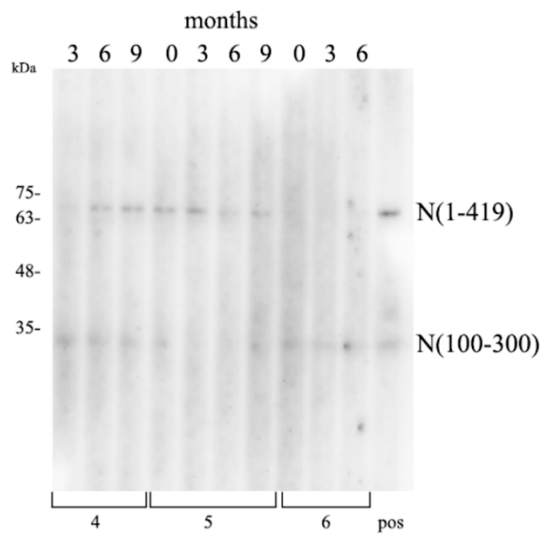


protein	virus	NCBI reference	aa number	% of identity
nucleocapsid	SARS-CoV-2	YP_009724397.2	419	100.00
nucleocapsid	SARS-CoV	AYV99827.1	422	89.74
nucleocapsid	HC OC43	YP_009555245.1	448	33.74
nucleocapsid	HUK1	ARU07581.1	441	33.59
nucleocapsid	HC NL63	ABI20791.1	377	29.25
nucleocapsid	HC E229	AGW80953.1	389	28.10

Supplementary Table S1. N-protein percentage of identity (% of identity) among human corona viruses. Identity was calculated using Clustal Omega at <https://www.ebi.ac.uk/Tools/msa/clustalo/> feeding the server with the indicated NCBI reference sequences.

