SUPPLEMENTARY INFORMATION

Structural dissection of human metapneumovirus phosphoprotein using small angle x-ray scattering

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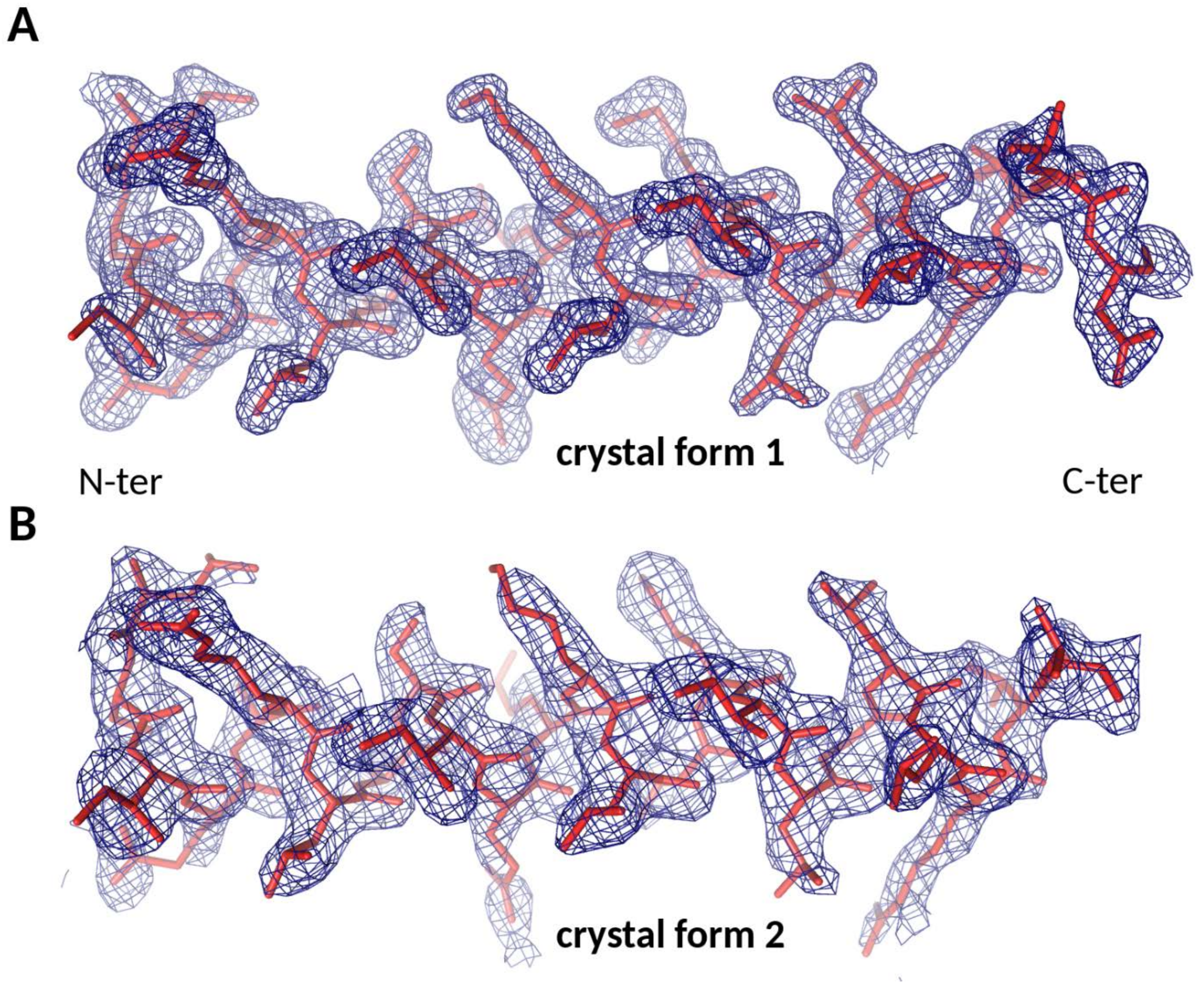
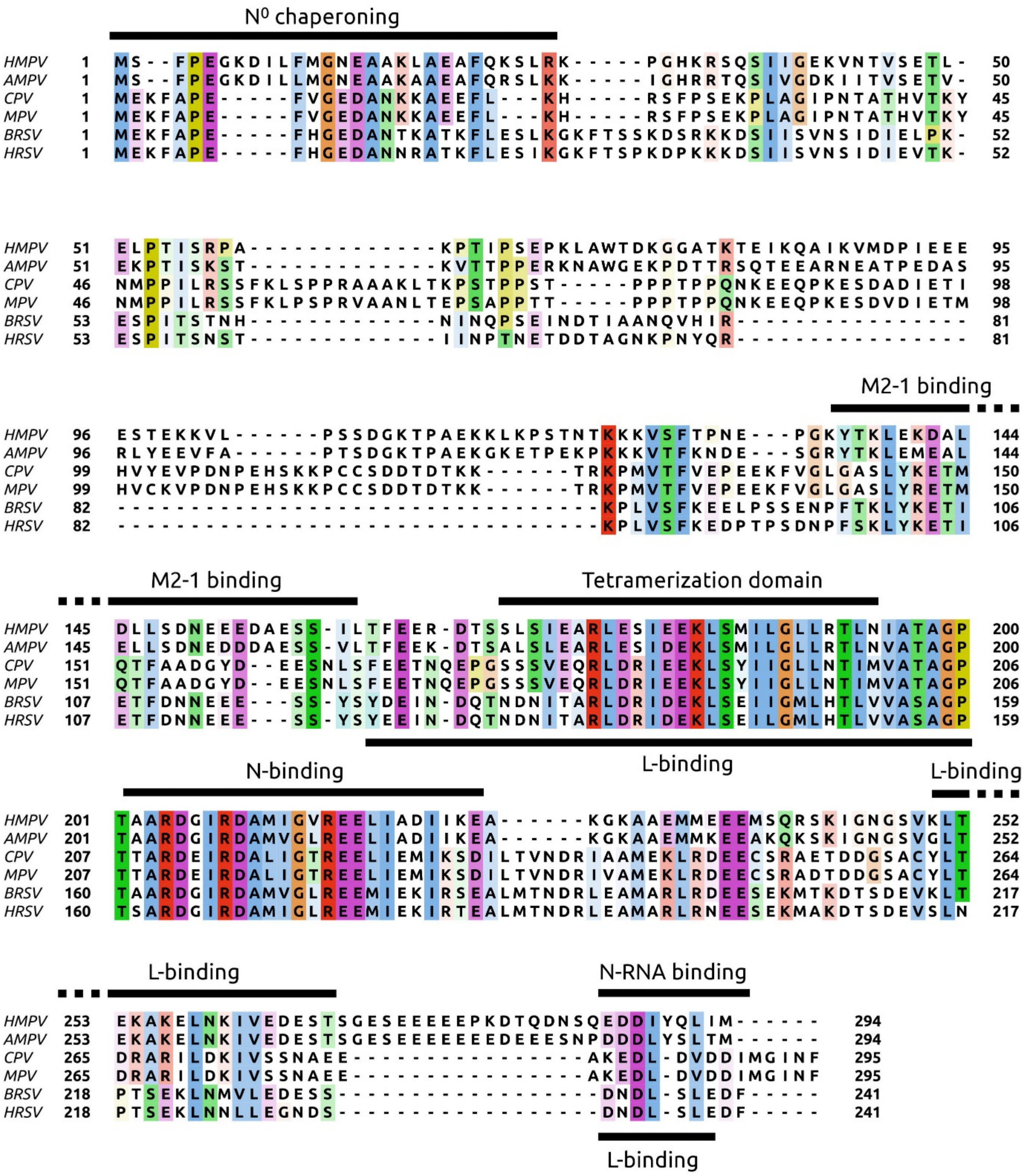


