQEDANESQLKTGASSLLSMLDKL  
SNKSSNAKKGPPQSPPPQALHSGKSPAVEQTQHGANQGRAQQETGHQAAPSPGPPGTGVNIA  
FPGQRGVSPQSVGATQPAPQSGQNQGSTPASADHVQPPVDFVQAMMSMMEAISQRVSKIDYQ  
LDLVLKQTSSIPTMRSEIQQLKTSVAVMEANLGMMKI**L**DPGCANVSS**L**SD**L**RAVAKSH**P**VLI  
**A**GPDPSPYVTQGGE**I**ALNKLSQ**P**VPHPSDLIKHATSGG**P**DIG**I**ERD**T**VR**A**L**I**LSR**P**MHPSS  
SSKLLSKLDSAGSVVEEIRKIKRLAL**NG**

>NDV\_P3 (BSA = 983 Å<sup>2</sup>)

MATF<sup>T</sup>DAEIDELFETSGTVIDSIIITAQGKPVETVGRSAIPQGKTKALSLAWEKHGNTNTPAA  
QESAGEQDQHGQNQASNSNRATPEEGPHSSQAQAATQPQEDANESQLKTGASSLLSMLDKL  
SNKSSNAKKGPPQSPPPQALHSGKSPAVEQTQHGANQGRAQQETGHQAAPSPGPPGTGVNIA  
FPGQRGVSPQSVGATQPAPQSGQNQGSTPASADHVQPPVDFVQAMMSMMEAISQRVSKIDYQ  
LDLVLKQTSSIPTMRSEIQQLKTSV**AV**MEAN**L**GM**M**K**I**L**D**PG**C**AN**V**SS**L**SD**L**RAVAKSH**P**VLI  
**A**GPDPSPYVTQGGE**I**ALNKLSQ**P**VPHPSDLIKHATSGG**P**DIG**I**ERD**T**VR**A**L**I**LSR**P**MHPSS  
SSKLLSKLDSAGSVVEEIRKIKRLAL**NG**

>NDV\_P4 (BSA = 923 Å<sup>2</sup>)

MATF<sup>T</sup>DAEIDELFETSGTVIDSIIITAQGKPVETVGRSAIPQGKTKALSLAWEKHGNTNTPAA  
QESAGEQDQHGQNQASNSNRATPEEGPHSSQAQAATQPQEDANESQLKTGASSLLSMLDKL  
SNKSSNAKKGPPQSPPPQALHSGKSPAVEQTQHGANQGRAQQETGHQAAPSPGPPGTGVNIA  
FPGQRGVSPQSVGATQPAPQSGQNQGSTPASADHVQPPVDFVQAMMSMMEAISQRVSKIDYQ  
LDLVLKQTSSIPTMRSEIQQLKTSVAV**MEAN**L**GM**M**K**I**L**D**PG**CAN**V**SS**L**SD**L**RAVAKSH**P**VLI  
**A**GPDPSPYVTQGGE**I**ALNKLSQ**P**VPHPSDLIKHATSGG**P**DIG**I**ERD**T**VR**A**L**I**LSR**P**MHPSS  
SSKLLSKLDSAGSVVEEIRKIKRLAL**NG**

Total BSA = 4583 Å<sup>2</sup>

>RSV\_P1 (BSA = 427 Å<sup>2</sup>)

MEKFÄPEFHGEDANNRATKFL<sup>2</sup>ESIKGKFTSPKDPKKKDSIISVNSIDIEVTKESPITSNSTI  
INPTNETDDTAGNKPNYQRKPLVSFKEDPTPSDNPFSKLYKETIETFDNNEEESSYSYEEIN  
DQTNDNITARLDRIDEKLSEILGMLHTLVVASAGPTSARDGIRDAMIGLREEMIEKIRTEAL  
MTNDRLEAMARLRNEESEKMAKDTSD<sup>2</sup>EVSLNPTSEKLNNLLEGNDSNDLSLEDFKGENKYF  
QG

>RSV\_P2 (BSA = 187 Å<sup>2</sup>)

MEKFÄPEFHGEDANNRATKFL<sup>2</sup>ESIKGKFTSPKDPKKKDSIISVNSIDIEVTKESPITSNSTI  
INPTNETDDTAGNKPNYQRKPLVSFKEDPTPSDNPFSKLYKETIETFDNNEEESSYSYEEIN  
DQTNDNITARLDRIDEKLSEILGMLHTLVVASAGPTSARDGIRDAMIGLREEMIEKIRTEAL  
MTNDRLEAMARLRNEESEKMAKDTSD<sup>2</sup>EVSLNPTSEKLNNLLEGNDSNDLSLEDFKGENKYF  
QG

>RSV\_P3 (BSA = 1526 Å<sup>2</sup>)

MEKFÄPEFHGEDANNRATKFL<sup>2</sup>ESIKGKFTSPKDPKKKDSIISVNSIDIEVTKESPITSNSTI  
INPTNETDDTAGNKPNYQRKPLVSFKEDPTPSDNPFSKLYKETIETFDNNEEESSYSYEEIN  
DQTNDNITARLDRIDEKLSEILGMLHTLVVASAGPTSARDGIRDAMIGLREEMIEKIRTEAL  
MTNDRLEAMARLRNEESEKMAKDTSD<sup>2</sup>EVSLNPTSEKLNNLLEGNDSNDLSLEDFKGENKYF  
QG

>RSV\_P4 (BSA = 2433 Å<sup>2</sup>)

MEKFÄPEFHGEDANNRATKFL<sup>2</sup>ESIKGKFTSPKDPKKKDSIISVNSIDIEVTKESPITSNSTI  
INPTNETDDTAGNKPNYQRKPLVSFKEDPTPSDNPFSKLYKETIETFDNNEEESSYSYEEIN  
DQTNDNITARLDRIDEKLSEILGM<sup>2</sup>LHTLVVASAGPTSARDGIRDAMIGLREEMIEKIRTEAL  
MTNDRLEAMARLRNEESEKMAKDTSD<sup>2</sup>EVSLNPTSEKLNNLLEGNDSNDLSLEDFKGENKYF  
QG

Total BSA = 3348 Å<sup>2</sup>

>EBOV\_P1  
MTTRTKGRGHTAATTQNDRMPGPELSGWISEQLMTGRIPVSDIFCDIENNPGLCYASQMQQT  
KPNPKTRNSQTQTDPICNHSFEEVVQTLASLATVVQQQTIASESLEQRITSLENGLKPVYDM  
AKTISSLNRVCAEMVAKYDLLVMTTGRATATAAATEAYWAEHGQPPPGPSLYEESAIRGKIE  
SRDETVPQSVREAFNNLNSTTSLTEENFGKPDISAKDLRNIMYDHLPGFGTAFHQLVQVICK  
LGKDSNSLDIIHAEFQASLAEGDSPQCALIQTITKRVPIFQDAAPPVIHIRSRGDI PRACQKS  
LRPVPPSPKIDRGWVCVFQLQDGKTLGLKI

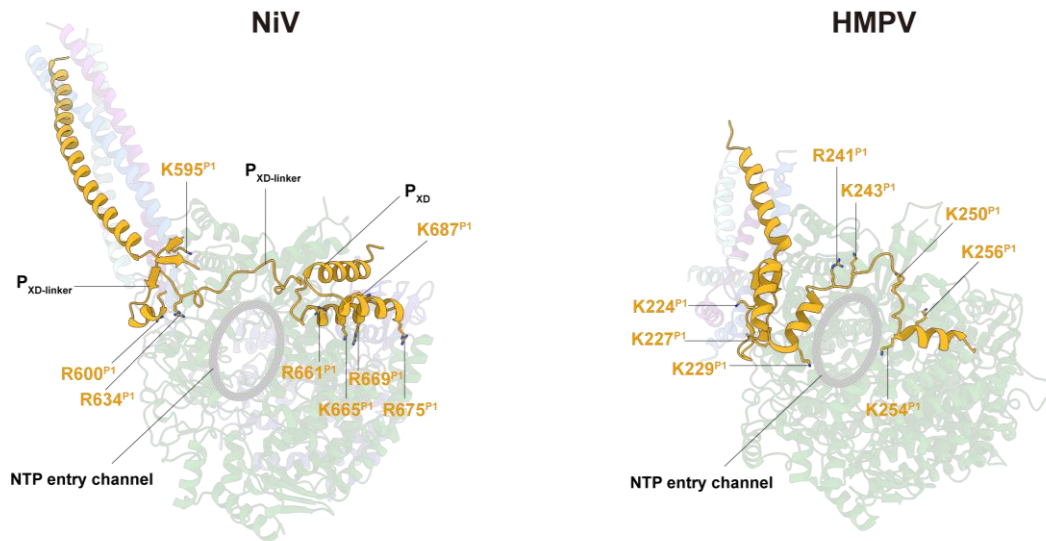
>EBOV\_P2 (BSA = 161 Å<sup>2</sup>)  
MTTRTKGRGHTAATTQNDRMPGPELSGWISEQLMTGRIPVSDIFCDIENNPGLCYASQMQQT  
KPNPKTRNSQTQTDPICNHSFEEVVQTLASLATVVQQQTIASESLEQRITSLENGLKPVYDM  
AKTISSLNRVCAEMVAKYDLLVMTTGRATATAAATEAYWAEHGQPPPGPSLYEESAIRGKIE  
SRDETVPQSVREAFNNLNSTTSLTEENFGKPDISAKDLRNIMYDHLPGFGTAFHQLVQVICK  
LGKDSNSLDIIHAEFQASLAEGDSPQCALIQTITKRVPIFQDAAPPVIHIRSRGDI PRACQKS  
LRPVPPSPKIDRGWVCVFQLQDGKTLGLKI

>EBOV\_P3 (BSA = 2093 Å<sup>2</sup>)  
MTTRTKGRGHTAATTQNDRMPGPELSGWISEQLMTGRIPVSDIFCDIENNPGLCYASQMQQT  
KPNPKTRNSQTQTDPICNHSFEEVVQTLASLATVVQQQTIASESLEQRITSLENGLKPVYDM  
AKTISSLNRVCAEMVAKYDLLVMTTGRATATAAATEAYWAEHGQPPPGPSLYEESAIRGKIE  
SRDETVPQSVREAFNNLNSTTSLTEENFGKPDISAKDLRNIMYDHLPGFGTAFHQLVQVICK  
LGKDSNSLDIIHAEFQASLAEGDSPQCALIQTITKRVPIFQDAAPPVIHIRSRGDI PRACQKS  
LRPVPPSPKIDRGWVCVFQLQDGKTLGLKI

>EBOV\_P4 (BSA = 1094 Å<sup>2</sup>)  
MTTRTKGRGHTAATTQNDRMPGPELSGWISEQLMTGRIPVSDIFCDIENNPGLCYASQMQQT  
KPNPKTRNSQTQTDPICNHSFEEVVQTLASLATVVQQQTIASESLEQRITSLENGLKPVYDM  
AKTISSLNRVCAEMVAKYDLLVMTTGRATATAAATEAYWAEHGQPPPGPSLYEESAIRGKIE  
SRDETVPQSVREAFNNLNSTTSLTEENFGKPDISAKDLRNIMYDHLPGFGTAFHQLVQVICK  
LGKDSNSLDIIHAEFQASLAEGDSPQCALIQTITKRVPIFQDAAPPVIHIRSRGDI PRACQKS  
LRPVPPSPKIDRGWVCVFQLQDGKTLGLKI

