

Gag_AF110965_BW_mod (SEQ ID NO: 63)

ATGGGCGCCCGCGCCAGCATCCTGCGCGGCGGCAAGCTGGACGCCTGGGAGCGCATCCGCC
TGCGCCCCGGCGGCAAGAAGTGCTACATGATGAAGCACCTGGTGTGGGCCAGCCGCGAGCT
GGAGAAGTTCGCCCTGAACCCCGGCCTGCTGGAGACCAGCGAGGGCTGCAAGCAGATCATC
CGCCAGCTGCACCCCGCCCTGCAGACCGGCAGCGAGGAGCTGAAGAGCCTGTTCAACACCG
TGGCCACCCTGTACTGCGTGACGAGAAGATCGAGGTCCGCGACACCAAGGAGGCCCTGGA
CAAGATCGAGGAGGAGCAGAACAAGTGCCAGCAGAAGATCCAGCAGGCCGAGGCCGCCGAC
AAGGGCAAGGTGAGCCAGAACTACCCCATCGTGCAACCTGCAGGGCCAGATGGTGCACC
AGGCCATCAGCCCCCGCACCCCTGAACGCCTGGGTGAAGGTGATCGAGGAGAAGGCCCTTCAG
CCCCGAGGTGATCCCCATGTTACCGCCCTGAGCGAGGGCGCCACCCCCCAGGACCTGAAC
ACGATGTTGAACACCGTGGGCGGCCACCGGCCCATGCAGATGCTGAAGGACACCATCA
ACGAGGAGGCCCGCGAGTGGGACCGCGTGACCCCGTGACGCCGGCCCCATCGCCCCGG
CCAGATGCGCGAGCCCCGCGGCAGCGACATCGCCGGCACCAACCAGCACCTGCAGGAGCAG
ATCGCCTGGATGACCAGCAACCCCCCATCCCCGTGGGCGACATCTACAAGCGGTGGATCA
TCCTGGGCCTGAACAAGATCGTGCGGATGTACAGCCCCGTGAGCATCCTGGACATCAAGCA
GGGCCCCAAGGAGCCCTTCCGCGACTACGTGGACCGCTTCTTCAAGACCCTGCGCGCCGAG
CAGAGCACCCAGGAGGTGAAGAACTGGATGACCGACACCCTGCTGGTGCAGAACGCCAACC
CCGACTGCAAGACCATCCTGCGCGCTCTCGGCCCCGGCGCCAGCCTGGAGGAGATGATGAC
CGCCTGCCAGGGCGTGGGCGGCCCCAGCCACAAGGCCCGCGTGCTGGCCGAGGCGATGAGC
CAGGCCAACACCAGCGTGATGATGCAGAAGAGCAACTTCAAGGGCCCCCGGCGCATCGTCA
AGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCCGCAACTGCCGCGCCCCCGCAAGAA
GGGCTGCTGGAAAGTGCGGCAAGGAGGGCCACCAGATGAAGGACTGCACCGAGCGCCAGGCC
AACTTCCTGGGCAAGATCTGGCCCAGCCACAAGGGCCGCCCCGGCAACTTCCTGCAGAGCC
GCCCCGAGCCCAACGCCCCCCCCCGCCGAGAGCTTCCGCTTCGAGGAGACCACCCCCGGCCA
GAAGCAGGAGAGCAAGGACCGCGAGACCCTGACCAGCCTGAAGAGCCTGTTCGGCAACGAC
CCCCTGAGCCAGTAA

FIG. 1

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Gag_AF110967_BW_mod (SEQ ID NO: 64)

