Figure 1. Light microscopy images of LLC-MK2 cells (A, B) and VERO cells (C, D) inoculated with phosphate-buffered saline (A, C) or novel human coronavirus HCoV-SA1 (B, D) 5 days after inoculation.

Figure 2. Results of pan-coronavirus PCR. Various samples (numbered 1-12) of cell culture supernatants infected with HCoV-SA1 reacted with a pair of primers specific for the coronavirus family. A positive control virus (HCoV-NL63) was also reactive.

```
                10        20        30        40        50        60        70        80
                .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1        GGGGTTGGGACTAATCCTAAGTGTGATAGAGCTAATGCCTAAATATGTGTAGAATCTTCGCTTCACTCATAATTAGCTCGTAAA

                90        100       110       120       130       140       150       160
                .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1        CATGGCACTTGTTGTACTACAAGGGACAGATTTTATCGCTTGGCAAATGAGTGTGCTCAGGTGCTAAGCGAATATGTTCT

                170       180       190       200       210       220       230       240
                .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1        ATGTGGTGGTGGTTACTACGTCAAACCTGGAGGTACCAGTAGCGGAGATGCCACCACTGCATATGCCAATAGTGTCTTTA

                250       260       270       280       290       300       310       320
                .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1        ACATTTTGCAGGCGACAACTGCTAATGTCAGTGCACTTATGGGTGCTAATGGCAACAAGATTGTTGACAAAGAAGTTAAA

                330       340       350       360       370       380       390       400
                .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1        GACATGCAGTTTGATTGTATGTCAATGTTTACAGGAGCACTAGCCCAGACCCCAAATTTGTTGATAAATACTATGCTTT

                410       420       430       440       450
                .....|.....|.....|.....|.....|.....|.....|
HCoV-SA1        TCTTAATAAGCACTTTTCTATGATGACTGTCTGACGACGGCGTTGTGTGTTAA
```

Figure 3. Partial open reading frame of HCoV-SA1.

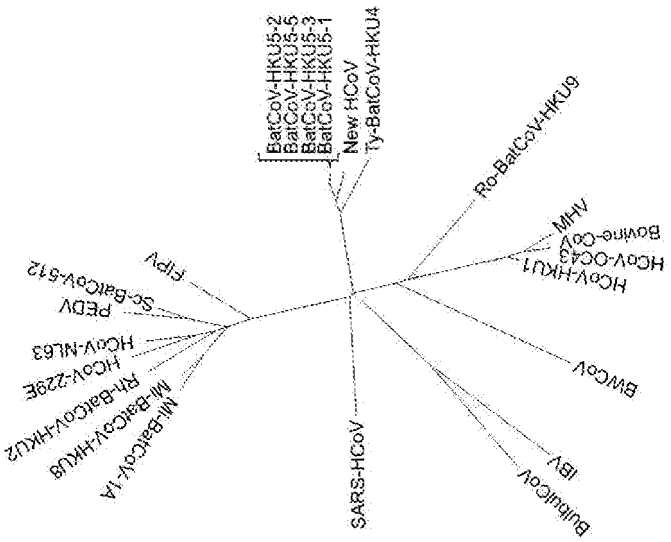


Figure 4. Maximum Likelihood tree of partial polymerase gene sequences of representative coronaviruses. HCoC-SA1 is shown in the cluster on the right hand side of the tree, labeled as "New HCoV". The cluster of viruses at the top represents viruses in the genus alphacoronavirus. The Beluga whale coronavirus (BWCoV) represents a gammacoronavirus, while the Bulbul-CoV and IBV represent a proposed new genus of the coronavirinae.

```
          10        20        30        40        50        60        70        80
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
N MASPAAAPRAVSFADNDITWTEILSRGRGRMPKPRAAPWNTVSWETCLEQHGKVPLTPPCQVVPLAAMSTPAQNGCRRR

          90       100       110       120       130       140       150       160
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
N QDRKINTCSMGIKQLAPRNTTNYTGTQPEAALPFRAVKDGIVWVHEDGATDAPSTFGTRNPNNDSAIVTQAAPHGTKLTKNT

          170       180       190       200       210       220       230       240
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
N AIETCCMSQSSSRAASLSRMSSRSSSQGSRSGNSTRGTSPGPSSIGAVEEDLLVLDLLNRLQALESGKVKQSQPKVITK

          250       260       270       280       290       300       310       320
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
N KDAAAKQKMRHKRTSTKSFNMVQAIGLRGPGDLQGNGDLQLAKLGTEDPRWPQIAELATSAAMSQVKLNHQGND

          330       340       350       360       370       380       390       400
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
N DRGNPVTLRASSTKLDPKMPTNMKLELLEQNIDAKTTPKKEKKQKAPKEESTDQMSEPPKREQRVQSSTQRTRTR2

          410
....|.....|....
N SVQPGPMIDVWTD

Figure 5 file N.rtf
```

```
          10        20        30        40        50        60        70        80
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
M   MSRMTQLTEAQIIAKITKDMRTANSLIFLLITTVLQAGYPSRSMTVYVAKMTVLALPSSMALSISAVTAPTDLASQIIS

          90       100       110       120       130       140       150       160
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
M   GTVAAVSAMMISTAVQSIRLAMRTGSNSSNPETNCLLMVPAGGTTVVRPLVEDSTSVTAVVTMGALKMAGMTGAACDY

          170       180       190       200       210
....|.....|.....|.....|.....|.....|.....|.....|.....
M   DRLPMEVTVAKPAVLIALKMVKRQSTGTNSGVAIYERKAGSTRSPPITADIELLLRA
```

Figure 6 file M.rtf

```
          10        20        30        40        50        60        70        80
 ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
E MLPFVQERIGLFIVNSLFIVVCQITLLVCMQELFETRLCVQCMTCSNTLAVQPALVLNETCRSVVKEQDSKPFLPPDE
          ..
E          SV
```

Figure 7 E.rtf

```
          10        20        30        40        50        60        70        80
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
NS3D      MAPISAFSPVQHMAVIIKRRHTSRRRSRSTVETLVRGMLVRGTCALIALMRCMVNLETFNLAYLAFTLLLVLPEFATVHGTLQAIFLFILSYTVGEVTTVSLFALLSLLTCLSTPHFYWLVDAYLKKCVYFLIHPLMMPLVVCGFEAIKLESIVLKVLVLFLLFGVVGMSLYKDVVCAVGGMSWITRGQGALHTGLDFMGSCVLLVGHSLLFKVPPEILQMLKMVAATLMSVVCVSNPVTLTAGVFLFLTLSFQPACALGLCLCGPRTHFREDSVAPVSDVLIAVATFFSSMFLLALGIPYTLTVVGACMFSCMQKKESMKLTVFVLTIQLCTVAVCTMAIYVYVESLKTHVEWPSSLRTPETKGETALLIKLLAVAYVLCPILLSLSLFSFILLAVWYMFQHRGSDIDVQKEATLTKPAETFFLDLDDKPLSIFFPTLGDPTSVETALKIFFDSQPCELQGFSFFQCAPKGQDIKLTFLRNETVIAVRDYTYHSRVLKPVCMEGSIGSLPQVVQGETHVGVLTGLGAFDKGELEVLSLKNVKRLTIMDGDCHSDSASKFRVSMVSIQVEEIHTSVDYMVYLTPQMVLRSGLLGLSHGPLSEVEIQKYGTLGVLFMAIHGKGKRSLATPSGTVTSTLVEGKSVSIGSTDLQPLVECDTWNGPKPKPIIIDSYTGEFILDDGCGGTKSSLSIEIESLVTLGEVRNVQVTSMLYTKENEWLVHKEWFHRDIPLPWTSGADTSSPHWNNKETLVTFKNPHAKKQDVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCRLRMDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEKRHVLGRLITVNPIVTEKDSPVNIEAEPPFGDSYIIIGVEPGQLKLNWFKKGSSIGQMFETTMRGAKRMAILGDTAWDFGSLGGVFTSVGKLVHQIFGTAYGVLFSGVSWTMKIGIGVLLTWLGLNSRSTSLSVSCIAVGMVTLYLGVMVQADSGCVVSWKNKELKCGSGIFITDNVHTWTEQYKFQPESPSKLASAIQKAHEEGICGIRSVTRLENLMWKQITPELNHILSENEVKLTIMTGDIKGIMQAGKRSLRPQPTELKYSWKTWGKAKMLSTESHNQTFLIDGPETAECPNTNRAWNSLEVEDYGFGVFTTNIWLKLKEKQDVFCDSKLMSAAIKDNRAVHADMGYWIESALNDTWKIEKASFIEVKNCHWPKSHTLWSNGVLESEMIIPKNFAGPVSQHNYRPGYHTQTAGPWHLGKLELDFDFCEGTTVVVTEDCGNRGPSLRTTTASGKLITEWCCRSCTLPPLRYRGEDGCWYGMEIRPLKEKEENLVNSLVTAGHGQVDNFSLGVLGMALFLEEMLRTRVGTKHAILLVAVSFVTLITGNMSFRDLGRVMVMVGATMTDDIGMGVTYLALLAAFKVRPTFAAGLLLRKLTSKELMMTTIGIVLSSQSSIPETILELTDALALGMMVLKMVRNMEKYQLAVTIMAILCVPNAVILQNAWKVSCTILAVVSVSPLFLTSSQQKTDWIPLALTIKGLNPTAIFLTTLSRTSKKKSWPLNEAIMAVGMVSILASSLLKNDIPMTGPLVAGGLLTVCYVLTGRSADLELERAADVKWEDQAEISGSSPILSITISEDGSMSIKNEEEEQTLTILIRTGLLVISGLFPVSIPITAAAWYLWEVKKQRAGVLWDVPSPPPMGKAELEDGAYRIKQKGILGYSQIGAGVYKEGTFHTMWHVTRGAVLMHKGKRIEPSWADVKKDLISYGGGWKLEGEWKEGEEVQVLALEPGKNPRAVQTKPGLFKTNAGTIGAVSLDFSPGTSGSPIVDKKGKVVGLYGNGVVTRSGAYVSAIAQTEKSIEDNPEIEDDIFRKKRLTIMDLHPGAGKTKRYLPAIVREAIKRGLRTLILAPTRVVAAEMEEALRGLPIRYQTPAIRAEHTGREIVDLMCHATFTMRLLSPVRVPNYNLIIMDEAHFTDPASIAARGYISTRVEMGEAAGIFMTATPPGSRDPFPQSNAPIIDEEREIPERSWNSGHEWVTDFKGKTVWFVPSIKAGNDIAACLRKNGKKVIQLSRKTFDSEYVKTRTNDWDFVVTTDISEMGANFKADRVIDSRRCLKPVILDGERVILAGPMPVTHASAAQRRGRIGRNPNKPGDEYLYGGGCAETDEDHAHWLEARMLLDNIYLQDGLIASLYRPEADKVAAIEGEFKLRTEQRKTFVELMKRGDLPVWLAYQVASAGITYTDRRWCFDGTTNNTIMEDSVPAEVWTRHGEKRVLKPRWMDARVCSDHAALKSFKEFAAGKRGAALGVMEALGTLPGHMTERFQEAIDNLAVLMRAETGSRPYKAAAAQLPETLETIMLLGLLGTVSLGIFFVLMRNKGIGKMGFGMVTLGASAWLMWLSEIEPARIACVLIVVFLLLVVLIPEPEKQRSPQDNQMAIIIMVAVGLLGLITANELGWLERTKSDLSHLMGRREEGATIGFSMDIDLRPASAWAIYAALTTFITPAVQHAVTTSYNNYSLMAMATQAGVLFGMGKGMPFYAWDFGVPLLMIGCYSQLTPLTLIVAIILLVAHYMYLIPGLQAAAARAAQKRTAAGIMKNPVVDGIVVTDIDTMTIDPQVEKKMGQVLLIAVAVSSAILSRTAWGWGEAGALITAATSTLWEGSPNKYWNSSTATSLCNIFRGSYLAGASLIYTVTRNAGLVKRRGGGTGETLGEKWKARLNQMSALEFYSYKKSGITEVCREEARRALKDGVATGGHAVSRGSAKLRWLVERGYLQPYGKVIDLGCGRGGWSYYAATIRKVQEVKGYTKGGPGHEEPVLVQSYGWNIVRLKSGVDVFHMAAEPCDTLLCDIGESSSSPEVEEARTLRVLSMVGDWLEKRPGAFCIKVLCPYTSTMMETLERLQRRYGGGLVRVPLSRNSTHEMYWVSGAKSNTIKSVSTTSQLLLGRMDGPRRPVKYEEDVNLGSGTRAVVSCAEAPNMKIIGNRIERIRSEHAETWFFDENHPYRTWAYHGSYEAPTQGSASSLINGVVRLLSKPWDVVTGVTGIAMTDTTPYGQQRVFKEKVDTRVPDPQEGTRQVMSMVSSWLWKELGKHKRPRVCTKEEFINKVRSNAALGAIFEEEKEWKTAVEAVNDPRFWALVDKEREHHLRGECQSCVYNMMGKREKKQGEFGKAKGSRAIWYMWLGARFLEFEALGFLNEDHWMGRENSGGGVEGLGLQRLGYVLEEMSRIPGGRMYADDTAGWDTRISRFDLENEALITNQMEKGHRALALAIIKYTYQNKVVKVLRPAEKGKTVMDIISRQDQRGSGQVVTYALNTFTNLVVQLIRNMEAEEVLEMQDLWLLRRSEKVTNWLQSNGWDRLKRMAVSGDDCVVKPIDDRFAHALRFLNDMGKVRKDTQEWKPSTGWDNWEEVPFCSHHFNKLHLKDGRSIVVPCRHQDELIGRARVSPGAGWSIRETACLAKSYAQMWQLLYFHRRDLRLMANAICSAVPVDWVPTGRTTWSIHGKGEWMTTEDMLVVWNRVWIEENDHMEDKTPVTKWTDIPYLGKREDLWCGSLIGHRPRTTWAENIKNTVNMVRRIIGDEEKYMDYLSTQVRYLGEEGSTPGVL
          90        100
....|.....|.....|.....|.....|..
NS3D      LATVLVACVTLCSRTAVSVSMVTRTSDGRLFFASAVIVLLIVL
```

Figure 8 file NS3d.rtf

```
          10        20        30        40        50        60        70        80
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
NS3C      MEESLMDVPSTSGMQVTSERKRRKRSASPTKKLRVKRRSLLRREDLSVIVQPTAVRVTSSDFMMSLRSGAALSVMM

          90        100       110       120       130       140       150       160
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
NS3C      KLKPSSSQPVSETATTLALLMLTDEDLRDLSPTALLLRSVRTELAESALLRKTLVLMNSEICNIARKPVCRVMTAT

          170       180       190       200       210       220       230       240
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
NS3C      PTTKDSLLVQSSLYSSLPLMMSLKLHALDDVTRMILTMPCRTTPQMTVTPLAVDVVSIRSSHQGMKQIVHSVPI

          ....|.
NS3C      LAEPSM
```

Figure 9 file NS3c.rtf

```
          10        20        30        40        50        60        70        80
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
NS3B      MDYVSLLMQIEQKLNSPVTPWCLAIFRPTAKVTPLVCISLMPVLACQLSPRSYTESMVSTKLAKQDMQRILKLMK

          90        100
....|.....|.....|.....|.....|.....|.....
NS3B      DGGIPDSCSLVLLAMSSLMQSEEEEPMSM
```

Figure 10 file NS3b.rtf

```
          10        20        30        40        50        60        70        80
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
NS3A      MEVQRPFLLLVASLSLLVTASSKPLYPEWCMLRCIKTQADTRAGLYWTRIDVPSASETCQSVSVDLESR

               90        100
....|.....|.....|.....|.....|....
NS3A      STRDSPTEWVTSVMLRDVGSSV
```

Figure 11 file NS3a.rtf

Figure 12 file S.rtf

```
        3210      3220      3230      3240      3250      3260      3270      3280
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
ORF1ab  SGMETNSVRFANSCITLAKHLQTVNENGSDLLYQPPMCSITSGVLQSGLVKMSHPSGDVEACMVQVTCGSMTLNGLWLD

        3290      3300      3310      3320      3330      3340      3350      3360
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
ORF1ab  NTVWCPRHVMCPADQLSDPWYDILLISMNNHSFSVQKHIGAPANLRVVGHAMQGTLLKLTVDVANPSTPAYTFVKPGA

        3370      3380      3390      3400      3410      3420      3430      3440
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
ORF1ab  ASSVLCWCRPTGTPTVVMRPNETIKSFLCSCSSVSFTKEGSVICMGHLANGTAFSFSDGTMVTGSSFSFDVMDKQV

        3450      3460      3470      3480      3490      3500      3510      3520
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
ORF1ab  EQVQLFDKCSAVVVNLRAFLMSCAVKPKRTSVVSSYNEFLLAQFTFVGTSVDMLAVKTSVYTEQLLFIQQLA

        3530      3540      3550      3560      3570      3580      3590      3600
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
ORF1ab  TGTQSKQILASTMLEDEYTPEDVNMQIMCVYSQSGVRKVTVGTANELKNGTLVSTVVTLLQATKTTLNMYLEFTQLAP

        3610      3620      3630      3640      3650      3660      3670      3680
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
ORF1ab  LLAVTMAVMLLVKHKHTFLMLLPVAICLTYNMIVFPTTPISSLIVAMGLAPWAMRTTMTDIGVPLISMSLVLV

        3690      3700      3710      3720      3730      3740      3750      3760
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
ORF1ab  IVVRRLMPSLSMNLLLCSCVMLPTYSICPASSPIALVLVYTLESDVPTIVLNVVMLACVCTMAIVSPQLTLVPP

        3770      3780      3790      3800      3810      3820      3830      3840
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
ORF1ab  EVKMILLLVTCLCPMCTCTCVSLLNLKLRPMCVYDKVSTQLRMTSNLTPRNSEMLANKLIGTGTPCIK

        3850      3860      3870      3880      3890      3900      3910      3920
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
ORF1ab  VAMQSKLTDLKCTSVVLLSVLQQLRLESSSKLWAQCVKCNDILGQTDPGFMEKYSLIFLMTFSGNVDLDALSDI

        3930      3940      3950      3960      3970      3980      3990      4000
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
ORF1ab  TDPSVLQATLSEISILGAFVIEEVKQLYQENMDSGDTSPQVLRKLQKVNITVKGKEVQLSTYKKWIEWDKYFMDV
```

