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Gag_AF110965_BW_mod (SEQ ID NO: 63)

ATGGGCGCCCGCGCCAGCATCCTGCGCGGCGGCAAGCTGGACGCCTGGGAGCGCATCCGCC
TGCGCCCCGGCGGCAAGAAGTGCTACATGATGAAGCACCTGGTGTGGGCCAGCCGCGAGCT
GGAGAAGTTCGCCCTGAACCCCGGCCTGCTGGAGACCAGCGAGGGCTGCAAGCAGATCATC
CGCCAGCTGCACCCCGCCCTGCAGACCGGCAGCGAGGAGCTGAAGAGCCTGTTCAACACCG
TGGCCACCCTGTACTGCGTGACGAGAAGATCGAGGTCCGCGACACCAAGGAGGCCCTGGA
CAAGATCGAGGAGGAGCAGAACAAGTGCCAGCAGAAGATCCAGCAGGCCGAGGCCGCCGAC
AAGGGCAAGGTGAGCCAGAATACTACCCATCGTGAGAACCTGCAGGGCCAGATGGTGCACC
AGGCCATCAGCCCCCGCACCTGAACGCCTGGGTGAAGGTGATCGAGGAGAAGGCCTTCAG
CCCCGAGGTGATCCCCATGTTTACCGCCCTGAGCGAGGGCGCCACCCCCCAGGACCTGAAC
ACGATGTTGAACACCGTGGGCGGCCACCAGGCCGCCATGCAGATGCTGAAGGACACCATCA
ACGAGGAGGCCCGCGAGTGGGACCGCGTGACCCCGTGACGCGCGCCCCATCGCCCCCGG
CCAGATGCGCGAGCCCCGCGGCAGCGACATCGCCGGCACCAACCAGCACCTGCAGGAGCAG
ATCGCCTGGATGACCAGCAACCCCCCATCCCCGTGGGCGACATCTACAAGCGGTGGATCA
TCCTGGGCCTGAACAAGATCGTGCGGATGTACAGCCCCGTGAGCATCCTGGACATCAAGCA
GGGCCCCAAGGAGCCCTTCCGCGACTACGTGGACCGCTTCTTCAAGACCCTGCGCGCCGAG
CAGAGCACCAGGAGGTGAAGAACTGGATGACCGACACCCTGCTGGTGCAGAACGCCAACC
CCGACTGCAAGACCATCCTGCGCGCTCTCGCCCCGGCGCCAGCCTGGAGGAGATGATGAC
CGCCTGCCAGGGCGTGGGCGGCCCCAGCCACAAGGCCCGCGTGCTGGCCGAGGCGATGAGC
CAGGCCAACACCAGCGTGATGATGCAGAAGAGCAACTTCAAGGGCCCCCGGCGCATCGTCA
AGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCCGCAACTGCCGCGCCCCCGCAAGAA
GGGCTGCTGGAAGTGCGGCAAGGAGGGCCACCAGATGAAGGACTGCACCGAGCGCCAGGCC
AACTTCCTGGGCAAGATCTGGCCCAGCCACAAGGGCCGCCCCGGCAACTTCCTGCAGAGCC
GCCCCGAGCCCAACGCCCCCCCCCGCCGAGAGCTTCCGCTTCGAGGAGACCACCCCCGGCCA
GAAGCAGGAGAGCAAGGACCGCGAGACCCTGACCAGCCTGAAGAGCCTGTTTCGGCAACGAC
CCCCTGAGCCAGTAA

FIG. 1

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Gag_AF110967_BW_mod (SEQ ID NO: 64)

