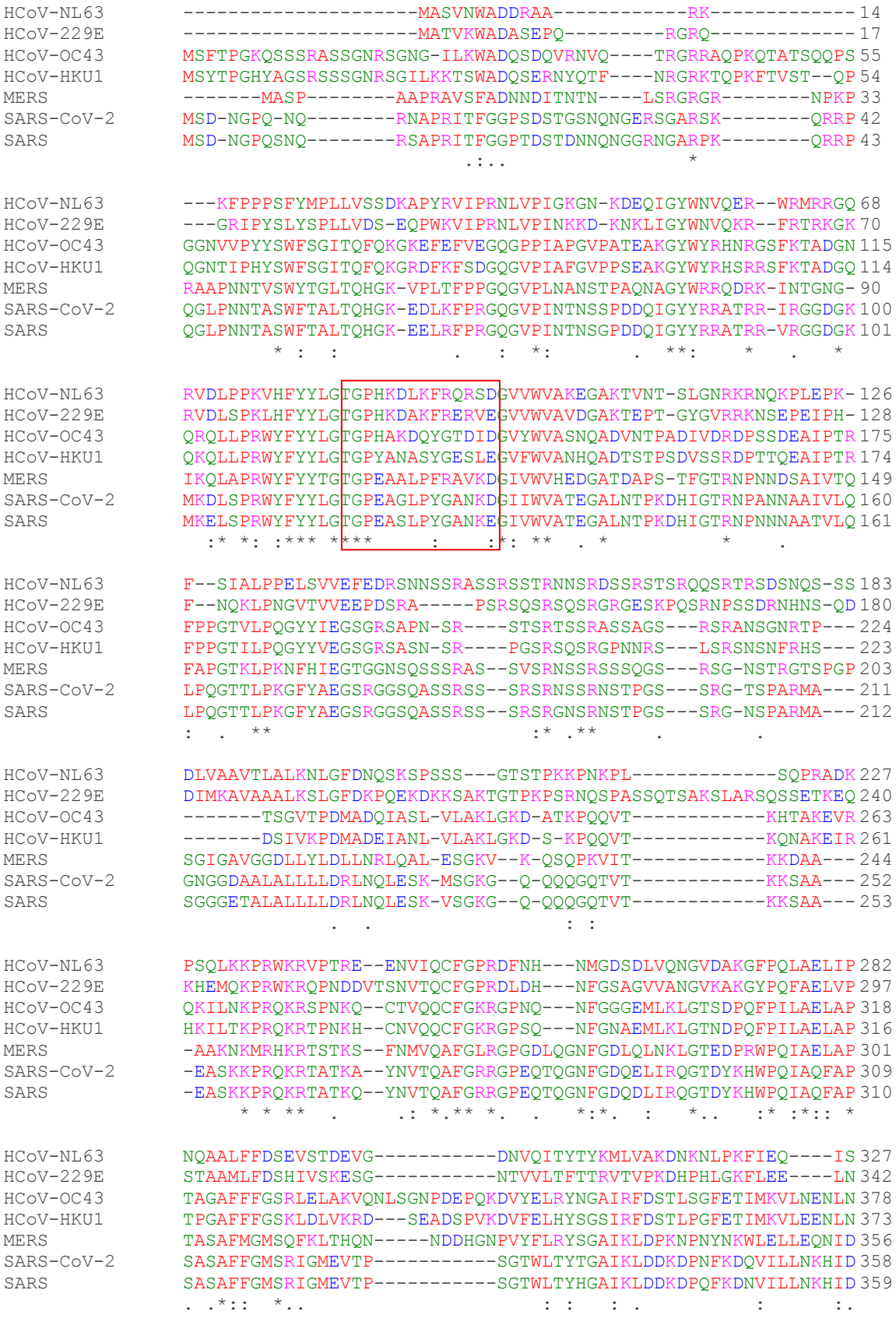
HCoV-NL63 ----------MASVNWADDRAA----------RK---------- 14
HCoV-229E ----------MATVKWADASEPQ---------RGRQ---------- 17
HCoV-OC43 MSFTPGKQSSSRASSGNRSGNG-ILKWADQSDQVRNVQ----TRGRRAQPKQTATSQQPS 55
HCoV-HKU1 MSYTPGHYAGSRSSSGNRSGILKKTSWADQSERNYQTF----NRGRKTQPKFTVST--QP 54
MERS -------MASP--------AAPRAVSFADNNDITNTN----LSRGRGR--------NPKP 33
SARS-CoV-2 MSD-NGPQ-NQ--------RNAPRITFGGPSDSTGSNQNGERSGARSK--------QRRP 42
SARS MSD-NGPQSNQ--------RSAPRITFGGPTDSTDNNQNGGRNGARPK--------QRRP 43
---KFPPPSFYMPLLVSSDKAPYRVIPRNLVPIGKGN-KDEQIGYWNVQER--WRMRRGQ 68
---GRIPYSLYSPLLVDS-EQPWKVIPRNLVPINKKD-KNKLIGYWNVQKR--FRTRKGK 70
GGNVVPYYSWFSGITQFQKGKEFEFVEGQGPPIAPGVPATEAKGYWYRHNRGSFKTADGN 115
QGNTIPHYSWFSGITQFQKGRDFKFSDGQGVPIAFGVPPSEAKGYWYRHSRRSFKTADGQ 114
RAAPNNTVSWYTGLTQHGK-VPLTFPPGQGVPLNANSTPAQNAGYWRRQDRK-INTGNG- 90
QGLPNNTASWFTALTQHGK-EDLKFPRGQGVPINTNSSPDDQIGYYRRATRR-IRGGDGK 100
QGLPNNTASWFTALTQHGK-EELRFPRGQGVPINTNSGPDDQIGYYRRATRR-VRGGDGK 101
RVDLPPKVHFYYLGTGPHKDLKFRQRSDGVVWVAKEGAKTVNT-SLGNRKRNQKPLEPK- 126
RVDLSPKLHFYYLGTGPHKDAKFRERVEGVVWVAVDGAKTEPT-GYGVRRKNSEPEIPH- 128
QRQLLPRWYFYYLGTGPHAKDQYGTDIDGVYWVASNQADVNTPADIVDRDPSSDEAIPTR 175
QKQLLPRWYFYYLGTGPYANASYGESLEGVFWVANHQADTSTPSDVSSRDPTTQEAIPTR 174
IKQLAPRWYFYYTGTGPEAALPFRAVKDGIVWVHEDGATDAPS-TFGTRNPNNDSAIVTQ 149
MKDLSPRWYFYYLGTGPEAGLPYGANKDGIIWVATEGALNTPKDHIGTRNPANNAAIVLQ 160
MKELSPRWYFYYLGTGPEASLPYGANKEGIVWVATEGALNTPKDHIGTRNPNNNAATVLQ 161
F--SIALPPELSVVEFEDRSNNSSRASSRSSTRNNSRDSSRSTSRQQSRTRSDSNQS-SS 183
F--NQKLPNGVTVVEEPDSRA-----PSRSQSRSQSRGRGESKPQSRNPSSDRNHNS-QD 180
FPPGTVLPQGYYIEGSGRSAPN-SR----STSRTSSRASSAGS---RSRANSGNRTP--- 224
FPPGTILPQGYYVEGSGRSASN-SR----PGSRSQSRGPNNRS---LSRSNSNFRHS--- 223
FAPGTKLPKNFHIEGTGGNSQSSSRAS--SVSRNSSRSSSQGS---RSG-NSTRGTSPGP 203
LPQGTTLPKGFYAEGSRGGSQASSRSS--SRSRNSSRNSTPGS---SRG-TSPARMA--- 211
LPQGTTLPKGFYAEGSRGGSQASSRSS--SRSRGNSRNSTPGS---SRG-NSPARMA--- 212