ABI20791.1	-----MANVNWADDRAA-----R-----	15
AGW80953.1	-----MATVKWADASEPQR-----GR-----	18
YP_009724397.2	MSD-NGPQ-NQR-----NAPRI TFGGSDSTGNSQNGERS----	46
AYV99827.1	MSD-NGPQSNQR-----SAPRI TFGGPTDSTDNNQNGGRN----	47
YP_009555245.1	MSF TPGKQSSSRASSGNRSGNG-ILKWADQSDQFRNVQTRGRRAQPKQTATSQQPSGGNV	59
ARU07581.1	MSYTPGHYAGSRSSSGNRSGILKKT\$WADQSERNYQT FNRGRKTQPKFTVST--QPQGN	58
	... *	
ABI20791.1	FPPPSFYMPLLVSSDKAPYRVI PRNLVPIGKGN-KDEQIGYWNVQE--RWRMRGRQVRDL	72
AGW80953.1	RIPYSLYSPLLVDS-EQPKWVI PRNLVPI NKKD-KNKLIGYWNVQK--RFRTKGRKRVDL	74
YP_009724397.2	NNTASWFTAL TQHGK-EDLK FPRGQGVPI NTNSSPDDQIGYYRRAT-RRIRGGDGKMKDL	104
AYV99827.1	NNTASWFTAL TQHGK-EELRFPRGQGVPI NTNSGPDQIGYYRRAT-RRVRGGDGKMKEL	105
YP_009555245.1	VPYYSWFSGITQFQKGKEFEFVEGQGVPIAPGVPATEAKGYWYRHNRRSFKTADGNQRQL	119
ARU07581.1	IPHYSWFSGITQFQKGRDFKFSDGQGVPIAFGVPPSEAKGYWYRHSRFSFKTADGQQKQL	118
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ABI20791.1	PPKVHFYLLGTGPHKDLKFRQRSDGVVWAKEGAKTVNTS-LGNRKRQKPLEPKFSIAL	131
AGW80953.1	SPKLHFYLLGTGPHKDAKFRERVEGVVWAVDGAKEPTG-YGVRRKNSEPEIPHFNQKL	133
YP_009724397.2	SPRWYFYLLGTGPEAGLPYGANKDGIWVATEGALNTPKDHIGTRNPANNAIIV---LQL	161
AYV99827.1	SPRWYFYLLGTGPEASLPYGANKEGIVWATEGALNTPKDHIGTRNPANNAATV---LQL	162
YP_009555245.1	LPRWYFYLLGTGPHAKDQYGTIDGVVWVASNQADVNTPADIVDRDPSSDEAIP---TRF	176
ARU07581.1	LPRWYFYLLGTGPYANASYGESLEGVFWANHQADTSTPSDVSSRDPTTQEAIP---TRF	175
	* : : ***** : : * : *** . * . : :	
ABI20791.1	PPELSVE--FEDRSNNSSRASSRSSTR--NNSRDSRSTSRQQSRTSDSNQSSSDLVA	187
AGW80953.1	PNGVTVVE--EPDSRA----PSRSQSR--SQSRGRGESK PQSRNPSSDRNHNSQDDIMK	184
YP_009724397.2	PQGTTLPKGFYAEGSRGGSQASSRSSRSRNSRNS---TPGS-SRGTS PARMAGNG---	214
AYV99827.1	PQGTTL PKGFYAEGSRGGSQASSRSSRSRGNRNS---TPGS-SRGNS PARMASGG---	215
YP_009555245.1	PPGTVL PQGYIEGSGRSAPN-SRSTSR--TSSRAS--SAGSRSRANSGNRTPTSGVTP	230
ARU07581.1	PPGTIL PQGYVEGSGRSASN-SRPGSR--SQSRGP--NNRSLSRNSNFRHSDSIVKP	229
	* : : : ** : * . **	
ABI20791.1	AVTLALKNLGFDNQSKSPSS--GTSTPKKPNKPL-----SQPRADKPSQL	231
AGW80953.1	AVAAALKS LGFDK PQEKDKKSAKTGT PKPSRNQSPASSQTSAKSLARSQSSE TKEQKH	244
YP_009724397.2	-GDAAALALLDLRLNQLESKMSGKQQQQ-----GQTVTKKSAEAS	255
AYV99827.1	-GETALALLDLRLNQLESKVSGKQQQQ-----GQTVTKKSAEAS	256
YP_009555245.1	DMADQIASLV LAKLGKDATK-----PQQV-----TKHTAKEVRQKIL	267
ARU07581.1	DMADEIANLV LAKLGKE-SK-----PQQV-----TKQNAKEIRHKIL	265
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ABI20791.1	KKPRWKRVPTRE--ENVIQCFGPRDFNH--NMGSDSLVQNGVDAGFPQLAELIPNQAA	286
AGW80953.1	KKPRWKRPNDVTSNVTQCFGPRDLDH--NFGSAGVVANGVKAGYQFAELVPS TAA	301
YP_009724397.2	KKPRQKRTATKA--YNV TQAFGRRGPEQTQGNFGDQELIRQGT DYKHWPQIAQFAPSASA	313
AYV99827.1	KKPRQKRTATKQ--YNV TQAFGRRGPEQTQGNFGDQELIRQGT DYKHWPQIAQFAPSASA	314
YP_009555245.1	NKPRQKRSPNKQ--CTVQQCFGKRGPNQ--NFGGGEMLKLGTS DPQFPILAELAPTAGA	322
ARU07581.1	TKPRQKRTPNKH--CNVQQCFGKRGPSQ--NFGNAEMLKLG TNDPQFPILAELAPTPGA	320
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ABI20791.1	LLFDSEVSTDEVG-----DNVQITYTYKMLVAKDNKNLPKF----IEQISAF TK	331
AGW80953.1	MLFDSHIVSKESG-----NTVVLFTTRVTVSKDHPHLGKF----LEELNAFTR	346
YP_009724397.2	FFGMSRIGMEVTP-----SGTWLTYTGAIKLDDKDPNFKDQVILLNKHIDAYKT	362
AYV99827.1	FFGMSRIGMEVTP-----SGTWLTYHGAIKLDDKDPQFQDNVILLNKHIDAYKT	363
YP_009555245.1	FFFGSRLE LAKVQNLSGNPDEPQKDVYELRYNGAIRFDSTLSGFETIMKVLNENLNAYQQ	382
ARU07581.1	FFFGSKLELVKRE---SEADSPVKDVFELRYSGSIRFDSTLPGFETIMKVLKENLDAYVN	377
	: : * : . : : : : : : : : : : *	
ABI20791.1	PSSIKEMQSQSS--HVVQNT-----VLNA-----SI-PESKPLADDDSAIIEIVNEVLH	377
AGW80953.1	EMQQHPLL NPSA--LEFNP-----SQT-----SP-ATAEPVRDEVSIETDIDEVN-	389
YP_009724397.2	FPPTEPKDKKKKDADETQALPQRQKQQT-----VTLLPAADLDDFSKQLQ-----	408
AYV99827.1	FPPTEPKDKKKKTDEAQPLPQRQKQQT-----VTLLPAADMDDFSRQLQ-----	409
YP_009555245.1	QDG---M-----MNMSPKPQRQRGHKNGQGENDNISVAVPKSRVQQNKSRELTAEDIS	432
ARU07581.1	SNQNTVS-----GSLSPKPQRKRGVKQSPLEFDSLNLN----ADTQHISNDFTPEDHS	426
	. : :	
ABI20791.1	-----	377
AGW80953.1	-----	389

Supplementary Figure S1. Nucleocapsid homology among SARS-Cov-2 and HCoV-NL63, HCoV-229E, HCoV-OC43, HCoV-HKU1. Amino acids identical are marked by*. Amino acid numbering is shown on the right, NCBI Reference Sequence number is indicated at the left. ABI20791.1 indicates HCoV-NL63, AGW80953.1 represents HCoV-229E, YP_009724397.2 represents SARS-Cov-2, represents SARS-CoV, YP_009555245.1 represents HCoV-OC43, ARU07581.1 represents HCoV-HKU1.



Supplementary Figure S2. Multiple slot immunoblotting against the N protein variants N(1-419) and N(100-300) in participants categorized as borderline positive by ELISA. Sera (diluted 1/100) from 3 donors at different time points (0, 3, 6 and 9 months) and a positive control were loaded into each slot. At the top of the blot is the time point of sample collection. The N protein variant is shown on the right and the numbers at the bottom indicate the individual donors.