ATGGGCGCCCGCGCCAGCATCCTGCGCGGCGAGAAGCTGGACAAGTGGGAGAAGATCCGCC
TGCGCCCGCGCGCAAGAAGCACTACATGCTGAAGCACCTGGTGTGGGCCAGCCGCGAGCT
GGAGGGCTTCGCCCTGAACCCCGGCCTGCTGGAGACCGCCGAGGGCTGCAAGCAGATCATG
AAGCAGCTGCAGCCCGCCCTGCAGACCGGCACCGAGGAGCTGCGCAGCCTGTACAACACCG
TGGCCACCCTGTACTGCGTGCACGCCGGCATCGAGGTCCGCGACACCAAGGAGGCCCTGGA
CAAGATCGAGGAGGAGCAGAACAAGTCCCAGCAGAAGACCCAGCAGGCCAAGGAGGCCGAC
GGCAAGGTGAGCCAGAACTACCCCATCGTGCAGAACCTGCAGGGCCAGATGGTGCACCAGG
CCATCAGCCCCCGCACCCCTGAACGCCTGGGTGAAGGTGATCGAGGAGAAGGCCTTCAGCCC
CGAGGTGATCCCCATGTTACCGCCCTGAGCGAGGGCGCCACCCCCCAGGACCTGAACACG
ATGTTGAACACCGTGGGCGGCCACCAGGCCGCCATGCAGATGCTGAAGGACACCATCAACG
AGGAGGCCGCCGAGTGGGACCGCCTGCACCCCGTGCAGGCCGGCCCCGTGGCCCCCGGCCA
GATGCGCGACCCCCGCGGCAGCGACATCGCCGGCGCCACCAGCACCCCTGCAGGAGCAGATC
GCCTGGATGACCAGCAACCCCCCGTGGCCGTGGGCGACATCTACAAGCGGTGGATCATCC
TGGGCCTGAACAAGATCGTGCGGATGTACAGCCCCGTGAGCATCCTGGACATCCGCCAGGG
CCCCAAGGAGCCCTTCGCGACTACGTGGACCGCTTCTTCAAGACCCCTGCGCGCCGAGCAG
GCCACCCAGGACGTGAAGAACTGGATGACCGAGACCCTGCTGGTGCAGAACGCCAACCCCG
ACTGCAAGACCATCCTGCGCGCTCTCGGCCCCGGCGCCACCCTGGAGGAGATGATGACCGC
CTGCCAGGGCGTGGGCGGCCCCGGCCACAAGGCCCGCGTCTGGCCGAGGCGATGAGCCAG
GCCAACAGCGTGAACATCATGATGCAGAAGAGCAACTTCAAGGGCCCCCGGCGCAACGTCA
AGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCAAGAACTGCCGCGCCCCCGCAAGAA
GGGCTGCTGGAAGTGCGGCAAGGAGGGCCACCAGATGAAGGACTGCACCGAGCGCCAGGCC
AACTTCCTGGGCAAGATCTGCCCCAGCCACAAGGGCGGCCCCGGCAACTTCCTGCAGAACC
GCAGCGAGCCCGCCGCCCCACCGTGCCACCGCCCCCCCCCGCGAGAGCTTCGCTTCGA
GGAGACCACCCCCGCCCCAAGCAGGAGCCCAAGGACCGCGAGCCCTACCGCGAGCCCCTG
ACCGCCCTGCGCAGCCTGTTCCGGCAGCGGCCCCCTGAGCCAGTAA

FIG. 2

Env_AF110968_C_BW_opt (SEQ ID NO 65)

--> signal peptide (1-81)

ATGCGCGTGATGGGCATCCTGAAGAACTACCAGCAGTGETGGATGTGGGGCATCCTGGGCTTCTGGATGCTGATCA
\/--> gp120/140/160 (82)