Figure S1: Electron density maps of P_{core} crytals. A, B. Sample 2Fo-Fc maps contoured at 1.0 σ for one helix each of the 4-helix bundles in the new crystal forms of P_{core}. N- and C-termini are labelled. The fitted models are shown in red in stick representation.



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HMPV   1  MS--FPEGKDILFMGNEAAKLAEAFQKSLRK-----PGHKRSQSIIGEKVNTVSETL-  50
AMPV   1  MS--FPEGKDILLMGNEAAKAAEAFQRSLKK-----IGHRRTQSIVGDKIITVSETV-  50
CPV    1  MEKFAPE-----FVGEDANKKAEEFL---KH-----RSFPSEKPLAGIPNTATHVTKY  45
MPV    1  MEKFAPE-----FVGEDANKKAEEFL---KH-----RSFPSEKPLAGIPNTATHVTKY  45
BRSV   1  MEKFAPE-----FHGEDANTKATKFLESLKGKFTSSKDSRKKDSIISVNSIDIELPK-  52
HRSV   1  MEKFAPE-----FHGEDANNRATKFLESIKGKFTSPKDPKKKDSIISVNSIDIEVTK-  52

HMPV  51  ELPTISRPA-------------KPTIPSEPKLAWTDKGGATKTEIKQAIKVMDPIEEE  95
AMPV  51  EKPTISKST-------------KVTTPPERKNAWGEKPDTTRSQTEEARNEATPEDAS  95
CPV   46  NMPPILRSSFKLSPPRAAAKLTKPSTPPST-----PPPTPPQNKEEQPKESDADIETI  98
MPV   46  NMPPILRSSFKLPSPRVAANLTEPSAPPTT-----PPPTPPQNKEEQPKESDVDIETM  98
BRSV  53  ESPITSTNH-------------NINQPSEINDTIAANQVHIR----------------  81
HRSV  53  ESPITSNST-------------IINPTNETDDTAGNKPNYQR----------------  81

HMPV  96  ESTEKKVL------PSSDGKTPAEKKLKPSTNTKKKVSFTPNE---PGKYTKLEKDAL 144
AMPV  96  RLYEEVFA------PTSDGKTPAEKGKETPEKPKKKVTFKNDE---SGRYTKLEMEAL 144
CPV   99  HVYEVPDNPEHSKKPCCSDDTDTKK------TRKPMVTFVEPEEKFVGLGASLYKETM 150
MPV   99  HVCKVPDNPEHSKKPCCSDDTDTKK------TRKPMVTFVEPEEKFVGLGASLYRETM 150
BRSV  82  ---------------------------------KPLVSFKEELPSSENPFTKLYKETI 106
HRSV  82  ---------------------------------KPLVSFKEDPTPSDNPFSKLYKETI 106

HMPV 145  DLLSDNEEEDAESS-ILTFEER-DTSSLSIEARLESIEEKLSMILGLLRTLNIATAGP 200
AMPV 145  ELLSDNEDDDAESS-VLTFEEK-DTSALSLEARLESIDEKLSMILGLLRTLNVATAGP 200
CPV  151  QTFAADGYD--EESNLSFEETNQEPGSSSVEQRLDRIEEKLSYIIGLLNTIMVATAGP 206
MPV  151  QTFAADGYD--EESNLSFEETNQEPGSSSVEQRLDRIEEKLSYIIGLLNTIMVATAGP 206
BRSV 107  ETFDNNEEE---SS-YSYDEIN-DQTNDNITARLDRIDEKLSEIIGMLHTLVVASAGP 159
HRSV 107  ETFDNNEEE---SS-YSYEEIN-DQTNDNITARLDRIDEKLSEILGMLHTLVVASAGP 159

HMPV 201  TAARDGIRDAMIGVREELIADIIKEA------KGKAAEMMEEEMSQRSKIGNGSVKLT 252
AMPV 201  TAARDGIRDAMVGLREELIADIIKEA------KGKAAEMMKEEAKQKSKIGNGSVGLT 252
CPV  207  TTARDEIRDALIGTREELIEMIKSDILTVNDRIAAMEKLRDEECSRAETDDGSACYLT 264
MPV  207  TTARDEIRDALIGTREELIEMIKSDILTVNDRIVAMEKLRDEECSRADTDDGSACYLT 264
BRSV 160  TAARDGIRDAMVGLREEMIEKIRSEALMTNDRLEAMARLRDEESEKMTKDTSDEVKLT 217
HRSV 160  TSARDGIRDAMIGLREEMIEKIRTEALMTNDRLEAMARLRNEESEKMAKDTSDEVSLN 217

