(SEQ ID NO:1)

```
1                                                                  22
A E T V E S C L A K P H T E N S F T N V W K
23                                                                 44
D D K T L D R Y A N Y E G C L W N A T G V V
45                                                                 66
V C T G D E T Q C Y G T W V P I G L A I P E
67                                                                 88
N E G G G S E G G G S E G G G S E G G G T K
89                                                                 110
P P E Y G D T P I P G Y T Y I N P L D G T Y
111                                                                132
P P G T E Q N P A N P N P S L E E S Q P L N
133                                                                154
T F M F Q N N R F R N R Q G A L T V Y T G T
155                                                                176
F T Q G T D P V K T Y Y Q Y T P V S S K A M
177                                                                198
Y D A Y W N G K F R D C A F H S G F N E D P
199                                                                220
F V C E Y Q G Q S S D L P Q P P V N A G G G
221                                                                242
S G G G S G G G S E G G G S E G G G S E G G
243                                                                264
G S E G G G S G G G S G S G A M V R S D K T
265                                                                286
H T C P P C P A P E L L G G P S V F L F P P
287                                                                308
K P K D T L M I S R T P E V T C V V V D V S
309                                                                330
H E D P E V K F N W Y V D G V E V H N A K T
331                                                                352
K P R E E Q Y N S T Y R V V S V L T V L H Q
353                                                                374
D W L N G K E Y K C K V S N K A L P A P I E
375                                                                396
K T I S K A K G Q P R E P Q V Y T L P P S R
397                                                                418
E E M T K N Q V S L T C L V K G F Y P S D I
419                                                                440
A V E W E S N G Q P E N N Y K T T P P V L D
441                                                                462
S D G S F F L Y S K L T V D K S R W Q Q G N
463                                                                484
V F S C S V M H E A L H N H Y T Q K S L S L
485
S P G K
```

FIG. 1

(SEQ ID NO:2)

```
1                                                                  22
A E T V E S C L A K P H T E N S F T N V W K
23                                                                 44
D D K T L D R Y A N Y E G C L W N A T G V V
45                                                                 66
V C T G D E T Q C Y G T W V P I G L A I P E
67                                                                 88
N E G G G S E G G G S E G G G S E G G G T K
89                                                                 110
P P E Y G D T P I P G Y T Y I N P L D G T Y
111                                                                132
P P G T E Q N P A N P N P S L E E S Q P L N
133                                                                154
T F M F Q N N R F R N R Q G A L T V Y T G T
155                                                                176
F T Q G T D P V K T Y Y Q Y T P V S S K A M
177                                                                198
Y D A Y W N G K F R D C A F H S G F N E D P
199                                                                220
F V C E Y Q G Q S S D L P Q P P V N A G G G
221                                                                242
S G G G S G G G S E G G G S E G G G S E G G
243                                                                262
G S E G G G S G G G S G S G A R S D K T
263                                                    284
H T C P P C P A P E L L G G P S V F L F P P
285                                                                306
K P K D T L M I S R T P E V T C V V V D V S
307                                                                328
H E D P E V K F N W Y V D G V E V H N A K T
329                                                                350
K P R E E Q Y N S T Y R V V S V L T V L H Q
351                                                                372
D W L N G K E Y K C K V S N K A L P A P I E
373                                                                394
K T I S K A K G Q P R E P Q V Y T L P P S R
395                                                                416
E E M T K N Q V S L T C L V K G F Y P S D I
417                                                                438
A V E W E S N G Q P E N N Y K T T P P V L D
439                                                                460
S D G S F F L Y S K L T V D K S R W Q Q G N
461                                                                482
V F S C S V M H E A L H N H Y T Q K S L S L
483
S P G K
```

