S1 Figure. Sequence alignments for key viruses and clones used in this study

A. BG505.T332N *vs*. B41

```
BG505.T332N     MRVMGIQRNCQHLFRWGTMILGMIIICSAAENLWVTVYYGVPVWKDAETTLFCASDAKAY
B41             MRVMEIRRNCQHLWRGGILLLGILMICSAAK-KWVTVYYGVPVWKEATTTLFCASDAKAY

                                        88
BG505.T332N     ETEKHNVWATHACVPTDPNPQEIHLENVTEEFNMWKNNMVEQMHTDIISLWDQSLKPCVK
B41             DTEVHNVWATHACVPTDPNPQEIVLGNVTENFNMWKNNMVEQMHEDIISLWDQSLKPCVK

                       130 133 137                  156 160
BG505.T332N     LTPLCVTLQCTNVTNNITDDMR----------GELKNCSFNMTTELRDKKQKVYSLFY
B41             LTPLCVTLNCNNVNTNNTNNSTNATISDWEKMETGEMKNCSFNVTTSIRDKIKKEYALFY

                            190 190c       197
BG505.T332N     RLDVVQINENQGNRSNNSNKEYRLINCNTSAITQACPKVSFEPIPIHYCAPAGFAILKCK
B41             KLDVVPLE-NKNNINNTNITNYRLINCNTSVITQACPKVSFEPIPIHYCAPAGFAILKCN

                230 234   241                  262           276          289
BG505.T332N     DKKFNGTGPCPSVSTVQCTHGIKPVVSTQLLLNGSLAEEEVMIRSENITNNAKNILVQFN
B41             SKTFNGSGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEEEIVIRSENITDNAKTIIVQLN

                    295   301                           332    339
BG505.T332N     TPVQINCTRPNNNTRKSIRIGPGQAFYATGDIIGDIRQAHCNVSKATWNETLGKVVKQLR
B41             EAVEINCTRPNNNTRKSIHIGPGRAFYATGDIIGNIRQAHCNISKARWNETLGQIVAKLE

                   355     363                    386   392   398    406  411
BG505.T332N     KHFGNNTIIRFANSSGGDLEVTTHSFNCGGEFFYCNTSGLFNSTWISNTSVQGSNSTGSN
B41             EQFPNKTII-FNHSSGGDPEIVTHSFNCGGEFFYCNTTPLFNSTW--NNTRTDDYPTGGE

                                                 448           462
BG505.T332N     DSITLPCRIKQIINMWQRIGQAMYAPPIQGVIRCVSNITGLILTRDGGSTNSTTETFRPG
B41             QNITLQCRIKQIINMWQGVGKAMYAPPIRGQIRCSSNITGLLLTRDGGRDQNGTETFRPG

                                                     Vcleavage
BG505.T332N     GGDMRDNWRSELYKYKVVKIEPLGVAPTRAKRRVVGREKRAVGIGAVFLGFLGAAGSTMG
B41             GGNMRDNWRSELYKYKVVKIEPLGIAPTAAKRRVVQREKRAVGLGAFILGFLGAAGSTMG

BG505.T332N     AASMTLTVQARNLLSGIVQQQSNLLRAIEAQQHLLKLTVWGIKQLQARVLAVERYLRDQQ
B41             AASMALTVQARLLLSGIVQQQNNLLRAIEAQQHMLQLTVWGIKQLQARVLAVERYLRDQQ

                                611    618    625         637
BG505.T332N     LLGIWGCSGKLICTTNVPWNSSWSNRNLSEIWDNMTWLQWDKEISNYTQIIYGLLEESQN
B41             LLGIWGCSGKIICTTNVPWNDSWSNKTINEIWDNMTWMQWEKEIDNYTQHIYTLLEVSQI
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                                SOSIP.664 truncation
BG505.T332N      QQEKNEQDLLALDKWASLWNWFDISNWLWYIKIFIMIVGGLIGLRIVFAVLSVIHRVRQG
B41              QQEKNEQELLELDKWDSLWNWFSISNWLWYIKIFIMIVGGLIGLRIVFTVLSIISRVRQG

BG505.T332N      YSPLSFQTHTPNPRGLDRPERIEEEDGEQDRGRSTRLVSGFLALAWDDLRSLCLFCYHRL
B41              YSPLSFQTLLPVPRGPDRPEGIEEEGGERDRDRSGPPVNGFLAIFWVDLRNLFLFLYHRL

BG505.T332N      RDFILIAARIVELLGHSSLKGLRLGWEGLKYLWNLLAYWGRELKISAINLFDTIAIAVAE
B41              RDLLLIAARIVELLGRR-------GWGILKYWWNLLQYWSQELKNSAVSLLNATAIAVAE

BG505.T332N      WTDRVIEIGQRLCRAFLHIPRRIRQGLERALL
B41              GTDRVIEVVQRIVRGILHIPTRIRQGLERALL
```