ATGGGCGCCCGCGCCAGCATCCTGCGCGGCGAGAAGCTGGACAAGTGGGAGAAGATCCGCC
TGCGCCCCGGCGGCAAGAAGCACTACATGCTGAAGCACCTGGTGTGGGCCAGCCGCGAGCT
GGAGGGCTTCGCCCTGAACCCCGGCCTGCTGGAGACCGCCGAGGGCTGCAAGCAGATCATG
AAGCAGCTGCAGCCCGCCCTGCAGACCGGCACCGAGGAGCTGCGCAGCCTGTACAACACCG
TGGCCACCCTGTACTGCGTGACGCGCGCATCGAGGTCCGCGACACCAAGGAGGCCCTGGA
CAAGATCGAGGAGGAGCAGAACAAGTCCCAGCAGAAGACCCAGCAGGCCAAGGAGGCCGAC
GGCAAGGTGAGCCAGAACTACCCCATCGTGCAAGAACCTGCAGGGCCAGATGGTGCACCAGG
CCATCAGCCCCCGCACCCCTGAACGCCTGGGTGAAGGTGATCGAGGAGAAGGCCTTCAGCCC
CGAGGTGATCCCCATGTTACCGCCCTGAGCGAGGGCGCCACCCCCCAGGACCTGAACACG
ATGTTGAACACCGTGGGCGGCCACCAGGCCGCCATGCAGATGCTGAAGGACACCATCAACG
AGGAGGCCGCCGAGTGGGACCGCCTGCACCCCGTGCAAGGCCGCCCCGCTGGCCCCCGGCA
GATGCGCGACCCCCGCGGCAGCGACATCGCCGCGGCCACCAGCACCTGCAGGAGCAGATC
GCCTGGATGACCAGCAACCCCCCGTGCCCGTGGGCGACATCTACAAGCGGTGGATCATCC
TGGGCCTGAACAAGATCGTGCGGATGTACAGCCCCGTGAGCATCCTGGACATCCGCCAGGG
CCCCAAGGAGCCCTTCGCGACTACGTGGACCGCTTCTTCAAGACCCTGCGCGCCGAGCAG
GCCACCCAGGACGTGAAGAACTGGATGACCGAGACCCTGCTGGTGCAAGCCCAACCCCG
ACTGCAAGACCATCCTGCGCGCTCTCGGCCCGGCGCCACCCTGGAGGAGATGATGACCGC
CTGCCAGGGCGTGGGCGGCCCCGGCCACAAGGCCCGCGTGCTGGCCGAGGCGATGAGCCAG
GCCAACAGCGTGAACATCATGATGCAGAAGAGCAACTTCAAGGGCCCCCGGCGCAACGTCA
AGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCAAGAACTGCCGCGCCCCCGCAAGAA
GGGCTGCTGGAAGTGCGGCAAGGAGGGCCACCAGATGAAGGACTGCACCGAGCGCCAGGCC
AACTTCCTGGGCAAGATCTGGCCCAGCCACAAGGGCCGCCCCGGCAACTTCCTGCAGAAC
GCAGCGAGCCCCGCCGCCCCACCGTGCCACCGCCCCCCCCCGCCGAGAGCTTCGCTTCGA
GGAGACCACCCCCGCCCCAAGCAGGAGCCCAAGGACCGCGAGCCCTACCGCGAGCCCCTG
ACCGCCCTGCGCAGCCTGTTCCGGCAGCGGCCCTGAGCCAGTAA

FIG. 2

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Env_AF110968_C_BW_opt (SEQ ID NO 65)

— → signal peptide (1-81)

ATGCGCGTGATGGGCATCCTGAAGAACTACCAGCAGTGETGGATGTGGGGCATCCTGGGCTTCTGGATGCTGATCA

\ / — → gp120/140/160 (82)