TCAGCAGCGTGTTGGGCAACCTGTGGGTGACCGTGACTACGGCGTGCCCGTGTGGAAGGAGGCCAAGACCACCT

GTTCTGCACCAGCGACGCCAAGGCCTACGAGACCGAGGTGCACAACGTGTGGGCCACCCACGCCTGCGTGCCCAAC

GACCCCAACCCCCAGGAGATCGTGCTGGAGAACGTGACCGAGAACTTCAACATGTGGAAGAACGACATGTTGGACC

AGATGCACGAGGACATCATCAGCCTGTGGGACCGAGCCTGAAGCCCTGCGTGAAGCTGACCCCCCTGTGCGTGAC

CCTGAAGTGCCGCAACGTGAACGCCACCAACAACATCAACAGCATGATCGACAACAGCAACAAGGGCGAGATGAAG

AACTGCAGCTTCAACGTGACCAACGAGCTGCGCGACCGCAAGCAGGAGGTGCACGCCCTGTTCTACCGCCTGGACG

TGTTGCCCTGACGGGCAACAACAGCAACGAGTACCGCCTGATCAACTGCAACACCAGCGCCATCACCAGGCCTG

CCCCAAGGTGAGCTTCGACCCCCATCCCCATCCACTACTGCACCCCCGCGGCTACGCCATCCTGAAGTGCAACAAC

CAGACCTTCAACGGCACCGCCCCCTGCAACAACGTGAGCAGCGTGCACTGCGCCCCACGGCATCAAGCCCGTGGTGA

GCACCCAGCTGCTGCTGAACGGCAGCCTGGCCAAGGGCGAGATCATCATCCGCGAGCGAGAACCTGGCCAACAACGC

CAAGATCATCATCGTGAGCTGAACAAGCCCGTGAAGATCGTGTGCGTGCGCCCCAACAACAACACCCGCAAGAGC

GTGCGCATCGGCCCCGCGCCAGACCTTCTACGCCACCGGCGAGATCATCGGCGACATCCGCCAGGCCTACTGCATCA

TCAACAAGACCGAGTGGAACAGCACCTGCAAGGCGTGAGCAAGAAGCTGGAGGAGCACTTCAGCAAGAAGGCCAT

CAAGTTGAGGCCAGCAGCGCGGCGACCTGGAGATCAACCCACAGCTTCAACTGCGCGGCGAGTTCTTCTAC

TGCGACACCAGCCAGCTGTTCAACAGCACCTACAGCCCCAGCTTCAACGGCACCGAGAACAAGCTGAACGGCACCA

TCACCATCACCTGCCGCATCAAGCAGATCATCAACATGTGGCAGAAGGTGGGCCCGGCCATGTACGCCCCCCCCAT

CGCCGGCAACCTGACCTGCGAGAGCAACATCAACGGCCTGTGCTGACCCGCGACGGCGCAAGACCGGCCCCAAC

GACACCGAGATCTTCCGCCCCGGCGGCGGACATGCGCGCAACTGGCGCAACGAGCTGTACAAGTACAAGGTGG

TGGAGATCAAGCCCCGTGGGCGTGCCCCCAACGAGGCCAAGCGCCGCTGTTGGAGCGCGAGAAGCGCGCGTGGG gp120 (1512)<\/-->(1513) gp41

CATCGGCGCCGTGTTCTGGGCTTCTGGGCGCGCGCGGCGAGCACCATGGGCGCGCCAGCATCACCTGACCGTG

CAGGCCCGCCTGCTGCTGAGCGGCATCGTGAGCAGCAGAACAACCTGCTGCGCGCCATCGAGGCCCGAGCAGCACC

TGCTGCAGCTGACCGTGTTGGGCATCAAGCAGCTGCAGACCCGCATCCTGGCCGTGGAGCGCTACCTGAAGGACCA

GCAGCTGCTGGGCATCTGGGCTGCAGCGGCAAGCTGATCTGCACACCGCCGTGCCCTGGAACAGCAGCTGGAGC

AACCGCAGCCACGACGAGATCTGGGACAACATGACCTGGATGCAGTGGGACCGCGAGATCAACAACCTACACCGACA

CCATCTACCGCCTGCTGGAGGAGAGCCAGAACGAGCAGGAGAGACGAGAGAGGACCTGCTGGCCCTGGACAGCTG

GCAGAACCTGTGGAACCTGTTTCAGCATCACCAACTGGCTGTGGTACATCAAGATCTTCATCATGATCGTGGGCGGC
gp140 (2025)<\/-->

CTGATCGSCCTGCGCATCATCTTCGCCCTGCTGAGCATCGTGAACCGCGTGCGCCAGGGCTACAGCCCCCTGCCCT

TCCAGACCCTGACCCCCAACCCCCGCGAGCCCGACCGCCTGGGCGCATCGAGGAGGAGGGCGGCGAGCAGGACCG

CGGCGCGAGCATCCGCTGTTGAGCGGCTTCTGGCCCTGGCCTGGGACGACCTGCGCAGCCTGTGCTGTTTCAGC

TACCACCGCCTGCGCGACTTCATCCTGATCGCCGCCCGCGTGTGGAGCTGCTGGGCCAGCGCGCTGGGAGGCC

TGAAGTACCTGGGCAGCCTGGTGCAGTACTGGGGCTGGAGCTGAAGAAGAGCGCCATCAGCCTGCTGGACACCAT

CGCCATCGCCGTGGCCGAGGGCACCGACCGCATCATCGAGTTTCATCCAGCGCATCTGCCGCGCCATCCGCAACATC

gp160, gp41 (2547)<\/-->
CCCCGCGCATCCGCCAGGGCTTCGAGGCCGCCCTGCAGTAA

Env_AF110975_C_BW_opt (SEQ ID NO: 66)
 --> signal peptide (1-72) \ / ->