B. BG505.T332N *vs.* MG505 cl.A2 and cl.H3

```
BG505.T332N      MRVMGIQRNCQHLFRWGTMILGMIIICSAAENLWVTVYYGVPVWKDAETTLFCASDAKAY
MG505.A2         MRVVGIQRNCQHLFRWGTMILGMIIICSAAENLWVTVYYGVPVWKDAETTLFCASDAKAY
MG505.H3         MRVMGIQMNCQHLFRWGTMILGMIIICSAAENLWVTVYYGVPVWKDAETTLFCASDAKAY

                                          88
BG505.T332N      ETEKHNVWATHACVPTDPNPQEIHLENVTEEFNMWKNNMVEQMHTDIISLWDQSLKPCVK
MG505.A2         ETEKHNVWATHACVPTDPNPQEIHLENVTEEFNMWKNSMVEQMHTDIISLWDQSLKPCVK
MG505.H3         KTEKHNVWATHACVPTDPNPQEIHLENVTEEFNMWKNSMVEQMHTDIISLWDQSLEPCVK

                        130 133  137         156 160
BG505.T332N      LTPLCVTLQCTN--VTNNITDDMRGELKNCSFNMTTELRDKKQKVYSLFYRLDVVQINEN
MG505.A2         LTPLCVTLQCTN--VTNNITDDMRGELKNCSFNMTTELRDKKQKVYSLFYRLDVIQINEN
MG505.H3         LTPLCVTLQCTNNVTNANITDDMRGELKNCSFNMTTELRDKKQKVYSLFYRLDVVQINEN

                  190 190c       197                                230 234
BG505.T332N      QGNRSNNSNKEYRLINCNTSAITQACPKVSFEPIPIHYCAPAGFAILKCKDKKFNGTGPC
MG505.A2         QGNGSNNSNKEYRLINCNTSAITQACPKVSFEPIPIHYCAPAGFAILKCKDKKFNGTGPC
MG505.H3         QGNSSKSSNKEYRLINCNTSAITQACPKVSFEPIPIHYCAPAGFAILKCKDKKFTGTGPC

                 241                   262           276           289   295
BG505.T332N      PSVSTVQCTHGIKPVVSTQLLLNGSLAEEEVMIRSENITNNAKNILVQFNTPVQINCTRP
MG505.A2         PKVSTVQCTHGIKPVVSTQLLLNGSLAEEEVMIRSENITNNAKNILVQFNTPVQINCTRP
MG505.H3         SNVSTVQCTHGIKPVVSTQLLLNGSLAEEEVMIRSENITNNAKNILVQFNTPVQINCTRP

                 301                           332    339             355
BG505.T332N      NNNTRKSIRIGPGQAFYATGDIIGDIRQAHCNVSKATWNETLGKVVKQLRKHFGNNTIIR
MG505.A2         NNNTRKSIRIGPGQAFYATGDIIGDIRQAHCTVSKATWNETLEKVVKQLRKHFGNNKTII
MG505.H3         NNNTRKSIHIGPGQAFYATGDIIGNIRQAQCTVSKATWNETLEKVVKQLREHFGNNTTII

                  363                    386   392   398    406  411
BG505.T332N      FANSSGGDLEVTTHSFNCGGEFFYCNTSGLFNSTWISNTSVQGSNSTGSNDSITLPCRIK
MG505.A2         FANSSGGDLEVTTHSFNCGGEFFYCNTSGLFNSTWNSNTSVQGSNSTGSNDSITLPCRIK
MG505.H3         FASSSGGDLEVTTHSFNCGGEFFYCNTSGLFNSTWISNTSVQGSNSTESSDTITLPCRIK
```

Unknown

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```
                                        448           462
BG505.T332N     QIINMWQRIGQAMYAPPIQGVIRCVSNITGLILTRDGGSTNSTTETFRPGGGDMRDNWRS
MG505.A2        QIINMWQRIGQAMYAPPIQGVIGCVSNITGLILTRDGGSTNSTTETFRPGGGDMRDNWRS
MG505.H3        QIINMWQRIGQAMYAPPIQGVIRCVSNITGLILTRDGGSNNSTNETFRPGGGDMRDNWRS

                                        Furin cleavage
BG505.T332N     ELYKYKVVKIEPLGVAPTRAKRRVVGREKRAVGIGAVFLGFLGAAGSTMGAASMTLTVQA
MG505.A2        ELYKYKVVKIEPLGVAPTRAKRRVVGREKRAVGIGAAFLGFLGAAGSTMGAASMTLTVQA
MG505.H3        ELYKYKVVKIEPLGVAPTRAKRRVVGREKRAVGIGAVFLGFLGAAGSTMGAASMTLTVQA

