US 20060053516A1

(19) **United States**

(12) **Patent Application Publication**

**Chye et al.**

(10) **Pub. No.: US 2006/0053516 A1**

(43) **Pub. Date: Mar. 9, 2006**

(54) **GENETICALLY MODIFIED PLANTS COMPRISING SARS-COV VIRAL NUCLEOTIDE SEQUENCES AND METHODS OF USE THEREOF FOR IMMUNIZATION AGAINST SARS**

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(21) Appl. No.: **11/004,399**

(22) Filed: **Dec. 3, 2004**

**Related U.S. Application Data**

(60) Provisional application No. 60/527,637, filed on Dec. 5, 2003.

**Publication Classification**

(51) **Int. Cl.**

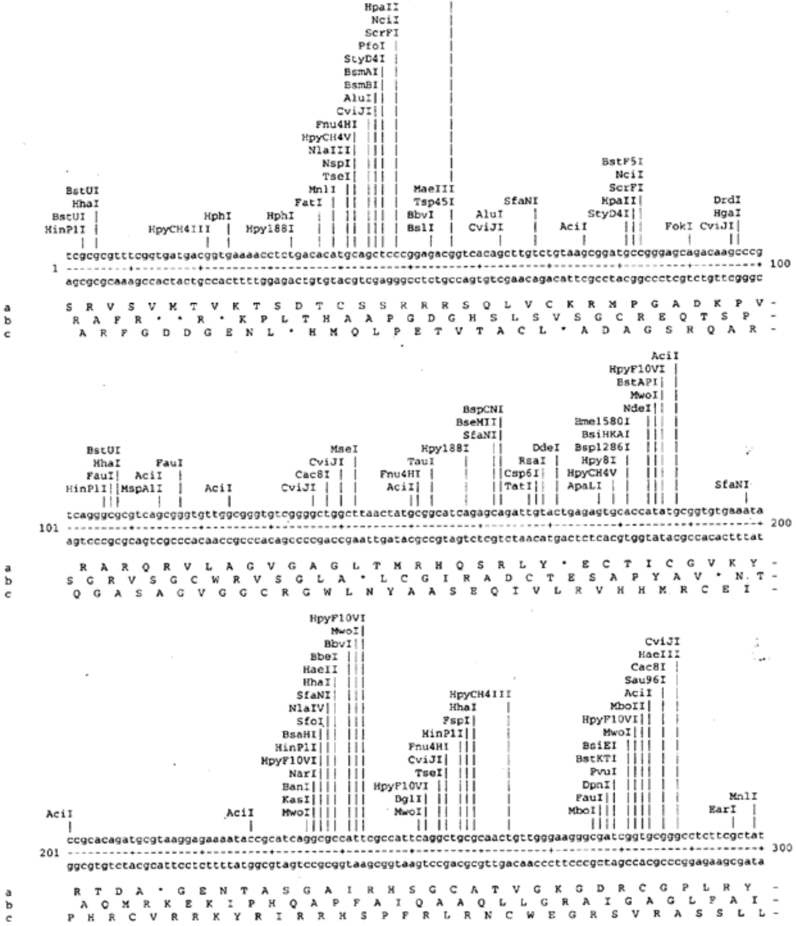
| | |
|---|---|
| *A61K 39/12* | (2006.01) |
| *C12N 5/04* | (2006.01) |
| *A01H 1/00* | (2006.01) |
| *C12N 15/82* | (2006.01) |
| *A61K 36/18* | (2006.01) |

(52) **U.S. Cl.** ......................... **800/288**; 435/419; 435/468; 424/186.1

(57) **ABSTRACT**

The invention relates to genetically modified plants and progeny thereof which constitute edible plant-derived mucosal vaccines and injectable plant-derived mucosal vaccines against Severe Acute Respiratory Syndrome (SARS). The invention relates to a recombinant vector that transforms specifically, but not limited to, the nuclei and/or plastids of tobacco, tomato and lettuce plants for antigen production. In specific embodiments, the plastid transformation vector expressing the nucleotide sequences are pCV1, pCV6 and pCV8, and their derivatives containing an S1 with nucleotide (but not amino acid) changes to optimize codon usage for expression in plants. The present invention relates to methods of making the modified plants which comprises transformation of plants with vectors for nuclear expression and/or plastid expression of nucleotide sequences of the SARS-CoV virus, fragments, derivatives, analogs, or variants thereof. The present invention also relates to methods of immunization against SARS and methods of antibody detection using the SARS-CoV antigens generated by the plastid and/or nuclear vector(s) transformed plants.

Figure 1-A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HpaII
NciI
ScrFI
PfoI
StyD4I
BsmAI
BsmBI
AluI
CviJI
Fnu4HI
HpyCH4V
NlaIII
NspI
TseI
MnlI
FatI
MaeIII
Tsp45I
BbvI
BslI
BstUI
HhaI
BstUI
HinP1I
HpyCH4III
HphI
HphI
Hpy188I
AluI
CviJI
SfaNI
AciI
BstF5I
NciI
ScrFI
HpaII
StyD4I
FokI
DrdI
HgaI
CviJI
tcgcgcgtttcggtgatgacggtgaaaacctctgacacatgcagctcccggagacggtcacagcttgtctgtaagcggatgccgggagcagacaagcccg
1
100
agcgcgcaaagccactactgccacttttggagactgtgtacgtcgagggcctctgccagtgtcgaacagacattcgcctacggccctcgtctgttcgggc
a S R V S V M T V K T S D T C S S R R R S Q L V C K R M P G A D K P V -
b R A F R * * R * K P L T H A A P G D G H S L S V S G C R E Q T S P -
c A R F G D D G E N L * H M Q L P E T V T A C L * A D A G S R Q A R -
AciI
HpyF10VI
BstAPI
MwoI
NdeI
BspCNI
BseMII
SfaNI
Bme1580I
BsiHKAI
Bsp1286I
Hpy8I
HpyCH4V
ApaLI
BstUI
HhaI
FauI
HinP1I
FauI
AciI
MspA1I
AciI
MseI
CviJI
Cac8I
CviJI
Hpy188I
TauI
Fnu4HI
AciI
DdeI
RsaI
Csp6I
TatI
SfaNI
tcagggcgcgtcagcgggtgttggcgggtgtcggggctggcttaactatgcggcatcagagcagattgtactgagagtgcaccatatgcggtgtgaaata
101
200
agtcccgcgcagtcgcccacaaccgcccacagccccgaccgaattgatacgccgtagtctcgtctaacatgactctcacgtggtatacgccacactttat
a R A R Q R V L A G V G A G L T M R H Q S R L Y * E C T I C G V K Y -
b S G R V S G C W R V S G L A * L C G I R A D C T E S A P Y A V * N T -
c Q G A S A G V G G C R G W L N Y A A S E Q I V L R V H H M R C E I -
HpyF10VI
MwoI
BbvI
BbeI
HaeII
HhaI
SfaNI
NlaIV
SfoI
BsaHI
HinP1I
HpyF10VI
NarI
BanI
KasI
MwoI
HpyCH4III
HhaI
FspI
HinP1I
Fnu4HI
CviJI
TseI
HpyF10VI
BglI
MwoI
CviJI
HaeIII
Cac8I
Sau96I
AciI
MboII
HpyF10VI
MwoI
BsiEI
BstKTI
PvuI
DpnI
FauI
MboI
AciI
AciI
MnlI
EarI
ccgcacagatgcgtaaggagaaaataccgcatcaggcgccattcgccattcaggctgcgcaactgttgggaagggcgatcggtgcgggcctcttcgctat
201
300
ggcgtgtctacgcattcctcttttatggcgtagtccgcggtaagcggtaagtccgacgcgttgacaacccttcccgctagccacgcccggagaagcgata
a R T D A * G E N T A S G A I R H S G C A T V G K G D R C G P L R Y -
b A Q M R K E K I P H Q A P F A I Q A A Q L L G R A I G A G L F A I -
c P H R C V R R K Y R I R R H S P F R L R N C W E G R S V R A S S L L -

Figure 1-B

```
                                                                                 TaiI
             Cac8I                                        BstNI               Hpy99I|
            AluI |                                        ScrFI           HpyCH4IV || 
           CviJI |             HpyCH4V                   BsaJI|     Hpy188III    | ||        CviJI|
          MspA1I |            Fnu4HI |                  PspGI||      MaeIII  |   | ||       HaeIII|
           PvuII |           BstF5I| |                 StyD4I||      Tsp45I  |   | ||      Hpy99I|| HindIII
        Cac8I  | |BbvI         TseI| |FokI MseI  MaeIII     |||BmrI  BsrI |  |   | ||       EaeI|||  TspRI|
             | | |   |            || |   |    |       |     |||   |     | |  |   | ||          ||||      ||
        tacgccagctggcgaaagggggatgtgctgcaaggcgattaagttgggtaacgccagggttttcccagtcacgacgttgtaaaacgacggccagtgccaa
301     ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 400
        atgcggtcgaccgctttccccctacacgacgttccgctaattcaacccattgcggtcccaaaagggtcagtgctgcaacattttgctgccggtcacggtt

a       Y  A  S  W  R  K  G  D  V  L  Q  G  D  *  V  G  *  R  Q  G  F  P  S  H  D  V  V  K  R  R  P  V  P  S -
b        T  P  A  G  E  R  G  M  C  C  K  A  I  K  L  G  N  A  R  V  F  P  V  T  T  L  *  N  D  G  Q  C  Q   -
c         R  Q  L  A  K  G  G  C  A  A  R  R  L  S  W  V  T  P  G  F  S  Q  S  R  R  C  K  T  T  A  S  A  K  -

                                                    BstF5I           BslI
      BceAI                                          RsaI|    Tsp509I   |
     AluI |          BsmFI                         Csp6I||  FokI     |  |               HpyCH4III
    CviJI |   Tsp509I    |                  BslI   TatI|||MseI  |    |  |          BceAI        | CviJI
        | |          |   |                  |         ||||   |  |    |  |              |        |     |
        gcttgaaagagataaattgaacaagtatggtcgtcccctgttgggatgtactattaaacctaaattggggttatctgctaaaaactacggtagagccgtt
401     ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 500
        cgaactttctctatttaacttgttcataccagcaggggacaaccctacatgataatttggatttaaccccaatagacgattttgatgccatctcggcaa

a         L  K  E  I  N  *  T  S  M  V  V  P  C  W  D  V  L  L  N  L  N  W  G  Y  L  L  K  T  T  V  E  P  F  -
b       A  *  K  R  *  I  E  Q  V  W  S  S  P  V  G  M  Y  Y  *  T  *  I  G  V  I  C  *  K  L  R  *  S  R  L -
c        L  E  R  D  K  L  N  K  Y  G  R  P  L  L  G  C  T  I  K  P  K  L  G  L  S  A  K  N  Y  G  R  A  V   -

                     Hpy8I                              MmeI
                  TspDTI  |                          Hpy8I |            PpiI       BstKTI
     BbsI         AciI  | |                           TaiI||            XcmI|       DpnI|
   MboII    XmnI BstUI  | |              PpiI  HpyCH4IV  |||         BsaXI ||     MboI ||          BsaXI
        |      |     |  | |                 |         |  |||             | ||        | ||              |
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501     ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 600
        atacttacagaagcgccacctgaactaaaatgatttctactactcttgcacttgagtgttggtaaatacgcaacctctctagcaaagaataaaacacggc

a        M  N  V  F  A  V  D  L  I  L  L  K  M  M  R  T  *  T  H  N  H  L  C  V  G  E  I  V  S  Y  F  V  P   -
b         *  M  S  S  R  W  T  *  F  Y  *  R  *  *  E  R  E  L  T  T  I  Y  A  L  E  R  S  F  L  I  L  C  R  -
c       Y  E  C  L  R  G  G  L  D  F  T  K  D  D  E  N  V  N  S  Q  P  F  M  R  W  R  D  R  F  L  F  C  A  E -

                                                                          NlaIII
                                                                        FatI    |
                                                                       RsaI |   |
                                                                     Csp6I ||   |         MboII
                                                                    PstI  |||   |     BstKTI  |
                                                               HpyCH4V | |||   |      DpnI | |     HpyF10VI
                                                                 SfcI | | |||   |     BclI || |  AluI      |
              PsiI      CviJI                 HphI       BspMI BsmI | | | |||NspI     MboI || | CviJI  MwoI|
                 |          |                    |           |    | | | | |||   |        | || |     |     ||
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601     ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 700
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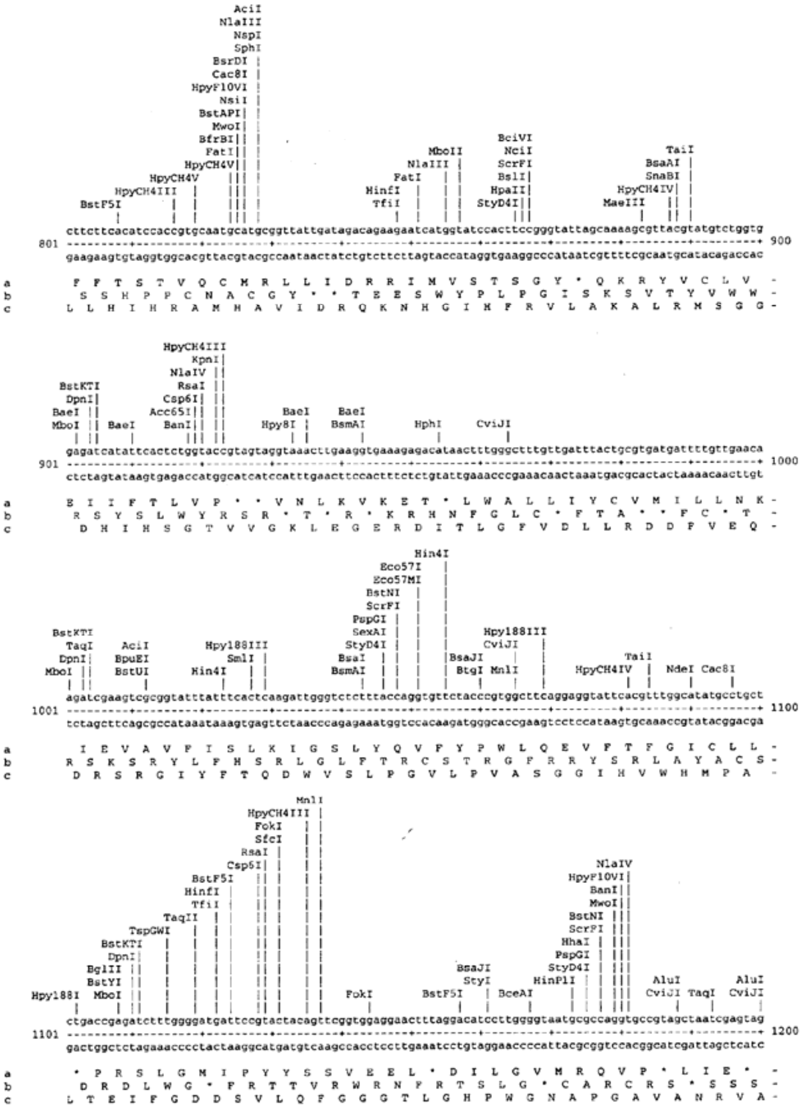
a       K  H  F  I  K  H  R  L  K  Q  V  K  S  K  G  I  T  *  M  L  L  Q  V  H  A  K  K  *  S  K  E  L  Y  L -
b        S  T  L  *  S  T  G  *  N  R  *  N  Q  R  A  L  L  E  C  Y  C  R  Y  M  R  R  N  D  Q  K  S  C  I   -
c         A  L  Y  K  A  Q  A  E  T  G  E  I  K  G  H  Y  L  N  A  T  A  G  T  C  E  E  M  I  K  R  A  V  F  -

                           BsiEI
                          BstKTI     NlaIII
                            PvuI     NsiI |                                                          Hpy8I
              BcgI         DpnI|  BfrBI | |       HphI                   AluI                        AccI|
         Tsp509I |    Hpy188I ||   FatI | |     BcgI |HinfI             CviJI                      FokI ||
      BfaI     | |       MboI ||HpyCH4V| |  MseI  | | TfiI  AciI     BfaI  |CviJI                MboII ||
          |    | |          | ||      | | |     |  | |    |     |        |  |    |                    | ||
        tgctagagaattgggcgttccgatcgtaatgcatgactacttaacggggggattcaccgcaaatactagcttggctcattattgccgagataatggtcta
701     ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 800
        acgatctcttaacccgcaaggctagcattacgtactgatgaattgcccccctaagtggcgtttatgatcgaaccgagtaataacggctctattaccagat

a         L  E  N  W  A  F  R  S  *  C  M  T  T  *  R  G  D  S  P  Q  I  L  A  W  L  I  I  A  E  I  M  V  Y  -
b       C  *  R  I  G  R  S  D  R  N  A  *  L  L  N  G  G  I  H  R  K  Y  *  L  G  S  L  L  P  R  *  W  S  T -
c        A  R  E  L  G  V  P  I  V  M  H  D  Y  L  T  G  G  F  T  A  N  T  S  L  A  H  Y  C  R  D  N  G  L   -
```

Figure 1-C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SphI
BsrDI
Cac8I
HpyF10VI
NsiI
BstAPI
MwoI
BfrBI
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HpyCH4V
HpyCH4III
BstF5I
MboII
NlaIII
FatI
HinfI
TfiI
BciVI
NciI
ScrFI
BslI
HpaII
StyD4I
TaiI
BsaAI
SnaBI
HpyCH4IV
MaeIII
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900
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a F F T S T V Q C M R L L I D R R I M V S T S G Y * Q K R Y V C L V -
b S S H P P C N A C G Y * * T E E S W Y P L P G I S K S V T Y V W W -
c L L H I H R A M H A V I D R Q K N H G I H F R V L A K A L R M S G G -
HpyCH4III
KpnI
NlaIV
RsaI
Csp6I
Acc65I
BanI
BstKTI
DpnI
BaeI
MboI
BaeI
BaeI
Hpy8I
BaeI
BsmAI
HphI
CviJI
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901
1000
ctctagtataagtgagaccatggcatcatccatttgaacttccactttctctgtattgaaacccgaaacaactaaatgacgcactactaaacaacttgt
a E I I F T L V P * * V N L K V K E T * L W A L L I Y C V M I L L N K -
b R S Y S L W Y R S R * T * R * K R H N F G L C * F T A * * F C * T -
c D H I H S G T V V G K L E G E R D I T L G F V D L L R D D F V E Q -
Hin4I
Eco57I
Eco57MI
BstNI
ScrFI
PspGI
SexAI
StyD4I
BsaI
BsmAI
BstKTI
TaqI
DpnI
MboI
AciI
BpuEI
BstUI
Hpy188III
SmlI
Hin4I
Hpy188III
CviJI
BsaJI
BtgI
MnlI
TaiI
HpyCH4IV
NdeI
Cac8I
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1001
1100
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a I E V A V F I S L K I G S L Y Q V F Y P W L Q E V F T F G I C L L -
b R S K S R Y L F H S R L G L F T R C S T R G F R R Y S R L A Y A C S -
c D R S R G I Y F T Q D W V S L P G V L P V A S G G I H V W H M P A -
MnlI
HpyCH4III
FokI
SfcI
RsaI
Csp6I
BstF5I
HinfI
TfiI
TaqII
TspGWI
BstKTI
DpnI
BglII
BstYI
Hpy188I
MboI
FokI
NlaIV
HpyF10VI
BanI
MwoI
BstNI
ScrFI
HhaI
PspGI
StyD4I
BsaJI
StyI
HinP1I
BstF5I
BceAI
AluI
CviJI
TaqI
AluI
CviJI
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1101
1200
gactggctctagaaacccctactaaggcatgatgtcaagccacctccttgaaatcctgtaggaaccccattacgcggtccacggcatcgattagctcatc
a * P R S L G M I P Y Y S S V E E L * D I L G V M R Q V P * L I E * -
b D R D L W G * F R T T V R W R N F R T S L G * C A R C R S * S S S -
c L T E I F G D D S V L Q F G G G T L G H P W G N A P G A V A N R V A -