FIG. 2

(SEQ ID NO:3)

```
1                                                                  22
A E T V E S C L A K P H T E N S F T N V W K
23                                                                 44
D D K T L D R Y A N Y E G C L W N A T G V V
45                                                                 66
V C T G D E T Q C Y G T W V P I G L A I P E
67                                                                 88
N E G G G S E G G G S E G G G S E G G G T K
89                                                                 110
P P E Y G D T P I P G Y T Y I N P L D G T Y
111                                                                132
P P G T E Q N P A N P N P S L E E S Q P L N
133                                                                154
T F M F Q N N R F R N R Q G A L T V Y T G T
155                                                                176
F T Q G T D P V K T Y Y Q Y T P V S S K A M
177                                                                198
Y D A Y W N G K F R D C A F H S G F N E D P
199                                                                220
F V C E Y Q G Q S S D L P Q P P A N A G G E
221                                                                242
S G G G S G G G S E G G G S E G G G S E G G
243                                                                262
G S E G G G S G G G S G S G A R S D K T
263                                                        284
H T C P P C P A P E L L G G P S V F L F P P
285                                                                306
K P K D T L M I S R T P E V T C V V V D V S
307                                                                328
H E D P E V K F N W Y V D G V E V H N A K T
329                                                                350
K P R E E Q Y N S T Y R V V S V L T V L H Q
351                                                                372
D W L N G K E Y K C K V S N K A L P A P I E
373                                                                394
K T I S K A K G Q P R E P Q V Y T L P P S R
395                                                                416
E E M T K N Q V S L T C L V K G F Y P S D I
417                                                                438
A V E W E S N G Q P E N N Y K T T P P V L D
439                                                                460
S D G S F F L Y S K L T V D K S R W Q Q G N
461                                                                482
V F S C S V M H E A L H N H Y T Q K S L S L
483
S P G K
```

FIG. 3

(SEQ ID NO:4)

ATGTACAGGATGCAACTCCTGTCTTGCACTTGTCACGAATTCGATGGCTGAAACTGTTGAAAG
TTGTTTAGCAAAACCCCATACAGAAAATTCATTTACTAACGTCTGGAAAGACGACAAAACTTTAGATCGTTACGCTAACT
ATGAGGGCTGTCTGTGGAATGCTACAGGCGTTGTAGTTTGTACTGGTGACGAAACTCAGTGTTACGGTACATGGGTTCCT
ATTGGGGCTTGCTATCCCTGAAAATGAGGGTGGTGGCTCTGAGGGTGGCGGTTCTGAGGGTGGCGGTGGCGGTCGG
TACTAAACCTCCTGAGTACGGTGATACACCTATTCCGGGCTATACTTATATCAACCCTCTCGACGGCACTTATCCGCCTGG
GTACTGAGCAAAACCCCGCTAATCCTTCTTGAGGAGTCTCAGCCTCTTAATACTTTCATGTTTCAGAATAAT
AGGTTCCGAAATAGGCAGGGGGCATTAACTGTTTATACGGGCACTTTTACTCAAGGCACTGACCCCGTTAAAACTTATTA
CCAGTACACTCCTGTATCATCAAAAGCCATGTATGACGCTTACTGGAACGGTAAATTCAGAGACTGCGCTTTCCATTCTG
GCTTTAATGAGGATCCATTCGTTTGTGAATATCAAGGCCAATCGTCTGACCTGCCTCAACCTCCTGTCAATGCTGGCGGC
GGCTCTGGTGGTGGTTCTGGTGGCGGCTCTGAGGGTGGTGGCGGTTCTGAGGGTGGCGGCTCTGAGGGT
AGGCGGTTCCGGTGGTGGCTCTGGTTCCGGTGCCATGGTTAGATCTGACAAAACTCACACATGCCCACCGTGCCCAGCAC
CTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG
GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCA
TAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGG
ACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA
GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCT
GACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACA
AGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
CAGGGGAACGTCTTCTCATGCTCCGTGATGCACGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCC
GGGTAAATGA

FIG. 4A

(SEQ ID NO:5)