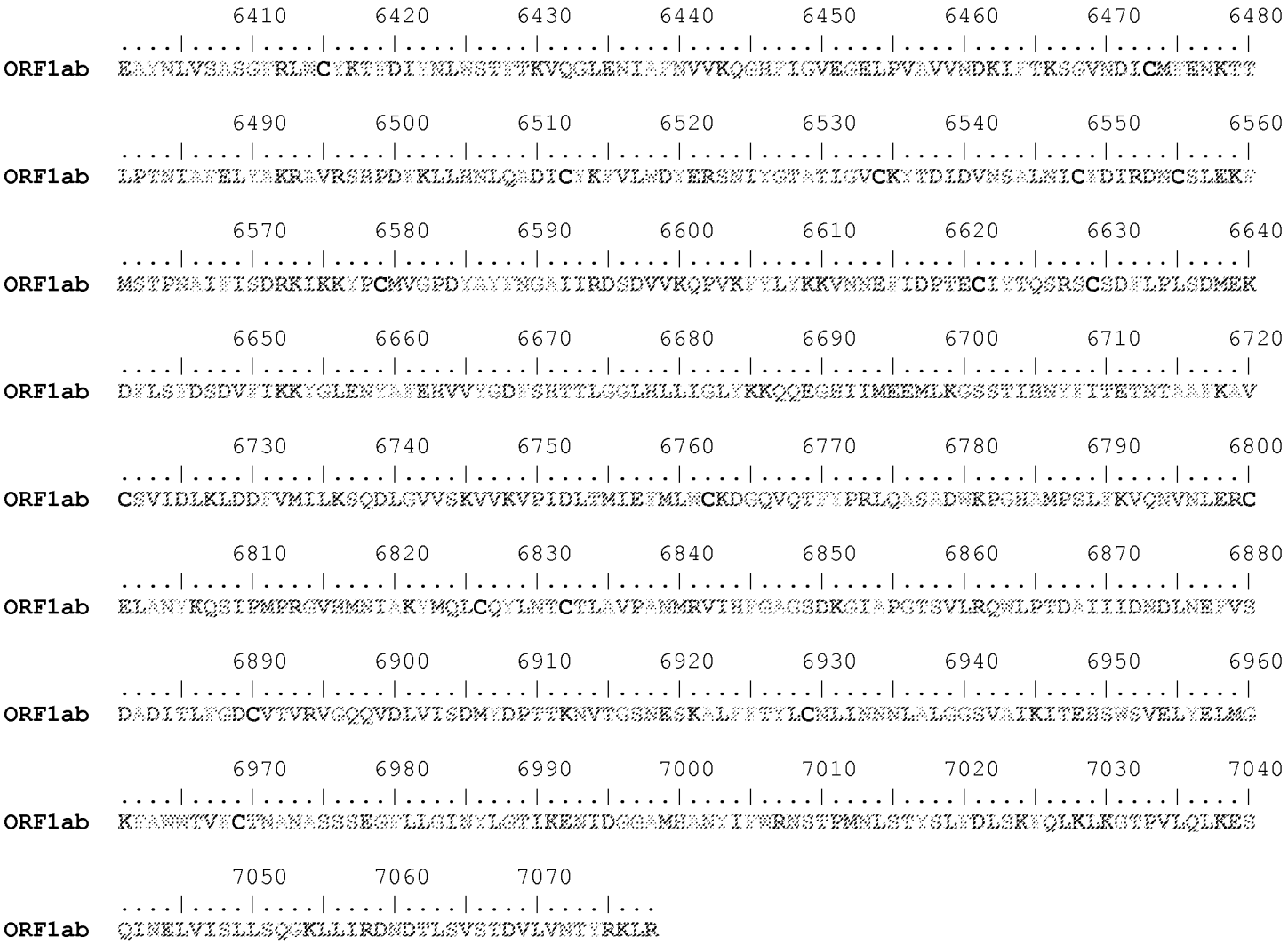


Figure 13 file Orf1ab.rtf

```
          10        20        30        40        50        60        70        80
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1 ATTTAAGTGAATAGCTTGGCTATCTCACTTCCCCTCGTTCTCTTGCAGAACTTTGATTTTAACGAACTTAAATAAAAAGCC

          90       100       110       120       130       140       150       160
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1 CTGTTGTTTAGCGTATCGTTGCACTTGTCTGGTGGGATTGTGGCATTAATTTGCCTGCTCATCTAGGCAGTGGACAATATG

         170       180       190       200       210       220       230       240
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1 CTCAACACTGGGTAATTCTAATTGAATACTATTTTTCAGTTAGAGCGTCGTGTCTCTTGTACGTCTCGGTCACAATAC

         250       260       270       280       290       300       310       320
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1 ACGGTTTCGTCCGGTGCGTGGCAATTCGGGGCACATCATGTCTTTCGTGGCTGGTGTGACCGCGCAAGGTGCGCGGTA

         330       340       350       360       370       380       390       400
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1 CGTATCGAGCAGCGCTCAACTCTGAAAAACATCAAGACCATGTGTCTCTAACTGTGCCACTCTGTGGTTCAGGAAACCTG

         410       420       430       440       450       460       470       480
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1 GTTGAAAAACTTTCACCATGGTTCATGGATGGCGAAAATGCCTATGAAGTGGTGAAGGCCATGTTACTTAAAAAGGAGCC

         490       500       510       520       530       540       550       560
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1 ACTTCTCTATGTGCCCATCCGGCTGGCACACACTAGACACCTCCCAGGTCCTCGTGTGTACCTGGTTGAGAGGCCTCA

         570       580       590       600       610       620       630       640
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1 TTGCTTGTGAAAATCCATTCATGGTTAACCAATTGGCTTATAGCTCTAGTGCAAATGGCAGCCTGGTTGGCACACTTTG

         650       660       670       680       690       700       710       720
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1 CAGGGCAAGCCTAATTGGTAATGTTCTTCCCTTATGACATCGAACTTGTCACAGGAAAGCAAAAATATTCTCCTGCGCAAGTA

         730       740       750       760       770       780       790       800
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1 TGGCCGTGGTGGTTATCACTACACCCCATTCCACATGAGCGAGACAACACCTCTTGCCCTGAGTGGATGGACGATTTTG
```

```
          810       820       830       840       850       860       870       880
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  AGGCGGATCCTAAAGGCAAATATGCCCAGAATCTGCTTAAGAAGTTGAATTGGCGGTGATGTCACTCCAGTTGACCAATAC

          890       900       910       920       930       940       950       960
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  ATGTGTGGCGTTGATGGAAAACCCATTAGTGCCTACGCATTTTTAATGGCCAAGGATGGAATAACCAAACTGGCTGATGT

          970       980       990       1000      1010      1020      1030      1040
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  TGAAGCGGACGTCGCAGCACGTGCTGATGACGAAGGCTTCATCACATTAAAGAACAATCTATATAGATTGGTTTGGCAATG

          1050      1060      1070      1080      1090      1100      1110      1120
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  TTGAGCGTAAAGACGTTCCAATATCCTAAGCAATCTATTTTTACTATTAATAGTGTGGTCCAAAAGGAAGGTGTTGAAAAC

          1130      1140      1150      1160      1170      1180      1190      1200
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  ACTCCTCCTCACTATTTTACTCTTGGATGCAAAATTTAACGCTCACCCCACGCAACAAGTGGAGTGGCGTTTCTGACTT

          1210      1220      1230      1240      1250      1260      1270      1280
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  GTCCCTCAAACAAAAACTCCTTTACACCTTCTAATGGTAAGGAGTCACTTGAGAACCCAACCTACATTTACCACTCCGCAT

          1290      1300      1310      1320      1330      1340      1350      1360
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  TCATTGAGTGTGGAAGTTGTGGTAATGATTCCTGGCTTACAGGGAATGCTATCCAAGGGTTTGCCTGTGGATGTGGGGCA

          1370      1380      1390      1400      1410      1420      1430      1440
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  TCATATACAGCTAATGATGTCGAAGTCCAATCATCTGGCATGATTAAGCCAAATGCTCTCTTTGTGCTACTTGCCCCTT

          1450      1460      1470      1480      1490      1500      1510      1520
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  TGCTAAGGGTGATAGCTGTTCTTCTAATTGCAAACATTCAGTTGCTCAGTTGGTTAGTTACCTTTCTGAACGCTGTTAATG

          1530      1540      1550      1560      1570      1580      1590      1600
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  TTATTGCTGATCTAAGTCCTTCACACTATCTTTGGTGGCGTAGCTTACGCCTACTTTGGAATGTGAGGAAGGTACTATG
```

```
                1610      1620      1630      1640      1650      1660      1670      1680
     ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1 TACTTTGTGCCTAGAGCTAAGTCTGTTGTCTCAAGGATTGGAGACTCCATCTTACAGGCTGTACTGGCTCTTGGAACAA

                1690      1700      1710      1720      1730      1740      1750      1760
     ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1 GGTCACTCAAATTGCTAACATGTTCTTGGAACAGACTCAGCATTCCCTTAACTTTGTGGGAGAGTTCGTTGTCAACGATG

                1770      1780      1790      1800      1810      1820      1830      1840
     ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1 TTGTCCTCGCAATTCTCTCTGGAACCACACAACTAATGTTGACAAAATACGCCAGCTTTCTCAAGGTGTCACCCTTGACAAG

                1850      1860      1870      1880      1890      1900      1910      1920
     ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1 TTGCGTGATTATTTTAGCTGACTATGACGAGCACTGCCGGCCCATTCATGGATAAATGCTATTAAATGTTGGTGGTAC

                1930      1940      1950      1960      1970      1980      1990      2000
     ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1 AGGATTACAGTATGCCGCCATTACTGCACCTTATGTAGTTCTCACTGGCTTAGGTGAGTCCTTTTAAGAAAGTTGCAACCA

                2010      2020      2030      2040      2050      2060      2070      2080
     ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1 TACCGTATAAGGTTTGCAACTCTGTTAAGGATACTCTGGCTTATTATGTCACAGCGTGTTGTACAGAGTTTTCCTTAT

                2090      2100      2110      2120      2130      2140      2150      2160
     ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1 GACATGGATTCTGGTGTCATCCTTAGTGAACTACTTTTTGATTGCGTTGATCTTTCAGTAGCTTCCTACCTATTTTT

                2170      2180      2190      2200      2210      2220      2230      2240
     ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1 AGTCCGCATCTTGCAAGATAAGACTGGCGACTTTATGTCTACAATTATTACTCCTGCCAAACTGCTGTTAGTAAGCTTC

                2250      2260      2270      2280      2290      2300      2310      2320
     ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1 TAGATACATGTTTTTGAAGCTACAGAAGCAACATTTAACTTCTTGTTAGATTTGGCAGGATTGTTCAGAATCTTTCTCGC

                2330      2340      2350      2360      2370      2380      2390      2400
     ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1 AATGCCTATGTGTACACTTCACAAGGGTTTGTGGTGGTCAATGGCAAAGTTTCTACACTTGTCAAACACAAGTGTTAGACTT
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          2410      2420      2430      2440      2450      2460      2470      2480
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  GCTTAAATAAGGGTATGCAACTTTTGCCATACAAAGGTCTCCTGGGCTGGTTCTAAAAATCATTGCTGTTATCTACAGCGGCA

          2490      2500      2510      2520      2530      2540      2550      2560
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  GGGAGTCTCTAAATATTCCCAATCGGGAACCTATTACTGTGTCACCACTAAGGCTAAGTCCGTTCAACAAGATCTTGACGTT

          2570      2580      2590      2600      2610      2620      2630      2640
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  ATTTTGCCTGGTGAGTTTTCCAAGAGCAGTTAGGACTGCTCCAACCTACTGACAATTCTACAACTGTTAGTGTTACTGT

          2650      2660      2670      2680      2690      2700      2710      2720
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  ATCCAGTAACATGGTTGAAACTGTTGTGGTCAACTTGAGCAAACTAATATGCATAGTCCTGATGTTATAGTAGGTGACT

          2730      2740      2750      2760      2770      2780      2790      2800
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  ATGTCATTATTAGTGAAAAATTGTTTGTGCGTAGTAAGGAAGAAGACGGATTTGCCTTCCTACCCTGCTTGCACTAAATGGT

          2810      2820      2830      2840      2850      2860      2870      2880
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  CATGCTGTACCGACTCTCTTTAGACTTAAGGGAGGTGCACCTAGTAAAAAAAGTAGCCTTTGGCGGTGATCAAGTACATGA

          2890      2900      2910      2920      2930      2940      2950      2960
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  GGTTGCTGCTGTAAGAAGTGTACTGTCGAGTACAACATTCATGCTGTATTAGACACACTACTTGCTTCTTTCTAGTCCTTA

          2970      2980      2990      3000      3010      3020      3030      3040
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  GAACTTTTGTTGTAGATAAGTCTTTGTCAATTGAGGAGTTTGCTGACGTAGTAAAGGAACAAGGTCTCAGACTTGCTTGTT

          3050      3060      3070      3080      3090      3100      3110      3120
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  AAATTACTGCGTGGAATGCCGATTCCAGATTTTGATTTTAGACGATTTTATTGACGCACCAATGCTATTGCTTTATAACGCTGA

          3130      3140      3150      3160      3170      3180      3190      3200
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  GGGTGATGCATCCTGGTCTTCTACTATGATCTTCTCTCTTCACCCCGTCGAGTGTGACGAGGAGTGTTCTGAAGTAGAGG
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                3210      3220      3230      3240      3250      3260      3270      3280
          ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  CTTCAGATTTAGAAGAGGTGAATCAGAGTGCATTTCTGAGACTTCAACTGAACAAGTTGACGTTTCTCATGAGACTTCT

                3290      3300      3310      3320      3330      3340      3350      3360
          ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  GACGACGAGTGGGCTGCTGCAGTTGATGAAGCGTTCCCTCTCGATGAAGCAGAAGATGTTACTGAATCTGTGCAAGAAGA

                3370      3380      3390      3400      3410      3420      3430      3440
          ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  AGCACAACCAGTAGAAGTACCTGTTGAAGATAATGCGCAGGTTGTCATAGCTGACACCTTACAGGAACTCCTGTTGTGC

                3450      3460      3470      3480      3490      3500      3510      3520
          ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  CTGATACTGTTGAAGTCCCACCGCAAGTGGTGAAACTTCCGTCTGCACCTCAGACTATCCAGCCCGAGGTAAAAGAAGTT

                3530      3540      3550      3560      3570      3580      3590      3600
          ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  GCACCTGTCTATGAGGCTGATACCGAACACAGACACAGAATGTTACTGTTAAACCTAAGAGGTTACGCAAAAAGCGTAATGT

                3610      3620      3630      3640      3650      3660      3670      3680
          ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  TGACCCTTTGTCCAATTTTGAACATAAGGTTAATTACAGAGTGCGTTACCATAGTTTTTAGGTGACGCAATTCAAGTAGCCA

                3690      3700      3710      3720      3730      3740      3750      3760
          ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  AGTGCTATGGGGAGTCTGTGTTAGTTAATGCTGCTAACACACATCTTAAGCATGGCGGTGGTATCGCTGGTGCTATTAAT

                3770      3780      3790      3800      3810      3820      3830      3840
          ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  GCGGCTTCAAAAGGGGCTGTCCAAAAAGAGTCAGATGATATTCTGGCTAAAGGGCCGTTACAAGTAGGAGATTCAGT

                3850      3860      3870      3880      3890      3900      3910      3920
          ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  TCTCTTGCAAGGCCATTCTCTAGCTAAGAATATCCTGCATGTCGTAGGCCCAGATGCCCGCGCTAAACAGGATGTTTCTC

                3930      3940      3950      3960      3970      3980      3990      4000
          ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  TCCTTAGTAAGTGCTATAAGGCTATGAATGCATATCCTCTTGTAGTCACTCCTCTTGTTTCAGCAGGCATATTTGGTGTA
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          4010      4020      4030      4040      4050      4060      4070      4080
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
AAACCAGCTGTGTCTTTTGATTATCTTATTAGGGAGGCTAAGACTAGAGTTTTAGTCGTTAATTCCCAAGATGTCTA
HCoV-SA1

          4090      4100      4110      4120      4130      4140      4150      4160
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
TAAGAGTCTTACCATAGTTGACATTCCACAGAGTTTTGACTTTTTTCATATGATGGGTTACGTGGCGCAATACGTAAAGCTA
HCoV-SA1

          4170      4180      4190      4200      4210      4220      4230      4240
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
AAGATTTATGGTTTTTACTGTTTTTTGTGTGCACAGACAACTCTGCTAACACTAAAGTTCTTAGGACAAGGGTGTTGATTAT
HCoV-SA1

          4250      4260      4270      4280      4290      4300      4310      4320
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
ACTAAGAAGTTTCTTACAGTTGACGGTGTGCAATATTATTGCTACACGTCTAAGGACACTTTAGATGATATCTTACAACA
HCoV-SA1

          4330      4340      4350      4360      4370      4380      4390      4400
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
GGCTAATAAGTCTGTTGGTTATTATATCTATGCCTTTGGGATATGTGTCTCATGGTTTAGACTTAATGCAAGCAGGGAGTG
HCoV-SA1

          4410      4420      4430      4440      4450      4460      4470      4480
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
TCGTGCGTAGAGTTAACGTGCCCTACGTGTGTCTCCTAGCTAATAAAGAGCAAGAAGCTATTTTGATGTCTGAAGACGTT
HCoV-SA1

          4490      4500      4510      4520      4530      4540      4550      4560
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
AAGTTAAAACCCTTCAGAAGATTTTATAAAAGCACGTCCGCACTAATGGTGGTTACAATTCTTGGCATTTAGTCGAGGGTGA
HCoV-SA1

          4570      4580      4590      4600      4610      4620      4630      4640
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
ACTATTGGTGCAAGACTTACGCTTAAATAAGCTCCTGCATTGGTCTGATCAAACCATATGCTACAAGGATAGTGTGTTTT
HCoV-SA1

          4650      4660      4670      4680      4690      4700      4710      4720
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
ATGTTGTAAAGAATAGTACAGCTTTTCCATTTGAAACACTTTCAGCATGTCGTGCGTATTTTGGATTCACGCACGACACAG
HCoV-SA1

          4730      4740      4750      4760      4770      4780      4790      4800
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
CAGTTAACAATCGAAGTCTTAGTGACTGTCGATGGTGTAAATTTTAGAACAGTCGTTCTAAATAATAAGAACACTTATAG
HCoV-SA1
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          4810      4820      4830      4840      4850      4860      4870      4880
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  ATCACAGCTTGGATGCGTTTTCTTTAATGGTGCTGATATTTCTGACACCATTCCTGATGAGAAACAGAATGGTCACAGTT

          4890      4900      4910      4920      4930      4940      4950      4960
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  TATATCTAGCAGACAATTTGACTGCTGATGAAACAAAGGCGCTTAAAGAGTTATATGGCCCCGTTGATCCTACTTTCTTA

          4970      4980      4990      5000      5010      5020      5030      5040
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  CACAGATTCTATTCACTTAAGGCTGCAGTCCATGGGTGGAAGATGGTTGTGTGTGATAAGGTACGTTCTCTCAAATTGAG

          5050      5060      5070      5080      5090      5100      5110      5120
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  TGATAATAATTGTTATCTTAATGCAGTTTATTATGACACTTGATTTATTGAAGGACATTAAATTTGTTTATACCTGCTCTAC

          5130      5140      5150      5160      5170      5180      5190      5200
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  AGCATGCATTTATGAAACATAAGGGCGGTGATTCAACTGACTTCATAGCCCTCATTATGGCTTATGGCAATTGCACATTT

          5210      5220      5230      5240      5250      5260      5270      5280
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  GGTGCTCCAGATGATGCCTCTCGGTTACTTCATACCGTGCTTGCAAAGGCTGAGTTATGCTGTTCTGCACGCATGGTTTG

          5290      5300      5310      5320      5330      5340      5350      5360
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  GAGAGAGTGGTGCAATGTCTGTGGCATAAAAGATGTTGTTCTACAAGGCTTAAAAGCTTGTTGTTACGTGGGTGTGCAAA

          5370      5380      5390      5400      5410      5420      5430      5440
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  CTGTTGAAGATCTGCGTGCTCCGCATGACATATTGTATGCCAGTGTGGTGGTGAACGTCATCGGCAATTAGTCGAACACACC

          5450      5460      5470      5480      5490      5500      5510      5520
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  ACCCCCTGGTTGCTGCTCTCAGGCACACCAAATGAAAAATTGGTGACAACCTCCACGGCGCCTGATTTTTGTAGCATTTTAA

          5530      5540      5550      5560      5570      5580      5590      5600
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  TGTCTTTCAGGGCATTGAAACGGCTGTGGCCATTATGTTCATGCTCGCCTGAAGGGTGGTCTTATTTTAAAGTTTGACT
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          5610      5620      5630      5640      5650      5660      5670      5680
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  CTGGCACCGTTAGCAAGACTTCAGACTGGAAGTGCAAGGTGACAGATGTACTTTCCCCGGCCAAAAATACAGTAGCGAT

          5690      5700      5710      5720      5730      5740      5750      5760
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  TGTAATGTCGTACGGTATTCTTTGGACGGTAATTTCAGAACAGAGGTTGATCCCGACCTACTCTGCTTCTATGTTAAGGA

          5770      5780      5790      5800      5810      5820      5830      5840
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  TGGTAAATACTTTACAAGTGAAACCACCCGTAACATATTCACCAGCTACAATTTTAGCTGGTAGTGTCTACACTAATAGCT

          5850      5860      5870      5880      5890      5900      5910      5920
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  GCCTTGTATCGTCTGATGGACAACCTGGCGGTGATGCTATTAGTTTGAGTTTTAATACCTTTTAGGGTTTGATTCTAGT

          5930      5940      5950      5960      5970      5980      5990      6000
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  AAACCAGTCACTAAGAAATACACTTACTCCTTCTTGCCTAAGAAGACGGCGATGTGTTGTTGGCTGAGTTTGACACTTA

          6010      6020      6030      6040      6050      6060      6070      6080
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  TGACCCTATTTATAAGAATGGTGCCATGTATAAAGGCAAACCAATTCTTTGGGTCAATAAAGCATCTTATGATACTAATC

          6090      6100      6110      6120      6130      6140      6150      6160
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  TTAATAAGTTCAATAGAGCTAGTTTGCGTCAAATTTTTGACGTAGCCCCCATTGAACTCGAAAATAAATTCACACCTTTG

          6170      6180      6190      6200      6210      6220      6230      6240
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  AGTGTGGAGTCTACACCAGTTGAACCTCCAACTGTAGATGTGGTAGCACTTCAACAGGAAATGACAATTGTCAAATGTAA

          6250      6260      6270      6280      6290      6300      6310      6320
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  GGGTTTAAATAAACCTTTCGTGAAGGACAATGTCAGTTTCGTTGCTGATGATTCAGGTACTCCCGTTGTTGAGTATCTGT

          6330      6340      6350      6360      6370      6380      6390      6400
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  CTAAAGAAGACCTACATACATTGTATGTAGACCCTAAGTATCAAGTCATTGTCTTTAAAAGACAATGTACTTTCTTCTATG
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          6410      6420      6430      6440      6450      6460      6470      6480
     ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1 CTTAGATTGCACACCGTTGAGTCAGGTGATATTAACGTTGTTGCAGCTTCCGGATCTTTTGACACGTAAAGTGAAGTTACT

          6490      6500      6510      6520      6530      6540      6550      6560
     ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1 ATTTAGGGCTTCATTTTATTTCAAAGAAATTTGCTACCCGCACATTTCACTGCTACCACACTGCTTGTAGGTAGTTGTATAAAGA

          6570      6580      6590      6600      6610      6620      6630      6640
     ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1 GTGTAGTGCGGCATCTAGGTGTTACTAAAGGCATATTGACAGGCTGTTTTTAGTTTTTGCCAAGATGTTATTTATGCTTCCA

          6650      6660      6670      6680      6690      6700      6710      6720
     ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1 CTAGCTTACTTTAGTGATTCAAACTCGGCACCACAGAGGTTAAAGTGAGTGCTTTGAAAACAGCGGCGTTGTGACAGG

          6730      6740      6750      6760      6770      6780      6790      6800
     ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1 TAATGTTGTAAAACAGTGTTGCACTGCTGCTTGATTTAAGTATGGATAAGTTGCGCCGTGTGGATTGGAAATCAACCC

          6810      6820      6830      6840      6850      6860      6870      6880
     ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1 TACGGTTGTTACTTATGTTATGCACAACTATGGTATTGTGTCTTCTGTGTATCACTTGTATGTCTTCAATCAGGTCTTA

          6890      6900      6910      6920      6930      6940      6950      6960
     ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1 TCAAGTGATGTTAATGTTTGAAGATGCCCAAGGTTTGAAAAAGTTCTACAAAGAAGTTAGAGCTTACCTAGGAATCTCTTC

          6970      6980      6990      7000      7010      7020      7030      7040
     ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1 TGCTTGTGACGGTCTTGCTTCAGCTTATAGGGCGAATTCCTTTGATGTACCTACATTCTGCGCAAACCGTTCTGCAATGT

          7050      7060      7070      7080      7090      7100      7110      7120
     ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1 GTAATTGGTGCTTTGATTAGCCAAGATTCCATAACTCACTACCCAGCTCTTAAGATGGTTCAAACACATCTTAGCCACTAT

          7130      7140      7150      7160      7170      7180      7190      7200
     ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1 GTTCTTAACATAGATTGGTTGTGGTTTGCATTTGAGACTGGTTTGGCATACATGCTCTATACCTCGGCGTTCAACTGGTT
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          7210      7220      7230      7240      7250      7260      7270      7280
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  GTTGTTGGCAGGTACATTGCATTATTTCTTTGCACAGACTTCCATATTTGTAGACTGGCGGTCATACAATTATGCTGTGT

          7290      7300      7310      7320      7330      7340      7350      7360
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  CTAGTGCCTTCTGGTTATTCACCCACAATCCAATGGCGGGTTTGGTACGAATGTATAATTTGTTAGCATGCCTTTGGCTT

          7370      7380      7390      7400      7410      7420      7430      7440
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  TTACGCAAGTTTTATCAGCATGTAATCAATGGTTGCAAAGATACGGCATGCTTGCTCTGCTATAAGAGGAACCGACTTAC

          7450      7460      7470      7480      7490      7500      7510      7520
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  TAGAGTTGAAGCTTCTACCGTTGTCTGTGGTGGAAAACGTACGTTTTATATCACAGCAAAATGGCGGTAATTTCATTCTGTC

          7530      7540      7550      7560      7570      7580      7590      7600
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  GTAGGCATAATTGGAATTGTGTGGATTGTGACACTGCAGGTGTGGGGAATACCTTCATCTGTGAAGAAGTCGCAAAATGAC

          7610      7620      7630      7640      7650      7660      7670      7680
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  CTCACTACCGCCCTACGCAGGCCTAATTAACGCTACGGATAGATCACATTATTATGTGGATTCCGTTACAGTTAAAGAGAC

          7690      7700      7710      7720      7730      7740      7750      7760
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  TGTTGTTCAGTTTAATTATCGTAGAGACGGTCAACCATTCTACGAGCGGTTTCCCCCTCTGCGCTTTACAAATCTAGATA

          7770      7780      7790      7800      7810      7820      7830      7840
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  AGTTGAAGTTCAAAGAGGTCTGTAAAACTACTACTGGTATACCTGAATACAACTTTATCATCTACGACTCATCAGATCGT

          7850      7860      7870      7880      7890      7900      7910      7920
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  GGCCAGGAAAGTTTAGCTAGGTCTGCAATGTGTTTTATTTCTCAAGTCTTGTGTAAATCAATTCTTTTGGTTGACTCAAG

          7930      7940      7950      7960      7970      7980      7990      8000
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  TTTGGTTACTTCTGTTGGTGATTCTAGTGAAATCGCCACTAAAATGTTTGATTCCTTTGTTAATAGTTTCGTCTCGCTGT
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          8010      8020      8030      8040      8050      8060      8070      8080
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  ATAATGTCACACGCGATAAGTTGGAAAACTTATCTCTACTGCTCGTGATGGCGTAAGGCGAGGCGATAACTTCCATAGT

          8090      8100      8110      8120      8130      8140      8150      8160
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  GTCTTAACAACATTCATTGACGCAGCACGAGGCCCCGCAGGTGTGGAGTCTGATGTTGAGACCAATGAAATTGTTGACTC

          8170      8180      8190      8200      8210      8220      8230      8240
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  TGTGCAGTATGCTCATAAACATGACATACAAATTACTAAATGAGCTACAATAAATTATGTACCCTCATATGTTAAACCTG

          8250      8260      8270      8280      8290      8300      8310      8320
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  ATAGTGTGTCTACCAGCGATTTAGGTAGTCTCATTGATTGTAATGCGGCTTCAGTTAACCAAATTGTCTTGCGTAATTCT

          8330      8340      8350      8360      8370      8380      8390      8400
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  AATGGTGCTTGCATTTGGAACGCTGCTGCATATATGAAACTCTCGGATGCACTTAAACGACAGATTCGCATTGCATGCCG

          8410      8420      8430      8440      8450      8460      8470      8480
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  TAAGTGTAATTTAGCTTTCCGGTTAACCACCTCAAAGCTACGCGCTAAATGATAAATATCTTATCAGTTAGATTCACTGCTA

          8490      8500      8510      8520      8530      8540      8550      8560
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  ACAAAATTGTTGGTGGTGCTCCCTACATGGTTTAATGCGTTGCGTGACTTTTACGTTTAAGGGTTATGTCTTGCTACCATT

          8570      8580      8590      8600      8610      8620      8630      8640
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  ATTGTGTTTCTGTGTGCTGTACTGATGTATTTGTGTTTACCTACATTTTCTATGGCACCTGTTGAATTTATTATGAAGACCG

          8650      8660      8670      8680      8690      8700      8710      8720
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  CATCTTGGACTTTAAAGTTCTTTGATAAATGGTATCATTTAGGGATGTAAATCCTGATGATAAGTGCTTTGCTAATAAGCACC

          8730      8740      8750      8760      8770      8780      8790      8800
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  GGTCCTTCACACAATGGTATCATGAGCAATGTTGGTGGTGTCTATGACAACTCTATCACATGCCCATTGACAGTTGCAGTA
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          8810      8820      8830      8840      8850      8860      8870      8880
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  ATTGCTGGAGTTGCTGGTGCTCGCATTCCAGACGTACCTACATTGGCTTGGGTGAACAATCAGATAATTTCTTTGT

          8890      8900      8910      8920      8930      8940      8950      8960
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  TTCTCGAGTCTTTGCTAATACAGGCAGTGTTGCTACACTCCTATAGATGAGATACCCTAAGAGTTTCTCTGATAGTG

          8970      8980      8990      9000      9010      9020      9030      9040
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  GTTGCATTCTTCCATCTGAGTGCACTATGTTTAGGGATGCAGAGGGCCGTATGACACCATACTGCCATGATCCTACTGTT

          9050      9060      9070      9080      9090      9100      9110      9120
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  TTGCCTGGGGCTTTTGCGTACAGTCAGATGAGGCCTCATGTTCGTTACGACTTGTATGATGGTAACAATGTTTATTAAATT

          9130      9140      9150      9160      9170      9180      9190      9200
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  TCCTGAAGTAGTATTTGAAAGTTACACTTAGGATTACTAGAACTCTGTCAACTCAGTACTGCCGGTTCGGTAGTTGTGAGT

          9210      9220      9230      9240      9250      9260      9270      9280
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  ATGCACAAGAGGGTGTTTGTATTACCACAAATGGCTCGTGGGCCATTTTTTAATGACCACCATCTTAAATAGACCTGGTGTC

          9290      9300      9310      9320      9330      9340      9350      9360
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  TATTGTGGCTCTGATTTTATTGACATTGTCAGGCGGTTAGCAGTATCACTGTTCCAGCCTATTACTTAATTTCCAATTGAC

          9370      9380      9390      9400      9410      9420      9430      9440
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  TACCTCATTGGTCTTGGGTATAGGTTTGTGCGTTCCTGACTTTGCTCTTCTATATTATTAAATAAAGTATAAAACGTGCTT

          9450      9460      9470      9480      9490      9500      9510      9520
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  TTGCAGATTACACCCAGTGTGCTGTAATTGCTGTTGCTGCTTCTTAAATAGCTTGTGCATCTGCTTTGTTACCTCT

          9530      9540      9550      9560      9570      9580      9590      9600
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  ATACCATTGTGTAATAGTACCTTACACTGCATTGTACTATTAGCTACATTCTATTTTACTAATGAGCCTGCATTTATTAT
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          9610      9620      9630      9640      9650      9660      9670      9680
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  GCATGTTTCTTGGTACATTATGTTCGGGCCTAATCGTTCCCATATGGATGACCTGCGTCTATACAGTTGCAATGTGCTTTA

          9690      9700      9710      9720      9730      9740      9750      9760
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  GACACTTCTTCTGGGTTTAGCTTATTTTAGTAAGAAACATGTAGAAGTTTTTACTGATGGTAAGCTTAATTGTAGTTTC

          9770      9780      9790      9800      9810      9820      9830      9840
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  CAGGACGCTGCCTCTAATATCTTTGTTATTAACAAGGACACTTATGCAGCTCTTAGAAACTCTTTAACTAATGATGCCTA

          9850      9860      9870      9880      9890      9900      9910      9920
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  TTCACGATTTTTGGGGTTGTTTAACAAGTATAAGTACTTCTCTGGTGCTATGGAAACAGCCGCTTATCGTGAAGCTGCAG

          9930      9940      9950      9960      9970      9980      9990      10000
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  CATGTCATCTTGCTAAAGCCTTACAAACATACAGCGAGACTGGTAGTGATCTCTTTTACCAACCACCCAACTGTAGCATA

          10010     10020     10030     10040     10050     10060     10070     10080
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  ACCTCTGGCGTGTTGCAAAGCGGTTTGGTGAAAATGTCACATCCCAGTGGAGATGTTGAGGCTTGTATGGTTCAGGTTAC

          10090     10100     10110     10120     10130     10140     10150     10160
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  CTGCGGTAGCATGACTCTTAATGGTCTTTGGCTTGACAACACAGTCTGGTGCCCACGACACGTAATGTGCCCGGCTGACC

          10170     10180     10190     10200     10210     10220     10230     10240
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  AGTTGTCTGATCCTAATTATGATGCCTTGTTGATTTCTATGACTAATCATAGTTTCAGTGTGCAAAAACACATTGGCGCT

          10250     10260     10270     10280     10290     10300     10310     10320
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  CCAGCAAACTTGCGTGTTGTTGGTCATGCCAAGGCACTCTTTTTGAAGTTGACTGTCGATGTTGCTAACCCTAAGCAC

          10330     10340     10350     10360     10370     10380     10390     10400
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  TCCAGCCTACACTTTTTACAACAGTGAAACCTGGCGCAGCATTTAGTGTGTTAGCAATGGTCGTCCGACTGGTA
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          10410     10420     10430     10440     10450     10460     10470     10480
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  CATTCACTGTTGTAATGCGCCCTAACTACACAATTAAGGGTTCCTTTCTGTGTGGTTCTTGTGGTAGTGTTGGTTACACC

          10490     10500     10510     10520     10530     10540     10550     10560
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  AAGGAGGGTAGTGTGATCAATTTCTGTTACATGCATCAAATGGAACTTGCTAATGGTACACATACCGGTTCAGCATTTGA

          10570     10580     10590     10600     10610     10620     10630     10640
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  TGGTACTATGTATGGTGCCTTTATGGATAAACAAGTGCACCAAGTTCAGTTAACAGACAAATACTGCAGTGTTAATGTAG

          10650     10660     10670     10680     10690     10700     10710     10720
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  TAGCTTGGCTTTACGCAGCAATACTTAATGGTTGCGTTGGTTTGTAAAACCTAATCGCACTAGTGTTGTTTCTTTTAAT

          10730     10740     10750     10760     10770     10780     10790     10800
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  GAATGGGCTCTTGCCAACCAATTCACTGAATTTGTTGGCACTCAATCCGTTGACATGTTAGCTGTCAAAACAGGCGTTGC

          10810     10820     10830     10840     10850     10860     10870     10880
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  TATTGAACAGCTGCTTTATGCGATCCAACAACTGTATACTGGTTCCAGGGAAGCAAATCCTTGGCAGTACCATGTTGG

          10890     10900     10910     10920     10930     10940     10950     10960
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  AAGATGAATTCACACCTGAGGATGTTAAATATGCAGATTATGGGTGTGGTTATGCAGAGTGGTGTGAGAAAAGTTACATAT

          10970     10980     10990     11000     11010     11020     11030     11040
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  GGTACTGCGCATTGGTTGTTTGCGACCCTTGTCTCAACCTATGTGATAAATCTTACAAGCCACTAAATTTACTTTGTGGAA

          11050     11060     11070     11080     11090     11100     11110     11120
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  CTACTTGTTTGAGACTATTCCCACACAGGTTGTTCCCACTCTTATTTGTGACTATGGCCTTCGTTATGTTGGTTTAAAC

          11130     11140     11150     11160     11170     11180     11190     11200
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  ACAAACACACCTTTTTGACACTTTTCTGTTGCCTGTGGCTATTTGTTTGACTTAATGCAAACATAGTCTACGAGCCCACT
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        11210     11220     11230     11240     11250     11260     11270     11280
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
ACTCCCATTTCGTCAGCGCTGATTGCAGTTGCAAATTGGCTTGCCCCCACTAATGCTTATATTGCGCACTACACTACTGA
HCoV-SA1

        11290     11300     11310     11320     11330     11340     11350     11360
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
TATTGGTGTCTACATTAGTAATGTCACTTGTATTAGTCATTGTAGTGAAGAGATTGTACAACCATCACTTTCTAACTTTTG
HCoV-SA1

        11370     11380     11390     11400     11410     11420     11430     11440
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
CGTTAGCAATTGTGCAGTGGTGTAATGTGGTTGTACACTTATAGCATTTGGAGAAGCCTCAAGCCCCATTGCCTATCTGGTT
HCoV-SA1

        11450     11460     11470     11480     11490     11500     11510     11520
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
TTTGTCACTACACTCACTAGTGATTATACGATTCAGTCTTTGTTACTGTCAACCTTGCAAAAGTTTGCACTTATGCCAT
HCoV-SA1

        11530     11540     11550     11560     11570     11580     11590     11600
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
CTTTGCTTACTCACCACCACAGCTTACACTTGTGTTTCCGGAAGTGATGAAGATGATACTTTTTATTATACACATGTTTAGGTTTTCA
HCoV-SA1

        11610     11620     11630     11640     11650     11660     11670     11680
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
TGTGTACTTGCTATTTTTGGTGTCTTCTCTCTTTTGAACCTTAAGCTTAGAGCACCTATGGGTGTCTATGACTTTAAGGTC
HCoV-SA1

        11690     11700     11710     11720     11730     11740     11750     11760
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
TCAACACAAGAGTTCAGATTCATGACTGCTAACAATCTAACTGCACCTAGAAATTCTTGGGAGGCTATGGCTCTGAACTT
HCoV-SA1

        11770     11780     11790     11800     11810     11820     11830     11840
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
TAAGTTTAATAGGTATTGGCGGTACACCTTGTATAAAGGTTGCTGCTATGCAGTCTTAAACTTACAGATCTTTAAATGCACAT
HCoV-SA1

        11850     11860     11870     11880     11890     11900     11910     11920
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
CTGTGGTTCTCCTCTCTGTGCTCCAACAGTTACACTTAGAGGCTAATAGTAGGGCCTGGGCTTTCTGTGTTAAATGCCAT
HCoV-SA1

        11930     11940     11950     11960     11970     11980     11990     12000
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
AATGATATATTGGCAGCAACAGTGAGGCTTTCGAGAAATTCGTAAGTCCTTGCTACTTTAAATGACTTTTTC
HCoV-SA1
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          12010     12020     12030     12040     12050     12060     12070     12080
..... | ..... | ..... | ..... | ..... | ..... | ..... | ..... | ..... | ..... |
HCoV-SA1 TGGTAATGTAGATCTTGATGCGTTAGCTAGTGATATTTTTGACACTCCTAGCGTACTTCAAGCTACTCTTTCTCTGAGTTTT

          12090     12100     12110     12120     12130     12140     12150     12160
..... | ..... | ..... | ..... | ..... | ..... | ..... | ..... | ..... | ..... |
HCoV-SA1 CACACTTAGCTACCTTTGCTGAGTTGGAAGCTGCGCAGAAAGCCTATCAGGAAGCTATGGACTCTGGTGACACCTCACCA

          12170     12180     12190     12200     12210     12220     12230     12240
..... | ..... | ..... | ..... | ..... | ..... | ..... | ..... | ..... | ..... |
HCoV-SA1 CAAGTTCTTTAAGGCTTTGCAGAAGGCTGTTAAATATAGCTTAAAAACGCCTATGAGAAGGATAAGGCAGTGGCCGTAAGTT

          12250     12260     12270     12280     12290     12300     12310     12320
..... | ..... | ..... | ..... | ..... | ..... | ..... | ..... | ..... | ..... |
HCoV-SA1 AGAACGTATGGCTGATCAGGCTATGACTTCTATGTATAAGCAAGCACGTGCTGAAGACAAGAAAGCAAAAATTGTCAGTG

          12330     12340     12350     12360     12370     12380     12390     12400
..... | ..... | ..... | ..... | ..... | ..... | ..... | ..... | ..... | ..... |
HCoV-SA1 CTATGCAAACTATGTTGTTTGGTATGATTAAGAAGCTCGACAACGATGTTCTTAATGGTATCATTTCTAACGCTAGGAAT

          12410     12420     12430     12440     12450     12460     12470     12480
..... | ..... | ..... | ..... | ..... | ..... | ..... | ..... | ..... | ..... |
HCoV-SA1 GGTTGTAATACCTCTTTAGTGTCATCCCACTGTGTGCTTCAAATAAACTTCGCGTTGTAATTCCTGACTTCACCGTCTGGAA

          12490     12500     12510     12520     12530     12540     12550     12560
..... | ..... | ..... | ..... | ..... | ..... | ..... | ..... | ..... | ..... |
HCoV-SA1 TCAGGTAGTCACAATATCCCTCGCTTAACTACGCTGGGGCTTTGTGGGACATTACAGTTATAAACAATGTGGACAATGAAA

          12570     12580     12590     12600     12610     12620     12630     12640
..... | ..... | ..... | ..... | ..... | ..... | ..... | ..... | ..... | ..... |
HCoV-SA1 TTGTTAAGTCTTCAGATGTTGTAGACAGCAATGAAAATTTAACATGGCCACTTGTTTTTAGAATGCACTAGGGCATCCACT

          12650     12660     12670     12680     12690     12700     12710     12720
..... | ..... | ..... | ..... | ..... | ..... | ..... | ..... | ..... | ..... |
HCoV-SA1 TCTGCCGTTAAGTTGCAAAATAATGAGATCAAACCTTCAGGTCTAAAAACCATGGTTGTGTCTGCGGGTCAAGAGCCAAAC

          12730     12740     12750     12760     12770     12780     12790     12800
..... | ..... | ..... | ..... | ..... | ..... | ..... | ..... | ..... | ..... |
HCoV-SA1 TAACTGTAATACTAGTTCCTTAGCTTATTACGAACCCTGTGCAGGGTCGTAAAATGCTGATGGCCTCTTCTTTCTGATAATG
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          12810     12820     12830     12840     12850     12860     12870     12880
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  CCTATCTCAAATGGGCGCGTGTTGAAGGTAGGACGGATTTGTCAGTGTAGAGCTACAACCTCCTTGCAAATTCTTGATT

          12890     12900     12910     12920     12930     12940     12950     12960
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  GCGGGACCAAAAGGACCTGAAATCCGATATCTCTAATTTGTTAAAAATCTTAACAACCTTCATCGCGGGCAAGTGTTAGG

          12970     12980     12990     13000     13010     13020     13030     13040
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  GCACATTGCTGCGACTGTTAGATTGCAAGCTGGTTCTAACACCGAGTTTGCCTCTAATTCCTCGGTGTTGTCACTTGTTA

          13050     13060     13070     13080     13090     13100     13110     13120
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  ACTTCACCGTTGATCCTCAAAAAGCTTATCTCGATTTCGTCAATGCGGGAGGTGCCCCATTGACAAATTGTGTTAAGATG

          13130     13140     13150     13160     13170     13180     13190     13200
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  CTTACTCCTAAAACTGGTACAGGTATAGCTATATCTGTTAAACCAGAGAGTACAGCTGATCAAGACTTATGGTGGAGC

          13210     13220     13230     13240     13250     13260     13270     13280
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  TTCAGTGTGTCTCTAATTGCCGTGCGCATATAGAACATCCTGATGTCTCTGGTGTTTGTAAATATAAAGGGTAAGTTTGTCC

          13290     13300     13310     13320     13330     13340     13350     13360
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  AAATCCCTGCTCAGTGTGTCCGTGACCCTGTGGGATTTTGTTTGTCAAATACCCCCTGTAATGTCTGTCAATATTGGATT

          13370     13380     13390     13400     13410     13420     13430     13440
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  GGATATGGGTGCAATTGTGACTCGCTTAGGCAAGCAGCACTGCCCCAAATCTAAAGATTCCAATTTTTTAAACGAGTCCGG

          13450     13460     13470     13480     13490     13500     13510     13520
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  GGTTCTATTGTAAATGCCCGAATAGAACCCTGTTCAAGTGGTTTGTCCACTGATGTCGTCTTTAGGGCATTTGACACTCTG

          13530     13540     13550     13560     13570     13580     13590     13600
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  CAACTATAAGGCTAAGGTTGTGGTATTGGAAAATACTACAAGACTAATACTTGTAGGTTTGTAGAATTAGATGACCAAG
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                13610     13620     13630     13640     13650     13660     13670     13680
           ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1   GGCATCATTTAGACTCCTATTTTGTCGTTAAGAGGCATACTATGGAGAATTATGAACTAGAGAAGCACTGTTACGACTTG

                13690     13700     13710     13720     13730     13740     13750     13760
           ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1   TTACGTGACTGTGATGCTGTAGCTCCCCATGATTTCTTCATCTTTGATGTAGACAAAGTTAAAACACCTCATATTGTACG

                13770     13780     13790     13800     13810     13820     13830     13840
           ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1   TCAGCGTTTAACTGAGTACACTATGATGGATCTTGTATATGCCCTGAGGCACTTTGATCAAAATAGCGAAGTGCTTAAGG

                13850     13860     13870     13880     13890     13900     13910     13920
           ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1   CTATCTTAGTGAAGTATGGTTGCTGTGATGTTACCTACTTTGAAAATAAACTCTGGTTTGATTTTGTTGAAAATCCCAGT

                13930     13940     13950     13960     13970     13980     13990     14000
           ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1   GTTATTGGTGTTTATCATAAACTTGGAGAACGTGTACGCCAAGCTATCTTAAACACTGTTAAATTTTGTGACCACATGGT

                14010     14020     14030     14040     14050     14060     14070     14080
           ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1   CAAGGCTGGTTTAGTCGGTGTGCTCACACTAGACAACCAGGACCTTAATGGCAAGTGGTATGATTTTGGTGACTTCGTAA

                14090     14100     14110     14120     14130     14140     14150     14160
           ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1   TCACTCAACCTGGTTCAGGAGTAGCTATAGTTGATAGCTACTATTCTTATTTGATGCCTGTGCTCTCAATGACCGATTGT

                14170     14180     14190     14200     14210     14220     14230     14240
           ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1   CTGGCCGCTGAGACACATAGGGATTGTGATTTTAATAAACCACTCATTGAGTGGCCACTTACTGAGTATGATTTTACTGA

                14250     14260     14270     14280     14290     14300     14310     14320
           ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1   TTATAAGGTACAACTCTTTGAGAAGTACTTTAAATATTGGGATCAGACGTATCACGCAAATTGCGTTAATTGTACTGATG

                14330     14340     14350     14360     14370     14380     14390     14400
           ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1   ACCGTTGTGTGTTACATTGTGCTAATTTCAATGTATTGTTTGCTATGACCATGCCTAAGACTTGTTTCGGACCCATAGTC
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      14410     14420     14430     14440     14450     14460     14470     14480
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1 CGAAAGATCTTTGTTGATGGCGTGCCATTTGTAGTATCTTGTGGTTATTCACTACAAAGAATTAGGTTTAGTCATGAATAT

      14490     14500     14510     14520     14530     14540     14550     14560
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1 GGATGTTAGTCTCCATAGACATAGGCTCTTCTCTTAAAGGAGTTGATGATGTATGCCGCTGATCCAGCCATGCACATTGCCT

      14570     14580     14590     14600     14610     14620     14630     14640
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1 CCTCTTAACGCTTTTCTTTGATTTTAGGACATCATGTTTTAGTGTCGCTGCACTTACAACTGGTTTGACTTTTTCAAACTGTG

      14650     14660     14670     14680     14690     14700     14710     14720
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1 CGGCCTGGCAATTTTAACCAAGACTTCTATGATTTCGTGGTAATCTAAAGGTTTCTTTTAAGGAGGGCTCTTTCAGTGACGCT

      14730     14740     14750     14760     14770     14780     14790     14800
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1 CAAACATTTTTTCTTTGCTCAAGATGGTAATGCTGCTATTACAGATTATAATTACTATTCTTATAATCTGCCTACTATGT

      14810     14820     14830     14840     14850     14860     14870     14880
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1 GTGACATCAAACAAATGTTGTTCTGCATGGAAGTTGTAAACAAGTACTTTCGAAATCTATGACGGTGGTTGTCTTAATGCT

      14890     14900     14910     14920     14930     14940     14950     14960
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1 TCTGAAGTGGTTGTTAATAATTTAGACAAGAGTGCTGGCCATCCTTTTAATAAGTTTGGCAAAGCTCGTGTCTATTATGA

      14970     14980     14990     15000     15010     15020     15030     15040
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1 GAGCATGTCTTACCAGGAGCAAGATGAACTTTTTGCCATGACAAAGCGTAACGTCATTCCTACCATGACTCAAATGAATC

      15050     15060     15070     15080     15090     15100     15110     15120
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1 TAAAATATGCTAATTAGTGCTTAAGAATTAGAGCTCGCACTGTTGCAGGCGTGTCCATACTTAGCACAATGACTAATCGCCAG

      15130     15140     15150     15160     15170     15180     15190     15200
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1 TACCATCAGAAAATGCTTAAGTCCATGGCTCGTGGAGCGACTTGCGTCATTGGTACTACAAAGATTCTACGGTGG
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          15210     15220     15230     15240     15250     15260     15270     15280
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  CTGGGATTTCATGCTTAAAACATTGTACAAAGATGTTGATAATCCGCATCTTATGGGTTGGGATTACCCTAAGTGTGATA

          15290     15300     15310     15320     15330     15340     15350     15360
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  GAGCTATGCCTAAATATGTGTAGAATCTTCGCTTCACTCATATTAGCTCGTAAACATGGCACTTGTTGTACTACAAGGGAC

          15370     15380     15390     15400     15410     15420     15430     15440
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  AGATTTTTATCGCTTGGCAAATGAGTGTGCTCAGGTGCTAAGCGAATATGTTCTAATGTGGTGGTTACTACGTCAAACC

          15450     15460     15470     15480     15490     15500     15510     15520
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  TGGAGGTACCAGTAGCGGAGATGCCACCACTGCATATGCCAATAGTGTCTTTAACATTTTGCAGGCGACAACTGCTAATG

          15530     15540     15550     15560     15570     15580     15590     15600
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  TCAGTGCACTTATGGGTGCTAATGGCAACAAGATTGTTGACAAAGAAGTTAAAGACATGCAGTTTGATTTGTATGTCAAT

          15610     15620     15630     15640     15650     15660     15670     15680
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  GTTTACAGGAGCACTAGCCCAGACCCCAAATTTGTTGATAAATACTATGCTTTTCTTAATAAGCACACTTTTCTATGATGAT

          15690     15700     15710     15720     15730     15740     15750     15760
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  ACTGTCTGATGACGGTGTCGTTTGCTAAAATAGTGATATTGCAGCTAAGGGTTACATTGCTGGAATACAGAATTTTAAGG

          15770     15780     15790     15800     15810     15820     15830     15840
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  AAACGCTGTATTATCAGAACAATGTCTTTATGTCTGAAGCTAAATGCTGGGTGGAAACCGATCTGAAGAAAGGGCCACAT

          15850     15860     15870     15880     15890     15900     15910     15920
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  GAATTCTGTTCACAGCATACGCTTTATATTAAGGATGGCGACGATGGTTACTTCCTTCCTTATCCAGACCCTTCAAGAAT

          15930     15940     15950     15960     15970     15980     15990     16000
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  TTTGTCEGCGGTTGCTTTGTAGATGAATCGTTAAGACTGACGGTACACTCATGGTAGAGCGGTTTGTGTCTTTGGCTA
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          16010     16020     16030     16040     16050     16060     16070     16080
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  TAGATGCTTACCCTCTCACAAAGCATGAAGATATAGAATGTATTCTGGGTCTACTTACAGTATATAGAAAAA

          16090     16100     16110     16120     16130     16140     16150     16160
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  CTGTATAAAGACCTTACAGGACACATGCTTTGACAGTTATTCTGTCATGCTATGGTGATAATTCTGCTAAGTTTTGGGA

          16170     16180     16190     16200     16210     16220     16230     16240
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  AGAGGCATTCTATAGAGATCTCTATAGTTCGCCTACCACTTTGCAGGCTGTCGGTTTCATGCGTTTGTATGCCATTCACACGA

          16250     16260     16270     16280     16290     16300     16310     16320
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  CTTCCCTACGCTGTGGGACATGCATCCGTAGACCATTTCTCTGCTGTAAATGCTGCTATGATCATGTTTATAGCAACTCCA

          16330     16340     16350     16360     16370     16380     16390     16400
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  CATAAGATGGTTTTGTCTGTTTCTCCTTACGTTTGTAATGCCCCTGGTTGTGGCGTTTCAGACGTTACTAAGCTATATTT

          16410     16420     16430     16440     16450     16460     16470     16480
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  AGGTGGTATGAGCTACTTTTGTGTAGATCATAGACCTGTGTGTAGTTTTTCCACTTTGCGCTAATGGTCTTGTATTCGGCT

          16490     16500     16510     16520     16530     16540     16550     16560
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  TATACAAGAATATGTGCACAGGTAGTCCTTCTATAGTTGAATTTAATAGGTTGGCTACCTGTGACTGGACTGAAAGTGGT

          16570     16580     16590     16600     16610     16620     16630     16640
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  GATTACACCCTTGCCAATACTACAACAGAACCACTCAAACTTTTTGCTGCTGAGACTTTACGTGCCACTGAAGAGGCGTC

          16650     16660     16670     16680     16690     16700     16710     16720
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  TAAGCAGTCTTAATGCTATTGCCACCATCAAAGAAATTGTTGGTGAGCGCCAACTATTACTTTGTGTGGGAGGCTGGCAAGT

          16730     16740     16750     16760     16770     16780     16790     16800
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  CCAAACCACCACTCAATCGTAATTATGTTTTTACTGGTTATCATATAACCAAAAAATAGTAAAGTGCAGCTCGGTGAGTAC
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          16810     16820     16830     16840     16850     16860     16870     16880
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  ATTTTCGAGCGCATTGATTATAGTGATGCTGTATCCCTACAAGTCTAGTACAACGTATAAACTGACTGTAGGTGACATCTT

          16890     16900     16910     16920     16930     16940     16950     16960
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  CGTACTTACCTCTCACTCTGTGGCTACCTTTGACGGCGCCCACAATTGTGAATCAAGAGAGGTATGTTAAAATTACTGGGT

          16970     16980     16990     17000     17010     17020     17030     17040
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  TGTACCCAACCATTACGGTACCTGAAGAGTTCGCAAGTCATGTTGCCAACTTCCAAAATCAGGTTATAGTAAATATGTC

          17050     17060     17070     17080     17090     17100     17110     17120
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  ACTGTTCAGGGACCACCTGGCACTGGCAAAAGTCATTTTGCTAAGGGTTAGCGATTTACTACCCTACAGCACGTGTTGT

          17130     17140     17150     17160     17170     17180     17190     17200
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  TTATACAGCATGTTCACACGCAGCTGTTGATGCTTTGTGTGAAAAAGCTTTTAAATATTTGAACATTGCTAAATGTTCCC

          17210     17220     17230     17240     17250     17260     17270     17280
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  GTATCATTCCTGCAAAGGCACGTGTTGAGTGCTATGACAGGTTTAAAGTTTAATGAGACAAATTCTCAATATTTGTTTAGT

          17290     17300     17310     17320     17330     17340     17350     17360
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  ACTATTAATGCTCTACCAGAAACTTCTGCCGATATTCTGGTGGTTGATGAGGTTATGTGCACTAAATTATGATCTTTC

          17370     17380     17390     17400     17410     17420     17430     17440
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  AATTATTAATGCACGTATTAAAGCTAAGCACATTGTCTATGTAGGAGATCCAGCACAGTTGCCAGCTCCTAGGACTTTGT

          17450     17460     17470     17480     17490     17500     17510     17520
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  TGACTAGAGGCACATTGGAACCAGAAAATTTCAAATAGTGTCACTAGATTGATGTGTAACTTAGGTCCTGACATAATTTTTA

          17530     17540     17550     17560     17570     17580     17590     17600
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  AGTATGTGCTACAGGTGTCCTAAGGAAATAGTAAGCACTGTGAGGCGCTCTTGTCTACAATAAATAAATTGTTAGCCAAGAA
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          17610     17620     17630     17640     17650     17660     17670     17680
..../.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|....
HCoV-SA1  GGAGCTTTCAGGCCAGTGCTTTAAAAATACTCTATAAAGGGCAATGTGACGCATGATGCTAGCTCTGCCATTAATAGACCAC

          17690     17700     17710     17720     17730     17740     17750     17760
..../.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|....
HCoV-SA1  AACTCACATTTGTGAAGAATTTTATTACTGCCAATCCGGCATGGAGTAAGGCAGTCTTTAATTTCGCCTTACAATTCACAG

          17770     17780     17790     17800     17810     17820     17830     17840
..../.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|....
HCoV-SA1  AATGCTGTGTCTCGTTCAATGCTGGGTCTTACCACTCAGACTGTTGATTCCTCACAGGGTTCAGAATACCAGTACGTTAT

          17850     17860     17870     17880     17890     17900     17910     17920
..../.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|....
HCoV-SA1  CTTCTGTCAAACAGCAGATACGGCACAGCTAACACATTAACAGATTTAATGTTGCAATCACTCGTGCCCAAAAAGGTA

          17930     17940     17950     17960     17970     17980     17990     18000
..../.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|....
HCoV-SA1  TTCTTTGTGTTATGACATCTCAGGCACTCTTTGAGTCCTTAGAGTTTACTGAATTGTCTTTTTACTAATTACAAGCTCCAG

          18010     18020     18030     18040     18050     18060     18070     18080
..../.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|....
HCoV-SA1  TCTCAGATTGTAACTGGCCTTTTTAAAGATTGCTCTAGAGAAACTTCTGGCCTCTCACCTGCTTATGCACCAACATATGT

          18090     18100     18110     18120     18130     18140     18150     18160
..../.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|....
HCoV-SA1  TAGTGTTGATGACAAGTATAAAGACGAGTGATGAGCTTTGCGTGAATCTTAATTTACCCGCAAATGTCCCATACTCTCGTG

          18170     18180     18190     18200     18210     18220     18230     18240
..../.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|....
HCoV-SA1  TTATTTCCAGGATGGGCTTTAAACTCGATGCAACAGTTCCTGGATATCCTAAGCTTTTTCATTACTCGTGAAGAGGCTGTA

          18250     18260     18270     18280     18290     18300     18310     18320
..../.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|....
HCoV-SA1  AGGCAAGTTCGAAGCTGGAATAGGCTTCGATGTTGAGGGTGCTCATGCTTCCCGTAATGCAATGTGGCACCAATGTGCCTCT

          18330     18340     18350     18360     18370     18380     18390     18400
..../.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|....
HCoV-SA1  ACAATTAGGATTTTCAACTGGTGTGAACTTTGTTTCAGCCAGTTGGTGTTGTAGACACTGAGTGGGGTAACATGTTAA
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          18410     18420     18430     18440     18450     18460     18470     18480
     .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1 CGGGCATTGCTGCACGTCCTCACCAGGTGAACAGTTAAGCACCTCGTGCCTCTTATGCATAAGGGGCTGCGTGGCCT

          18490     18500     18510     18520     18530     18540     18550     18560
     .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1 ATTGTTAGACGACGTATAGTGCAAATGTTGTCAGACACTTTAGACAAATTGTCTGATTACTGTACGTTTGTTTGGGC

          18570     18580     18590     18600     18610     18620     18630     18640
     .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1 TCATGGCTTTGAATTAACGTCTGCATCATACTTTTGCAAGATAGGTAAGGAACAGAAGTGTTGCATGTGCAATAGACGCG

          18650     18660     18670     18680     18690     18700     18710     18720
     .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1 CTGCAGCGTACTCTTCACCTCTGCAATCTTATGCCTGCTGGACTCATTCCTGCGGTTATGATTATGTCTACAACCCTTTC

          18730     18740     18750     18760     18770     18780     18790     18800
     .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1 TTTGTCGATGTTCAACAGTGGGGTTATGTAGGCAATCTTGCTACTAATCACGATCGTTATTGCTCTGTCCATCAAGGAGC

          18810     18820     18830     18840     18850     18860     18870     18880
     .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1 TCATGTGGCTTCTAATGATGCAATAAATGACTCGTTGTTTAGCTATTCATTCTTGTTTTTATAGAACGTGTGGATTGGGATA

          18890     18900     18910     18920     18930     18940     18950     18960
     .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1 TAGAGTATCCTTATATCTCACATGAAAAGAAATTGAATTCCTGTTGTAGAATCGTTGAGCGCAACGTCGTACGTGCTGCT

          18970     18980     18990     19000     19010     19020     19030     19040
     .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1 CTTCTTGCCGGTTCATTTGACAAAGTCTATGATATTGGCAATCCTAAAGGAATTCCTATTGTTGATGACCCTGTGGTTGA

          19050     19060     19070     19080     19090     19100     19110     19120
     .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1 TTGGCATTATTTTTGATGCACAGCCCTTGACCAGGAAGGTACAACAGCTTTTCTATACAGAGGACATGGCCTCAAGAATTTG

          19130     19140     19150     19160     19170     19180     19190     19200
     .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1 CTGATGGGCTCTGCTTATTTTGGAACTGTAATGTACCAAAAATATCCTAATAATGCAATTGTATGCAGGTTTGACACACGT
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          19210     19220     19230     19240     19250     19260     19270     19280
          ....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  GTGCATTCTGAGTTCAATTTGCCAGGTTGTGATGGCGGTAGTTTGTATGTTAACAAGCACGCTTTTCATACCAGCATA

          19290     19300     19310     19320     19330     19340     19350     19360
          ....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  TGAATGTGAGTGCATTCCGTGATCTGAAACCTTACCATCTTTTATTATCTACACCATGTGAAGTGCATGGTAATG

          19370     19380     19390     19400     19410     19420     19430     19440
          ....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  GTAGTTATGATAGAGGATATTGATTATGTACCCCTAAAATCTGCAGTCTGTATTACAGCTTGTAATTTAGGGGGCGCTGTT

          19450     19460     19470     19480     19490     19500     19510     19520
          ....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  TGTAGGAAGCATGCTACAGAGAGTATATGGAAGCATATAATCTTGTCTCTGCATCAGGTTTCCGCCTTTGGTG

          19530     19540     19550     19560     19570     19580     19590     19600
          ....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  TTATAAGACCTTTGATATTTATAATCTCTGGTCTACTTTTACAAAAGTTCAAGGTTTGGAAAACATTGCTTTTTAATGTTG

          19610     19620     19630     19640     19650     19660     19670     19680
          ....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  TTAAACAAGGCCATTTTTATTGGTGTTGAGGGTGAACTACCTGTAGCTGTGATCAATGATAAGATCTTCACCAAGAGTGGC

          19690     19700     19710     19720     19730     19740     19750     19760
          ....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  GTTAATGACATTTGTATGTTTGAGAATAAAACCACATTTGCCTACTAATATAGCTTTTTGAACTCTATGCTAAGCGTGCTGT

          19770     19780     19790     19800     19810     19820     19830     19840
          ....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  ACGCTCGCATCCCGATTTCAAATTGCTACACAATTTACAAGCAGACATTTGCTACAAGTTCGTCCTTTGGGATTATGAAC

          19850     19860     19870     19880     19890     19900     19910     19920
          ....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  GTAGCAATATTTTATGGTACTGCTACTATTTGGTGTTATAAGTACACTGATATTTGATGTTAAATTCAGCTTTTGAATATTATGT

          19930     19940     19950     19960     19970     19980     19990     20000
          ....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  TTTGACATACGCGATAATTGTTCATTGGAGAAGTTCATGTCTACTCCCAATGCCACTCTTATTTCTGATAGAAAAATCAA
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          20010     20020     20030     20040     20050     20060     20070     20080
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  GAAATACCCTTGTATGGTAGGTCCTGATTATGCTTACTTCAATGGTGCTATCATCCGTGATAGTGATGTTGTTAAACAAC

          20090     20100     20110     20120     20130     20140     20150     20160
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  CAGTGAAGTTCTACTTGTATAAGAAAGTCAATAAATGAGTTTATTGATCCTACTGAGTGTATTTACACTCAGAGTCGCTCT

          20170     20180     20190     20200     20210     20220     20230     20240
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  TGTAGTGACTTCCTACCCCTTTCTGACATGGAGAAAGACTTTCTATCTTTTGATAGTGATGTTTTCATTAAGAAGTATGG

          20250     20260     20270     20280     20290     20300     20310     20320
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  CTTGGAAAACTATGCTTTTGAGCACGTAGTCTATGGAGACTTCTCTCATACTACGTTAGGCGGTCTTCACTTGCTTATTG

          20330     20340     20350     20360     20370     20380     20390     20400
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  GTTTATACAAGAAGCAACAGGAAGGTCATATTATTATGGAAGAAATGCTAAAAGGTAGCTCAACTATTCATACTATTTT

          20410     20420     20430     20440     20450     20460     20470     20480
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  ATTACTGAGACTAACACAGCGGCTTTTAAGGCGGTGTTCTGTTATAGATTTAAAGCTTGACGACTTTGTTATGATTTT

          20490     20500     20510     20520     20530     20540     20550     20560
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  AAAGAGTCAAGACCTTGGCGTAGTATCCAAGGTTGTCCTATTGACTTAACAATGATTGAGTTTATGTTAGGT

          20570     20580     20590     20600     20610     20620     20630     20640
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  GTAAGGATGGACAGGTTCAAACCTTCTACCCTCGACTCCAGGCTTCTGCAGATTGGAAACCTGGTCATGCAATGCCATCC

          20650     20660     20670     20680     20690     20700     20710     20720
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  CTCTTTAAAGTTCAAAATGTAAACCTTGAACGTTGTGAGCTTGCTAATTTACAAGCAATCTTATTCCTATGCCTCGCGGTGT

          20730     20740     20750     20760     20770     20780     20790     20800
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  GCACATGAACATCGCTAAATATATGCAATTGTGCCAGTATTTAAATACTTGCACATTATGCCGTGCCTGCCAATATGCGTG
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          20810     20820     20830     20840     20850     20860     20870     20880
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|....
TTATACATTTTGGCGCTGGTTCTGATAAAGGTATCGCTCCTGGTACCTCAGTTTTACGACAGTGGCTTCCTACAGATGCC
HCoV-SA1

          20890     20900     20910     20920     20930     20940     20950     20960
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|....
ATTATTATAGATAAATGATTTAAATGAGTTCGTGTCAGATGCTGACATAACTTTATTTGGAGATTGTGTAACTGTACGTGT
HCoV-SA1

          20970     20980     20990     21000     21010     21020     21030     21040
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|....
CGGCCAACAAGTGGATCTTGTTATTTCCGACATGTATGATCCTACTACTAAGAATGTAACAGGTAGTAATGAGTCAAAGG
HCoV-SA1

          21050     21060     21070     21080     21090     21100     21110     21120
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|....
CTTTATTCTTTACTTACCTGTGTAACCTCATTAATAATCTTGCTCTTGGTGGGTCTGTTGCTATTAAAATAACAGAA
HCoV-SA1

          21130     21140     21150     21160     21170     21180     21190     21200
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|....
CACTCTTGGAGCGTTGAACTTTATGGGAAATTTGCTTGGTGGACTGTTTTCTGCACCAATGCAAATGCATC
HCoV-SA1

          21210     21220     21230     21240     21250     21260     21270     21280
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|....
CTCATCTGAAGGATTCCTCTTAGGTAATTAACTTGGGTACTATTAAAGAAAATATAGATGGTGGTGCTATGCACGCCA
HCoV-SA1

          21290     21300     21310     21320     21330     21340     21350     21360
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|....
ACTATATATTTTGGAGAAATTCCACTCCTATGAATCTGAGTACTTACTCACTTTTTGATTTATCCAAGTTTCAATTAAAA
HCoV-SA1

          21370     21380     21390     21400     21410     21420     21430     21440
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|....
TTAAAAGGAACACCAGTTCTTCAATTAAAGGAGAGGTCAAATTAACGAACTCGTAAATATCTCTCCTGTCGCAGGGTAAGTT
HCoV-SA1

          21450     21460     21470     21480     21490     21500     21510     21520
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|....
ACTTTATCCGTGACAATGATACACTCAGTGTTTCTTACTGATGTTCTTGTTACACCTACAGAAAGTTACGTTGATGTTGGG
HCoV-SA1

          21530     21540     21550     21560     21570     21580     21590     21600
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|....
CCAGATTCTGTTAAGTCTGCTTGTTATTGAGGTTGATATACAACAGACTTTCTTTGATAAAACTTGGCCTAGGCCAATTGA
HCoV-SA1
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          21610     21620     21630     21640     21650     21660     21670     21680
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  TGTTTCTAAGGCTGACGGTATTATATACCCTCAAGGCCGTACATATTCTAACATAAACTATCACTTATCAAGGTCTTTTTC

          21690     21700     21710     21720     21730     21740     21750     21760
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  CCTATCAGGGAGACCATGGTGATATGTAATGTTACTCTGCAGGACATGCTACAGGCACAACTCCACAAAAGTTGTTTGTA

          21770     21780     21790     21800     21810     21820     21830     21840
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  GCTAACTATTCTCAGGACGTCAAACAGTTTGCTAATGGGTTTGTCGTCCGTATAGGAGCAGCTGCCAATTCCACTGGCAC

          21850     21860     21870     21880     21890     21900     21910     21920
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  TGTTATTATTAGCCCATCTACCAGCGCTACTATACGAAAAATTTACCCTGCTTTTATGCTGGGTTCTTCAGTTGGTAATT

          21930     21940     21950     21960     21970     21980     21990     22000
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  TCTCAGATGGTAAAATGGGCCGCTTCTTCAATCATACTCTAGTTCTTTTGCCCGATGGATGTGGCACTTTACTTAGAGCT

          22010     22020     22030     22040     22050     22060     22070     22080
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  TTTTATTGTATTCTAGAGCCTCGCTCTGGAAATCATTGTCCTGCTGGCAATTCCTATACTTCTTTTGCCACTTATCACAC

          22090     22100     22110     22120     22130     22140     22150     22160
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  TCCTGCAACAGATTGTTCTGATGGCAATTACAATCGTAATGCCAGTCTGAACTCTTTTAAGGAGTATTTTAATTTACGTA

          22170     22180     22190     22200     22210     22220     22230     22240
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  ACTGCACCTTTATGTACACTTATAACATTACCGAAGATGAGATTTTAGAGTGGTTTGGCATTACACAAACTGGCTCAAGGT

          22250     22260     22270     22280     22290     22300     22310     22320
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  GTTCACCTCTTCTCATCTCGGTATGTTGATTTGTACGGCGGCAATATGTTTCAATTTGCCACCTTGCCTGTTTATGATAC

          22330     22340     22350     22360     22370     22380     22390     22400
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  TATTAAGTATTATTCTATCATTCCTCACAGTATTCGTTCTATCCAAAGTGATAGAAAAGCTTGGGCTGCCTTCTACGTAT
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          22410     22420     22430     22440     22450     22460     22470     22480
          ....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  ATAAACTTCAACCGTTAACTTTCCTGTTGGATTTTTTCTGTTGATGGTTATATACGCAGAGCTATAGACTGTGGTTTTTAAT

          22490     22500     22510     22520     22530     22540     22550     22560
          ....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  GATTTGTCACAACTCCACTGCTCATAGAATCCTTCGATGTTGAATCTGGAGTTTATTCAGTTTCGTCTTTCGAAGCAAA

          22570     22580     22590     22600     22610     22620     22630     22640
          ....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  ACCTTCTGGCTCAGTTGTGGAACAGGCTGAAGGTGATTTTTTCACCTCTTCTGTCTGGCACACCTCCTCAGG

          22650     22660     22670     22680     22690     22700     22710     22720
          ....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  TTTATAATTTCAAGCGTTTGGTTTTTACCAATTGCAATTATAACTTACCAAATTGCTTTCACTTTTTTCTGTGAATGAT

          22730     22740     22750     22760     22770     22780     22790     22800
          ....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  TTTACTTGTAGTCAAATATCTCCAGCAGCAATTGCTAGCAACTGTTATTCTTCACTGATTTTGGATTACTTTTTCATACCC

          22810     22820     22830     22840     22850     22860     22870     22880
          ....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  ACTTAGTATGAAATCCGATCTCAGTGTTAGTTCTGCTGGTCCAATATCCCAGTTTAATTATAAACAGTCCTTTTCTAATC

          22890     22900     22910     22920     22930     22940     22950     22960
          ....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  CCACATGTTTGATTTTAGCGACTGTTCCTCATAACCTTACTACTATTACTAAGCCCTCTTAAGTACAGCTATATTAACAAG

          22970     22980     22990     23000     23010     23020     23030     23040
          ....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  TGCTCTCGTCTCTTTTCTGATGATCGTACTGAAGTACCTCAGTTAGTGAACGCTAAATCAATACTCACCCTGTGTATCCAT

          23050     23060     23070     23080     23090     23100     23110     23120
          ....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  TGTCCCATCCACTGTGTGGGAAGACGGTGATTATTATAGGAAACAACTATCTCCACTTGAAGGTGGTGGCTGGCTTTGTTG

          23130     23140     23150     23160     23170     23180     23190     23200
          ....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  CTAGTGGCTCAACTGTTGCCATGACTGAGCAATTACAGATGGGCTTTGGTATTACAGTTCAATATGGTTACAGACACCAAT
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                23210     23220     23230     23240     23250     23260     23270     23280
            ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1    AGTGTTTGCCCCAAGCTTGAATTTGCTAATGACACAAAAATTGCCTCTCAATTAGGCAATTGCGTGGAATATTCCCTCTA

                23290     23300     23310     23320     23330     23340     23350     23360
            ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1    TGGTGTTTCGGGCCGTGGTGTTTTTCAGAATTGCACAGCTGTAGGTGTTCGACAGCAGCGCTTTGTTTATGATGCGTACC

                23370     23380     23390     23400     23410     23420     23430     23440
            ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1    AGAATTTAGTTGGCTATTATTCTGATGATGGCAACTACTACTGTTTGCGTGCTTGTGTTAGTGTTCCTGTTTCTGTCATC

                23450     23460     23470     23480     23490     23500     23510     23520
            ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1    TATGATAAAGAAACTAAAACCCACGCTACTCTATTTGGTAGTGTTGCATGTGAACACATTTCTTCTACCATGTCTCAATA

                23530     23540     23550     23560     23570     23580     23590     23600
            ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1    CTCCCGTTCTACGCGATCAATGCTTAAACGGCGAGATTCTACATATGGCCCCCTTCAGACACCTGTTGGTTGTGTCCTAG

                23610     23620     23630     23640     23650     23660     23670     23680
            ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1    GACTTGTTAATTCCTCTTTGTTCGTAGAGGACTGCAAGTTGCCTCTTGGTCAATCTCTCTGTGCTCTTCCTGACACACCT

                23690     23700     23710     23720     23730     23740     23750     23760
            ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1    AGTACTCTCACACCTCGCAGTGTGCGCTCTGTTCCAGGTGAAATGCGCTTGGCATCCATTGCTTTTAATCATCCTATTCA

                23770     23780     23790     23800     23810     23820     23830     23840
            ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1    GGTTGATCAACTTAATAGTAGTTATTTAAATTAAGTATACCCACTAATTTTTCCTTTGGTGTGACTCAGGAGTACATTC

                23850     23860     23870     23880     23890     23900     23910     23920
            ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1    AGACAACCATTCAGAAAGTTACTGTTGATTGTAAACAGTACGTTTGCAATGGTTTCCAGAAGTGTGAGCAATTACTGCGC

                23930     23940     23950     23960     23970     23980     23990     24000
            ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1    GAGTATGGCCAGTTTTGTTCCAAAATAAACCAGGCTCTCCATGGTGCCAATTTACGCCAGGATGATTCTGTACGTAATTT
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                24010     24020     24030     24040     24050     24060     24070     24080
                    |.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  GTTTGCGAGCGTGAAAAGCTCTCAATCATCTCCTATACCAGGTTTTGGAGGTGACTTTAATTTGACACTTCTAGAAC

                24090     24100     24110     24120     24130     24140     24150     24160
                    |.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  CTGTTTCTATATCTACTGGCAGTCGTAGTGCACGTAGTGCTATTGAGGATTTGCTATTTGACAAAGTCACTATAGCTTGAT

                24170     24180     24190     24200     24210     24220     24230     24240
                    |.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  CCTGGTTTATATGCAAGGTTACGATGATTGCATGCAGCAAGGTCCAGCATCAGCTCGTGATCTTATTTGTGCTCAATATGT

                24250     24260     24270     24280     24290     24300     24310     24320
                    |.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  GGCTTGGTTACAAAGTATTACCTCCTCTTATGGATGTTAATATGGAAGCCGCGTATACTTCATCTTTGCTTGGCAGCATAG

                24330     24340     24350     24360     24370     24380     24390     24400
                    |.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  CAGGTGTTGGCTGGACTGCTGGCTTATCCTCCTTTGCTGCTATTCCATTTGCACAGAGTATCTTTTATAGGTTAAACGGT

                24410     24420     24430     24440     24450     24460     24470     24480
                    |.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  GTTGGCATTACTCAACAGGTTCTTTCAGAGAACCAAAAGCTTATTGCCAATAAGTTTAATCAGGCTCTGGGAGCTATGCA

                24490     24500     24510     24520     24530     24540     24550     24560
                    |.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  AACAGGCTTCACTACAACTAATGAAGCTTTTCAGAAGGTTCAGGATGCTGTGAACAACAATGCACAGGCTCTATCCAAAT

                24570     24580     24590     24600     24610     24620     24630     24640
                    |.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  TAGCTAGCGAGCTATCTAATACTCTTTGGTGCTATTTCCGCCTCTATTGGAGACATCATACAACGTCTTGATGTTCTCGAA

                24650     24660     24670     24680     24690     24700     24710     24720
                    |.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  CAGGACGCCCAAATAGACAGACTTATTAATGGCCGTTTGACAACACTAAATGCTTTTGTTGCACAGCAGCTTGTTCGTTC

                24730     24740     24750     24760     24770     24780     24790     24800
                    |.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  CGAATCAGCTGCTCTTTCCGCAATTGGCTAAAGATAAAGTCAATGAGTGTGTCAAGGCACAATCCAAGCGTTCTGGAT
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                24810     24820     24830     24840     24850     24860     24870     24880
           ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1   TTTGCGGTCAAGGCACACATATAGTGTCCTTTGTTGTAAAATGCCCCTAATGGCCTTTACTTCATGCATGTTGGTTATTAC

                24890     24900     24910     24920     24930     24940     24950     24960
           ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1   CCTAGCAACCACATTGAGGTTGTTTCTGCTTATGGTCTTTGCGATGCAGCTAACCCTACTAATTGTATAGCCCCTGTTAA

                24970     24980     24990     25000     25010     25020     25030     25040
           ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1   TGGCTACTTTATTAAAACTAATAACACTAGGATTGTTGATGAGTGGTCATATACTGGCTCGTCCTTCTATGCACCTGAGC

                25050     25060     25070     25080     25090     25100     25110     25120
           ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1   CCATTACCTCCCTTAATACTAAGTATGTTGCACCACAGGTGACATACCAAAACATTTCTACTAACCTCCCTCCTCCTCTT

                25130     25140     25150     25160     25170     25180     25190     25200
           ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1   CTCGGCAATTCCACCGGGATTGACTTCCAAGATGAGTTGGATGAGTTTTTCAAAAATGTTAGCACCAGTATACCTAATTT

                25210     25220     25230     25240     25250     25260     25270     25280
           ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1   TGGTTCCCTAACACAGATTAATACTACATTACTCGATCTTACCTACGAGATGTTGTCTCTTCAACAAGTTGTTAAAGCCC

                25290     25300     25310     25320     25330     25340     25350     25360
           ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1   TTAATGAGTCTTACATAGACCTTAAAGAGCTTGGCAATTATACTTATTACAACAAATGGCCGTGGTACATTTGGCTTGGT

                25370     25380     25390     25400     25410     25420     25430     25440
           ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1   TTCATTGCTGGGCTTGTTGCCTTAGCTCTATGCGTCTTCTTCATACTGTGCTGCACTGGTTGTGGCACAAACTGTATGGG

                25450     25460     25470     25480     25490     25500     25510     25520
           ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1   AAAACTTAAGTGTAATCGTTGTTGTGATAGATACGAGGAATACGACCTCGAGCCGCATAAGGTTCATGTTCACTAATTAA

                25530     25540     25550     25560     25570     25580     25590     25600
           ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1   CGAACTATTAATGAGAGTTCAAAGACCACCCACTCTCTTGTTAGTGTTTTCACTCTCTCTTTTGGTCACTGCATCCTCAA
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          25610     25620     25630     25640     25650     25660     25670     25680
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  AACCTCTCTATGTACCTGAGCATTGTCAGAATTATTCTGGTTGCATGCTTAGGGCTTGTATTAAAACTGCCCAAGCTGAT

          25690     25700     25710     25720     25730     25740     25750     25760
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  ACAGCTGGTCTTTATACAAAATTTTCGAATTGACGTCCCATCTGCAGAATCAACTGGTACTCAATCAGTTTCTGTCGATCT

          25770     25780     25790     25800     25810     25820     25830     25840
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  TGAGTCAACTTCAACTCATGATGGTCCTACCGAACATGTTACTAGTGTGAATCTTTTTTGACGTTGGTTACTCAGTTAATT

          25850     25860     25870     25880     25890     25900     25910     25920
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  AACGAACTCTAATGGATTACGTGTCTCTGCTTAATCAAATTTGGCAGAAGTACCTTACTCACCGTACTACTTGTTTGT

          25930     25940     25950     25960     25970     25980     25990     26000
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  ACATCCCTAAACCCACAGCTAAGTATACACCTTTAGTTGGCACTTCATTGCACCCTGTGCTGTGGAACTGTCAGCTATCC

          26010     26020     26030     26040     26050     26060     26070     26080
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  TTTGCTGGTTATACTGAATCTGCTGTTAATTCTACAAAAGCTTTTGGCCAAACAGGACGCAGCTCAGCGAATCGCTTGGTT

          26090     26100     26110     26120     26130     26140     26150     26160
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  GCTACATAAGGATGGAGGAAACCCTGATGGATGTTCCCTCTACCTCCGGCACTCAAGTTTATTCGCGCAAAGCGAGGAAG

          26170     26180     26190     26200     26210     26220     26230     26240
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  AGGAGCCATTCTCCAACTAAGAAACTGCGCTACGTTAAGCGTAGATTTTCTCTTCTGCGCCATGAAGACCTTAGTGTTAT

          26250     26260     26270     26280     26290     26300     26310     26320
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  TGTCCAACCAACACACTAATGTCAGGGTTTACATTTTTCAGACCCCAACATGTGGTATCTACGTTCGGGTCATCATTTTACACT

          26330     26340     26350     26360     26370     26380     26390     26400
..........|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  CAGTTCACAATTGGCTTAAACCTTATGGCGGCCAACCTGTTTCTGAGTACCATATTACTCTAGCTTTGCTAAATCTCACT
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          26410     26420     26430     26440     26450     26460     26470     26480
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  GATGAAGATTTAGCTAGAGATTTTTCACCCATTGCGCTCTTTTTGCGCAATGTCAGATTTGAGCTACATGAGTTCGCCTT

          26490     26500     26510     26520     26530     26540     26550     26560
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  GCTGCGCAAAACTCTTGTTCTTAATGCATCAGAGATCTACTGTGCTAACATACATAGATTTAAGCCTGTGTATAGAGGTTA

          26570     26580     26590     26600     26610     26620     26630     26640
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  ACACGGCAATCCCTACTATTAAGGATTGGCTTCTCGTTCAGGGATTTTCCCTTTACCATAGTGGCCTCCCTTTACATATG

          26650     26660     26670     26680     26690     26700     26710     26720
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  TCAATCTCTAAATTGCATGCACTGGATGATGTTACTCGCAATTACATCATTACAATGCCATGCTTTAGAACTTACCCTCA

          26730     26740     26750     26760     26770     26780     26790     26800
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  ACAAATGTTTGTTACTCCTTTGGCCGTAGATGTTGTCTCCATACGGTCTTCCAATCAGGGTAATAAACAAATTGTTCATT

          26810     26820     26830     26840     26850     26860     26870     26880
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  CTTATCCCATTTTACATCATCCAGGATTTTTAACGAACTAATGGCTTTCTCTGGCGTCTTTATTTTAAACCCGTCCAGCTAGTC

          26890     26900     26910     26920     26930     26940     26950     26960
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  CCAGTTTCTCCTGCATTTCAACGCATTGAGTCTACTGACTCTATTGTTTTCACATACATTCCTGCTAGCGGCTATGTAGC

          26970     26980     26990     27000     27010     27020     27030     27040
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  TGCTTTAGCTGTCAATGTGTGTCTCATTCCCCTATTATTACTGCTACGTCAAGATACTTGTCGTCGCAGCATTATCAGAA

          27050     27060     27070     27080     27090     27100     27110     27120
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  CTATGGTTCTCTATTTCCTTGTTCTGTATAACTTTTTTATTAGCCATTGTACTAGTCAATGGTGTACAATTATCCAACTGGA

          27130     27140     27150     27160     27170     27180     27190     27200
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  AGTTGCCTGATAGCCTTCTAGTTATCCACATAATACTTTAGTTGTAGATAGAATTCGTTCGTCTCATGCTGGAATTC
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                27210     27220     27230     27240     27250     27260     27270     27280
                .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1        CTACATTCCACTGTTTGACATGCGTTCCCACTTTATTCGTGTTAGTACAGTTTCTTCTCATGGTATGGTTCCCTGTAATAC

                27290     27300     27310     27320     27330     27340     27350     27360
                .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1        ACACCAAACCATTATTTATTTAGAAACTTCGATCAGCGTTGCAGCTGTTCTCGTTGTTTTTATTTGCACTCTTCCACTTAT

                27370     27380     27390     27400     27410     27420     27430     27440
                .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1        ATAGAGTGCACTTTATATTAGCCGTTTTAGTAAGATTAGCCTAGTTTCTGTAACTGACTTCTCCTTTAAACGGCAATGTTTC

                27450     27460     27470     27480     27490     27500     27510     27520
                .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1        CACTGTTTTCGTGCCTGCAACGCGCGATTTCAGTTCCTCTTCACATAATCGCCCCGAGCTCGCTTATCGTTTAAGCAGCTC

                27530     27540     27550     27560     27570     27580     27590     27600
                .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1        TGCGCTACTATGGGTCCCGTGTAGAGGCTAATCCATTAGTCTCTCTTTGGACATATGGAAAACGAACTATGTTACCCTTT

                27610     27620     27630     27640     27650     27660     27670     27680
                .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1        GTCCAAGAACGAATAGGGTTGTTCATAGTAAACTTTTTTCATTTTTACCGTAGTATGTGCTATAACACTCTTGGTGTGTAT

                27690     27700     27710     27720     27730     27740     27750     27760
                .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1        GGCTTTCCTTACGGCTACTAGATTATGTGTGCAATGTATGACAGGCTTCAATACCCTGTTAGTTCAGCCCGCATTATACT

                27770     27780     27790     27800     27810     27820     27830     27840
                .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1        TGTATAAATACTGGACGTTCAGTCTATGTAAAATTCCAGGATAGTAACCCCCTCTACCACCTGACGAGTGGGTTTAACGA

                27850     27860     27870     27880     27890     27900     27910     27920
                .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1        ACTCCTTCATAAATGTCTAAATATGACGCAACTCACTGAGGCGCAGATTATTGCCATTATTAAAGACTGGAACTTTGCATGG

                27930     27940     27950     27960     27970     27980     27990     28000
                .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1        TCCCTGATCTTTCTCTTAATTACTATCGTACTACAGTATGGATACCCATCCCGTAGTATGACTGTCTATGTCTTTAAAAT
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          28010     28020     28030     28040     28050     28060     28070     28080
          |....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  GTTTGTTTTTATGGCTCCTATGGCCATCTTCCATGGCGCTATCAATTTAGCGCCGTTTATCCAATTGATCTAGCTTCCC

          28090     28100     28110     28120     28130     28140     28150     28160
          |....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  AGATAAATCTCTGGCATTGTAGCAGCTGTTTTCAGCTATGATGTGGATTTCCTACTTTGTGCAGATCCGGCTGTTTATG

          28170     28180     28190     28200     28210     28220     28230     28240
          |....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  AGAACTGGATCATGGTGGTCATTCAATCCTGAGACTAATTGCCTTTTGAACGTTCCATTTGGTGGTACAACTGTCGTACG

          28250     28260     28270     28280     28290     28300     28310     28320
          |....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  TCCACTCGTAGAGGACTCTACCAGTGTAACTGCTGTTGTAACCAATGGCCACCTCAAAATGGCTGGCATGCATTTCGGTG

          28330     28340     28350     28360     28370     28380     28390     28400
          |....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  CTTGTGACTACGACAGACTTCCTAATGAAGTCACCGTGGCCAAACCCAATGTGCTGATTGCTTTTAAAAATGGTGAAGCGG

          28410     28420     28430     28440     28450     28460     28470     28480
          |....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  CAAAGCTACGGAACTAATTCCGGCGTTGCCATTTACCATAGATATAAGGCAGGTAAATTACAGGAGTCCGCCTATTACGGC

          28490     28500     28510     28520     28530     28540     28550     28560
          |....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  GGATATTGAACTTGCATTGCTTCGAGCTTAGGCTCTTTAGTAAGAGTATCTTAATTGATTTTAACGAAATCTCAATTTCAT

          28570     28580     28590     28600     28610     28620     28630     28640
          |....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  TGTTATGGCATCCCCCTGCTGACCTCGTGCTGTTTCCTTTGCCGATAACAATGATATAACAAATACAAACCTATCTCGAG

          28650     28660     28670     28680     28690     28700     28710     28720
          |....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  GTAGAGGACGTAATCCAAAACCACGAGCTGCACCAAATAACACTGTCTCTTGGTACACTGGGCTTACCCAACACGGGAAA

          28730     28740     28750     28760     28770     28780     28790     28800
          |....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
HCoV-SA1  GTCCCTCTTACCTTTCCACCTGGGCAGGGTGTACCTCTTAATGCCAATTCTACCCCTGCGCAAAATGCTGGGTATTGGCG
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          28810     28820     28830     28840     28850     28860     28870     28880
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  GAGACAGGACAGAAAAATTATACCGGGAATTAAGCAACTGGCTCCCAGGTGGTACTTCTACTACTGGAACTG

          28890     28900     28910     28920     28930     28940     28950     28960
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  GACCCGAAGCAGCACTCCCATTCCGGGCTGTTAAGGATGGCATCGTTTGGGTCCATGAAGATGGCGCCACTGATGCTCCT

          28970     28980     28990     29000     29010     29020     29030     29040
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  TCAACTTTTTGGGACGCGGAACCCTAACAATGATTCAGCTATTGTTACACAATTCGCGCCCGGTACTAAGCTTCCTAAAAA

          29050     29060     29070     29080     29090     29100     29110     29120
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  CTTCCACATTGAGGGGACTGGAGGCAAAAGTCAACATCTTCAAGAGCCTCTAGCTTAAGCAGAAACTCTTCCAGAACTA

          29130     29140     29150     29160     29170     29180     29190     29200
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  GTTCACAAGGTTCAAGATCAGGAAACTCTACCCGCGGCACTTCTCCAGGTCCATCTGGAATCGGAGCAGTAGGAGGTGAT

          29210     29220     29230     29240     29250     29260     29270     29280
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  CTACTTTACCTTGATCTTCTGAACAGACTACAAGCCCTTGAGTCTGGCAAAGTAAAGCAATCGCAGCCAAAAGTAATCAC

          29290     29300     29310     29320     29330     29340     29350     29360
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  TAAGAAAGATGCTGCTGCTAAAAAATAAGATGCGCCACAAGCGCACTTCCACCAAAAGTTTCAACATGGTGCAAGCTT

          29370     29380     29390     29400     29410     29420     29430     29440
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  TTGGTCTTCGCGGACCAGGAGACCTCCAGGGAAACTTTGGTGATCTTCAATTGAATAACTCGGCACTGAGGACCCACGT

          29450     29460     29470     29480     29490     29500     29510     29520
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  TGGCCCCAAATTGCTGAGCTTTGCTCCTACAGCCAGTGCTTTTTATGGGTATGTCGCAATTTTAAACTTACCCATCAGAACAA

          29530     29540     29550     29560     29570     29580     29590     29600
....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  TGATGATCATGGCAACCCTGTGTACTTCCTTCGGTACAGTGGAGCCATTAAACTTGACCCAAAGAATCCCAACTACAATA
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          29610     29620     29630     29640     29650     29660     29670     29680
          ....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  AGTGGTTGGAGCTTCTTGAGCAAAAATATTGATGCCTACAAAACCTTCCCTAAGAAGGAAAGAAACAAAAGGCACCAAAA

          29690     29700     29710     29720     29730     29740     29750     29760
          ....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  GAAGAATCAACAGACCAAATGTCTGAACCTCCAAAGGAGCAGCGTGTGCAAGGTAGCATCACTCAGCGCACTCGCACCCG

          29770     29780     29790     29800     29810     29820     29830     29840
          ....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  TCCAAGTGTTCAGCCTGGTCCAATGATTGATGTTAACACTGATTAGTGTCACTCAAGTAACAAGATCGGCAATCGTT

          29850     29860     29870     29880     29890     29900     29910     29920
          ....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  TGTGTTTGGCAACCCCATCTCACCATCGCTTGTCCACTCTTGCACAGAATGGAATCATGTTGTAATTACAGTGCAATAAG

          29930     29940     29950     29960     29970     29980     29990     30000
          ....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  GTAATTATAACCCATTTAATTGATAGCTATGCTTTATTAAAGTGTGTAGCTGTGAGAGAATGTTAAAGACTGTCACCTC

          30010     30020     30030     30040     30050     30060     30070     30080
          ....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
HCoV-SA1  TGCTTGATTGCAAGTGAACAGTGCCCCCGGGAAGAGCTCTACAGTGTGAAATGTTAAATAAAAAATAGCTATTATTCAat

          30090     30100     30110     30120
          ....|.....|.....|.....|.....|.....|.....
HCoV-SA1  tagattaggctaattagatgatttgcaaaaaaaaaaaaaaaaaaaa
```