Figure 1-D

```
                                                                                             BanII
                                                                                          Bsp1286I
                                                                                             HpaII
                                                                                              NciI
                                                                                             ScrFI
                                                                                              BbvI|
                                                                                            CviJI||
                                                                                           StyD4I||
                                                                                            NlaIV|||
                                                                                             BbvI||||
                                                                                      HpyF10VI||||
                                                                                HpyCH4V      |||||
                                                                                Cac8I |      |||||
                                                                             HpyF10VI |      |||||
                                                                                MwoI| |      |||||
                                               Hpy188III                      CviJI|| |      |||||
                                                Bpu10I |                   TspDTI ||| |      |||||
                                                  DdeI |                 BstUI  | ||| |      |||||
              NlaIII                        TspDTI   | |                  NruI  | ||| |      |||||
            FatI    |                      BstKTI |  | |            Hpy188III|  | ||| |      |||||
      HpyF10VI  |   |                       DpnI| |  | |             MnlI   ||  | ||| |      |||||    Fnu4HI
          MwoI| |   |                     MboI || |  | |            XmnI|   ||  | ||| |      |||||     AluI|
      BfaI   || |   |                     TaiI || |  | |      Tsp509I  ||   ||  | ||| |      |||||    CviJI|
  Hpy188III  || |   |   AluI           BmgBI | || |  | |      BseMII|  ||   ||  | ||| |      |||||     TseI|
      XbaI|  || |NspI  CviJI       HpyCH4IV| | || |  | |     BspCNI||  ||   ||  | ||| | MwoI |||||  BfaI  ||
         ||  || |   |       |             || | || |  | |          |||  ||   ||  | ||| |     ||||||     |  ||
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1201    ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 1300
        gagatcttcgtacacattttcgagcattacttcctgcactagaacgagtccttccattactttaataagcgctccgaacgtttacctcgggccttgatcg

a       L  *  K  H  V  *  K  L  V  M  K  D  V  I  L  L  R  K  V  M  K  L  F  A  R  L  A  N  G  A  R  N  *  L-
b        S  R  S  M  C  K  S  S  *  *  R  T  *  S  C  S  G  R  *  *  N  Y  S  R  G  L  Q  M  E  P  G  T  S  -
c         L  E  A  C  V  K  A  R  N  E  G  R  D  L  A  Q  E  G  N  E  I  I  R  E  A  C  K  W  S  P  E  L  A -

                                                          TaiI
                                                         BbvI|
                                           Fnu4HI      BtsI ||
                            BstKTI        HpyCH4V| HpyCH4IV ||                Hpy8I
     Fnu4HI                  DpnI|Tsp509I       ||    TspRI ||                AccI|
      TseI|                MboI  ||  MseI|   TseI|  Hpy8I | ||         HpyCH4III ||       Tsp509I
         ||                    | ||     ||      ||      | | ||                 | ||             |
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1301    ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 1400
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a         L  L  V  K  Y  G  K  R  S  Y  L  I  L  Q  Q  W  T  F  W  I  S  K  N  S  R  H  *  Q  I  N  *  Q  E -
b       C  C  L  *  S  M  E  R  D  R  I  *  F  C  S  S  G  R  F  G  *  V  K  T  V  D  I  S  R  *  I  S  R  K-
c        A  A  C  E  V  W  K  E  I  V  F  N  F  A  A  V  D  V  L  D  K  *  K  Q  *  T  L  A  D  K  L  A  G  -

                                                                     MseI
                                                               Tsp509I  |
                                                              HpyCH4V|  |
                                                         Tsp509I    ||  |    CviJI
                                 Tsp509I            Tsp509I    |    ||  |   HaeIII
             BpuEI           SmlI      |              MseI|    |    ||  |  Sau96I|                     CviJI
                  |              |     |                 ||    |    ||  |       ||                         |
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1401    ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 1500
        ttatttcttcctattcctctttcttgagttcattaataggaagcaagagaattaacttaacgttaatttgagccgggttagaaaatgattttcctaactc

a        I  K  K  D  K  E  K  E  L  K  *  L  S  F  V  L  L  I  E  L  Q  L  N  S  A  Q  S  F  T  K  R  I  E  -
b         *  R  R  I  R  R  K  N  S  S  N  Y  P  S  F  S  *  L  N  C  N  *  T  R  P  N  L  L  L  K  G  L  S -
c       N  K  E  G  *  G  E  R  T  Q  V  I  I  L  R  S  L  N  *  I  A  I  K  L  G  P  I  F  Y  *  K  D  *  A-

                                                                                      BfaI
                  HinfI                                                          Hpy188III              MlyI
                   TfiI  HpyCH4V         DdeI            BfaI                        XbaI|              PleI
                      |        |            |               |                           ||                 |
        ccgaatacaacaaagattctattgcatatattttgactaagtatatacttacctagatatacaagatttgaaatacaaaatctagaaaactaaatcaaaa
1501    ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 1600
        ggcttatgttgtttctaagataacgtatataaaactgattcatatatgaatggatctatatgttctaaactttatgttttagatcttttgatttagtttt

a       P  N  T  T  K  I  L  L  H  I  F  *  L  S  I  Y  L  P  R  Y  T  R  F  E  I  Q  N  L  E  N  *  I  K  I-
b        R  I  Q  Q  R  F  Y  C  I  Y  F  D  *  V  Y  T  Y  L  D  I  Q  D  L  K  Y  K  I  *  K  T  K  S  K  -
c         E  Y  N  K  D  S  I  A  Y  I  L  T  K  Y  I  L  T  *  I  Y  K  I  *  N  T  K  S  R  K  L  N  Q  N -
```

Figure 1-E

```
                                                             HincII
                                                              Hpy8I|
                                                              AccI |
                                                              TaqI||
                                                             SalI ||
                                                            PstI |||
                                                        HpyCH4V ||||
                                                        Cac8I  |||||
                                                         SfcI| |||||
                                                     NlaIII  | |||||
                                                       NspI| | |||||
                                                       SphI| | |||||
                                                    Cac8I  | | |||||
                                                   FatI  | | | |||||
                                                HpyCH4V| | | | |||||
                                                Cac8I  | | | | |||||
                                               AluI  | | | | | |||||
                                            CviJI  | | | | | | |||||
                                           AlwI  | | | | | | | |||||
                                         TaqI  | | | | | | | | |||||
                                    BstKTI   | | | | | | | | | |||||                             RsaI
        HinfI                        DpnI |  | | | | | | | | | |||||                           Csp6I |
     DdeI    |                     MboI  ||  | | | | | | | | | ||||| HpyCH4III  Hpy188I        TatI ||
         |   |                         | ||  | | | | | | | | | |||||        |          |           |||
        tctaagactcaaatctttctattgttgtcttggatcatcgagcttgcatgcctgcagtcgactttcacagtttccattctgaaatgttctctgtactata
1601    ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 1700
        agattctgagtttagaaagataacaacagaacctagtagctcgaacgtacggacgtcagctgaaagtgtcaaaggtaagactttacaagagacatgatat

a         *  D  S  N  L  S  I  V  V  L  D  H  R  A  C  M  P  A  V  D  F  H  S  F  H  S  E  M  F  S  V  L  *  -
b       S  K  T  Q  I  F  L  L  L  S  W  I  I  E  L  A  C  L  Q  S  T  F  T  V  S  I  L  K  C  S  L  Y  Y  N -
c        L  R  L  K  S  F  Y  C  C  L  G  S  S  S  L  H  A  C  S  R  L  S  Q  F  P  F  *  N  V  L  C  T  I   -

                                            Hpy8I           MnlI
                HinfI                      MboII |        EarI   |
                 TfiI             Tsp509I   AccI |     Hpy188I   |   CviJI                     HpyCH4V
                     |                   |      ||            |  |        |                           |
        ataaatagtaagtgaatcaacttactactaaaaaattagtagacttcctcttcggaatagaaatagcctatttctacatagggaaagtcgtgtgcaatg
1701    ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 1800
        tatttatcattcacttagttgaatgatgatttttttaatcatctgaaggagaagccttatctttatcggataaagatgtatccctttcagcacacgttac

a        *  I  V  S  E  S  T  Y  Y  *  K  N  *  *  T  S  S  S  E  *  K  *  P  I  S  T  *  G  K  S  C  A  M   -
b         K  *  *  V  N  Q  L  T  T  K  K  I  S  R  L  P  L  R  N  R  N  S  L  F  L  H  R  E  S  R  V  Q  *  -
c       I  N  S  K  *  I  N  L  L  L  K  K  L  V  D  F  L  F  G  I  E  I  A  Y  F  Y  I  G  K  V  V  C  N  E -

                                                                                                   MlyI
                                                                                                   PleI|
                                                                                                  MmeI |
                                                                                                NciI  ||
                                                                                               ScrFI| ||
                                                                                                SmaI| ||
                                                                                   NciI       HpaII | ||
                                                                                  ScrFI|       NciI|| ||
                                                                                 HpaII |      ScrFI|| ||
                                                                               StyD4I ||      AvaI || ||
                                                                            BsmFI    |||     BsaJI||| ||
                                                                             BccI|   |||    StyD4I||| ||
              TspDTI                                                        BfaI |   |||      XmaI||| ||
           Cac8I    |                                                      SpeI ||   |||   StyD4I ||| ||
       HpyCH4V  |   |                                Tsp509I          Hpy188I  |||   |||HinfI    |||| ||
    BsrDI     | |   |MnlI                 MaeIII       FokI |     BstF5I     | |||   |||   TaqI  |||| ||
         |    | |   |    |                      |          ||           |    | |||   |||     | | |||| ||
        aaaaatgcaagcacgatttggggagaggttttttctctattgtaacaaggaataattatctactccatccgactagttccgggttcgagtcccgggcaac
1801    ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 1900
        tttttacgttcgtgctaaacccctctccaaaaaagagataacattgttccttattaatagatgaggtaggctgatcaaggcccaagctcagggcccgttg

a       K  N  A  S  T  I  W  G  E  V  F  S  L  L  *  Q  G  I  I  I  Y  S  I  R  L  V  P  G  S  S  P  G  Q  P -
b        K  M  Q  A  R  F  G  E  R  F  F  L  Y  C  N  K  E  *  L  S  T  P  S  D  *  F  R  V  R  V  P  G  N   -
c         K  C  K  H  D  L  G  R  G  F  F  S  I  V  T  R  N  N  Y  L  L  H  P  T  S  S  G  F  E  S  R  A  T  -

                    BspCNI
                   BseMII | Hpy188I                            ApoI             ApoI
      NdeI     BfaI      ||   DdeI |     TspDTI             Tsp509I          Tsp509I
          |        |     ||       ||           |                   |                |
        ccatatggaaactagaaaggagcaatctgagttttgatttttcactcacttcatttacaaaattttttggtttggtaaattttgttgtatggatatacaa
1901    ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 2000
        ggtataccttttgatctttcctcgttagactcaaaactaaaaagtgagtgaagtaaatgttttaaaaaaccaaaccatttaaaacaacatacctatatgtt

a         I  W  K  L  E  R  S  N  L  S  F  D  F  S  L  T  S  F  T  K  F  F  G  L  V  N  F  V  V  W  I  Y  N  -
b       P  Y  G  N  *  K  G  A  I  *  V  L  I  F  H  S  L  H  L  Q  N  F  L  V  W  *  I  L  L  Y  G  Y  T  T -
c        H  M  E  T  R  K  E  Q  S  E  F  *  F  F  T  H  F  I  Y  K  I  F  W  F  G  K  F  C  C  M  D  I  Q   -
```

Figure 1-F

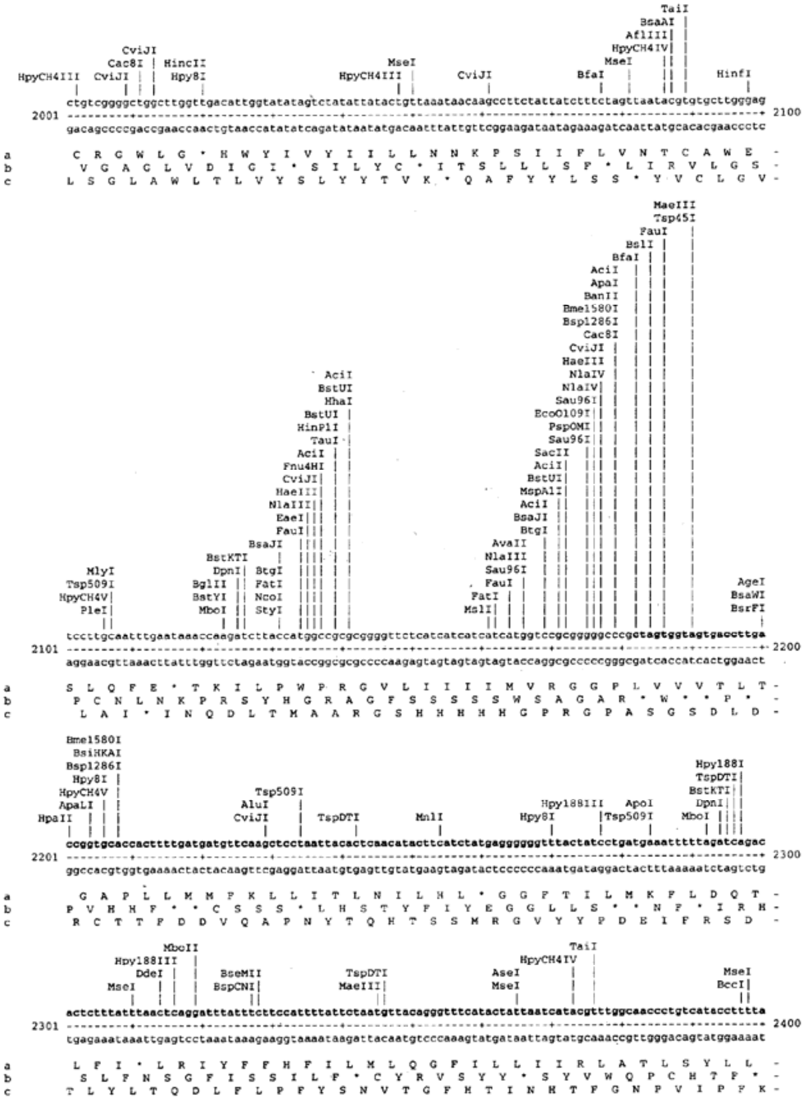

TaiI
BsaAI
AflIII
HpyCH4IV
MseI
CviJI
Cac8I
HincII
HpyCH4III
CviJI
Hpy8I
MseI
HpyCH4III
CviJI
BfaI
HinfI
ctgtcggggctggcttggttgacattggtatatagtctatattatactgttaaataacaagccttctattatctttctagttaatacgtgtgcttggag
2001
2100
gacagccccgaccgaaccaactgtaaccatatatcagatataatatgacaatttattgttcggaagataatagaaagatcaattatgcacacgaaccctc
a C R G W L G * H W Y I V Y I I L L N N K P S I I F L V N T C A W E -
b V G A C L V D I G I * S I L Y C * I T S L L L S F * L I R V L G S -
c L S G L A W L T L V Y S L Y Y T V K * Q A F Y Y L S S * Y V C L G V -
MaeIII
Tsp45I
FauI
BslI
BfaI
AciI
ApaI
BanII
Bme1580I
Bsp1286I
Cac8I
CviJI
HaeIII
NlaIV
NlaIV
Sau96I
EcoO109I
PspOMI
Sau96I
SacII
AciI
BstUI
MspA1I
AciI
BsaJI
BtgI
AvaII
NlaIII
Sau96I
FauI
FatI
MslI
AciI
BstUI
HhaI
BstUI
HinP1I
TauI
AciI
Fnu4HI
CviJI
HaeIII
NlaIII
EaeI
FauI
BsaJI
BstKTI
DpnI
BtgI
BglII
FatI
BstYI
NcoI
MboI
StyI
MlyI
Tsp509I
HpyCH4V
PleI
AgeI
BsaWI
BsrFI
tccttgcaatttgaataaaccaagatcttaccatggccgcgcggggttctcatcatcatcatcatggtccgcgggggcccgctagtggtagtgaccttga
2101
2200
aggaacgttaaacttatttggttctagaatggtaccggcgcgccccaagagtagtagtagtagtaccaggcgcccccgggcgatcaccatcactggaact
a S L Q F E * T K I L P W P R G V L I I I I M V R G G P L V V V T L T -
b P C N L N K P R S Y H G R A G F S S S S S W S A G A R * W * * P * -
c L A I * I N Q D L T M A A R G S H H H H H G P R G P A S G S D L D -
Bme1580I
BsiHKAI
Bsp1286I
Hpy8I
HpyCH4V
ApaLI
HpaII
Tsp509I
AluI
CviJI
TspDTI
MnlI
Hpy188III
Hpy8I
ApoI
Tsp509I
Hpy188I
TspDTI
BstKTI
DpnI
MboI
ccggtgcaccactttttgatgatgttcaagctcctaattacactcaacatacttcatctatgaggggggtttactatcctgatgaaatttttagatcagac
2201
2300
ggccacgtggtgaaaactactacaagttcgaggattaatgtgagttgtatgaagtagatactccccccaaatgataggactactttaaaaatctagtctg
a G A P L L M M F K L L I T L N I L H L * G G F T I L M K F L D Q T -
b P V H H F * * C S S S * L H S T Y F I Y E G G L L S * * N F * I R H -
c R C T T F D D V Q A P N Y T Q H T S S M R G V Y Y P D E I F R S D -
MboII
Hpy188III
DdeI
MseI
BseMII
BspCNI
TspDTI
MaeIII
TaiI
HpyCH4IV
AseI
MseI
MseI
BccI
actctttatttaactcaggatttatttcttccatttattctaatgttacagggtttcatactattaatcatacgtttggcaaccctgtcatacctttta
2301
2400
tgagaaataaattgagtcctaaataaagaaggtaaaataagattacaatgtcccaaagtatgataattagtatgcaaaccgttgggacagtatggaaaat
a L F I * L R I Y F F H F I L M L Q G F I L L I I R L A T L S Y L L -
b S L F N S G F I S S I L F * C Y R V S Y Y * S Y V W Q P C H T F * -
c T L Y L T Q D L F L P F Y S N V T G F H T I N H T F G N P V I P F K -