BG505.T332N     RNLLSGIVQQQSNLLRAIEAQQHLLKLTVWGIKQLQARVLAVERYLRDQQLLGIWGCSGK
MG505.A2        RNLLSGIVQQQSNLLRAIEAQQHLLKLTVWGIKQLQARVLAVERYLRDQQLLGIWGCSGK
MG505.H3        RNLLSGIVQQQSNLLRAIEAQQHLLKLTVWGIKQLQARVLAVERYLRDQQLLGIWGCSGK

                        611     618     625         637
BG505.T332N     LICTTNVPWNSSWSNRNLSEIWDNMTWLQWDKEISNYTQIIYGLLEESQNQQEKNEQDLL
MG505.A2        LICTTNVPWNSSWSNKNLSEIWDNMTWLQWDKEISNYTQIIYGLLEESQNQQEKNEQDLL
MG505.H3        LICTTNVPWNSSWSNRNLSEIWDNMTWLQWDKEISNYTQIIYGLLEESQNQQEKNEQDLL

                   SOSIP.664 truncation
BG505.T332N     ALDKWASLWNWFDISNWLWYIKIFIMIVGGLIGLRIVFAVLSVIHRVRQGYSPLSFQTHT
MG505.A2        ALDKWASLWNWFDISNWLWYIKIFIMIVGGLIGLRIVFAMLSVIHRVRQGYSPLSFQTHT
MG505.H3        ALDKWASLWNWFDISNWLWYIKIFIMIVGGLIGLRIVFAVLSVIHRVRQGYSPLSFQTHT

BG505.T332N     PNPRGLDRPERIEEEDGEQDRGRSTRLVSGFLALAWDDLRSLCLFCYHRLRDFILIAARI
MG505.A2        PNPRGLDRPERIEEEDGEQDRGRSTRLVSGFLALAWDDLRSLCFFCYHRLRDFILIAARI
MG505.H3        PNPRGLDRPERIEEEDGEQDRGRSTRLVSGFLALAWDDLRGLCLFSYHRLRDFILIAARI

BG505.T332N     VELLGHSSLKGLRLGWEGLKYLWNLLAYWGRELKISAINLFDTIAIAVAEWTDRVIEIGQ
MG505.A2        VELLGHSSLKGLRLGWEGLKYLWNLLAYWGRELKISAINLFDTIAIAVAGWTDRVIEIGQ
MG505.H3        VELLGHSSLKGLRLGWEGLKYLWNLLAYWGQELKISAINLFDTIAIAVAGWTDRVIEIGQ

BG505.T332N     RLCRAFLHIPRRIRQGLERALL
MG505.A2        RLCRAFLHIPRRIRQGFERALL
MG505.H3        RLCRAFLHIPRRIRQGFERALL
```

C. CZA97 cl.29 *vs.* cl.12

```
97.29           MRVRGIPRNWPQWWIWGILGFWMIIICRVVGNMWVTVYYGVPVWTDAKTTLFCASDAKAY
97.12           MRVRGIPRNWPQWWMWGILGFWMIIICRVVGNMWVTVYYGVPVWTDAKTTLFCASDTKAY

                                        88
97.29           DREVHNVWATHACVPTDPNPQEIVLENVTENFNMWKNDMVDQMHEDIISLWDQSLKPCVK
97.12           DREVHNVWATHACVPTDPNPQEIVLENVTENFNMWKNDMVDQMHEDIISLWDQSLKPCVK