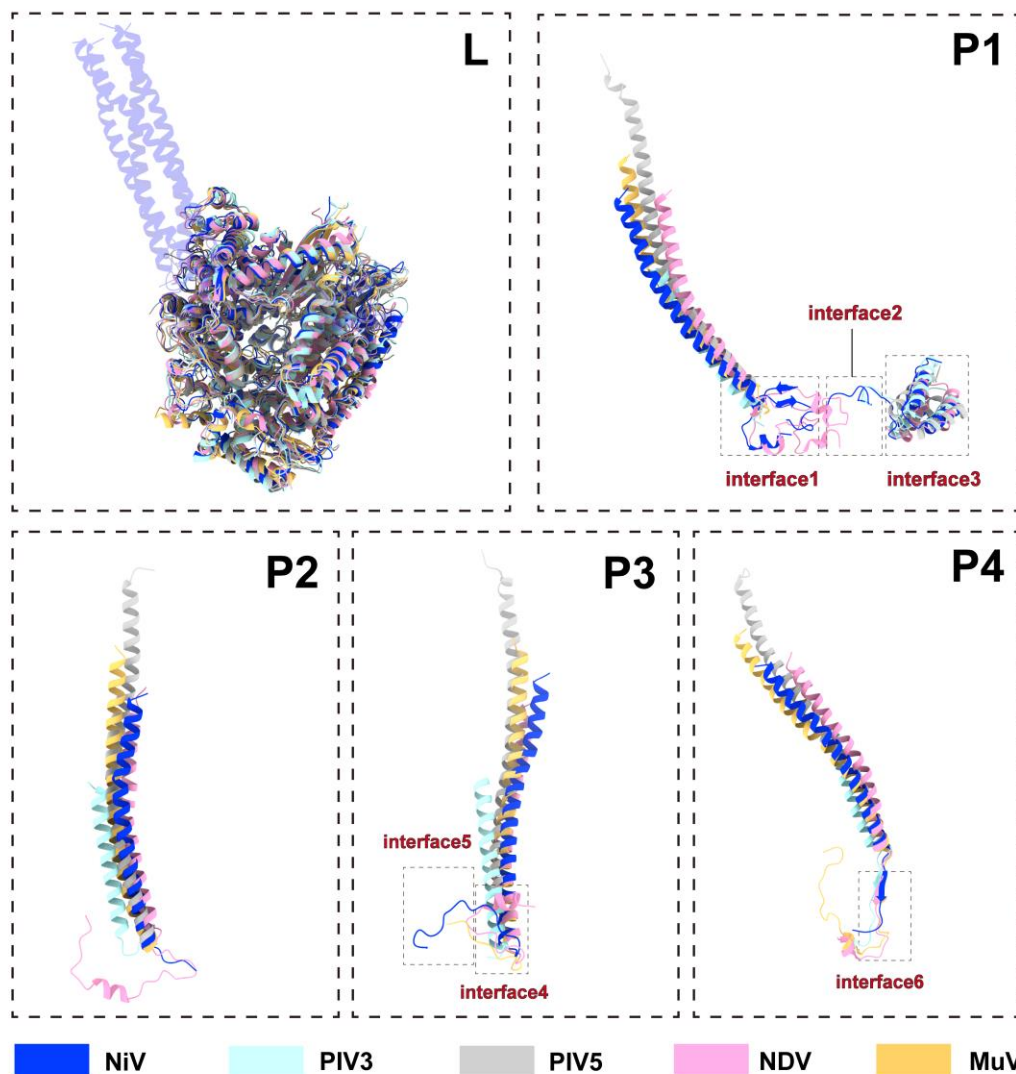
**Figure S12 | NiV, NDV, RSV, and EBOV P protein sequences and their L protein interacting residues.**

Hydrophobic residues in P1 (yellow), P2 (cyan), P3 (magenta) and P4 (blue) monomers of the P tetramers contacting the L proteins are colored.



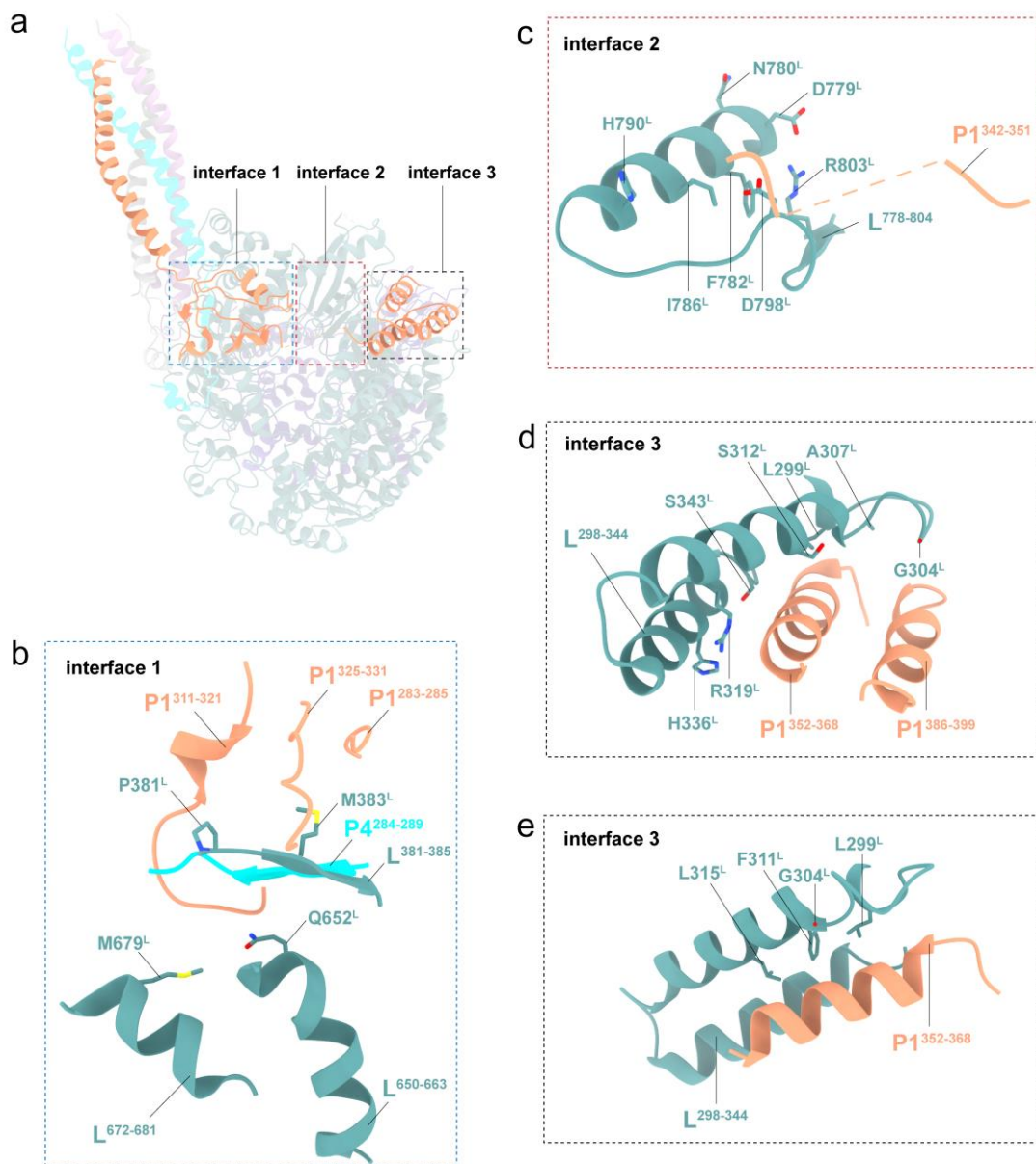
**Figure S13 | The NiV P1<sub>XD</sub> domain and P1<sub>XD</sub> linker may play a potential role in NTP entry.**

For HMPV, basic residues (K224<sup>P1</sup>, K227<sup>P1</sup>, K229<sup>P1</sup>, R241<sup>P1</sup>, K243<sup>P1</sup>, K250<sup>P1</sup>, K254<sup>P1</sup> and K256<sup>P1</sup>) in the C-terminal region of subunit P1, located around the polymerase NTP entry tunnel, form a positively charged arch that may attract NTPs to the NTP entry tunnel. Similarly, for NiV, we observe several basic amino acids (K595<sup>P1</sup>, R600<sup>P1</sup>, R634<sup>P1</sup>, R661<sup>P1</sup>, K665<sup>P1</sup>, R669<sup>P1</sup>, R675<sup>P1</sup> and K687<sup>P1</sup>) present in the P1<sub>XD</sub> domain and P1<sub>XD</sub> linker.



**Figure S14 | Comparison of P protein structures among paramyxovirus L–P complexes.**

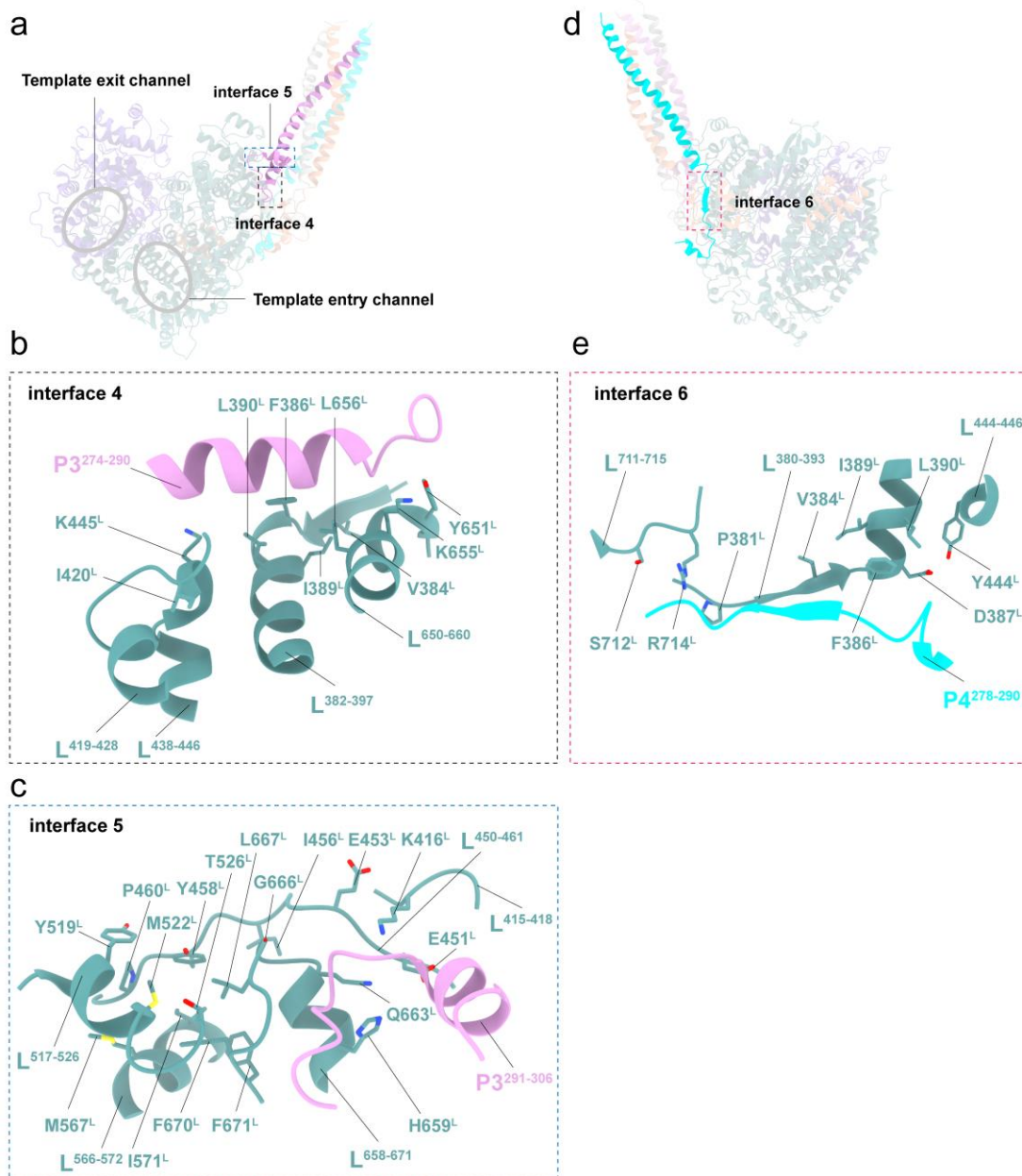
Structural superposition of the paramyxoviruses L–P complexes reveals that P (P1, P2, P3 and P4) proteins from different viruses exhibit conformational dynamics on the surface of the L proteins (NiV: blue; PIV3: cyan, 8KDC; PIV5: gray, 6V85; NDV: pink, 7YOV; MuV: yellow, 8IZL).



**Figure S15 | Structural features of the L-P interactions in interfaces 1-3 of the NDV polymerase complex.**

**a.** The overall structure of the NDV L-P complex (PDB: 7YOV). The locations of the interfaces 1-3, equivalent to those in the NiV L-P complex, are indicated by the dashed boxes. **b-e.** Structural details in the NDV L-P interfaces. The L residues in NDV, equivalent to those involved in the NiV

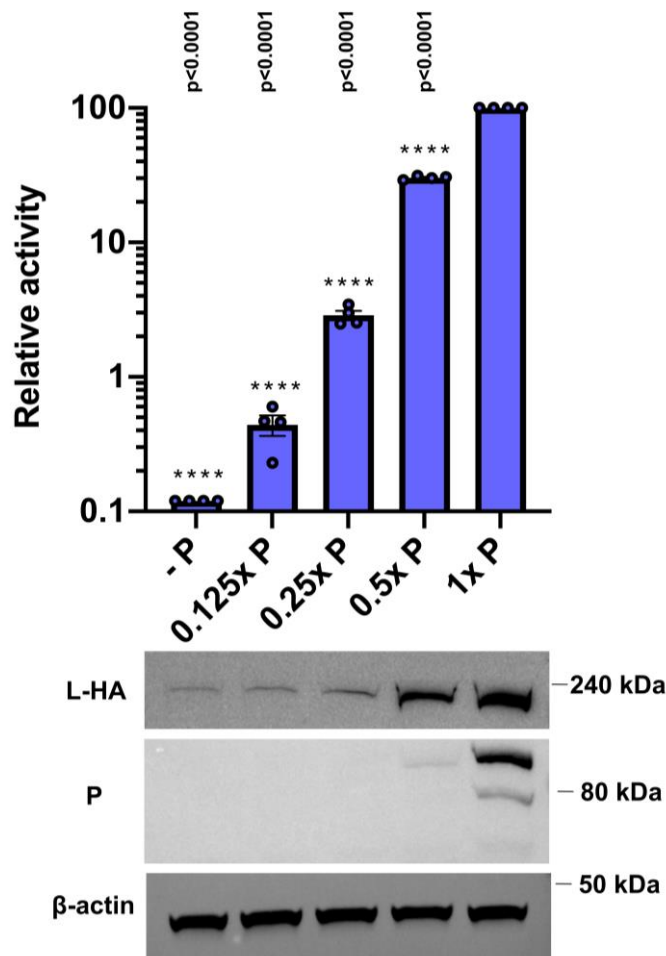
L-P interaction, are shown as sticks and labeled. These residues exhibit substantial variations when compared to those in NiV (see **Fig. 4**).