Figure 1-G

```
                                                                                      HpyCH4III
                   Fnu4HI                                                            TspDTI|
        BstF5I      TseI|                    BsaJI                     NlaIII  MaeIII    ||
       BbvI  |   FokI  ||        TspGWI       BtgI  BslI             FatI   |  Tsp45I    ||           MseI
          |  |      |  ||             |          |     |                |   |       |    ||              |
      aggatggtatttattttgctgccacagagaaatcaaatgttgtccgtggttgggtttttggttctaccatgaacaacaagtcacagtcggtgattattat
2401  ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 2500
      tcctaccataaataaaacgacggtgtctctttagtttacaacaggcaccaacccaaaaaccaagatggtacttgttgttcagtgtcagccactaataata

a     R  M  V  F  I  L  L  P  Q  R  N  Q  M  L  S  V  V  G  F  L  V  L  P  *  T  T  S  H  S  R  *  L  L  L -
b      G  W  Y  L  F  C  C  H  R  E  I  K  C  C  P  W  L  G  F  W  F  Y  H  E  Q  Q  V  T  V  G  D  Y  Y   -
c       D  G  I  Y  F  A  A  T  E  K  S  N  V  V  R  G  W  V  F  G  S  T  M  N  N  K  S  Q  S  V  I  I  I  -

                                                                                       Hpy8I
                                                                                       RsaI|
                                                                                     Csp6I||
                                                                                  NlaIII |||
                                                                               BsaJI   | |||
                                 NlaIII                                         BtgI   | |||
                                   NspI        MaeIII                           FatI   | |||
   Tsp509I                      MaeIII|        Tsp45I                           NcoI   | |||
   HphI  |                     FatI  || Tsp509I     |                           StyI   | |||
      |  |                        |  ||       |     |                              |   | |||
      taacaattctactaatgttgttatacgagcatgtaactttgaattgtgtgacaaccctttctttgctgtttctaaacccatgggtacacagacacatact
2501  ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 2600
      attgttaagatgattacaacaatatgctcgtacattgaaacttaacacactgttgggaaagaaacgacaaagatttgggtacccatgtgtctgtgtatga

a       T  I  L  L  M  L  L  Y  E  H  V  T  L  N  C  V  T  T  L  S  L  L  F  L  N  P  W  V  H  R  H  I  L  -
b     *  Q  F  Y  *  C  C  Y  T  S  M  *  L  *  I  V  *  Q  P  F  L  C  C  F  *  T  H  G  Y  T  D  T  Y  Y -
c      N  N  S  T  N  V  V  I  R  A  C  N  F  E  L  C  D  N  P  F  F  A  V  S  K  P  M  G  T  Q  T  H  T   -

                         HpyCH4V
                           Hin4I|
                    Tsp509I    ||      RsaI
                      MseI|    ||    Csp6I|
                    NsiI ||    ||    SfaNI|
                 BfrBI | ||    ||    TatI||                                              DraI
          TaqI HpyCH4V | ||    || TaqI  ||| Hpy188I       Hin4I     Hpy188I     Tsp509I MseI|
             |       | | ||    ||    |  |||       |           |           |           |    ||
      atgatattcgataatgcatttaattgcactttcgagtacatatctgatgccttttcgcttgatgtttcagaaaagtcaggtaattttaaacacttacgag
2601  ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 2700
      tactataagctattacgtaaattaacgtgaaagctcatgtatagactacggaaaagcgaactacaaagtcttttcagtccattaaaatttgtgaatgctc

a      *  Y  S  I  M  H  L  I  A  L  S  S  T  Y  L  M  P  F  R  L  M  F  Q  K  S  Q  V  I  L  N  T  Y  E   -
b       D  I  R  *  C  I  *  L  H  F  R  V  H  I  *  C  L  F  A  *  C  F  R  K  V  R  *  F  *  T  L  T  R  -
c     M  I  F  D  N  A  F  N  C  T  F  E  Y  I  S  D  A  F  S  L  D  V  S  E  K  S  G  N  F  K  H  L  R  E -

                                                                          BstKTI
                                                                           DpnI|
             DraI                                                        MboI ||
            MseI|BccI                     PsiI CviJI     SfcI     Hpy188III | ||          MseI
               ||   |                        |     |        |            |  | ||             |
      agtttgtgtttaaaaataaagatgggtttctctatgtttataagggctatcaacctatagatgtagttcgtgatctaccttctggttttaacactttgaa
2701  ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 2800
      tcaaacacaaatttttatttctacccaaagagatacaaatattcccgatagttggatatctacatcaagcactagatggaagaccaaaattgtgaaactt

a     S  L  C  L  K  I  K  M  G  F  S  M  F  I  R  A  I  N  L  *  M  *  F  V  I  Y  L  L  V  L  T  L  *  N -
b      V  C  V  *  K  *  R  W  V  S  L  C  L  *  G  L  S  T  Y  R  C  S  S  *  S  T  F  W  F  *  H  F  E   -
c       F  V  F  K  N  K  D  G  F  L  Y  V  Y  K  G  Y  Q  P  I  D  V  V  R  D  L  P  S  G  F  N  T  L  K  -
```

Figure 1-H

```
                                                                                                PstI
                                                                                           Fnu4HI|
                                                                                         HpyCH4V||
                                                                                            TseI||
                                                                                      Fnu4HI |||
                                                                                        SfcI |||
                                                                                     AluI| |||
                                                                                    CviJI| |||
                                                                                   MspA1I| |||
                                                                                    PvuII| |||
                                                                                     TseI| |||
                                                                                TaiI  || |||
                                                                           BmgBI |   || |||
                                                    AarI       Bmc1580I|  |   || |||
                                  CviJI            BspMI       Bsp1286I|  |   || |||
            MnlI    ApoI          BpuEI |   Hpy188III |        HpyCH4IV|  |   || |||
     MseI   MseI   Tsp509I  CviJI  HphI |       SmlI | |    BbvI      ||  |   || |||
       |      |       |       |      | |            | | |      |      ||  |   || |||
    acctatttttaagttgcctcttggtattaacattacaaattttagagccattcttacagccttttcacctgctcaagacatttggggcacgtcagctgca
2801 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 2900
    tggataaaaattcaacggagaaccataattgtaatgtttaaaatctcggtaagaatgtcggaaaagtggacgagttctgtaaaccccgtgcagtcgacgt

a      L  F  L  S  C  L  L  V  L  T  L  Q  I  L  E  P  F  L  Q  P  F  H  L  L  K  T  F  G  A  R  Q  L  Q  -
b     T  Y  F  *  V  A  S  W  Y  *  H  Y  K  F  *  S  H  S  Y  S  L  F  T  C  S  R  H  L  G  H  V  S  C  S -
c      P  I  F  K  L  P  L  G  I  N  I  T  N  F  R  A  I  L  T  A  F  S  P  A  Q  D  I  W  G  T  S  A  A  -

                  BpuEI                                          TspDTI
                  CviJI|                                     RsaI  |
            CviJI  DraI ||                                  SfaNI  |
CviJI  BbvI   |  MseI| ||            SmlI                   Csp6I| |     AlwNI
  |      |    |    || ||               |                        || |       |
    gcctatttgttggctatttaaagccaactacatttatgctcaagtatgatgaaaatggtacaatcacagatgctgttgattgttctcaaatccacttg
2901 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 3000
    cggataaaacaaccgataaatttcggttgatgtaaatacgagttcatactactttaccatgttagtgtctacgacaactaacaagagtttaggtgaac

a      P  I  L  L  A  I  *  S  Q  L  H  L  C  S  S  M  M  K  M  V  Q  S  Q  M  L  L  I  V  L  K  I  H  L  -
b      L  F  C  W  L  F  K  A  N  Y  I  Y  A  Q  V  *  *  K  W  Y  N  H  R  C  C  *  L  F  S  K  S  T  C  -
c     A  Y  F  V  G  Y  L  K  P  T  T  F  M  L  K  Y  D  E  N  G  T  I  T  D  A  V  D  C  S  Q  N  P  L  A -

                                                                                             HinfI
                                                                    Hpy188III                 TfiI
                                                                     Bsu36I |        BseMII   |
                AluI               ApoI                                DdeI |       BspCNI|   |
           MseI CviJI            Tsp509I         Tsp509I  MnlI   BsaXI    | |   MnlI     ||   |
              |   |                  |                |     |       |     | |     |      ||   |
    ctgaactcaaatgctctgttaagagctttgagattgacaaaggaatttaccagacctctaatttcagggttgttccctcaggagatgttgtgagattccc
3001 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 3100
    gacttgagtttacgagacaattctcgaaactctaactgtttccttaaatggtctggagattaaagtcccaacaagggagtcctctacaacactctaaggg

a     L  N  S  N  A  L  L  R  A  L  R  L  T  K  E  F  T  R  P  L  I  S  G  L  F  P  Q  E  M  L  *  D  S  L -
b     *  T  Q  M  L  C  *  E  L  *  D  *  Q  R  N  L  P  D  L  *  F  Q  G  C  S  L  R  R  C  C  E  I  P  -
c      E  L  K  C  S  V  K  S  F  E  I  D  K  G  I  Y  Q  T  S  N  F  R  V  V  P  S  G  D  V  V  R  F  P  -

                                                             NlaIII
                                                              NsiI |
                                                            BfrBI | |
  SspI                                       ApoI            FatI | |        ApoI      Tsp509I
BsaXI|            MnlI        MseI         Tsp509I        HpyCH4V | |      Tsp509I        |
    ||              |            |             |                | | |          |          |
    taatattacaaacttgtgtccttttggagaggtttttaatgctactaaattcccttctgtctatgcatgggagagaaaaaaatttctaattgtgttgct
3101 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 3200
    attataatgtttgaacacaggaaaacctctccaaaaattacgatgatttaagggaagacagatacgtaccctctctttttttaaagattaacacaacga

a      I  L  Q  T  C  V  L  L  E  R  F  L  M  L  L  N  S  L  L  S  M  H  G  R  E  K  K  F  L  I  V  L  L  -
b     *  Y  Y  K  L  V  S  F  W  R  G  F  *  C  Y  *  I  P  F  C  L  C  M  G  E  K  K  N  F  *  L  C  C  * -
c      N  I  T  N  L  C  F  F  G  E  V  F  N  A  T  K  F  P  S  V  Y  A  W  E  R  K  K  I  S  N  C  V  A  -

                                                                        BstKTI
       BsiHKAI                                                         DpnI|
      Bsp1286I                MseI                    DdeI       MboI ||                 HpyCH4V
           |                    |                       |           | ||                      |
    gattactctgtgctctacaactcaacatttttttcaacctttaagtgctatggcgtttctgccactaagttgaatgatctttgcttctccaatgtctatg
3201 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 3300
    ctaatgagacacgagatgttgagttgtaaaaaaagttggaaattcacgataccgcaaagacggtgattcaacttactagaaacgaagaggttacagatac

a      I  T  L  C  S  T  T  Q  H  F  F  Q  P  L  S  A  M  A  F  L  P  L  S  *  M  I  F  A  S  P  M  S  M  -
b      L  L  C  A  L  Q  L  N  I  F  F  N  L  *  V  L  W  R  F  C  H  *  V  E  *  S  L  L  L  Q  C  L  C  -
c     D  Y  S  V  L  Y  N  S  T  F  F  S  T  F  K  C  Y  G  V  S  A  T  K  L  N  D  L  C  F  S  N  V  Y  A -
```

Figure 1-I

```
                                              BstNI
                                              ScrFI
                                             HaeII|
                                             HhaI||
                                            PspGI||                                  TspDTI
                                           StyD4I||                            Tsp509I    |
   HinfI                                   BsaXI|||                     Tsp509I      |    |
    TfiI     BsaXI                       HinP1I||||         BsrI          PsiI| PsiI |    |       FatI
        |        |                            |||||            |             ||    | |    |          |
     cagattcttttgtagtcaagggagatgatgtaagacaaatagcgccaggacaaactggtgttattgctgattataattataaattgccagatgatttcat
3301 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 3400
     gtctaagaaaacatcagttccctctactacattctgtttatcgcggtcctgtttgaccacaataacgactaatattaatatttaacggtctactaaagta

a    Q  I  L  L  *  S  R  E  M  M  *  D  K  *  R  Q  D  K  L  V  L  L  L  I  I  I  I  N  C  Q  M  I  S  W -
b     R  F  F  C  S  Q  G  R  *  C  K  T  N  S  A  R  T  N  W  C  Y  C  *  L  *  L  *  I  A  R  *  F  H    -
c      D  S  F  V  V  K  G  D  D  V  R  Q  I  A  P  G  Q  T  G  V  I  A  D  Y  N  Y  K  L  P  D  D  F  M   -

                                                                                                 CviJI
                                                                                                HaeIII
                                                                                             EcoO109I|
                                                                                               Sau96I|
                                                                                           Bpu10I   ||
                                                                                             DdeI   ||
                                                                                            AluI|   ||
                                                                                           CviJI|   ||
                                                                                         Cac8I ||   ||
                                                        Tsp509I                        HindIII ||   ||
                         SfaNI                     BsrI     |                      NlaIII  |  ||   ||
NlaIII                   BfaI|                Tsp509I PsiI| PsiI          DdeI FatI   |  |  ||   ||
     |                      ||                           |    ||    |             |    |   |  |  ||   ||
     gggttgtgtccttgcttggaatactaggaacattgatgctacttcaactggtaattataattataaatataggtatcttagacatggcaagcttaggccc
3401 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 3500
     cccaacacaggaacgaaccttatgatccttgtaactacgatgaagttgaccattaatattaatatttatatccatagaatctgtaccgttcgaatccggg

a      V  V  S  L  L  G  I  L  G  T  L  M  L  L  Q  L  V  I  I  I  I  N  I  G  I  L  D  M  A  S  L  G  P   -
b    G  L  C  P  C  L  E  Y  *  E  H  *  C  Y  F  N  W  *  L  *  L  *  I  *  V  S  *  T  W  Q  A  *  A  L -
c     G  C  V  L  A  W  N  T  R  N  I  D  A  T  S  T  G  N  Y  N  Y  K  Y  R  Y  L  R  H  G  K  L  R  P    -

                                                HpyCH4V            AarI       CviJI
                                             HpyF10VI |           BspMI      HaeIII
                                              BstAPI| |         Tsp509I        MscI
  BsmAI                         BccI            MwoI| |           MseI|      EaeI |MseI
      |                            |               || |              ||         | |   |
     tttgagagagacatatctaatgtgcctttctcccctgatggcaaaccttgcaccccacctgctcttaattgttattggccattaaatgattatggtttt
3501 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 3600
     aaactctctctgtatagattacacggaaagaggggactaccgtttggaacgtggggtggacgagaattaacaataaccggtaatttactaataccaaaaa

a     L  R  E  T  Y  L  M  C  L  S  P  L  M  A  N  L  A  P  H  L  L  L  I  V  I  G  H  *  M  I  M  V  F    -
b      *  E  R  H  I  *  C  A  F  L  P  *  W  Q  T  L  H  P  T  C  S  *  L  L  L  A  I  K  *  L  W  F  L   -
c    F  E  R  D  I  S  N  V  P  F  S  P  D  G  K  P  C  T  P  P  A  L  N  C  Y  W  P  L  N  D  Y  G  F  Y -

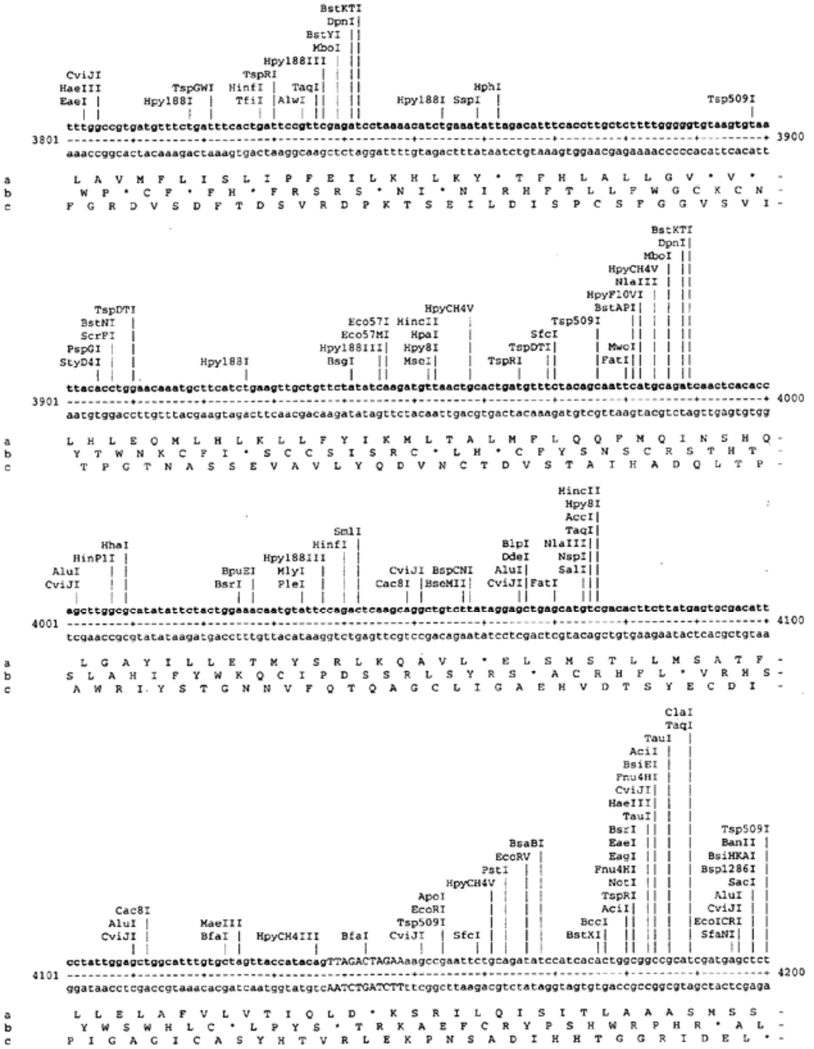
                                                                         HpyCH4III
                                                                         BsaJI   |
                                                                          BtgI   |
                                                                        CviJI|   |
                                                                       HaeIII|   |
                                                                       EaeI ||   |
                                                                     HpaII| ||   |
                                            RsaI                    BsrFI|| ||   |      Tsp509I
                                            ScaI                HpyCH4V ||| ||   |  AvaII     |
                   CviJI                  Csp6I|              DraI    | ||| ||   |  Hpy8I     |
               BsrI    |                  TatI||             MseI|    | ||| ||   | Sau96I     |
                  |    |                     |||             ||    | ||| ||   |      |     |
     acaccactactggcattggctaccaaccttacagagttgtagtactttcttttgaactttaaatgcaccggccacggtttgtggaccaaaattatccac
3601 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 3700
     tgtggtgatgaccgtaaccgatggttggaatgtctcaacatcatgaaagaaaacttgaaatttacgtggccggtgccaaacacctggttttaataggtg

a    T  P  L  L  A  L  A  T  N  L  T  E  L  *  Y  F  L  L  N  F  *  M  H  R  P  R  F  V  D  Q  N  Y  P  L -
b     H  H  Y  W  H  W  L  P  T  L  Q  S  C  S  T  F  F  *  T  F  K  C  T  G  H  G  L  W  T  K  I  I  H    -
c      T  T  T  G  I  G  Y  Q  P  Y  R  V  V  V  L  S  F  E  L  L  N  A  P  A  T  V  C  G  P  K  L  S  T   -

                                                              HincII
                                                                HpaI
                                                     BsrI      Hpy8I
                             Tsp509I MlyI            RsaI      MboII
                       Tsp509I     | MseI  BaeI     TspRI      MseI|
    TspRI MseI   BsrI  TspRI | MseI| PleI HinfI    Csp6I| BsrI   ||        BaeI          BceAI Tsp509I
        |    |      |      | |    ||    |     |        ||     |   ||           |              |       |
     tgaccttattaagaaccagtgtgtcaattttaattttaatggactcactggtactggtgtgttaactccttcttcaaagagatttcaaccatttcaacaa
3701 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 3800
     actggaataattcttggtcacacagttaaaattaaaattacctgagtgaccatgaccacacaattgaggaagaagtttctctaaagttggtaaagttgtt

a      T  L  L  R  T  S  V  S  I  L  I  L  M  D  S  L  V  L  V  C  *  L  L  L  Q  R  D  F  N  H  F  N  N   -
b    *  P  Y  *  E  P  V  C  Q  F  *  F  *  W  T  H  W  Y  W  C  V  N  S  F  F  K  E  I  S  T  I  S  T  I -
c     D  L  I  K  N  Q  C  V  N  F  N  F  N  G  L  T  G  T  G  V  L  T  P  S  S  K  R  F  Q  P  F  Q  Q    -
```