                      130 133  139        156 160
97.29           LTPLCVTLHCTNATFKNNVTNDMNKEIRNCSFNTTTEIRDKKQQGYALFYRPDIVLLKEN
97.12           LTPLCVTLHCTNATFKNNVTNDMNKEIRNCSFNTTTEIRDKKQQGYALFYRPDIVLLKEN
```

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Unknown
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```
                183 186      197                                230        241
97.29           RNNSNNSEYILINCNASTITQACPKVNFDPIPIHYCAPAGYAILKCNNETFSGKGPCNNV
97.12           RNNSNNSEYILINCNASTITQACPKVNFDPIPIHYCAPAGYAILKCNNKTFSGKGPCNNV

                                262           276          289         301
97.29           STVQCTHGIKPVVSTQLLLNGSLAEKEIIIRSENLTDNVKTIIVHLNKSVEIVCTRPNNN
97.12           STVQCTHGIKPVVSTQLLLNGSLAEKEIIIRSENLTDNVKTIIVHLNKSVEIVCTRPNNN

                                          332    339              355
97.29           TRKSMRIGPGQTFYATGDIIGDIRQAYCNISESMWKETLERVKEKLKENYNNNKTIKFAP
97.12           TRKSMRIGPGQTFYATGDIIGDIRQAYCNISGSKWNETLKRVKEKLQENYNNNKTIKFAP

                                     386     392 411
97.29           SSGGDLEITTHSFNCRGEFFYCNTSKLFSYNGTGNETIILPCRIKQIINMWQGVGRAMYA
97.12           SSGGDLEITTHSFNCRGEFFYCNTTRLFNNNATEDETITLPCRIKQIINMWQGVGRAMYA

                    442   448           462
97.29           PPIAGNITCKSNITGLLLVRDGGEDNKTEETFRPGGGNMKDNWRSELYKYKVIELKPLGI
97.12           PPIAGNITCKSNITGLLLVRDGGEDNKTEEIFRPGGGNMKDNWRSELYKYKVIELKPLGI

                              furin cleavage
97.29           APTGAKRRVVEREKRAVGIGAVFLGFLGAAGSTMGAASLALTVQARQLLSGIVQQQSNLL
97.12           APTGAKRRVVEREKRAVGIGAVFLGFLGAAGSTMGAASLTLTVQARQLLSSIVQQQSNLL

                                                                611  616
97.29           RAIEAQQHMLQLTVWGIKQLQTRVLAIERYLKDQQLLGIWGCSGKLICTTNVPWNSSWSN
97.12           RAIEAQQHMLQLTVWGIKQLQTRVLAIERYLKDQQLLGIWGCSGKLICTTNVPWNSSWSN

                       625         637                        SOSIP.664 truncation
97.29           KSQTDIWNNMTWMEWDREISNYTDTIYRLLEDSQTQQEKNEKDLLALDSWKNLWNWFDIT
97.12           KSQTDIWNNMTWMEWDREISNYTDTIYRLLEDSQTQQEKNEKDLLALDSWKNLWSWFDIS

97.29           NWLWYIKIFIMIVGGLIGLRIIFAVLSIVNRVRQGYSPLSFQTLTPNPRGLDRLGRIEEE
97.12           NWLWYIKIFIMIVGGLIGLRIIFAVLSIVNRVRQGYSPLSFQTLTPNPRELDRLGRIEEE

97.29           GGEQDRDRSIRLVNGFLALAWDDLRSLCLFIYHQLRDFILLTARAVELLGRSSLRGLQRG
97.12           GGEQDRDRSIRLVNGFLALAWDDLRSLCLFIYHQLRDFILLTARAVELLGRSSLRGLQRG

97.29           WEALKYLGNLVQYWGLELKKSAISLLDTIAITVAEGTDRIIEVVQRICRAIRNIPRRIRQ
97.12           WEALKYLGNLVQYWGLELKKSAISLLDTIAITVAEGTDRIIEVVQRICRAIRNIPRRIRQ

97.29           GFEAALL
97.12           GFEAALP
```

Unknown
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Ian Wilson 6/12/2016 7:43 AM
Comment [1]: Sorry cant seem to move over slightly to be between D and S – Help!!