**Figure S16 | Structural features of the L-P interactions in interfaces 4-6 of the NDV polymerase complex.**

**a.** The overall structure of the NDV L-P complex (PDB: 7YOV). The locations of the interfaces 4 and 5, equivalent to those in the NiV L-P complex, are indicated by the dashed boxes. **d.** The overall structure of the

NDV L-P complex (PDB: 7YOV) in a different view. The location of the interfaces 6 is indicated by the dashed box. **b-c and e.** Structural details in the NDV L-P interfaces. The L residues in NDV, equivalent to those involved in the NiV L-P interaction, are shown as sticks and labeled. These residues exhibit substantial variations when compared to those in NiV (see **Fig. 5**).



**Figure S17 | P protein expression titration experiment showing P protein expression dependent L protein expression and mini-replicon activity.**

1×P, 0.5×P, 0.25×P, 0.125×P and -P lanes represent protein expression levels in mini-replicon experiments, where 0.5 $\mu$ g, 0.25  $\mu$ g, 0.125  $\mu$ g, 0.0625  $\mu$ g and 0  $\mu$ g of P protein expression plasmid were transfected.

Corresponding mini-replicon activities are reported as mean  $\pm$  SEM from four independent experiments (n = 4). All statistics used one-way ANOVA

Dunnett's multiple comparisons test. (ns,  $p > 0.05$ ; \*,  $p < 0.05$ ; \*\*,  $p < 0.01$ ; \*\*\*,  $p < 0.001$ ; \*\*\*\*,  $p < 0.0001$ ).

```

1      10      20      30      40      50      60
NiV_L .....MADELSISDILVPEHLSPVGGKLSIAIEYAQLRHNPQSDDKRLSENIRLNHLGKRRSLYLRSQKO
HeV_L .....MAHELSISDIIIPVPEHLSPVGGKLSIAIEYAQLRHNPQNGDKRLTENIKINLQGRKRSVYISRSQRL
CedV_L .....MESDFDISVSDVLPVPEHLSPVGGKLSITSEYANLTHNQPHEDQTLTININVKKKIKRSPGISQOSLF
MoJ_V_L .....MNFSDVSVSDILVPECHLSPVGGKLSIVQVVRFSIDIPCNQILIDPTLNEIIDIKLRSNKQGLIRRRQKEY
Lay_V_L .....MNFSDVSVSDILVPECHLSPVGGKLSIVQAVRFSEIPCNQILIDPTLNDVIDIKLRSNKQGLIRRRQKEY
FIV3_L MISNQSDSNGQKENIKNLGAKRARKMDTESNNGTVSDILVPECHLSPVGGKLSIAQLHTIMSLEPQYDMDDDSLVI TRQKIKLNKLDKRRQRSIRRL
NDV_L .....MAGSSEAEHQILPEHLSPVGGKLSLYWKLTLPLDECDPDHILSRQWKIKLESSTPDIERMIKL
FIV5_L .....MAGSRDILVPEVHLSPVGGKLSYIYLLGNLNEIDLDLGLPHNQWNGIAHESLSLAQRVNVV
MuV_L .....MAGLNEILVPEVHLSPVGGKLSYIYLLHGQLFNLEPDDLGLPLANQWKAIAEESQVHARLKQI

70      80      90      100     110     120     130
NiV_L .....GDIYIRNNIKHL.....KEFMHIANDECNNILFSITSGQMTSKLDNIMKKSFKAYNIISKKVIGMLQNIIRNLTIT.....
HeV_L .....GNYIRDNIKHL.....KEFLHVSYPECNKSLFSLKSPGMTSKLSNIMKKSFKAYNIVSRKIIEMLQNIIRNLTIT.....
CedV_L .....GNEVNKEIFDL.....KNYHVPYPECNRDLPISDDKIAFKLSKIMDNSNKLFDGLERKLSRLISVNDVQLLNATSLHNSSEMDRKGKHPFPPE
MoJ_V_L .....GILLKQVAGDI.....TSYQHIPPYECNTRLFYISDSSLVCLSEIMTHANQCYLKISSRILDLLDKTECNLTG.....
Lay_V_L .....GILLKQVAGDI.....TSYQHIPPYECNTRLFYIHDPFLVCLTEIMTHANQCYLKISSRILDLLDKTECNLTG.....
FIV3_L .....KLLTEKVNLDL.....GKYTFIRYPEMSKEMFKLPIPGINSKVTELLKADRTYSQMTDGLRDLWINVLSKPLAS.....
NDV_L .....GRSVHQVLSH.....SKRITGLLPECLDEDVGLDIDPSTNPKFRIRIEKKIQHNRTRYGEPFTRLSYVEKLLGOSWT.....
FIV5_L .....RNFLITHIPDLRKGHQEYVNVLLWPERILPLIPDFKINDQLPLLNKWDKLVKESCSVINAGTSQICQNLVSYLGTGRGNL.....
MuV_L .....RVELIARIPSLWRTRSORETAILWPERILPLIQAYDLRQSMQLPTWWEKLTQSTVNLISDGLERVVLHISNQLTGFPNL.....

140     150
NiV_L .....QDRRDEIINIECRRL.....
HeV_L .....QDQKDEVLGIYEQDRIL.....
CedV_L .....KSTIDDRVQRQTRDFPKNSTREGRSPKHPDAGPTPENSANKDLHRDNTNMPIGHSSSTMMKPKISGEEYLSMWLDSDDLGSKRISAQLGKDVSVCK
MoJ_V_L .....IGSRDDDETRIIYNNV.....
Lay_V_L .....IGSRDDDETRIIYNNI.....
FIV3_L .....KNDGSNYDLNEEFNNI.....
NDV_L .....HKRR.....SEEDSL.....
FIV5_L .....FTSRR.....ELSGDRRDDIDL.....
MuV_L .....PTRSRAGQDTKDYISIPST.....

160     170     180     190     200
NiV_L .....GDLGNMSSQSKWVECFLEWFTLTEMRAVIKNSQKPKFRSDSCIIHHRDKSTEI
HeV_L .....SNIGKYMSSQSKWVECFLEWFTLTEMRAVIKNSQKPKFRSDSCIIHMKDNMEI
CedV_L .....GHLHTTEDKPIIVPDRYIQNHESNNDIFPKKEKFKLPPSSDNLTKIMVNSKWNYPFLWFTVTEIRACQKENYKRNKRLGIIITSIKGSCYKL
MoJ_V_L .....ETLPRKIMAQSRWYKSFLEWFTVTEMRNNIKENKKYSRHNRPHITQLSGKLIYV
Lay_V_L .....ETLPRKIMAQSRWYKSFLEWFTVTEMRNNIKENKKYSRHNRPHITQLSGKLIYV
FIV3_L .....SKVHTTYKSDKWYKSFLEWFTLTEMRRRLQKARNEITFVQKDYINLLEDQKNFL
NDV_L .....KTDPAFWPHSSWTAKFALWVLCIQRLIYAAR.....TRSAENKLVLSHRSQVY
FIV5_L .....KTVVAAWHSDWKRISDFWIMLQFONROLIVROT.....DHDSDLLTYIENREGII
MuV_L .....RELSQIWFNNEWGSVKTWLMLRYMRROLITNQK.....TGLTDLVTVDRTRSLTC

210     220     230     240     250     260     270     280     290
NiV_L .....ILNPEKCIPIKSDKGTG.....KKCYLTPVLMVCDVLEGRMMMEITVKSQDIKYQPLISRSNALWGLDPLFPVGNRIINIVSMIDPLVLAL
HeV_L .....VMNPNWCYIKKNDKDG.....KRCYLTPEVLMVCDVLEGRMMMEITVKSQDIKYQSLITRSNALWTFIDPLFPVGNRIINIVSMIDPLVLAL
CedV_L .....ILNONLVAIFEDDSSGYSDDHKKRKRKYLTPEVLMVSDVTEGRLMIDVAMRFDKRYKTEKKAKLWFLDPLFPVGNRIINIVSMIDPLVLAI
MoJ_V_L .....QLNMMNISIEWKK.....KCIYHLTPVLMVCDVLEGRLMIDVAMRFDKRYHPLYNRAHQLWLDLDMFEELGNMNYNIIISLIEPLTLGI
Lay_V_L .....QINMMNISIEWKK.....KCIYHLTPVLMVCDVLEGRLMIDVAMRFDKRYHPLCERAHQLWLDLDMFEELGNMNYNIIISLIEPLTLGI
FIV3_L .....LIHPEVWILDKGN.....NGYLITPEVLMVCDVLEGRNNTISACAKLDFKLOSMYQRGNLWLEVIDPLFPVGNRIINIVSMIDPLVLALS
NDV_L .....FITPELVVTHNE.....NKFTCLSCVLMVADWVGRBMVNIISSTAVHRCLEKIDDIRLVDRARDGNQVDDWALMEFAYGA
FIV5_L .....IITPELVALENEN.....HTLYMTPVLMVSDVTEGRNNTISLCTVSTYLNPKKRIITYLLSLVDNLAFQGDVAWYNIJALLESFVYVQ
MuV_L .....IITPELVALYSSEH.....KALTYLTPVLMVTDVLEGRNNTISLCTVSTYLNPKKRIIEVLLTLDLALLGDKVYGVVSSLEFVYVQ

300     310     320     330     340     350     360     370     380     390
NiV_L .....LQDKDEARILR...LPHHCIEKMOELSECGFTDQKIRSMFTDOLLILNIDNIHLVAE...FFSFFRTGHP...LBAKVAA...BVR...HMA...KVL...EAP...TMMK
HeV_L .....LQDKDEARILR...LPHHCIEKIQEELIGCGFTDQKIRSMFTDOLLILNIDNIHLVAE...FFSFFRTGHP...LBAKVAA...BVR...HMA...KVL...EAP...TMMK
CedV_L .....LQDKDEARILR...LPHHCIEKIQEELRESKNYFDEIKRFANOLINVMTCRDIHLVAE...FFSFFRTGHP...LBAKVAA...BVR...HMA...KVL...EAP...TMMK
MoJ_V_L .....LQDKDAVALV...SFLSFCINIEKEELIKNGFNDEQDINEFTSRIINIMSIPDIHLVAE...FFSFFRTGHP...LBAKVAA...BVR...HMA...KVL...EAP...TMMK
Lay_V_L .....LQDKDAVALV...SFLSFCINIEKEELIKNGFNDEQDINEFTSRIINIMSIPDIHLVAE...FFSFFRTGHP...LBAKVAA...BVR...HMA...KVL...EAP...TMMK
FIV3_L .....LQDKDPVQQLR...AFENHVLSEMLLIFESGESINFLSDVYIDKILDFNESTIDE...AE...FFSFFRTGHP...LBAKVAA...BVR...HMA...KVL...EAP...TMMK
NDV_L .....VGLPESSTFA...DFSNVQMLRDLTI...CLLQRIADSVTAIRAINISFLEQONQAEMLCL...L...GHP...LESRAAK...VRA...Q...CAF...K...VLD...E...MLO
FIV5_L .....LQMSDFELR...Q...HAFVCS...I...DALRGTNSFTQDELRTVTINLISPPDLDL...AE...L...C...M...L...GHP...L...TASQA...A...G...V...R...S...C...A...K...V...L...D...E...MLO
MuV_L .....LQGD...PV...DI...K...TF...YGF...IC...E...I...LDLLTEDNIF...TE...EANKVLLDLSQ...F...D...N...L...S...P...L...AE...L...C...M...L...GHP...L...TASQA...A...G...V...R...S...C...A...K...V...L...D...E...MLO