TCAGCAGCGTGGTGGGCAACCTGTGGGTGACCGTGTACTACGGCGTGCCCGTGTGGAAGGAGGCCAAGACCACCCCT

GTTCTGCACCAGCGACGCCAAGGCCTACGAGACCGAGGTGCACAACGTGTGGGCCACCCACGCCTGCGTGCCACC

GACCCCAACCCCCAGGAGATCGTGCTGGAGAACGTGACCGAGAACTTCAACATGTGGAAGAACGACATGGTGGACC

AGATGCACGAGGACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGAAGCTGACCCCCCTGTGCGTGAC

CCTGAAGTGCCGCAACGTGAACGCCACCAACAACATCAACAGCATGATCGACAACAGCAACAAGGGCGAGATGAAG

AACTGCAGCTTCAACGTGACCAACCGAGCTGCGCGACCGCAAGCAGGAGGTGCACGCCCTGTTCTACCGCCTGGACG

TGGTGCCCTGCAGGGCAACAACAGCAACGAGTACCGCCTGATCAACTGCAACACCAGCGCCATCACCAGGCCTG

CCCCAAGGTGAGCTTCGACCCCATCCCCATCCACTACTGACCCCCGCGGCTACGCCATCCTGAAGTGCAACAAC

CAGACCTTCAACGGCACCGGCCCTTGCAACAACGTGAGCAGCGTGCACTGCGCCACGGCATCAAGCCCCTGGTGA

GCACCCAGCTGTGCTGAACGGCAGCCTGGCCAAGGGCGAGATCATCATCCGCGAGGAGAACCTGGCCAACAACGC

CAAGATCATCATCGTGAGCTGAACAAGCCCTGAAGATCGTGTGCGTGCGCCCCAACACAACACCCGCAAGAGC

GTGCGCATCGGCCCCGGCCAGACCTTCTACGCCACCGCGCAGATCATCGGCGACATCCGCCAGGCCTACTGCATCA

TCAACAAGACCGAGTGGAACAGCACCTGCGAGGCGTGAGCAAGAAGCTGGAGGAGCACTTCAGCAAGAAGGCCAT

CAAGTTTCGAGCCAGCAGCGGCGGCGACCTGGAGATCACCACCCACAGCTTCAACTGCCGCGGCGAGTTCTTCTAC

TGCGACACCAGCCAGCTGTTCAACAGCACCTACAGCCCCAGCTTCAACGGCACCGAGAACAGCTGAACGGCACCA

TCACCATCACCTGCCGATCAAGCAGATCATCAACATGTGGCAGAAGGTGGGCCGCGCCATGTACGCCCCCCCCAT

CGCCGGCAACCTGACCTGCGAGAGCAACATCACCGGCCTGCTGCTGACCCGCGACGGCGGCAAGACCGGCCCCAAC

GACACCGAGATCTTCGCCCCGCGGCGGCGACATGCGCGACAACCTGGCGCAACGAGCTGTACAAGTACAAGGTGG

TGGAGATCAAGCCCCTGGGCGTGGCCCCACCGAGGCCAAGCGCCGCTGGTGGAGCGCGAGAAGCGCGCCGTGGG gp120 (1512)←\ /→(1513) gp41

CATCGGCGCCGTGTTCTCTGGGCTTCTCTGGGCGCCGCGGCGAGCAACATGGGCGCCGCCAGCATCACCTGACCGTG

CAGGCCCCGCTGCTGCTGAGCGGCATCGTGAGCAGCAGAACCACTGCTGCGCGCCATCGAGGCCAGCAGCACCC

TGCTGCAGCTGACCGTGTGGGGCATCAAGCAGCTGCAGACCCGCATCCTGGCCGTGGAGCGCTACCTGAAGGACCA

GCAGCTGCTGGGCATCTGGGGTGCAGCGGCAAGCTGATCTGCACCAACCGCGTGCCTGGAACAGCAGCTGGAGC

AACCAGCAGCCACGACGAGATCTGGGACAACATGACCTGGATGCAGTGGGACCGCGAGATCAACAACCTACACCGACA

CCATCTACCGCTGCTGGAGGAGAGCCAGAACCGAGCAGGAGAAGAACGAGAAGGACCTGTGGCCCTGGACAGCTG

GCAGAACCTGTGGAACCTGTTTCTGAGCATCACCAACTGGCTGTGGTACATCAAGATCTTCATCATGATCGTGGGCGGC

CTGATCGGCGCTGCGCATCATCTTCGCGCTGCTGAGCATCGTGAACCGCGTGCGCCAGGGTACAGCCCCCTGCCCT

TCCAGACCCCTGACCCCCAACCCCCGCGAGCCCCGACCGCCTGGGCCGATCGAGGAGGAGGGCGGCGAGCAGGACCG

CGGCCGCGCATCCGCTGGTGGAGCGGCTTCTGGCCCTGGCCTGGGACGACCTGCGCAGCCTGTGCTGTTTCTGAG

TACCACCGCCTGCGCGACTTCATCCTGATCGCCGCCCCGCTGCTGGAGCTGCTGGGCCAGCGCGGCTGGGAGGCC

TGAAGTACCTGGGCGAGCCTGGTGCAGTACTGGGGCCTGGAGCTGAAGAAGAGCGCCATCAGCCTGCTGGACACCAT

CGCCATCGCCGTGGCCGAGGGCACCGACCGCATCATCGAGTTTATCCAGCGCATCTGCCGCGCCATCCGCAACATC

CCCCGCGCATCCGCCAGGGCTTCGAGGCCGCCCTGCAGTAA gp160, gp41 (2547)←- \

FIG. 3

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Env_Af110975_C_BW_opt (SEQ ID NO: 66)
 -> signal peptide (1-72) \ / ->