Figure 1-J



```
     tttggccgtgatgtttctgatttcactgattccgttcgagatcctaaaacatctgaaatattagacatttcaccttgctcttttggggtgtaagtgtaa
3801 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 3900
     aaaccggcactacaaagactaaagtgactaaggcaagctctaggattttgtagactttataatctgtaaagtggaacgagaaaaccccacattcacatt

a     L  A  V  M  F  L  I  S  L  I  P  F  E  I  L  K  H  L  K  Y  *  T  F  H  L  A  L  L  G  V  *  V  *  -
b      W  P  *  C  F  *  F  H  *  F  R  S  R  S  *  N  I  *  N  I  R  H  F  T  L  L  F  W  G  C  K  C  N  -
c     F  G  R  D  V  S  D  F  T  D  S  V  R  D  P  K  T  S  E  I  L  D  I  S  P  C  S  F  G  G  V  S  V  I -

     ttacacctggaacaaatgcttcatctgaagttgctgttctatatcaagatgttaactgcactgatgtttctacagcaattcatgcagatcaactcacacc
3901 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 4000
     aatgtggaccttgtttacgaagtagacttcaacgacaagatatagttctacaattgacgtgactacaaagatgtcgttaagtacgtctagttgagtgtgg

a     L  H  L  E  Q  M  L  H  L  K  L  L  F  Y  I  K  M  L  T  A  L  M  F  L  Q  Q  F  M  Q  I  N  S  H  Q -
b      Y  T  W  N  K  C  F  I  *  S  C  C  S  I  S  R  C  *  L  H  *  C  F  Y  S  N  S  C  R  S  T  H  T  -
c      T  P  G  T  N  A  S  S  E  V  A  V  L  Y  Q  D  V  N  C  T  D  V  S  T  A  I  H  A  D  Q  L  T  P  -

     agcttggcgcatatattctactggaaacaatgtattccagactcaagcaggctgtcttataggagctgagcatgtcgacacttcttatgagtgcgacatt
4001 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 4100
     tcgaaccgcgtatataagatgacctttgttacataaggtctgagttcgtccgacagaatatcctcgactcgtacagctgtgaagaatactcacgctgtaa

a      L  G  A  Y  I  L  L  E  T  M  Y  S  R  L  K  Q  A  V  L  *  E  L  S  M  S  T  L  L  M  S  A  T  F  -
b     S  L  A  H  I  F  Y  W  K  Q  C  I  P  D  S  S  R  L  S  Y  R  S  *  A  C  R  H  F  L  *  V  R  H  S -
c      A  W  R  I  Y  S  T  G  N  N  V  F  Q  T  Q  A  G  C  L  I  G  A  E  H  V  D  T  S  Y  E  C  D  I  -

     cctattggagctggcatttgtgctagttaccatacagTTAGACTAGAAagccgaattctgcagatatccatcacactggcggccgcatcgatgagctct
4101 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 4200
     ggataacctcgaccgtaaacacgatcaatggtatgtcAATCTGATCTTtcggcttaagacgtctataggtagtgtgaccgccggcgtagctactcgaga

a     L  L  E  L  A  F  V  L  V  T  I  Q  L  D  *  K  S  R  I  L  Q  I  S  I  T  L  A  A  A  S  M  S  S  -
b      Y  W  S  W  H  L  C  *  L  P  Y  S  *  T  R  K  A  E  F  C  R  Y  P  S  H  W  R  P  H  R  *  A  L  -
c     P  I  G  A  G  I  C  A  S  Y  H  T  V  R  L  E  K  P  N  S  A  D  I  H  H  T  G  G  R  I  D  E  L  * -
```

Figure 1-K

```
        MseI
        PacI                                          BfaI
  Tsp509I  |                                         AluI|
    AseI|  |                                        CviJI|                                    Eco57I
    MseI|  |CviJI             Tsp509I               MboII|                                   Eco57MI
       ||  |    |                   |                   ||                                         |
     aattaattaaggcttttctgctaacatatagcaatttttgaagaaaggaaagctagaaatacccaatatcttgctgaagcaagatattgggtatttcttt
4201 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 4300
     ttaattaattccgaaaagacgattgtatatcgttaaaaacttctttcctttcgatctttatgggttatagaacgacttcgttctataacccataaagaaa

a    N  *  L  R  L  F  C  *  H  I  A  I  F  E  E  R  K  A  R  N  T  Q  Y  L  A  E  A  R  Y  W  V  F  L  F  -
b     I  N  *  G  F  S  A  N  I  *  Q  F  L  K  K  G  K  L  E  I  P  N  I  L  L  K  Q  D  I  G  Y  F  F    -
c      L  I  K  A  F  L  L  T  Y  S  N  F  *  R  K  E  S  *  K  Y  P  I  S  C  *  S  K  I  L  G  I  S  F   -

                                     Hin4I                                                           ApoI
                             ApoI   HincII                                                          EcoRI
                            EcoRI     HpaI                    HpyCH4V                             Tsp509I
             HinfI        Tsp509I    Hpy8I                     BciVI|     Hpy188III              RsaI   |
              TfiI       Hpy188I|    MseI| Hpy99I         TspDTI   ||Hin4I  BssSI |            Csp6I|   |
                 |             ||       ||      |              |   ||    |      | |                ||   |
     tttttttattttgaatctttctattctgaattcagttaacgacgagatttagtatcctttcttgcactttcataactcgtgaaatgccgagttggtacga
4301 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 4400
     aaaaaaataaaacttagaaagataagacttaagtcaattgctgctctaaatcataggaaagaacgtgaaagtattgagcactttacggctcaaccatgct

a      F  L  F  *  I  F  L  F  *  I  Q  L  T  T  R  F  S  I  L  S  C  T  F  I  T  R  E  M  P  S  W  Y  E   -
b    F  F  Y  F  E  S  F  Y  S  E  F  S  *  R  R  D  L  V  S  F  L  A  L  S  *  L  V  K  C  R  V  G  T  N  -
c     F  F  I  L  N  L  S  I  L  N  S  V  N  D  E  I  *  Y  P  F  L  H  F  H  N  S  *  N  A  E  L  V  R    -

                                                                                        BsrDI
                                                                                       FauI |
                                                                        BstUI     CviJI    | |
                                                                         NruI    HaeIII    | |
                                                                   Hpy188III|      MscI    | |
                         BslI                                      HinfI   ||     EaeI |   | |    SfaNI
      Tsp509I         EcoNI |                                       TfiI   ||  TspDTI| |   | | AciI   |
            |             | |                                          |   ||       || |   | |    |   |
     attcccccaatttgcgacctaccataggatttgttatgtaaataggtatatgttcctttccattatgaatcgcgattgtatggccaaccattgcgggtag
4401 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 4500
     taagggggttaaacgctggatggtatcctaaacaatacatttatccatatacaaggaaaggtaatacttagcgctaacataccggttggtaacgcccatc

a     F  P  Q  F  A  T  Y  H  R  I  C  Y  V  N  R  Y  M  F  L  S  I  M  N  R  D  C  M  A  N  H  C  G  *    -
b      S  P  N  L  R  P  T  I  G  F  V  M  *  I  G  I  C  S  F  P  L  *  I  A  I  V  W  P  T  I  A  G  R   -
c    I  P  P  I  C  D  L  P  *  D  L  L  C  K  *  V  Y  V  P  F  H  Y  E  S  R  L  Y  G  Q  P  L  R  V  E  -

                         TaiI
                     MaeIII |
                  HpyCH4IV| |
                 NlaIV   || |
                AvaII|   || |
               Sau96I|   || |
               NciI ||   || |
              ScrFI ||   || |
               SmaI ||   || |
             HpaII| ||   || |
              NciI| ||   || |
             ScrFI| ||   || |
             AvaI|| ||   || |
            BsaJI|| ||   || |                                                             KpnI
           StyD4I|| ||   || |                                                         NlaIV  |
             XmaI|| ||   || |                                                           RsaI |
          StyD4I||| ||   || |                             AluI                        Csp6I| |
       BsmI   |||| ||   || |  BseRI                     CviJI              BccI    Acc65I|| |      MnlI
      BfaI|    |||| ||   || |BsmFI |TspDTI           MnlI    |          Hin4I  |      BanI|| |  AciI   |
         ||    |||| ||   || |    | |     |              |    |              |  |         ||| |      |  |
     aatgctagatgcccgggaccacgttactattgtttctttctcctccttcatattgagcttttctatttttgccaataaatgatggtacctccccccgcca
4501 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 4600
     ttacgatctacgggccctggtgcaatgataacaaagaaagaggaggaagtataactcgaaaagataaaaacggttatttactaccatggaggggggcggt

a    N  A  R  C  P  G  P  R  Y  Y  C  F  F  L  L  L  H  I  E  L  F  Y  F  C  Q  *  M  M  V  P  P  P  A  T  -
b     M  L  D  A  R  D  H  V  T  I  V  S  F  S  S  F  I  L  S  F  S  I  F  A  N  K  *  W  Y  L  P  P  P    -
c      C  *  M  P  G  T  T  L  L  L  F  L  S  P  P  S  Y  *  A  F  L  F  L  P  I  N  D  G  T  S  P  R  H   -
```

Figure 1-L

```
        BsiEI
       BstKTI
        Hin4I
         PvuI                                                                          CviJI            HaeII
         TaqI                                                                       BstNI  |            HhaI|
        DpnI|                                 TaiI                 BpmI             ScrFI  |           AfeI||
       FauI||                              BmgBI |              Eco57MI           PspGI  | |        HinP1I|||
      MboI|||       MnlI     CviJI     HpyCH4IV| |           CviJI    |          StyD4I  | |   Hpy188I   ||||
         ||||          |         |            || |               |    |                | | |         |   ||||
         cgatcgaacgggaatggataagaggcttgtgggattgacgtgatagggtagggttggctatactgctggtggcgaactccaggctaataatctgaagcgc
    4601 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 4700
         gctagcttgcccttacctattctccgaacaccctaactgcactatcccatcccaaccgatatgacgaccaccgcttgaggtccgattattagacttcgcg

a          I  E  R  E  W  I  R  G  L  W  D  *  R  D  R  V  G  L  A  I  L  L  V  A  N  S  R  L  I  I  *  S  A  -
b        R  S  N  G  N  G  *  E  A  C  G  I  D  V  I  G  *  G  W  L  Y  C  W  W  R  T  P  G  *  *  S  E  A  L -
c         D  R  T  G  M  D  K  R  L  V  G  L  T  *  *  G  R  V  G  Y  T  A  G  G  E  L  Q  A  N  N  L  K  R   -

                       BstKTI
                        DpnI|               HpyF10VI                                                     BccI
                       NlaIV|            AciI      |                                                    BceAI|
                     BamHI ||      HpyF10VI |      |                                                  TaqI ||
                     BstYI ||         MwoI| |      |                                            Hpy188III| ||
                Eco57I   | || Hpy188III  || |      |        HinfI                               HaeII   || ||
               Eco57MI   | ||   BssSI |  || |      |       TaqI |        HgaI                   HhaI|   || ||
                 AlwI|   | ||  CviJI| |  || |      |   MlyI   | |   Hpy188I               HinP1I ||   || ||
             MnlI   ||MboI || AlwI || |  || | MwoI|   PleI   | | MnlI     |     BsaHI  TaqI   | ||   || ||
                |   ||   | ||    | || |  || |     ||      |   | |     |     |          |     |   | ||   || ||
         ttggaagttgtagggaggatcctatggctcgtgaagcggttatcgccgaagtatcgactcaactatcagaggtagttggcgtcatcgagcgccatctcga
    4701 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 4800
         aaccttcaacatccctcctaggataccgagcacttcgccaatagcggcttcatagctgagttgatagtctccatcaaccgcagtagctcgcggtagagct

a         W  K  L  *  G  G  S  Y  G  S  *  S  G  Y  R  R  S  I  D  S  T  I  R  G  S  W  R  H  R  A  P  S  R   -
b          G  S  C  R  E  D  P  M  A  R  E  A  V  I  A  E  V  S  T  Q  L  S  E  V  V  G  V  I  E  R  H  L  E  -
c        L  E  V  V  G  R  I  L  W  L  V  K  R  L  S  P  K  Y  R  L  N  Y  Q  R  *  L  A  S  S  S  A  I  S  N -

                                                    CviJI
                       RsaI                        HaeIII
                     Csp6I|                          TauI
                  CviJI  ||             BccI     BstF5I |                                  HpyCH4III
                 HaeIII  ||           AciI |     Fnu4HI |                               BstEII     |
                Cac8I |  ||        NlaIV | |      AciI| |        DraIII              HpyCH4III     |
             TaiI   | |  ||       CviJI| | |   BceAI || |     HpyCH4III   Eco57I        MaeIII     |
          Hpy99I|   | |  ||    RsaI   || | |   BtsI| || |  CviJI      | Eco57MI         Tsp45I     | CviJI
      HpyCH4IV ||EaeI |  ||  Csp6I|   || | |  TspRI| || | FokI |      |TspRI   |  MaeIII     |     |  HphI
             | ||   | |  ||      ||   || | |      || || |    | |      |    |   |       |     |     |     |
         accgacgttgctggccgtacatttgtacggctccgcagtggatggcggcctgaagccacacagtgatattgatttgctggttacggtgaccgtaaggctt
    4801 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 4900
         tggctgcaacgaccggcatgtaaacatgccgaggcgtcacctaccgccggacttcggtgtgtcactataactaaacgaccaatgccactggcattccgaa

a        T  D  V  A  G  R  T  F  V  R  L  R  S  G  W  R  P  E  A  T  Q  *  Y  *  F  A  G  Y  G  D  R  K  A  * -
b         P  T  L  L  A  V  H  L  Y  G  S  A  V  D  G  G  L  K  P  H  S  D  I  D  L  L  V  T  V  T  V  R  L   -
c          R  R  C  W  P  Y  I  C  T  A  P  Q  W  M  A  A  *  S  H  T  V  I  L  I  C  W  L  R  *  P  *  G  L  -

                        AluI
                       CviJI
                     Cac8I |                                                         HphI
                    TspDTI |                                BstNI                   HhaI||
                    TauI | |                                ScrFI                 BpmI |||
                Fnu4HI | | | BstKTI                       BsaJI |                BstUI |||
                 AciI| | | |  DpnI|                       PspGI |              Eco57MI |||
                BstUI| | | |BclI ||                      StyD4I |        HinfI  HinP1I |||MaeIII        ApaLI
            Hin4I   || | | |MboI ||         Hin4I    CviJI    | |         TfiI  AciI | |||Tsp45I      MslI  |
                |   || | | |   ||             |        |    | |            |     | | |||     |         |  |
         gatgaaacaacgcggcgagctttgatcaacgaccttttggaaacttcggcttcccctggagagagcgagattctccgcgctgtagaagtcaccattgttg
    4901 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 5000
         ctactttgttgcgccgctcgaaactagttgctggaaaacctttgaagccgaaggggacctctctcgctctaagaggcgcgacatcttcagtggtaacaac

a          *  N  N  A  A  S  F  D  Q  R  P  F  G  N  F  G  F  P  W  R  E  R  D  S  P  R  C  R  S  H  H  C  C  -
b        D  E  T  T  R  R  A  L  I  N  D  L  L  E  T  S  A  S  P  G  E  S  E  I  L  R  A  V  E  V  T  I  V  V -
c         M  K  Q  R  G  E  L  *  S  T  T  F  W  K  L  R  L  P  L  E  R  A  R  F  S  A  L  *  K  S  P  L  L   -
```