```

400 410 420 430 440 450 460 470 480 490

NiV\_L AHAHPCGTLINGRDRRHGGWPPDLYLPAHASKHIIRLKNSESLTIDDCVKNWESFCGIQDFCPMELIKDSDLSMYMKDKALSPKIDEDSVYPPREV  
 HeV\_L AHAHPCGTLINGRDRRHGGWPPDLYLPAHASKHIIRLKNSESLTIDDCVKNWESFCGIQDFCPMELIKDSDLSMYMKDKALSPKIDEDSVYPPREV  
 CedV\_L AHAHPCGTLINGRDRRHGGWPPDLYLPAHASKHIIRLKNSESLTIDDCVKNWESFCGIQDFCPMELIKDSDLSMYMKDKALSPKIDEDSVYPPREV  
 MojV\_L AHAHPCGTLINGRDRRHGGWPPDLYLPAHASKHIIRLKNSESLTIDDCVKNWESFCGIQDFCPMELIKDSDLSMYMKDKALSPKIDEDSVYPPREV  
 LayV\_L AHAHPCGTLINGRDRRHGGWPPDLYLPAHASKHIIRLKNSESLTIDDCVKNWESFCGIQDFCPMELIKDSDLSMYMKDKALSPKIDEDSVYPPREV  
 PIV3\_L CHAHPCTIINGRDRRHGGWPPDLYLPAHASKHIIRLKNSESLTIDDCVKNWESFCGIQDFCPMELIKDSDLSMYMKDKALSPKIDEDSVYPPREV  
 NDV\_L VLSEPKGTINGRDRRHGGWPPDLYLPAHASKHIIRLKNSESLTIDDCVKNWESFCGIQDFCPMELIKDSDLSMYMKDKALSPKIDEDSVYPPREV  
 PIV5\_L TLAPFHITLINGRDRRHGGWPPDLYLPAHASKHIIRLKNSESLTIDDCVKNWESFCGIQDFCPMELIKDSDLSMYMKDKALSPKIDEDSVYPPREV  
 MuV\_L TLAPFHITLINGRDRRHGGWPPDLYLPAHASKHIIRLKNSESLTIDDCVKNWESFCGIQDFCPMELIKDSDLSMYMKDKALSPKIDEDSVYPPREV

500 510 520 530 540 550 560 570 580

NiV\_L LSYTPPKSTEP.....RRLVDVFNVDENDDPPNMIDVYVLSGAYLDEQFNVSYSYLKEDEKQAGRIFAKMTYKMRACQVIAEALIASGVGKYPKEN  
 HeV\_L LNYTPPKSTEP.....RRLVDVFNVDENDDPPNMIDVYVLSGAYLDEQFNVSYSYLKEDEKQAGRIFAKMTYKMRACQVIAEALIASGVGKYPKEN  
 CedV\_L MSYQPPRSTK.....RRLVDVFNVDENDDPPNMIDVYVLSGAYLDEQFNVSYSYLKEDEKQAGRIFAKMTYKMRACQVIAEALIASGVGKYPKEN  
 MojV\_L MCVNPPASTS.....RRLVDVFNVDENDDPPNMIDVYVLSGAYLDEQFNVSYSYLKEDEKQAGRIFAKMTYKMRACQVIAEALIASGVGKYPKEN  
 LayV\_L MCVNPPASTS.....RRLVDVFNVDENDDPPNMIDVYVLSGAYLDEQFNVSYSYLKEDEKQAGRIFAKMTYKMRACQVIAEALIASGVGKYPKEN  
 PIV3\_L LLYRTNASNES.....RRLVDVFNVDENDDPPNMIDVYVLSGAYLDEQFNVSYSYLKEDEKQAGRIFAKMTYKMRACQVIAEALIASGVGKYPKEN  
 NDV\_L LSEEQKHNVDQSTSTNRLLIFLSENDPDKKEMVLTLEYLDDSDVAVSYSYLKEDEKQAGRIFAKMTYKMRACQVIAEALIASGVGKYPKEN  
 PIV5\_L IKQRVYRANRPLFPQFNRLNLEDDRDFDKKEMVLTLEYLDDSDVAVSYSYLKEDEKQAGRIFAKMTYKMRACQVIAEALIASGVGKYPKEN  
 MuV\_L IKQRVYRANRPLFPQFNRLNLEDDRDFDKKEMVLTLEYLDDSDVAVSYSYLKEDEKQAGRIFAKMTYKMRACQVIAEALIASGVGKYPKEN

590 600 610 620 630

NiV\_L GVMKDEHELEKTLFQLSISVPRGNSQGN.....DPQSINNTERDFQYFKGVITN  
 HeV\_L GVMKDEHELEKTLFQLSISVPRGNSQGN.....DPQSINNTERDFQYFKGVITN  
 CedV\_L GVMKDEHELEKTLFQLSISVPRGNSQGN.....DPQSINNTERDFQYFKGVITN  
 MojV\_L GVMKDEHELEKTLFQLSISVPRGNSQGN.....DPQSINNTERDFQYFKGVITN  
 LayV\_L GVMKDEHELEKTLFQLSISVPRGNSQGN.....DPQSINNTERDFQYFKGVITN  
 PIV3\_L GVMKDEHELEKTLFQLSISVPRGNSQGN.....DPQSINNTERDFQYFKGVITN  
 NDV\_L GVMKDEHELEKTLFQLSISVPRGNSQGN.....DPQSINNTERDFQYFKGVITN  
 PIV5\_L GVMKDEHELEKTLFQLSISVPRGNSQGN.....DPQSINNTERDFQYFKGVITN  
 MuV\_L GVMKDEHELEKTLFQLSISVPRGNSQGN.....DPQSINNTERDFQYFKGVITN

640 650 660 670 680 690

NiV\_L VKDKKNSFNKVSALNN.....PCQADGVHNNMSPNT.....RNRYKCSNTS.KSFLDYHTEFNPHNYKSDN.....  
 HeV\_L LLNNEVPCRNIMMSALID.....KNQSDQKKNHILPNT.....RNRYKCSNTS.QTFLDYHTEFNPHNYKSDN.....  
 CedV\_L SMIRRQKSHREVKINKLDIGSDNEEQGKEIDAAYKIIDNPNPHINPDQDPGICQEDKQEGAKSDLTGEMSFLEMHITFNPNKSKSETIGIFSRATEKSS  
 MojV\_L SKENKTLNLSKVIINTIG.....HNTFNTLQNKQPT.....PRINPQLNKKNSLQDTISNYISKDYTIQDY.....DNWKISKRFKRIEGRDLSL  
 LayV\_L SKENKTLNLSKVIINTIG.....HNTFNTLQNKQPT.....PRINPQLNKKNSLQDTISNYISKDYTIQDY.....DNWKISKRFKRIEGRDLSL  
 PIV3\_L SHTDLLKTYNKI.....QNHFTSLQNKQPT.....PRINPQLNKKNSLQDTISNYISKDYTIQDY.....DNWKISKRFKRIEGRDLSL  
 NDV\_L .....ERV.....SSRNHDLKGGH.....QRNKSHTSQQVN.....  
 PIV5\_L NIN..QPFGQNI.....QRNKSHTSQQVN.....  
 MuV\_L NMTLAHSQSNKH.....RINNQQFKKND.....

700 710 720 730 740 750 760 770

NiV\_L .....TEAAVLSRYEDNTGTFDVSAPFTTDLKPKLNRWESMAIFARLDEIYLPGFNWHRRLRSVIVYVDDPCPPDI  
 HeV\_L .....TETSDFSKYDDGIGIKFDIVSAPFTTDLKPKLNRWESMAIFARLDEIYLPGFNWHRRLRSVIVYVDDPCPPDI  
 CedV\_L LSNPFGISQKERRKTYNESHSLGKFSKDEERYDVISAPFTTDLKPKLNRWESMAIFARLDEIYLPGFNWHRRLRSVIVYVDDPCPPDI  
 MojV\_L .....TSKAFDRSDKYDTISSAPFTTDLKPKLNRWESMAIFARLDEIYLPGFNWHRRLRSVIVYVDDPCPPDI  
 LayV\_L .....TNTAVDKSEERYDTISSAPFTTDLKPKLNRWESMAIFARLDEIYLPGFNWHRRLRSVIVYVDDPCPPDI  
 PIV3\_L .....KSTDIYNDGYEIVSCFTTDLKPKLNRWESMAIFARLDEIYLPGFNWHRRLRSVIVYVDDPCPPDI  
 NDV\_L .....RRR.....VATFTTDLKPKLNRWESMAIFARLDEIYLPGFNWHRRLRSVIVYVDDPCPPDI  
 PIV5\_L .....QRD..PSDDFELAASF...TTLKPKLNRWESMAIFARLDEIYLPGFNWHRRLRSVIVYVDDPCPPDI  
 MuV\_L .....NKHEMPDDGFETIACFTTDLKPKLNRWESMAIFARLDEIYLPGFNWHRRLRSVIVYVDDPCPPDI

780 790 800 810 820 830 840 850 860 870

NiV\_L DKHMLLEKTPEDDIFIHSPKGGIEGYSQKWTIATPFLISAYETNRRAAIVQGDNESTADIKORVHPNLPYKVKKEICARQAOLYERLRLMNLRA  
 HeV\_L GKHINLDDTPEDDIFIHSPKGGIEGYSQKWTIATPFLISAYETNRRAAIVQGDNESTADIKORVHPNLPYKVKKEICARQAOLYERLRLMNLRA  
 CedV\_L NEHIDLNDSPEDDIFIHSPKGGIEGYSQKWTIATPFLISAYETNRRAAIVQGDNESTADIKORVHPNLPYKVKKEICARQAOLYERLRLMNLRA  
 MojV\_L TDHLLDEVDEGIFIRHSPKGGIEGYSQKWTIATPFLISAYETNRRAAIVQGDNESTADIKORVHPNLPYKVKKEICARQAOLYERLRLMNLRA  
 LayV\_L TAHIDLDDVDEGIFIRHSPKGGIEGYSQKWTIATPFLISAYETNRRAAIVQGDNESTADIKORVHPNLPYKVKKEICARQAOLYERLRLMNLRA  
 PIV3\_L KEHIDLDDVDEGIFIRHSPKGGIEGYSQKWTIATPFLISAYETNRRAAIVQGDNESTADIKORVHPNLPYKVKKEICARQAOLYERLRLMNLRA  
 NDV\_L TDYDLKVPNDGIFIVSAPGGIEGYSQKWTIATPFLISAYETNRRAAIVQGDNESTADIKORVHPNLPYKVKKEICARQAOLYERLRLMNLRA  
 PIV5\_L TSQDLKVINDDGIFIVSAPGGIEGYSQKWTIATPFLISAYETNRRAAIVQGDNESTADIKORVHPNLPYKVKKEICARQAOLYERLRLMNLRA  
 MuV\_L PQQLDLTALMDDGIFIVSAPGGIEGYSQKWTIATPFLISAYETNRRAAIVQGDNESTADIKORVHPNLPYKVKKEICARQAOLYERLRLMNLRA

880 890 900 910 920 930 940 950 960  
 Nav\_L LCHLKKKTEETI STHLFFVYSKRIHYDCAVLSQALKEMSRCCCFWSETLVD ETRASACSNISTTIAKAHEBNGHSRNVGTCINILVKVIOQLLISTEFSFINE  
 HeV\_L LCHLKKKTEETI STHLFFVYSKRIHYDCAVLSQALKEMSRCCCFWSETLVD ETRASACSNISTTIAKAHEBNGHSRNVGTCINILVKVIOQLLISTEFSFINE  
 CedV\_L LCHLKKKTEETI STHLFFVYSKRIHYDCAVLSQALKEMSRCCCFWSETLVD ETRASACSNISTTIAKAHEBNGHSRNVGTCINILVKVIOQLLISTEFSFINE  
 MoJV\_L LCHLKKKTEETI STHLFFVYSKRIHYDCAVLSQALKEMSRCCCFWSETLVD ETRASACSNISTTIAKAHEBNGHSRNVGTCINILVKVIOQLLISTEFSFINE  
 LayV\_L LCHLKKKTEETI STHLFFVYSKRIHYDCAVLSQALKEMSRCCCFWSETLVD ETRASACSNISTTIAKAHEBNGHSRNVGTCINILVKVIOQLLISTEFSFINE  
 FIV3\_L LCHLKKKTEETI STHLFFVYSKRIHYDCAVLSQALKEMSRCCCFWSETLVD ETRASACSNISTTIAKAHEBNGHSRNVGTCINILVKVIOQLLISTEFSFINE  
 NDV\_L LCHLKKKTEETI STHLFFVYSKRIHYDCAVLSQALKEMSRCCCFWSETLVD ETRASACSNISTTIAKAHEBNGHSRNVGTCINILVKVIOQLLISTEFSFINE  
 FIV5\_L LCHLKKKTEETI STHLFFVYSKRIHYDCAVLSQALKEMSRCCCFWSETLVD ETRASACSNISTTIAKAHEBNGHSRNVGTCINILVKVIOQLLISTEFSFINE  
 MuV\_L LCHLKKKTEETI STHLFFVYSKRIHYDCAVLSQALKEMSRCCCFWSETLVD ETRASACSNISTTIAKAHEBNGHSRNVGTCINILVKVIOQLLISTEFSFINE