DLVAAVTLALKNLGFDNQSKSPSSS---GTSTPKKPNKPL----------SQPRADK 227
DIMKAVAAALKSLGFDKPQEKDKKSAKTGTPKPSRNQSPASSQTSAKSLARSQSSETKEQ 240
-------TSGVTPDMADQIASL-VLAKLGKD-ATKPQQVT----------KHTAKEVR 263
-------DSIVKPDMADEIANL-VLAKLGKD-S-KPQQVT----------KQNAKEIR 261
SGIGAVGGDLLYLDLLNRLQAL-ESGKV--K-QSQPKVIT----------KKDAA--- 244
GNGGDAALALLLLDRLNQLESK-MSGKG--Q-QQQGQTVT----------KKSAA--- 252
SGGGETALALLLLDRLNQLESK-VSGKG--Q-QQQGQTVT----------KKSAA--- 253
PSQLKKPRWKRVPTRE--ENVIQCFGPRDFNH---NMGDSDLVQNGVDAKGFPQLAELIP 282
KHEMQKPRWKRQPNDDVTSNVTQCFGPRDLDH---NFGSAGVVANGVKAKGYPQFAELVP 297
QKILNKPRQKRSPNKQ--CTVQQCFGKRGPNQ---NFGGGEMLKLGTSDPQFPILAELAP 318
HKILTKPRQKRTPNKH--CNVQQCFGKRGPSQ---NFGNAEMLKLGTNDPQFPILAELAP 316
-AAKNKMRHKRTSTKS--FNMVQAFGLRGPGDLQGNFGDLQLNKLGTEDPRWPQIAELAP 301
-EASKKPRQKRTATKA--YNVTQAFGRRGPEQTQGNFGDQELIRQGTDYKHWPQIAQFAP 309
-EASKKPRQKRTATKQ--YNVTQAFGRRGPEQTQGNFGDQDLIRQGTDYKHWPQIAQFAP 310
NQAALFFDSEVSTDEVG-----------DNVQITYTYKMLVAKDNKNLPKFIEQ----IS 327
STAAMLFDSHIVSKESG-----------NTVVLTFTTRVTVPKDHPHLGKFLEE----LN 342
TAGAFFFGSRLELAKVQNLSGNPDEPQKDVYELRYNGAIRFDSTLSGFETIMKVLNENLN 378
TPGAFFFGSKLDLVKRD---SEADSPVKDVFELHYSGSIRFDSTLPGFETIMKVLEENLN 373
TASAFMGMSQFKLTHQN-----NDDHGNPVYFLRYSGAIKLDPKNPNYNKWLELLEQNID 356
SASAFFGMSRIGMEVTP-----------SGTWLTYTGAIKLDDKDPNFKDQVILLNKHID 358
SASAFFGMSRIGMEVTP-----------SGTWLTYHGAIKLDDKDPQFKDNVILLNKHID 359

Supplementary figure 1. shows a sequence alignment depicting the conserved complement-activating sequence in high-consequence coronaviruses; depicted high consequence coronaviruses include SARS-CoV-2, SARS, and MERS; depicted endemic coronaviruses include HCoV-NL63, 229E, OC43, and HKU1; alignment generated with clustal omega 1.2.4; box: conserved complement-activating sequence; *: fully conserved residues; : (colon):conservation between groups of strongly similar properties; (period): conservation between groups of weakly similar properties.