Figure 1-M

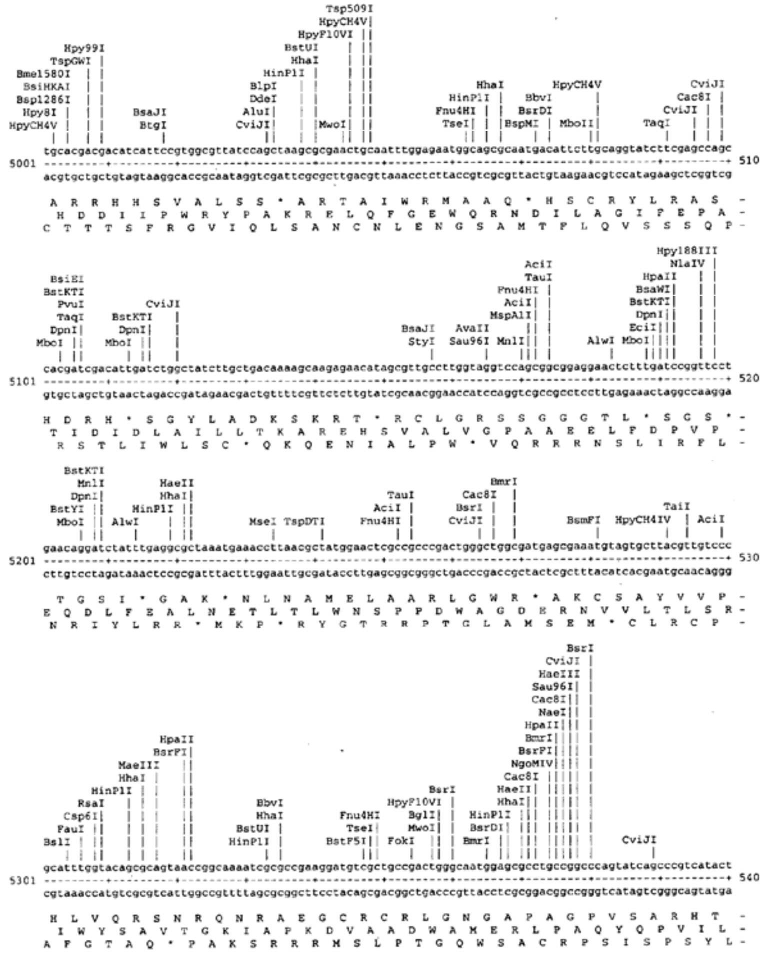

Tsp509I
HpyCH4V
HpyF10VI
BstUI
HhaI
HinP1I
BlpI
DdeI
AluI
CviJI
MwoI
Hpy99I
TspGWI
Bme1580I
BsiHKAI
Bsp1286I
Hpy8I
HpyCH4V
BsaJI
BtgI
HhaI
HinP1I
Fnu4HI
TseI
BbvI
BsrDI
BspMI
HpyCH4V
MboII
CviJI
Cac8I
CviJI
TaqI
tgcacgacgacatcattccgtggcgttatccagctaagcgcgaactgcaatttggagaatggcagcgcaatgacattcttgcaggtatcttcgagccagc
5001
5100
acgtgctgctgtagtaaggcaccgcaataggtcgattcgcgcttgacgttaaacctcttaccgtcgcgttactgtaagaacgtccatagaagctcggtcg
a A R R H H S V A L S S * A R T A I W R M A A Q * H S C R Y L R A S -
b H D D I I P W R Y P A K R E L Q F G E W Q R N D I L A G I F E P A -
c C T T T S F R G V I Q L S A N C N L E N G S A M T F L Q V S S S Q P -
Hpy188III
NlaIV
AciI
TauI
HpaII
BsaWI
BstKTI
DpnI
EciI
MboI
AlwI
Fnu4HI
AciI
MspA1I
AvaII
Sau96I
MnlI
BsaJI
StyI
BsiEI
BstKTI
PvuI
TaqI
DpnI
MboI
CviJI
BstKTI
DpnI
MboI
cacgatcgacattgatctggctatcttgctgacaaaagcaagagaacatagcgttgccttggtaggtccagcggcggaggaactctttgatccggttcct
5101
5200
gtgctagctgtaactagaccgatagaacgactgttttcgttctcttgtatcgcaacggaaccatccaggtcgccgcctccttgagaaactaggccaagga
a H D R H * S G Y L A D K S K R T * R C L G R S S G G G T L * S G S * -
b T I D I D L A I L L T K A R E H S V A L V G P A A E E L F D P V P -
c R S T L I W L S C * Q K Q E N I A L P W * V Q R R R N S L I R F L -
BstKTI
MnlI
DpnI
BstYI
MboI
AlwI
HaeII
HhaI
HinP1I
MseI
TspDTI
TauI
AciI
Fnu4HI
BmrI
Cac8I
BsrI
CviJI
BsmFI
HpyCH4IV
TaiI
AciI
gaacaggatctatttgaggcgctaaatgaaaccttaacgctatggaactcgccgcccgactgggctggcgatgagcgaaatgtagtgcttacgttgtccc
5201
5300
cttgtcctagataaactccgcgatttactttggaattgcgataccttgagcggcgggctgacccgaccgctactcgctttacatcacgaatgcaacaggg
a T G S I * G A K * N L N A M E L A A R L G W R * A K C S A Y V V P -
b E Q D L F E A L N E T L T L W N S P P D W A G D E R N V V L T L S R -
c N R I Y L R R * M K P * R Y G T R R P T G L A M S E M * C L R C P -
BsrI
CviJI
HaeIII
Sau96I
Cac8I
NaeI
HpaII
BmrI
BsrFI
NgoMIV
Cac8I
HaeII
HhaI
HinP1I
BsrDI
BmrI
BsrI
HpyF10VI
BglI
MwoI
FokI
Fnu4HI
TseI
BstF5I
BbvI
HhaI
BstUI
HinP1I
HpaII
BsrFI
MaeIII
HhaI
HinP1I
RsaI
Csp6I
FauI
BslI
CviJI
gcatttggtacagcgcagtaaccggcaaaatcgcgccgaaggatgtcgctgccgactgggcaatggagcgcctgccggcccagtatcagcccgtcatact
5301
5400
cgtaaaccatgtcgcgtcattggccgttttagcgcggcttcctacagcgacggctgacccgttacctcgcggacggccgggtcatagtcgggcagtatga
a H L V Q R S N R Q N R A E G C R C R L G N G A P A G P V S A R H T -
b I W Y S A V T G K I A P K D V A A D W A M E R L P A Q Y Q P V I L -
c A F G T A Q * P A K S R R R M S L P T G Q W S A C R P S I S P S Y L -

Figure 1-N

```
                                                                 BstKTI
                                                                  DpnI|
                                                                MboI ||
                                                                MnlI ||
                                                              HhaI | ||
                                                           BstUI | | ||
                                                           Cac8I | | ||
                                                            HhaI | | ||
                                                          HinP1I | | ||
                                                        HpyF10VI | | ||
                                                           MwoI| | | ||
                                                        BssHII|| | | ||
                                                         BstUI|| | | ||
                                                        HinP1I|| | | ||
                                                    CviJI    ||| | | ||
                                                   HaeIII    ||| | | ||
                                                    MboII    ||| | | ||                      TaiI
                      CviJI                        MmeI |    ||| | | ||                   BsaAI |            BcgI
                 HpyF10VI |                      MboII| |    ||| | | ||                  DraIII |           DdeI|
               BfaI     | |                 BstKTI   || |    ||| | | ||               HpyCH4IV| |      BstKTI  ||
              AluI|     | |                  DpnI|   || |    ||| | | ||      ApoI    MboII   || |       DpnI|  ||
             CviJI| MwoI| |                MboI ||   || |    ||| | | ||   Tsp509I   Hpy8I|   || |     MboI ||  ||
                 ||    || |                   | ||   || |    ||| | | ||         |       ||   || |        | ||  ||
            tgaagctagacaggcttatcttggacaagaagaagatcgcttggcctcgcgcgcagatcagttggaagaatttgtccactacgtgaaaggcgagatcact
       5401 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 5500
            acttcgatctgtccgaatagaacctgttcttcttctagcgaaccggagcgcgtctagtcaaccttcttaaacaggtgatgcactttccgctctagtga

   a        *  S  *  T  G  L  S  W  T  R  R  R  S  L  G  L  A  R  R  S  V  G  R  I  C  P  L  R  E  R  R  D  H  *  -
   b         E  A  R  Q  A  Y  L  G  Q  E  E  D  R  L  A  S  R  A  D  Q  L  E  E  F  V  H  Y  V  K  G  E  I  T    -
   c          K  L  D  R  L  I  L  D  K  K  K  I  A  W  P  R  A  Q  I  S  W  K  N  L  S  T  T  *  K  A  R  S  L   -

                         Hpy188III
                             TaqI|
                            AvaI||                                                           BstKTI
                            SmlI||                                                            DpnI|
                            XhoI||         Tsp509I                                          MboI ||
                        BsmAI  ||| DdeI    BcgI  |                       EarI      Hin4I MboII | ||   MaeIII
                            |  |||    |       |  |                          |          |     | | ||        |
            aaggtagttggcaaataactcgagactaagtggataaaattagatagaaaaaaggtctaaataaaaaagaagagaaatagaaagatcaaaaatcagttac
       5501 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 5600
            ttccatcaaccgtttattgagctctgattcacctattttaatctatctttttttccagatttattttttcttctctttatctttctagtttttagtcaatg

   a          G  S  W  Q  I  T  R  D  *  V  D  K  I  R  *  K  K  G  L  N  K  K  E  E  K  *  K  D  Q  K  S  V  T   -
   b        K  V  V  G  K  *  L  E  T  K  W  I  K  L  D  R  K  K  V  *  I  K  K  K  R  N  R  K  I  K  N  Q  L  R  -
   c         R  *  L  A  N  N  S  R  L  S  G  *  N  *  I  E  K  R  S  K  *  K  R  R  E  I  E  R  S  K  I  S  Y    -

                 Tsp509I
               Hin4I   |                            MseI          Hpy188I                                    DpnI
             HpyCH4V   |                      Tsp509I  |        BsmAI   |                  DraI            BsmAI|
               MboII   | MboII      Tsp509I  HpyCH4V|  |        BsmBI   |         CviJI   MseI|            MboI||
                   |   |     |            |        ||  |            |   |             |      ||               |||
            gaaaatgcagtaattcttcttttttcttctaattgattgcaattaaactcgtctcaatctgaaaaaagattgagccgagtttaaatagattttgatacga
       5601 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 5700
            cttttacgtcattaagaagaaaaaagaagattaactaacgttaatttgagcagagttagactttttttctaactcggctcaaatttatctaaaactatgct

   a         K  M  Q  *  F  F  F  F  L  L  I  D  C  N  *  T  R  L  N  L  K  K  D  *  A  E  F  K  *  I  L  I  R    -
   b          K  C  S  N  S  S  F  F  F  *  L  I  A  I  K  L  V  S  I  *  K  K  I  E  P  S  L  N  R  F  *  Y  D   -
   c        E  N  A  V  I  L  L  F  S  S  N  *  L  Q  L  N  S  S  Q  S  E  K  R  L  S  R  V  *  I  D  F  D  T  I  -

            NlaIII                                                                                        Bsu36I
      Hpy188III  |                                                                                 TaqI     DdeI
         BspHI|  |            HinfI                                                        BfaI   AlwI| BstKTI |
        BstKTI|  |             TfiI                                                   Hpy188III  AluI||  DpnI| |
          FatI|  |     Hpy188III  |          MnlI                MboII                    XbaI| CviJI||MboI || |
             ||  |             |  |             |                    |                       ||     |||   | || |
            tcatgagacttgacaaatcgggattcctctattctatatatttagaagatataaaggtataatacaataaataaatacaatctagaagctcgatgatcct
       5701 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 5800
            agtactctgaactgtttagccctaaggagataagatatataaatcttctatatttccatattatgttatttatttatgttagatcttcgagctactagga

   a        S  *  D  L  T  N  R  D  S  S  I  L  Y  I  *  K  I  *  R  Y  N  T  I  N  K  Y  N  L  E  A  R  *  S  L  -
   b         H  E  T  *  Q  I  G  I  P  L  F  Y  I  F  R  R  Y  K  G  I  I  Q  *  I  N  T  I  *  K  L  D  D  P    -
   c          M  R  L  D  K  S  G  F  L  Y  S  I  Y  L  E  D  I  K  V  *  Y  N  K  *  I  Q  S  R  S  S  M  I  L   -
```

Figure 1-O

```
                                                                                BstF5I
                                                 HinfI                          BsmFI|
                                SfcI              TfiI  CviJI       FokI        MnlI||    BccI TspGWI
                                  |                   |     |          |            ||       |      |
        taggattggtatattcttttctatcctgtagtttgtagtttccctgaatcaagccaagtatcacacctctttctacccatcctgtatattgtcccctttg
   5801 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 5900
        atcctaaccatataagaaaagataggacatcaaacatcaaagggacttagttcggttcatagtgtggagaaagatgggtaggacatataacaggggaaac

a          G  L  V  Y  S  F  L  S  C  S  L  *  F  P  *  I  K  P  S  I  T  P  L  S  T  H  P  V  Y  C  P  L  C  -
b         *  D  W  Y  I  L  F  Y  P  V  V  C  S  F  P  E  S  S  Q  V  S  H  L  F  L  P  I  L  Y  I  V  P  F  V -
c         R  I  G  I  F  F  S  I  L  *  F  V  V  S  L  N  Q  A  K  Y  H  T  S  F  Y  P  S  C  I  L  S  P  L   -

                                                   ApoI
                     Tsp509I                    Tsp509I                                                     Tsp509I
                        MseI|                      MseI |                                                         |
                            ||                         | |                                                        |
        ttccgtgttgaaatagaaccttaatttattacttatttttttattaaattttagatttgttagtgattagatattagtattagacgagattttacgaaac
   5901 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 6000
        aaggcacaactttatcttggaattaaataatgaataaaaaaataatttaaaatctaaacaatcactaatctataatcataatctgctctaaaatgctttg

a         S  V  L  K  *  N  L  N  L  L  L  I  F  L  L  N  F  R  F  V  S  D  *  I  L  V  L  D  E  I  L  R  N   -
b          P  C  *  N  R  T  L  I  Y  Y  L  F  F  Y  *  I  L  D  L  L  V  I  R  Y  *  Y  *  T  R  F  Y  E  T  -
c        F  R  V  E  I  E  P  *  F  I  T  Y  F  F  I  K  F  *  I  C  *  *  L  D  I  S  I  R  R  D  F  T  K  Q -

                                                          ApoI                     TauI
                                                       Tsp509I                   AciI |
                   MnlI                                 Hin4I |                Fnu4HI |      Tsp509I
                 Hin4I |                SfaNI      TaqI      | |                CviJI| |    MseI    |   FalI
                      | |                 |       |           | |                    || |       |    |      |
        aattatttttttatttctttataggagaggacaaatctcttttttcgatgcgaatttgacacgacataggagaagccgccctttattaaaaattatatta
   6001 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 6100
        ttaataaaaaaataaagaaatatcctctcctgtttagagaaaaaagctacgcttaaactgtgctgtatcctcttcggcgggaaataattttaatataat

a        N  Y  F  F  I  S  L  *  E  R  T  N  L  F  F  R  C  E  F  D  T  T  *  E  K  P  P  F  I  K  N  Y  I  I -
b         I  I  F  L  F  L  Y  R  R  G  Q  I  S  F  F  D  A  N  L  T  R  H  R  R  S  R  P  L  L  K  I  I  L   -
c          L  F  F  Y  F  F  I  G  E  D  K  S  L  F  S  M  R  I  *  H  D  I  G  E  A  A  L  Y  *  K  L  Y  Y -

                                                                    Hpy188I
         DraI                        AseI                    HinfI      |
        MseI|              NlaIV     MseI            MmeI     TfiI      |                                  MseI
           ||                  |        |               |        |      |                                  |
        ttttaaataatataaagggggttccaacatattaatatatagtgaagtgttcccccagattcagaactttttttcaatactcacaatccttattagttaa
   6101 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 6200
        aaaatttattatatttcccccaaggttgtataattatatatcacttcacaagggggtctaagtcttgaaaaaaagttatgagtgttaggaataatcaatt

a          L  N  N  I  K  G  V  P  T  Y  *  Y  I  V  K  C  S  P  R  F  R  T  F  F  Q  Y  S  Q  S  L  L  V  N  -
b        F  *  I  I  *  R  G  F  Q  H  I  N  I  *  *  S  V  P  P  D  S  E  L  F  F  N  T  H  N  P  Y  *  L  I -
c         F  K  *  Y  K  G  G  S  N  I  L  I  Y  S  E  V  F  P  Q  I  Q  N  F  F  S  I  L  T  I  L  I  S  *  -

                                    Hpy188I                                 TspDTI                     Hin4I
          BfaI                 DdeI       |                     Tsp509I  Hin4I    |             TspDTI     FatI |
             |                    |       |                           |        |    |                  |         ||
        taatcctagtgattggatttctatgcttagtctgataggaaataagatattcaaataaataattttatagcgaatgactattcatctattgtattttcat
   6201 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 6300
        attaggatcactaacctaaagatacgaatcagactatcctttattctataagtttatttattaaaatatcgcttactgataagtagataacataaaagta

a         N  P  S  D  W  I  S  M  L  S  L  I  G  N  K  I  F  K  *  I  I  L  *  R  M  T  I  H  L  L  Y  F  H   -
b          I  L  V  I  G  F  L  C  L  V  *  *  E  I  R  Y  S  N  K  *  F  Y  S  E  *  L  F  I  Y  C  I  F  M -
c        *  S  *  *  L  D  F  Y  A  *  S  D  R  K  *  D  I  Q  I  N  N  F  I  A  N  D  Y  S  S  I  V  F  S  C -

                                                                          BstBI
                                                                           TaqI
                                                                      AarI |
 HpyCH4V                                Tsp509I                      BspMI |
 NlaIII                      BccI          MseI|TaqI        MseI     XmnI| |                    CviJI
        |                         |              || |            |        || |                      |
        gcaaatagggggcaagaaaactctatggaaagatggtggtttaattcgatgttgtttaagaaggagttcgaacgcaggtgtgggctaaataaatcaatgg
   6301 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 6400
        cgtttatccccccgttcttttgagatacctttctaccaccaaattaagctacaacaaattcttcctcaagcttgcgtccacacccgatttatttagttacc

a        A  N  R  G  Q  E  N  S  M  E  R  W  W  F  N  S  M  L  F  K  K  E  F  E  R  R  C  G  L  N  K  S  M  G -
b         Q  I  G  G  K  K  T  L  W  K  D  G  G  L  I  R  C  C  L  R  R  S  S  N  A  G  V  G  *  I  N  Q  W   -
c          K  *  G  A  R  K  L  Y  G  K  M  V  V  *  F  D  V  V  *  E  G  V  R  T  Q  V  W  A  K  *  I  N  G -
```

Figure 1-P

```
                                                                              Tsp509I
                                     BsaBI     TspDTI                  Hpy188III    |
                                  BstKTI |    MmeI  |                     MaeIII    |
                                   DpnI| |TspDTI |  |                     Tsp45I    |    HpyCH4V
         AvaII                  BstYI || |MboII| |  |         MnlI     HinfI   |    |    BsaXI |
        Sau96I              AlwI MboI || |TaqI|| |  |      BsaXI |      TfiI   |    | BfaI   | |
             |                 |    | || |   ||| |  |          | |         |   |    |    |   | |
     gcagtcttggtcctattgaaaataccaatgaagatccaaatcgaaaagtgaaaaacattcatagttggaggaatcgtgacaattctagttgcagtaatgt
6401 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 6500
     cgtcagaaccaggataacttttatggttacttctaggtttagcttttcactttttgtaagtatcaacctccttagcactgttaagatcaacgtcattaca

a      S  L  G  P  I  E  N  T  N  E  D  P  N  R  K  V  K  N  I  H  S  W  R  N  R  D  N  S  S  C  S  N  V  -
b    A  V  L  V  L  L  K  I  P  M  K  I  Q  I  E  K  *  K  T  F  I  V  G  G  I  V  T  I  L  V  A  V  M  L -
c     Q  S  W  S  Y  *  K  Y  Q  *  R  S  K  S  K  S  E  K  H  S  *  L  E  E  S  *  Q  F  *  L  Q  *  C   -

                                ApoI
                             Tsp509I
                            Hpy188I|
                   MseI TspDTI    ||     Hpy188I                     BsmAI  HpyCH4III           BccI
                      |      |    ||           |                         |          |              |
     tgattatttattcggcgttaaagacattcggaatttcatctctgatgacacttttttagttagtgataggaatggagacagttattccatctattttgat
6501 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 6600
     actaataaataagccgcaatttctgtaagccttaaagtagagactactgtgaaaaaatcaatcactatccttacctctgtcaataaggtagataaaacta

a     D  Y  L  F  G  V  K  D  I  R  N  F  I  S  D  D  T  F  L  V  S  D  R  N  G  D  S  Y  S  I  Y  F  D   -
b      I  I  Y  S  A  L  K  T  F  G  I  S  S  L  M  T  L  F  *  L  V  I  G  M  E  T  V  I  P  S  I  L  I  -
c    *  L  F  I  R  R  *  R  H  S  E  F  H  L  *  *  H  F  F  S  *  *  *  E  W  R  Q  L  F  H  L  F  *  Y -

                                  BspCNI
                                 BseMII|
                                BstKTI||
                                 DpnI|||  Hpy188I    BfaI                         Tsp509I
                               MboI ||||    DdeI|Hpy8I  |                   TaqI   TaqI | Hpy188I
                                  | ||||       ||    |  |                      |      | |       |
     attgaaaatcatatttttgagattgacaacgatcattcttttctgagtgaactagaaagttctttttatagttatcgaaactcgaattatcggaataatg
6601 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 6700
     taacttttagtataaaaactctaactgttgctagtaagaaaagactcacttgatctttcaagaaaaatatcaatagctttgagcttaatagccttattac

a    I  E  N  H  I  F  E  I  D  N  D  H  S  F  L  S  E  L  E  S  S  F  Y  S  Y  R  N  S  N  Y  R  N  N  G -
b     L  K  I  I  F  L  R  L  T  T  I  I  L  F  *  V  N  *  K  V  L  F  I  V  I  E  T  R  I  I  G  I  M   -
c      *  K  S  Y  F  *  D  *  Q  R  S  F  F  S  E  *  T  R  K  F  F  L  *  L  S  K  L  E  L  S  E  *  W  -

                                     NlaIII
                                       NspI
                BstKTI               MmeI |
                 DpnI|           AflIII | |                                  HpyCH4V
              BstYI ||  Tsp509I    FatI | |                            AseI  Eco57I|    BsaBI
          AlwI MboI ||  MboII |    PciI | |                            MseI Eco57MI|MboII   |
             |    | ||      | |       | | |                               |       ||    |   |
     gatttaggggcgaagatccctactataattcttacatgtatgatactcaatatagttggaataatcacattaatagttgcattgatagttatcttcagtc
6701 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 6800
     ctaaatccccgcttctagggatgatattaagaatgtacatactatgagttatatcaaccttattagtgtaattatcaacgtaactatcaatagaagtcag

a      F  R  G  E  D  P  Y  Y  N  S  Y  M  Y  D  T  Q  Y  S  W  N  N  H  I  N  S  C  I  D  S  Y  L  Q  S  -
b    D  L  G  A  K  I  P  T  I  I  L  T  C  M  I  L  N  I  V  G  I  I  T  L  I  V  A  L  I  V  I  F  S  L -
c     I  *  G  R  R  S  L  L  *  F  L  H  V  *  Y  S  I  *  L  E  *  S  H  *  *  L  H  *  *  L  S  S  V   -

                                                     BceAI
                                                 HpyCH4III
                                                    MaeIII
                                           HpyCH4III     |          CviJI
                                              MaeIII     |         HaeIII                    HphI
   BsmAI                   PsiI       Tsp509I Tsp45I     |  HphI Sau96I |                TaqI   |    MnlI
       |                      |             |      |     |     |      | |                   |   |       |
     tcaaatctgtatagatacttccattataagtggtagtgagaattacggtgacagttacatttatagggccgtttgtggtggtgaaagtcgaaatagtagt
6801 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 6900
     agtttagacatatctatgaaggtaatattcaccatcactcttaatgccactgtcaatgtaaatatcccggcaaacaccaccactttcagctttatcatca

a     Q  I  C  I  D  T  S  I  I  S  G  S  E  N  Y  G  D  S  Y  I  Y  R  A  V  C  G  G  E  S  R  N  S  S   -
b      K  S  V  *  I  L  P  L  *  V  V  V  R  I  T  V  T  V  T  F  I  G  P  F  V  V  V  K  V  E  I  V  V  -
c    S  N  L  Y  R  Y  F  H  Y  K  W  *  *  E  L  R  *  Q  L  H  L  *  G  R  L  W  W  *  K  S  K  *  *  * -
```