970 980 990 1000 1010 1020 1030 1040 1050 1060  
 Nav\_L LTLDDVTSPIFNNDLWLTAAALPAPGCFNYLNRSRFFRNIGDDPVASADIKRMIDHSIMFESVTLQKVNQEPDASFLDWDASDPFSGCDDPDSO  
 HeV\_L LTLDDVTSPIFNNDLWLTAAALPAPGCFNYLNRSRFFRNIGDDPVASADIKRMIDHSIMFESVTLQKVNQEPDASFLDWDASDPFSGCDDPDSO  
 CedV\_L CMTDDIRPFRDNPWIKHAALIPASIGGLNYMNSRFLVNRNIGDDPVASADIKRMIDHSIMFESVTLQKVNQEPDASFLDWDASDPFSGCDDPDSO  
 MoJV\_L TMTPDVTNPLIQNVNLLTACLIPASIGGFNYLNRSRFLVNRNIGDDPVASADIKRMIDHSIMFESVTLQKVNQEPDASFLDWDASDPFSGCDDPDSO  
 LayV\_L TMTPDVTNPLIQNVNLLTACLIPASIGGFNYLNRSRFLVNRNIGDDPVASADIKRMIDHSIMFESVTLQKVNQEPDASFLDWDASDPFSGCDDPDSO  
 FIV3\_L TITONIKDQYFNNSNMQYASLLIPASIGGFNYLNRSRFLVNRNIGDDPVASADIKRMIDHSIMFESVTLQKVNQEPDASFLDWDASDPFSGCDDPDSO  
 NDV\_L STQSGSQWINDIPFHSVLLPQALGGLNPLSRFLVNRNIGDDPVASADIKRMIDHSIMFESVTLQKVNQEPDASFLDWDASDPFSGCDDPDSO  
 FIV5\_L IPGDDITLXYINPHLVSRLALPQALGGLNPLSRFLVNRNIGDDPVASADIKRMIDHSIMFESVTLQKVNQEPDASFLDWDASDPFSGCDDPDSO  
 MuV\_L SLSQDITLXYINPHLVSRLALPQALGGLNPLSRFLVNRNIGDDPVASADIKRMIDHSIMFESVTLQKVNQEPDASFLDWDASDPFSGCDDPDSO

1070 1080 1090 1100 1110 1120 1130 1140 1150 1160  
 Nav\_L SITKTIKRNITARTILRNSFNPDKGFHDKSFFDELEASFLMDRNVILPRAAHELDNSLTGAREEIGGLDITKGLIRSGLRKSGIQPKLVSRLS  
 HeV\_L SITKTIKRNITARTILRNSFNPDKGFHDKSFFDELEASFLMDRNVILPRAAHELDNSLTGAREEIGGLDITKGLIRSGLRKSGIQPKLVSRLS  
 CedV\_L SITKTIKRNITARTILRNSFNPDKGFHDKSFFDELEASFLMDRNVILPRAAHELDNSLTGAREEIGGLDITKGLIRSGLRKSGIQPKLVSRLS  
 MoJV\_L SITKTIKRNITARTILRNSFNPDKGFHDKSFFDELEASFLMDRNVILPRAAHELDNSLTGAREEIGGLDITKGLIRSGLRKSGIQPKLVSRLS  
 LayV\_L SITKTIKRNITARTILRNSFNPDKGFHDKSFFDELEASFLMDRNVILPRAAHELDNSLTGAREEIGGLDITKGLIRSGLRKSGIQPKLVSRLS  
 FIV3\_L NITTKIKRNITARTILRNSFNPDKGFHDKSFFDELEASFLMDRNVILPRAAHELDNSLTGAREEIGGLDITKGLIRSGLRKSGIQPKLVSRLS  
 NDV\_L SPISIVLKHTRVLETCRNPDLKGFHDKSFFDELEASFLMDRNVILPRAAHELDNSLTGAREEIGGLDITKGLIRSGLRKSGIQPKLVSRLS  
 FIV5\_L PPTTALRKHQAQYLMERSVNPDLKGFHDKSFFDELEASFLMDRNVILPRAAHELDNSLTGAREEIGGLDITKGLIRSGLRKSGIQPKLVSRLS  
 MuV\_L PPTTALRKHQAQYLMERSVNPDLKGFHDKSFFDELEASFLMDRNVILPRAAHELDNSLTGAREEIGGLDITKGLIRSGLRKSGIQPKLVSRLS

1170 1180 1190 1200 1210 1220 1230 1240 1250  
 Nav\_L HDYDQFVFNFLMRNKNMSPY...IKPTICSVELAKYLRSHMWRRLSOGRLIYGLVPPDESMGGSIIRGSEBGS...ASEKSPYQWFFIFKDG  
 HeV\_L HDYDQFVFNFLMRNKNMSPY...IKPTICSVELAKYLRSHMWRRLSOGRLIYGLVPPDESMGGSIIRGSEBGS...ASEKSPYQWFFIFKDG  
 CedV\_L HDYDQFVFNFLMRNKNMSPY...IKPTICSVELAKYLRSHMWRRLSOGRLIYGLVPPDESMGGSIIRGSEBGS...ASEKSPYQWFFIFKDG  
 MoJV\_L HDYDQFVFNFLMRNKNMSPY...IKPTICSVELAKYLRSHMWRRLSOGRLIYGLVPPDESMGGSIIRGSEBGS...ASEKSPYQWFFIFKDG  
 LayV\_L HDYDQFVFNFLMRNKNMSPY...IKPTICSVELAKYLRSHMWRRLSOGRLIYGLVPPDESMGGSIIRGSEBGS...ASEKSPYQWFFIFKDG  
 FIV3\_L HDYDQFVFNFLMRNKNMSPY...IKPTICSVELAKYLRSHMWRRLSOGRLIYGLVPPDESMGGSIIRGSEBGS...ASEKSPYQWFFIFKDG  
 NDV\_L HDYDQFVFNFLMRNKNMSPY...IKPTICSVELAKYLRSHMWRRLSOGRLIYGLVPPDESMGGSIIRGSEBGS...ASEKSPYQWFFIFKDG  
 FIV5\_L HDYDQFVFNFLMRNKNMSPY...IKPTICSVELAKYLRSHMWRRLSOGRLIYGLVPPDESMGGSIIRGSEBGS...ASEKSPYQWFFIFKDG  
 MuV\_L HDYDQFVFNFLMRNKNMSPY...IKPTICSVELAKYLRSHMWRRLSOGRLIYGLVPPDESMGGSIIRGSEBGS...ASEKSPYQWFFIFKDG

1260 1270 1280 1290 1300 1310 1320 1330 1340 1350  
 Nav\_L SLDQVDRHSSIRVYVCGSDRERSEIKLGHVKSRRALKSAIRATVYTWAGDDEESWLEAWYLASQRNNDLEVRRAITPISNSNLAHRRD  
 HeV\_L SLDQVDRHSSIRVYVCGSDRERSEIKLGHVKSRRALKSAIRATVYTWAGDDEESWLEAWYLASQRNNDLEVRRAITPISNSNLAHRRD  
 CedV\_L SLDQVDRHSSIRVYVCGSDRERSEIKLGHVKSRRALKSAIRATVYTWAGDDEESWLEAWYLASQRNNDLEVRRAITPISNSNLAHRRD  
 MoJV\_L SLDQVDRHSSIRVYVCGSDRERSEIKLGHVKSRRALKSAIRATVYTWAGDDEESWLEAWYLASQRNNDLEVRRAITPISNSNLAHRRD  
 LayV\_L SLDQVDRHSSIRVYVCGSDRERSEIKLGHVKSRRALKSAIRATVYTWAGDDEESWLEAWYLASQRNNDLEVRRAITPISNSNLAHRRD  
 FIV3\_L SLDQVDRHSSIRVYVCGSDRERSEIKLGHVKSRRALKSAIRATVYTWAGDDEESWLEAWYLASQRNNDLEVRRAITPISNSNLAHRRD  
 NDV\_L SLDQVDRHSSIRVYVCGSDRERSEIKLGHVKSRRALKSAIRATVYTWAGDDEESWLEAWYLASQRNNDLEVRRAITPISNSNLAHRRD  
 FIV5\_L SLDQVDRHSSIRVYVCGSDRERSEIKLGHVKSRRALKSAIRATVYTWAGDDEESWLEAWYLASQRNNDLEVRRAITPISNSNLAHRRD  
 MuV\_L SLDQVDRHSSIRVYVCGSDRERSEIKLGHVKSRRALKSAIRATVYTWAGDDEESWLEAWYLASQRNNDLEVRRAITPISNSNLAHRRD

1360 1370 1380 1390 1400 1410 1420 1430 1440  
 Nav\_L KCFPKFAGSVLNRVSRVYVNSDNDLDFRIEKGKVDNLIYQVMMLLGLSABQRVRYKTCGTGKENVIVHLHARENCCVIEMSTGNVPSLEPPFY  
 HeV\_L KCFPKFAGSVLNRVSRVYVNSDNDLDFRIEKGKVDNLIYQVMMLLGLSABQRVRYKTCGTGKENVIVHLHARENCCVIEMSTGNVPSLEPPFY  
 CedV\_L KCFPKFAGSVLNRVSRVYVNSDNDLDFRIEKGKVDNLIYQVMMLLGLSABQRVRYKTCGTGKENVIVHLHARENCCVIEMSTGNVPSLEPPFY  
 MoJV\_L KCFPKFAGSVLNRVSRVYVNSDNDLDFRIEKGKVDNLIYQVMMLLGLSABQRVRYKTCGTGKENVIVHLHARENCCVIEMSTGNVPSLEPPFY  
 LayV\_L KCFPKFAGSVLNRVSRVYVNSDNDLDFRIEKGKVDNLIYQVMMLLGLSABQRVRYKTCGTGKENVIVHLHARENCCVIEMSTGNVPSLEPPFY  
 FIV3\_L KCFPKFAGSVLNRVSRVYVNSDNDLDFRIEKGKVDNLIYQVMMLLGLSABQRVRYKTCGTGKENVIVHLHARENCCVIEMSTGNVPSLEPPFY  
 NDV\_L KCFPKFAGSVLNRVSRVYVNSDNDLDFRIEKGKVDNLIYQVMMLLGLSABQRVRYKTCGTGKENVIVHLHARENCCVIEMSTGNVPSLEPPFY  
 FIV5\_L KCFPKFAGSVLNRVSRVYVNSDNDLDFRIEKGKVDNLIYQVMMLLGLSABQRVRYKTCGTGKENVIVHLHARENCCVIEMSTGNVPSLEPPFY  
 MuV\_L KCFPKFAGSVLNRVSRVYVNSDNDLDFRIEKGKVDNLIYQVMMLLGLSABQRVRYKTCGTGKENVIVHLHARENCCVIEMSTGNVPSLEPPFY

1450 1460 1470 1480 1490 1500 1510 1520 1530 1540

Niv\_L TEVDNHLIYDPPVSEIDCSRISNQESKSRLEDFLWSTEELHVDLAKTVAQTVEIITKADKDVVKQHLAIDSDDNINSITTEFLIVDPELFALY  
HeV\_L TEVDNHLIYDPPVSEIDCDRLSKQESKARELDFFLWSTEELHVDLAKTVAQTVEIITKADKDVVKQHLAIDSDDNINSITTEFLMVDPELFALY  
CedV\_L TEVRNRLIYDPPVSEIDDELRLAQQTKRVLDLEFSLWDTKELHENLAQSLAITVTDMTKSDKDHKQDRSDVDNKTITTEFLMVDPELFALY  
MoJV\_L KEIRENRLIYDPPVSEIDDLRKLRLQAMYSADVDFSNWKSDDLHCVLAQSLAHTIISISKSDNDVLKQFVITSSDINSITTEFLMVDVNLISVY  
LayV\_L KEIRENRLIYDPPVSEIDDLRKLRLQAMYSADVDFSNWKSDDLHCVLAQSLAHTIISISKSDNDVLKQFVITSSDINSITTEFLMVDVNLISVY  
PIV3\_L RYPEENFEIYDPPVSEIDLSKLMVVKDHSYTDIMNWDVTDIHAISICTAITIADTMSQDLRDLNKEIVITANDDINSITTEFLMVDVNLISVY  
NDV\_L RVVAENKFMVYDPPVSEIDFARLDLAIKFSYELNLESYSYVLMNLSISSGKLIQSVVSYDEETSINKNDIIVDNTNRWITTEAQNSDVVRLFEY  
PIV5\_L TVPYSNKFVYDPPVSEIDTAKLESLSFQAQLGNIDAVDMTGKLLTLQSQTARQIINAITGLDESVELTNDIIVASDYSVSNWITTECMYTKLDELDFMY  
Miv\_L NVPQNNKRVYDPPVSEIDLSLEMERKEDIAYQTRIGGLDQPLLEKIFLPLAHLAKQMVNSITGLDEATSIMNDAMVQADYSVSNWITTECCYTYIDSVFVY