 ATGCGCGTGC GCGCATCCTGCGCAGCTGGCAGCAGTGGTGGATCTGGGGCATCCTGGGCTTCTGGATCTGCAGCG
 gp120/140/160 (72)
 GCCTGGGCAACCTGTGGGTGACCGTGTACGACGGCGTGCCCGTGTGGCGGAGGCCAGCACCACCTGTTCTGCGC
 CAGCGACGCCAAGGCCTACGAGAAGGAGGTGCACAACGTGTGGGCCACCCACGCCTGCGTGCCACCGACCCCAAC
 CCCAGGAGATCGAGCTGGACAACGTGACCGAGAACTTCAACATGTGGAAGAACGACATGGTGGACCAGATGCACG
 AGGACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCCGCGTGAAGCTGACCCCCCTGTGCGTGACCCTGAAGTG
 CACCAACTACAGCACCAACTACAGCAACCCATGAACGCCACCAGCTACAACAACAACACCCAGGAGATCAAG
 AACTGCACCTTCAACATGACCACCGAGCTGCGCGACAAGAAGCAGCAGGTGTACGCCCTGTTCTACAAGCTGGACA
 TCGTGCCCTGAACAGCAACAGCAGCGAGTACCGCTGATCAACTGCAACACCAGCGCCATCACCAGGCCTGCCC
 CAAGGTGAGCTTCGACCCCATCCCATCCACTACTGCGCCCCCGCGGCTACGCCATCCTGAAGTGCAAGAACAAC
 ACCAGCAACGGCACCGGCCCTGCCAGAACGTGAGCACCGTGCAGTGCACCCAGGCATCAAGCCCGTGGTGAGCA
 CCCCCCTGCTGCTGAACGGCAGCCTGGCCGAGGGCGGCGAGATCATCATCCGCGAGCAAGAACCTGAGCAACACGC
 CTACACCATCATCGTGACCTGAACGACAGCGTGGAGATCGTGTGCACCCGCCCAACAACAACACCCGCAAGGGC
 ATCCGATCGGCCCCGGCCAGACCTTCTACGCCACCAGAACATCATCGGCGACATCCGCCAGGCCCACTGCAACA
 TCAGCGCCGGCGAGTGGAACAAGGCCGTGAGCGCGTGCAGCGCAAGCTGCGCGAGCACTTCCCCAACAAGACCAT
 CGAGTTCAGCCAGCAGCGGGCGGACCTGGAGATCACCACCCACAGCTTCAACTGCCGCGGCGAGTTCTTCTAC
 TGCAACACCAGCAAGCTGTTCAACAGCAGCTACAACGGCACCAGCTACCGGGCACCGAGAGCAACAGCAGCATCA
 TCACCCTGCCCTGCCGATCAAGCAGATCATCGACATGTGGCAGAAGGTGGGCCGCGCCATCTACGCCCCCCCCAT
 CGAGGGCAACATCACCTGCAGCAGCAGCATCACCGGCTGCTGCTGGCCGCGACGGCGGCTGGACAACATCACC
 ACCGAGATCTTCCGCCCCAGGGCGGCGACATGAAGGACAACCTGGCGCAACGAGCTGTACAAGTACAAGTGGTGG
 gp120 (1509) <- \ / -> (1510) gp41
 AGATCAAGCCCTGGGCGTGGCCCCACCGAGGCCAAGCGCCGCTGGTGGAGCGGAGAAGCGCGCCGTGGGCAT
 CGGCGCGTGATCTTCGGCTTCTGGGCGCCCGGGCAGCAACATGGGCGCCGCGAGCATCACCTGACCGCCAG
 GCCCGCCAGCTGCTGAGCGGCATCGTGAGCAGCAGAGCAACCTGCTGCGGCCATCGAGGCCAGCAGCACATGC
 TGCAGCTGACCGTGTGGGGCATCAAGCAGCTGCAGGCCCGCGTGTGGCCATCGAGCGCTACCTGAAGGACCAGCA
 GCTGCTGGGCATCTGGGGCTGCAGCGCAAGCTGATCTGCACCACCACCGTGGCTGGAACAGCAGCTGGAGCAAC
 AAGACCCAGGGCGAGATCTGGGAGAACATGACCTGGATGCAGTGGGACAAGGAGATCAGCAACTACACCGGCATCA
 TCTACCGCTGCTGGAGGAGAGCCAGAACCAGCAGGAGCAGAACGAGAAGGACCTGCTGGCCCTGGACAGCCGCAA
 gp140 (2022) <- \ /
 CAACCTGTGGAGCTGGTTCAACATCAGCAACTGGCTGTGGTACATCAAGATCTTCATCATGATCGTGGGCGGCTG
 ATCGGCCTGCGCATCATCTTCGCCGTGCTGAGCATCGTGAACCGCGTGCGCCAGGGCTACAGCCCCCTGAGCTTCC
 AGACCCTGACCCCCAACCCCGCGGCTGGACCGCCTGGGCCGATCGAGGAGGAGGGCGGCGAGCAGGACCGCGA
 CCGCAGCATCCGCTGGTGCAGGGCTTCTGGCCCTGGCCTGGGACGACCTGCGCAGCCTGTGCTTCTAGCTAC
 CACCGCTGCGGACCTGATCCTGGTGACCGCCCGTGGTGGAGCTGCTGGGCCGAGCAGCCCCCGGGCCTGC
 AGCGCGGTGGGAGGCCCTGAAGTACCTGGGCGCCTGGTGCAGTACTGGGCCCTGGAGCTGAAGAAGAGCGCCAC
 CAGCCTGCTGGACAGCATCGCCATCGCGTGGCCGAGGGCACCGACCGCATCATCGAGGTGATCCAGCGCATCTAC
 gp160, gp41 (2565) <- \ /
 CGCGCCTTCTGCAACATCCCCCGCGGTGCGCCAGGGCTTCGAGGCCGCGCTGCAGTAA