Figure 14 file HCoV-SA1.rtf

Figure 15

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HCoV-SA1 translation 3 frames

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5'    ATTTAAGTGAATAGCTTGGCTATCTCACTTCCCCTCGTTCTCTTGCAGAACTTTGATTTTAACGAACTTA
o     +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++ 70
1      I  .  V  N  S  L  A  I  S  L  P  L  V  L  L  Q  N  F  D  F  N  E  L
2       F  K  .  I  A  W  L  S  H  F  P  S  F  S  C  R  T  L  I  L  T  N  L
3      N  L  S  E  .  L  G  Y  L  T  S  P  R  S  L  A  E  L  .  F  .  R  T  .
o
5'    AATAAAAGCCCTGTTGTTTAGCGTATCGTTGCACTTGTCTGGTGGGATTGTGGCATTAATTTGCCTGCTC
o     +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++ 140
1     K  .  K  P  C  C  L  A  Y  R  C  T  C  L  V  G  L  W  H  .  F  A  C  S
2      N  K  S  P  V  V  .  R  I  V  A  L  V  W  W  D  C  G  I  N  L  P  A
3       I  K  A  L  L  F  S  V  S  L  H  L  S  G  G  I  V  A  L  I  C  L  L
o
5'    ATCTAGGCAGTGGACATATGCTCAACACTGGGTATAATTCTAATTGAATACTATTTTTCAGTTAGAGCGT
o     +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++ 210
1      S  R  Q  W  T  Y  A  Q  H  W  V  .  F  .  L  N  T  I  F  Q  L  E  R
2     H  L  G  S  G  H  M  L  N  T  G  Y  N  S  N  .  I  L  F  F  S  .  S  V
3       I  .  A  V  D  I  C  S  T  L  G  I  I  L  I  E  Y  Y  F  S  V  R  A
o
5'    CGTGTCTCTTGTACGTCTCGGTCACAATACACGGTTTCGTCCGGTGCGTGGCAATTCGGGGCACATCATG
o     +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++ 280
1      R  V  S  C  T  S  R  S  Q  Y  T  V  S  S  G  A  W  Q  F  G  A  H  H
2       V  S  L  V  R  L  G  H  N  T  R  F  R  P  V  R  G  N  S  G  H  I  M
3     S  C  L  L  Y  V  S  V  T  I  H  G  F  V  R  C  V  A  I  R  G  T  S  C
o
5'    TCTTTCGTGGCTGGTGTGACCGCGCAAGGTGCGCGCGGTACGTATCGAGCAGCGCTCAACTCTGAAAAAC
o     +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++ 350
1     V  F  R  G  W  C  D  R  A  R  C  A  R  Y  V  S  S  S  A  Q  L  .  K  T
2      S  F  V  A  G  V  T  A  Q  G  A  R  G  T  Y  R  A  A  L  N  S  E  K
3       L  S  W  L  V  .  P  R  K  V  R  A  V  R  I  E  Q  R  S  T  L  K  N
o
5'    ATCAAGACCATGTGTCTCTAACTGTGCCACTCTGTGGTTCAGGAAACCTGGTTGAAAAACTTTCACCATG
o     +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++ 420
1      S  R  P  C  V  S  N  C  A  T  L  W  F  R  K  P  G  .  K  T  F  T  M
2     H  Q  D  H  V  S  L  T  V  P  L  C  G  S  G  N  L  V  E  K  L  S  P  W
3       I  K  T  M  C  L  .  L  C  H  S  V  V  Q  E  T  W  L  K  N  F  H  H
o
5'    GTTCATGGATGGCGAAAATGCCTATGAAGTGGTGAAGGCCATGTTACTTAAAAAGGAGCCACTTCTCTAT
o     +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++ 490
1     V  H  G  W  R  K  C  L  .  S  G  E  G  H  V  T  .  K  G  A  T  S  L
2      F  M  D  G  E  N  A  Y  E  V  V  K  A  M  L  L  K  K  E  P  L  L  Y
3     G  S  W  M  A  K  M  P  M  K  W  .  R  P  C  Y  L  K  R  S  H  F  S  M
o
5'    GTGCCCATCCGGCTGGCTGGACACACTAGACACCTCCCAGGTCCTCGTGTGTACCTGGTTGAGAGGCTCA
o     +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++ 560
1     C  A  H  P  A  G  W  T  H  .  T  P  P  R  S  S  C  V  P  G  .  E  A  H
2      V  P  I  R  L  A  G  H  T  R  H  L  P  G  P  R  V  Y  L  V  E  R  L
3       C  P  S  G  W  L  D  T  L  D  T  S  Q  V  L  V  C  T  W  L  R  G  S
o
5'    TTGCTTGTGAAAATCCATTCATGGTTAACCAATTGGCTTATAGCTCTAGTGCAAATGGCAGCCTGGTTGG
o     +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++ 630
1      C  L  .  K  S  I  H  G  .  P  I  G  L  .  L  .  C  K  W  Q  P  G  W
2     I  A  C  E  N  P  F  M  V  N  Q  L  A  Y  S  S  S  A  N  G  S  L  V  G
3       L  L  V  K  I  H  S  W  L  T  N  W  L  I  A  L  V  Q  M  A  A  W  L
o
5'    CACAACTTTGCAGGGCAAGCCTATTGGTATGTTCTTCCCTTATGACATCGAACTTGTCACAGGAAAGCAA
o     +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++ 700
1      H  N  F  A  G  Q  A  Y  W  Y  V  L  P  L  .  H  R  T  C  H  R  K  A
2       T  T  L  Q  G  K  P  I  G  M  F  F  P  Y  D  I  E  L  V  T  G  K  Q
3     A  Q  L  C  R  A  S  L  L  V  C  S  S  L  M  T  S  N  L  S  Q  E  S  K
o
```

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HCoV-SA1 translation 3 frames

```
5'    AATATTCTCCTGCGCAAGTATGGCCGTGGTGGTTATCACTACACCCCATTCCACTATGAGCGAGACAACA
o     +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++ 770
1     K  Y  S  P  A  Q  V  W  P  W  W  L  S  L  H  P  I  P  L  .  A  R  Q  H
2      N  I  L  L  R  K  Y  G  R  G  G  Y  H  Y  T  P  F  H  Y  E  R  D  N
3       I  F  S  C  A  S  M  A  V  V  V  I  T  T  P  H  S  T  M  S  E  T  T
o
5'    CCTCTTGCCCTGAGTGGATGGACGATTTTGAGGCGGATCCTAAAGGCAAATATGCCCAGAATCTGCTTAA
o     +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++ 840
1      L  L  P  .  V  D  G  R  F  .  G  G  S  .  R  Q  I  C  P  E  S  A  .
2     T  S  C  P  E  W  M  D  D  F  E  A  D  P  K  G  K  Y  A  Q  N  L  L  K
3      P  L  A  L  S  G  W  T  I  L  R  R  I  L  K  A  N  M  P  R  I  C  L
o
5'    GAAGTTGATTGGCGGTGATGTCACTCCAGTTGACCAATACATGTGTGGCGTTGATGGAAAACCCATTAGT
o     +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++ 910
1     E  V  D  W  R  .  C  H  S  S  .  P  I  H  V  W  R  .  W  K  T  H  .
2      K  L  I  G  G  D  V  T  P  V  D  Q  Y  M  C  G  V  D  G  K  P  I  S
3     R  S  .  L  A  V  M  S  L  Q  L  T  N  T  C  V  A  L  M  E  N  P  L  V
o
5'    GCCTACGCATTTTTAATGGCCAAGGATGGAATAACCAAACTGGCTGATGTTGAAGCGGACGTCGCAGCAC
o     +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++ 980
1     C  L  R  I  F  N  G  Q  G  W  N  N  Q  T  G  .  C  .  S  G  R  R  S  T
2      A  Y  A  F  L  M  A  K  D  G  I  T  K  L  A  D  V  E  A  D  V  A  A
3       P  T  H  F  .  W  P  R  M  E  .  P  N  W  L  M  L  K  R  T  S  Q  H
o
5'    GTGCTGATGACGAAGGCTTCATCACATTAAAGAACAATCTATATAGATTGGTTTGGCATGTTGAGCGTAA
o     +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++ 1050
1      C  .  .  R  R  L  H  H  I  K  E  Q  S  I  .  I  G  L  A  C  .  A  .
2     R  A  D  D  E  G  F  I  T  L  K  N  N  L  Y  R  L  V  W  H  V  E  R  K
3      V  L  M  T  K  A  S  S  H  .  R  T  I  Y  I  D  W  F  G  M  L  S  V
o
5'    AGACGTTCCATATCCTAAGCAATCTATTTTTACTATTAATAGTGTGGTCCAAAAGGATGGTGTTGAAAAC
o     +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++ 1120
1     R  R  S  I  S  .  A  I  Y  F  Y  Y  .  .  C  G  P  K  G  W  C  .  K
2      D  V  P  Y  P  K  Q  S  I  F  T  I  N  S  V  V  Q  K  D  G  V  E  N
3     K  T  F  H  I  L  S  N  L  F  L  L  L  I  V  W  S  K  R  M  V  L  K  T
o
5'    ACTCCTCCTCACTATTTTACTCTTGGATGCAAAATTTTAACGCTCACCCCACGCAACAAGTGGAGTGGCG
o     +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++ 1190
1     H  S  S  S  L  F  Y  S  W  M  Q  N  F  N  A  H  P  T  Q  Q  V  E  W  R
2      T  P  P  H  Y  F  T  L  G  C  K  I  L  T  L  T  P  R  N  K  W  S  G
3       L  L  L  T  I  L  L  L  D  A  K  F  .  R  S  P  H  A  T  S  G  V  A
o
5'    TTTCTGACTTGTCCCTCAAACAAAAACTCCTTTACACCTTCTATGGTAAGGAGTCACTTGAGAACCCAAC
o     +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++ 1260
1      F  .  L  V  P  Q  T  K  T  P  L  H  L  L  W  .  G  V  T  .  E  P  N
2     V  S  D  L  S  L  K  Q  K  L  L  Y  T  F  Y  G  K  E  S  L  E  N  P  T
3      F  L  T  C  P  S  N  K  N  S  F  T  P  S  M  V  R  S  H  L  R  T  Q
o
5'    CTACATTTACCACTCCGCATTCATTGAGTGTGGAAGTTGTGGTAATGATTCCTGGCTTACAGGGAATGCT
o     +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++ 1330
1      L  H  L  P  L  R  I  H  .  V  W  K  L  W  .  .  F  L  A  Y  R  E  C
2      Y  I  Y  H  S  A  F  I  E  C  G  S  C  G  N  D  S  W  L  T  G  N  A
3     P  T  F  T  T  P  H  S  L  S  V  E  V  V  V  M  I  P  G  L  Q  G  M  L
o
5'    ATCCAAGGGTTTGCCTGTGGATGTGGGGCATCATATACAGCTAATGATGTCGAAGTCCAATCATCTGGCA
o     +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++ 1400
1     Y  P  R  V  C  L  W  M  W  G  I  I  Y  S  .  .  C  R  S  P  I  I  W  H
2      I  Q  G  F  A  C  G  C  G  A  S  Y  T  A  N  D  V  E  V  Q  S  S  G
3       S  K  G  L  P  V  D  V  G  H  H  I  Q  L  M  M  S  K  S  N  H  L  A
o
```

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HCoV-SA1 translation 3 frames

```
5' TGATTAAGCCAAATGCTCTTCTTTGTGCTACTTGCCCCTTTGCTAAGGGTGATAGCTGTTCTTCTAATTG
o                                                                          1470
1   D . A K C S S L C Y L P L C . G . . L F F . L
2  M I K P N A L L C A T C P F A K G D S C S S N C
3   . L S Q M L F F V L L A P L L R V I A V L L I
o
5' CAAACATTCAGTTGCTCAGTTGGTTAGTTACCTTTCTGAACGCTGTAATGTTATTGCTGATTCTAAGTCC
o                                                                          1540
1   Q T F S C S V G . L P F . T L . C Y C . F . V
2   K H S V A Q L V S Y L S E R C N V I A D S K S
3  A N I Q L L S W L V T F L N A V M L L L I L S P
o
5' TTCACACTTATCTTTGGTGGCGTAGCTTACGCCTACTTTGGATGTGAGGAAGGTACTATGTACTTTGTGC
o                                                                          1610
1  L H T Y L W W R S L R L L W M . G R Y Y V L C A
2   F T L I F G G V A Y A Y F G C E E G T M Y F V
3   S H L S L V A . L T P T L D V R K V L C T L C
o
5' CTAGAGCTAAGTCTGTTGTCTCAAGGATTGGAGACTCCATCTTTACAGGCTGTACTGGCTCTTGGAACAA
o                                                                          1680
1   . S . V C C L K D W R L H L Y R L Y W L L E Q
2  P R A K S V V S R I G D S I F T G C T G S W N K
3   L E L S L L S Q G L E T P S L Q A V L A L G T
o
5' GGTCACTCAAATTGCTAACATGTTCTTGGAACAGACTCAGCATTCCCTTAACTTTGTGGGAGAGTTCGTT
o                                                                          1750
1   G H S N C . H V L G T D S A F P . L C G R V R
2   V T Q I A N M F L E Q T Q H S L N F V G E F V
3  R S L K L L T C S W N R L S I P L T L W E S S L
o
5' GTCAACGATGTTGTCCTCGCAATTCTCTCTGGAACCACAACTAATGTTGACAAAATACGCCAGCTTCTCA
o                                                                          1820
1  C Q R C C P R N S L W N H N . C . Q N T P A S Q
2   V N D V V L A I L S G T T T N V D K I R Q L L
3   S T M L S S Q F S L E P Q L M L T K Y A S F S
o
5' AAGGTGTCACCCTTGACAAGTTGCGTGATTATTTAGCTGACTATGACGTAGCAGTCACTGCCGGCCCATT
o                                                                          1890
1   R C H P . Q V A . L F S . L . R S S H C R P I
2  K G V T L D K L R D Y L A D Y D V A V T A G P F
3   K V S P L T S C V I I . L T M T . Q S L P A H
o
5' CATGGATAATGCTATTAATGTTGGTGGTACAGGATTACAGTATGCCGCCATTACTGCACCTTATGTAGTT
o                                                                          1960
1   H G . C Y . C W W Y R I T V C R H Y C T L C S
2   M D N A I N V G G T G L Q Y A A I T A P Y V V
3  S W I M L L M L V V Q D Y S M P P L L H L M . F
o
5' CTCACTGGCTTAGGTGAGTCCTTTAAGAAAGTTGCAACCATACCGTATAAGGTTTGCAACTCTGTTAAGG
o                                                                          2030
1  S H W L R . V L . E S C N H T V . G L Q L C . G
2   L T G L G E S F K K V A T I P Y K V C N S V K
3   S L A . V S P L R K L Q P Y R I R F A T L L R
o
5' ATACTCTGGCTTATTATGCTCACAGCGTGTTGTACAGAGTTTTTCCTTATGACATGGATTCTGGTGTGTC
o                                                                          2100
1   Y S G L L C S Q R V V Q S F S L . H G F W C V
2  D T L A Y Y A H S V L Y R V F P Y D M D S G V S
3   I L W L I M L T A C C T E F F L M T W I L V C
o
```

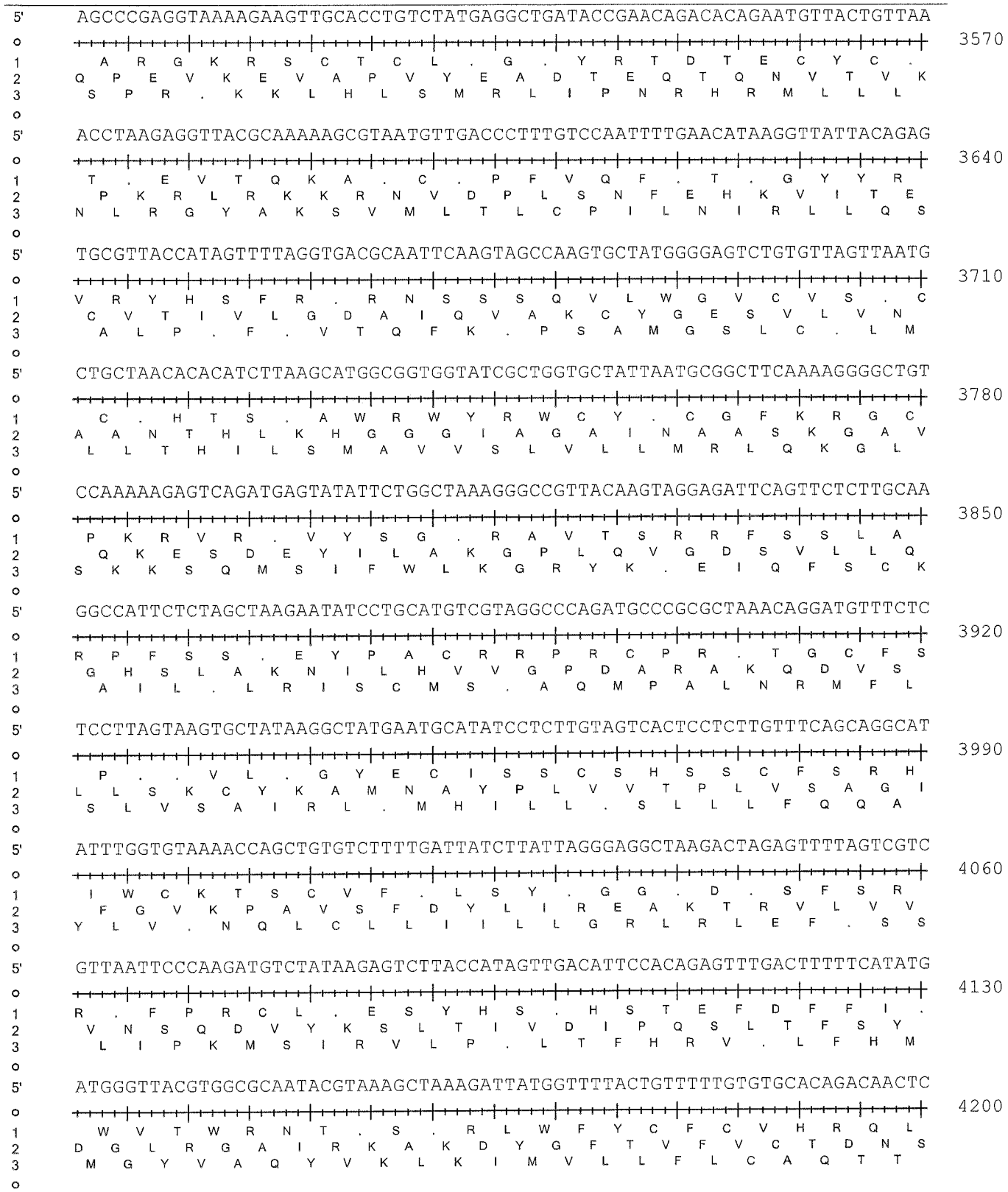
Sunday, September 23, 2012 1:41 PM
HCoV-SA1 translation 3 frames