 ATGCGCGTGGCGCGCATCCTGCGCAGCTGGCAGCAGTGGTGGATCTGGGGCATCCTGGGCTTCTGGATCTGCAGCG
 gp120/140/160 (72)
 GCCTGGGCAACCTGTGGGTGACCGGTACGACGGCGTGCCCGTGTGGCGCGAGGCCAGCACCACCTGTTCTGCGC
 CAGCGACGCCAAGGCCTACGAGAAGGAGGTGCACAACGTGTGGGCCACCCACGCCTGCGTGCCACCGACCCCAAC
 CCCCAGGAGATCGAGCTGGACAACGTGACCGAGAACTTCAACATGTGGAAGAACGACATGGTGGACCAGATGCACG
 AGGACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCCCGCGTGAAGCTGACCCCCCTGTGCGTGACCCCTGAAGTG
 CACCAACTACAGCACCAACTACAGCAACACCATGAACGCCACCAGCTACAACAACAACACCACCGAGGAGATCAAG
 AACTGCACCTTCAACATGACCAACCGAGCTGCGCGACAAGAAGCAGCAGGTGTACGCCCTGTTCTACAAGCTGGACA
 TCGTGCCCTGAACAGCAACAGCAGCGAGTACCGCCTGATCAACTGCAACACCAGCGCCATCACCCAGGCCTGCCC
 CAAGGTGAGCTTCGACCCCATCCCATCCACTACTGCGCCCCCGCGGCTACGCCATCCTGAAGTGAAGAACAAC
 ACCAGCAACGGCACCGGCCCTGCCAGAACGTGAGCACCGTGCAGTGCACCCACGGCATCAAGCCCGTGGTGAACA
 CCCCCCTGTGCTGAACGGCAGCCTGGCCGAGGGCGGCGAGATCATCATCCGAGCAAGAACCTGAGCAACAACGC
 CTACACCATCATCGTGACCTGAACGACAGCGTGGAGATCGTGTGACCCCGCCCCAACACAACACCCGCAAGGGC
 ATCCGCATCGGCCCCGGCCAGACCTTCTACGCCACCGAGAACATCATCGGCGACATCCGCCAGGCCCCACTGCAACA
 TCAGCGCCGGCGAGTGAACAAGGCCGTGAGCGCGTGAGCGCAAGCTGCGCGAGCACTTCCCCAACAGACCAT
 CGAGTTCCAGCCAGCAGCGGCGGCGACCTGGAGATCACCAACCCACAGCTTCAACTGCCGCGGCGAGTTCTTCTAC
 TGCAACACCAGCAAGCTGTTCAACAGCAGCTACAACGGCACCGCTACCGCGGCACCGAGAGCAACAGCAGCATCA
 TCACCCTGCCCTGCCGCATCAAGCAGATCATCGACATGTGGCAGAAGGTGGGCGCGCCATCTACGCCCCCCCCAT
 CGAGGGCAACATCACCTGCAGCAGCAGCATCACCGCCTGCTGCTGGCCCGCAGCGGCGCCTGGACAACATCACC
 ACCGAGATCTTCCGCCCCAGGGCGGCGCATGAAGGCAACTGGCGCAACGAGCTGTACAAGTACAAGGTGGTGG
 gp120 (1509) <- \ / -> (1510) gp41
 AGATCAAGCCCTGGGCGTGGCCCCACCGAGGCCAAGCGCGCGTGGTGGAGCGGAGAGCGCGCGTGGGCAT
 CGGCGCGTGATCTTCGGCTTCTGGGCGCGCCCGCAGCAACATGGGCGCCGCCAGCATCACCTGACCGCCAG
 GCCCGCCAGCTGCTGAGCGGCATCGTGACGAGCAGAGCAACCTGCTGCGCGCCATCGAGGCCAGCAGCATGC
 TGCAGCTGACCGTGTGGGGCATCAAGCAGCTGCAGGCCCGCGTGTGGCCATCGAGCGCTACCTGAAGGACCAGCA
 GCTGCTGGGCATCTGGGCTGCAGCGGCAAGCTGATCTGCACCACCACCGTGGCCCTGGAACAGCAGCTGGAGCAAC
 AAGACCCAGGGCGAGATCTGGGAGAACATGACCTGGATGCAGTGGGACAAGGAGATCAGCAACTACACCGGCATCA
 TCTACCGCCTGCTGGAGGAGAGCCAGAACAGCAGGAGCAGAACGAGAAGGACCTGCTGGCCCTGGACAGCCGCAA
 CAACCTGTGGAGCTGGTTCAACATCAGCAACTGGCTGTGGTACATCAAGATCTTCATCATGATCGTGGGCGGCCGTG
 ATCGGCCTGCGCATCATCTTCGCCGTGCTGAGCATCGTGAACCGGTGCGCCAGGGCTACAGCCCCCTGAGCTTCC
 AGACCCTGACCCCCAACCCCGCGGCCTGGACCGCCTGGGCCGCATCGAGGAGGAGGGCGGCGAGCAGGACCGCGA
 CCGCAGCATCCGCTGGTGAGGGCTTCTGGCCCTGGCCTGGGACGACCTGCGCAGCCTGTGCTGTTTCAAGTAC
 CACCGCCTGCGCGACCTGATCCTGGTGACCGCCCGCGTGGTGGAGCTGCTGGGCCGAGCAGCCCCCGCGCCTGC
 AGCGCGGCTGGGAGGCCCTGAAGTACCTGGGCGACCTGGTGCAGTACTGGGCCCTGGAGCTGAAGAAGAGCGCCAC
 CAGCCTGCTGGACAGCATCGCCATCGCCGTGGCCGAGGGCACCGACCGCATCATCGAGGTGATCCAGCGCATCTAC
 gp160, gp41 (2565) <- \ /
 CGCGCCTTCTGCAACATCCCCCGCGCGTGCAGGAGGGCTTCGAGGCCCGCCTGCAGTAA