Unknown
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D. Heterologous Tier-2 viruses

```
Ce703010217_B6      MRVTGTQRNYPRWWIWGWWIWGILGFWMLLNCNG--AKDMWVTVYYGVPVWREAKTTLFC
246_F3_C10_2        MRARGMLRTW-----QHWWIWGILGFWMLMICN---MQDLWVTVYYGVPVWKDAKTTLFC
CNE55x2             MRVKETQMNW-----PNLWKWGVLILGLVIICSA--SDKLWVTVYYGVPVWRDADTTLFC
TRO11x3             MRAKGIRKNC-----QHLWIWGTMLLGMLMIYSAAEQGQLWVTVYYGVPVWKDASTTLFC
X1632_S2_B10        MKVKGTQRDW-----HSLWNWGILILGLVIICSA--SNNLWVTVYYGVPVWEDADTTLFC
BJ0X002000032       MRVTGIRKNY-----WHLWRWGTMLLGMLMICST--VGNLWVTVYYGVPVWKEATTTLFC
CH11910             MRVTGIRKNY-----RHLWRWGTMLLGMLMICSA--VGNLWVTVYYGVPVWKEATTTLFC
25710_243           MRVRGTLRNY-----QQWWIWGVLGFWMLMICNV--GGNLWVTVYYGVPVWKEATTTLFC
Ce1176_A3           MRAKGILRNY-----QQWWIWGILGFWMLMVCNV--VGNLWVTVYYGVPVWKEAKTTLFC

                                                   88
Ce703010217_B6      ASDAKAYEREVHNVWATHACVPTDPNPQERVLENVTENFNMWKNNMVDQMHEDIISLWDE
246_F3_C10_2        ASDAKAYEKEVHNVWATHACVPTDPNPQEIVMANVTEEFNMWKNNMVEQMHTDIISLWDQ
CNE55x2             ASDAKAHETEVHNVWATHACVPTDPNPQEIHLVNVTENFNMWKNKMVEQMQEDVISLWDE
TRO11x3             ASDAKAYDTEVHNVWATHACVPTDPNPQEVVLGNVTENFNMWKNNMVDQMHEDIISLWDQ
X1632_S2_B10        ASDAKAYSTESHNVWATHACVPTDPNPQEIYLENVTEDFNMWENNMVEQMQEDIISLWDE
BJ0X002000032       ASDAKAYDTEVHNVWATHACVPTDPDPQEMFLENVTENFNMWKNNMVDQMHEDVISLWDQ
CH11910             ASDAKAYDTEVHNVWATHACVPTDPSPQELVLENVTENFNMWKNEMVNQMHEDVISLWDQ
25710_243           ASDAKAYDKEVHNVWATHACVPTDPNPQEMVLGNVTENFNMWKNEMVNQMHEDVISLWDQ
Ce1176_A3           ASDAKAYEKEVHNVWATHACVPTDPNPQEMVLENVTENFNMWKNDMVDQMHEDVISLWDQ

                                130                                156 160
Ce703010217_B6      SLKPCIKLTPLCVTLNCGNAIV--N---------------ESTIEGMKNCSFNVTTELKD
246_F3_C10_2        SLKPCVKLTPLCVTLDCKDYNY--S-ITNNS---------TGMEGEIKNCSYNITTELRD
CNE55x2             SLKPCVKLTPLCVTLNCTTAN--TNETKNNTT-------DDNIKDEMKNCTFNMTTEIRD
TRO11x3             SLKPCVKLTPLCVTLNCTDNIT--NTNTNSSKNSSTHSYNNSLEGEMKNCSFNITAGIRD
X1632_S2_B10        SLKPCVKLTPLCVTLTCTNVTNVTDSVGTNSR-------LKGYKEELKNCSFNTTTEIRD
BJ0X002000032       SLKPCVKLTPLCVTLECKNVNS--SS-SDTK---------NGTDPEMKNCSFNATTELRD
CH11910             SLKPCVKLTPLCVTLECSKVSN--NE-TDKY---------NGTE-EMKNCSFNATTVVRD
25710_243           SLKPCVKLTPLCVTLECSNVT---------Y---------NESMKEVKNCSFNLTTELRD
Ce1176_A3           SLKPCVKLTPLCVTLTCTNTTV--SNGSSNS---------NANFEEMKNCSFNATTEIKD

                                                   197
Ce703010217_B6      KKKKEYALFYKLDVVPLNGENNNSNSKNFSEYRLINCNTSTITQACPKVSFDPIPIHYCA
246_F3_C10_2        KRQKVYSLFYRLDVVQINDSNDRNNSQ----YRLINCNTTTMTQACPKVTFDPIPIHYCA
CNE55x2             KKQRVSALFYKLDIVPIDDSKNNSE------YRLINCNTSVIKQACPKVSFDPIPIHYCT
TRO11x3             KVKKEYALFYKLDVVPIEEDKDTNKTT----YRLRSCNTSVITQACPKVTFEPIPIHYCA
X1632_S2_B10        KKKQEYALFYKLDIVPINDNSNNSNG-----YRLINCNVSTIKQACPKVSFDPIPIHYCA
BJ0X002000032       RKQKVYALFYKLDIVPLNEKNSSE-------YRLINCNTSTITQACPKVTFDPIPIHYCT