ATGTACAGGATGCAACTCCTGTCTTGCATTGCACTAAGTCTTGCACGAATTCGATGGCTGAAACTGTTGAAAG
TTGTTTAGCAAAACCCCATACAGAAAATTCATTTACTAACGTCTGGAAAGACGACAAAACTTTAGATCGTTACGCTAACT
ATGAGGGCTGTCTGTGGAATGCTACAGGCGTTGTAGTTTGTACTGGTGACCGAAACTCAGTGTTACGGTACATGGGTTCCT
ATTGGGCTTGCTATCCCTGAAAATGAGGGTGGTGGCTCTGAGGGTGGCGGTTCTGAGGGTGGCGGTGGCGGG
TACTAAACCTCCTGAGTACGGTGATACACCTATTCCGGGCTATACTTATATCAACCCTCTCGACGGCACTTATCCGCCTG
GTACTGAGCAAAACCCCGCTAATCCTTCTTCTTGAGGAGTCTCAGCCTCTTAATACTTTCATGTTTCAGAATAAT
AGGTTCCGAAATAGGCAGGGGGGCATTAACTGTTTATACGGGCACTTTTACTCAAGGCACTGACCCCGTTAAAACTTATTA
CCAGTACACTCCTGTATCATCAAAAGCCATGTATGACGCTTACTGGAACGGTAAATTCAGAGACTGCGCTTTCCATTCTG
GCTTTAATGAGGATCCATTCGTTTGTGAATATCAAGGCCAATCGTCTGACCTGCCTCAACCTCCTGTCAATGCTGGCGGC
GGCTCTGGTGGTGGTTCTGGTGGCGGCTCTGAGGGTGGTGGCTCTGAGGGTGGCGGCTCTGAGGG
AGGCGGTTCCGGTGGTGGCTCTGGTTCCGGTGCCAGATCTGACAAAACTCACACACATGCCCACCGTGCCCAGCACCTGAAC
TCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA
TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGC
CAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGC
TGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA
GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTG
CCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCA
CGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGGGG
AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAA
ATGA

FIG. 4B

(SEQ ID NO:6)

ATGTACAGGATGCAACTCCTGTCTTGCATTGCACTAAGTCTTGCACTTGTCACGAATTCGATGGCTGAAACTGTTGAAAG
TTGTTTAGCAAAACCCCATACAGAAAATTCATTTACTAACGTCTGGAAAGACGACAAAACTTTAGATCGTTACGCTAACT
ATGAGGGCTGTCTGTGGAATGCTACAGGCGTTGTAGTTTGTACTGGTGACGAACTCAGTGTCACGTACGGTTACGATGGT
ATTGGGCTTGCTATCCCTGAAAATGAGGGTGGTGGCGGTTCTGAGGGTGGCGGTTCTGAGGGTGGCGGTTCTGAGGGTG
TACTAAACCTCCTGAGTACGGTGATACACCTATTCCGGGCTATACTTATCAACCCTCTCGACGGCACTTATCCGCCTG
GTACTGAGCAAAACCCCGCCTAATCCTTCTTCTTGAGGAGTCTCAGCCTCTTAATACTTTCATGTTTCAGAATAAT
AGGTTCCGAAATAGGCAGGGGGCATTAACTGTTTATACGGGCACTTTTACTCAAGGCACTGACCCCGTTAAAACTTATTA
CCAGTACACTCCTGTATCATCAAAAGCCATGTATGACGCTTACTGGAACGGTAAATTCAGAGACTGCGCTTTCCATTCTG
GCTTTAATGAGGATCCATTCGTTTTGTGAATATCAAGGCCAATCGTCTGACCTGCCTCAACCTCCTGcCAATGCTGGCGGC
GagTCTGGTGGTGGTTCTGGTGGCGGCTCTGAGGGTGGTGGCGGTTCTGAGGGTGGCGGCTCTGAGGG
AGGCGGTTCCGGTGGTGGCTCTGGTTCCGGTGCCAGATCTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAC
TCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA
TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGC
CAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGC
TGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA
GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTG
CCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCA
CGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG
AACGTCTTCTCATGCTCCGTGATGCACGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAA
ATGA