Figure 1-Q

```
                                                                              MaeIII
                                                                            TaqI   |
                                                                           AvaI|   |
                                                                      Hpy188III|   |
                                                                           SmlI|   |
                                                                           XhoI|   |
                                                                        BstKTI||   |
                    Hpy8I                       MseI                     DpnI|||   |
                BsrI    |         HpyF10VI     BtsI|                   MboI ||||   |
             NlaIV |AccI|            MwoI|    TspRI|                   MnlI ||||   |
                 | |   ||               ||        ||                      | ||||   |
      gaaaacgagggttccagtagacgaactcgcacgaagggcagtgatttaactataagagaaagttctaatgatctcgaggtaactcaaaaatacaggcatt
 6901 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 7000
      cttttgctcccaaggtcatctgcttgagcgtgcttcccgtcactaaattgatattctctttcaagattactagagctccattgagtttttatgtccgtaa

a     E  N  E  G  S  S  R  R  T  R  T  K  G  S  D  L  T  I  R  E  S  S  N  D  L  E  V  T  Q  K  Y  R  H  L -
b      K  T  R  V  P  V  D  E  L  A  R  R  A  V  I  *  L  *  E  K  V  L  M  I  S  R  *  L  K  N  T  G  I  -
c       K  R  G  F  Q  *  T  N  S  H  E  G  Q  *  F  N  Y  K  R  K  F  *  *  S  R  G  N  S  K  I  Q  A  F -

                                            ApoI
                               Tsp509I   Tsp509I                           TspDTI
                Tsp509I         MseI | PsiI    |                   SspI  Hpy8I  |    EcoRV
                      |            | |    |    |                      |      |  |        |
      tgtgggttcaatgcgaaaattgttatggattaaattataagaaattttgaaatcaaaaatgaatatttgtgaacaatgtggatatcatttgaaaatgag
 7001 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 7100
      acacccaagttacgcttttaacaatacctaatttaatattctttaaaactttagtttttacttataaacacttgttacacctatagtaaacttttactc

a       W  V  Q  C  E  N  C  Y  G  L  N  Y  K  K  F  L  K  S  K  M  N  I  C  E  Q  C  G  Y  H  L  K  M  S  -
b     C  G  F  N  A  K  I  V  M  D  *  I  I  R  N  F  *  N  Q  K  *  I  F  V  N  N  V  D  I  I  *  K  *  V -
c      V  G  S  M  R  K  L  L  W  I  K  L  *  E  I  F  E  I  K  N  E  Y  L  *  T  M  W  I  S  F  E  N  E  -

              ApoI
             EcoRI                                              Tsp509I
           Tsp509I        NlaIII   AluI                      BsrBI    |                HpaII
      Hpy188I    |      FatI   |  CviJI        Tsp509I      AciI |    |               CviJI|
            |    |         |   |      |              |         | |    |                   ||
      tagttcagatagaattcgtaatcatggtcatagctgtttcctgtgtgaaattgttatccgctcacaattccacacaacatacgagccggaagcataaagt
 7101 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 7200
      atcaagtctatcttaagcattagtaccagtatcgacaaaggacacactttaacaataggcgagtgttaaggtgtgttgtatgctcggccttcgtatttca

a      S  S  D  R  I  R  N  H  G  H  S  C  P  L  C  E  I  V  I  R  S  Q  F  H  T  T  Y  E  P  E  A  *  S  -
b       V  Q  I  E  F  V  I  M  V  I  A  V  S  C  V  K  L  L  S  A  H  N  S  T  Q  H  T  S  R  K  H  K  V -
c     *  F  R  *  N  S  *  S  W  S  *  L  F  P  V  *  N  C  Y  P  L  T  I  P  H  N  I  R  A  G  S  I  K  C -

                                                                                                    AseI
                                                                                                    MseI
               NlaIV                                       AciI                           HpyCH4V  |
           HpyF10VI|                                      Cac8I                          Fnu4HI |  |
         BstNI    ||                                      TspRI                           AluI| |  |
         ScrFI    ||                                   HpyF10VI   |                      CviJI| |  |
        BsaJI|    ||                                      MwoI|   |                     MspA1I| |  |
       CviJI||    ||                   Tsp509I          BtsI ||   |   Hpy188III              PvuII| |  |
       PspGI||BanI||          AluI       AseI|        HhaI | ||   |   BsrI    |               TseI| |  |
      StyD4I||MwoI||         CviJI       MseI|    HinP1I | | ||   |   FauI    |  BbvI      Cac8I || |  |
           |||   |||             |          ||         | | | ||   |      |    |     |          | || |  |
      gtaaagcctggggtgcctaatgagtgagctaactcacattaattgcgttgcgctcactgcccgctttccagtcgggaaacctgtcgtgccagctgcatta
 7201 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 7300
      catttcggaccccacggattactcactcgattgagtgtaattaacgcaacgcgagtgacgggcgaaaggtcagccctttggacagcacggtcgacgtaat

a     V  K  P  G  V  P  N  E  *  A  N  S  H  *  L  R  C  A  H  C  P  L  S  S  R  E  T  C  R  A  S  C  I  N -
b      *  S  L  G  C  L  M  S  E  L  T  H  I  N  C  V  A  L  T  A  R  F  P  V  G  K  P  V  V  P  A  A  L  -
c       K  A  W  G  A  *  *  V  S  *  L  T  L  I  A  L  R  S  L  P  A  F  Q  S  G  N  L  S  C  Q  L  H  * -
```

Figure 1-R

```
                     AciI
                    BstUI
                     HhaI
                     MnlI
                    BslI|
                  TspDTI|
                  BstUI||                                                         BbvI
                 HinP1I||                                                         HhaI
                BsaXI |||                        HaeII                        HinP1I  |              Cac8I
              FauI  | |||                         HhaI|                     Fnu4HI  | |              TauI  |
            CviJI|  | |||                     BsaXI  ||                       TseI| | |          Fnu4HI  | |
           HaeIII|  | |||                    HinP1I  ||                   TaqII   || | |            AciI | | |
          EaeI  ||  | |||                  HpyF10VI  | ||  EarI      MlyI   TspRI   || | |      Fnu4HI  || | |
      HinfI   |  ||  | |||                    MwoI| | ||  SapI      PleI HinfI  |  || | |       CviJI| || | |
       TfiI   |  ||  | |||      AciI        MboII|| | || AciI|  BbvI | MnlI| |  || | |  BsiEI   TseI| || | |
          |   |  ||  | |||         |         ||| | ||    ||      | |   || |  || | |     |      || || | |
        atgaatcggccaacgcgcggggagaggcggtttgcgtattgggcgctcttccgcttcctcgctcactgactcgctgcgctcggtcgttcggctgcggcga
   7301 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 7400
        tacttagccggttgcgcgcccctctccgccaaacgcataacccgcgagaaggcgaaggagcgagtgactgagcgacgcgagccagcaagccgacgccgct

a        E  S  A  N  A  R  G  E  A  V  C  V  L  G  A  L  P  L  P  R  S  L  T  R  C  A  R  S  F  G  C  G  E  -
b       M  N  R  P  T  R  G  E  R  R  F  A  Y  W  A  L  F  R  F  L  A  H  *  L  A  A  L  G  R  S  A  A  A  S -
c         *  I  G  Q  R  A  G  R  G  G  L  R  I  G  R  S  S  A  S  S  L  T  D  S  L  R  S  V  V  R  L  R  R  -

                                                                                                       NlaIV
                                                                                                   BstNI    |
                                                                                                   ScrFI    |
              AluI                                                        NlaIII                 CviJI  |   |
             CviJI                                                          NspI                HaeIII  |   |
        HpyF10VI |                                                      AflIII  |        Cac8I   PspGI  |   |
     AciI     ¦ |                             HinfI                       FatI  |      CviJI |  StyD4I  |   |
    BsrBI MwoI|| |        AciI HpyCH4III       TfiI                       PciI  |     HaeIII | BslI  |  |   |
        |     || |            |         |          |                        |   |           |  |    |   |   |
        gcggtatcagctcactcaaaggcggtaatacggttatccacagaatcaggggataacgcaggaaagaacatgtgagcaaaaggccagcaaaaggccagga
   7401 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 7500
        cgccatagtcgagtgagtttccgccattatgccaataggtgtcttagtcccctattgcgtcctttcttgtacactcgttttccggtcgttttccggtcct

a        R  Y  Q  L  T  Q  R  R  *  Y  G  Y  P  Q  N  Q  G  I  T  Q  E  R  T  C  E  Q  K  A  S  K  R  P  G  -
b         G  I  S  S  L  K  G  G  N  T  V  I  H  R  I  R  G  *  R  R  K  E  H  V  S  K  R  P  A  K  G  Q  E -
c       A  V  S  A  H  S  K  A  V  I  R  L  S  T  E  S  G  D  N  A  G  K  N  M  *  A  K  G  Q  Q  K  A  R  N -

                        Cac8I
                     HpyF10VI
                  BstUI       |                                                    Hpy188I
                   TauI       |                                                    HgaI  |
                 AciI |       |                                                DrdI   |  |
               Fnu4HI |       |                                                MnlI   |  |
               CviJI| |       |                 AciI                         SmlI |   |  |
              HaeIII| |       |                NlaIV |                    Hpy99I| |   |  |
  HpyCH4III BslI   || |   MwoI|     EciI     CviJI| |             BpuEI SfaNI  |  || |   |  |
          |    |   || |     ||       |        || |                  |     |  |  || |   |  |
        accgtaaaaaggccgcgttgctggcgtttttccataggctccgcccccctgacgagcatcacaaaaatcgacgctcaagtcagaggtggcgaaacccgac
   7501 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 7600
        tggcatttttccggcgcaacgaccgcaaaaaggtatccgaggcggggggactgctcgtagtgtttttagctgcgagttcagtctccaccgctttgggctg

a       T  V  K  R  P  R  C  W  R  F  S  I  G  S  A  P  L  T  S  I  T  K  I  D  A  Q  V  R  G  G  E  T  R  Q -
b        P  *  K  G  R  V  A  G  V  F  P  *  A  P  P  P  *  R  A  S  Q  K  S  T  L  K  S  E  V  A  K  P  D  -
c         R  K  K  A  A  L  L  A  F  F  H  R  L  R  P  P  D  E  H  H  K  N  R  R  S  S  Q  R  W  R  N  P  T  -

                                                                                EciI
                                                                              HpaII|
                                                                             BsaWI||
                                                      MnlI                    BslI||
                                 BstNI              HhaI |                  BciVI |||
                    BstNI        ScrFI           HinP1I| |                   TauI| |||
                    ScrFI      BsaJI |     BssSI     | | |                     || |||
                  PspGI |      PspGI |  AluI    |    | | |             AciI || |||          AciI
                 StyD4I |     StyD4I | CviJI    |    | | |    Hpy188I Fnu4HI || |||     MmeI   |
                      | |          | |     |    |    | | |         |       | || |||       |   |
        aggactataaagataccaggcgtttccccctggaagctccctcgtgcgctctcctgttccgaccctgccgcttaccggatacctgtccgcctttctccct
   7601 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 7700
        tcctgatatttctatggtccgcaaagggggaccttcgagggagcacgcgagaggacaaggctgggacggcgaatggcctatggacaggcggaaagaggga

a        D  Y  K  D  T  R  R  F  P  L  E  A  P  S  C  A  L  L  F  R  P  C  R  L  P  D  T  C  P  P  F  S  L  -
b       R  T  I  K  I  P  G  V  S  P  W  K  L  P  R  A  L  S  C  S  D  P  A  A  Y  R  I  P  V  R  L  S  P  P -
c         G  L  *  R  Y  Q  A  F  P  P  G  S  S  L  V  R  S  P  V  P  T  L  P  L  T  G  Y  L  S  A  P  L  P  -
```

Figure 1-S

```
                                                                                      Bme1580I
                                                                                       BsiHKAI
                                                                                CviJI Bsp1286I
                   HaeII                                                    AluI    |  Hpy8I |
                   HhaI|      AluI                         BseMII          BseYI    |HpyCH4V |
 Hpy188III     HinP1I ||     CviJI   SfcI      DdeI       BspCNI|          CviJI    |ApaLI | |       BbvI
         |          | ||         |      |         |            ||              |    |    | | |          |
        tcgggaagcgtggcgctttctcatagctcacgctgtaggtatctcagttcggtgtaggtcgttcgctccaagctgggctgtgtgcacgaaccccccgttc
   7701 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 7800
        agcccttcgcaccgcgaaagagtatcgagtgcgacatccatagagtcaagccacatccagcaagcgaggttcgacccgacacacgtgcttggggggcaag

a        R  E  A  W  R  F  L  I  A  H  A  V  G  I  S  V  R  C  R  S  F  A  P  S  W  A  V  C  T  N  P  P  F  -
b         G  K  R  G  A  F  S  *  L  T  L  *  V  S  Q  F  G  V  G  R  S  L  Q  A  G  L  C  A  R  T  P  R  S -
c       S  G  S  V  A  L  S  H  S  S  R  C  R  Y  L  S  S  V  *  V  V  R  S  K  L  G  C  V  H  E  P  P  V  Q -

                                                                                              BbvI
                                                                                             BsrI|
                                                                                            TspRI|
                                                                                           BbvI ||
                                                                                         MaeIII ||
                                                                                       AlwNI  | ||
                   HhaI                                                             CviJI  |  | ||
               HinP1I |                            HpaII                             Fnu4HI |  |  | ||
             Fnu4HI | |                             MlyI                              TseI| |  |  | ||
            MspA1I| | |                             NciI                            BsrI || |  |  | ||
              TseI| | |   MaeIII          HinfI    ScrFI                          Fnu4HI || |  |  | ||
            AciI || | | HpaII  |   Hpy188III  |    PleI|                           TspRI || |  |  | ||
    CviJI  BsiEI || | | BsaWI| |        SmlI  | StyD4I||    BpuEI      MmeI    TseI| || |  |  | ||      MnlI
         |     | || | |     || |           |  |      |||        |         |       || || |  |  | ||         |
        agcccgaccgctgcgccttatccggtaactatcgtcttgagtccaacccggtaagacacgacttatcgccactggcagcagccactggtaacaggattag
   7801 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 7900
        tcgggctggcgacgcggaataggccattgatagcagaactcaggttgggccattctgtgctgaatagcggtgaccgtcgtcggtgaccattgtcctaatc

a       S  P  T  A  A  P  Y  P  V  T  I  V  L  S  P  T  R  *  D  T  T  Y  R  H  W  Q  Q  P  L  V  T  G  L  A -
b        A  R  P  L  R  L  I  R  *  L  S  S  *  V  Q  P  G  K  T  R  L  I  A  T  G  S  S  H  W  *  Q  D  *  -
c         P  D  R  C  A  L  S  G  N  Y  R  L  E  S  N  P  V  R  H  D  L  S  P  L  A  A  A  T  G  N  R  I  S -

                                                 CviJI      CviJI       HpyCH4III          HhaI
                      AciI  SfcI Hpy188III      HaeIII   BslI   |  BfaI  BceAI  |        HinP1I |      CviJI
                         |     |         |           |      |   |     |      |  |             | |          |
        cagagcgaggtatgtaggcggtgctacagagttcttgaagtggtggcctaactacggctacactagaaggacagtatttggtatctgcgctctgctgaag
   7901 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 8000
        gtctcgctccatacatccgccacgatgtctcaagaacttcaccaccggattgatgccgatgtgatcttcctgtcataaaccatagacgcgagacgacttc

a         E  R  G  M  *  A  V  L  Q  S  S  *  S  G  G  L  T  T  A  T  L  E  G  Q  Y  L  V  S  A  L  C  *  S -
b       Q  S  E  V  C  R  R  C  Y  R  V  L  E  V  V  A  *  L  R  L  H  *  K  D  S  I  W  Y  L  R  S  A  E  A -
c        R  A  R  Y  V  G  G  A  T  E  F  L  K  W  W  P  N  Y  G  Y  T  R  R  T  V  F  G  I  C  A  L  L  K  -

                                         HpaII
                                       BstKTI|                                                       BpuEI
                                        DpnI||                                                        HhaI
                                      MboI |||                                                    BbvI |
                               Hpy188III | |||                                         Fnu4HI      BstUI |
                  Eco57I         AluI  | | |||                                          TseI|     HinP1I |
     MaeIII      Eco57MI         AlwI  | | |||           MspA1I                      Cac8I || HpyF10VI | |
     BsrI |    Hpy188I  |       CviJI  | | |||           AciI |   AciI           HpyCH4V | ||   MwoI|| | |
        | |         |  |            |  | | |||              | |      |                 | | ||       || | |
        ccagttaccttcggaaaaagagttggtagctcttgatccggcaaacaaaccaccgctggtagcggtggtttttttgtttgcaagcagcagattacgcgca
   8001 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 8100
        ggtcaatggaagcctttttctcaaccatcgagaactaggccgtttgtttggtggcgaccatcgccaccaaaaaaacaaacgttcgtcgtctaatgcgcgt

a        Q  L  P  S  E  K  E  L  V  A  L  D  P  A  N  K  P  P  L  V  A  V  V  F  L  F  A  S  S  R  L  R  A  -
b         S  Y  L  R  K  K  S  W  *  L  L  I  R  Q  T  N  H  R  W  *  R  W  F  F  C  L  Q  A  A  D  Y  A  Q -
c       P  V  T  F  G  K  R  V  G  S  S  *  S  G  K  Q  T  T  A  G  S  G  G  F  F  V  C  K  Q  Q  I  T  R  R -
```