FIG. 4

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Gag_AF110965_BW_opt (SEQ ID NO: 67)
ATGGGCGCCCGCGCCAGCATCCTGCGCGGGCGCAAGCTGGACGCCTGGGAGCGCATCCGCTGCGCCCCGG
CGGCAAGAAGTGCTACATGATGAAGCACCTGGTGTGGGCCAGCCGCGAGCTGGAGAAGTTCGCCCTGAACC
CCGCGCTGCTGGAGACCAGCGAGGGCTGCAAGCAGATCATCCGCCAGCTGCACCCCGCCCTGCAGACCGGC
AGCGAGGAGCTGAAGAGCCTGTTCAACACCGTGGCCACCCTGTACTGCGTGCACGAGAAGATCGAGGTGCG
CGACACCAAGGAGGCCCTGGACAAGATCGAGGAGGAGCAGAACAAGTGCCAGCAGAAGATCCAGCAGGCCG
AGGCCCGCGACAAGGGCAAGGTGAGCCAGAACTACCCCATCGTGCAGAACCTGCAGGGCCAGATGGTGCAC
CAGGCCATCAGCCCCCGCACCCCTGAACGCCTGGGTGAAGGTGATCGAGGAGAAGGCCTTCAGCCCCGAGGT
GATCCCCATGTTTACCGCCCTGAGCGAGGGCGCCACCCCCAGGACCTGAACACCATGCTGAACACCGTGG
GCGGCCACCAGGCCCGCCATGCAGATGCTGAAGGACACCATCAACGAGGAGGCCGCCGAGTGGGACCGCGTG
CACCCCGTGACGCGCGGCCCATCGCCCCCGGCCAGATGCGCGAGCCCCGCGGCAGCGACATCGCCGGCAC
CACCAGCACCCCTGCAGGAGCAGATCGCCTGGATGACCAGCAACCCCCCATCCCCGTGGGCGACATCTACA
AGCCCTGGATCATCCTGGGCCTGAACAAGATCGTGCGCATGTACAGCCCCGTGAGCATCCTGGACATCAAG
CAGGGCCCCAAGGAGCCCTTCCGCGACTACGTGGACCGCTTCTTCAAGACCCTGCGCGCCGAGCAGAGCAC
CCAGGAGGTGAAGAACTGGATGACCGACACCCTGCTGTTGCAGAACGCCAACCCCGACTGCAAGACCATCC
TGCGCGCCCTGSGCCCCGGCGCCAGCCTGGAGGAGATGATGACCGCCTGCCAGGGCGTGGGCGGCCCCAGC
CACAAGGCCCGCGTGTCTGGCCGAGGCCATGAGCCAGGCCAACACCAGCGTGATGATGCAGAAGAGCAACTT
CAAGGGCCCCCGCGCATCGTGAAGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCCGCAACTGCCGCG
CCCCCGCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAGGGCCACCAGATGAAGGACTGCACCGAGCGCCAG
GCCAACTTCTGGGCAAGATCTGGCCCAGCCACAAGGGCCGCCCGGCAACTTCTGTCAGAGCCGCCCCGA
GCCACCGCCCCCCCCCGCCGAGAGCTTCCGCTTCGAGGAGACCACCCCGGCCAGAAGCAGGAGAGCAAGG
ACCGCGAGACCCTGACCAGCCTGAAGAGCCTGTTTCGGCAACGACCCCTGAGCCAGTAA

