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       ON991821
                   ACAPFRRLSLCDRNLELMN---RKKTKARHKLLLDVCLAAKFEAESLIPDHAHYVAKYG-
                                                                                                 56
       ON991924
                    ACAPYRRLSLCNKNFQKIN---NYSSNAKHNLLLDVCMAANYEAQSLIPYHAQYDEQYP-
                                                                                                 56
                    ACAPYRRI SI CNKNEOKTN --- NYSSKAKHNI LI DVCI AANHEGOSTKTHI KOYDAEYPS
        PFF0005C
                                                                                                 57
                   ACAPFRRLHLCDOHLEHIKH--D-KI-TRHNLLADVCLAAKFEAESLEKHRAKYOLTNP-
       ON991927
                                                                                                 55
                    ACAPFRRLNLCVTNLENINN--YGKI-NNDTLLADVCLAALHEGVLISADHARYKETNN-
       ON991930
                                                                                                 56
        PFF0845C
                   ACAPYRRLHVCVRNLENIND--YSKINNKHNLLVEVCLAAKYEGESITGRYPQHQETNP-
                   ACAPFRRLHLCDKNLEQIKA--QI-TTHNLLADVCMAAKFEQSIRGYHPQYDEQYP-
ACAPFRRLHVCDKNLEQIEP--I-KITNTHNLLVDVCQAAKYEGQSITRYYQQYRAQYG-
                                                                                                 55
       ON991938
       ON991943
                                                                                                 56
                   ACAPFRRLHLCDYNLEKITD--T-NTTTTHNLLVDVCLAAKYEGESLKGYHDKYNATYS-
       ON991949
                                                                                                 56
                                                                **
                                                           : *
                                   ::: :
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                                                                                                 115
                   DTNSQLCTVLARSFADIGDIVRGKDLYLGNPQE---STQRIILENNLKDIFAKIHSDVMS
DSGSTICTVLARSFADIGDIIRGKDLYLGNPQE---SAQREKLEENLKKIFEKIHDDVMK
       PFΔ0015C
                                                                                                 116
       ON991821
                                                                                                 113
       ON991924
                   GSGSTMCTMLARSFADIGDIIRGRDLFRGNNKE---KTKREKLEENLKRIFGDIYEELK-
                                                                                                 112
        PFF0005C
                   GSGHTTCTALARSFADIGDIIRGKDLYRRDKGE-----KKKLEEHLKTIFGKIHSDVT-
                                                                                                 110
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DVNANICTMLARSFADIGDIVRGKDLYRGVNGN------DKLENKLKEIFKKIHEGLTS
       ON991927
                                                                                                 108
       ON991930
                                                                                                 109
        PFF0845C
                    DTKSQLCTVLARSFADIGDIIRGKDLYRGGNTKEK--KKRKKLEENLKTIFGHIYDELKN
                                                                                                 115
       ON991938
                   GSVSTMCTMLARSFADIGDIIRGKDLYNGNNRKG-----EKLENKLKEYFEKIYKDVTR
DSPSQICTVLARSFADIGDIIRGKDLYLGDKKEK-----LKLEKKLKKYFKELHNHLEL
                                                                                                 100
       ON991943
                                                                                                 110
                   DSRSQLCTVLARSFADIGDIIRGKDLYRGNRKKNQNVTEREKLEQKLKEIFAKIHEELKN
       ON991949
                                                                                                 116
                                                                     : . ::
       PFD1245C
                   GR----N--GVKDHYQD-DNGGNYFQLREDWMTANRATVWKAITCKAD---TGNAYFR
                                                                                                 163
                   TSGSN--GR--ALQKRYK---DTDNYYELREDWWALNRDQVWKAITCNAG---GGNRYFR
TRGSN--GE--ALKTRYEN--DTGNYYKLREDWWTANRETVWKAMTCSD--DLKDASYFR
       PFΔ0015C
                                                                                                 166
       ON991821
                                                                                                165
                    ----N--EK--TLQARYKK-DEDPNFFQLREYWYANRHTVWKAMTCSD--KLANYKYFR
       ON991924
                                                                                                161
        PFF0005C
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                                                                                                164
       ON991927
                   DLKNYPTKS--AEAEERYK-DNEGNHYQLREDWWEANRQEVWKAITCDAK---G-SQYFR
                                                                                                 161
       ON991930
                   TNGRN--GE--AP-KKYYF-DPKGNFYOLREDWJYANRETVWKAIRCSAP---TDANYFR
                                                                                                 160
        PFF0845C
                   GKTNG--EE--ELQKRYRG-DKDNDFYQLREDWIDANRETVWKAITCNAG---S-YQYSQ
                                                                                                 166
                   TSTRE--KR--SALQTRYG--GDPNYYKLREDWINNNRLMWWYAITCGVK---G-NKYFR
-----R--S-KNHYOS--NDTNYFELREDWIALNRKDWKALTCEAS---G--TYFR
       ON991938
                                                                                                159
       ON991943
                                                                                                152
       ON991949
                   GKTNK--EA--A-KDHYKD--DGDNFFQLREDWWDANRETVWKALTCDAD---G--SYFR
                                                                                                164
                  PT-CSNRQGP---SQAHHYCRCNGDKPDDDK----PNTDPPTYFDYVPQYLRWFEEWA
        PFD1245C
                                                                                                213
        PFA0015C
                  QT-CGSG-----EWAKDKCRCKD------DKVPTYFDYVPQYLRWFEEWA
                                                                                                204
                  QT-CDDD---GTSSRANHKCRCKDKKGQH-----DTDQVPTYFDYVPQYLRWFEEWA
PT-CDSVDGKGP-SQAQNRCRCD--GA-----KADQVPTYFDYVPQYLRWFEEWA
       ON991821
                                                                                                213
       ON991924
                                                                                                207
                  AT-CSDSDGKGSFSQANDKCRCKDKKGK-----NTDQVPTYFDYVPQYLRWFEEWA
        PFF0005C
                                                                                                214
                  RT-CGSGNN-A--SPTQDNCRCAT------NYVPTYFDYVPQYLRWFEEWA
       ON991927
                                                                                                202
                  QTVCSGGKT----PTQGKCRCID-----FSVPTYFDYVPQYLRWFEEWA
       ON991930
                                                                                                200
                  PT-CGRGEI-P--YVTLSKCQCIA------GEVPTYFDYVPQYLRWFEEWA
        PFF0845C
                                                                                                207
                  QA-CGSGKT----PTQDDCRCPI-------YKVPTYFDYVPQYLRWFEEWA
       ON991938
                                                                                                198
       ON991943
                                                                                                192
                  AT-CGGDNK-KTTIRTPSQCRCIN-----FSVPTYFDYVPQYLRWFEEWA
       ON991949
                                                                                                207
Supplementary Fig. S1. Alignment of the DBLa sequences of Myanmar population and 3D7 strain.
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