FIG. 5

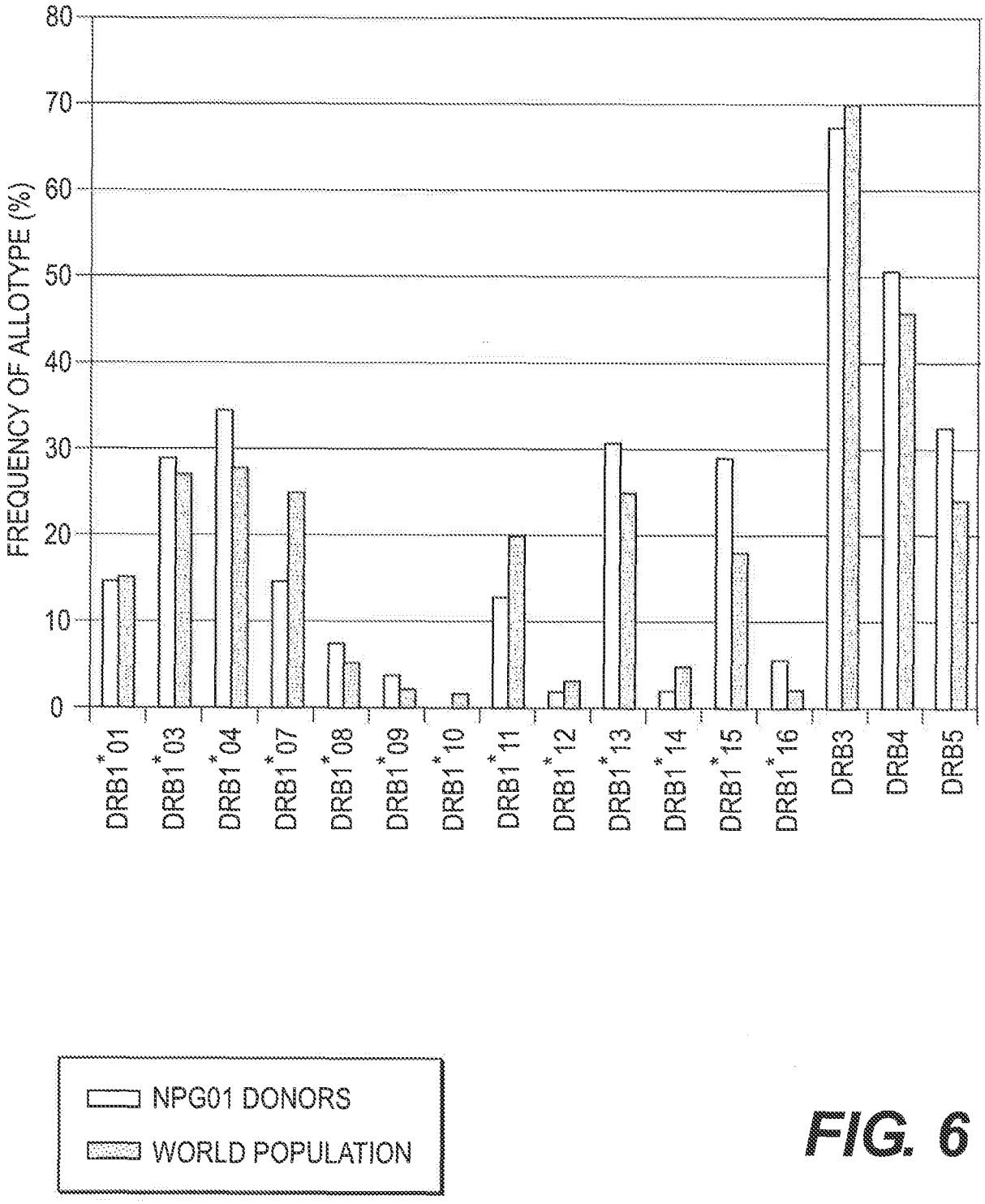

FREQUENCY OF ALLOTYPE (%)
80
70
60
50
40
30
20
10
0
DRB1*01
DRB1*03
DRB1*04
DRB1*07
DRB1*08
DRB1*09
DRB1*10
DRB1*11
DRB1*12
DRB1*13
DRB1*14
DRB1*15
DRB1*16
DRB3
DRB4
DRB5
NPG01 DONORS
WORLD POPULATION