HMPV 253  EKAKELNKIVEDESTSGESEEEEEPKDTQDNSQEDDIYQLIM------ 294
AMPV 253  EKAKELNKIVEDESTSGESEEEEEEEDEEESNPDDDLYSLTM------ 294
CPV  265  DRARILDKIVSSNAEE----------------AKEDL-DVDDIMGINF 295
MPV  265  DRARILDKIVSSNAEE----------------AKEDL-DVDDIMGINF 295
BRSV 218  PTSEKLNMVLEDESS------------------DNDL-SLEDF----- 241
HRSV 218  PTSEKLNNLLEGNDS------------------DNDL-SLEDF----- 241
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Figure S2: Sequence alignment of *Pneumoviridae* P proteins with approximate and putative annotation of functional regions. The multiple sequence alignment was generated using PROMALS3D [97] and Jalview [98]. Residues are colored using the ClustalX scheme, as implemented in Jalview. The putative functional regions have been assigned based on homology and previously reported studies [16, 26, 27, 42, 60, 66, 99, 100] . HMPV, human metapneumovirus, AMPV, avian metapneumovirus, CPV, canine pneumonia virus, MPV, murine pneumonia virus, BRSV, bovine respiratory syncytial virus, HRSV, human respiratory syncytial virus.

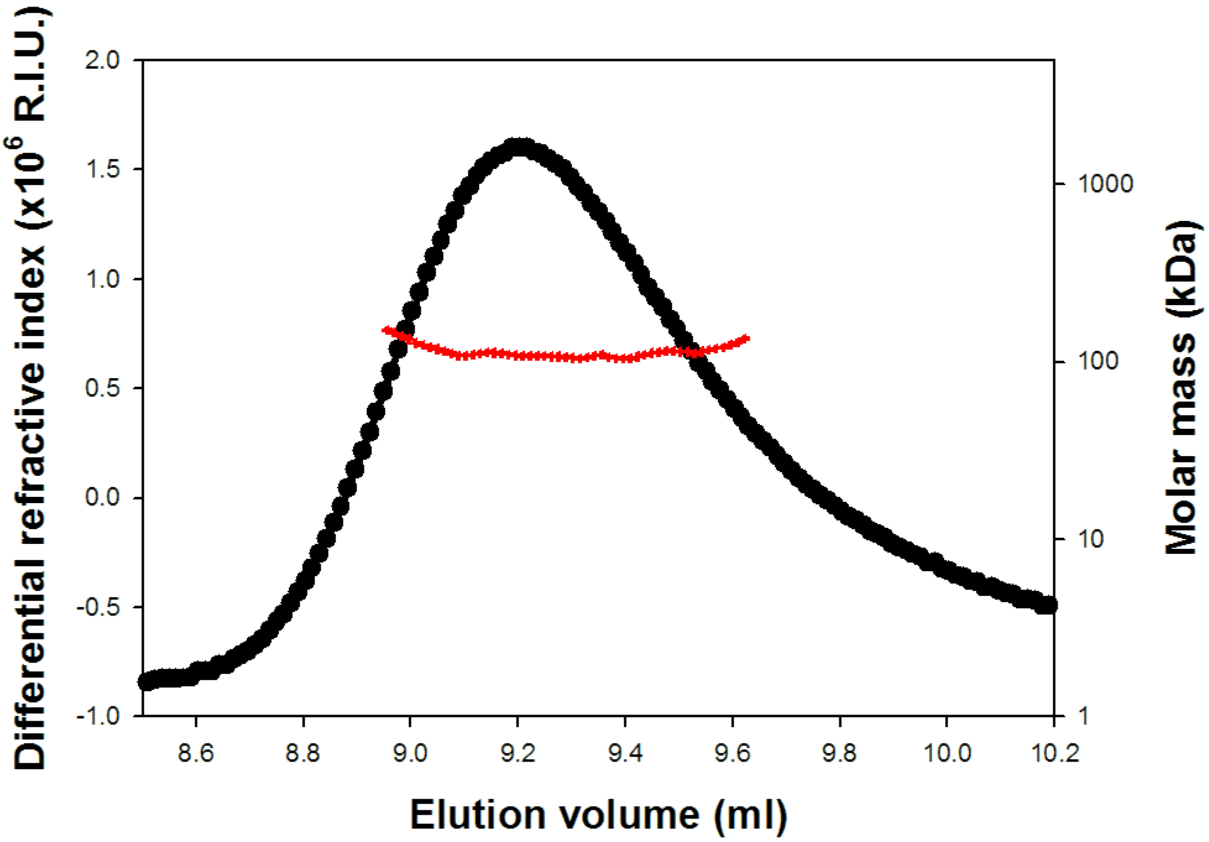

Figure S3: Characterization of full-length HMPV P by size exclusion chromatography (SEC) combined with detection by multi-angle laser light scattering (MALLS) and refractometry (RI). The black line shows the SEC elution profile as monitored by refractometry. The red line shows the molecular weight calculated from light scattering and refractometry data.