```
5'  ATCCTTTAGTGAACTACTTTTTGATTGCGTTGATCTTTCAGTAGCTTCTACCTATTTTTTAGTCCGCATC
o   +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++  2170
1    I  L  .  .  T  T  F  .  L  R  .  S  F  S  S  F  Y  L  F  F  S  P  H
2     S  F  S  E  L  L  F  D  C  V  D  L  S  V  A  S  T  Y  F  L  V  R  I
3    H  P  L  V  N  Y  F  L  I  A  L  I  F  Q  .  L  L  P  I  F  .  S  A  S
o
5'  TTGCAAGATAAGACTGGCGACTTTATGTCTACAATTATTACTTCCTGCCAAACTGCTGTTAGTAAGCTTC
o   +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++  2240
1    L  A  R  .  D  W  R  L  Y  V  Y  N  Y  Y  F  L  P  N  C  C  .  .  A  S
2     L  Q  D  K  T  G  D  F  M  S  T  I  I  T  S  C  Q  T  A  V  S  K  L
3     C  K  I  R  L  A  T  L  C  L  Q  L  L  L  P  A  K  L  L  L  V  S  F
o
5'  TAGATACATGTTTTGAAGCTACAGAAGCAACATTTAACTTCTTGTTAGATTTGGCAGGATTGTTCAGAAT
o   +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++  2310
1    R  Y  M  F  .  S  Y  R  S  N  I  .  L  L  V  R  F  G  R  I  V  Q  N
2    L  D  T  C  F  E  A  T  E  A  T  F  N  F  L  L  D  L  A  G  L  F  R  I
3     .  I  H  V  L  K  L  Q  K  Q  H  L  T  S  C  .  I  W  Q  D  C  S  E
o
5'  CTTTCTCCGCAATGCCTATGTGTACACTTCACAAGGGTTTGTGGTGGTCAATGGCAAAGTTTCTACACTT
o   +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++  2380
1    L  S  P  Q  C  L  C  V  H  F  T  R  V  C  G  G  Q  W  Q  S  F  Y  T
2     F  L  R  N  A  Y  V  Y  T  S  Q  G  F  V  V  V  N  G  K  V  S  T  L
3    S  F  S  A  M  P  M  C  T  L  H  K  G  L  W  W  S  M  A  K  F  L  H  L
o
5'  GTCAAACAAGTGTTAGACTTGCTTAATAAGGGTATGCAACTTTTGCATACAAAGGTCTCCTGGGCTGGTT
o   +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++  2450
1    C  Q  T  S  V  R  L  A  .  .  G  Y  A  T  F  A  Y  K  G  L  L  G  W  F
2     V  K  Q  V  L  D  L  L  N  K  G  M  Q  L  L  H  T  K  V  S  W  A  G
3     S  N  K  C  .  T  C  L  I  R  V  C  N  F  C  I  Q  R  S  P  G  L  V
o
5'  CTAAAATCATTGCTGTTATCTACAGCGGCAGGGAGTCTCTAATATTCCCATCGGGAACCTATTACTGTGT
o   +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++  2520
1     .  N  H  C  C  Y  L  Q  R  Q  G  V  S  N  I  P  I  G  N  L  L  L  C
2    S  K  I  I  A  V  I  Y  S  G  R  E  S  L  I  F  P  S  G  T  Y  Y  C  V
3     L  K  S  L  L  L  S  T  A  A  G  S  L  .  Y  S  H  R  E  P  I  T  V
o
5'  CACCACTAAGGCTAAGTCCGTTCAACAAGATCTTGACGTTATTTTGCCTGGTGAGTTTTCCAAGAAGCAG
o   +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++  2590
1     H  H  .  G  .  V  R  S  T  R  S  .  R  Y  F  A  W  .  V  F  Q  E  A
2     T  T  K  A  K  S  V  Q  Q  D  L  D  V  I  L  P  G  E  F  S  K  K  Q
3    S  P  L  R  L  S  P  F  N  K  I  L  T  L  F  C  L  V  S  F  P  R  S  S
o
5'  TTAGGACTGCTCCAACCTACTGACAATTCTACAACTGTTAGTGTTACTGTATCCAGTAACATGGTTGAAA
o   +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++  2660
1    V  R  T  A  P  T  Y  .  Q  F  Y  N  C  .  C  Y  C  I  Q  .  H  G  .  N
2     L  G  L  L  Q  P  T  D  N  S  T  T  V  S  V  T  V  S  S  N  M  V  E
3     .  D  C  S  N  L  L  T  I  L  Q  L  L  V  L  L  Y  P  V  T  W  L  K
o
5'  CTGTTGTGGGTCAACTTGAGCAAACTAATATGCATAGTCCTGATGTTATAGTAGGTGACTATGTCATTAT
o   +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++  2730
1     C  C  G  S  T  .  A  N  .  Y  A  .  S  .  C  Y  S  R  .  L  C  H  Y
2    T  V  V  G  Q  L  E  Q  T  N  M  H  S  P  D  V  I  V  G  D  Y  V  I  I
3     L  L  W  V  N  L  S  K  L  I  C  I  V  L  M  L  .  .  V  T  M  S  L
o
5'  TAGTGAAAAATTGTTTGTGCGTAGTAAGGAAGAAGACGGATTTGCCTTCTACCCTGCTTGCACTAATGGT
o   +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++  2800
1     .  .  K  I  V  C  A  .  .  G  R  R  R  I  C  L  L  P  C  L  H  .  W
2     S  E  K  L  F  V  R  S  K  E  E  D  G  F  A  F  Y  P  A  C  T  N  G
3    L  V  K  N  C  L  C  V  V  R  K  K  T  D  L  P  S  T  L  L  A  L  M  V
o
```

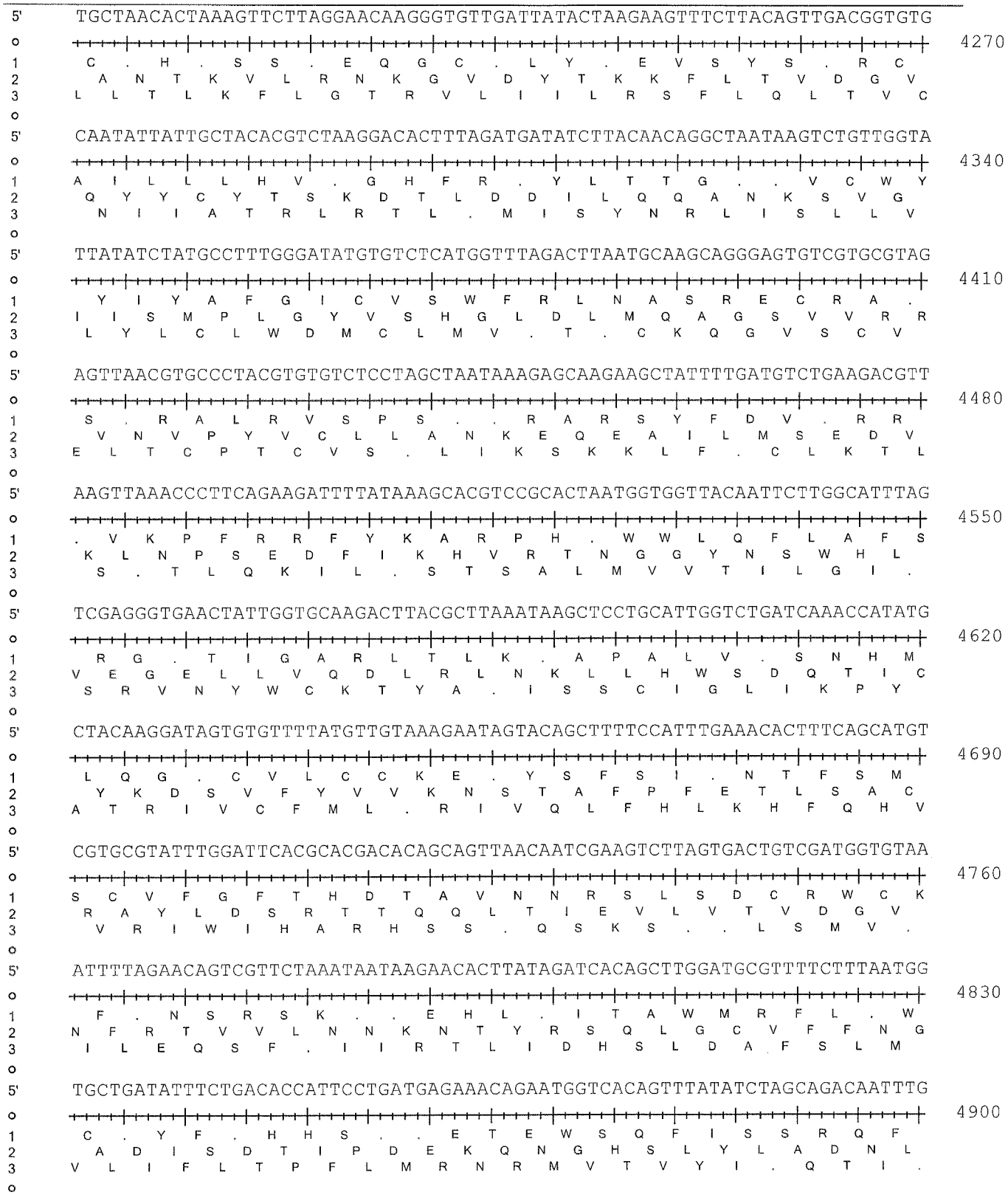
Sunday, September 23, 2012 1:41 PM
HCoV-SA1 translation 3 frames

```
5'  CATGCTGTACCGACTCTCTTTAGACTTAAGGGAGGTGCACCTaGTAAAAAAGTAGCCTTTGGCGGTGATC
o   +----|----+----|----+----|----+----|----+----|----+----|----+----|----+ 2870
1    S   C   C   T   D   S   L   .   T   .   G   R   C   T   .   .   K   S   S   L   W   R   .   S
2      H   A   V   P   T   L   F   R   L   K   G   G   A   P   S   K   K   V   A   F   G   G   D
3        M   L   Y   R   L   S   L   D   L   R   E   V   H   L   V   K   K   .   P   L   A   V   I
o
5'  AAGTACATGAGGTTGCTGCTGTAAGAAGTGTTACTGTCGAGTACAACATTCATGCTGTATTAGACACACT
o   +----|----+----|----+----|----+----|----+----|----+----|----+----|----+ 2940
1        S   T   .   G   C   C   C   K   K   C   Y   C   R   V   Q   H   S   C   C   I   R   H   T
2      Q   V   H   E   V   A   A   V   R   S   V   T   V   E   Y   N   I   H   A   V   L   D   T   L
3        K   Y   M   R   L   L   L   .   E   V   L   L   S   S   T   T   F   M   L   Y   .   T   H
o
5'  ACTTGCTTCTTCTAGTCTTAGAACCTTTGTTGTAGATAAGTCTTTGTCAATTGAGGAGTTTGCTGACGTA
o   +----|----+----|----+----|----+----|----+----|----+----|----+----|----+ 3010
1        T   C   F   F   .   S   .   N   L   C   C   R   .   V   F   V   N   .   G   V   C   .   R
2          L   A   S   S   S   L   R   T   F   V   V   D   K   S   L   S   I   E   E   F   A   D   V
3      Y   L   L   L   L   V   L   E   P   L   L   .   I   S   L   C   Q   L   R   S   L   L   T   .
o
5'  GTAAAGGAACAAGTCTCAGACTTGCTTGTTAAATTACTGCGTGGAATGCCGATTCCAGATTTTGATTTAG
o   +----|----+----|----+----|----+----|----+----|----+----|----+----|----+ 3080
1    S   K   G   T   S   L   R   L   A   C   .   I   T   A   W   N   A   D   S   R   F   .   F   R
2      V   K   E   Q   V   S   D   L   L   V   K   L   L   R   G   M   P   I   P   D   F   D   L
3        .   R   N   K   S   Q   T   C   L   L   N   Y   C   V   E   C   R   F   Q   I   L   I   .
o
5'  ACGATTTTATTGACGCACCATGCTATTGCTTTAACGCTGAGGGTGATGCATCCTGGTCTTCTACTATGAT
o   +----|----+----|----+----|----+----|----+----|----+----|----+----|----+ 3150
1        R   F   Y   .   R   T   M   L   L   L   .   R   .   G   .   C   I   L   V   F   Y   Y   D
2      D   D   F   I   D   A   P   C   Y   C   F   N   A   E   G   D   A   S   W   S   S   T   M   I
3        T   I   L   L   T   H   H   A   I   A   L   T   L   R   V   M   H   P   G   L   L   L   .
o
5'  CTTCTCTCTTCACCCCGTCGAGTGTGACGAGGAGTGTTCTGAAGTAGAGGCTTCAGATTTAGAAGAAGGT
o   +----|----+----|----+----|----+----|----+----|----+----|----+----|----+ 3220
1        L   L   S   S   P   R   R   V   .   R   G   V   F   .   S   R   G   F   R   F   R   R   R
2          F   S   L   H   P   V   E   C   D   E   E   C   S   E   V   E   A   S   D   L   E   E   G
3      S   S   L   F   T   P   S   S   V   T   R   S   V   L   K   .   R   L   Q   I   .   K   K   V
o
5'  GAATCAGAGTGCATTTCTGAGACTTCAACTGAACAAGTTGACGTTTCTCATGAGACTTCTGACGACGAGT
o   +----|----+----|----+----|----+----|----+----|----+----|----+----|----+ 3290
1        .   I   R   V   H   F   .   D   F   N   .   T   S   .   R   F   S   .   D   F   .   R   R   V
2          E   S   E   C   I   S   E   T   S   T   E   Q   V   D   V   S   H   E   T   S   D   D   E
3        N   Q   S   A   F   L   R   L   Q   L   N   K   L   T   F   L   M   R   L   L   T   T   S
o
5'  GGGCTGCTGCAGTTGATGAAGCGTTCCCTCTCGATGAAGCAGAAGATGTTACTGAATCTGTGCAAGAAGA
o   +----|----+----|----+----|----+----|----+----|----+----|----+----|----+ 3360
1        G   C   C   S   .   .   S   V   P   S   R   .   S   R   R   C   Y   .   I   C   A   R   R
2      W   A   A   A   A   V   D   E   A   F   P   L   D   E   A   E   D   V   T   E   S   V   Q   E   E
3        G   L   L   Q   L   M   K   R   S   L   S   M   K   Q   K   M   L   L   N   L   C   K   K
o
5'  AGCACAACCAGTAGAAGTACCTGTTGAAGATATTGCGCAGGTTGTCATAGCTGACACCTTACAGGAAACT
o   +----|----+----|----+----|----+----|----+----|----+----|----+----|----+ 3430
1        S   T   T   S   R   S   T   C   .   R   Y   C   A   G   C   H   S   .   H   L   T   G   N
2          A   Q   P   V   E   V   P   V   E   D   I   A   Q   V   V   I   A   D   T   L   Q   E   T
3        K   H   N   Q   .   K   Y   L   L   K   I   L   R   R   L   S   .   L   T   P   Y   R   K   L
o
5'  CCTGTTGTGCCTGATACTGTTGAAGTCCCACCGCAAGTGGTGAAACTTCCGTCTGCACCTCAGACTATCC
o   +----|----+----|----+----|----+----|----+----|----+----|----+----|----+ 3500
1        S   C   C   A   .   Y   C   .   S   P   T   A   S   G   E   T   S   V   C   T   S   D   Y   P
2          P   V   V   P   D   T   V   E   V   P   P   Q   V   V   K   L   P   S   A   P   Q   T   I
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o
```

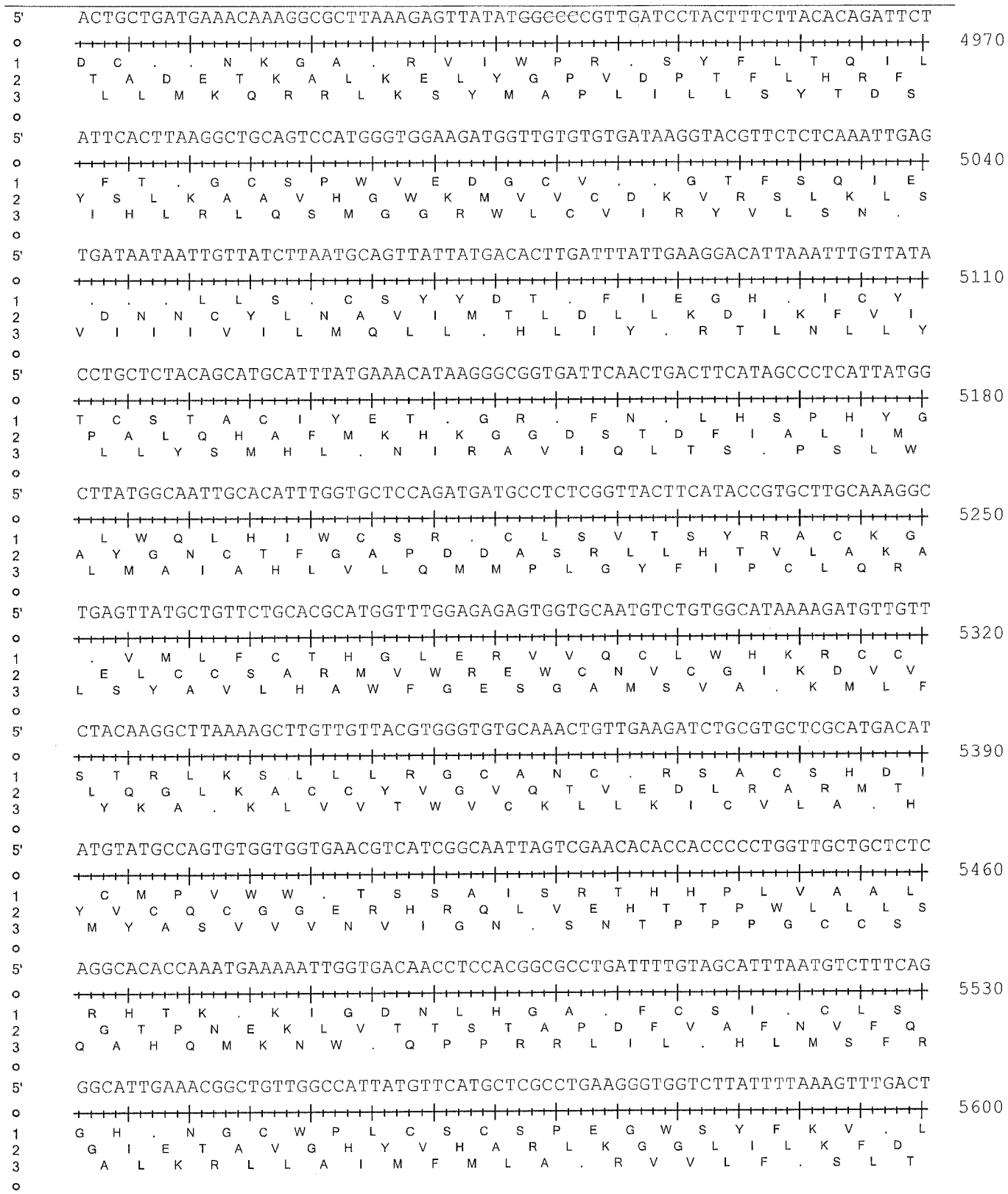
Sunday, September 23, 2012 1:41 PM
HCoV-SA1 translation 3 frames



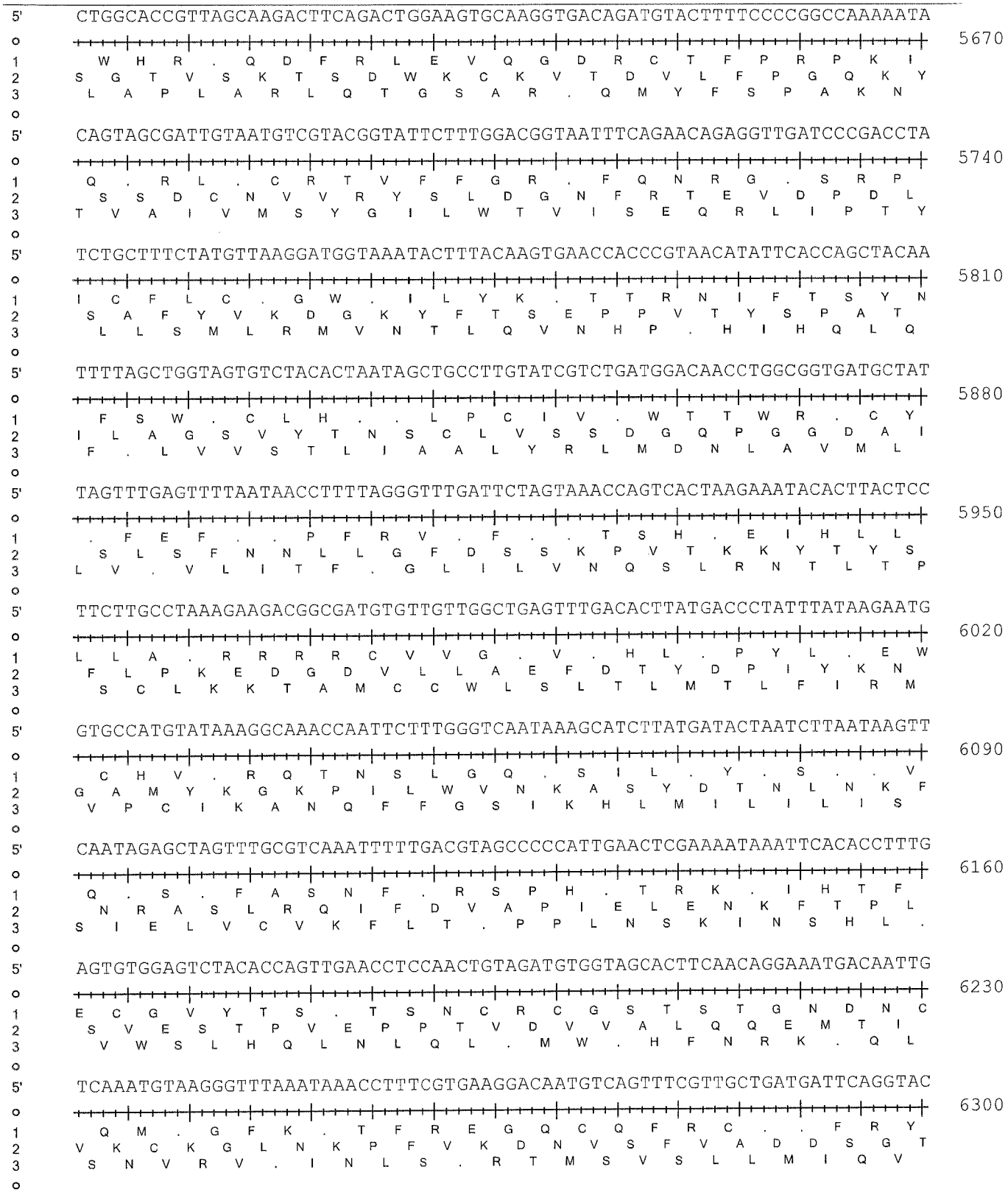
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HCoV-SA1 translation 3 frames



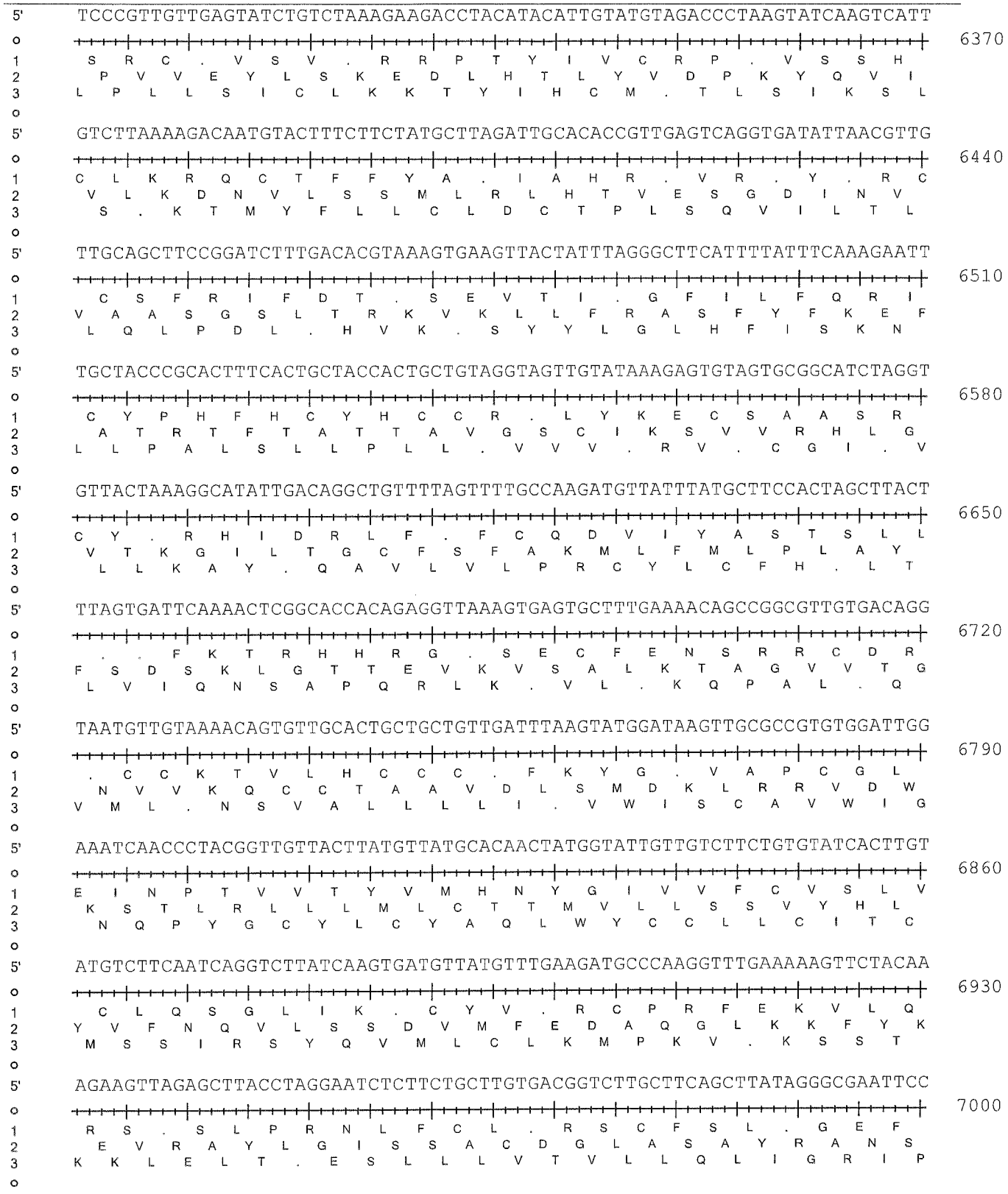
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HCoV-SA1 translation 3 frames



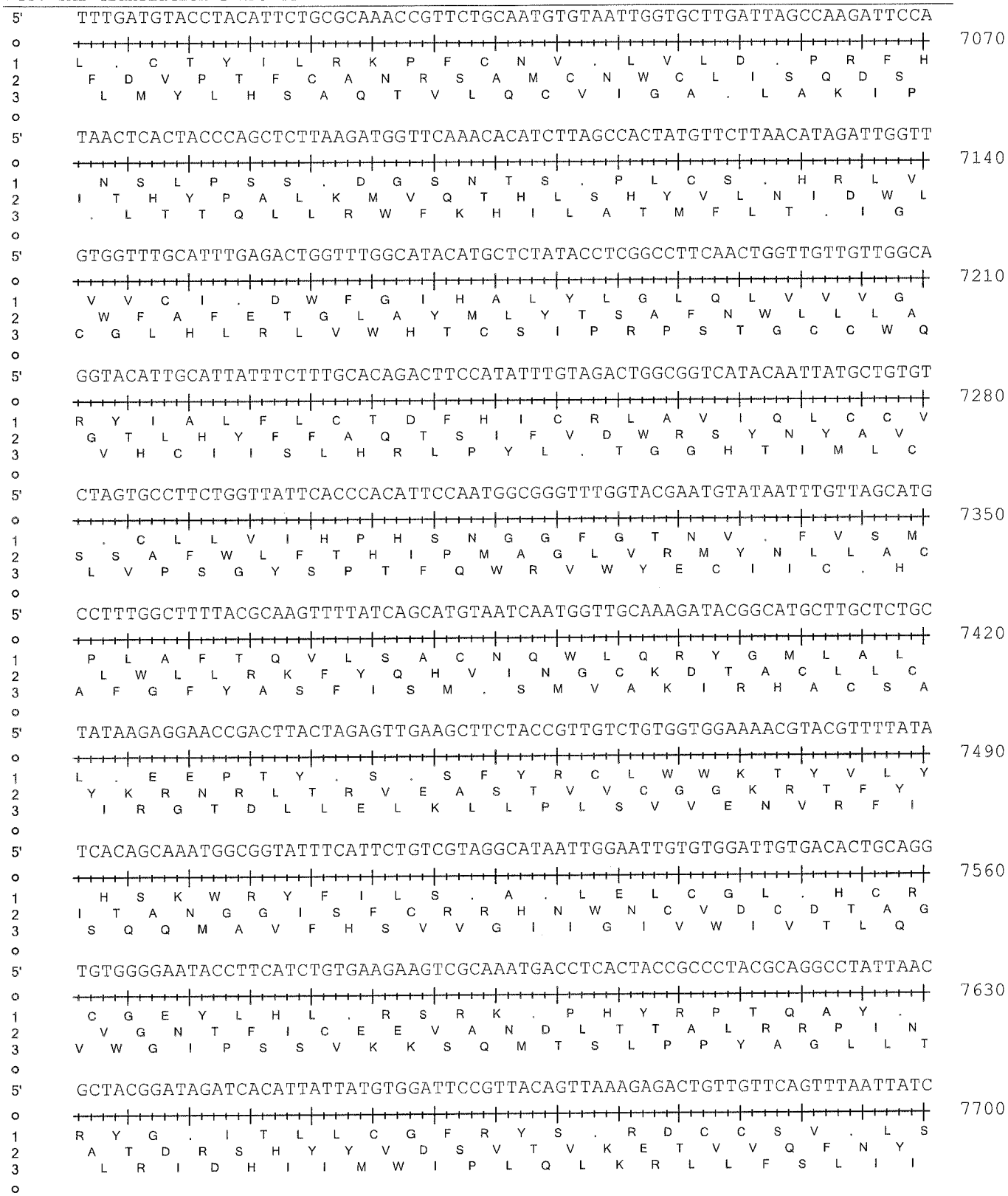
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HCoV-SA1 translation 3 frames



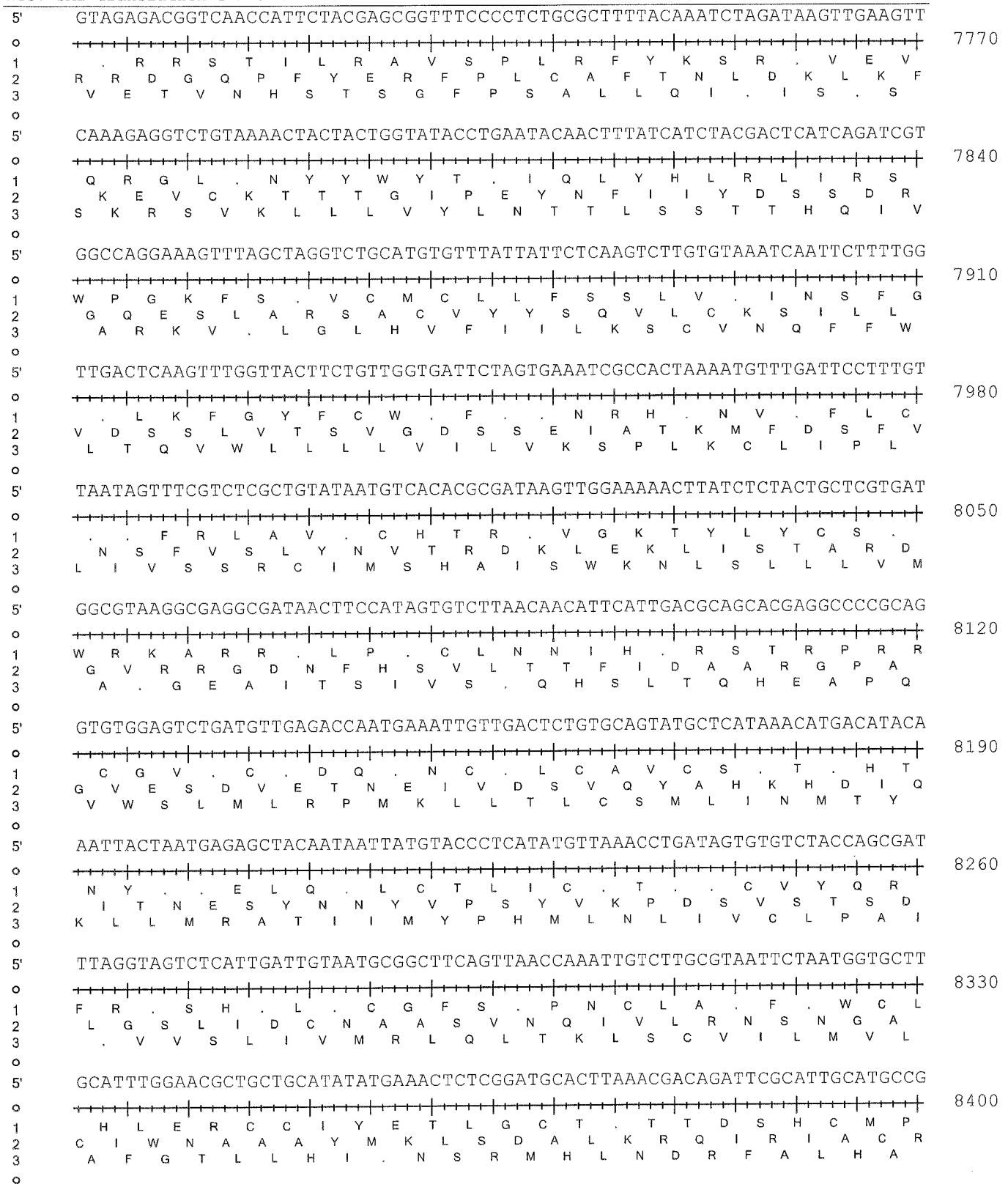
Sunday, September 23, 2012 1:41 PM
HCoV-SA1 translation 3 frames



Sunday, September 23, 2012 1:41 PM
HCoV-SA1 translation 3 frames



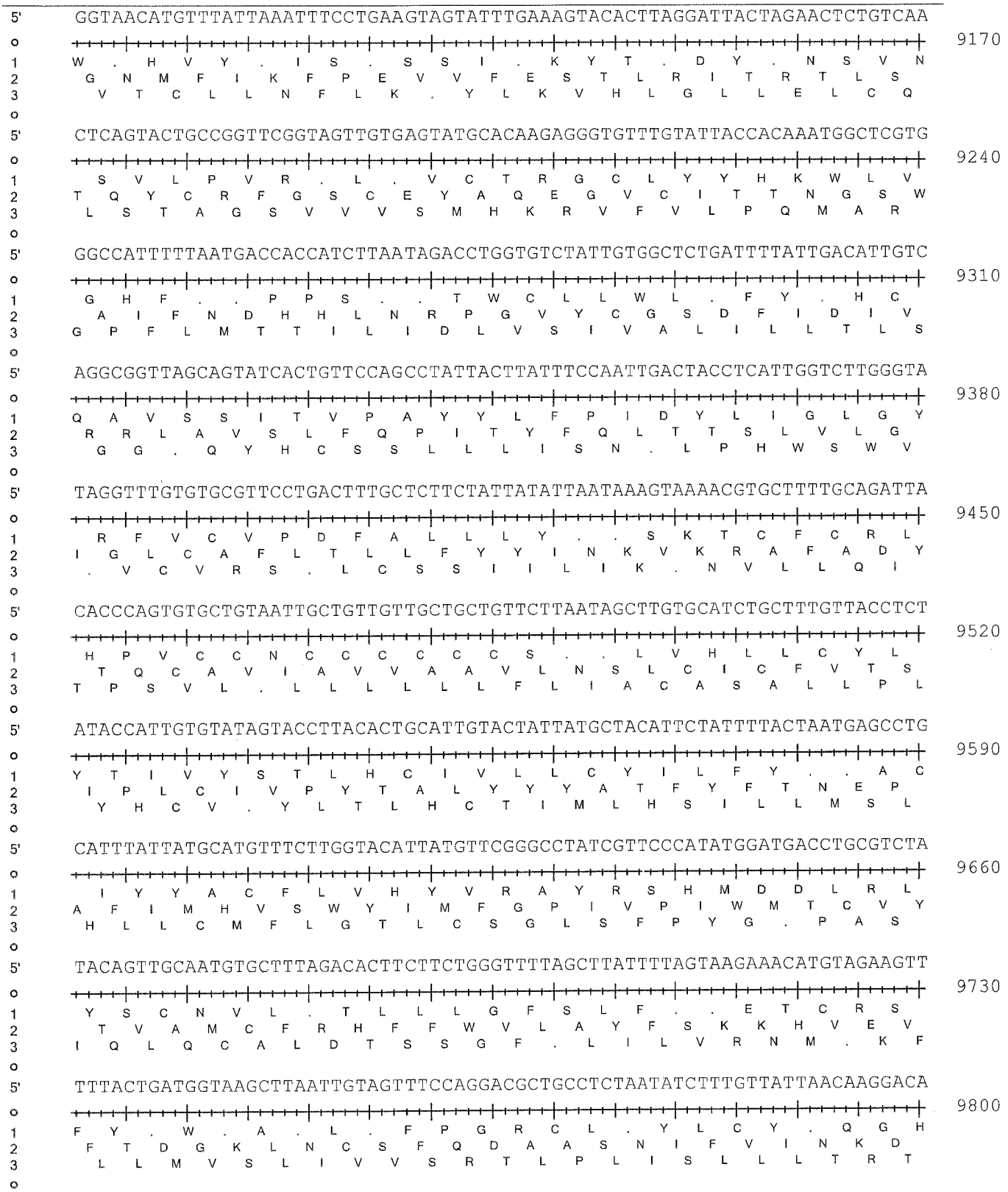
Sunday, September 23, 2012 1:41 PM
HCoV-SA1 translation 3 frames



Sunday, September 23, 2012 1:41 PM
HCoV-SA1 translation 3 frames