CH11910             RQQKVYALFYRLDIVPLTEKNSSENSS--KYYRLINCNTSAITQACPKVSFEPIPIHYCT
25710_243           KKQKVHALFYRLDIVPLNDTEKKN-SS--RPYRLINCNTSAITQACPKVTFDPIPIHYCT
Ce1176_A3           KKKNEYALFYKLDIVPLNNSSGKY-------R-LINCNTSAIAQACPKVTFEPIPIHYCA

                          230 234    241                  262           276
Ce703010217_B6      PAGFAILKCNNETFNGTGPCNNVSTVQCTHGIKPVVSTQLLLNGSLAEKEIIIRSENLTN
246_F3_C10_2        PAGFAILKCNNKTFNGKGPCNNVSSVQCTHGIKPVVSTQLLLNGSLAEKEIVIRSENLTD
CNE55x2             PAGYVILKCNDKNFNGTGPCKNVSSVQCTHGIKPVVSTQLLLNGSLAEEEIIIRSENLTD
TRO11x3             PAGFAILKCNDKKFNGTGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSENFTN
X1632_S2_B10        PAGFAILKCRDKEFNGTGTCRNVSTVQCTHGIKPVVSTQLLLNGSLAEGDIVIRSENITD
BJ0X002000032       PAGYAILKCNDEKFNGTGPCSNVSTVQCTHGIKPVVSTQLLLNGSLAEKGIVIRSENLTN
CH11910             PAGYAILKCNDKTFNGTGPCHNVSTVQCTHGIKPVVSTQLLLNGSLAEGEIIIRSENLTN
25710_243           PAGYAILKCNDKKFNGTGPCHKVSTVQCTHGIKPVVSTQLLLNGSLAEGEIIIRSENLTN
Ce1176_A3           PAGYAILKCNNKTFNGTGPCNNVSTVQCTHGIKPVVSTQLLLNGSLAEKEIIIRSENLTN

                         289   295   301                          332   339
Ce703010217_B6      NAKIIIVHLNNPVKIICTRPGNNTRKSMRIGPGQTFYATGDIIGDIRRAYCNISEKTWYD
246_F3_C10_2        NVKTIIVHLNESVEINCTRPNNNTRKSVRIGPGQTFYATGDIIGNIRQAHCTVNKTEWNT
```

```
CNE55x2             NAKNIIVHLNKSVEINCTRPSNNTRTSVRIGPGQVFYRTGDITGDIRKAYCEIDGTEWNK
TRO11x3             NAKTIIVQLNESIAINCTRPNNNTRRSIHIGPGRAFYATGDIIGDIRQAHCNISRTEWNS
X1632_S2_B10        NAKTIIVHLNKTVSITCTRPNNNTRKSIRIGPGQALYATGAIIGDTRQAHCNINGSEWYE
BJ0X002000032       NVKTIIVHLNQSVEILCIRPNNNTRKSIRIGPGQTFYATGEIIGDIRQAHCNISGKVWNE
CH11910             NVKTILVHLNQSVEIVCTRPNNNTRKSIRIGPGQTFYATGDIIGDIRQAHCNIS--KWHE
25710_243           NAKTIIVHLNQSVEIVCARPSNNTRTSIRIGPGQTFYATGAITGDIRQAHCNISKDKWNE
Ce1176_A3           NAKTIIIHFNESVGIVCTRPSNNTRKSIRIGPGQTFYATGDIIGDIRQAHCNVSKQNWNR

                                    355   363                     386   392
Ce703010217_B6      TLKNVSDKFQEHF--PNASIEFKPSAGGDLEITTHSFNCRGEFFYCDTSELFNGTYN---
246_F3_C10_2        ALTRVSKKLKEYF--PNKTIAFQPSSGGDLEITTFSFNCRGEFFYCNTSDLFNGTFN---
CNE55x2             TLTQVAEKLKEHF---NKTIVYQPPSGGDLEITMHHFNCRGEFFYCNTTQLFNNS-----
TRO11x3             TLRQIVTKLREQLGDPNKTIIFNQSSGGDTEITMHSFNCGGEFFYCNTTKLFNSTWN--G
X1632_S2_B10        MIQNVKNKLNETF---KKNITFNPSSGGDLEITTHSFNCRGEFFYCNTSELFNSSHL---
BJ0X002000032       TLQRVGEKLAEYF--PNKTIKFNSSSGGDLEITTHSFNCGGEFFYCNTSKLFNGTFN--G
CH11910             TLKRVSEKLAEHF--PNKTINFTSSSGGDLEITTHSFTCRGEFFYCNTSGLFNSTYMPNG
25710_243           TLQRVGEKLAEHF--PNKTIKFNSSSGGDLEITTHSFNCRGEFFYCNTSGLFNGTFN--G
Ce1176_A3           TLQQVGRKLAEHF--PNRNITFNHSSGGDLEITTHSFNCRGEFFYCNTSGLFNGTYHPNG

                                  411                         442   448
Ce703010217_B6      --N-STYN---SSNNITLQCKIKQIINMWQGVGRAMYAPPIAGNITCESNITGLLLTRDG
246_F3_C10_2        -ETSGQFN---STFNSTLQCRIKQIINMWQEVGQAMYAPPIAGSITCISNITGLILTRDG
CNE55x2             ----------VGNSTIKLPCRIKQIINMWQGVGQAMYAPPISGAINCLSNITGILLTRDG