FIG. 5

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Gag AF110967_BW_Opt (SEQ ID NO: 68)

ATGGGCGCCCGCGCCAGCATCCTGCGCGGCGAGAAGCTGGACAAGTGGGAGAAGATCCGCCTGCGCCCCGG
CGGCAAGAAGCACTACATGCTGAAGCACCTGGTGTGGGCCAGCCGCGAGCTGGAGGGCTTCGCCCTGAACC
CCGGCCTGCTGGAGACCGCCGAGGGCTGCAAGCAGATCATGAAGCAGCTGCAGCCCGCCCTGCAGACCGGC
ACCGAGGAGCTGCGCAGCCTGTACAACACCGTGGCCACCCTGTACTGCGTGACGCCGGCATCGAGGTGCG
CGACACCAAGGAGGCCCTGGACAGATCGAGGAGGAGCAGAACAAGAGCCAGCAGAAGACCCAGCAGGCCA
AGGAGGCCGACGGCAAGGTGAGCCAGAACTACCCCATCGTGCAAGAACCTGCAGGGCCAGATGGTGCACCAG
GCCATCAGCCCCCGCACCTGAACGCCTGGGTGAAGGTGATCGAGGAGAAGGCCTTCAGCCCCGAGGTGAT
CCCCATGTTACCGCCCTGAGCGAGGGCGCCACCCCCAGGACCTGAACACCATGCTGAACACCGTGGGCG
GCCACCAGGCCGCCATGCAGATGCTGAAGGACACCATCAACGAGGAGGCCGCCGAGTGGGACCGCCTGCAC
CCCGTGCAAGGCCGCCCGCCCGTGGCCCCCGGCCAGATGCGCGACCCCCGCGGCAGCGACATCGCCGGCGCCAC
CAGCACCTGCAGGAGCAGATCGCCTGGATGACCAGCAACCCCCCGTGCCCGTGGGCGACATCTACAAGC
GCTGGATCATCCTGGGCCTGAACAAGATCGTGCGCATGTACAGCCCCGTGAGCATCCTGGACATCCGCCAG
GGCCCCAAGGAGCCCTTCGCGACTACGTGGAACCGCTTCTTCAAGACCTGCGCGCCGAGCAGGCCACCCA
GGACGTGAAGAACTGGATGACCGAGACCCTGCTGGTGCAGAACGCCAACCCGACTGCAAGACCATCCTGC
GCGCCCTGGGCCCCGGCGCCACCCTGGAGGAGATGATGACCGCCTGCCAGGGCGTGGGCGGCCCCGGCCAC
AAGGCCCCGCTGCTGGCCGAGGCCATGAGCCAGGCCAACAGCGTGACATCATGATGCAGAAGAGCAACTT
CAAGGGCCCCCGCGCAACGTGAAGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCAAGAACTGCCGCG
CCCCCGCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAGGGCCACCAGATGAAGGACTGCACCGAGCGCCAG
GCCAACTTCTGGGCAAGATCTGGCCAGCCACAAGGGCCGCCCGGCAACTTCTGCAGAACCGCAGCGA
GCCCCGCGCCCCACCCTGCCACCGCCCCCCCCCGCGAGAGCTTCCGCTTCGAGGAGACCACCCCCGCC
CCAAGCAGGAGCCCAAGGACCGCGAGCCCTACCGCGAGCCCCTGACCGCCCTGCGCAGCCTGTTCCGGCAGC
GGCCCCCTGAGCCAGTAA

FIG. 6