```
5'    TAAGTGTAATTTAGCTTTCCGGTTAACCACCTCAAAGCTACGCGCTAATGATAATATCTTATCAGTTAGA
o     +---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+  8470
1      .   V   .   F   S   F   P   V   N   H   L   K   A   T   R   .   .   Y   L   I   S   .
2        K   C   N   L   A   F   R   L   T   T   S   K   L   R   A   N   D   N   I   L   S   V   R
3      V   S   V   I   .   L   S   G   .   P   P   Q   S   Y   A   L   M   I   I   S   Y   Q   L   D
o
5'    TTCACTGCTAACAAAATTGTTGGTGGTGCTCCTACATGGTTTAATGCGTTGCGTGACTTTACGTTAAAGG
o     +---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+  8540
1      I   H   C   .   Q   N   C   W   W   C   S   Y   M   V   .   C   V   A   .   L   Y   V   K   G
2        F   T   A   N   K   I   V   G   G   A   P   T   W   F   N   A   L   R   D   F   T   L   K
3        S   L   L   T   K   L   L   V   V   L   L   H   G   L   M   R   C   V   T   L   R   .   R
o
5'    GTTATGTTCTTGCTACCATTATTGTGTTTCTGTGTGCTGTACTGATGTATTTGTGTTTACCTACATTTTC
o     +---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+  8610
1        L   C   S   C   Y   H   Y   C   V   S   V   C   C   T   D   V   F   V   F   T   Y   I   F
2      G   Y   V   L   A   T   I   I   V   F   L   C   A   V   L   M   Y   L   C   L   P   T   F   S
3        V   M   F   L   L   P   L   L   C   F   C   V   L   Y   .   C   I   C   V   Y   L   H   F
o
5'    TATGGCACCTGTTGAATTTTATGAAGACCGCATCTTGGACTTTAAAGTTCTTGATAATGGTATCATTAGG
o     +---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+  8680
1      Y   G   T   C   .   I   L   .   R   P   H   L   G   L   .   S   S   .   .   W   Y   H   .
2        M   A   P   V   E   F   Y   E   D   R   I   L   D   F   K   V   L   D   N   G   I   I   R
3      L   W   H   L   L   N   F   M   K   T   A   S   W   T   L   K   F   L   I   M   V   S   L   G
o
5'    GATGTAAATCCTGATGATAAGTGCTTTGCTAATAAGCACCGGTCCTTCACACAATGGTATCATGAGCATG
o     +---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+  8750
1      G   C   K   S   .   .   .   V   L   C   .   .   A   P   V   L   H   T   M   V   S   .   A   C
2        D   V   N   P   D   D   K   C   F   A   N   K   H   R   S   F   T   Q   W   Y   H   E   H
3        M   .   I   L   M   I   S   A   L   L   I   S   T   G   P   S   H   N   G   I   M   S   M
o
5'    TTGGTGGTGTCTATGACAACTCTATCACATGCCCATTGACAGTTGCAGTAATTGCTGGAGTTGCTGGTGC
o     +---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+  8820
1        W   W   C   L   .   Q   L   Y   H   M   P   I   D   S   C   S   N   C   W   S   C   W   C
2      V   G   G   V   Y   D   N   S   I   T   C   P   L   T   V   A   V   I   A   G   V   A   G   A
3        L   V   V   S   M   T   T   L   S   H   A   H   .   Q   L   Q   .   L   L   E   L   L   V
o
5'    TCGCATTCCAGACGTACCTACTACATTGGCTTGGGTGAACAATCAGATAATTTTCTTTGTTTCTCGAGTC
o     +---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+  8890
1        S   H   S   R   R   T   Y   Y   I   G   L   G   E   Q   S   D   N   F   L   C   F   S   S
2          R   I   P   D   V   P   T   T   L   A   W   V   N   N   Q   I   I   F   F   V   S   R   V
3        L   A   F   Q   T   Y   L   L   H   W   L   G   .   T   I   R   .   F   S   L   F   L   E   S
o
5'    TTTGCTAATACAGGCAGTGTTTGCTACACTCCTATAGATGAGATACCCTATAAGAGTTTCTCTGATAGTG
o     +---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+  8960
1      L   C   .   Y   R   Q   C   L   L   H   S   Y   R   .   D   T   L   .   E   F   L   .   .   W
2        F   A   N   T   G   S   V   C   Y   T   P   I   D   E   I   P   Y   K   S   F   S   D   S
3          L   L   I   Q   A   V   F   A   T   L   L   .   M   R   Y   P   I   R   V   S   L   I   V
o
5'    GTTGCATTCTTCCATCTGAGTGCACTATGTTTAGGGATGCAGAGGGCCGTATGACACCATACTGCCATGA
o     +---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+  9030
1        L   H   S   S   I   .   V   H   Y   V   .   G   C   R   G   P   Y   D   T   I   L   P   .
2      G   C   I   L   P   S   E   C   T   M   F   R   D   A   E   G   R   M   T   P   Y   C   H   D
3        V   A   F   F   H   L   S   A   L   C   L   G   M   Q   R   A   V   .   H   H   T   A   M
o
5'    TCCTACTGTTTTGCCTGGGGCTTTTGCGTACAGTCAGATGAGGCCTCATGTTCGTTACGACTTGTATGAT
o     +---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+  9100
1        S   Y   C   F   A   W   G   F   C   V   Q   S   D   E   A   S   C   S   L   R   L   V   .
2          P   T   V   L   P   G   A   F   A   Y   S   Q   M   R   P   H   V   R   Y   D   L   Y   D
3        I   L   L   F   C   L   G   L   L   R   T   V   R   .   G   L   M   F   V   T   T   C   M   M
o
```

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HCoV-SA1 translation 3 frames



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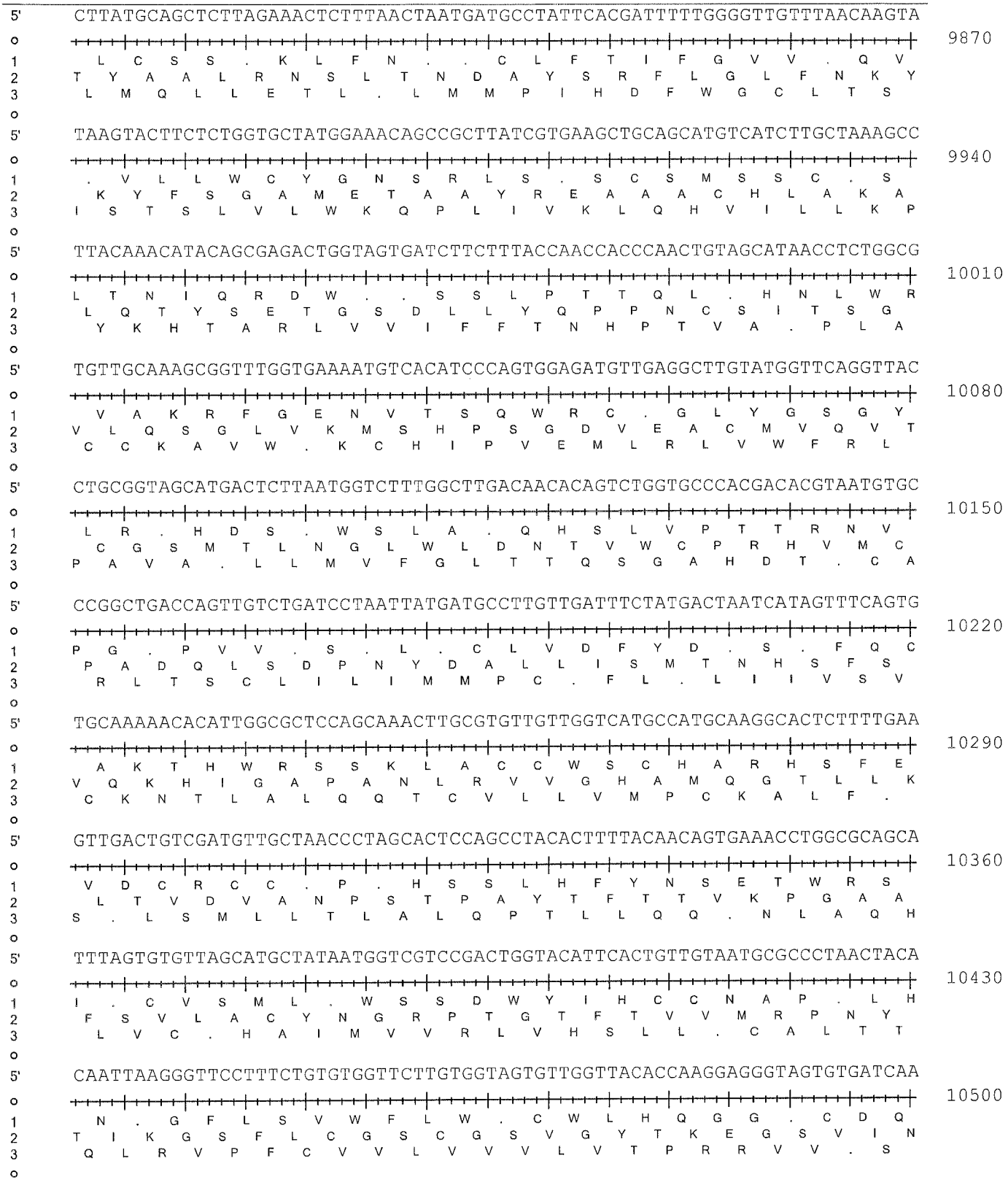
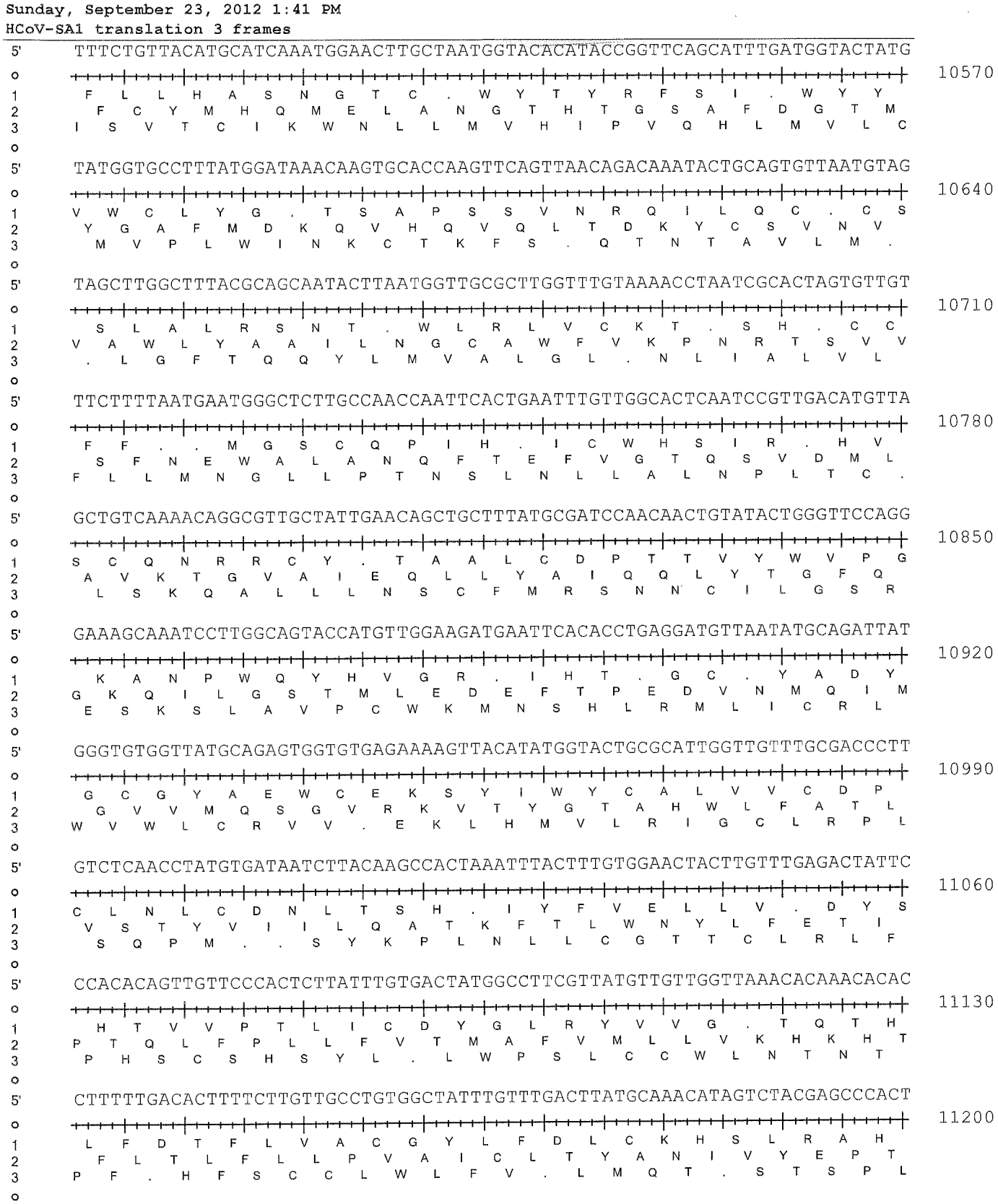


Figure 15 continued



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```
5'  ACTCCCATTTCGTCAGCGCTGATTGCAGTTGCAAATTGGCTTGCCCCCACTAATGCTTATATGCGCACTA
o  +---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+  11270
1   Y   S   H   F   V   S   A   D   C   S   C   K   L   A   C   P   H   .   C   L   Y   A   H   Y
2     T   P   I   S   S   A   L   I   A   V   A   N   W   L   A   P   T   N   A   Y   M   R   T
3       L   P   F   R   Q   R   .   L   Q   L   Q   I   G   L   P   P   L   M   L   I   C   A   L
o
5'  CACATACTGATATTGGTGTCTACATTAGTATGTCACTTGTATTAGTCATTGTAGTGAAGAGATTGTACAA
o  +---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+  11340
1     T   Y   .   Y   W   C   L   H   .   Y   V   T   C   I   S   H   C   S   E   E   I   V   Q
2   T   H   T   D   I   G   V   Y   I   S   M   S   L   V   L   V   I   V   V   K   R   L   Y   N
3     H   I   L   I   L   V   S   T   L   V   C   H   L   Y   .   S   L   .   .   R   D   C   T
o
5'  CCCATCACTTTCTAACTTTGCGTTAGCATTGTGCAGTGGTGTAATGTGGTTGTACACTTATAGCATTGGA
o  +---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+  11410
1     P   I   T   F   .   L   C   V   S   I   V   Q   W   C   N   V   V   V   H   L   .   H   W
2       P   S   L   S   N   F   A   L   A   L   C   S   G   V   M   W   L   Y   T   Y   S   I   G
3   T   H   H   F   L   T   L   R   .   H   C   A   V   V   .   C   G   C   T   L   I   A   L   E
o
5'  GAAGCCTCAAGCCCCATTGCCTATCTGGTTTTTGTCACTACACTCACTAGTGATTATACGATTACAGTCT
o  +---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+  11480
1   R   S   L   K   P   H   C   L   S   G   F   C   H   Y   T   H   .   .   L   Y   D   Y   S   L
2     E   A   S   S   P   I   A   Y   L   V   F   V   T   T   L   T   S   D   Y   T   I   T   V
3       K   P   Q   A   P   L   P   I   W   F   L   S   L   H   S   L   V   I   I   R   L   Q   S
o
5'  TTGTTACTGTCAACCTTGCAAAAGTTTGCACTTATGCCATCTTTGCTTACTCACCACAGCTTACACTTGT
o  +---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+  11550
1     C   Y   C   Q   P   C   K   S   L   H   L   C   H   L   C   L   L   T   T   A   Y   T   C
2   F   V   T   V   N   L   A   K   V   C   T   Y   A   I   F   A   Y   S   P   Q   L   T   L   V
3     L   L   L   S   T   L   Q   K   F   A   L   M   P   S   L   L   T   H   H   S   L   H   L
o
5'  GTTTCCGGAAGTGAAGATGATACTTTTATTATACACATGTTTAGGTTTCATGTGTACTTGCTATTTTGGT
o  +---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+  11620
1   V   S   G   S   E   D   D   T   F   I   I   H   M   F   R   F   H   V   Y   L   L   F   W
2     F   P   E   V   K   M   I   L   L   L   Y   T   C   L   G   F   M   C   T   C   Y   F   G
3   C   F   R   K   .   R   .   Y   F   Y   Y   T   H   V   .   V   S   C   V   L   A   I   L   V
o
5'  GTCTTCTCTCTTTTGAACCTTAAGCTTAGAGCACCTATGGGTGTCTATGACTTTAAGGTCTCAACACAAG
o  +---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+  11690
1   C   L   L   S   F   E   P   .   A   .   S   T   Y   G   C   L   .   L   .   G   L   N   T   R
2     V   F   S   L   L   N   L   K   L   R   A   P   M   G   V   Y   D   F   K   V   S   T   Q
3       S   S   L   F   .   T   L   S   L   E   H   L   W   V   S   M   T   L   R   S   Q   H   K
o
5'  AGTTCAGATTCATGACTGCTAACAATCTAACTGCACCTAGAAATTCTTGGGAGGCTATGGCTCTGAACTT
o  +---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+  11760
1     V   Q   I   H   D   C   .   Q   S   N   C   T   .   K   F   L   G   G   Y   G   S   E   L
2   E   F   R   F   M   T   A   N   N   L   T   A   P   R   N   S   W   E   A   M   A   L   N   F
3     S   S   D   S   .   L   L   T   I   .   L   H   L   E   I   L   G   R   L   W   L   .   T
o
5'  TAAGTTAATAGGTATTGGCGGTACACCTTGTATAAAGGTTGCTGCTATGCAGTCTAAACTTACAGATCTT
o  +---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+  11830
1     .   V   N   R   Y   W   R   Y   T   L   Y   K   G   C   C   Y   A   V   .   T   Y   R   S
2       K   L   I   G   I   G   G   T   P   C   I   K   V   A   A   M   Q   S   K   L   T   D   L
3   L   S   .   .   V   L   A   V   H   L   V   .   R   L   L   L   C   S   L   N   L   Q   I   L
o
5'  AAATGCACATCTGTGGTTCTCCTCTCTGTGCTCCAACAGTTACACTTAGAGGCTAATAGTAGGGCCTGGG
o  +---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+  11900
1     .   M   H   I   C   G   S   P   L   C   A   P   T   V   T   L   R   G   .   .   .   G   L   G
2       K   C   T   S   V   V   L   L   S   V   L   Q   Q   L   H   L   E   A   N   S   R   A   W
3         N   A   H   L   W   F   S   S   L   C   S   N   S   Y   T   .   R   L   I   V   G   P   G
o
```

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```
5'    CTTTCTGTGTTAAATGCCATAATGATATATTGGCAGCAACAGACCCCAGTGAGGCTTTCGAGAAATTCGT
o     +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++ 11970
1       F   L   C   .   M   P   .   .   Y   I   G   S   N   R   P   Q   .   G   F   R   E   I   R
2     A   F   C   V   K   C   H   N   D   I   L   A   A   T   D   P   S   E   A   F   E   K   F   V
3       L   S   V   L   N   A   I   M   I   Y   W   Q   Q   Q   T   P   V   R   L   S   R   N   S
o
5'    AAGTCTCTTTGCTACTTTAATGACTTTTTCTGGTAATGTAGATCTTGATGCGTTAGCTAGTGATATTTTT
o     +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++ 12040
1       K   S   L   C   Y   F   N   D   F   F   W   .   C   R   S   .   C   V   S   .   .   Y   F
2         S   L   F   A   T   L   M   T   F   S   G   N   V   D   L   D   A   L   A   S   D   I   F
3       .   V   S   L   L   L   .   .   L   F   L   V   M   .   I   L   M   R   .   L   V   I   F   L
o
5'    GACACTCCTAGCGTACTTCAAGCTACTCTTTCTGAGTTTTCACACTTAGCTACCTTTGCTGAGTTGGAAG
o     +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++ 12110
1       .   H   S   .   R   T   S   S   Y   S   F   .   V   F   T   L   S   Y   L   C   .   V   G   S
2         D   T   P   S   V   L   Q   A   T   L   S   E   F   S   H   L   A   T   F   A   E   L   E
3           T   L   L   A   Y   F   K   L   L   F   L   S   F   H   T   .   L   P   L   L   S   W   K
o
5'    CTGCGCAGAAAGCCTATCAGGAAGCTATGGACTCTGGTGACACCTCACCACAAGTTCTTAAGGCTTTGCA
o     +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++ 12180
1       C   A   E   S   L   S   G   S   Y   G   L   W   .   H   L   T   T   S   S   .   G   F   A
2     A   A   Q   K   A   Y   Q   E   A   M   D   S   G   D   T   S   P   Q   V   L   K   A   L   Q
3       L   R   R   K   P   I   R   K   L   W   T   L   V   T   P   H   H   K   F   L   R   L   C
o
5'    GAAGGCTGTTAATATAGCTAAAAACGCCTATGAGAAGGATAAGGCAGTGGCCCGTAAGTTAGAACGTATG
o     +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++ 12250
1       E   G   C   .   Y   S   .   K   R   L   .   E   G   .   G   S   G   P   .   V   R   T   Y
2         K   A   V   N   I   A   K   N   A   Y   E   K   D   K   A   V   A   R   K   L   E   R   M
3       R   R   L   L   I   .   L   K   T   P   M   R   R   I   R   Q   W   P   V   S   .   N   V   W
o
5'    GCTGATCAGGCTATGACTTCTATGTATAAGCAAGCACGTGCTGAAGACAAGAAAGCAAAAATTGTCAGTG
o     +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++ 12320
1       G   .   S   G   Y   D   F   Y   V   .   A   S   T   C   .   R   Q   E   S   K   N   C   Q   C
2         A   D   Q   A   M   T   S   M   Y   K   Q   A   R   A   E   D   K   K   A   K   I   V   S
3           L   I   R   L   .   L   L   C   I   S   K   H   V   L   K   T   R   K   Q   K   L   S   V
o
5'    CTATGCAAACTATGTTGTTTGGTATGATTAAGAAGCTCGACAACGATGTTCTTAATGGTATCATTTCTAA
o     +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++ 12390
1       Y   A   N   Y   V   V   W   Y   D   .   E   A   R   Q   R   C   S   .   W   Y   H   F   .
2     A   M   Q   T   M   L   F   G   M   I   K   K   L   D   N   D   V   L   N   G   I   I   S   N
3       L   C   K   L   C   C   L   V   .   L   R   S   S   T   T   M   F   L   M   V   S   F   L
o
5'    CGCTAGGAATGGTTGTATACCTCTTAGTGTCATCCCACTGTGTGCTTCAAATAAACTTCGCGTTGTAATT
o     +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++ 12460
1       R   .   E   W   L   Y   T   S   .   C   H   P   T   V   C   F   K   .   T   S   R   C   N
2         A   R   N   G   C   I   P   L   S   V   I   P   L   C   A   S   N   K   L   R   V   V   I
3       T   L   G   M   V   V   Y   L   L   V   S   S   H   C   V   L   Q   I   N   F   A   L   .   F
o
5'    CCTGACTTCACCGTCTGGAATCAGGTAGTCACATATCCCTCGCTTAACTACGCTGGGGCTTTGTGGGACA
o     +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++ 12530
1       S   .   L   H   R   L   E   S   G   S   H   I   S   L   A   .   L   R   W   G   F   V   G   H
2         P   D   F   T   V   W   N   Q   V   V   T   Y   P   S   L   N   Y   A   G   A   L   W   D
3           L   T   S   P   S   G   I   R   .   S   H   I   P   R   L   T   T   L   G   L   C   G   T
o
5'    TTACAGTTATAAACAATGTGGACAATGAAATTGTTAAGTCTTCAGATGTTGTAGACAGCAATGAAAATTT
o     +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++ 12600
1       Y   S   Y   K   Q   C   G   Q   .   N   C   .   V   F   R   C   C   R   Q   Q   .   K   F
2     I   T   V   I   N   N   V   D   N   E   I   V   K   S   S   D   V   V   D   S   N   E   N   L
3       L   Q   L   .   T   M   W   T   M   K   L   L   S   L   Q   M   L   .   T   A   M   K   I
o
```

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```
5'  AACATGGCCACTTGTTTTAGAATGCACTAGGGCATCCACTTCTGCCGTTAAGTTGCAAAATAATGAGATC
o  +----|----|----|----|----|----|----|----|----|----|----|----|----|----|  12670
1    N   M   A   T   C   F   R   M   H   .   G   I   H   F   C   R   .   V   A   K   .   .   D
2      T   W   P   L   V   L   E   C   T   R   A   S   T   S   A   V   K   L   Q   N   N   E   I
3    .   H   G   H   L   F   .   N   A   L   G   H   P   L   L   P   L   S   C   K   I   M   R   S
o
5'  AAACCTTCAGGTCTAAAAACCATGGTTGTGTCTGCGGGTCAAGAGCAAACTAACTGTAATACTAGTTCCT
o  +----|----|----|----|----|----|----|----|----|----|----|----|----|----|  12740
1  Q   T   F   R   S   K   N   H   G   C   V   C   G   S   R   A   N   .   L   .   Y   .   F   L
2    K   P   S   G   L   K   T   M   V   V   S   A   G   Q   E   Q   T   N   C   N   T   S   S
3      N   L   Q   V   .   K   P   W   L   C   L   R   V   K   S   K   L   T   V   I   L   V   P
o
5'  TAGCTTATTACGAACCTGTGCAGGGTCGTAAAATGCTGATGGCTCTTCTTTCTGATAATGCCTATCTCAA
o  +----|----|----|----|----|----|----|----|----|----|----|----|----|----|  12810
1    S   L   L   R   T   C   A   G   S   .   N   A   D   G   S   S   F   .   .   C   L   S   Q
2  L   A   Y   Y   E   P   V   Q   G   R   K   M   L   M   A   L   L   S   D   N   A   Y   L   K
3    .   L   I   T   N   L   C   R   V   V   K   C   .   W   L   F   F   L   I   M   P   I   S
o
5'  ATGGGCGCGTGTTGAAGGTAAGGACGGATTTGTCAGTGTAGAGCTACAACCTCCTTGCAAATTCTTGATT
o  +----|----|----|----|----|----|----|----|----|----|----|----|----|----|  12880
1    M   G   A   C   .   R   .   G   R   I   C   Q   C   R   A   T   T   S   L   Q   I   L   D
2      W   A   R   V   E   G   K   D   G   F   V   S   V   E   L   Q   P   P   C   K   F   L   I
3  N   G   R   V   L   K   V   R   T   D   L   S   V   .   S   Y   N   L   L   A   N   S   .   L
o
5'  GCGGGACCAAAAGGACCTGAAATCCGATATCTCTATTTTGTTAAAAATCTTAACAACCTTCATCGCGGGC
o  +----|----|----|----|----|----|----|----|----|----|----|----|----|----|  12950
1  C   G   T   K   R   T   .   N   P   I   S   L   F   C   .   K   S   .   Q   P   S   S   R   A
2    A   G   P   K   G   P   E   I   R   Y   L   Y   F   V   K   N   L   N   N   L   H   R   G
3      R   D   Q   K   D   L   K   S   D   I   S   I   L   L   K   I   L   T   T   F   I   A   G
o
5'  AAGTGTTAGGGCACATTGCTGCGACTGTTAGATTGCAAGCTGGTTCTAACACCGAGTTTGCCTCTAATTC
o  +----|----|----|----|----|----|----|----|----|----|----|----|----|----|  13020
1    S   V   R   A   H   C   C   D   C   .   I   A   S   W   F   .   H   R   V   C   L   .   F
2  Q   V   L   G   H   I   A   A   T   V   R   L   Q   A   G   S   N   T   E   F   A   S   N   S
3    K   C   .   G   T   L   L   R   L   L   D   C   K   L   V   L   T   P   S   L   P   L   I
o
5'  CTCGGTGTTGTCACTTGTTAACTTCACCGTTGATCCTCAAAAAGCTTATCTCGATTTCGTCAATGCGGGA
o  +----|----|----|----|----|----|----|----|----|----|----|----|----|----|  13090
1    L   G   V   V   T   C   .   L   H   R   .   S   S   K   S   L   S   R   F   R   Q   C   G
2      S   V   L   S   L   V   N   F   T   V   D   P   Q   K   A   Y   L   D   F   V   N   A   G
3  P   R   C   C   H   L   L   T   S   P   L   I   L   K   K   L   I   S   I   S   S   M   R   E
o
5'  GGTGCCCCATTGACAAATTGTGTTAAGATGCTTACTCCTAAAACTGGTACAGGTATAGCTATATCTGTTA
o  +----|----|----|----|----|----|----|----|----|----|----|----|----|----|  13160
1  R   C   P   I   D   K   L   C   .   D   A   Y   S   .   N   W   Y   R   Y   S   Y   I   C   .
2    G   A   P   L   T   N   C   V   K   M   L   T   P   K   T   G   T   G   I   A   I   S   V
3      V   P   H   .   Q   I   V   L   R   C   L   L   L   K   L   V   Q   V   .   L   Y   L   L
o
5'  AACCAGAGAGTACAGCTGATCAAGAGACTTATGGTGGAGCTTCAGTGTGTCTCTATTGCCGTGCGCATAT
o  +----|----|----|----|----|----|----|----|----|----|----|----|----|----|  13230
1    T   R   E   Y   S   .   S   R   D   L   W   W   S   F   S   V   S   L   L   P   C   A   Y
2  K   P   E   S   T   A   D   Q   E   T   Y   G   G   A   S   V   C   L   Y   C   R   A   H   I
3    N   Q   R   V   Q   L   I   K   R   L   M   V   E   L   Q   C   V   S   I   A   V   R   I
o
5'  AGAACATCCTGATGTCTCTGGTGTTTGTAAATATAAGGGTAAGTTTGTCCAAATCCCTGCTCAGTGTGTC
o  +----|----|----|----|----|----|----|----|----|----|----|----|----|----|  13300
1    R   T   S   .   C   L   W   C   L   .   I   .   G   .   V   C   P   N   P   C   S   V   C
2      E   H   P   D   V   S   G   V   C   K   Y   K   G   K   F   V   Q   I   P   A   Q   C   V
3  .   N   I   L   M   S   L   V   F   V   N   I   R   V   S   L   S   K   S   L   L   S   V   S
o
```

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HCoV-SA1 translation 3 frames

```
5' CGTGACCCTGTGGGATTTTGTTTGTCAAATACCCCCTGTAATGTCTGTCAATATTGGATTGGATATGGGT 13370
1  P . P C G I L F V K Y P L . C L S I L D W I W V
2  R D P V G F C L S N T P C N V C Q Y W I G Y G
3  V T L W D F V C Q I P P V M S V N I G L D M G

5' GCAATTGTGACTCGCTTAGGCAAGCAGCACTGCCCCAATCTAAAGATTCCAATTTTTAAACGAGTCCGG 13440
1  Q L . L A . A S S T A P I . R F Q F F K R V R
2  C N C D S L R Q A A L P Q S K D S N F L N E S G
3  A I V T R L G K Q H C P N L K I P I F . T S P

5' GGTTCTATTGTAAATGCCCGAATAGAACCCTGTTCAAGTGGTTTGTCCACTGATGTCGTCTTTAGGGCAT 13510
1  G S I V N A R I E P C S S G L S T D V V F R A
2  V L L . M P E . N P V Q V V C P L M S S L G H
3  G F Y C K C P N R T L F K W F V H . C R L . G I

5' TTGACATCTGCAACTATAAGGCTAAGGTTGCTGGTATTGGAAAATACTACAAGACTAATACTTGTAGGTT 13580
1  F D I C N Y K A K V A G I G K Y Y K T N T C R F
2  L T S A T I R L R L L V L E N T T R L I L V G
3  . H L Q L . G . G C W Y W K I L Q D . Y L . V

5' TGTAGAATTAGATGACCAAGGGCATCATTTAGACTCCTATTTTGTCGTTAAGAGGCATACTATGGAGAAT 13650
1  V E L D D Q G H H L D S Y F V V K R H T M E N
2  L . N . M T K G I I . T P I L S L R G I L W R I
3  C R I R . P R A S F R L L F C R . E A Y Y G E

5' TATGAACTAGAGAAGCACTGTTACGACTTGTTACGTGACTGTGATGCTGTAGCTCCCCATGATTTCTTCA 13720
1  Y E L E K H C Y D L L R D C D A V A P H D F F
2  M N . R S T V T T C Y V T V M L . L P M I S S
3  L . T R E A L L R L V T . L . C C S S P . F L H

5' TCTTTGATGTAGACAAAGTTAAAACACCTCATATTGTACGTCAGCGTTTAACTGAGTACACTATGATGGA 13790
1  I F D V D K V K T P H I V R Q R L T E Y T M M D
2  S L M . T K L K H L I L Y V S V . L S T L . W
3  L . C R Q S . N T S Y C T S A F N . V H Y D G

5' TCTTGTATATGCCCTGAGGCACTTTGATCAAAATAGCGAAGTGCTTAAGGCTATCTTAGTGAAGTATGGT 13860
1  L V Y A L R H F D Q N S E V L K A I L V K Y G
2  I L Y M P . G T L I K I A K C L R L S . . S M V
3  S C I C P E A L . S K . R S A . G Y L S E V W

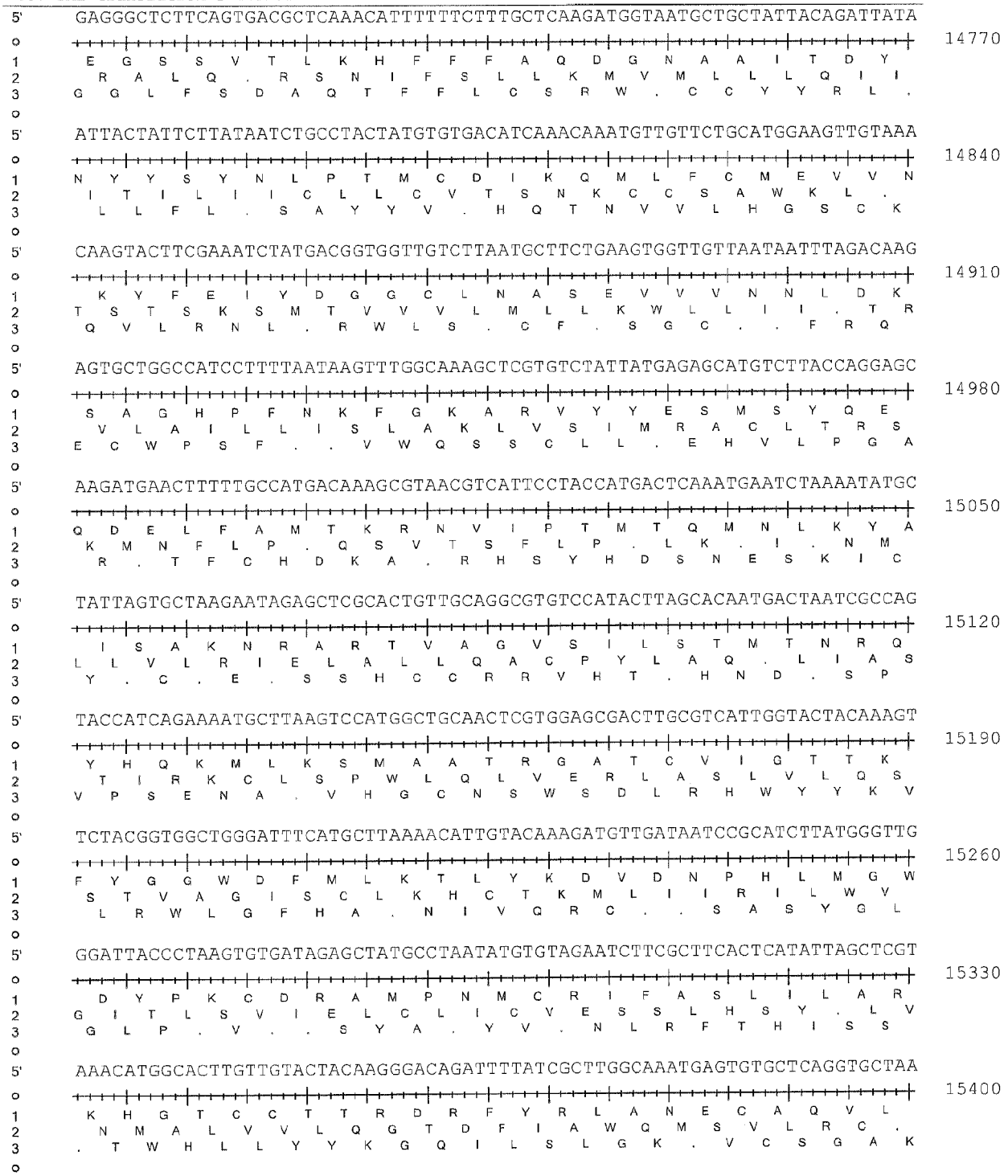
5' TGCTGTGATGTTACCTACTTTGAAAATAAACTCTGGTTTGATTTTGTTGAAAATCCCAGTGTTATTGGTG 13930
1  C C D V T Y F E N K L W F D F V E N P S V I G
2  A V M L P T L K I N S G L I L L K I P V L L V
3  L L . C Y L L . K . T L V . F C . K S Q C Y W C

5' TTTATCATAAACTTGGAGAACGTGTACGCCAAGCTATCTTAAACACTGTTAAATTTTGTGACCACATGGT 14000
1  V Y H K L G E R V R Q A I L N T V K F C D H M V
2  F I I N L E N V Y A K L S . T L L N F V T T W
3  L S . T W R T C T P S Y L K H C . I L . P H G
```

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HCoV-SA1 translation 3 frames

```
5'    CAAGGCTGGTTTAGTCGGTGTGCTCACACTAGACAACCAGGACCTTAATGGCAAGTGGTATGATTTTGGT
o     +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++  14070
1       K   A   G   L   V   G   V   L   T   L   D   N   Q   D   L   N   G   K   W   Y   D   F   G
2     S   R   L   V   .   S   V   C   S   H   .   T   T   R   T   L   M   A   S   G   M   I   L   V
3       Q   G   W   F   S   R   C   A   H   T   R   Q   P   G   P   .   W   Q   V   V   .   F   W
o
5'    GACTTCGTAATCACTCAACCTGGTTCAGGAGTAGCTATAGTTGATAGCTACTATTCTTATTTGATGCCTG
o     +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++  14140
1       D   F   V   I   T   Q   P   G   S   G   V   A   I   V   D   S   Y   Y   S   Y   L   M   P
2         T   S   .   S   L   N   L   V   Q   E   .   L   .   L   I   A   T   I   L   I   .   C   L
3       .   L   R   N   H   S   T   W   F   R   S   S   Y   S   .   .   L   L   F   L   F   D   A   C
o
5'    TGCTCTCAATGACCGATTGTCTGGCCGCTGAGACACATAGGGATTGTGATTTTAATAAACCACTCATTGA
o     +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++  14210
1     V   L   S   M   T   D   C   L   A   A   E   T   H   R   D   C   D   F   N   K   P   L   I   E
2       C   S   Q   .   P   I   V   W   P   L   R   H   I   G   I   V   I   L   I   N   H   S   L
3       A   L   N   D   R   L   S   G   R   .   D   T   .   G   L   .   F   .   .   T   T   H   .
o
5'    GTGGCCACTTACTGAGTATGATTTTACTGATTATAAGGTACAACTCTTTGAGAAGTACTTTAAATATTGG
o     +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++  14280
1       W   P   L   T   E   Y   D   F   T   D   Y   K   V   Q   L   F   E   K   Y   F   K   Y   W
2     S   G   H   L   L   S   M   I   L   L   I   I   R   Y   N   S   L   R   S   T   L   N   I   G
3       V   A   T   Y   .   V   .   F   Y   .   L   .   G   T   T   L   .   E   V   L   .   I   L
o
5'    GATCAGACGTATCACGCAAATTGCGTTAATTGTACTGATGACCGTTGTGTGTTACATTGTGCTAATTTCA
o     +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++  14350
1       D   Q   T   Y   H   A   N   C   V   N   C   T   D   D   R   C   V   L   H   C   A   N   F
2         I   R   R   I   T   Q   I   A   L   I   V   L   M   T   V   V   C   Y   I   V   L   I   S
3     G   S   D   V   S   R   K   L   R   .   L   Y   .   .   P   L   C   V   T   L   C   .   F   Q
o
5'    ATGTATTGTTTGCTATGACCATGCCTAAGACTTGTTTCGGACCCATAGTCCGAAAGATCTTTGTTGATGG
o     +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++  14420
1     N   V   L   F   A   M   T   M   P   K   T   C   F   G   P   I   V   R   K   I   F   V   D   G
2       M   Y   C   L   L   .   P   C   L   R   L   V   S   D   P   .   S   E   R   S   L   L   M
3       C   I   V   C   Y   D   H   A   .   D   L   F   R   T   H   S   P   K   D   L   C   .   W
o
5'    CGTGCCATTTGTAGTATCTTGTGGTTATCACTACAAAGAATTAGGTTTAGTCATGAATATGGATGTTAGT
o     +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++  14490
1       V   P   F   V   V   S   C   G   Y   H   Y   K   E   L   G   L   V   M   N   M   D   V   S
2     A   C   H   L   .   Y   L   V   V   I   T   T   K   N   .   V   .   S   .   I   W   M   L   V
3       R   A   I   C   S   I   L   W   L   S   L   Q   R   I   R   F   S   H   E   Y   G   C   .
o
5'    CTCCATAGACATAGGCTCTCTCTTAAGGAGTTGATGATGTATGCCGCTGATCCAGCCATGCACATTGCCT
o     +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++  14560
1       L   H   R   H   R   L   S   L   K   E   L   M   M   Y   A   A   D   P   A   M   H   I   A
2         S   I   D   I   G   S   L   L   R   S   .   .   C   M   P   L   I   Q   P   C   T   L   P
3     S   P   .   .   T   .   A   L   S   .   G   V   D   D   V   C   R   .   S   S   H   A   H   C   L
o
5'    CCTCTAACGCTTTTCTTGATTTGAGGACATCATGTTTTAGTGTCGCTGCACTTACAACTGGTTTGACTTT
o     +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++  14630
1     S   S   N   A   F   L   D   L   R   T   S   C   F   S   V   A   A   L   T   T   G   L   T   F
2       P   L   T   L   F   L   I   .   G   H   H   V   L   V   S   L   H   L   Q   L   V   .   L
3       L   .   R   F   S   .   F   E   D   I   M   F   .   C   R   C   T   Y   N   W   F   D   F
o
5'    TCAAACTGTGCGGCCTGGCAATTTTAACCAAGACTTCTATGATTTCGTGGTATCTAAAGGTTTCTTTAAG
o     +++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++|+++  14700
1       Q   T   V   R   P   G   N   F   N   Q   D   F   Y   D   F   V   V   S   K   G   F   F   K
2     F   K   L   C   G   L   A   I   L   T   K   T   S   M   I   S   W   Y   L   K   V   S   L   R
3       S   N   C   A   A   W   Q   F   .   P   R   L   L   .   F   R   G   I   .   R   F   L   .
o
```

Sunday, September 23, 2012 1:41 PM
HCoV-SA1 translation 3 frames



Sunday, September 23, 2012 1:41 PM
HCoV-SA1 translation 3 frames

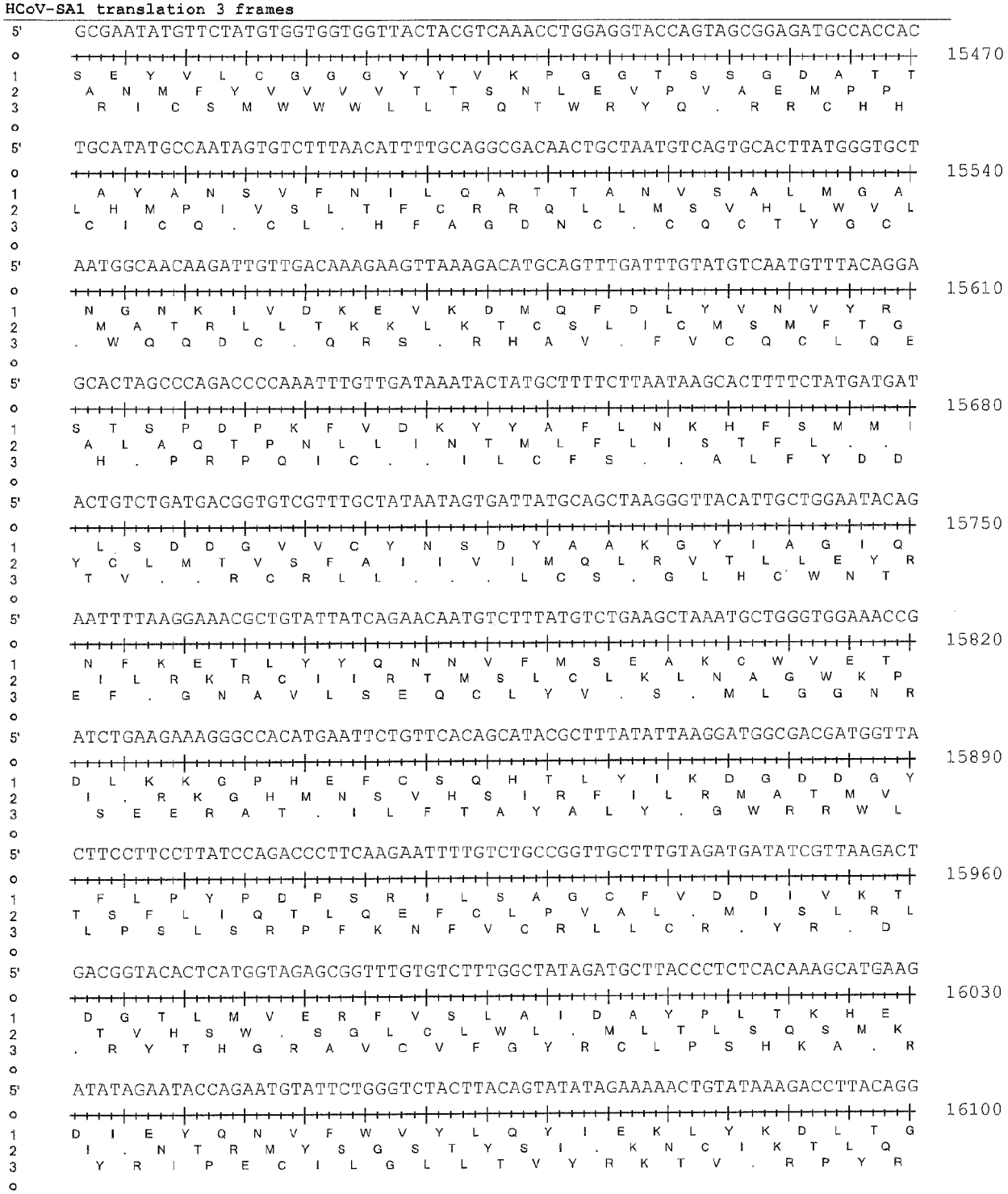
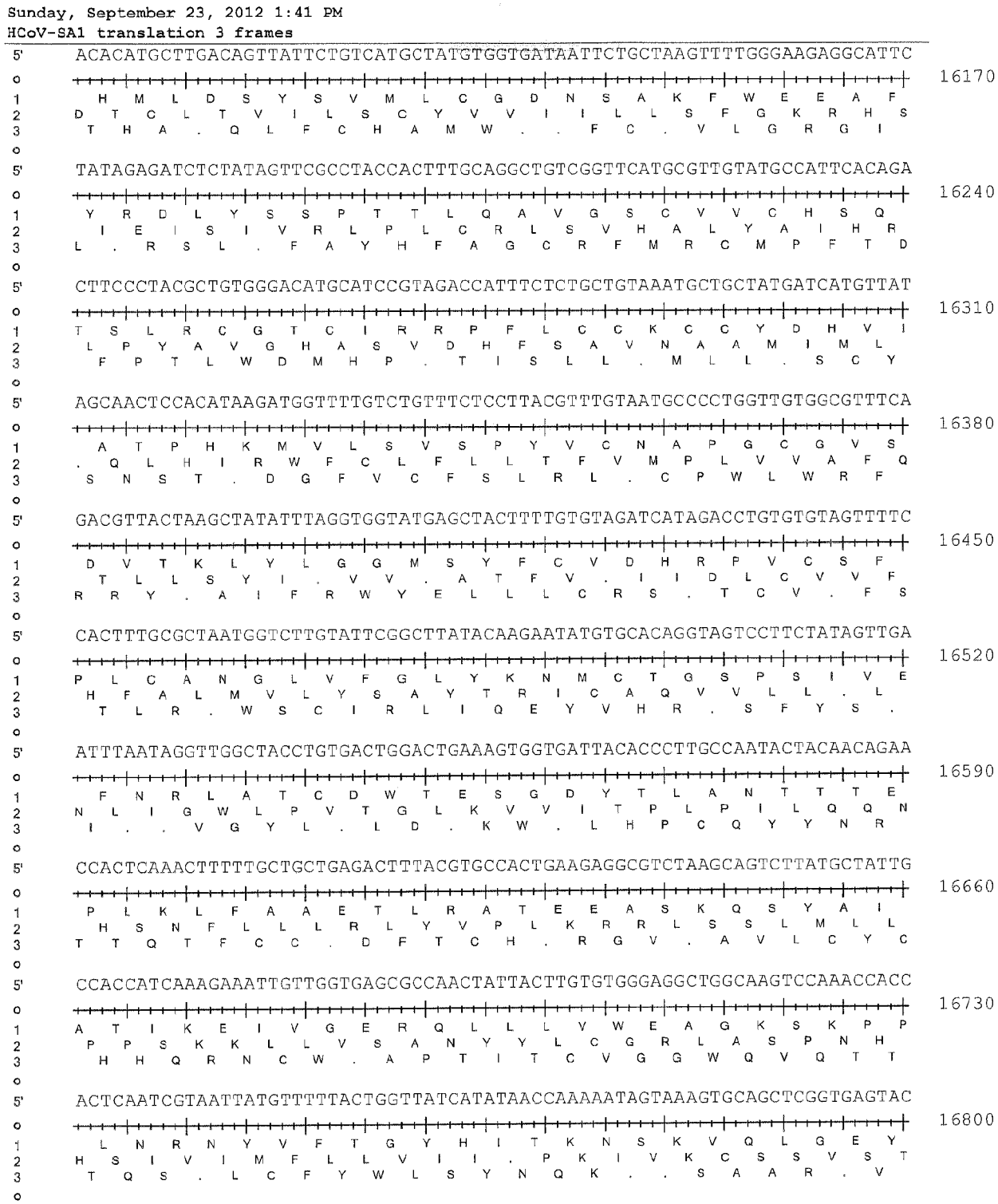
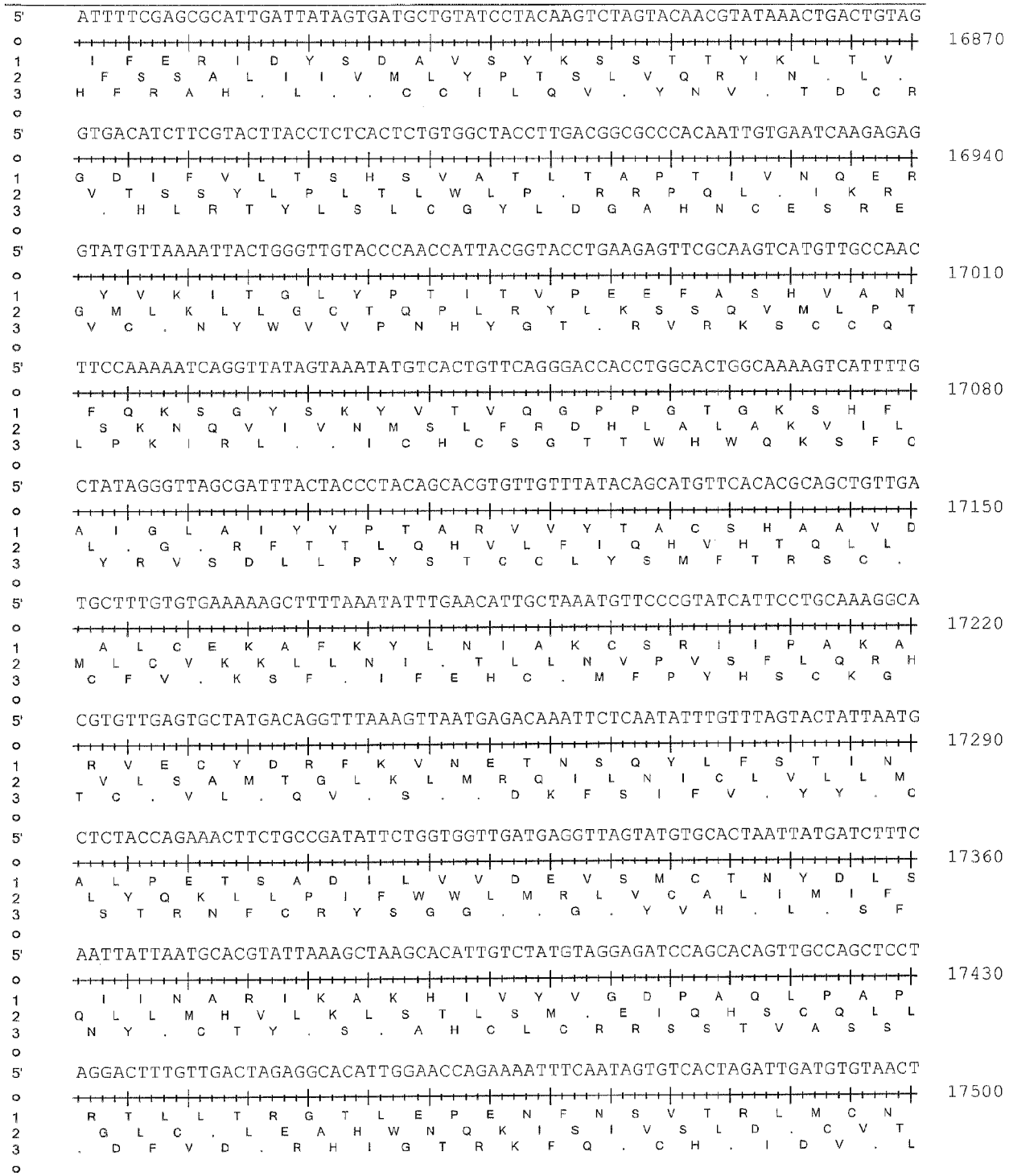