TRO11x3             NNTTESDS---TGENITLPCRIKQIINLWQEVGKAMYAPPIKGQISCSSNITGLLLTRDG
X1632_S2_B10        --FNGSTL--STNGTITLPCRIKQIVRMWQRVGQAMYAPPIAGNITCRSNITGLLLTRDG
BJ0X002000032       TYMPNVTE---GNSTISIPCRIKQIINMWQKVGRAMYAPPIEGNITCKSKITGLLLERDG
CH11910             TYLHGDTN---SNSSITIPCRIKQIINMWQEVGRAMYAPPIEGNITCKSNITGLLLVRDG
25710_243           TYVSPNSTDSNSSSIITIPCRIKQIINMWQEVGRAMYAPPIAGNITCKSNITGLLLVRDG
Ce1176_A3           TYNETAVN---SSDTITLQCRIKQIINMWQEVGRAMYAPPIAGNITCNSTITGLLLTRDG

                          462                                   furin cleavage
Ce703010217_B6      GNN-----KSTPETFRPGGGDMRDNWRSELYKYKVVEIKPLGIAPTKAKRRVVEREKRAV
246_F3_C10_2        GNT-----NSTKETFRPGGGNMRDNWRSELYKYKVVKIEPLGVAPTKARRRVVEREKRAV
CNE55x2             GGNN---RSNE--TFRPGGGNIKDNWRSELYKYKVVEIEPLGIAPTKAKRRVVEREKRAV
TRO11x3             GNNN----SSGPETFRPGGGNMKDNWRSELYKYKVIKIEPLGVAPTRAKRRVVQREKRAV
X1632_S2_B10        GTNK---DTNEAETFRPGGGDMRDNWRSELYKYKVVKIKPLGVAPTRARRRVVEREKRAI
BJ0X002000032       GPE------NDTEIFRPGGGDMRNNWRSELYKYKVVEIKPLGVAPTEAKRRVVERERRAV
CH11910             GTESNNTETNNTEIFRPGGGDMRDNWRSELYKYKVVEIKPLGVAPTAAKRRVVEREKRAV
25710_243           GTGS---ESNKTEIFRPGGGDMRDNWRSELYKYKVVEIKPLGVAPTKAKRRVVEREKRAV
Ce1176_A3           GIN-----QTGEEIFRPGGGDMRDNWRNELYKYKVVEIKPLGIAPTKAKRRVVEREKRAV

Ce703010217_B6      G-MGAVFLGFLGAAGSTMGAASLTLTVQARQLLSGIVQQQNNLLRAIEAQQHMLQLTVWG
246_F3_C10_2        G-IGAVFIGFLGAAGSTMGAASITLTVQARQLLSGIVQQQSNLLRAIEAQQHLLKLTVWG
CNE55x2             G-IGAMIFGFLGAAGSTMGAASITLTVQARQLLSGIVQQQSNLLRAIEAQQHMLQLTVWG
TRO11x3             GTLGAMFLGFLGAAGSTMGAASVTLTVQARLLLSGIVQQQNNLLRAIEAQQHMLQLTVWG
X1632_S2_B10        G-LGTVLLGFLGTAGSTMGAASITLTVQVRQLLSGIVQQQSNLLRAIEAQQHLLQLTVWG
BJ0X002000032       G-IGAVFLGFLGVAGSTMGAASMALTVQARQLLSGIVQQQSNLLRAIEAQQHLLQLTVWG
CH11910             G-IGAVFLGFLGVAGSTMGAASMTLTVQARQLLSGIVQQQSNLLRAIEAQQHLLQLTVWG
25710_243           G-IGAVFLGFLGAAGSTMGAASITLTVQARQLLSGIVQQQSNLLRAIEAQQHLLQLTVWG
Ce1176_A3           G-IGAVFLGFLGAAGSTMGAASITLTVQARQLLSGIVQQQSNLLRAIEAQQHMLQLTVWG

                                                        611  618       625
Ce703010217_B6      IKQLQARVLAIERYLTDQQLLGIWGCSGKLICTTNVPWNNSWSNKSYEDIWGRNMTWMQW
246_F3_C10_2        IKQLQARVLAVERYLKDQQLLGIWGCSGKLICTTNVPWNSSWSNKSQDEIWD-NMTWLQW
CNE55x2             IKQLQARVLAVERYLKDQRFLGLWGCSGKTICTTAVPWNSTWSNKTYEEIWD-NMTWTQW
TRO11x3             IKQLQARVLAVERYLRDQQLLGIWGCSGKLICTTNVPWNASWSNKSLNNIWE-NMTWMEW
X1632_S2_B10        IKQLQARVLAVERYLKDQQILGIWGCSGKLICTTNVPWNSSWSNKSYSDIWD-NLTWIQW
BJ0X002000032       IKQLQTRVLAIERYLKDQQLLGIWGCSGKLICTTAVPWNSSWSNKSQEEIWE-NMTWMQW
CH11910             IKQLQTRVLAIERYLKDQQLLGIWGCSGKLICTTAVPWNSSWSNKSQKEIWD-NMTWMQW
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Unknown

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25710_243           IKQLQTRVLAIERYLKDQQLLGIWGCSGKLICTTAVPWNYSWSNRSQDDIWD-NMTWMQW
Ce1176_A3           IKQLQARVLAIERYLKDQQLLGIWGCSGKLICTTNVPWNSSWSNRSQEDIWN-NMTWMEW