Figure 1-T

```
                          BstKTI
                           DpnI|
                        BstYI ||
                         MboI ||
                      AlwI  | ||
                    AlwI |  | ||                                               MseI
               Hpy188III |  | ||                                               TaiI
                  SmlI | |  | ||                                        HpyCH4IV  |
               BstKTI| | |  | ||  BstKTI                             BseMII    |  |            NlaIII
                DpnI|| | |  | ||   DpnI|                 DdeI       BspCNI|    |  |      Hpy188III  |
             BstYI ||| | |  | ||  MboII|                PpiI|   TspRI    ||    |  |         BspHI|  |
              MboI ||| | |  | || MboI ||         Hpy188I   || HgaI  |    ||    |  |     PpiI FatI|  |
                 | ||| | |  | ||    | ||               |   ||    |  |    ||    |  |        |    ||  |
         gaaaaaaaggatctcaagaagatcctttgatcttttctacggggtctgacgctcagtggaacgaaaactcacgttaagggattttggtcatgagattatc
    8101 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 8200
         cttttttcctagagttcttctaggaaactagaaaagatgccccagactgcgagtcaccttgcttttgagtgcaattccctaaaaccagtactctaatag

a        E  K  K  D  L  K  K  I  L  *  S  F  L  R  G  L  T  L  S  G  T  K  T  H  V  K  G  F  W  S  *  D  Y  Q -
b         K  K  R  I  S  R  R  S  F  D  L  F  Y  G  V  *  R  S  V  E  R  K  L  T  L  R  D  F  G  H  E  I  I    -
c          K  K  G  S  Q  E  D  P  L  I  F  S  T  G  S  D  A  Q  W  N  E  N  S  R  *  G  I  L  V  M  R  L  S   -

                        BstKTI
            BstKTI       DpnI|
             DpnI|    BstYI ||
          BstYI ||     MboI ||      MseI
           MboI ||   BfaI | ||Tsp509I  |                                              HpyCH4III
         HphI | || AlwI | | ||  DraI|  |           DraI                                  MaeIII          MnlI
     MboII  | | ||AlwI| | | || MseI||  |          MseI|TspDTI               Hpy8I   Hpy188I   |        MseI |
         |  | | ||   || | | ||    |||  |             ||     |                   |         |   |           | |
         aaaaaggatcttcacctagatccttttaaattaaaaatgaagttttaaatcaatctaaagtatatatgagtaaacttggtctgacagttaccaatgctta
    8201 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 8300
         ttttcctagaagtggatctaggaaaatttaatttttacttcaaaatttagttagatttcatatatactcatttgaaccagactgtcaatggttacgaat

a          K  G  S  S  P  R  S  F  *  I  K  N  E  V  L  N  Q  S  K  V  Y  M  S  K  L  G  L  T  V  T  N  A  *  -
b        K  K  D  L  H  L  D  P  F  K  L  K  M  K  F  *  I  N  L  K  Y  I  *  V  N  L  V  *  Q  L  P  M  L  N -
c         K  R  I  F  T  *  I  L  L  N  *  K  *  S  F  K  S  I  *  S  I  Y  E  *  T  W  S  D  S  Y  Q  C  L    -

                                   BseMII
                                  BspCNI|
                                TspDTI ||
                                FokI | ||
               NlaIV         BstKTI| | ||              MlyI
              BanI |          DpnI|| | ||              PleI           Hpy99I          MnlI
             TspRI |   DdeI MboI ||| | ||  BstF5I  Hin4I  | HinfI AhdI     |       Hin4I |      CviJI   BbvI
                 | |      |    | ||| | ||       |      |  |     |    |     |           | |          |      |
         atcagtgaggcacctatctcagcgatctgtctatttcgttcatccatagttgcctgactccccgtcgtgtagataactacgatacgggagggcttaccat
    8301 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 8400
         tagtcactccgtggatagagtcgctagacagataaagcaagtaggtatcaacggactgaggggcagcacatctattgatgctatgccctcccgaatggta

a         S  V  R  H  L  S  Q  R  S  V  Y  F  V  H  P  *  L  P  D  S  P  S  C  R  *  L  R  Y  G  R  A  Y  H    -
b          Q  *  G  T  Y  L  S  D  L  S  I  S  F  I  H  S  C  L  T  P  R  R  V  D  N  Y  D  T  G  G  L  T  I  -
c        I  S  E  A  P  I  S  A  I  C  L  F  R  S  S  I  V  A  *  L  P  V  V  *  I  T  T  I  R  E  G  L  P  S -

                                                                                                        HhaI
                                    BpmI                                                    HinP1I |
            BsrI                 Eco57MI                                                CviJI    | |
          BccI |              BstUI    |                                               HaeIII    | |
         NlaIV |             AciI |    |        Hpy188III                          HpyF10VI |    | |
        CviJI| | HpyCH4V   BsaI | |    |          NlaIV |                       HpaII     | |    | |
       HaeIII| |  TspRI|  BsmAI | |    |         CviJI| |                      CviJI|Sau96I |    | |
      Sau96I|| |Fnu4HI||  BsrDI | |    |      HpaII  || |                    Cac8I || BglI| |    | |   AvaII
      BmrI ||| | TseI||| Hin4I| | | HphI     BsrFI|  || |Hin4I             CviJI | || MwoI| |    | |  Sau96I
         | ||| |    ||||     || | |    |         ||  || |    |                 | | ||    || |    | |       |
         ctggccccagtgctgcaatgataccgcgagacccacgctcaccggctccagatttatcagcaataaaccagccagccggaagggccgagcgcagaagtgg
    8401 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 8500
         gaccggggtcacgacgttactatggcgctctgggtgcgagtggccgaggtctaaatagtcgtttatttggtcggtcggccttcccggctcgcgtcttcacc

a        L  A  P  V  L  Q  *  Y  R  E  T  H  A  H  R  L  Q  I  Y  Q  Q  *  T  S  Q  P  E  G  P  S  A  E  V  V -
b         W  P  Q  C  C  N  D  T  A  R  P  T  L  T  G  S  R  F  I  S  N  K  P  A  S  R  K  G  R  A  Q  K  W    -
c          G  P  S  A  A  M  I  P  R  D  P  R  S  P  A  P  D  L  S  A  I  N  Q  P  A  G  R  A  E  R  R  S  G   -
```

Figure 1-U

```
                                                                                             TaiI
                                                                                       AclI  |
                           Tsp509I     NciI                                        HpyCH4IV  |
         FokI          BccI      |    ScrFI   BfaI                                   HhaI |  |
  HpyCH4V  |       BstF5I   MnlI|AseI|   HpaII| AluI|                   MseI       FspI|  |  |
     EciI| |   AciI     |BsrI ||MseI|  StyD4I|| CviJI|              BsrI |      HinP1I||  |  |  BsrDI
        || |      |     |   | ||   ||       |||     ||                 |   |        |||  |  |    |
      tcctgcaactttatccgcctccatccagtctattaattgttgccgggaagctagagtaagtagttcgccagttaatagtttgcgcaacgttgttgccatt
 8501 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 8600
      aggacgttgaaataggcggaggtaggtcagataattaacaacggcccttcgatctcattcatcaagcggtcaattatcaaacgcgttgcaacaacggtaa

a       L  Q  L  Y  P  P  P  S  S  L  L  I  V  A  G  K  L  E  *  V  V  R  Q  L  I  V  C  A  T  L  L  P  L  -
b     S  C  N  F  I  R  L  H  P  V  Y  *  L  L  P  G  S  *  S  K  *  F  A  S  *  *  F  A  Q  R  C  C  H  C  -
c      P  A  T  L  S  A  S  I  Q  S  I  N  C  C  R  E  A  R  V  S  S  S  P  V  N  S  L  R  N  V  V  A  I  -

                                                                                  BstKTI
                                                                                    DpnI|
                                                      NlaIV                      NlaIII||
                                                   HpaII  |                        MboI|||
             MaeIII                               BsaWI|  |       BstKTI       FatI   ||||            HpyCH4V
              SfaNI                              AluI ||  |        DpnI|     AlwI |   ||||    NlaIII      |
             Tsp45I           TspDTI            CviJI·||  |       MboI ||  MaeIII | |  ||||[FatI   |      |
   SfcI      MslI |         Hpy99I |    CviJI        | ||  |          | ||      | | |  ||||    |   |       |
      |          | |              | |        |        | ||  |          | ||      | | |  |||||   |   |       |
      gctacaggcatcgtggtgtcacgctcgtcgtttggtatggcttcattcagctccggttcccaacgatcaaggcgagttacatgatcccccatgttgtgca
 8601 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 8700
      cgatgtccgtagcaccacagtgcgagcagcaaaccataccgaagtaagtcgaggccaagggttgctagttccgctcaatgtactagggggtacaacacgt

a       L  Q  A  S  W  C  H  A  R  R  L  V  W  L  H  S  A  P  V  P  N  D  Q  G  E  L  H  D  P  P  C  C  A  -
b        Y  R  H  R  G  V  T  L  V  V  W  Y  G  F  I  Q  L  R  F  P  T  I  K  A  S  Y  M  I  P  H  V  V  Q  -
c     A  T  G  I  V  V  S  R  S  S  F  G  M  A  S  F  S  S  G  S  Q  R  S  R  R  V  T  *  S  P  M  L  C  K  -

                                    Hpy188I
                                 MnlI     |
                             BsiEI   |     |
                            BstKTI   |     |                                                          BbvI
                              PvuI   |     |             TauI                                     Tsp509I|
                              DpnI|  |     |           AciI |                                      TspRI||
             AluI                 ||  |     |          Fnu4HI |                                 HpyCH4V |||
            CviJI        Hpy188I ||  |     |          CviJI| |            MslI     BtsI          | |||
       TaqII  |    AvaII       | ||  |     |         HaeIII| |    BtsI   NlaIII| Fnu4HI |        | |||
    AciI  |   |   Sau96I   MboI | ||  |     |          EaeI ||| |  TspRI  FatI  || TseI| |        | |||  FokI
        |  |   |        |      | ||  |     |             | ||| |      |     |  ||    || |        | |||     |
      aaaaagcggttagctccttcggtcctccgatcgttgtcagaagtaagttggccgcagtgttatcactcatggttatggcagcactgcataattctcttac
 8701 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 8800
      tttttcgccaatcgaggaagccaggaggctagcaacagtcttcattcaaccggcgtcacaatagtgagtaccaataccgtcgtgacgtattaagagaatg

a     K  K  R  L  A  P  S  V  L  R  S  L  S  E  V  S  W  P  Q  C  Y  H  S  W  L  W  Q  H  C  I  I  L  L  L  -
b      K  S  G  *  L  L  R  S  S  D  R  C  Q  K  *  V  G  R  S  V  I  T  H  G  Y  G  S  T  A  *  F  S  Y   -
c       K  A  V  S  S  F  G  P  P  I  V  V  R  S  K  L  A  A  V  L  S  L  M  V  M  A  A  L  H  N  S  L  T  -

                                                                                                    BcgI
                                                                                              BsaHI  |
      BstF5I                                                                               HpaII  |  |
       SfaNI                               RsaI                                              NciI  |  |
     NlaIII|                               ScaI                                 BsiEI       ScrFI  |  |
   FatI   ||                              Csp6I|   BspCNI                      TauI   |     TaqII|  |  |
HpyCH4III |   ||                MaeIII     TatI||  BseMII|  Hpy188I           Fnu4HI |   |    StyD4I||  |  |
  TspGWI |   ||       BccI      Tsp45I   BsrI |||  HphI ||     DdeI|    BcgI   AciI| |   |  HgaI  |||  |  |
       | |   ||          |           |      | |||     | ||        ||       |      || |   |     |   |||  |  |
      tgtcatgccatccgtaagatgcttttctgtgactggtgagtactcaaccaagtcattctgagaatagtgtatgcggcgaccgagttgctcttgcccggcg
 8801 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 8900
      acagtacggtaggcattctacgaaaagacactgaccactcatgagttggttcagtaagactcttatcacatacgccgctggctcaacgagaacgggccgc

a       S  C  H  P  *  D  A  F  L  *  L  V  S  T  Q  P  S  H  S  E  N  S  V  C  G  D  R  V  A  L  A  R  R  -
b     C  H  A  I  R  K  M  L  F  C  D  W  *  V  L  N  Q  V  I  L  R  I  V  Y  A  A  T  E  L  L  L  P  G  V  -
c      V  M  P  S  V  R  C  F  S  V  T  G  E  Y  S  T  K  S  F  *  E  *  C  M  R  R  P  S  C  S  C  P  A  -

                                                          BpuEI
                                                        TaiI  |                                     AlwI
                 HhaI                                 AclI |  |                     BstKTI MspAlI  |
                BstUI |                           HpyCH4IV |  |                       DpnI| AciI |  |
               HinP1I |          DraI  BsiHKAI         XmnI |  |                     BstYI || AlwI |  |
                 AciI | |         MseI| Bsp1286I    MboII  | |  |               SmlI MboI ||PpiI| |  |
                    | | |             ||        |        |  | |  |                  |    | ||   || |  |
      tcaatacgggataataccgcgccacatagcagaactttaaaagtgctcatcattggaaaacgttcttcggggcgaaaactctcaaggatcttaccgctgt
 8901 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 9000
      agttatgccctattatggcgcggtgtatcgtcttgaaattttcacgagtagtaaccttttgcaagaagccccgcttttgagagttcctagaatggcgaca

a       Q  Y  G  I  I  P  R  H  I  A  E  L  *  K  C  S  S  L  E  N  V  L  R  G  E  N  S  Q  G  S  Y  R  C  -
b        N  T  G  *  Y  R  A  T  *  Q  N  F  K  S  A  H  H  W  K  T  F  F  G  A  K  T  L  K  D  L  T  A  V  -
c     S  I  R  D  N  T  A  P  H  S  R  T  L  K  V  L  I  I  G  K  R  S  S  G  R  K  L  S  R  I  L  P  L  L  -
```

Figure 1-V

```
                                    MboII
                               Bme1580I |
                                BsiHKAI |
                               Bsp1286I |
                                Hpy8I | |
                              HpyCH4V | |
          BsrI                ApaLI | | |
       BstKTI|               Eco57I | | |
        DpnI||              Eco57MI | | |  BstKTI
     BstYI |||   MaeIII     BssSI | | | |   DpnI|          SfaNI
      MboI ||| TaqI   |     PpiI  | | | | MboI ||TaqII  HphI   |  TaqII                     HphI
         | |||    |   |        |  | | | |    | ||    |     |   |      |                        |
       tgagatccagttcgatgtaacccactcgtgcacccaactgatcttcagcatctttactttcaccagcgtttctgggtgagcaaaaacaggaaggcaaaa
9001   ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 9100
       actctaggtcaagctacattgggtgagcacgtgggttgactagaagtcgtagaaatgaaagtggtcgcaaagacccactcgtttttgtccttccgtttt

a      *  D  P  V  R  C  N  P  L  V  H  P  T  D  L  Q  H  L  L  L  S  P  A  F  L  G  E  Q  K  Q  E  G  K  M -
b       E  I  Q  F  D  V  T  H  S  C  T  Q  L  I  F  S  I  F  Y  F  H  Q  R  F  W  V  S  K  N  R  K  A  K   -
c        R  S  S  S  M  *  P  T  R  A  P  N  *  S  S  A  S  F  T  F  T  S  V  S  G  *  A  K  T  G  R  Q  N  -

                                                                                                     NlaIII
                                                                                                    BciVI |
                                                                                                    BsmAI |
        TauI                                                                                   Hpy188III| |
      AciI |                                 MboII                                                BspHI|| |
    Fnu4HI |                      MslI      TspGWI         EarI     SspI                           FatI|| |
         | |                         |           |            |        |                              ||| |
       tgccgcaaaaaagggaataagggcgacacggaaatgttgaatactcatactcttcctttttcaatattattgaagcatttatcagggttattgtctcatg
9101   ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 9200
       acggcgtttttttcccttattcccgctgtgcctttacaacttatgagtatgagaaggaaaaagttataataacttcgtaaatagtcccaataacagagtac

a        P  Q  K  R  E  *  G  R  H  G  N  V  E  Y  S  Y  S  S  F  F  N  I  I  E  A  F  I  R  V  I  V  S  *  -
b      C  R  K  K  G  N  K  G  D  T  E  M  L  N  T  H  T  L  P  F  S  I  L  L  K  H  L  S  G  L  L  S  H  E -
c       A  A  K  K  G  I  R  A  T  R  K  C  *  I  L  I  L  F  L  F  Q  Y  Y  *  S  I  Y  Q  G  Y  C  L  M   -

                                                                                        DdeI
                                                        HhaI                          AatII|
                                                     BstUI |                           TaiI|
                                                    HinP1I |                         ZraI ||
     AciI                                           AciI | |                       BsaHI| ||
    BsrBI                                        NlaIV | | |                    HpyCH4IV| ||
        |                                            | | | |                           || ||
       agcggatacatatttgaatgtatttagaaaaataaacaaataggggttccgcgcacatttccccgaaaagtgccacctgacgtctaagaaaccattatta
9201   ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 9300
       tcgcctatgtataaacttacataaatctttttatttgtttatccccaaggcgcgtgtaaaggggcttttcacggtggactgcagattctttggtaataat

a       A  D  T  Y  L  N  V  F  R  K  I  N  K  *  G  F  R  A  H  F  P  E  K  C  H  L  T  S  K  K  P  L  L   -
b        R  I  H  I  *  M  Y  L  E  K  *  T  N  R  G  S  A  H  I  S  P  K  S  A  T  *  R  L  R  N  H  Y  Y  -
c      S  G  Y  I  F  E  C  I  *  K  N  K  Q  I  G  V  P  R  T  F  P  R  K  V  P  P  D  V  *  E  T  I  I  I -

                                        CviJI
                                       HaeIII
                                   EcoO109I|
      NlaIII                         Sau96I|
Hpy188III  |                      BssSI    ||
   BspHI|  |                  Hpy188III    ||
    FatI|  |MseI               MnlI   |    ||
       ||  |   |                  |   |    ||
       tcatgacattaacctataaaaataggcgtatcacgaggccctttcgtc
9301   ---------+---------+---------+---------+-------- 9348
       agtactgtaattggatatttttatccgcatagtgctccgggaaagcag

a      S  *  H  *  P  I  K  I  G  V  S  R  G  P  F  V    -
b       H  D  I  N  L  *  K  *  A  Y  H  E  A  L  S      -
c        M  T  L  T  Y  K  N  R  R  I  T  R  P  F  R     -
```