1550 1560 1570 1580 1590 1600 1610 1620 1630 1640

Niv\_L LQGSISIKWAFDEIHRRRPHGRHTMVDLLSDLVSNSTSKHTYKVLNSALSHPRVFKRFVNCGLLLPTQGPYLHQDPEKLSQNLVTSYMIYLMNWCDF  
HeV\_L LQGSISIKWAFDEIHRRRPHGRHTMVDLLSDLVSNSTSKHTYKVLNSALSHPRVFKRFVNCGLLLPTQGPYLHQDPEKLSQNLVTSYMIYLMNWCDF  
CedV\_L LGLHISIKWAFDEIHRRRPHGRYSMEIYLLDNTSSHVYRITLNVLSHPVVMKRFNAGLLVFKYGPYLTSDPKKMAVDFITATYTFLLTNWCNN  
MoJV\_L LQACSNKWAFFDIHFKRFQGRWQMIELTLDLSDTSVHFRVLTNALSHPRVFKRFVNCGLLLPTQGPYLHQDPEKLSQNLVTSYMIYLMNWCDF  
LayV\_L LQACSNKWAFFDIHFKRFQGRWQMIELTLDLSDTSVHFRVLTNALSHPRVFKRFVNCGLLLPTQGPYLHQDPEKLSQNLVTSYMIYLMNWCDF  
PIV3\_L FGGLLVQNFAMTLYSLKIEGRDLINDYIMRTLRDTSHSILKVLNSALSHPRVFKRFVNCGLLLPTQGPYLHQDPEKLSQNLVTSYMIYLMNWCDF  
NDV\_L AALEVLLDCSYQLYLVRVGNVNVLYMSDLYKNMFGILLNSAATITSHPIHSRLHTVGLISHDGHQLADTFEELSAKLLVSCTRRVVSGLYAG  
PIV5\_L CGWELLLELSYQMYLVRVGNVNVLYMSDLYKNMFGILLNSAATITSHPIHSRLHTVGLISHDGHQLADTFEELSAKLLVSCTRRVVSGLYAG  
Miv\_L CSEWALLLELSYQMYLVRVGNVNVLYMSDLYKNMFGILLNSAATITSHPIHSRLHTVGLISHDGHQLADTFEELSAKLLVSCTRRVVSGLYAG

1650 1660 1670 1680 1690 1700 1710 1720 1730

Niv\_L KKSPFLIAEQDETVISLREDIITSKHLCVIIDLYANHHKPFWIIDLNQPKICVLDKDFISKRHVDTSRWSW.....NTSDLFVFVYASLTVLR  
HeV\_L KKSPFLIAEQDEAVVELREDIITSKHLCVIIDLYANHHKPFWIIDLNQPKICVLDKDFISKRHVDTSRWSW.....NTSDLFVFVYASLTVLR  
CedV\_L NKFSLLIPEQDPIELRKHDIHARHLCMIISDLYCYSFKQWIKELTQPKICVLMEDFIANCVANQTSAGW.....NITPLRVVNLPASTTVLR  
MoJV\_L RTVSPFLMAEQSDVAVDIRSCTVQAKHLCMLCDLYCNEQGFHIRDLMHPKIDILSDFFKTRLNIVGSDSW.....NIHMLHINVPASTTVLR  
LayV\_L RTVSPFLMAEQSDVAVDIRSCTVQAKHLCMLCDLYCNEQGFHIRDLMHPKIDILSDFFKTRLNIVGSDSW.....NIHMLHINVPASTTVLR  
PIV3\_L VSLLEYLDCSYQLYLVRVGNVNVLYMSDLYKNMFGILLNSAATITSHPIHSRLHTVGLISHDGHQLADTFEELSAKLLVSCTRRVVSGLYAG  
NDV\_L NKFSLLIPEQDPIELRKHDIHARHLCMIISDLYCYSFKQWIKELTQPKICVLMEDFIANCVANQTSAGW.....NITPLRVVNLPASTTVLR  
PIV5\_L GDELLVTVSEDSLILSDRSMNLIARLKLTLHLRHNGLELPIKIGFSPDEKCFALTEFLRVVNSGLSSIENLSNFMVNVENPRLAFAFASNNYVTR  
Miv\_L IDYEIVVPSSEQLTISDRVNLVARKLSLLAIITWANYNPFVKGKSPDEKCFALTEFLRVVNSGLSSIENLSNFMVNVENPRLAFAFASNNYVTR

1740 1750 1760 1770 1780 1790 1800

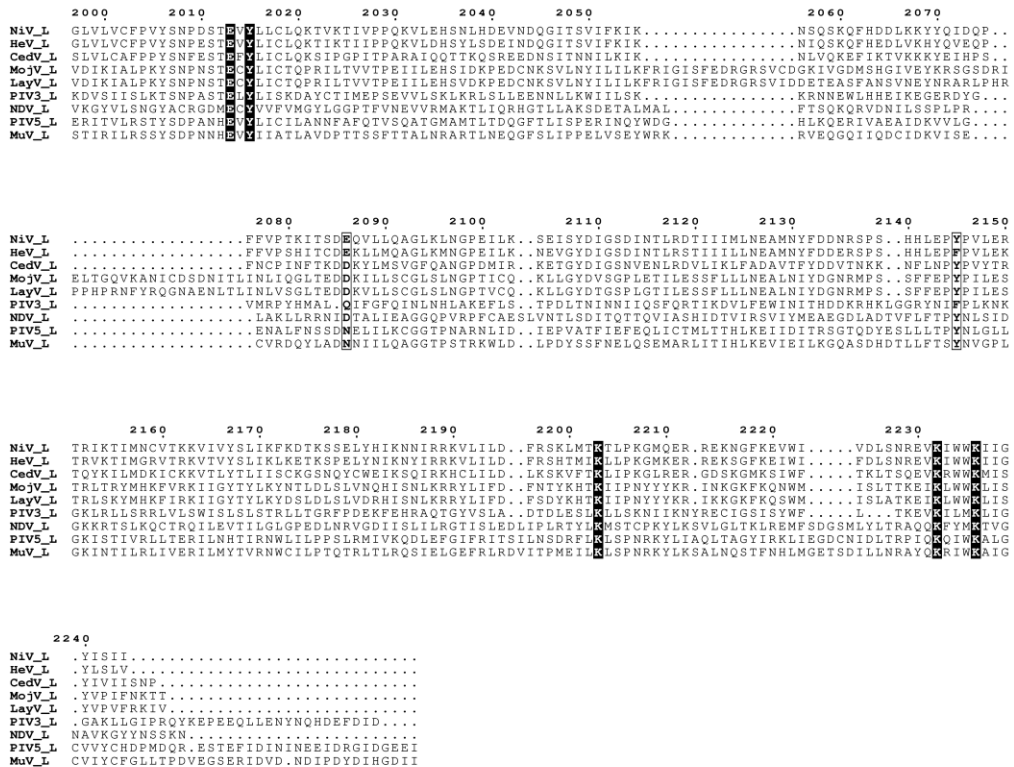
Niv\_L GIICKQLRIRQ.VT.EVIDTTMLRD.NII.VENPPIKTGVLDIRGCIINYLEEILSMNTKASAKKIFNLNSRPSVE.....NHK  
HeV\_L GIICKQLRIRQ.VT.EVIDTTMLRD.NII.VENPPIKTGVLDIRGCIINYLEEILSMNTKASAKKIFNLNSRPSVE.....NHK  
CedV\_L GIICKQLRIRQ.SN.EPFDLEDIRIQDNP.D.FVNKPIEFCSSEF.GITTYNLEEILSQSNVHLSVNMNIDSTSNNTE.....NHL  
MoJV\_L GVIKQLRIRQDIG.EMFDIEMDRKYHKF..MVETAINYKFRS..SCTVNLNIDIRPLNSTLYIDLEDSVFPVNGW.....ACTV.....SHK  
LayV\_L GVIKQLRIRQDIG.EMFDIEMDRKYHKF..MVETAINYKFRS..SCTVNLNIDIRPLNSTLYIDLEDSVFPVNGW.....ACTV.....SHK  
PIV3\_L TAIKYLIRGISPPVEIDDWPIEDENMLDNVKTINDONCKNKGKINNFVGLAKLYQVLRKIRITSDDNDRLDASTGLTLPQGGNYLSHQ  
NDV\_L KSLNLIREREDRDSILALMFPQEPLEFPLVQD..IGARVKDOLTMKPAALHELDLSAPARYDAYTLEQARSDCALAMDGEDL.....VRYL  
PIV5\_L KLLNSIRTESGQAVTSYYESLEYDSLKLTPLHVPGTSCIEDDSLCTNDYIWIIESNANLEKYIPNSPEDDSNFHFKLNP.....SHHT  
Miv\_L KLLNLRDESSEGGFLIASYNSFGYLEPILMESKIFNLSSSEASLTFDFPILNLELSDASLEKYSPLSLLMATAENMNDPFPQP.....LHHV

1810 1820 1830 1840 1850 1860 1870 1880 1890

Niv\_L YRRIGDINSSSCYKALNLSPLIQRYLPSGAQRFLVGGGSGMMLLYQSTLGGQISFVNSGIDGDYIPGQRELKLPSE.....YSIAEEDDPSQSDKGL  
HeV\_L YRRIGDINSSSCYKALNLSPLIQRYLPSGAQRFLVGGGSGMMLLYQSTLGGQISFVNSGIDGDYIPGQRELKLPSE.....YSIAEEDDPSQSDKGL  
CedV\_L FRRVIGDINSSTYKALSPLTPVIRYHQNTNRDLFVGGGSGMMLLYQSTLGGQISFVNSGIDGDYIPGQRELKLPSE.....YSIAEEDDPSQSDKGL  
MoJV\_L YRRIGDINSSTYKALSPLTPVIRYHQNTNRDLFVGGGSGMMLLYQSTLGGQISFVNSGIDGDYIPGQRELKLPSE.....YSIAEEDDPSQSDKGL  
LayV\_L YRRIGDINSSTYKALSPLTPVIRYHQNTNRDLFVGGGSGMMLLYQSTLGGQISFVNSGIDGDYIPGQRELKLPSE.....YSIAEEDDPSQSDKGL  
PIV3\_L LRIFGINSSTYKALSPLTPVIRYHQNTNRDLFVGGGSGMMLLYQSTLGGQISFVNSGIDGDYIPGQRELKLPSE.....YSIAEEDDPSQSDKGL  
NDV\_L FRRVIGDINSSTYKALSPLTPVIRYHQNTNRDLFVGGGSGMMLLYQSTLGGQISFVNSGIDGDYIPGQRELKLPSE.....YSIAEEDDPSQSDKGL  
PIV5\_L LRIFGINSSTYKALSPLTPVIRYHQNTNRDLFVGGGSGMMLLYQSTLGGQISFVNSGIDGDYIPGQRELKLPSE.....YSIAEEDDPSQSDKGL  
Miv\_L LRIFGINSSTYKALSPLTPVIRYHQNTNRDLFVGGGSGMMLLYQSTLGGQISFVNSGIDGDYIPGQRELKLPSE.....YSIAEEDDPSQSDKGL

1900 1910 1920 1930 1940 1950 1960 1970 1980 1990

Niv\_L KGLVVPENGRPETTWIGNLDSYEIINRTAGRSIGLWHSQMGSGIDKNVEEILVEHSHLSIAINVMMDGLLVSIAIYTFGFPISRLFNMYRSYF  
HeV\_L KGLVVPENGRPETTWIGNLDSYEIINRTAGRSIGLWHSQMGSGIDKNVEEILVEHSHLSIAINVMMDGLLVSIAIYTFGFPISRLFNMYRSYF  
CedV\_L TGHVTPENGRPETTWIGNDSDSKYIIEHTINRDIQLWHSQMGSGIDKNVEEILVEHSHLSIAINVMMDGLLVSIAIYTFGFPISRLFNMYRSYF  
MoJV\_L LOSIIPENGRPETTWIGNMDCFIIMRMKSHSLGLWHSQMGSGIDKNVEEILVEHSHLSIAINVMMDGLLVSIAIYTFGFPISRLFNMYRSYF  
LayV\_L LKSIIVPENGRPETTWIGNMDCFIIMRMKSHSLGLWHSQMGSGIDKNVEEILVEHSHLSIAINVMMDGLLVSIAIYTFGFPISRLFNMYRSYF  
PIV3\_L LNRVVPENGNPNSTWIGNMECESIIVSELNDSIGLWHSQMGSGIDKNVEEILVEHSHLSIAINVMMDGLLVSIAIYTFGFPISRLFNMYRSYF  
NDV\_L VQEFRTWRENTESDLSKAVGIVTSVVPYRSVSLWHSQMGSGIDKNVEEILVEHSHLSIAINVMMDGLLVSIAIYTFGFPISRLFNMYRSYF  
PIV5\_L FDFPFTWNGNAAMTDIGMTACVEIINRVGPRCTSLWHSQMGSGIDKNVEEILVEHSHLSIAINVMMDGLLVSIAIYTFGFPISRLFNMYRSYF  
Miv\_L VQEFRTWRENTESDLSKAVGIVTSVVPYRSVSLWHSQMGSGIDKNVEEILVEHSHLSIAINVMMDGLLVSIAIYTFGFPISRLFNMYRSYF



**Figure S18 | Multiple sequence alignment of the L proteins from different paramyxovirus.**

Residues in the NiV L protein interacting with the P proteins were identified. These residues and their equivalent residues in L proteins of the other paramyxoviruses are highlighted in the brown boxes. The NiV L sequences involved in interfaces 1, 2, 3, 4, 5 and 6 are indicated by red, orange, yellow, green, blue and purple overlines. Highly conserved amino acid residues are shaded black. L protein sequences used are NiV (Nipah virus), HeV (Hendra virus), CedV (Cedar virus), MojV

(Mojiang virus), LayV (Langya virus), PIV3 (Parainfluenza virus type 3), NDV (Newcastle disease virus), PIV5 (Parainfluenza virus 5), MuV (Mumps virus), EBOV (Ebola virus), RSV (Respiratory syncytial virus), HMPV (Human metapneumovirus), VSV (Vesicular stomatitis virus) and RABV (Rabies virus).