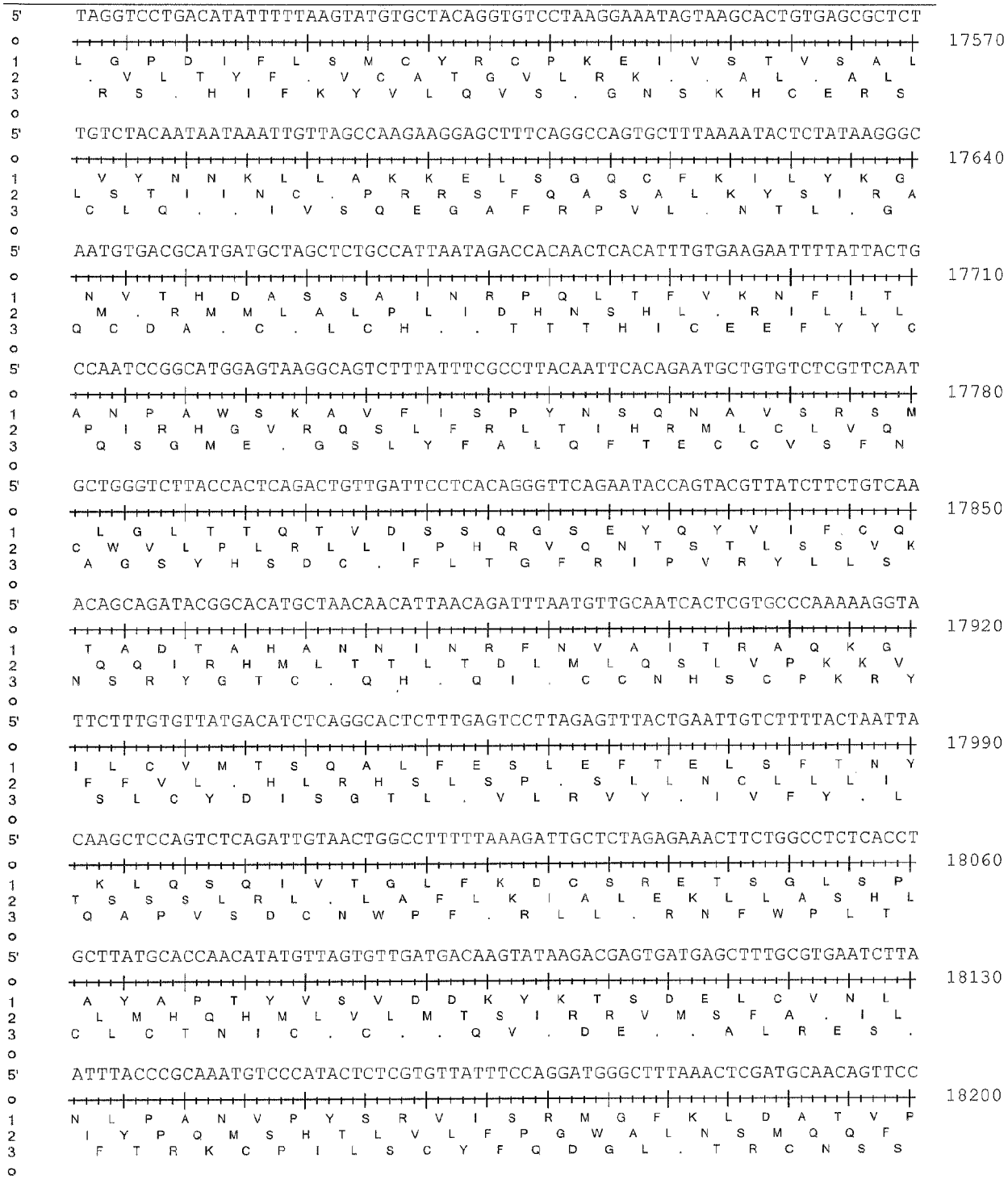
Figure 15 continued



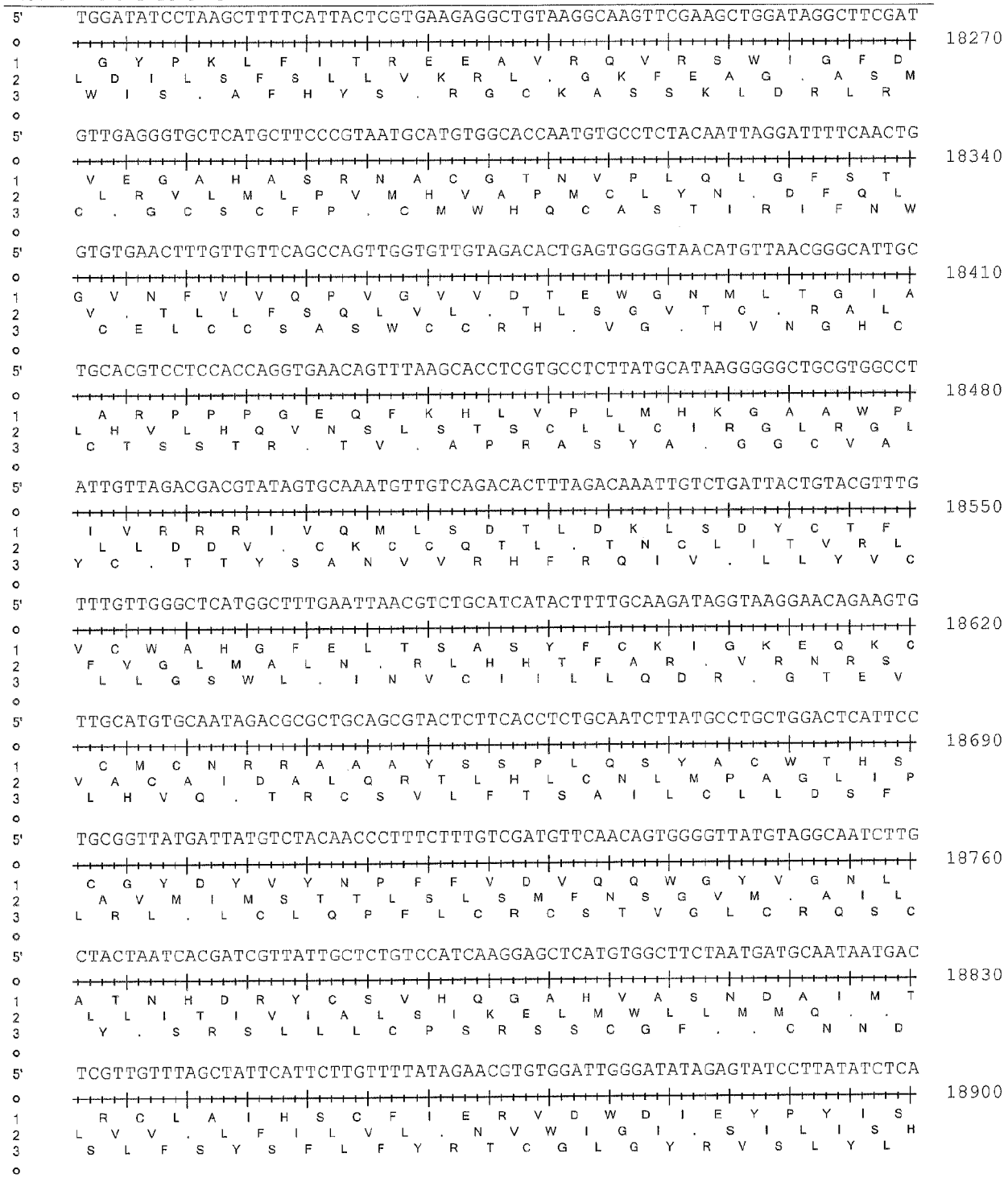
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HCoV-SA1 translation 3 frames



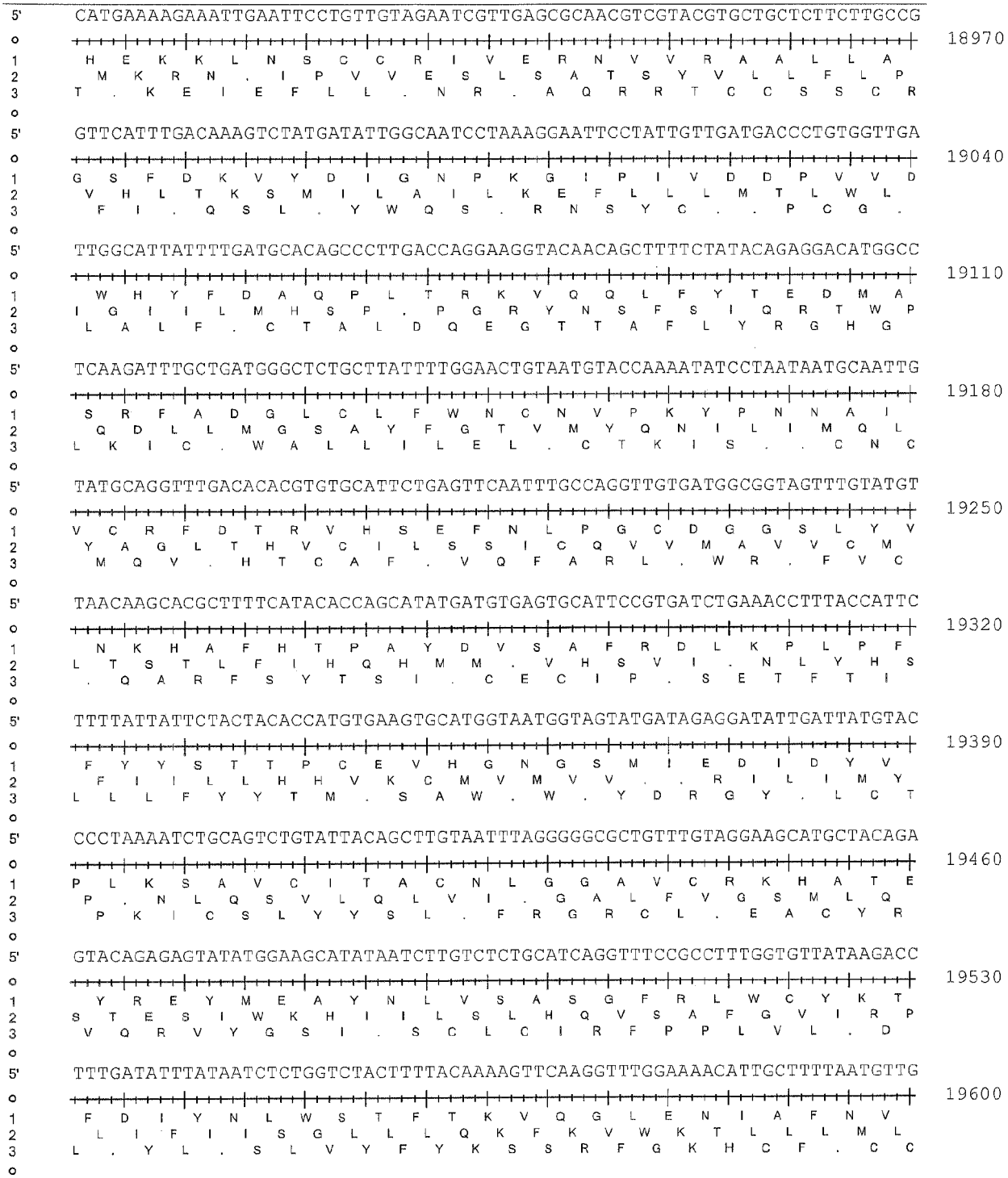
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HCoV-SA1 translation 3 frames



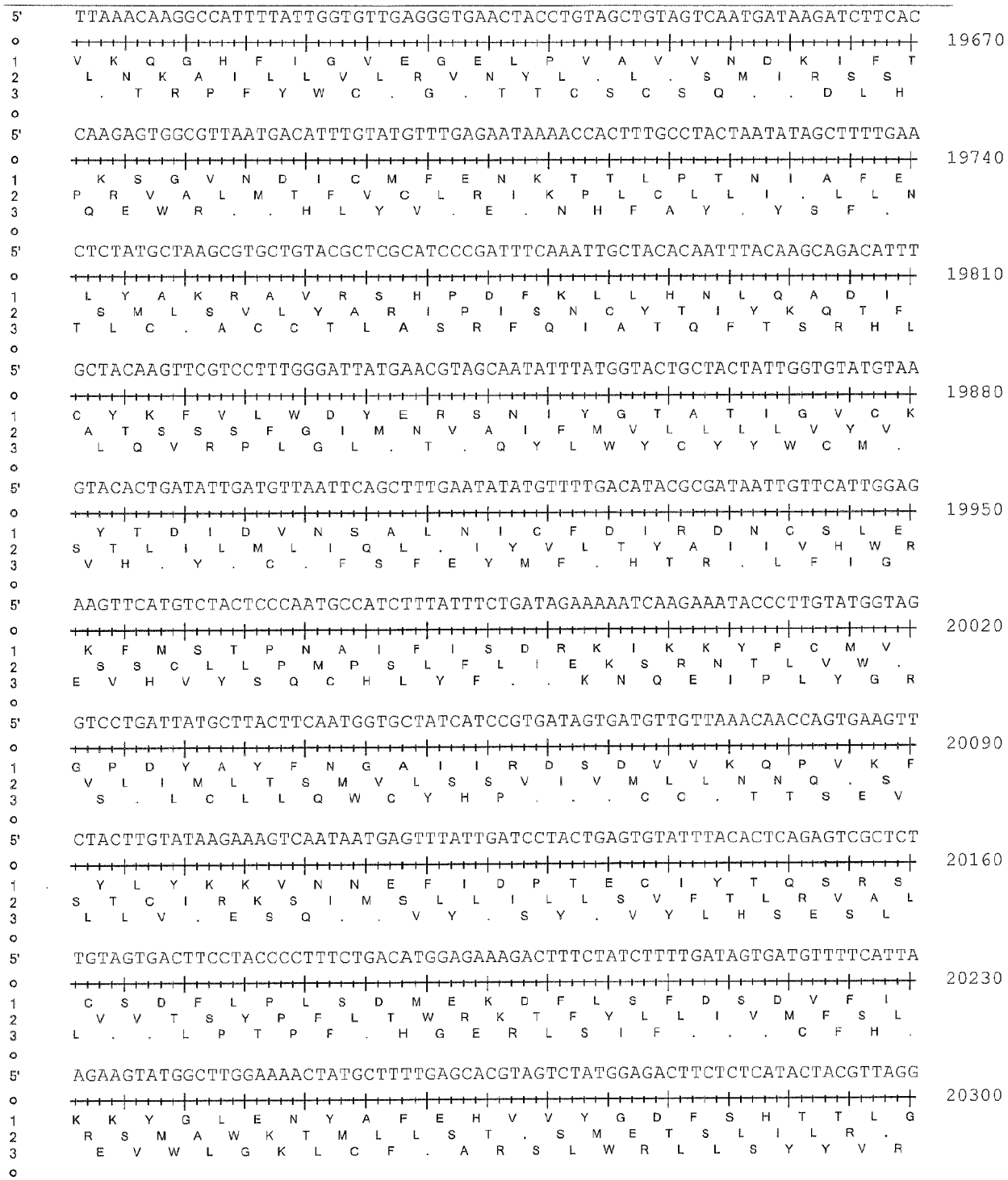
Sunday, September 23, 2012 1:41 PM
HCoV-SA1 translation 3 frames



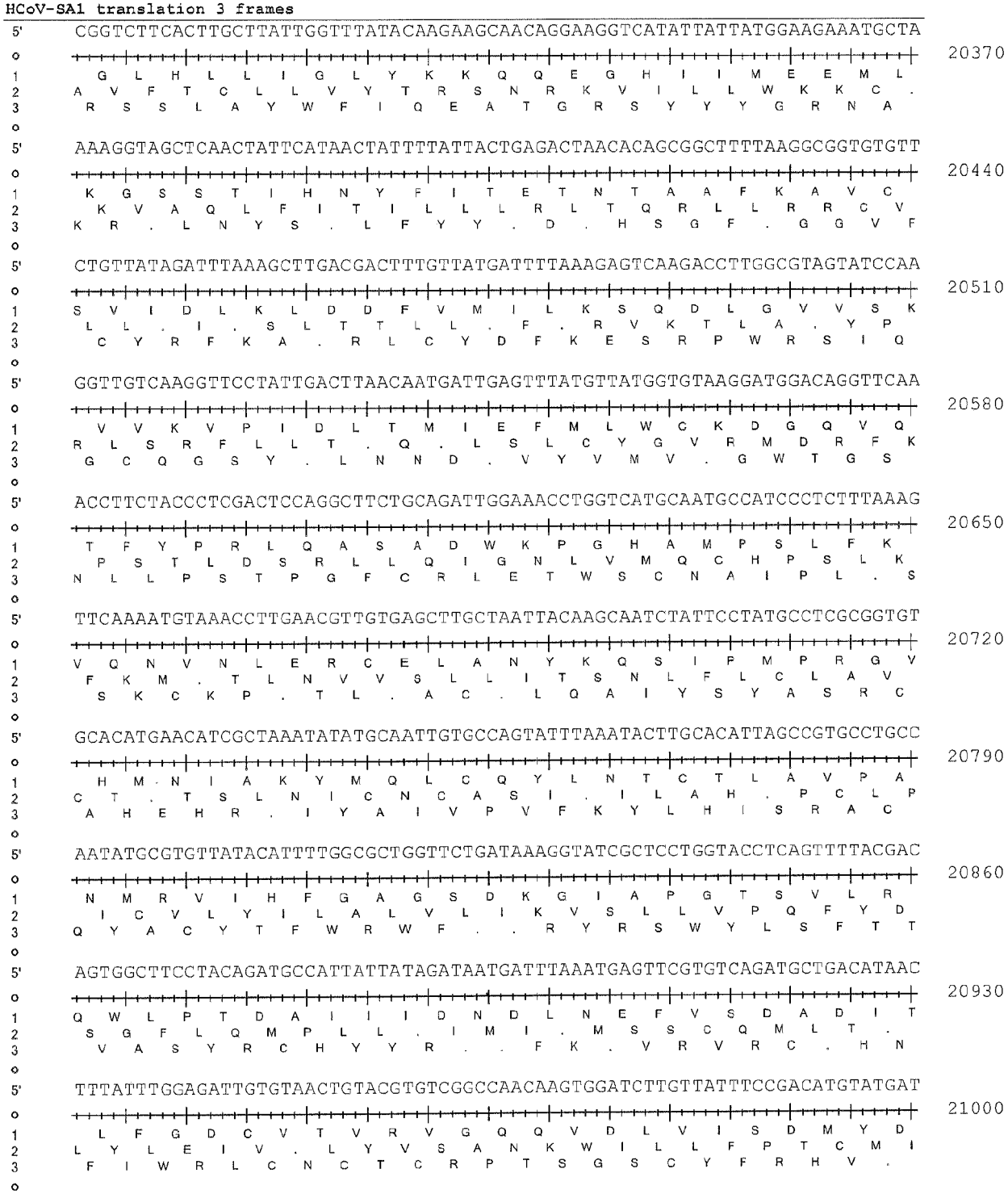
Sunday, September 23, 2012 1:41 PM
HCoV-SA1 translation 3 frames



Sunday, September 23, 2012 1:41 PM
HCoV-SA1 translation 3 frames



Sunday, September 23, 2012 1:41 PM
HCoV-SA1 translation 3 frames



Sunday, September 23, 2012 1:41 PM
HCoV-SA1 translation 3 frames

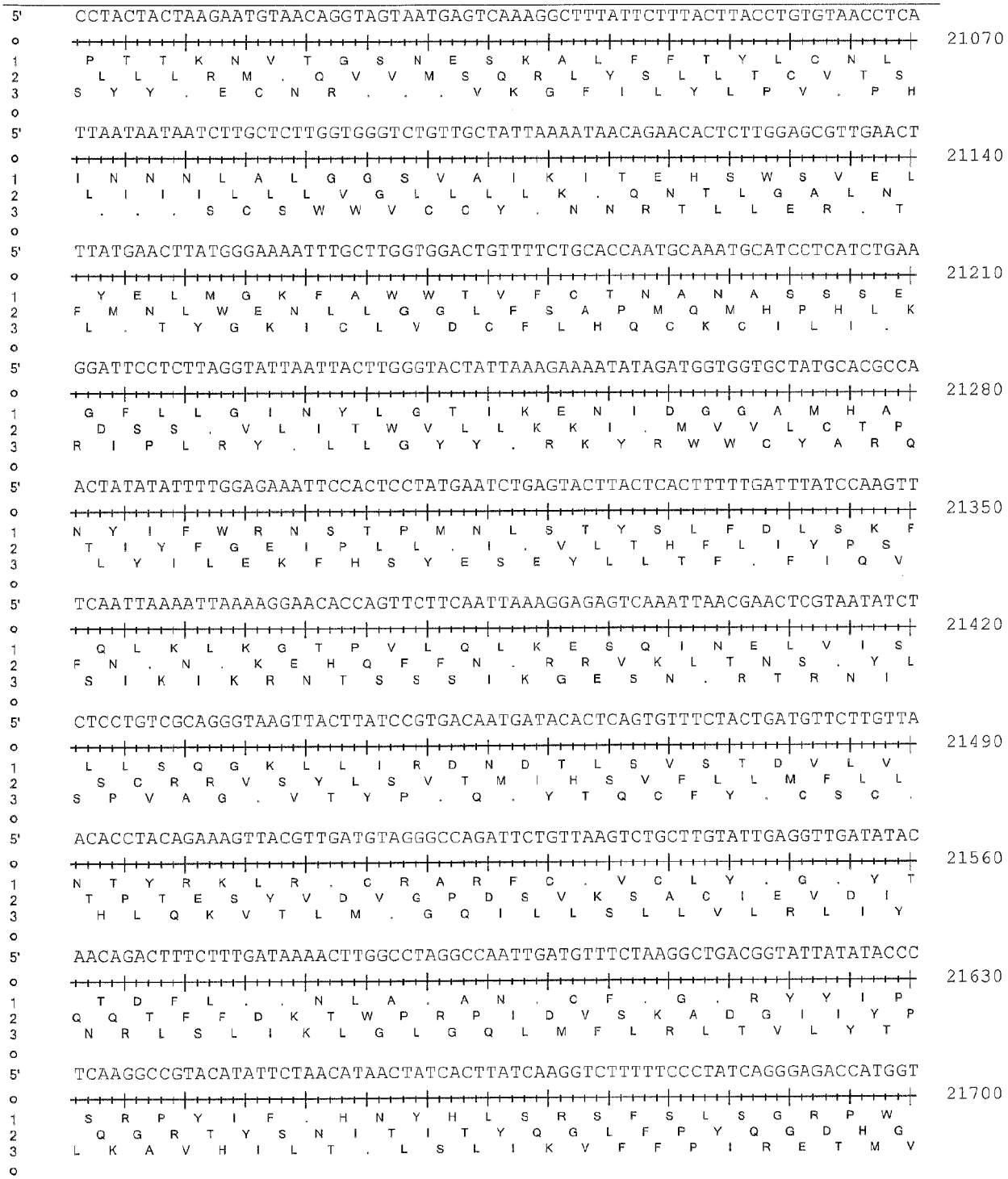
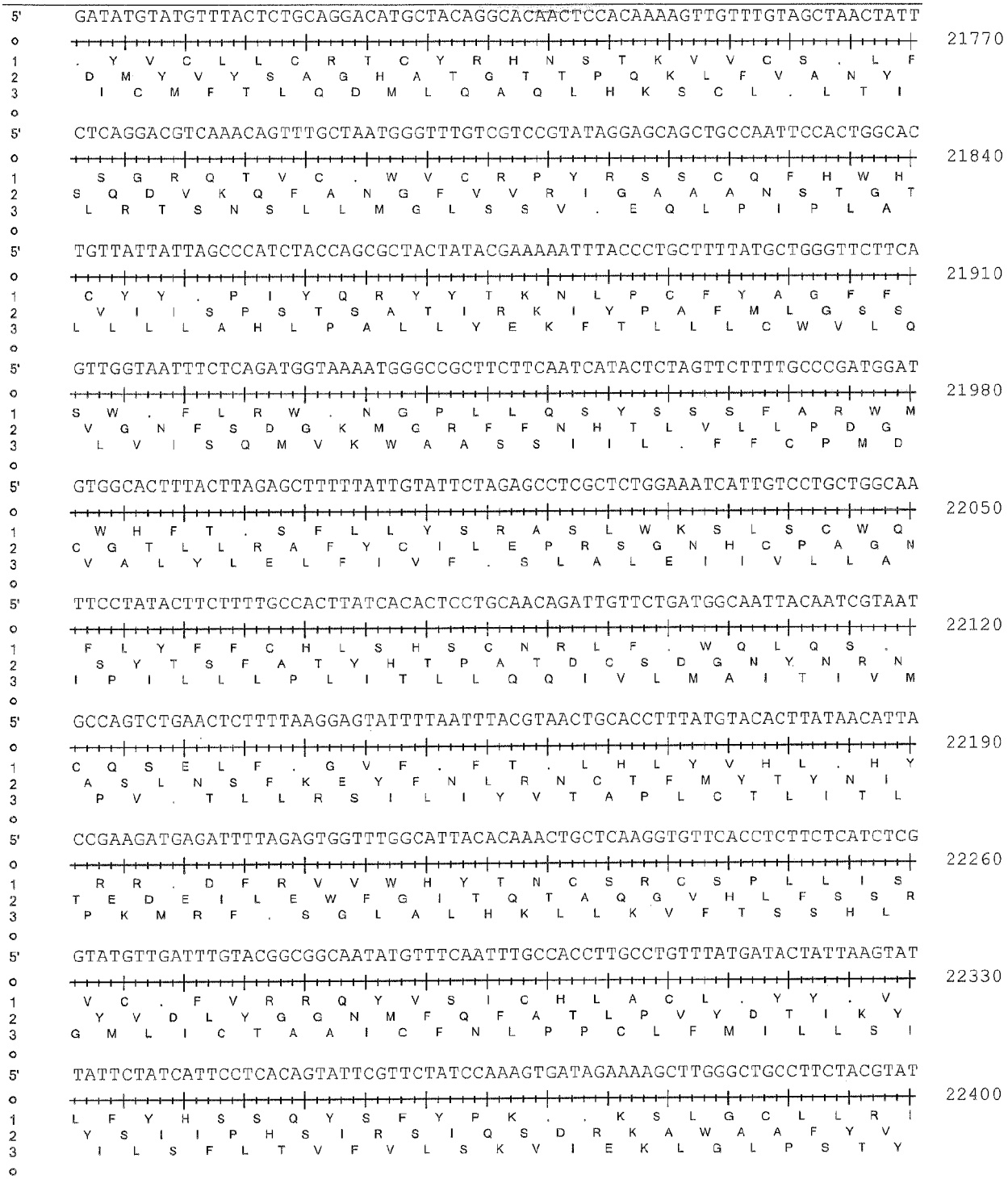
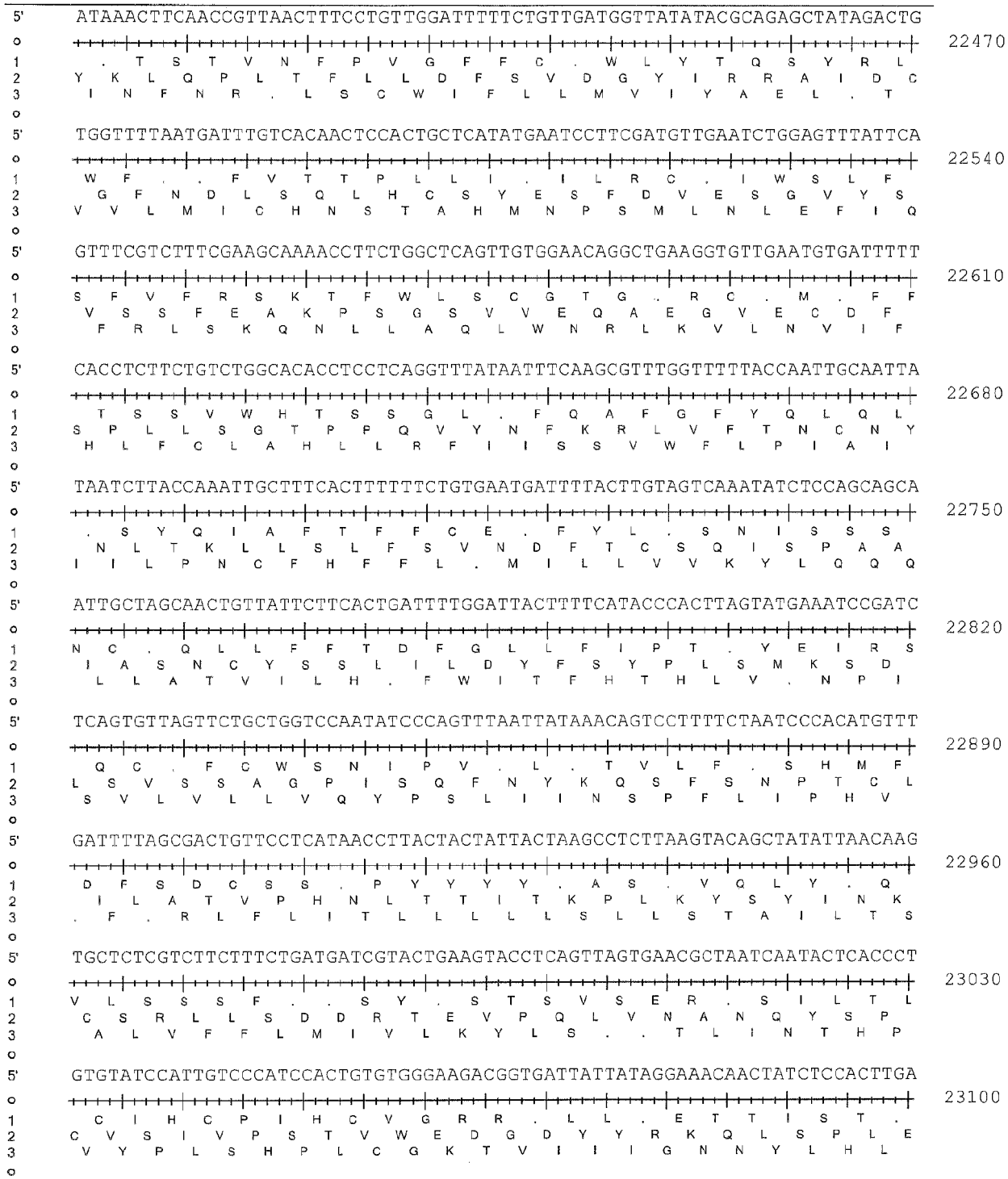


Figure 15 continued

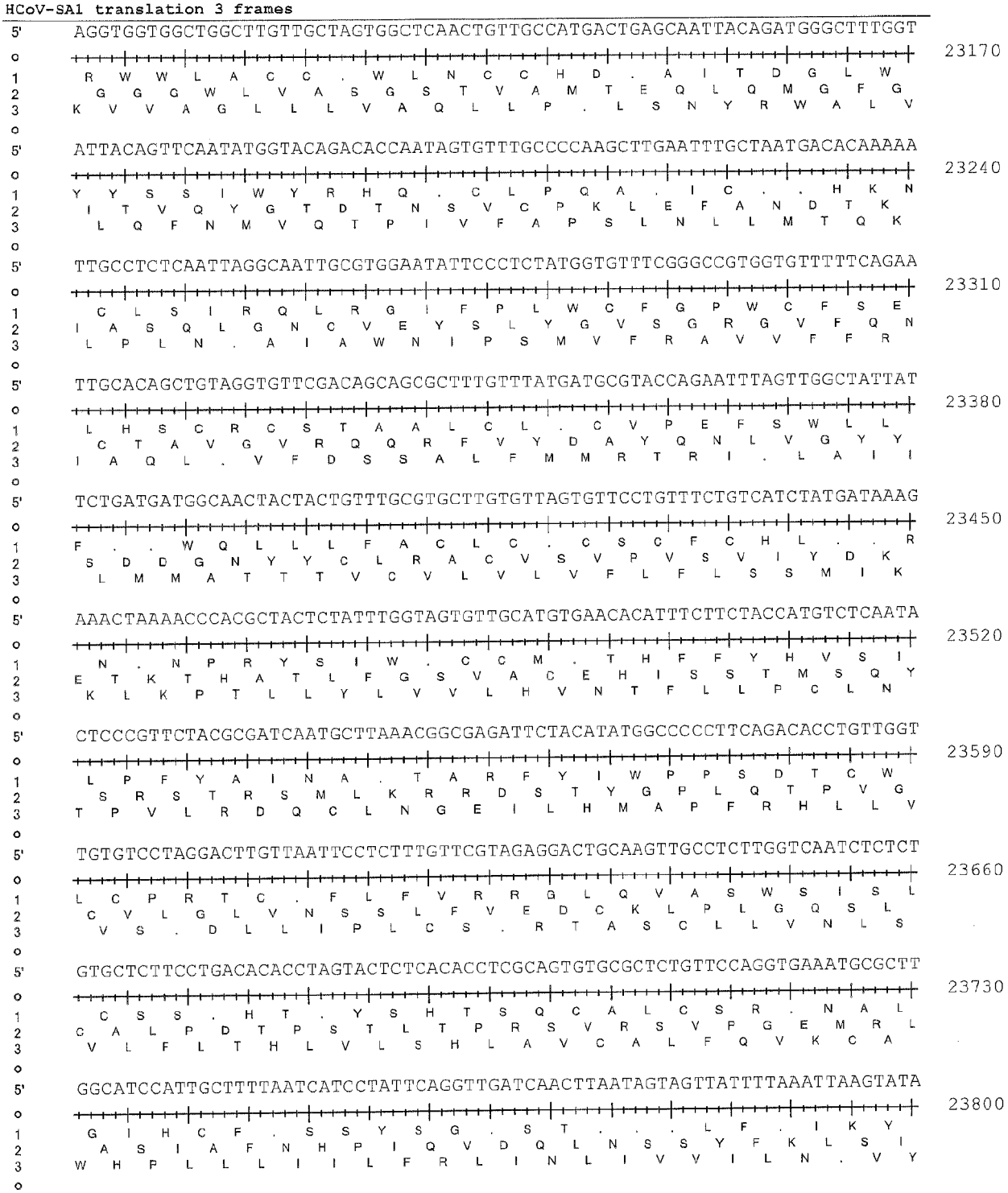
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HCoV-SA1 translation 3 frames



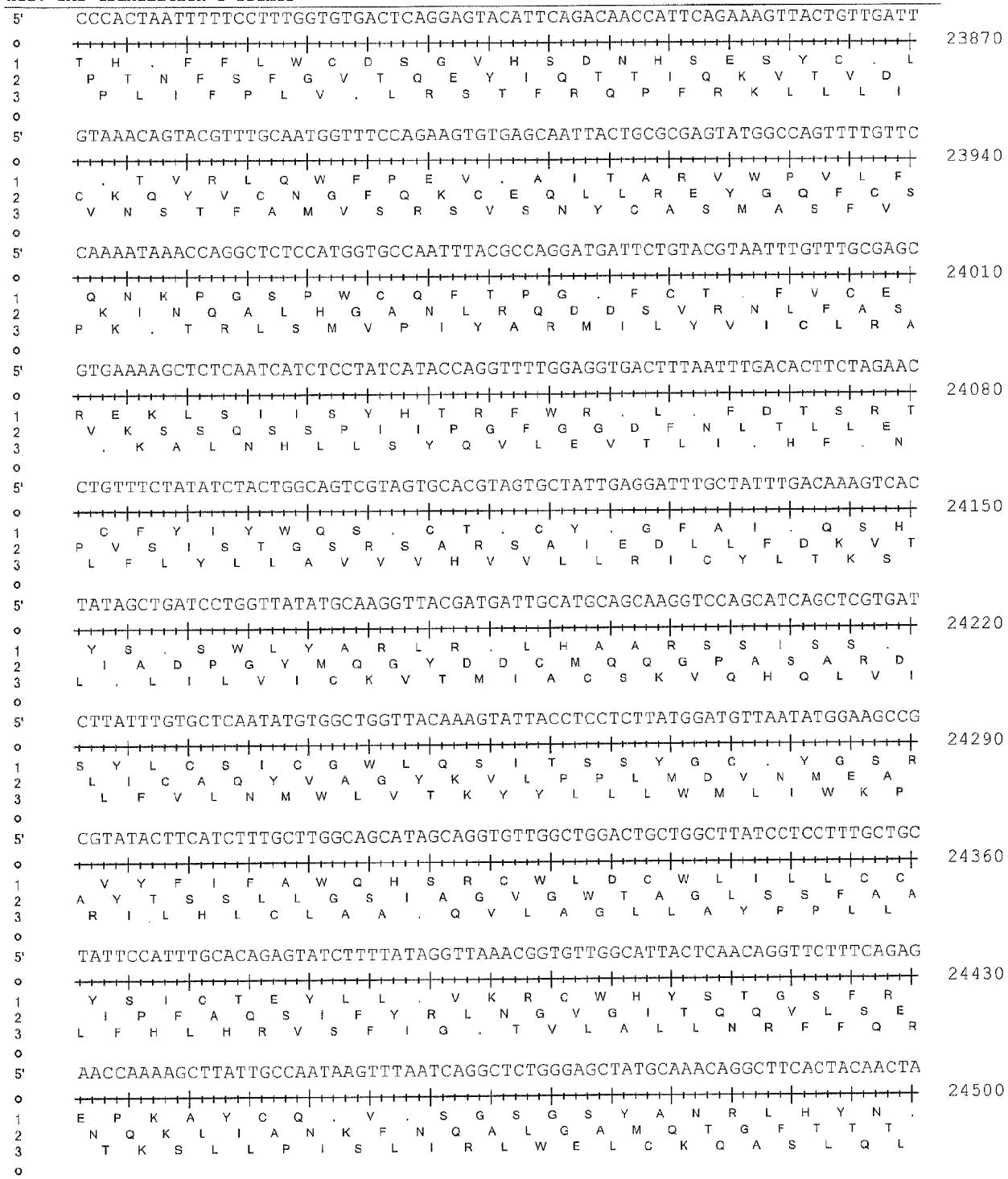
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HCoV-SA1 translation 3 frames



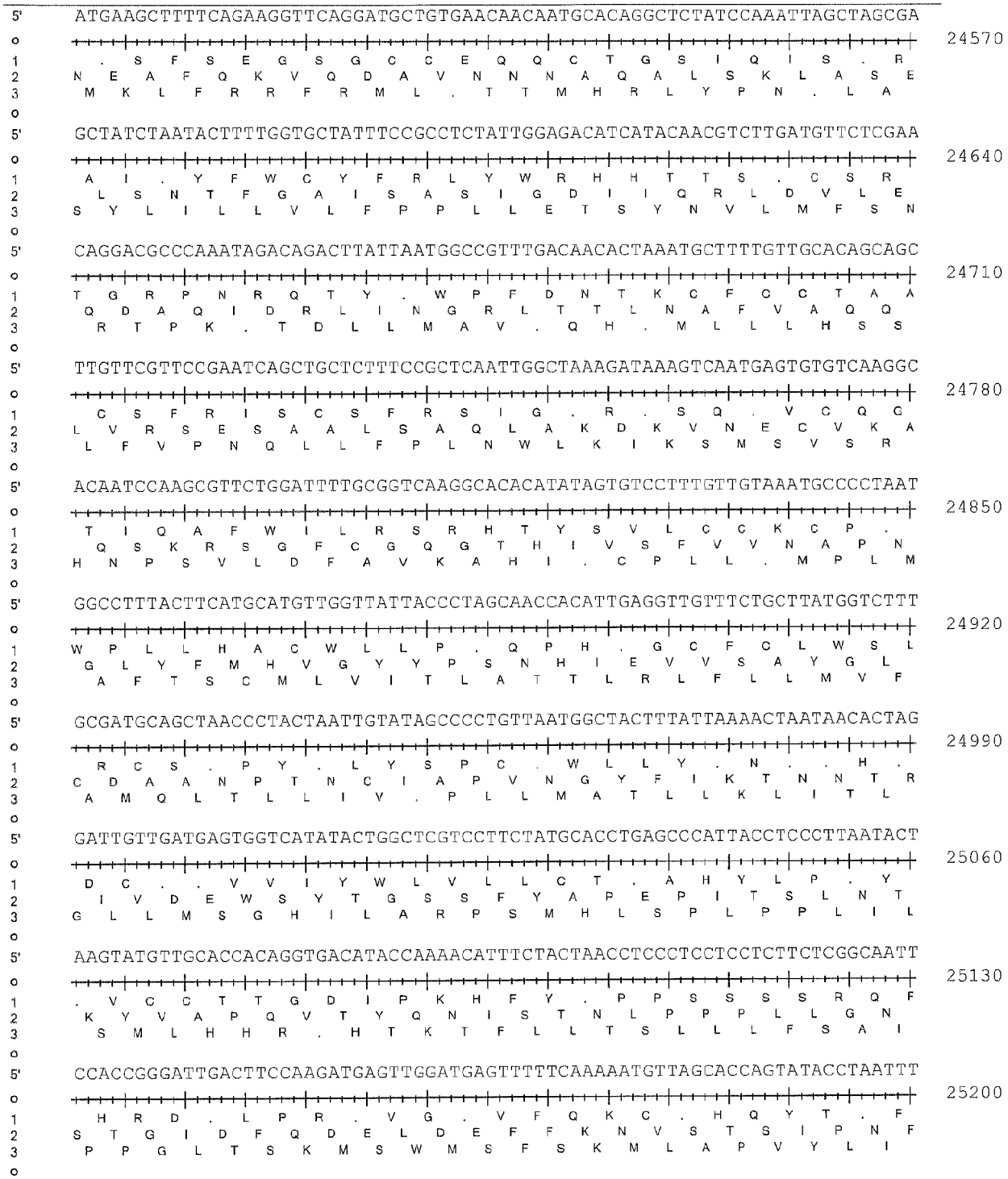
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HCoV-SA1 translation 3 frames