FIG. 6

(SEQ ID NO:7)

```
1                                                                  22
A E T V E S C L A K P H T E N S F T N V W K
23                                                                 44
D D K T L D R Y A N Y E G C L W N A T G V V
45                                                                 66
V C T G D E T Q C Y G T W V P I G L A I P E
67                                                                 88
N E G G G S E G G G S E G G G S E G G G T K
89                                                                110
P P E Y G D T P I P G Y T Y I N P L D G T Y
111                                                               132
P P G T E Q N P A N P N P S L E E S Q P L N
133                                                               154
T F M F Q N N R F R N R Q G A L T V Y T G T
155                                                               176
F T Q G T D P V K T Y Y Q Y T P V S S K A M
177                                                               198
Y D A Y W N G K F R D C A F H S G F N E D P
199                                                               220
F V C E Y Q G Q S S D L P Q P P G N A G G G
221                                                               242
S G G G S G G G S E G G G S E G G G S E G G
243                                                               264
G S E G G G S G G G S G S G A M V R S D K T
265                                                               286
H T C P P C P A P E L L G G P S V F L F P P
287                                                               308
K P K D T L M I S R T P E V T C V V V D V S
309                                                               330
H E D P E V K F N W Y V D G V E V H N A K T
331                                                               352
K P R E E Q Y N S T Y R V V S V L T V L H Q
353                                                               374
D W L N G K E Y K C K V S N K A L P A P I E
375                                                               396
K T I S K A K G Q P R E P Q V Y T L P P S R
397                                                               418
E E M T K N Q V S L T C L V K G F Y P S D I
419                                                               440
A V E W E S N G Q P E N N Y K T T P P V L D
441                                                               462
S D G S F F L Y S K L T V D K S R W Q Q G N
463                                                               484
V F S C S V M H E A L H N H Y T Q K S L S L
485
S P G K
```

FIG. 7

(SEQ ID NO:8)

ATGTACAGGATGCAACTCCTGTCTTGCATTGCACTTGTCACGAATTCGATGGCTGAAACTGTTGAAAG
TTGTTTAGCAAAACCCCATACAGAAAATTCATTTACTTAACGTCTGGAAAGACGACAAAACTTTAGATCGTTACGCTAACT
ATGAGGGCCTGTCTGTGGAATGCTACAGGCGTTGTAGTTTGTACTGGTGACGAAACTCAGTGTGTTACGGTACATGGGTTCCT
ATTGGGCTTGCTATCCCTGAAAATGAGGGTGGTGGCTCTGAGGGTGGCGGTTCTGAGGGTGGCGG
TACTAAACCTCCTGAGTACGGTGATACACCTATTCCGGGCCTATACTTATCAACCCTCTCGACGGCACTTATCCGCCTC
GTACTGAGCAAAACCCCGCTAATCCTAATCCTTCTCTTGAGGAGTCTCAGCCTCTTTAATACTTTCATGTTTCAGAATAAT
AGGTTCCGAAATAGGCAGGGGGCATTAACTGTTTATACGGGCACTTTTACTCAAGGCACTGACCCCGTTAAAACTTATTA
CCAGTACACTCCTGTATCATCAAAAGCCATGTATGACGCTTACTGGAACGGTAAATTCAGAGACTGCGCTTTCCATTCTG
GCTTTAATGAGGATCCATTCGTTTGTGAATATCAAGGCCAATCGTCTGACCTGCCTCAACCTCCTGGCAATGCTGGCGGC
GGCTCTGGGTGGTGGTTCTGGTGGCGGCTCTGAGGGTGGTGGCGGTTCTGAGGGTGGCGGCTCTGAGGGG
AGGCGGTTCCGGTGGTGGCTCTGGTTCCGGTGCCATGGTTAGATCTGACAAAACTCACACATGCCCACCGTGCCCAGCAC
CTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG
GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCA
TAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGG
ACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA
GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCT
GACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACA
AGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
CAGGGGAACGTCTTCTCATGCTCCGTGATGCACGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCC
GGGTAAATGA

FIG. 8