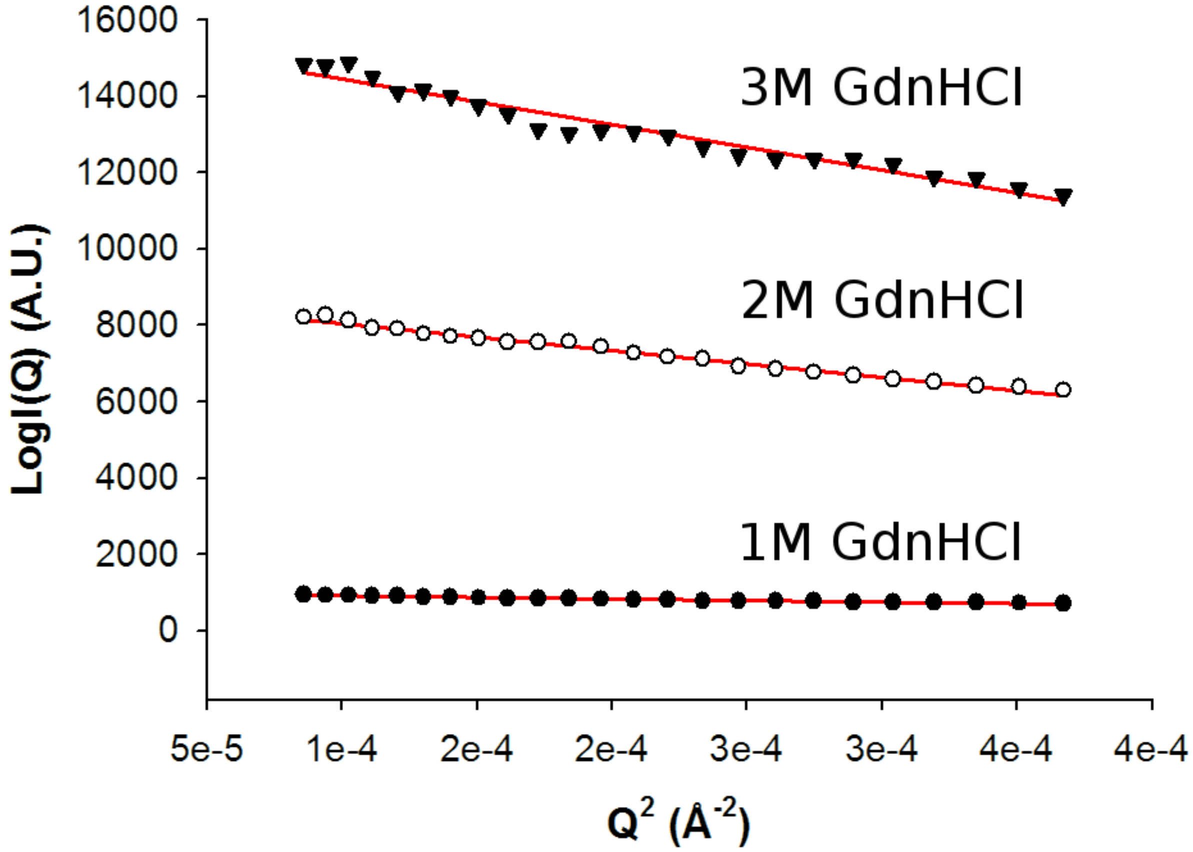

Figure S4: Guinier plots for $P_{135\text{-}237}$ SAXS profiles measured in the presence of guanidinum hydrochloride, showing linear behavior in the low Q range.

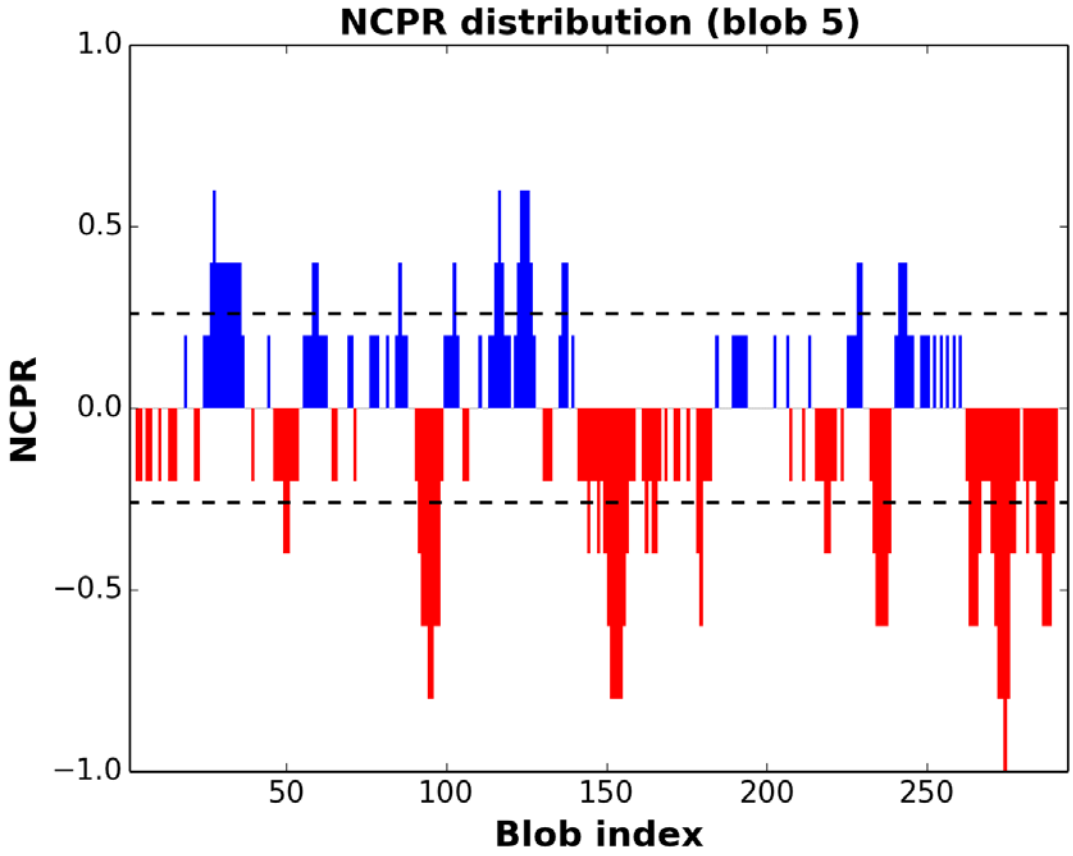

Figure S5: Linear net charge per residue (NCPR) for HMPV P. Plot of NCPR over 5 residue windows for the HMPV P sequence. The plot was obtained using the Classification of Intrinsically Disordered Ensemble Regions (CIDER) webserver [101].