                         637
Ce703010217_B6      DREINNYTNTIYRLLEKSQNQQEKNEKELLELDNWKNLWSWFNISNWLWYIKIFIMIVGG
246_F3_C10_2        DKEISNYTQIIYNLIEESQTQQELNERDLLALDKWANLWNWFDITKWLWYIKIFIMIVGG
CNE55x2             EREISNYTNQIYSILTESQSQQDKNEKDLLELDKWASLWNWFTLSRWLWYIKIFIMIVGG
TRO11x3             EREIDNYTDLIYILLEKSQIQQEKNEQELLELDSWASLWNWFDISKWLWYIKIFIMIVGG
X1632_S2_B10        EREISNYTQQIYTLLEESQNQQEKNEQELLALDKWASLWNWFDITNWLWYIKIFIMIVGG
BJ0X002000032       DKEISNYTDTIYRLLEDSQNQQERNEKDLLALDSWKNLWSWFDITNWLWYIRIFIMIVGG
CH11910             DKEISNYTNTIYKLLEDSQNQQESNEKDLLALDSWNNLWNWFNITQWLWYIKIFIIIVGG
25710_243           DKEISNYTNTIYKLLEDSQIQQEKNEKDLLALDSWENLWNWFNITNWLWYIKIFIIIVGG
Ce1176_A3           EREIDNYTHTIYSLLEESQIQQEKNEKDLLALDSWQNLWSWFSITKWLWYIKIFIMIVGG


Ce703010217_B6      LIGLRIIFAVLSIVNRVRQGYSPLSFQTLLPNPRG-PDRLGGIEEEGGEQDRDRSVRLVN
246_F3_C10_2        LIGLRIIFAVLSIVNRVRQGYSPLSFQTLTPNPRG-PDRPGGIEEEGGEQGRNSYTRLVS
CNE55x2             LIGLRIIFAVLSIVNRVRQGYSPLSFQTPILQQRE-PDRPERIEEGGGEQGRDTSVRFVS
TRO11x3             LVGLRIVFAVLSIANRVRQGYSPLSFQTRLPTPRG-PDRPEGIEKEGGGRDRDGSRPLVH
X1632_S2_B10        LIGLRIVFAVLSIINRVRKGYSPLSFQTLTRHQRE-PDRPGGIEEEDGEQDRDKSVRFVS
BJ0X002000032       LIGLRIIFAVLSIVNRVRQGYSPLSFQTLTPNPGG-PDRLGRIEEEGGKQDRDRSVRLVS
CH11910             LIGLRIIFAVLSIVNRVRQGYSPLSFQTLTPTSGGRPDRLERIEEEGGEQDRDRSIRLVN
25710_243           LIGLRIIFAVLPIVNRVRQGYSPLSFQTHTPTPGG-PDRLGRIEEEGGEQDNVRSIRLVN
Ce1176_A3           LIGLRIIFAVLSIVNRVRQGYSPLSLQTLIPNPRG-PDRLGRIEEEGGEQDRDRSIRLVN


Ce703010217_B6      GFLALAWDDLRNLCLFSYRQLRDFILIVARAVQLLGHSSLRGIQRGWEALKYLGSLVQYW
246_F3_C10_2        GFLPLAWDDLRSLCLFSYHLLRDFILIAARAAELLGRSSLRGLQRGWETLKYLGSLVQYW
CNE55x2             RFLALAWEDLRNLCLFSYHRLRDLLLIATRTVEILGHYSLKGLRRGWEVLKYLGNLLLYW
TRO11x3             GLLALIWDDLRSLCLFSYHRLRDLLLIVTRTVELLGR-------RGWELLKYWWNLLQYW
X1632_S2_B10        GFLSPVWDDLRSLCLFSYRRLRDFILVAARTVELLGRSSLKGLRLGWEGLKYLWNLLLYW
BJ0X002000032       GFLALAWDDLRNLCLFSYHRLRDFILVAVRVVELLGRNSLKGLQRGWEALKYLGSLVQYW
CH11910             GFLALAWDDLRNLCLFSYHRLRDFILVAARVVELLGRTSLRGLQRGWEALKYLGSLVQYW
25710_243           GFLALAWDDLRNLCLFSYHRLRDFILVAARVVELLGRNSLRGLQKGWEALKYLGSLVQYW
Ce1176_A3           GFLALAWDDLRSLCLFSYHQLRDFILVIARAVELLG-------QRGWEALKYLGSLVQYW


Ce703010217_B6      GLELKKSAISLLDTIAITVAEGTDRIIEVVQVIWRAILNIPRRIRQGFEAALQ
246_F3_C10_2        GLELKKSAISLLDTIAIQVAEGTDRIIELIQGIYRAIRNIPRRIRQGAETALV
CNE55x2             GQELKTSAISLLDATAIATAEWTDRVIEVAQRAWRAFIHIPRRIRQGFERALL
TRO11x3             SQELKNSAVSLLNTTAIAVAEGTDRVIEVVQRAFRAILHIPARIRQGLERALL
X1632_S2_B10        GRELKSSAINLLDTTAIAVANWTDRVIEVGQRIVRAFLHIPVRIRQGLERALL
BJ0X002000032       GQELKKSIISLVDTIAIAVAEGTDRIIELVQRFCRGIYHIPRRIRQGFEAALQ
CH11910             GQELKKSAISLVDTIAIVVAEGTDRIIDIVQAFCRAIYNIPRRIRQGFEAALQ
25710_243           GLELKRSAISLLDTIAIAVAEGTDRIIQLGQGICRAICNIPRRIRQGLEAALQ
Ce1176_A3           GIELKKSATSLLDTTAIVVVEGTDRIIGIIQAICRALLNLPRRIRQGFEAALL
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