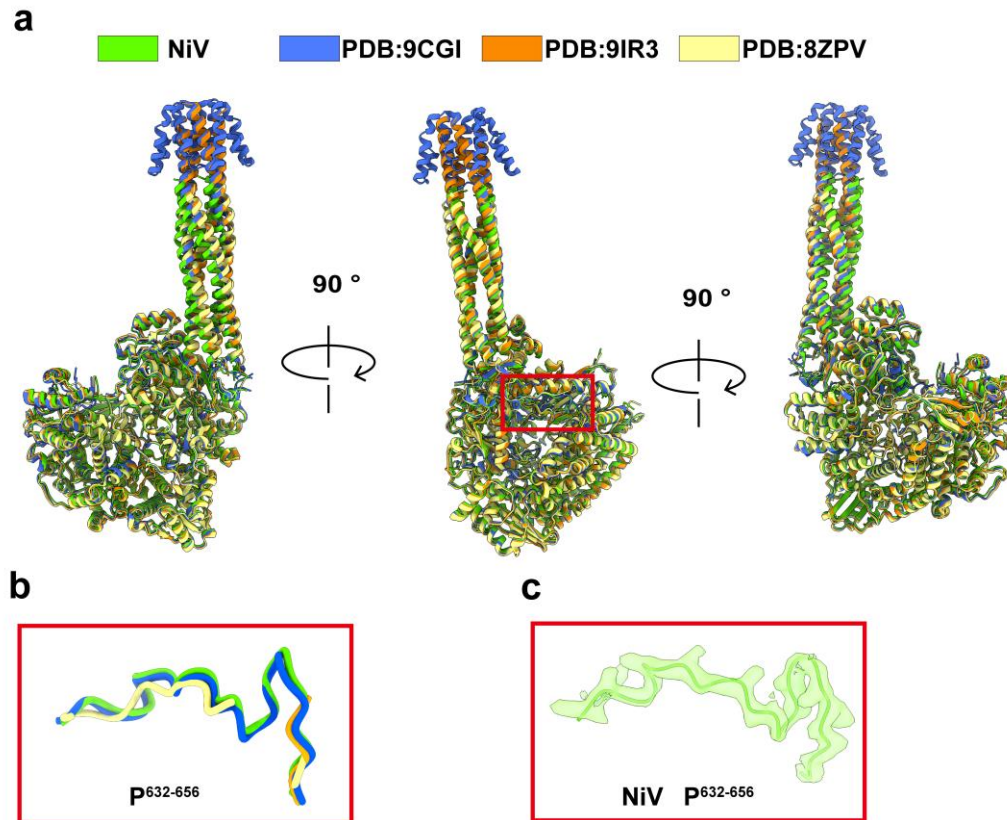
NiV_P1	MDKLELVNDGLNIIDFIQKNQKEIQKTYGRSSIQQPSIKDQTKAWEDFLQCTSGESEQVE	60
NDV_P1	-----	0
NiV_P1	GGMSKDDGDVERRNLEDLSSTSPTDGTIGKRVSNTRDWAEGSDDIQLDPVVTDVVYHDHG	120
NDV_P1	-----	0
NiV_P1	GECTGYGFTSSPERGWSDYTSGANNNGNVLVSDAKMLSYAPEIAVSKEDRETDLVHLENK	180
NDV_P1	-----	0
NiV_P1	LSTTGLNPTAVPFTLRNLSDPKADSPVIAEHYYGLGVKEQNVGFPQTSRNVNLDLSIKLYTS	240
NDV_P1	-----MATF--	4
	: :	
NiV_P1	DDEEADQLEFEDEFAGSSSEVIVGISPEDEEPPSSVGGKPNESIGRTIEGQSIRDNLQ---	297
NDV_P1	TDAE-----IDELFE-TSGTVIDSII-----TAQGKPVETVGRSAIPQGKTKALS LAW	51
	* * : : * : * . * * . * : . * * * * : * * : * . . * .	
NiV_P1	-----AKDNKSTDVPGAGPKDSAVKEE-PPQKRLPMLAEEF	332
NDV_P1	EKHGNTNTPAAQESAGEQDQHGQNGQASNSNRATPEEGPHSSQAQAATQPQEDAN--ESQ	108
	. * . . . * * * . * . : : * * : * .	
NiV_P1	ECSGSEDPIIRELLK-ENSLINCQQGKDAQPPYHWSIERSISDPKTEIVNGAVQTADRQR	391
NDV_P1	LKTGASSLLSMLDKLSNKNKSGPPQPPQ-ALHSGKSPAVEQTQHGANQGRAQQE	167
	* : * . . : : * * * . * . : : * * : : * * * : : * * * : * .	
NiV_P1	PGTTPMKSRGPIKKGTDKAKYPSAGTENVPKSGKSGATHRVGRSPPYQEGKSVNAENVQLN	451
NDV_P1	TGHQAAPSPGPP-GTGVNIAFPG--QRGVSPQSVGATQP-----APQSGQNQG-----	212
	* * * * . * : : * . . * . * * * : * * : . .	
NiV_L	ASTAVKETDKSEVNPVDDNDSLDDKYIMPSDDFSNTFFPHDTRDLNYHADHLGDYDLETL	511
NDV_L	-----STP-----ASADHVQPPVDFVQAMMSMM-----	235
	. * . . : : * * : : :	
NiV_P1	CEESVLMGVINSIKLINLDMRLNHIEEQVKEIPKIINKLESIDRVLAKTNTALSTIEGHL	571
NDV_P1	-----E-AISQRVSKIDYQLDLVLKQTSSIPTMRSEIQQLK-----TSVAVMEANL	280
	* : : : * * : : * . . * * . : : : : . * : : : : *	
NiV_P1	VSMIMIPGKGGKERK-----GKNNPCLKPVIGRDI---LEQQSLFSFD	612
NDV_P1	GMMKILDPCCANVSSLSDLRAVAKSHPVLIAGP GDPSFYVTQGGELALNKLSQFVPHPSD	340
	* * : * * : . . * . : * . * * : * * . * .	
NiV_P1	NVKNFRDGLTNEPYGAAVQLREDLILPELNEEETNASQFVPMADDSSRDVIKTLIRTHI	672
NDV_P1	LIKHATSG-----G-----EDIGIE-----RDTVRAILLSRE	367
	: * : . * * * : : * * : : * * : : * * : : *	
NiV_P1	KDRELRSSELIGYLNKAENDEEIQEIANTVNDI IDGNI	709
NDV_P1	MHPSSSSKLLSKLDSAGSVVEIRKIKR--LALNG--	399
	. . * * . * : * . * * * : * . : * : *	

NiV_P2	MDKLELVNDGLNIIDFIQKNQKEIQKTYGRSSIQQPSIKDQTKAWEDFLQCTSGESEQVE	60
NDV_P2	-----	0
NiV_P2	GGMSKDDGDVERRNLEDLSSTSPTDGTIGKRVSNTRDWAEGSDDIQLDPVVTDVVYHDHG	120
NDV_P2	-----	0
NiV_P2	GECTGYGFTSSPERGWSDYTSGANNNGNVLVSDAKMLSYAPEIAVSKEDRETDLVHLENK	180
NDV_P2	-----	0
NiV_P2	LSTTGLNPTAVPFTLRNLSDPKADSPVIAEHYYGLGVKEQNVGPQTSRNVNLDSEIKLYTS	240
NDV_P2	-----MATF--	4
	: :	
NiV_P2	DDEEADQLEFEDEFAGSSSEVIVGISPEDEEPPSSVGGKPNESIGRTIEGQSIRDNLQ---	297
NDV_P2	TDAE-----IDELFE-TSGTVIDSII-----TAQGKPVETVGRSAIPQGKTKALS LAW	51
	* * : : * : * . * * . * : . * * * * : * : * * : * . . * .	
NiV_P2	-----AKDNKSTDVPGAGPKDSAVKEE-PPQKRLPMLAEFF	332
NDV_P2	EKHGNTNTPAAQESAGEQDQHGQNGQASNSNRATPEEGPHSSQAQAATQPQEDAN--ESQ	108
	. * . . . * * * . * . : : * * : * .	
NiV_P2	ECSGSEDPIIRELLK-ENSLINCQQGKDAQPPYHWSIERSISDPKTEIVNGAVQTADRQR	391
NDV_P2	LKTGASSLLSMLDKLSNKKSSNAKGPQPPQ-ALHSGKSPAVEQTQHGANQGRAQQE	167
	* : * . . : : * * * . * . * : * * : : . . * * : : * * * * : *	
NiV_P2	PGTTPMKSRGPIPKKGTDAKYP SAGTENVP GSKSGATHRVGRSPPYQEGKSVNAENVQLN	451
NDV_P2	TGHQAAPSPGPP-GTGVNIAFPG--QRGVSPQSVGATQP-----APQSGQNQG-----	212
	* * * * . * : : * . . * . . * * * : * * : * . .	
NiV_P2	ASTAVKETDKSEVNPVDDNDSLDDKYIMP SDDF SNTFFPHDTDRLN YHADHLGDYDLETL	511
NDV_P2	-----STP-----ASADHVQPPVDFVQAMMSMM-----	235
	. * . . : : * * * : : :	
NiV_P2	CEESVLMGVINSIKLINLDMRLNHIEEQVKEIPKIINKLESIDRVLAKTNTALSTIEGHL	571
NDV_P2	-----E-AISQRVSKIDYQLDLVLKQTS S IPTMRSEIQQLK-----TSVAVMEANL	280
	* : : : * * : : * * . * * . : : : : * * : : : * * : * * : *	
NiV_P2	VSMIMI PGKGGKERK-----GKNNPELKPVI GRDI-----LEQQSLFSFD	612
NDV_P2	GMMKI LDPGCANVSS LSDLRAVA KSHFVLIAGPGDPSPYVTQGGEIALNKLSQVPHPSPD	340
	* * : * * . : . * . : * . . * * : * * * * . * . * .	
NiV_P2	NVKNFRDGLTNEPYGAAVQLREDLILPELNFEETNASQFVPMADDSSRDVIKTLIRTHI	672
NDV_P2	LIKHATSG-----G-----PDIGIE-----RDTVRALILSRP	367
	: * : . * * * * : : * * : : * * : : * * : : * * : :	
NiV_P2	KDREL RSELIGYLNKAENDEEIQEIAN TVNDI DGNI	709
NDV_P2	MHPSSSKLLSKLDSAGSV E EIRKIKR--LALNG--	399
	. . * * . * : * * . * * : * * . : * * : * *	