Gag_AF110965_BW_opt (SEQ ID NO: 67)

ATGGGCGCCCCGCGCCAGCATCCTGCGCGGCGGCAAGCTGGACGCCTGGGAGCGCATCCGCGCTGCGCCCCGG
CGGCAAGAAGTGCTACATGATGAAGCACCTGGTGTGGGCCAGCCGCGAGCTGGAGAAGTTGCGCCCTGAACC
CCGGCCTGCTGGAGACCAGCGAGGGCTGCAAGCAGATCATCCGCCAGCTGCACCCCGCCCTGCAGACCGGC
AGCGAGGAGCTGAAGAGCCTGTTCAACACCGTGGCCACCCTGTACTGCGTGACGAGAAGATCGAGGTGCG
CGACACCAAGGAGGCCCTGGACAAGATCGAGGAGGAGCAGAACAGTGCCAGCAGAAGATCCAGCAGGCCG
AGGCCGCGGACAAGGGCAAGGTGAGCCAGAACTACCCCATCGTGAGAACCTGCAGGGCCAGATGGTGAC
CAGGCCATCAGCCCCCGCACCCCTGAACGCCTGGGTGAAGGTGATCGAGGAGAAGGCCCTTCAGCCCCGAGGT
GATCCCCATGTTACCGCCCTGAGCGAGGGCGCCACCCCCAGGACCTGAACACCATGCTGAACACCGTGG
GCGGCCACCAGGCCCGCCATGCAGATGCTGAAGGACACCATCAACGAGGAGGCCCGCCGAGTGGGACCGCGTG
CACCCCGTGACGCGCGGCCCATCGCCCCCGGCCAGATGCGCGAGCCCCGCGGCAGCGACATCGCCGGCAC
CACCAGCACCTGCAGGAGCAGATCGCCTGGATGACCAGCAACCCCCCATCCCGTGGGCGACATCTACA
AGCCTTGATCATCCTGGGCCTGAACAAGATCGTGCGCATGTACAGCCCCGTGAGCATCCTGGACATCAAG
CAGGGCCCCAAGGAGCCCTTCGCGACTACGTGGACCGCTTCTTCAAGACCCTGCGCGCCGAGCAGAGCAC
CCAGGAGGTGAAGAACTGGATGACCGACACCCTGCTGGTGCAGAACGCCAACCCCGACTGCAAGACCATCC
TGCGCGCCCTGGGCCCCGCGCCAGCCTGGAGGAGATGATGACCGCCTGCCAGGGCGTGGGCGGCCCCAGC
CACAAGGCCCGCGTGCTGGCCGAGGCCATGAGCCAGGCCAACACCAGCGTGATGATGCAGAAGAGCAACTT
CAAGGGCCCCCGCGCATCGTGAAGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCCGCAACTGCCCGG
CCCCCGCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAGGGCCACCAGATGAAGGACTGCACCGAGCGCCAG
GCCAACTTCCTGGGCAAGATCTGGCCCAGCCACAAGGGCCGCCCCGGCAACTTCCTGCAGAGCCGCCCCGA
GCCACCGCCCCCCCCGCGGAGAGCTTCGCTTCGAGGAGACCAACCCCGGCCAGAAGCAGGAGAGCAAGG
ACCGCGAGACCCTGACCAGCCTGAAGAGCCTGTTGGGCAACGACCCCTGAGCCAGTAA