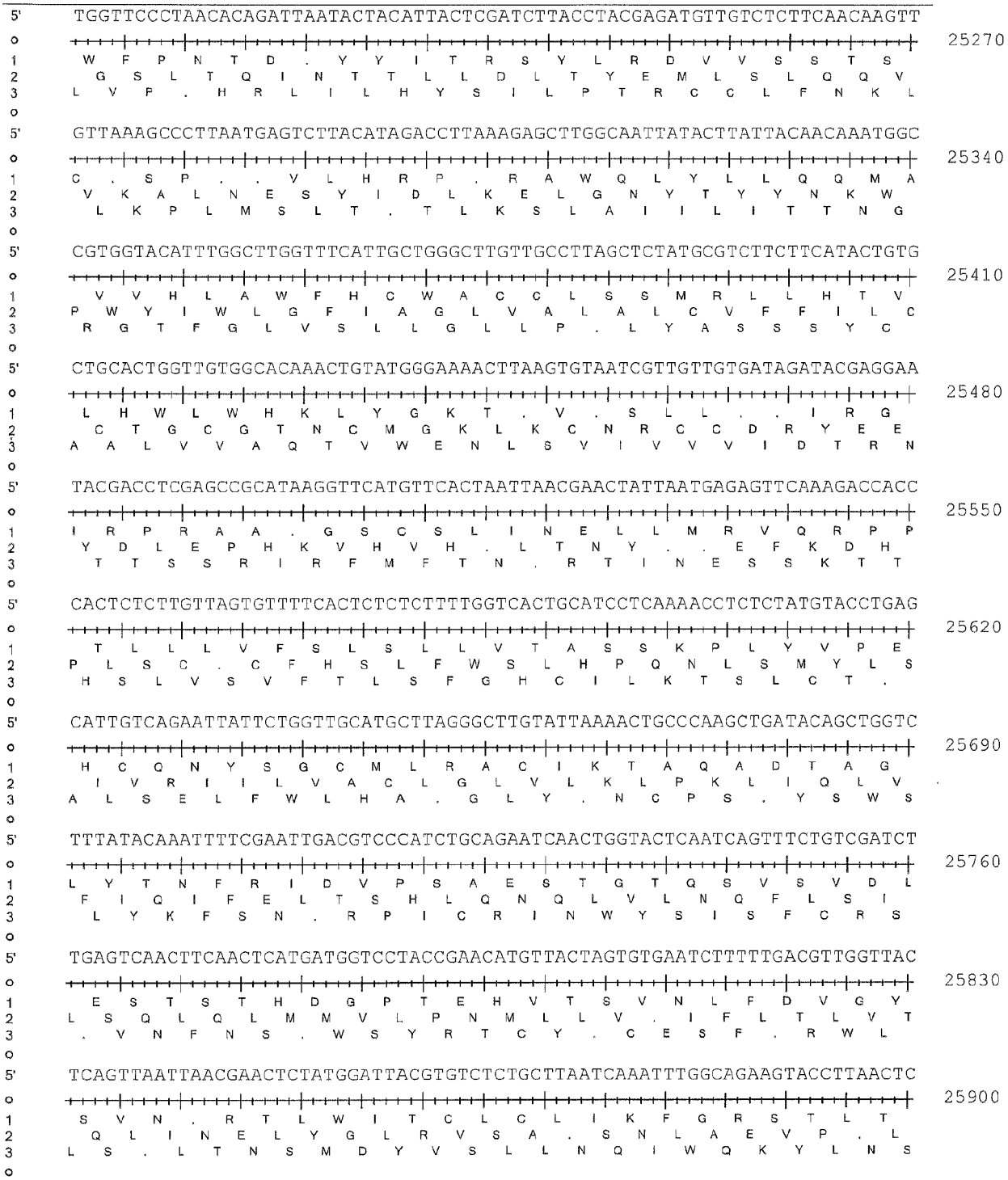
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HCoV-SA1 translation 3 frames



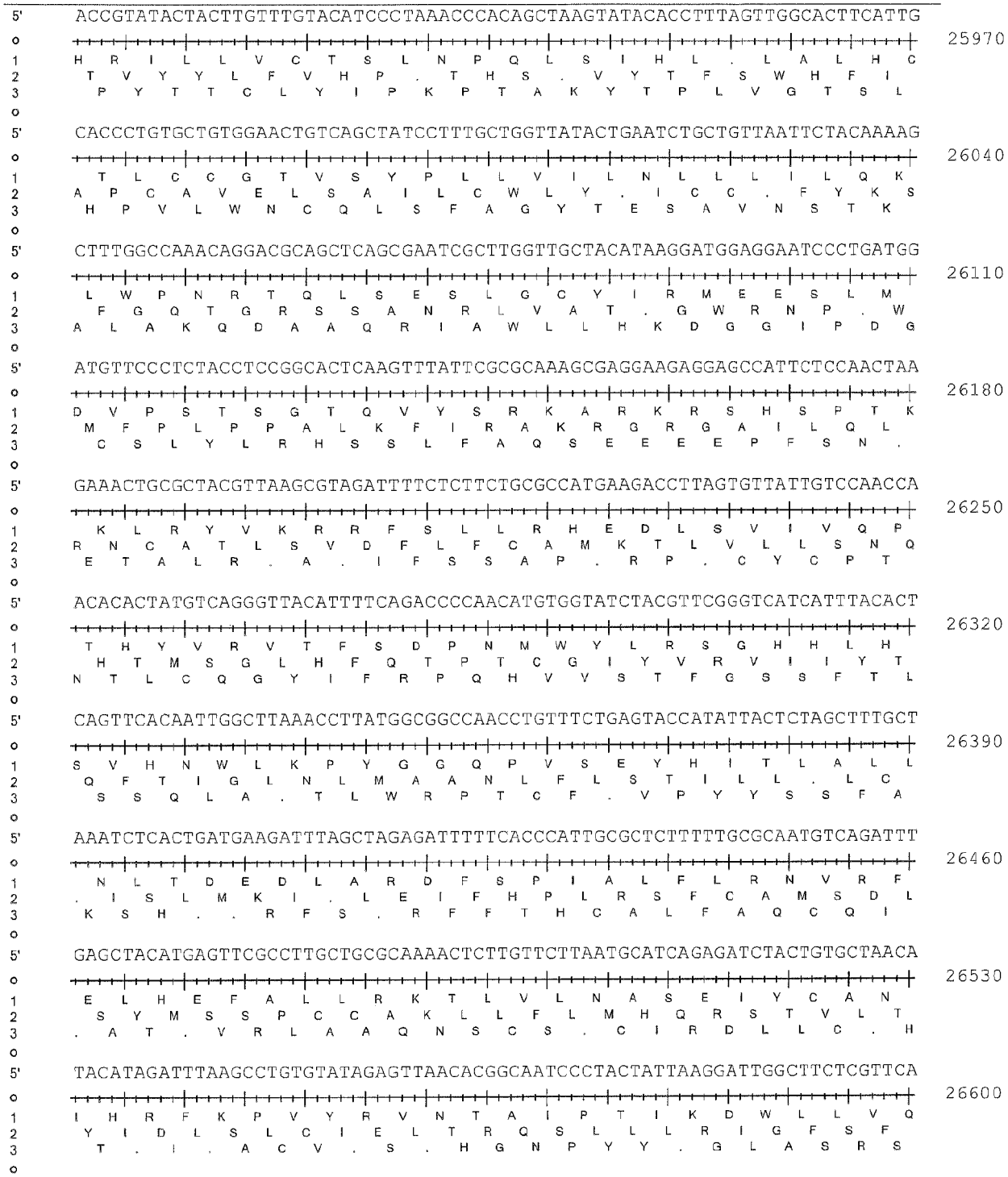
Sunday, September 23, 2012 1:41 PM
HCoV-SA1 translation 3 frames



Sunday, September 23, 2012 1:41 PM
HCoV-SA1 translation 3 frames



Sunday, September 23, 2012 1:41 PM
HCoV-SA1 translation 3 frames



Sunday, September 23, 2012 1:41 PM
HCoV-SA1 translation 3 frames

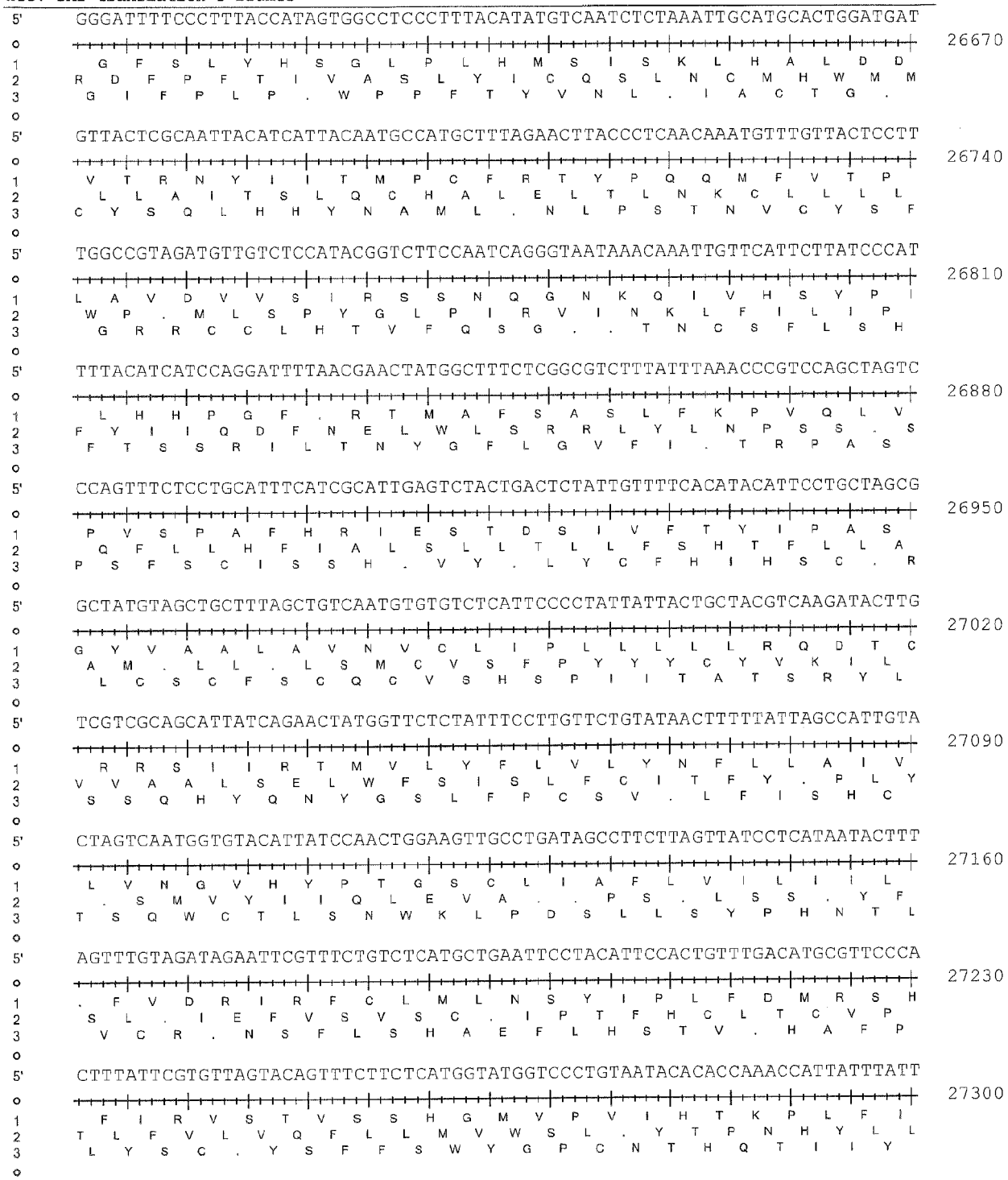
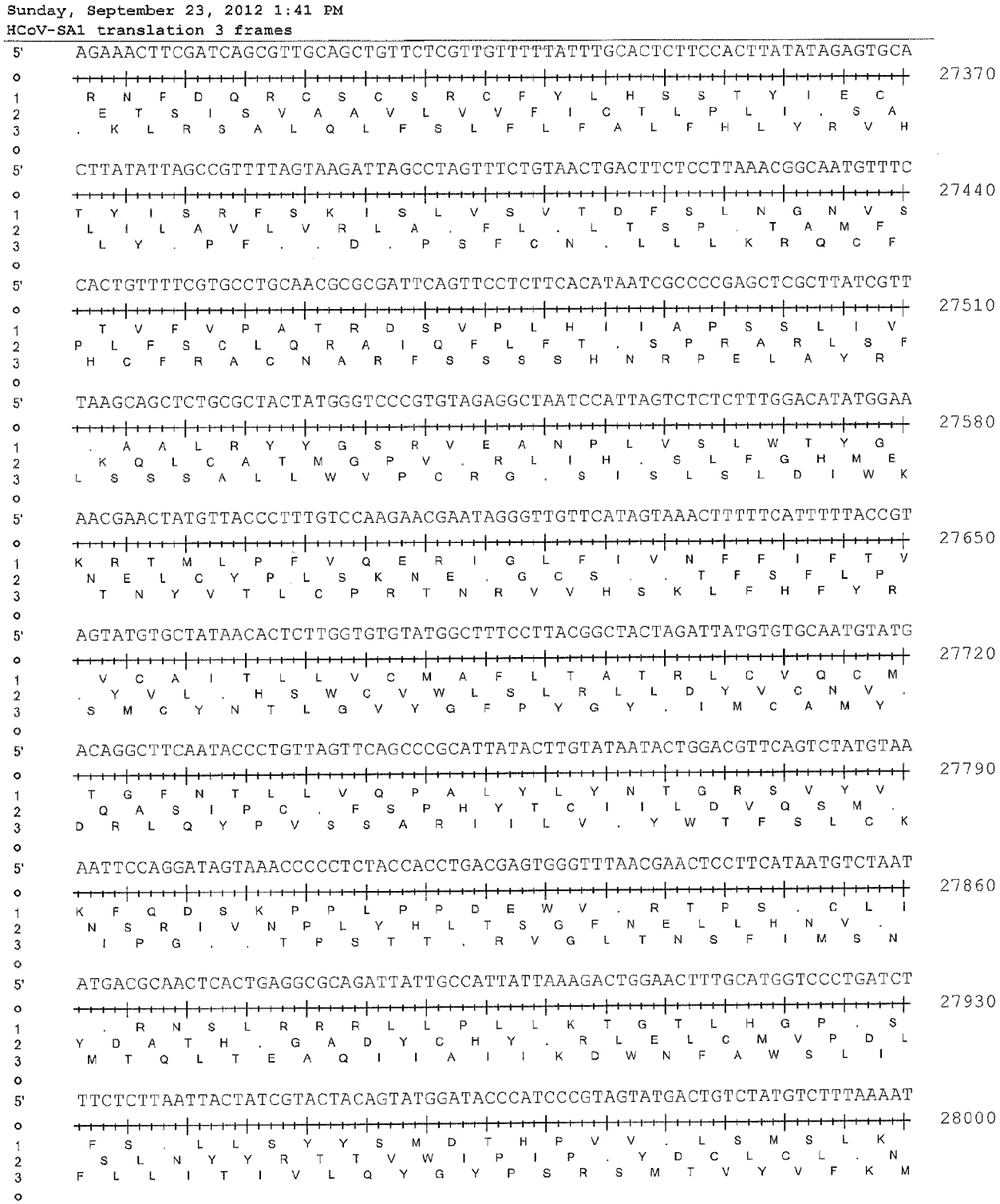
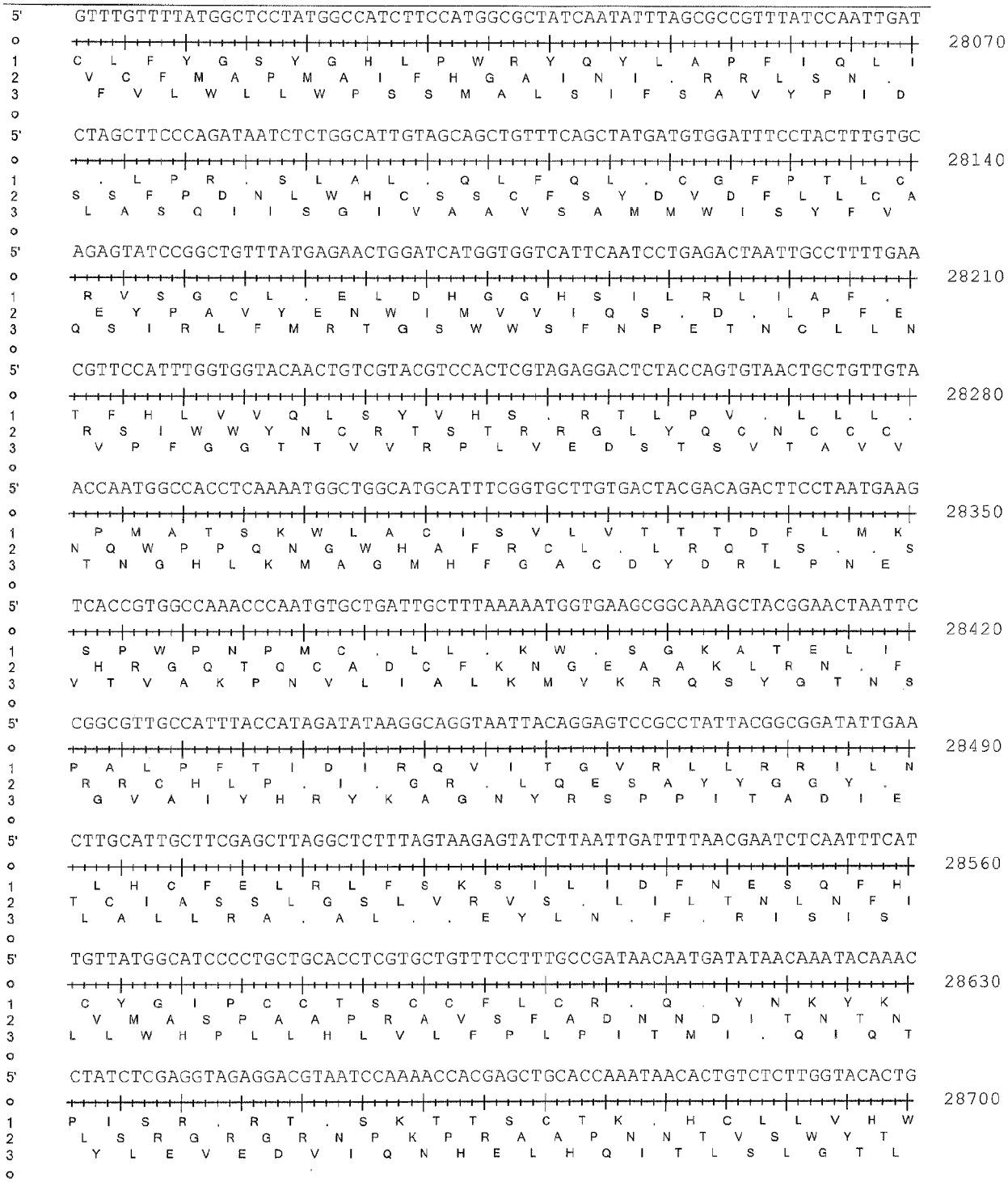


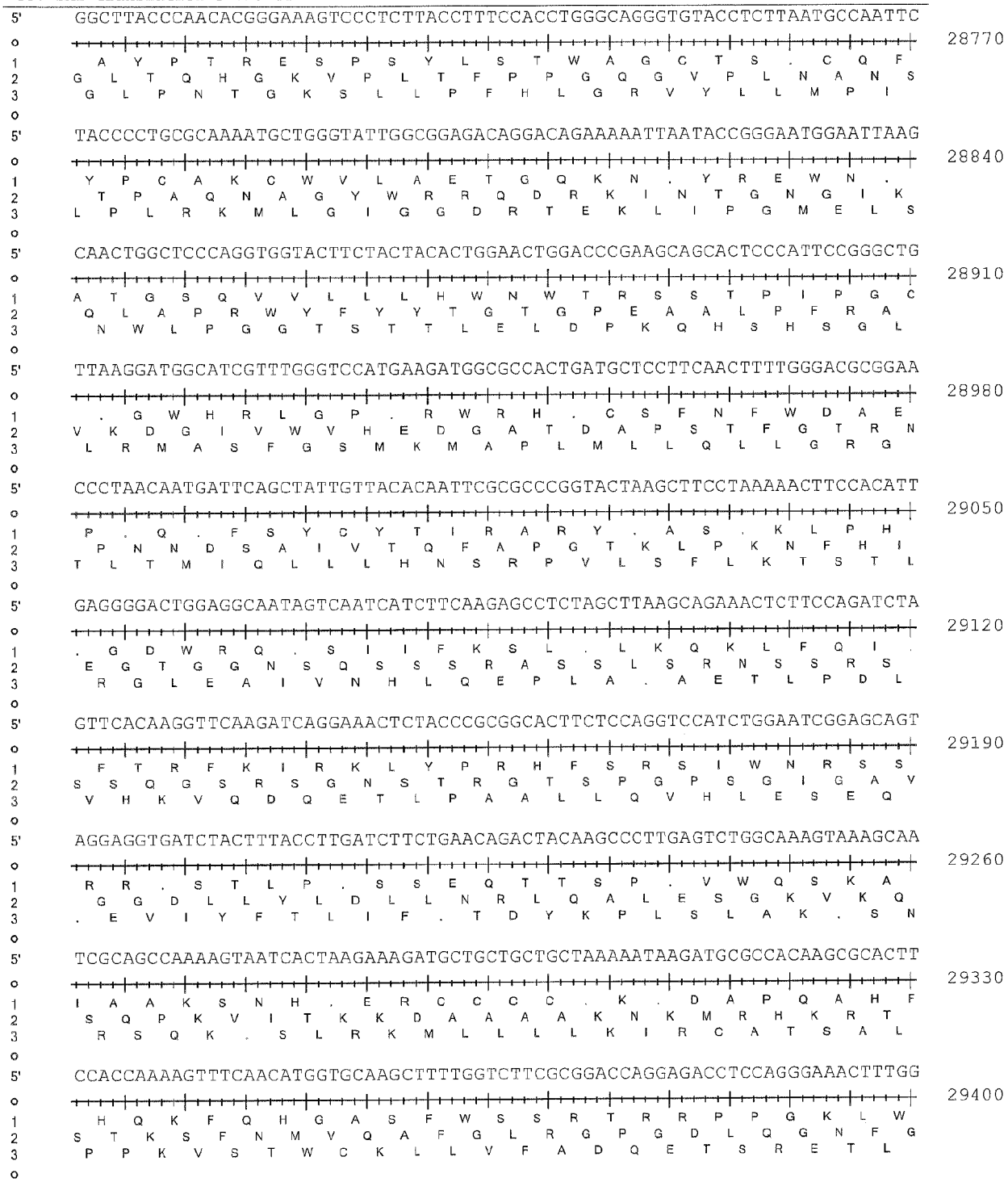
Figure 15 continued



Sunday, September 23, 2012 1:41 PM
HCoV-SA1 translation 3 frames



Sunday, September 23, 2012 1:41 PM
HCoV-SA1 translation 3 frames



Sunday, September 23, 2012 1:41 PM
HCoV-SA1 translation 3 frames

```
5'  TGATCTTCAATTGAATAAACTCGGCACTGAGGACCCACGTTGGCCCCAAATTGCTGAGCTTGCTCCTACA
o  +----|----|----|----|----|----|----|----|----|----|----|----|----|----|  29470
1   .  S  S  I  E  .  T  R  H  .  G  P  T  L  A  P  N  C  .  A  C  S  Y
2    D  L  Q  L  N  K  L  G  T  E  D  P  R  W  P  Q  I  A  E  L  A  P  T
3   V  I  F  N  .  I  N  S  A  L  R  T  H  V  G  P  K  L  L  S  L  L  L  Q
o
5'  GCCAGTGCTTTTATGGGTATGTCGCAATTTAAACTTACCCATCAGAACAATGATGATCATGGCAACCCTG
o  +----|----|----|----|----|----|----|----|----|----|----|----|----|----|  29540
1  S  Q  C  F  Y  G  Y  V  A  I  .  T  Y  P  S  E  Q  .  .  S  W  Q  P  C
2   A  S  A  F  M  G  M  S  Q  F  K  L  T  H  Q  N  N  D  D  H  G  N  P
3    P  V  L  L  W  V  C  R  N  L  N  L  P  I  R  T  M  M  I  M  A  T  L
o
5'  TGTACTTCCTTCGGTACAGTGGAGCCATTAAACTTGACCCAAAGAATCCCAACTACAATAAGTGGTTGGA
o  +----|----|----|----|----|----|----|----|----|----|----|----|----|----|  29610
1    V  L  P  S  V  Q  W  S  H  .  T  .  P  K  E  S  Q  L  Q  .  V  V  G
2  V  Y  F  L  R  Y  S  G  A  I  K  L  D  P  K  N  P  N  Y  N  K  W  L  E
3   C  T  S  F  G  T  V  E  P  L  N  L  T  Q  R  I  P  T  T  I  S  G  W
o
5'  GCTTCTTGAGCAAAATATTGATGCCTACAAAACCTTCCCTAAGAAGGAAAAGAAACAAAAGGCACCAAAA
o  +----|----|----|----|----|----|----|----|----|----|----|----|----|----|  29680
1   A  S  .  A  K  Y  .  C  L  Q  N  L  P  .  E  G  K  E  T  K  G  T  K
2    L  L  E  Q  N  I  D  A  Y  K  T  F  P  K  K  E  K  K  Q  K  A  P  K
3   S  F  L  S  K  I  L  M  P  T  K  P  S  L  R  R  K  R  N  K  R  H  Q  K
o
5'  GAAGAATCAACAGACCAAATGTCTGAACCTCCAAAGGAGCAGCGTGTGCAAGGTAGCATCACTCAGCGCA
o  +----|----|----|----|----|----|----|----|----|----|----|----|----|----|  29750
1  R  R  I  N  R  P  N  V  .  T  S  K  G  A  A  C  A  R  .  H  H  S  A  H
2   E  E  S  T  D  Q  M  S  E  P  P  K  E  Q  R  V  Q  G  S  I  T  Q  R
3    K  N  Q  Q  T  K  C  L  N  L  Q  R  S  S  V  C  K  V  A  S  L  S  A
o
5'  CTCGCACCCGTCCAAGTGTTCAGCCTGGTCCAATGATTGATGTTAACACTGATTAGTGTCACTCAAAGTA
o  +----|----|----|----|----|----|----|----|----|----|----|----|----|----|  29820
1   S  H  P  S  K  C  S  A  W  S  N  D  .  C  .  H  .  L  V  S  L  K  V
2  T  R  T  R  P  S  V  Q  P  G  P  M  I  D  V  N  T  D  .  C  H  S  K  .
3    L  A  P  V  Q  V  F  S  L  V  Q  .  L  M  L  T  L  I  S  V  T  Q  S
o
5'  ACAAGATCGCGGCAATCGTTTGTGTTTGGCAACCCCATCTCACCATCGCTTGTCCACTCTTGCACAGAAT
o  +----|----|----|----|----|----|----|----|----|----|----|----|----|----|  29890
1   T  R  S  R  Q  S  F  V  F  G  N  P  I  S  P  S  L  V  H  S  C  T  E
2    Q  D  R  G  N  R  L  C  L  A  T  P  S  H  H  R  L  S  T  L  A  Q  N
3   N  K  I  A  A  I  V  C  V  W  Q  P  H  L  T  I  A  C  P  L  L  H  R  M
o
5'  GGAATCATGTTGTAATTACAGTGCAATAAGGTAATTATAACCCATTTAATTGATAGCTATGCTTTATTAA
o  +----|----|----|----|----|----|----|----|----|----|----|----|----|----|  29960
1  W  N  H  V  V  I  T  V  Q  .  G  N  Y  N  P  F  N  .  .  L  C  F  I  K
2   G  I  M  L  .  L  Q  C  N  K  V  I  I  T  H  L  I  D  S  Y  A  L  L
3    E  S  C  C  N  Y  S  A  I  R  .  L  .  P  I  .  L  I  A  M  L  Y  .
o
5'  AGTGTGTAGCTGTAGAGAGAATGTTAAAGACTGTCACCTCTGCTTGATTGCAAGTGAACAGTGCCCCCCG
o  +----|----|----|----|----|----|----|----|----|----|----|----|----|----|  30030
1   V  C  S  C  R  E  N  V  K  D  C  H  L  C  L  I  A  S  E  Q  C  P  P
2  K  C  V  A  V  E  R  M  L  K  T  V  T  S  A  .  L  Q  V  N  S  A  P  R
3   S  V  .  L  .  R  E  C  .  R  L  S  P  L  L  D  C  K  .  T  V  P  P
o
5'  GGAAGAGCTCTACAGTGTGAAATGTAAATAAAAAATAGCTATTATTCA
o  +----|----|----|----|----|----|----|----|----|----|----|  30078
1   G  R  A  L  Q  C  E  M  .  I  K  N  S  Y  Y  S
2    E  E  L  Y  S  V  K  C  K  .  K  I  A  I  I  Q
3   G  K  S  S  T  V  .  N  V  N  K  K  .  L  L  F
o
```

Figure 16

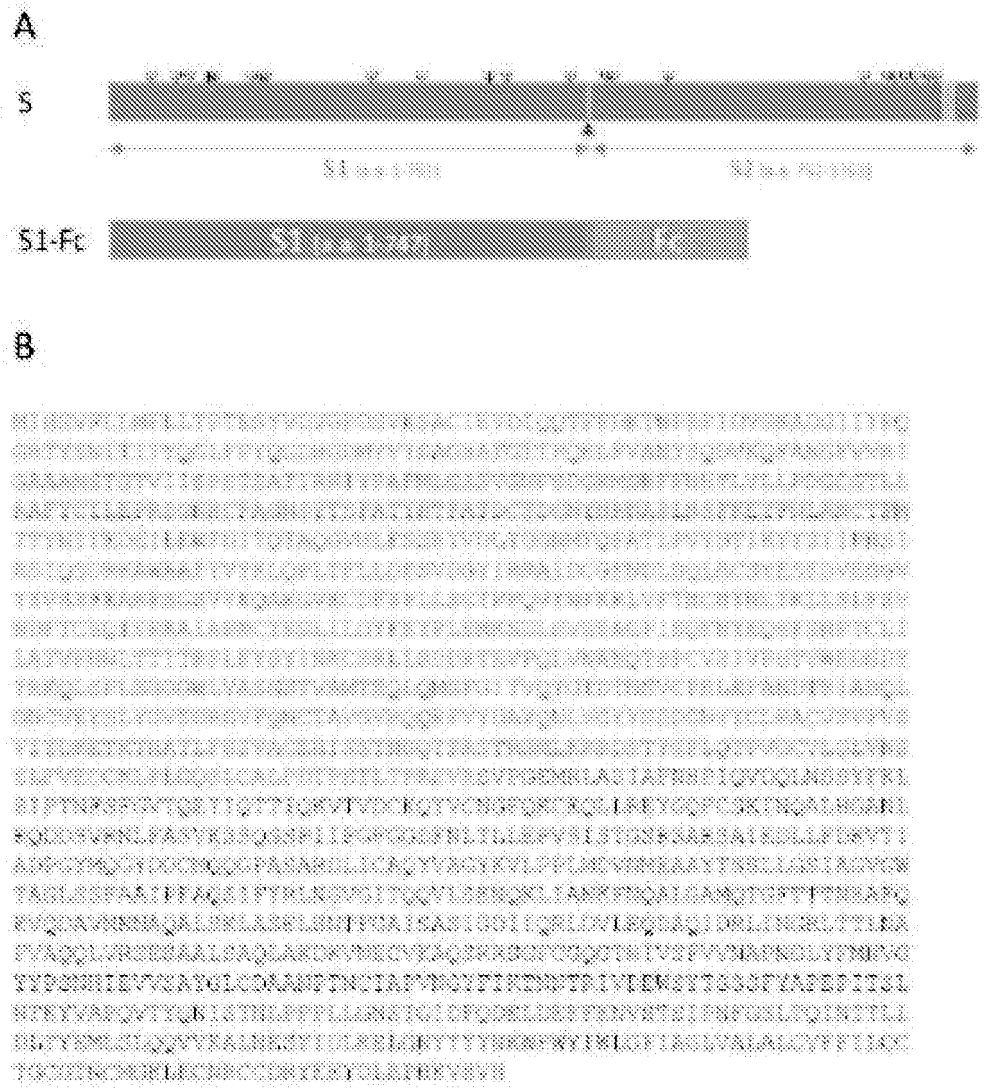
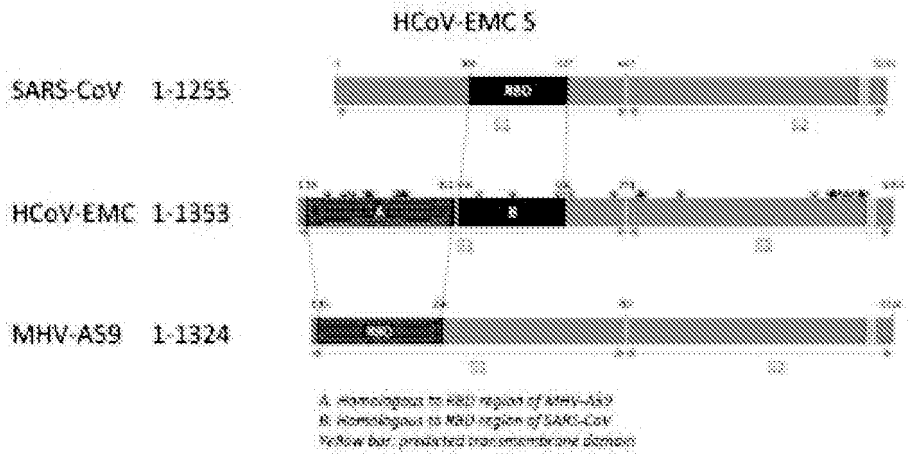


Figure 17




HCoV-EMC S
SARS-CoV 1-1255
RBD
HCoV-EMC 1-1353
A
B
MHV-A59 1-1324
A
B. Homologous to RBD region of SARS-CoV
Yellow bar: predicted transmembrane domain

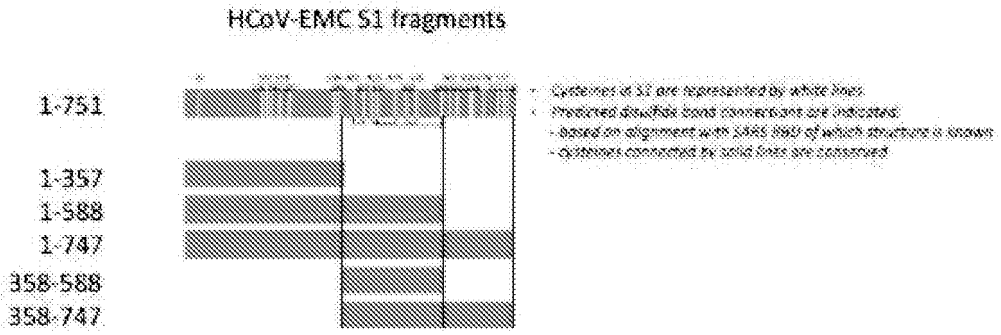
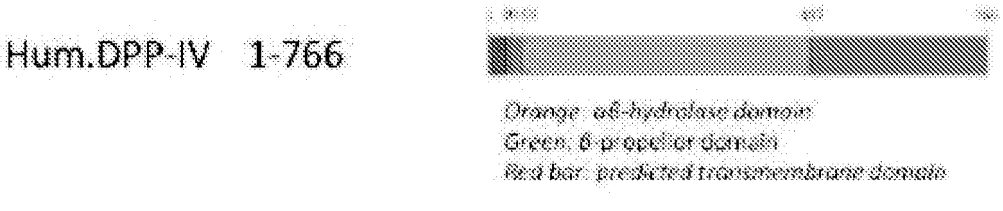
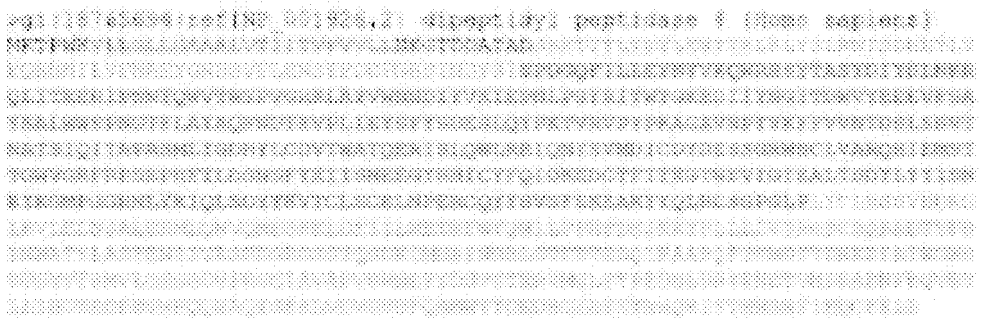

HCoV-EMC S1 fragments
1-751
1-357
1-588
1-747
358-588
358-747
Cysteines in S1 are represented by white lines
Predicted disulfide bond connectivity are indicated
based on alignment with SARS RBD of which structure is known
Cysteines connected by solid lines are conserved

Figure 18



Domain structure human DPP-IV:



Residues 1-766: human DPP-IV
Residues 1-6: cytoplasmic tail
Residues 7-28: transmembrane region human DPP-IV
Residues 29-39: region connecting transmembrane region and αβ-hydrolase domain
Residues 40-766: Naturally occurring soluble form of DPP-IV

Domains in the DPP-IV ectodomain:
Residues 55-497: β-propeller domain in green
Residues 39-51 and 504-766: αβ-hydrolase domain in grey

Domain borders based on crystal structure (Rasmussen Nat.Struct.Biol. 2003)

Figure 19

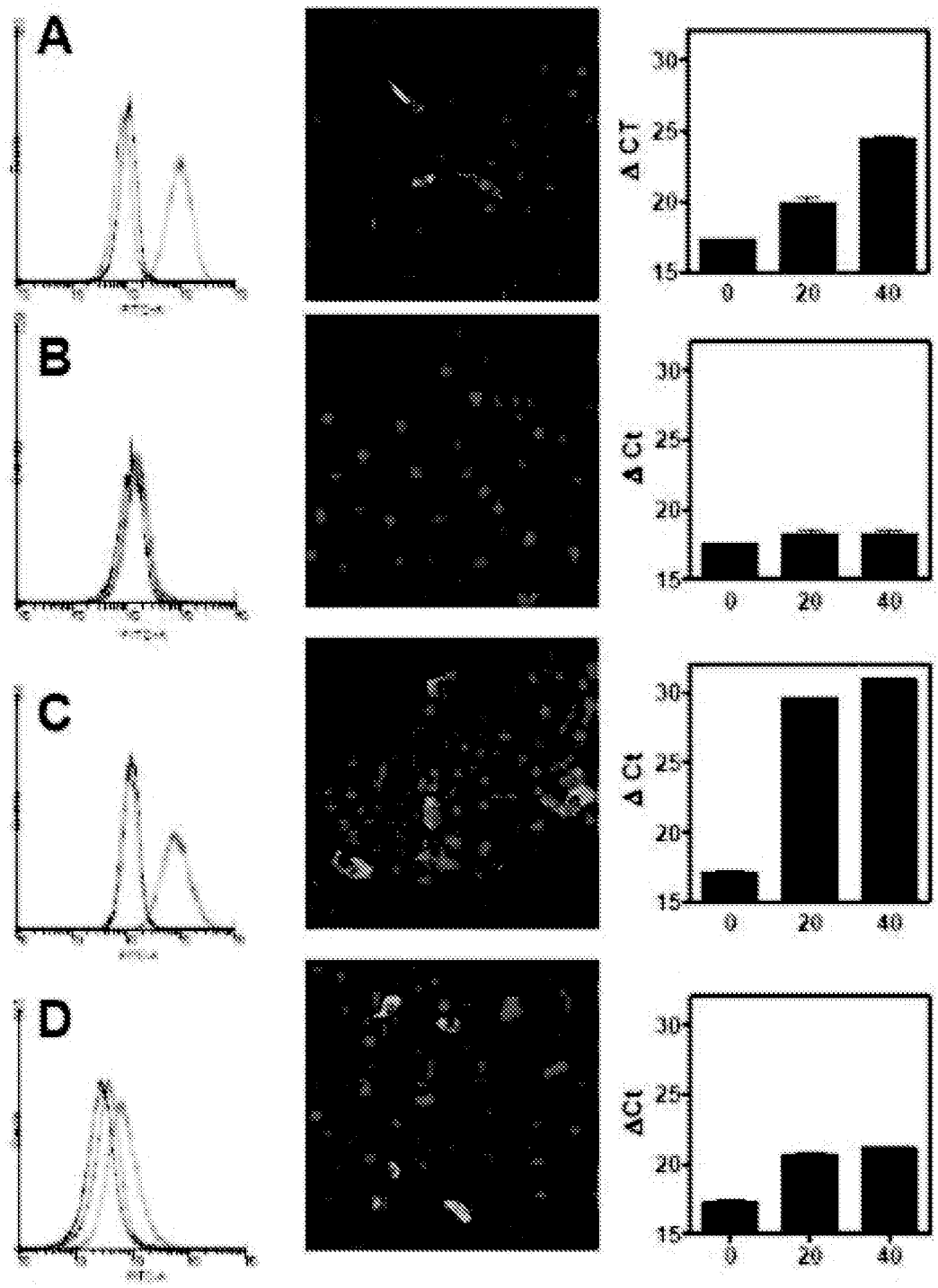


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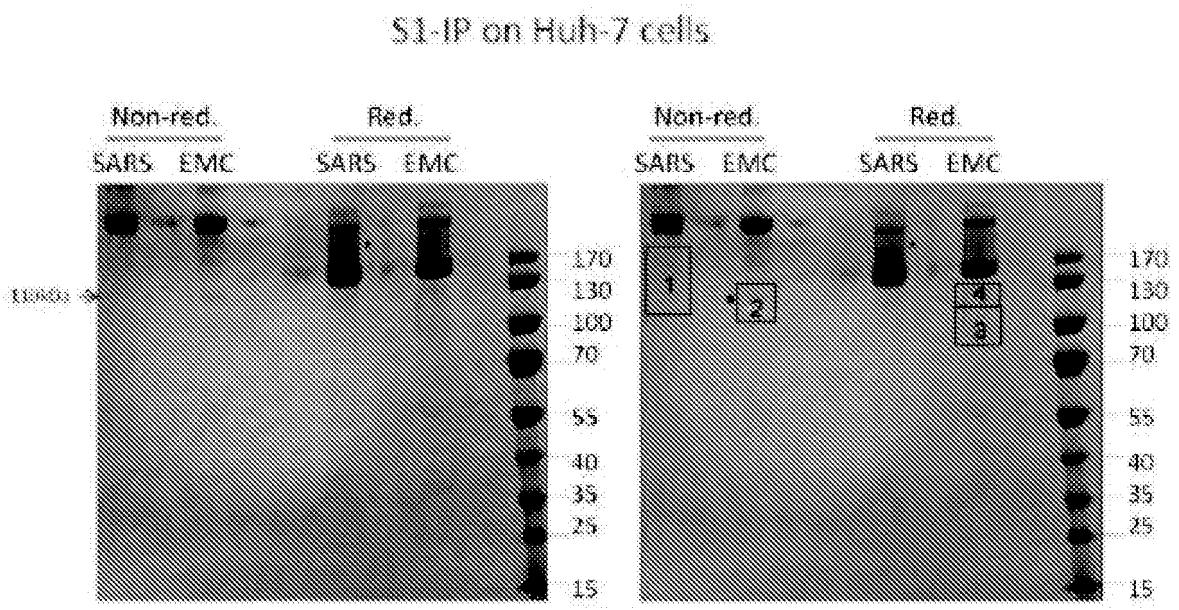

S1-IP on Huh-7 cells
Non-red.
Red.
SARS EMC SARS EMC
Non-red.
Red.
SARS EMC SARS EMC
170
130
100
70
55
40
35
25
15
1
2
3
4
5