NiV_P3	MDKLELVNDGLNIIDFIQKNQKEIQKTYGRSSIQQPSIKDQTKAWEDFLQCTSGESEQVE	60
NDV_P3	-----	0
NiV_P3	GGMSKDDGDVERRNLEDLSSTSPTDGTIGKRVSNTRDWAEGSDDIQLDPVVTDVVYHDHG	120
NDV_P3	-----	0
NiV_P3	GECTGYGFTSSPERGWSDYTSGANNNGNVLVSDAKMLSYAPEIAVSKEDRETDLVHLENK	180
NDV_P3	-----	0
NiV_P3	LSTTGLNPTAVPFTLRNLSDPKADSPVIAEHYYGLGVKEQNVGFPQTSRNVNLDLSIKLYTS	240
NDV_P3	-----MATF--	4
	: :	
NiV_P3	DDEEADQLEFEDEFAGSSSEVIVGISPEDEEPPSSVGGKPNESIGRTIEGQSIRDNLQ---	297
NDV_P3	TDAE-----IDELFE-TSGTVIDSII-----TAQGKPVETVGRSAIPQGKTKALS LAW	51
	* * : : * : * . * * . * : . * * * * : * * : * . . * .	
NiV_P3	-----AKDNKSTDVPGAGPKDSAVKEE-PPQKRLPMLAEFF	332
NDV_P3	EKHGNTNTPAAQESAGEQDQHGQNGQASNSNRATPEEGPHSSQAQAATQPQEDAN--ESQ	108
	. * . . . * * * . * . : : * * : * .	
NiV_P3	ECSGSEDPIIRELLK-ENSLINCQQGKDAQPPYHWSIERSISDPKTEIVNGAVQTADRQR	391
NDV_P3	LKTGASSLLSMLDKLSNKNKSGPPQPPQ-ALHSGKSPAVEQTQHGANQGRAQQE	167
	* : * . . : : * * * . * . : : * * : : * * * : : * * * * : *	
NiV_P3	PGTPMPKSRGPIKKGTDKYPKPSAGTENVPKSGKSGATHRVGRSPPYQEGKSVNAENVQLN	451
NDV_P3	TGHQAAPSPGPP-GTGVNIAFPG--QRGVSPQSVGATQP-----APQSGQNQG-----	212
	* * * * . * : : * . . * . . * * * : * * : * . .	
NiV_P3	ASTAVKETDKSEVNPVDDNDSLDDKYIMPDDFSNTFFPHDTDRLNHYHADHLGDYDLETL	511
NDV_P3	-----STP-----ASADHVQPPVDFVQAMMSM-----	235
	. * . . : : * * * : : :	
NiV_P3	CEESVLMGVINSIKLINLDMRLNHIEEQVKEIPKIINKLESIDRVLAKTNTALSTIEGHL	571
NDV_P3	-----E-AISQRVSKIDYQLDLVLKQTSSIPTMRSEIQQLK-----TSVAVMEANL	280
	* : : * * : : * * . . * . . : : * * . . : : * * : * * : *	
NiV_P3	VSMIMIPGKKGGERK-----GKNNPEIKPVIGRDI---LEQQSLFSFD	612
NDV_P3	GMMKILDEGCANVSSLSDLRAVAKSHPVLIAGPGDPSPYVTQGGGEIALNKLSQVPHPSD	340
	* * : * * . : . * . : * . . * * * * * . * . *	
NiV_P3	NVKNFRDGLTNEPYGAAVQLREDLILPELNFEETNASQFVPMADDSSRDVIKTLIRTHI	672
NDV_P3	LIKHATSG-----G-----PDIGIE-----RDTVRALILSRP	367
	* : . * * * * : : * * * : * * : : *	
NiV_P3	KDRELRSSELIGYLNKAENDEEIQEIANTVNDIIDGNI	709
NDV_P3	MHPSSSSKLLSKLDSAGSVVEEIRKIKR---LALNG--	399
	. . * * . * : * . * * * : * . : *	

NiV_P4	MDKLELVNDGLNIIDFIQKNQKEIQKTYGRSSIQQPSIKDQTKAWEDFLQCTSGESEQVE	60
NDV_P4	-----	0
NiV_P4	GGMSKDDGDVERRNLEDLSSTSPDTGTIGKRVSNTRDWAEGSDDIQLDPVVTDVVYHDHG	120
NDV_P4	-----	0
NiV_P4	GECTGYGFTSSPERGWSDYTSGANNNGNVLVSDAKMLSYAPEIAVSKEDRETDLVHLENK	180
NDV_P4	-----	0
NiV_P4	LSTTGLNPTAVPFTLRNLSDPKADSPVIAEHYYGLGVKEQNVGFPQTSRNVNLDLSIKLYTS	240
NDV_P4	-----MATF--	4
	: :	
NiV_P4	DDEEADQLEFEDEFAGSSSEVIVGISPEDEEPPSSVGGKPNESIGRTIEGQSIRDNLQ---	297
NDV_P4	TDAE-----IDELFE-TSGTVIDSII-----TAQGKPVETVGRSAIPQGKTKALSLAW	51
	* * : : * : * . * * . * : . * * * * : * : * * : * . . * .	
NiV_P4	-----AKDNKSTDVPGAGPKDSAVKEE-PPQKRLPMLAEFF	332
NDV_P4	EKHGNTNTPAAQESAGEQDQHGQNGQASNSNRATPEEGPHSSQAQAATQPQEDAN---ESQ	108
	. * . . . * * * . * . : : * * : * .	
NiV_P4	ECSGSEDPIIRELLK-ENSLINCQQGKDAQPPYHWSIERSISPKDTEIVNGAVQTADRQR	391
NDV_P4	LKTGASSLLSMLDKLSNKNKSNKGGPPQPPQ-ALHSGKSPAVEQTQHGANQGRAQQE	167
	: * . . . : * * * . * . : : * * : * * : : * * * : : * * * * : *	
NiV_P4	PGTTPMPKSRGIPKKGTDKYPKPSAGTENVPKSGKSGATHRVGRSPPYQEGKSVNAENVQLN	451
NDV_P4	TGHQAAPSPGPP-GTGVNIAFPG--QRGVSPQSVGATQP-----APQSGQNQG-----	212
	* * * * . * : : * . . * . * * * : * * : * . .	
NiV_P4	ASTAVKETDKSEVNPVDDNDSLDDKYIMPDDFSNTFFPHDTDRLNHYHADHLGDYDLETL	511
NDV_P4	-----STP-----ASADHVQPPVDFVQAMMSMM-----	235
	. * . . : : * * : : :	
NiV_P4	CEESVLMGVINSIKLINLDMRLNHIEEQVKEIPKIINKLESIDRVLAKTNTALSTIEGHI	571
NDV_P4	-----E-AISQRVSKIDYQLDLVLKQTSSIPTMRSEIQQLK-----TSVAVMEANI	280
	* : : * * : * : : * * . . * . : : : : * * : * : * : *	
NiV_P4	VSMIMIPGKCKGERK-----GKNNPELKPVIGRDI---LEQQSLFSFD	612
NDV_P4	GMMKILDPGCANVSSLSLRAVAKSHPVLIAGPGDPSPYVTQGGEIALNKLSPVPHPSD	340
	* * : * * . : . * . : * . * * * * * * . * . *	
NiV_P4	NVKNFRDGLTNEPYGAAVQLREDLILPELNFEETNASQFVPMADDSSRDVIKTLIRTHI	672
NDV_P4	LIKHATSG-----G-----PDIGIE-----RDTVRALILSRP	367
	: * : . * * * * : : : * * : : * * : : * * : : *	
NiV_P4	KDRELRSSELIGYLNKAENDEEIQEIANTVNDIIDGNI	709
NDV_P4	MHPSSSSKLLSKLDSAGSVVEEIRKIKR---LALNG--	399
	. . * * . * : * . * * * : * . : * : *	

**Figure S19 | Hydrophobic residues in P1 (yellow), P2 (cyan), P3 (magenta) and P4 (blue) monomers contacting the L proteins are compared between NiV and NDV.**



**Figure S20 | A comparison of the reported NiV L-P complex structures.**

**a.** Three different views of our NiV L<sub>1-1451</sub>-P complex structure superposed onto the released NiV L-P complex structures (9CGI, 9IR3 and 8ZPV). **b.** Close-up view of the modelled structures for the residues P<sup>632-656</sup>. **c.** The cryo-EM density for the residues P<sup>632-656</sup> in the NiV L<sub>1-1451</sub>-P complex structure.

**Supplementary Table 1. Cryo-EM data collection, refinement and validation statistics.**

	NiV L <sub>1-1451</sub> -P complex	NiV L-P complex
<b>Data collection and processing</b>		
Magnification	165000	165000
Voltage (kV)	300	300
Electron exposure (e <sup>-</sup> /Å <sup>2</sup> )	50	50
Defocus range (µm )	0.6-2.4	0.6-2.4
Pixel size (Å)	0.73	0.73
Movies (no.)	16735	10073
Initial particle images (no.)	4390986	7475406
Symmetry imposed	<i>C1</i>	<i>C1</i>
Final particle images (no.)	674945	224424
Map resolution (Å)	2.31	2.52
FSC threshold	0.143	0.143
Map resolution range (Å)	2.30-37.23	2.15-38.17
<b>Refinement</b>		
Initial model used	PDB 6EB8	PDB 9IV9
Model resolution (Å)	2.56	2.87
FSC threshold	0.5	0.5
Map sharpening <i>B</i> factor (Å <sup>2</sup> )	-88	-89
Model composition		
Non-hydrogen atoms	13048	12944
Protein residues	1624	1611
Ligands	2	2
<i>B</i> factors (Å <sup>2</sup> )		
Protein	104.83	101.08
Ligand	146.19	124.50
R.m.s. deviations		
Bond lengths (Å)	0.004	0.004
Bond angles (°)	0.798	0.669
<b>Validation</b>		
MolProbity score	1.34	1.34
Clash score	3.69	3.45
Poor rotamers (%)	0	0
Ramachandran plot		
Favored (%)	96.94	96.73
Allowed (%)	3.06	3.27
Disallowed (%)	0	0

**Supplementary Table 2. Interactions between L and P proteins.**

Interface	Molecule	Sites	L	Interaction Pattern		
Interface1	P1	I576 <sup>P1</sup> I578 <sup>P1</sup> L608 <sup>P1</sup> L633 <sup>P1</sup> L637 <sup>P1</sup> I638 <sup>P1</sup>	V386 <sup>L</sup>	Hydrophobic interactions		
		R634 <sup>P1</sup>	D384 <sup>L</sup>	long-range electrostatic interaction		
	P4	R600 <sup>P1</sup>	E733 <sup>L</sup> E760 <sup>L</sup>	salt bridges		
		M575 <sup>P4</sup> M577 <sup>P4</sup> P579 <sup>P4</sup>	V386 <sup>L</sup>	Hydrophobic interactions		
Interface2	P1	L639 <sup>P1#</sup>	R871 <sup>L</sup>	hydrogen bond		
		P640 <sup>P1#</sup>	R867 <sup>L</sup>	hydrogen bond		
		Q651 <sup>P1</sup>	Q860 <sup>L</sup>	hydrogen bond		
		L642 <sup>P1</sup> F644 <sup>P1</sup>	L861 <sup>L</sup> F863 <sup>L</sup> A879 <sup>L</sup> I884 <sup>L</sup>	Hydrophobic interactions		
Interface3	P1	D658 <sup>P1#</sup> D662 <sup>P1</sup>	H320 <sup>L</sup>	hydrogen bond salt bridge		
		S660 <sup>P1</sup>	H313 <sup>L</sup>	hydrogen bond		
		K665 <sup>P1</sup> R669 <sup>P1</sup>	D339 <sup>L</sup>	salt bridges		
		T670 <sup>P1</sup> H671 <sup>P1</sup>	N346 <sup>L</sup> L300 <sup>L#</sup>	hydrogen bond hydrogen bond		
		N702 <sup>P1</sup> D706 <sup>P1</sup>	R308 <sup>L</sup>	hydrogen bond salt bridge		
		D706 <sup>P1</sup> D703 <sup>P1</sup>	R305 <sup>L</sup>	salt bridges		
		F652 <sup>P1</sup> V663 <sup>P1</sup> L667 <sup>P1</sup>	L300 <sup>L</sup> G309 <sup>L</sup> L312 <sup>L</sup> I316 <sup>L</sup>	Hydrophobic interactions		
		interface4	P3	S565 <sup>P3</sup>	H423 <sup>L</sup>	hydrogen bond
				H570 <sup>P3</sup>	Y389 <sup>L</sup> E448 <sup>L</sup>	hydrogen bond salt bridge
				I576 <sup>P3</sup> M577 <sup>P3</sup> P579 <sup>P3</sup>	L387 <sup>L</sup> I392 <sup>L</sup> M393 <sup>L</sup> Y732 <sup>L</sup> A736 <sup>L</sup> I737 <sup>L</sup>	Hydrophobic interactions
Interface5	P3	K583 <sup>P3</sup>	E740 <sup>L</sup> E744 <sup>L</sup>	salt bridges		
		E585 <sup>P3#</sup> K587 <sup>P3</sup>	Q454 <sup>L</sup> Y419 <sup>L</sup>	hydrogen bond cation- $\pi$ interaction		
		K589 <sup>P3#</sup>	D456 <sup>L</sup>	salt bridge		
		N591 <sup>P3</sup>	M459 <sup>L#</sup> Y746 <sup>L#</sup>	hydrogen bonds		

		E593 <sup>P3</sup>	L461 <sup>L#</sup> Y518 <sup>L</sup>	hydrogen bonds
		L594 <sup>P3</sup>	L461 <sup>L</sup> L463 <sup>L</sup> Y518 <sup>L</sup> L521 <sup>L</sup> L525 <sup>L</sup> I566 <sup>L</sup> L570 <sup>L</sup> L748 <sup>L</sup> F751 <sup>L</sup> F752 <sup>L</sup>	Hydrophobic interactions
		G580 <sup>P4#</sup>	D384 <sup>L</sup>	hydrogen bond
		G582 <sup>P4#</sup>	K795 <sup>L</sup>	hydrogen bond
		K583 <sup>P4</sup>	Y793 <sup>L</sup>	cation- $\pi$ interaction
Interface6	P4	V572 <sup>P4</sup> M574 <sup>P4</sup> I576 <sup>P4</sup> I578 <sup>P4</sup>	L387 <sup>L</sup> Y389 <sup>L</sup> A390 <sup>L</sup> I392 <sup>L</sup> M393 <sup>L</sup> W447 <sup>L</sup>	Hydrophobic interactions

The "#" symbol indicates the formation of hydrogen bonds with nitrogen or oxygen in the main chain.