FIG. 5

Gag AF110967_BW_Opt (SEQ ID NO: 68)

ATGGGCGCCCGCGCCAGCATCCTGCGCGGCGAGAAGCTGGACAAGTGGGAGAAGATCCGCCTGCGCCCCGG
CGGCAAGAAGCACTACATGCTGAAGCACCTGGTGTGGGCCAGCCGCGAGCTGGAGGGCTTCGCCCTGAACC
CCGGCCTGCTGGAGACCGCCGAGGGCTGCAAGCAGATCATGAAGCAGCTGCAGCCCCGCTTCAGACCGGC
ACCGAGGAGCTGCGCAGCCTGTACAACACCGTGGCCACCCTGTACTGCGTGACGCCGGCATCGAGGTGCG
CGACACCAAGGAGGCCCTGGACAAGATCGAGGAGGAGCAGAACAAGAGCCAGCAGAAGACCCAGCAGGCCA
AGGAGGCCGACGGCAAGGTGAGCCAGAATAACCCATCGTGCAAGACCTGCAGGGCCAGATGCTGCACCAG
GCCATCAGCCCCCGCACCCCTGAACGCCCTGGGTGAAGGTGATCGAGGAGAAGGCTTCAGCCCCGAGGTGAT
CCCCATGTTTACCGCCCTGAGCGAGGGCGCCACCCCCAGGACCTGAACACCATGCTGAACACCGTGGGCG
GCCACCAGGCCCGCCATGCAGATGCTGAAGGACACCATCAACGAGGAGGCCCGCGAGTGGGACCGCCTGCAC
CCCGTGAGGCCGGCCCCCGTGGCCCCCGGCCAGATGCGCGACCCCCGCGGCAGCGACATCGCCGGCGCCAC
CAGCACCCCTGCAGGAGCAGATCGCCTGGATGACCAGCAACCCCCCGTGGCCGTGGGCGACATCTACAAGC
GCTGGATCATCCTGGGCCCTGAACAAGATCGTGCGCATGTACAGCCCCGTGAGCATCCTGGACATCCGCCAG
GGCCCCAAGGAGCCCTTCCGCGACTACGTGGACCGCTTCTTCAAGACCCTGCGCGCCGAGCAGGCCACCCA
GGACGTGAAGAACTGGATGACCGAGACCCTGCTGGTGCAGAACGCCAACCCCGACTGCAAGACCATCCTGC
GCGCCCTGGGCCCCGGCGCCACCCCTGGAGGAGATGATGACCGCCTGCCAGGGCGTGGGCGGCCCCGGCCAC
AAGGCCCCGCGTGGTGGCCGAGGCCATGAGCCAGGCCAACAGCGTGAACATCATGATGCAGAAGAGCAACTT
CAAGGGCCCCCGCGCAACGTGAAGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCAAGAACTGCCGCG
CCCCCGCAAGAAGGGCTGCTGGAAGTGGGSCAAGGAGGGCCACCAGATGAAGGACTGCACCGAGCGCCAG
GCCAACTTCTGGGCAAGATCTGGCCAGCCACAAGGCGGCCCGGCAACTTCTGCAGAACCGCAGCGA
GCCCCGCGCCCCACCGTGCCACCGCCCCCCCCCGCGAGAGCTTCCGCTTCGAGGAGACCACCCCCGCCC
CCAAGCAGGAGCCCCAAGGACCGCGAGCCCTACCGCGAGCCCCCTGACCGCCCTGCGCAGCCTGTTCCGGCAGC
GGCCCCCTGAGCCAGTAA

FIG. 6