Figure 21

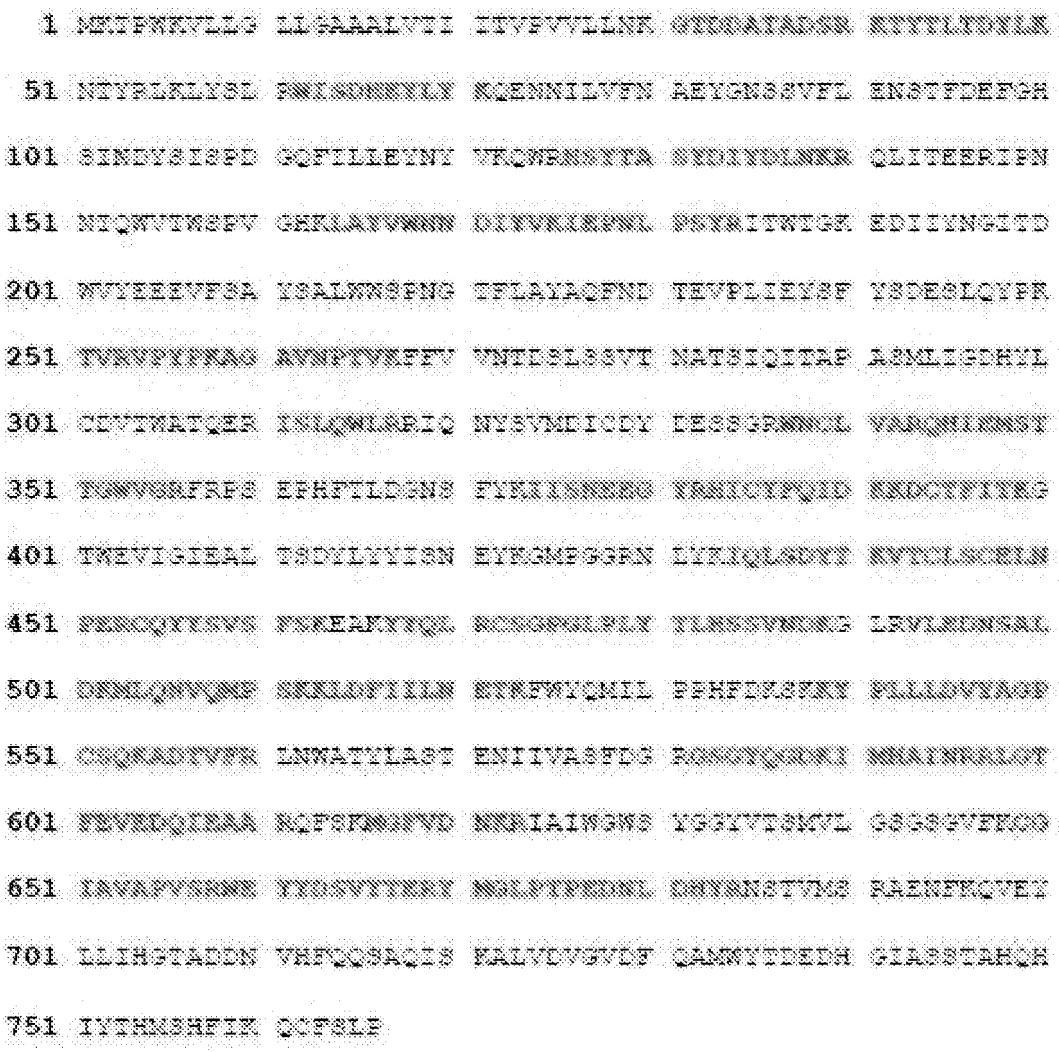


Figure 22

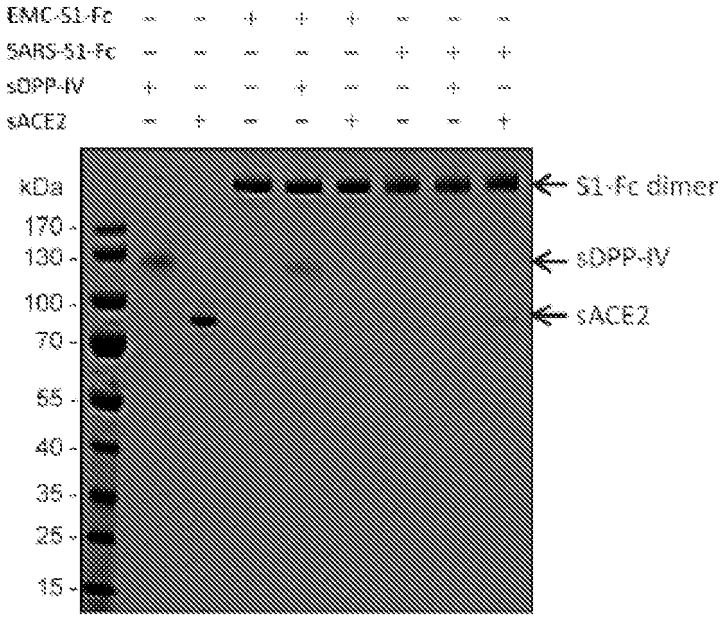

EMC-S1-Fc
SARS-S1-Fc
sDPP-IV
sACE2
kDa
170
130
100
70
55
40
35
25
15
S1-Fc dimer
sDPP-IV
sACE2

Figure 23

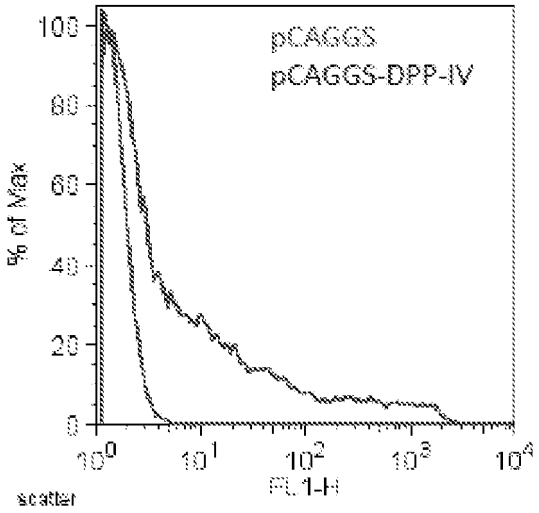

pCAGGS
pCAGGS-DPP-IV
% of Max
100
80
60
40
20
0
10^0
10^1
10^2
10^3
10^4
FL1-H
scatter

Figure 24

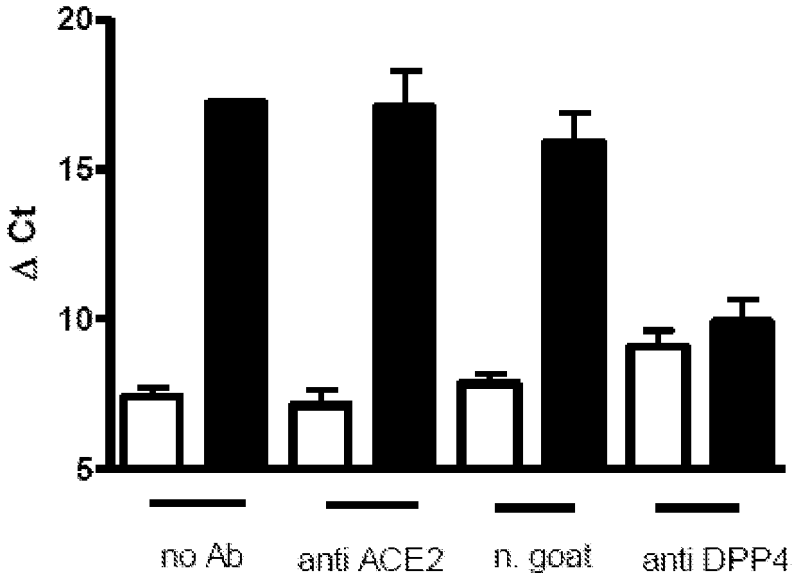


Figure 25

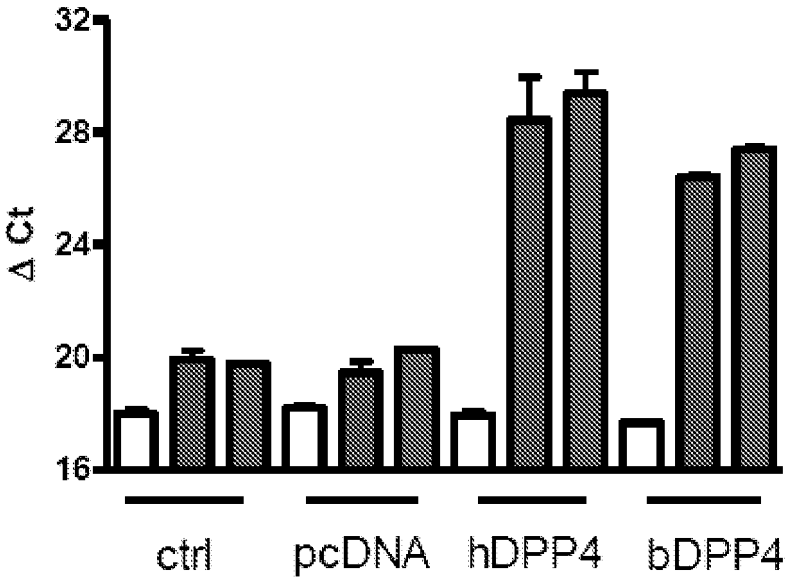


Figure 26

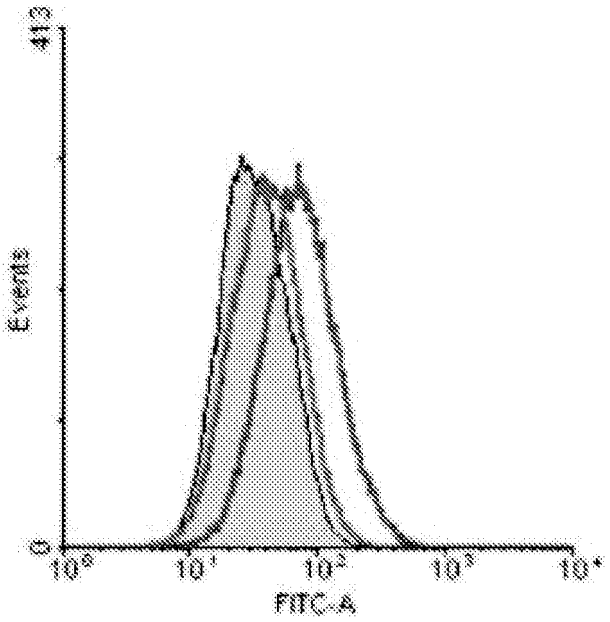


Figure 27

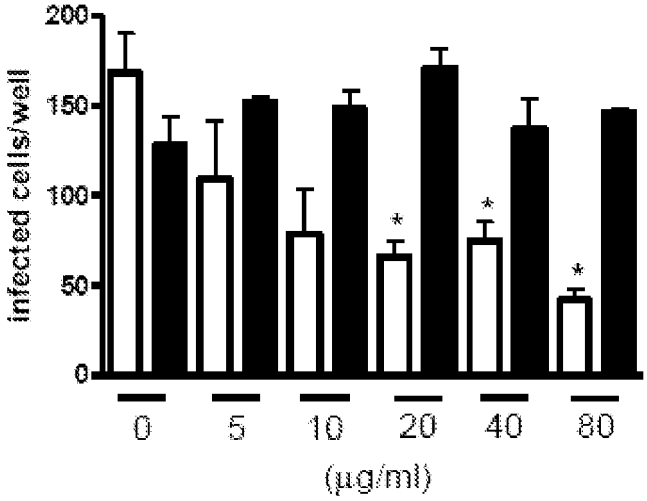


Figure 28

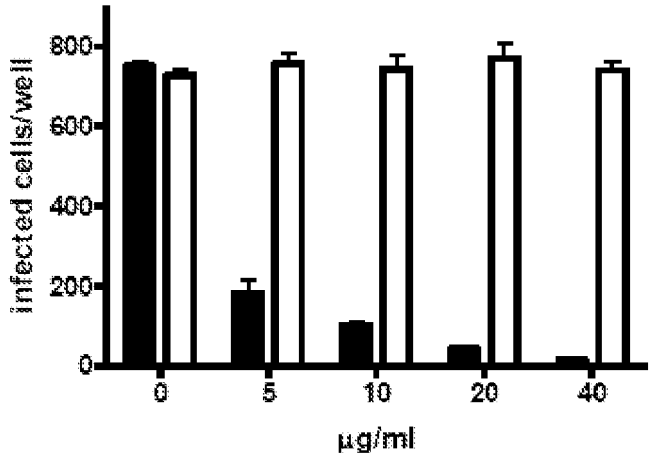


Figure 29

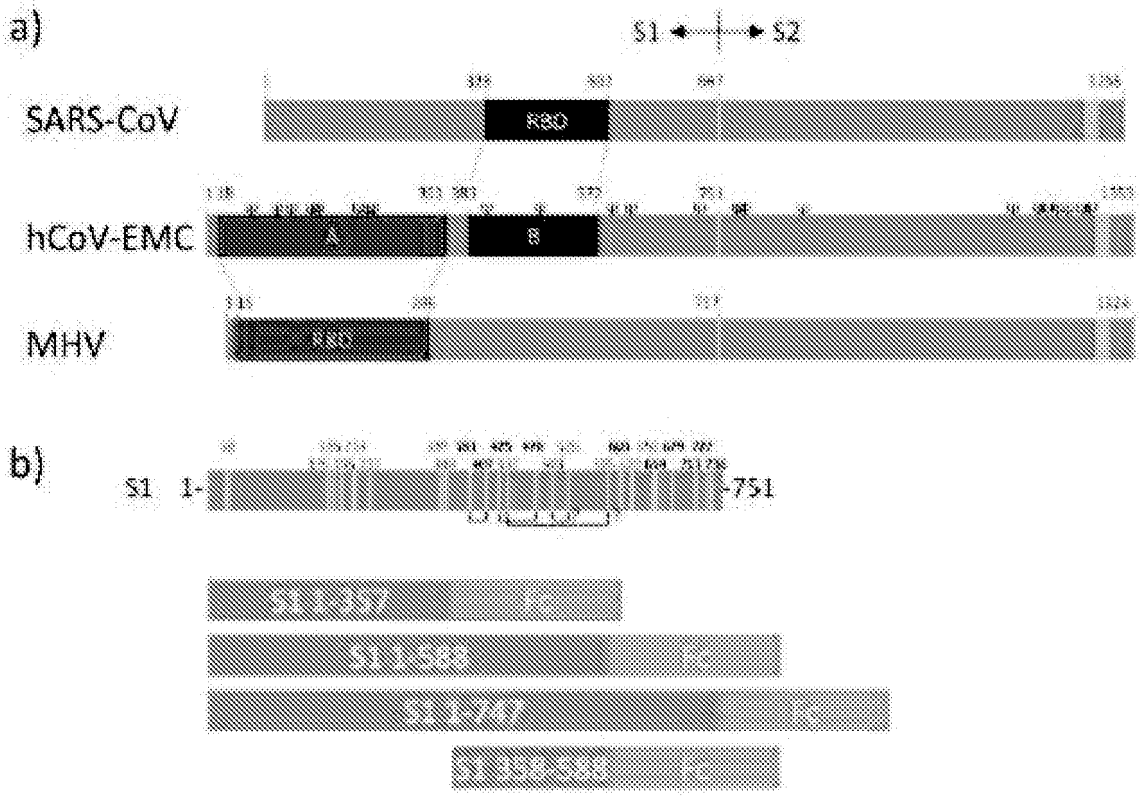


Figure 30

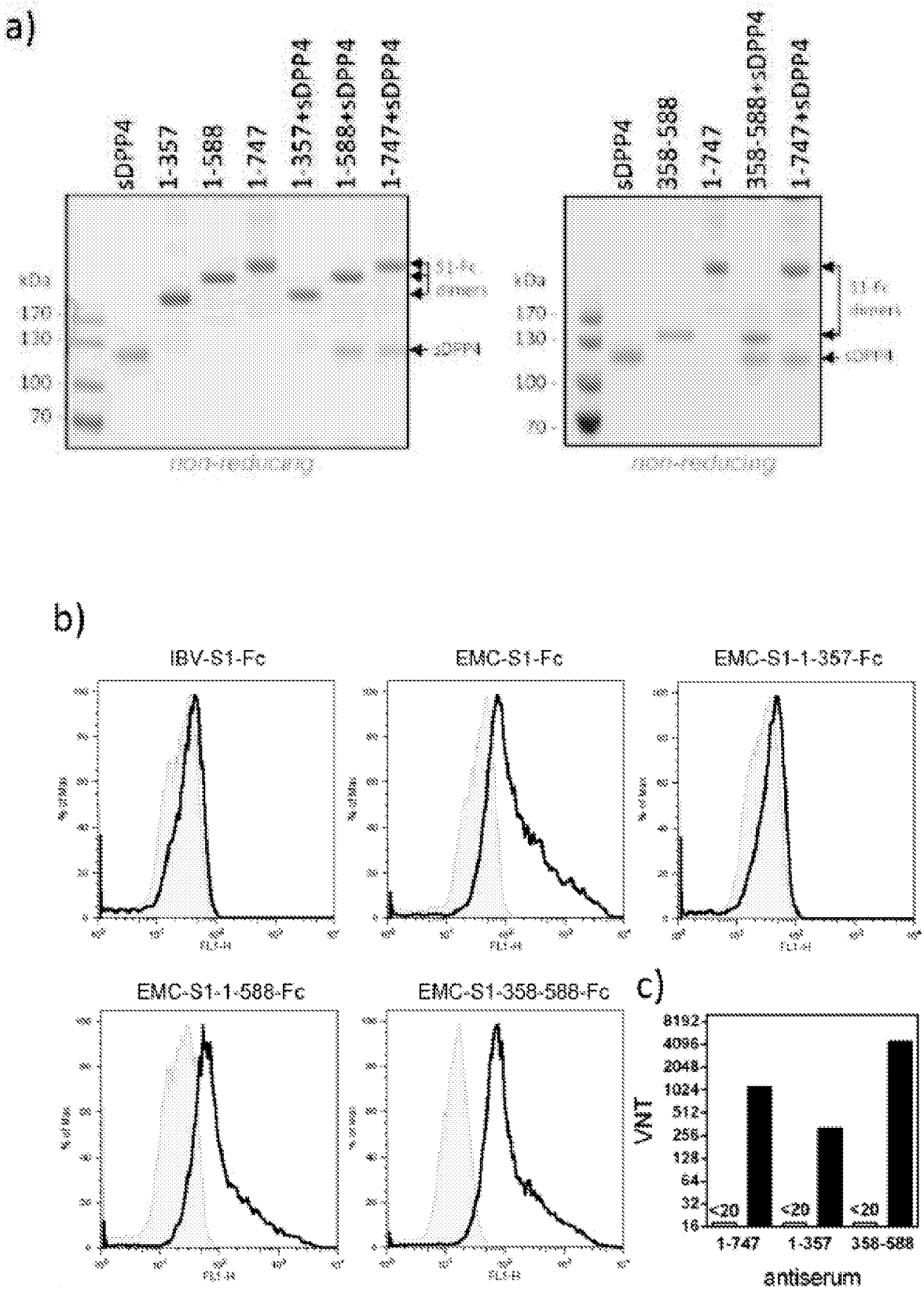

a)
sDPP4
1-357
1-588
1-747
1-357+sDPP4
1-588+sDPP4
1-747+sDPP4
kDa
170
130
100
70
non-reducing
sDPP4
358-588
358-588+sDPP4
b)
IBV-S1-Fc
EMC-S1-Fc
EMC-S1-1-357-Fc
EMC-S1-1-588-Fc
EMC-S1-358-588-Fc
c)
VNT
8192
4096
2048
1024
512
256
128
64
32
16
<20
1-747
1-357
358-588
antiserum

Figure 31

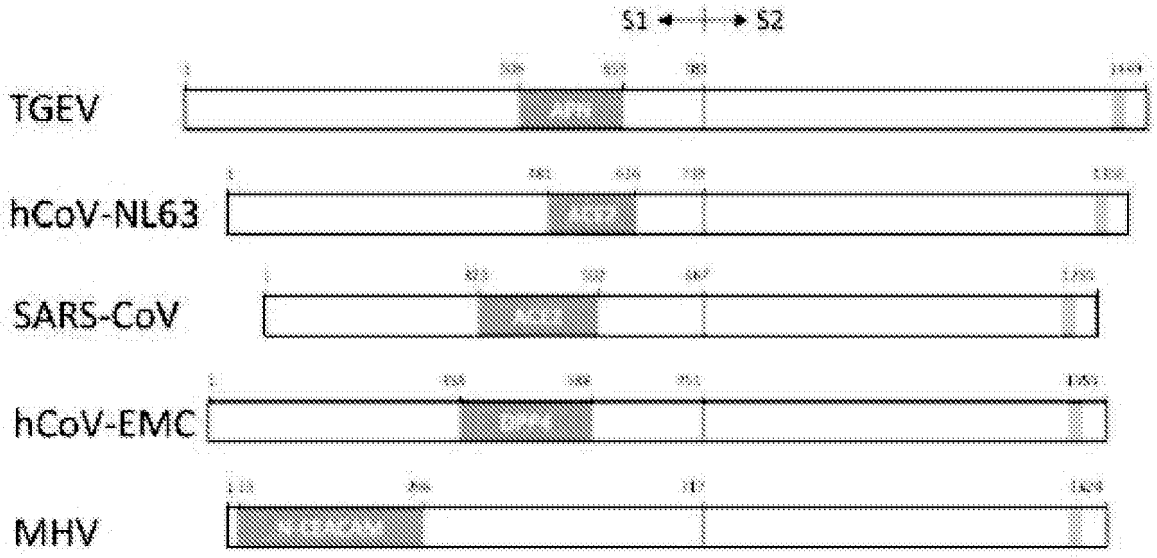
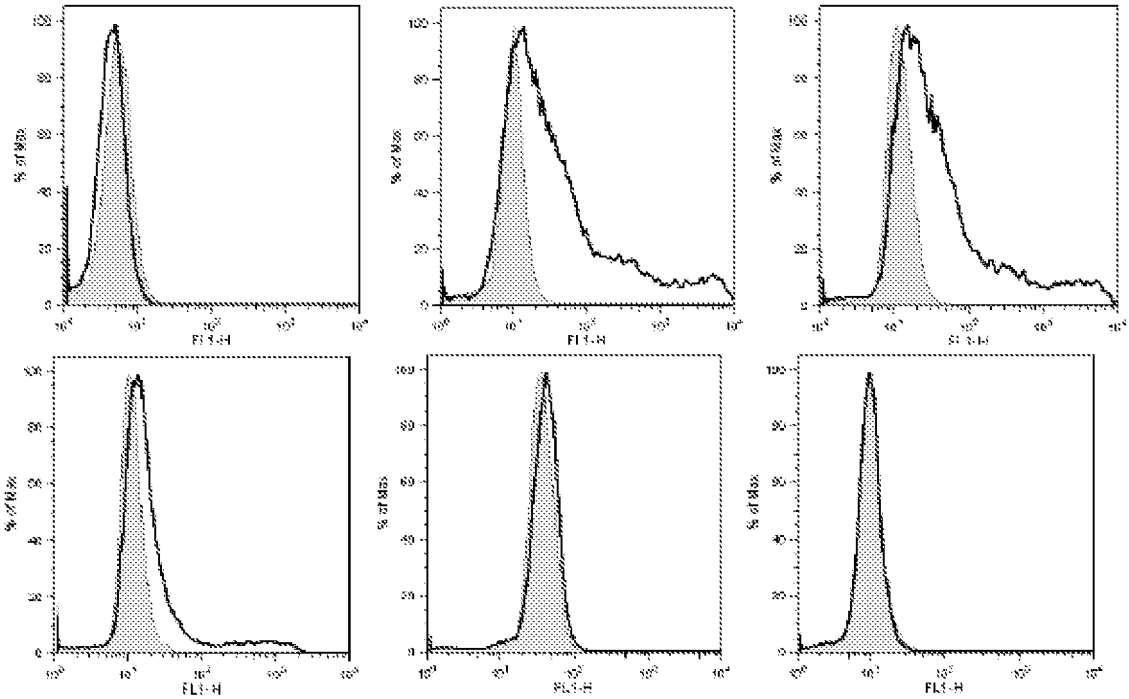


Figure 32



>EMC_8
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GAAANSTGTVIISPSTSATIRKIYPAFMLGSSVGNFSDGKMGRFFNHTLVLLPDGCGTLL
RAFYCILEPRSGNHCPAGNSYTSFATYHTPATDCSDGNYNRNASLNSFKEYFNLRNNTFN
YTYNITEDEILEWFGITQTAQGVHLFSSRYVDLYGGNMFQFATLPVYDTIKYYSITPHSI
RSIQSDRKAWAAFYVYKLQPLTFLLDFSVDGYIRRAIDCGFNDLSQLHCSYESFDVESGV
YSVSSFEAKPSGSVVEQAEGVECDFSPLLSGTPPQVYNFKRLVFTNCNYNLTKLLSLFSV
NDFTCSQISPAAIASNCYSSLILDYFSYPLSMKSDLSVSSAGPISQFNYKQSFSNPTCLI
LATVPHNLTTITKPLKYSYINKCSRLLSDDRTEVPQLVNANQYSPCVSIVPSTVWEDGD
YRKQLSPLEGGGWLVASGSTVAMTEQLQMGFGITVQYGTDTNSVCPKLEFANDTFIASQL
GNCVEYSLVGVSGRGVFQNCTAVGVRQQRFVYDAYQNLVGYYSDDGNYYCLRACVSVPVS
VIYDKETKTHATLFGSVACEHISSTMSQYSRSTRSMLKRRDSTYGPLQTPVGCVLGLVNS
SLFVEDCKLPLGQSLCALPDTPSTLTPRSVRSVPGEMRLASIAFNHPIQVDQLNSSYFKL
SIPTNFSFGVTQEYIQTTIQKVTVDCKQYVCNGFQKCEQLLREYGQFCSKINQALHGANL
RQDDSVRNLFASVKSSQSSPIIPGFGGDFNLTLLAPVSISTGSRSARSAIEDLLFDKVTI
ADPGYMQGYDDCMQQGPASARDLICAQYVAGYKVLPPLMDVNMEAAYTSSLLGSIAGVGW
TAGLSSFAAIPFAQSIFYRLNGVGITQQVLSENQKLIANKFNQALGAMQTGFTTTNEAFQ
KVQDAVNNNAQALSKLASELSNTFGAISASIGDIIQRLDVLEQDAQIDRLINGRLTTLNA
FVAQQLVRSESAALSAQLAKDKVNECVKAQSKRSGFCGQGTHIVSFVVNAPNGLYFNHVG
YYPSNHIEVYSAYGLCDAANPTNCIAPVNGYFIKTNNTRIVDEWSYTGSSFYAPEPITSL
NTKYVAPQVTYQNISTNLPPPLLGNSTGIDFQDELDEFFKNVSTSIPNFGSLTQINTTLL
DLTYEMLSLQQVVKALNESYIDLKELGNYTYYNKWPWYIWLGFIAGLVALALCVFFILCC
TGCGTNCMGKLKCNRCCDRYEEYDLEPHKVHVH

>HKU5_8
MIRSVLVLMCSLTFISNLTRQQSVDMGHNSTGSCLDSQVQPDIFESVHITNPNPIDTSFAEGVIYPNGRS
VSNITLTYTGLYPYKANDLGWQVLFSSDGHSAPGRLNNLFVSNTSSQVESFDDGFVVRIGAAANNTGTTVIS
QSTFSPIPEIYPAFLLGHSVGNYTPSNPTGPVLNHTLVILPDGCGTILHAFYCVLHPRTQQNCAGETNFK
SLSLMDTFAGLCVSGSYNQEATLGAFYVYSLLINCTFPVNITTEIENAENFGITQSITQDVHLYSSFKEN
VFPNNMFHFATLPVTQKILYYTVIPPSIRSFFNCPFLANAAFYIPKLHPLTYLLNFIVEGVITKAVLDGVD
SLAQLQCSYESFEVETGNYSVSSFEASPRGEFIEQATTQECDFTPMLTGTPFFSINFKFLVFTNCNYNLT
KLLSLFSVSEFSCHQVSPSSLATGCYSSLIVDYFAYSSLMSSYLQPGSASAIVQFNIKQSFSNPTCPVLA
TVPQNLTTITKPSKYAYLTECIKTGAVSKNYILVNAPSGAYIPCLSLASRSFSTKYQSHSDSELTTTGYIYP
VTGNLQMAFTSVQVSSLTNSVSFMQALPNDTSYIELKLDVCVEYSLHGITSRGVFHNCTSVGLRNQRFVY
DTFDNLVGYHSEDNSNYYCYRFCVSVPVSVIYDKASNSHATLFGSVACSHVTTDSSQCFSRASPSRNLLLARTT
PSPLQTTVGGAMGFINSSNVTYETQLPLQSSLCAIPPTTSSRVRPATSSASIVFQIATLNFTSFLTLAPI
NSTGFTVAVPTNFTFSVTQEFIETTIQKITVDCKQYVCNGFQKCEDLLKEYGQFCSKINQALHGANLRQD
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GITQQVLSENQKLIANKFNQALSAMQTGFTTTNLAFNKVQDAVNANAMALSKLAAELSNTFGAISASIGD
ILARLDTVEQEAQIDRLINGRLTSLNAFVAQQLVRTEAAARSAQLAQDKVNECVKSQSSRFNGAGTHLI
VSFAINAPNGLYFFHSVGYYPTSHVNATAAYGLCNTENSQAKCIAPIDGYFVLNKTTSTVADSDQGMYTTGS
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Figure 32 continued

>HKU4_S
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NITLAYTGLFPLQGDLGSQVLYSVSHAVSHDGDPTPAYISNVSLLVNDFDNGFVVRIGAAANSTGTIVI
PSVNTKIKPAVPAFILGSSLTNTSASQPLVANVSLTIIPDGCGTVLHAFYCILKPRTVNRCPSGTGVYSV
FIVETVHNDCQSTINRNASLNSFKSFFDLVNCTFFNSNDITALEIYENFGITQDTQGVHLVSSRFGGLVG
GNMFRFATLPVYEGIKVYTVIPSSFRSNANFREANAAFYVTRLHQLTYLLDFSVDGYIRRAIDCGRDDLS
QLHCSYTSFEVDTGVYSVSSIEASATGTFIEQFNATECDFSPMLIGVAPQVINFNRLVTSNCNINLTKLL
SLFAVLEFSCNGISPDSIARGCVSTLTVDYFAIPLSMKSYIRPGSAGNIPLINIRQSFANFTCRVTGASVL
ANVTITKSHAVSYISKLSRLTGANQDVETSLVINNSEYSICRDFSSPSGFSEIGQVTFRCLTQFEGGGLLI
GVSTRVFNTINLQNSFIISVQVGTSTDSVCPMLILGDSLTITMPLGRCVDYSLIFVTGSGVFQNCTAVGV
RQQPFVTDSFDNLVGYYSDDGNYYCVRPCVSVPVSVIYDNSTNLHATLFGSVACEHVTTNMSCFSRLTQS
NLPRRDSNIPLQTAVGCVIGLSNNSLVVSDCKLPLGQSLCAVPPVSTFRSYSRSQFQLAVLNITSPITVT
PINSSGFTAAIPTNFSFSVTQEYIETSIQKVTVLCRQIYCNGFTRCEYLLVEYGQFCSKINQALHGANLR
QDESVYSLYSNIKTTSTQTLEYGLNGLPNLTLLQVFQIGGSSSSYRSAIELLLFDKVTIADPGYMQGYDD
CMKQGPQSARDLICAQYVSGYKVLPPLVDPNMEAAYTSSLLGSIAGAGWTAGLSSFAAIPFAQSMFYRLN
GVGITQQVLSENQKLIANKFNQALGAMQTGFTTSNLAFSKVQDAVNANAQALSELASELSNTFGAISSSI
SDILARLDTVEQDAQIDRLINGRLISLNAFVSQQLVRSETAARSAQLAGDMVNECVKSQSSRINFCGNGT
HIVSFVVNAPNGFYFFHVGYYPTNYVTARVGLCNNNNPFLCIAPIDGYFITNTTTYSVDTEWYYTGS
SFYRPEPITQAMPRIVSSDVEFDPLEKNKLPPPLLENSTDVDFTDELEEFFLNVTSHGPNFAEISNKINTTL
LDLSDEMAMLQEVVKQLNDSYIDLPELGNYTYYNKWPWYVWLGFIAGLVALLLCVFFLLCCTGCGTSCLG
FMKCFNDCDSVEEYDVEPHVH

>EMC_S_RBD_359-588
SGV
YSVSSFEADPSGSVVEQAEGVECDFSPLLSGTPPQVYNFKRLVFTNCNYNLTKLLSLFSV
NDFTCSQISPAAIASNCYSSLILDYFSYPLSMKSDLSVSSAGPISQFNYKQSFSNPTCLI
LATVPHNLTTITKPLKYSYINKCSRLLSDDRTEVPQLVNANQYSPCVSITPSTVWEDGDY
YRKQLSPLEGGGWLVASGSTVAMTEQLQMGFGITVQYGTDTNSVCPKL

>HKU4_S_RBD_363-593
TGVLSVSSFEASPRGEFIEQATTQECDFTPNLDTPPSIINFTRLVFTKCNYNLT
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EVPQNLTTITKPSNYAYLTECYNTSASYGKNVLVNAPSGAVTPCLSSLASRSFSSTRVQSHSDGELTTTSYIYP
VTSNLQMAFIISYQYSTDTNSVCPMQ

>HKU5_S_RBD_366-596
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SLFAVLEFSCNGISPDSIARGCVSTLTVDYFAYPLSMKSYIRPGSAGNIPLVNIRQSFANFTCRVMASVL
ANVTITKSHAVSYISKLSRLTGANQDVETSLVINNSEYSICRDFSSPSGFSEIGQVTFRCLTQFEGGGLLI
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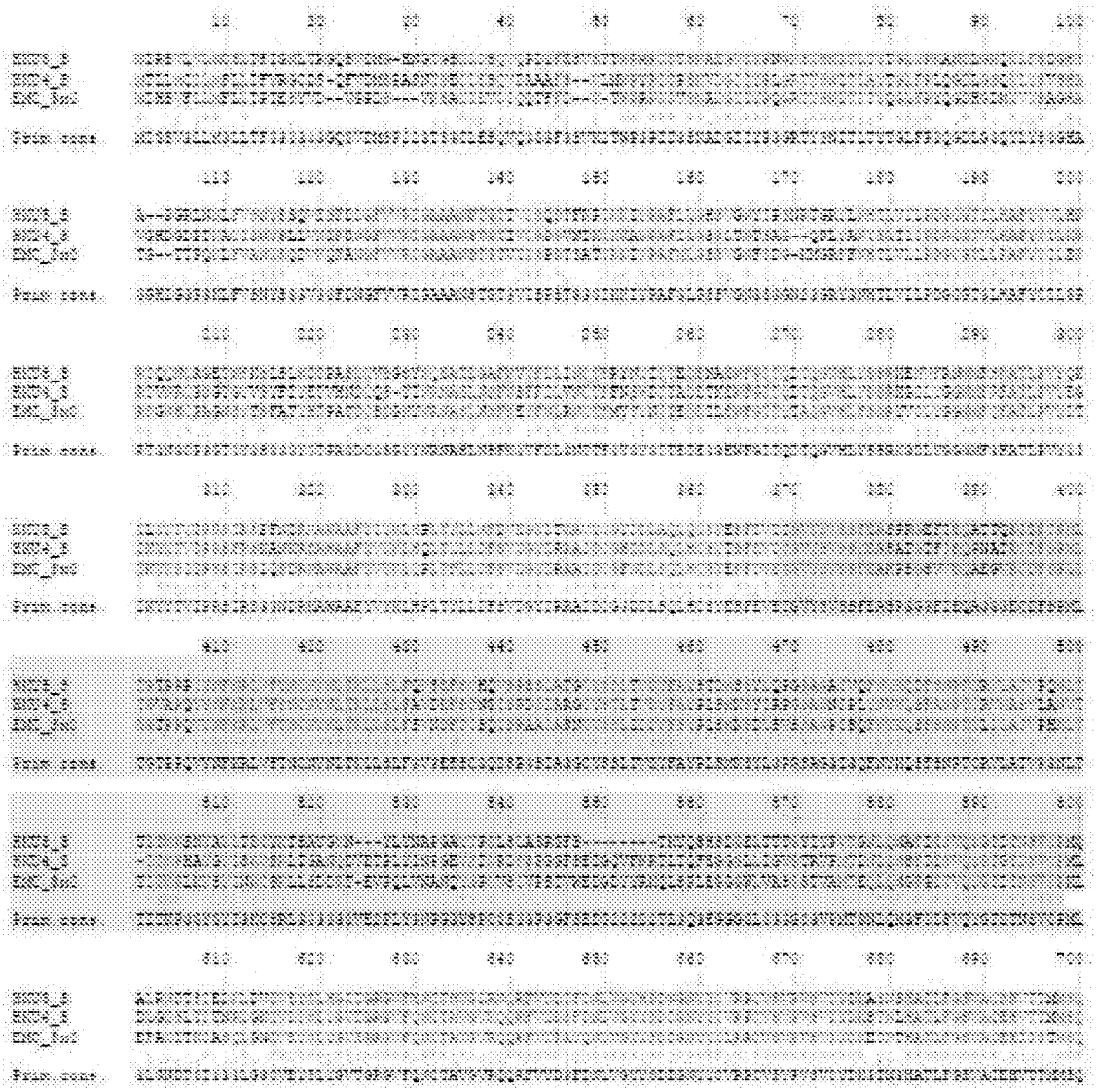
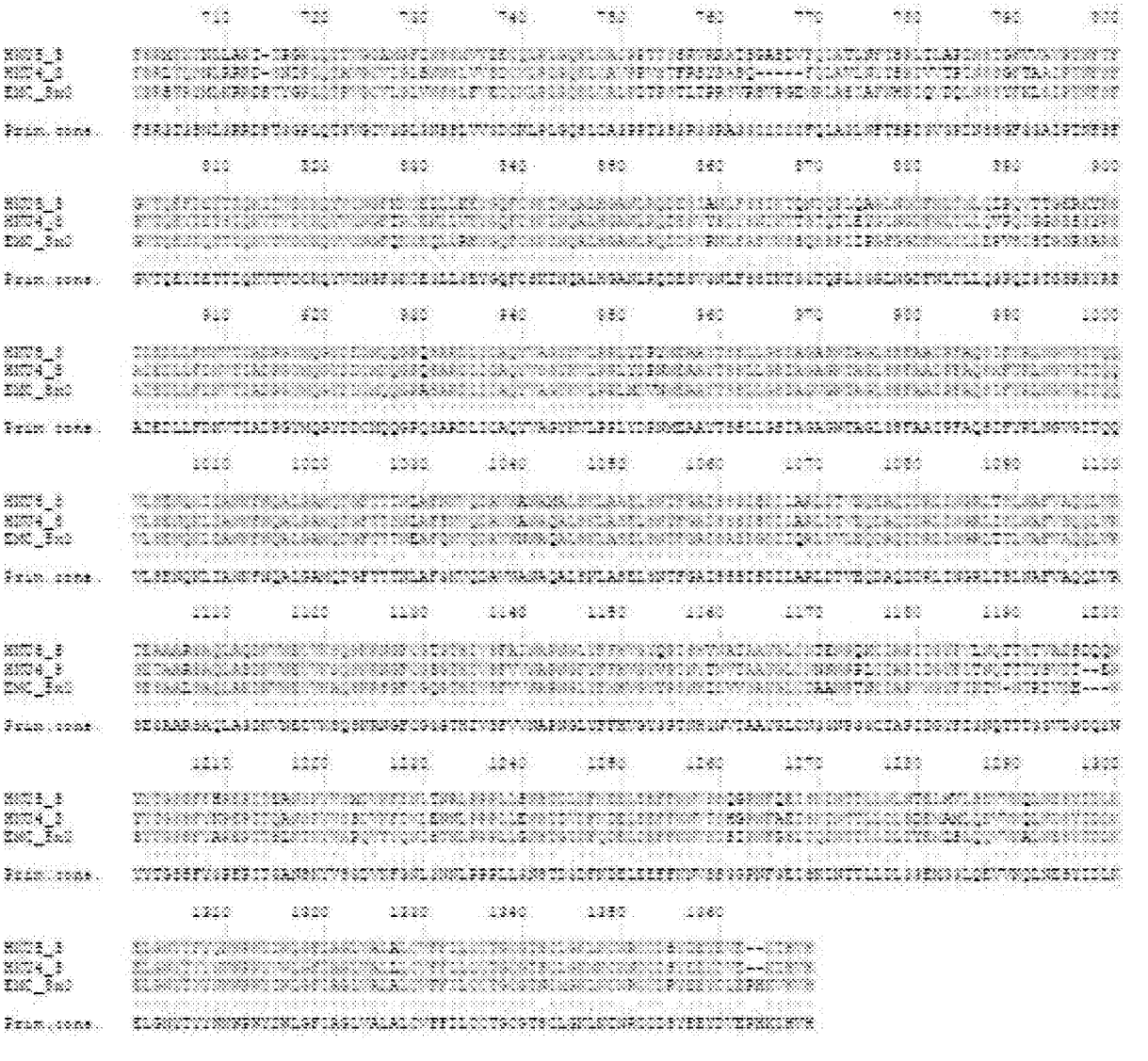
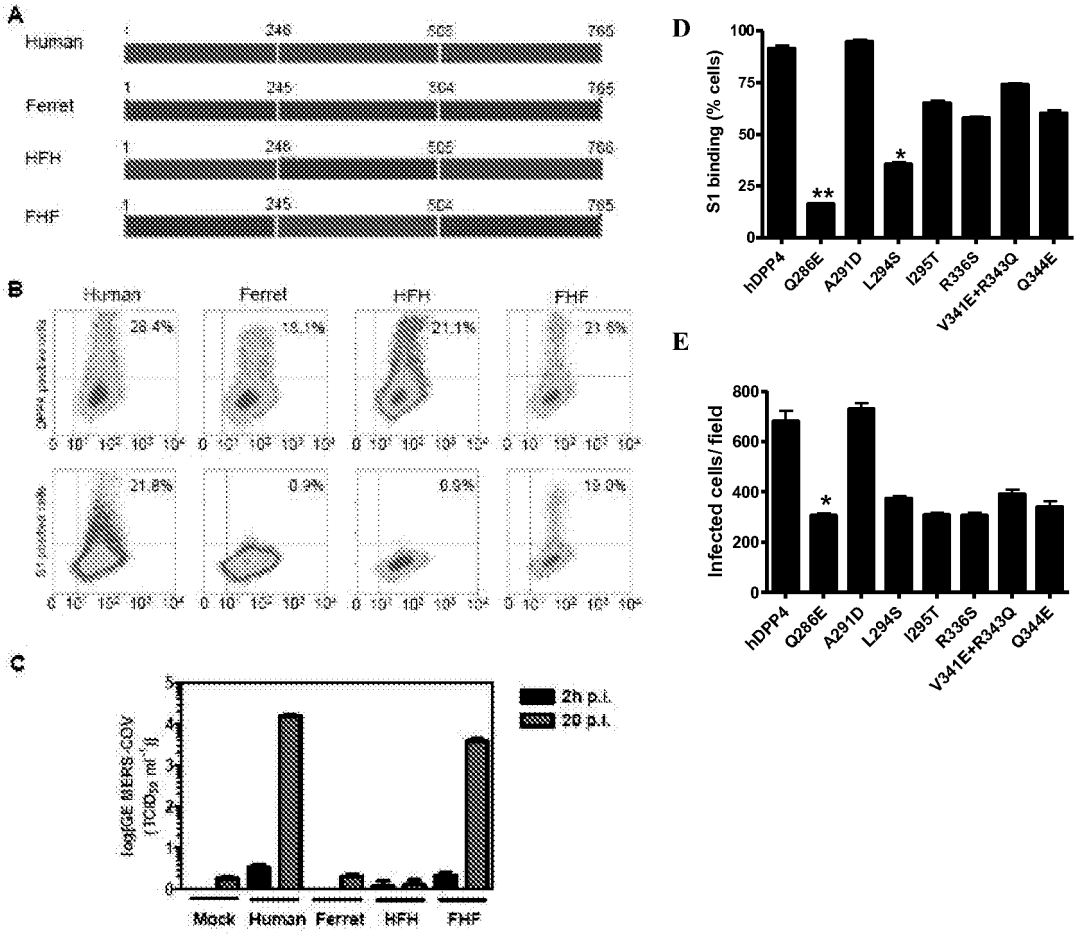


Figure 32 continued



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Alignment length : 1369
Identity (*) : 766 is 55.95 %
Strongly similar (:) : 233 is 17.02 %
Weakly similar (.) : 110 is 8.04 %
Different : 260 is 18.99 %
Sequence 0001 : HXU5_S (1352 residues)
Sequence 0002 : HXU4_S (1352 residues)
Sequence 0003 : EMC_Sx0 (1353 residues)

Figure 33


A
Human
Ferret
HFH
FHF
1
246
505
765
1
245
504
765
B
Human
Ferret
HFH
FHF
28.4%
18.1%
21.1%
21.6%
21.8%
0.9%
0.8%
19.0%
C
log(GE MERS-COV (TCID50 ml-1))
2h p.i.
20 p.i.
Mock
Human
Ferret
HFH
FHF
D
S1 binding (% cells)
hDPP4
Q286E
A291D
L294S
I295T
R336S
V341E+R343Q
Q344E
E
Infected cells/ field
hDPP4
Q286E
A291D
L294S
I295T
R336S
V341E+R343Q
Q344E