Figure 1-W

```
 Enzymes that do cut and were not excluded:

AarI      AatII      AccI    Acc65I      AciI      AclI      AfeI    AflIII      AgeI      AhdI      AluI      AlwI     AlwNI
ApaI      ApaLI      ApoI      AseI      AvaI     AvaII      BaeI     BamHI      BanI     BanII      BbeI      BbsI      BbvI
BccI      BceAI      BcgI     BciVI      BclI      BfaI     BfrBI      BglI     BglII      BlpI  Bme1580I     BmgBI      BmrI
BpmI     Bpu10I     BpuEI      BsaI     BsaAI     BsaBI     BsaHI     BsaJI     BsaWI     BsaXI    BseMII     BseRI     BseYI
BsgI      BsiEI   BsiHKAI      BslI      BsmI     BsmAI     BsmBI     BsmFI  Bsp1286I    BspCNI     BspHI     BspMI      BsrI
BsrBI     BsrDI     BsrFI    BssHII     BssSI    BstAPI     BstBI    BstEII    BstF5I    BstKTI     BstNI     BstUI     BstXI
BstYI    Bsu36I      BtgI      BtsI     Cac8I      ClaI     Csp6I     CviJI      DdeI      DpnI      DraI    DraIII      DrdI
EaeI       EagI      EarI      EciI    Eco57I   EcoICRI   Eco57MI     EcoNI  EcoO109I     EcoRI     EcoRV      FalI      FatI
FauI     Fnu4HI      FokI      FspI     HaeII    HaeIII      HgaI      HhaI     Hin4I    HinP1I    HincII   HindIII     HinfI
HpaI      HpaII      HphI     Hpy8I    Hpy99I   Hpy188I Hpy188III HpyCH4III  HpyCH4IV   HpyCH4V  HpyF10VI      KasI      KpnI
MaeIII     MboI     MboII      MlyI      MmeI      MnlI      MscI      MseI      MslI    MspA1I      MwoI      NaeI      NarI
NciI       NcoI      NdeI    NgoMIV    NlaIII     NlaIV      NotI      NruI      NsiI      NspI      PacI      PciI      PfoI
PleI       PpiI      PsiI     PspGI    PspOMI      PstI      PvuI     PvuII      RsaI      SacI     SacII      SalI      SapI
Sau96I     ScaI     ScrFI     SexAI     SfaNI      SfcI      SfoI      SmaI      SmlI     SnaBI      SpeI      SphI      SspI
StyI     StyD4I      TaiI      TaqI     TaqII      TatI      TauI      TfiI      TseI    Tsp45I   Tsp509I    TspDTI    TspGWI
TspRI      XbaI      XcmI      XhoI      XmaI      XmnI      ZraI

 Enzymes that do not cut:

AflII      AleI      AloI      AscI     AsiSI     AvrII     BbvCI      BmtI      BplI     BsiWI     BspEI     BsrGI   BstZ17I
FseI      FspAI      MfeI      MluI      NheI     PflMI      PmeI      PmlI     PpuMI     PshAI      PsrI     RsrII     SanDI
SbfI       SfiI     SgrAI      SrfI      StuI      SwaI   Tth111I

 Enzymes excluded; MinCuts: 1  MaxCuts: 100000

   NONE
```

Figure 2-A

pCV1 sequence

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Figure 2-B

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Figure 2-C

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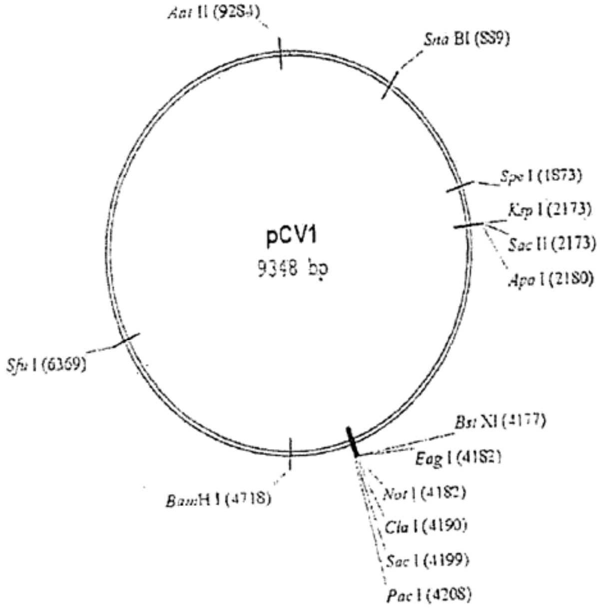
Figure 3-A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*Bst* XI (4177)
*Eag* I (4182)
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*Sac* I (4199)
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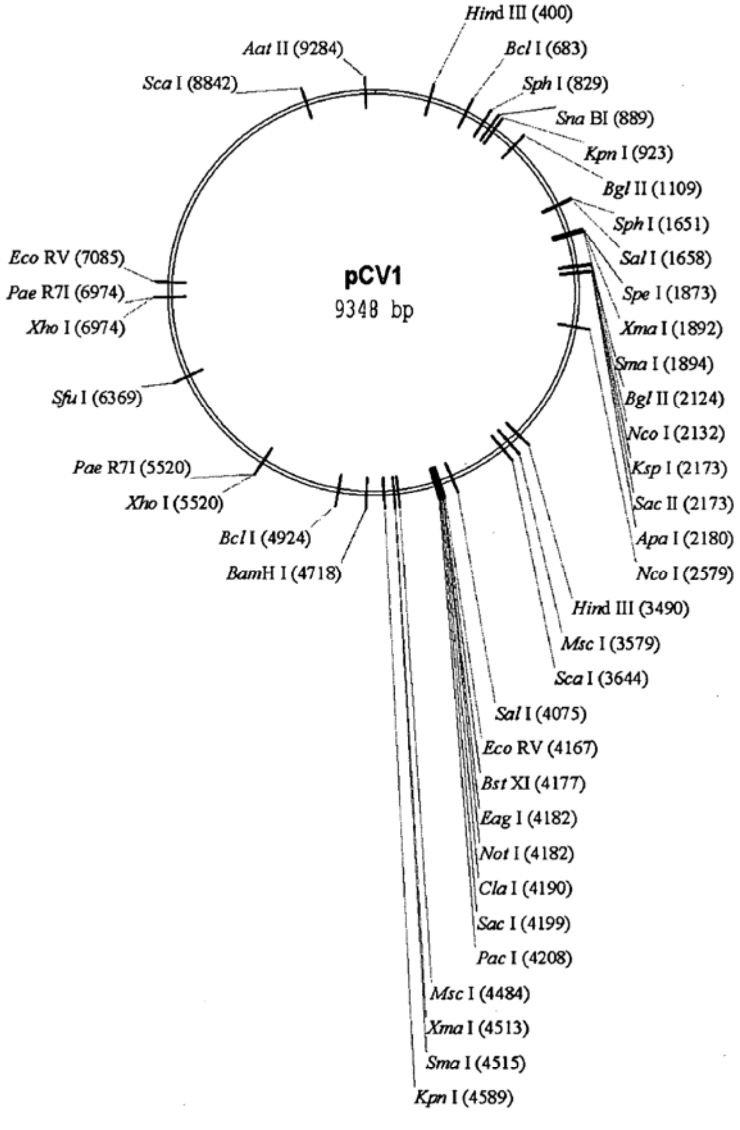
*Bam*H I (4718)

Figure 3-B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Sal I (1658)
Spe I (1873)
Xma I (1892)
Sma I (1894)
Bgl II (2124)
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Pae R7I (5520)
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Figure 3-C

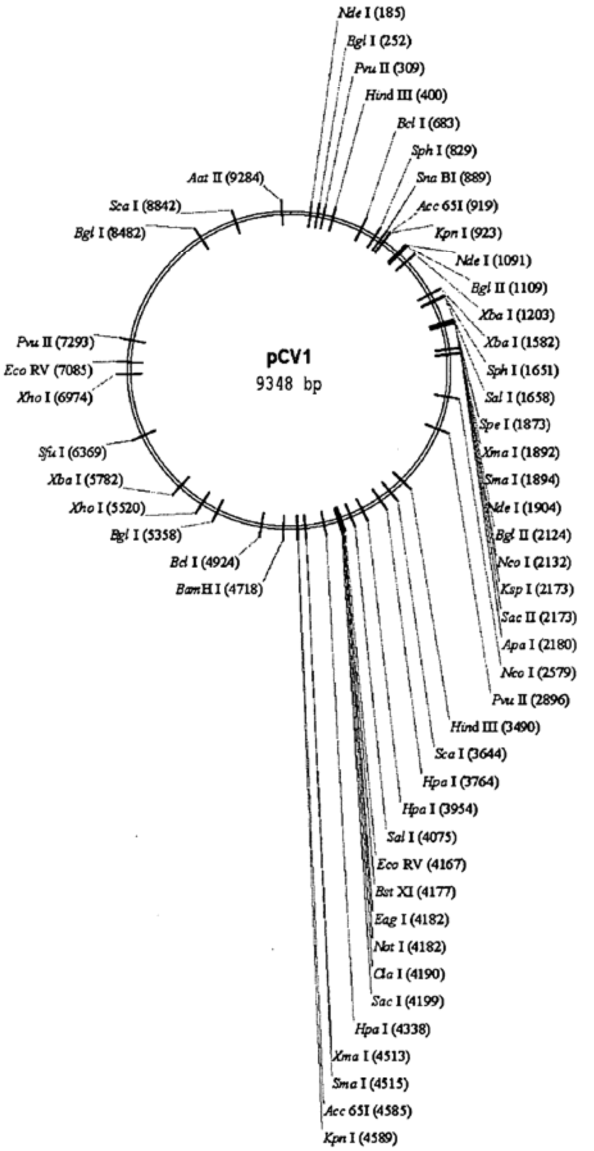
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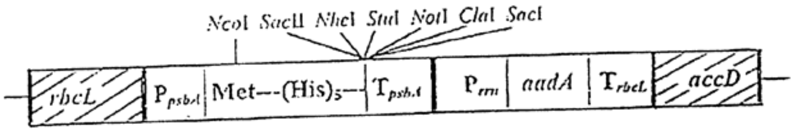
Figure 4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accD

Figure 5

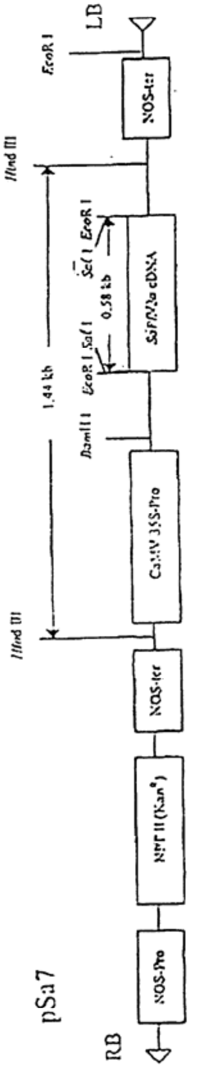
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Figure 6-A

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241     GTCCGGGTGT  GACCGAAAGG  TAAGATGGAG  AGCCTTGTTC  TTGGTGTCAA  CGAGAAAACA
301     CACGTCCAAC  TCAGTTTGCC  TGTCCTTCAG  GTTAGAGACG  TGCTAGTGCG  TGGCTTCGGG
361     GACTCTGTGG  AAGAGGCCCT  ATCGGAGGCA  CGTGAACACC  TCAAAAATGG  CACTTGTGGT
421     CTAGTAGAGC  TGGAAAAAGG  CGTACTGCCC  CAGCTTGAAC  AGCCCTATGT  GTTCATTAAA
481     CGTTCTGATG  CCTTAAGCAC  CAATCACGGC  CACAAGGTCG  TTGAGCTGGT  TGCAGAAATG
541     GACGGCATTC  AGTACGGTCG  TAGCGGTATA  ACACTGGGAG  TACTCGTGCC  ACATGTGGGC
601     GAAACCCCAA  TTGCATACCG  CAATGTTCTT  CTTCGTAAGA  ACGGTAATAA  GGGAGCCGGT
661     GGTCATAGCT  ATGGCATCGA  TCTAAAGTCT  TATGACTTAG  GTGACGAGCT  TGGCACTGAT
721     CCCATTGAAG  ATTATGAACA  AAACTGGAAC  ACTAAGCATG  GCAGTGGTGC  ACTCCGTGAA
781     CTCACTCGTG  AGCTCAATGG  AGGTGCAGTC  ACTCGCTATG  TCGACAACAA  TTTCTGTGGC
641     CCAGATGGGT  ACCCTCTTGA  TTGCATCAAA  GATTTTCTCG  CACGCGCGGG  CAAGTCAATG
901     TGCACTCTTT  CCGAACAACT  TGATTACATC  GAGTCGAAGA  GAGGTGTCTA  CTGCTGCCGT
961     GACCATGAGC  ATGAAATTGC  CTGGTTCACT  GAGCGCTCTG  ATAAGAGCTA  CGAGCACCAG
1021    ACACCCTTCG  AAATTAAGAG  TGCCAAGAAA  TTTGACACTT  TCAAAGGGGA  ATGCCCAAAG
1081    TTTGTGTTTC  CTCTTAACTC  AAAAGTCAAA  GTCATTCAAC  CACGTGTTGA  AAAGAAAAAG
1141    ACTGAGGGTT  TCATGGGGCG  TATACGCTCT  GTGTACCCTG  TTGCATCTCC  ACAGGAGTGT
1201    AACAATATGC  ACTTGTCTAC  CTTGATGAAA  TGTAATCATT  GCGATGAAGT  TTCATGGCAG
1261    ACGTGCGACT  TTCTGAAAGC  CACTTGTGAA  CATTGTGGCA  CTGAAAATTT  AGTTATTGAA
1221    GGACCTACTA  CATGTGGGTA  CCTACCTACT  AATGCTGTAG  TGAAAATGCC  ATGTCCTGCC
1381    TGTCAAGACC  CAGAGATTGG  ACCTGAGCAT  AGTGTTGCAG  ATTATCACAA  CCACTCAAAC
1441    ATTGAAACTC  GACTCCGCAA  GGGAGGTAGG  ACTAGATGTT  TTGGAGGCTG  TGTGTTTGCC
1501    TATGTTGGCT  GCTATAATAA  GCGTGCCTAC  TGGGTTCCTC  GTGCTAGTGC  TGATATTGGC
1561    TCAGGCCATA  CTGGCATTAC  TGGTGACAAT  GTGGAGACCT  TGAATGAGGA  TCTCCTTGAG
1621    ATACTGAGTC  GTGAACGTGT  TAACATTAAC  ATTGTTGGCG  ATTTTCATTT  GAATGAAGAG
1681    GTTGCCATCA  TTTTGGCATC  TTTCTCTGCT  TCTACAAGTG  CCTTTATTGA  CACTATAAAG
1741    AGTCTTGATT  ACAAGTCTTT  CAAAACCATT  GTTGAGTCCT  GCGGTAACTA  TAAAGTTACC
1801    AAGGGAAAGC  CCGTAAAAGG  TGCTTGGAAC  ATTGGACAAC  AGAGATCAGT  TTTAACACCA
1661    CTGTGTGGTT  TTCCCTCACA  GGCTGCTGGT  GTTATCAGAT  CAATTTTTGC  GCGCACACTT
1921    GATGCAGCAA  ACCACTCAAT  TCCTGATTTG  CAAAGAGCAG  CTGTCACCAT  ACTTGATGGT
1981    ATTTCTGAAC  AGTCATTACG  TCTTGTCGAC  GCCATGGTTT  ATACTTCAGA  CCTGCTCACC
2041    AACAGTGTCA  TTATTATGGC  ATATGTAACT  GGTGGTCTTG  TACAACAGAC  TTCTCAGTGG
2101    TTGTCTAATC  TTTTGGGCAC  TACTGTTGAA  AAACTCAGGC  CTATCTTTGA  ATGGATTGAG
2161    GCGAAACTTA  GTGCAGGAGT  TGAATTTCTC  AAGGATGCTT  GGGAGATTCT  CAAATTTCTC
2221    ATTACAGGTG  TTTTTGACAT  CGTCAAGGGT  CAAATACAGG  TTGCTTCAGA  TAACATCAAG
2281    GATTGTGTAA  AATGCTTCAT  TGATGTTGTT  AACAAGGCAC  TCGAAATGTG  CATTGATCAA
2341    GTCACTATCG  CTGGCGCAAA  GTTGCGATCA  CTCAACTTAG  GTGAAGTCTT  CATCGCTCAA
2401    AGCAAGGGAC  TTTACCGTCA  GTGTATACGT  GGCAAGGAGC  AGCTGCAACT  ACTCATGCCT
2461    CTTAAGGCAC  CAAAAGAAGT  AACCTTTCTT  GAAGGTGATT  CACATGACAC  AGTACTTACC
2521    TCTGAGGAGG  TTGTTCTCAA  GAACGGTGAA  CTCGAAGCAC  TCGAGACGCC  CGTTGATAGC
2581    TTCACAAATG  GAGCTATCGT  CGGCACACCA  GTCTGTGTAA  ATGGCCTCAT  GCTCTTAGAG
2641    ATTAAGGACA  AAGAACAATA  CTGCGCATTG  TCTCCTGGTT  TACTGGCTAC  AAACAATGTC
2701    TTTCGCTTAA  AAGGGGGTGC  ACCAATTAAA  GGTGTAACCT  TTGGAGAAGA  TACTGTTTGG
2761    GAAGTTCAAG  GTTACAAGAA  TGTGAGAATC  ACATTTGAGC  TTGATGAACG  TGTTGACAAA
2821    GTGCTTAATG  AAAAGTGCTC  TGTCTACACT  GTTGAATCCG  GTACCGAAGT  TACTGAGTTT
2881    GCATGTGTTG  TAGCAGAGGC  TGTTGTGAAG  ACTTTACAAC  CAGTTTCTGA  TCTCCTTACC
2941    AACATGGGTA  TTGATCTTGA  TGAGTGGAGT  GTAGCTACAT  TCTACTTATT  TGATGATGCT
3001    GGTGAAGAAA  ACTTTTCATC  ACGTATGTAT  TGTTCCTTTT  ACCCTCCAGA  TGAGGAAGAA
3061    GAGGACGATG  CAGAGTGTGA  GGAAGAAGAA  ATTGATGAAA  CCTGTGAACA  TGAGTACGGT
3121    ACAGAGGATG  ATTATCAAGG  TCTCCCTCTG  GAATTTGGTG  CCTCAGCTGA  AACAGTTCGA
3181    GTTGAGGAAG  AAGAAGAGGA  AGACTGGCTG  GATGATACTA  CTGAGCAATC  AGAGATTGAG
3241    CCAGAACCAG  AACCTACACC  TGAAGAACCA  GTTAATCAGT  TTACTGGTTA  TTTAAAACTT
3301    ACTGACAATG  TTGCCATTAA  ATGTGTTGAC  ATCGTTAAGG  AGGCACAAAG  TGCTAATCCT
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Figure 6-B

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3361   ATGGTGATTG   TAAATGCTGC   TAACATACAC   CTGAAACATG   GTGGTGGTGT   AGCAGGTGCA
3421   CTCAACAAGG   CAACCAATGG   TGCCATGCAA   AAGGAGAGTG   ATGATTACAT   TAAGCTAAAT
34B1   GGCCCTCTTA   CAGTAGGAGG   GTCTTGTTTG   CTTTCTGGAC   ATAATCTTGC   TAAGAAGTGT
3541   CTGCATGTTG   TTGGACCTAA   CCTAAATGCA   GGTGAGGACA   TCCAGCTTCT   TAAGGCAGCA
3601   TATGAAAATT   TCAATTCACA   GGACATCTTA   CTTGCACCAT   TGTTGTCAGC   AGGCATATTT
3661   GGTGCTAAAC   CACTTCAGTC   TTTACAAGTG   TGCGTGCAGA   CGGTTCGTAC   ACAGGTTTAT
3721   ATTGCAGTCA   ATGACAAAGC   TCTTTATGAG   CAGGTTGTCA   TGGATTATCT   TGATAACCTG
3781   AAGCCTAGAG   TGGAAGCACC   TAAACAAGAG   GAGCCACCAA   ACACAGAAGA   TTCCAAAACT
3841   GAGGAGAAAT   CTGTCGTACA   GAAGCCTGTC   GATGTGAAGC   CAAAAATTAA   GGCCTGCATT
3901   GATGAGGTTA   CCACAACACT   GGAAGAAACT   AAGTTTCTTA   CCAATAAGTT   ACTCTTGTTT
3961   GCTGATATCA   ATGGTAAGCT   TTACCATGAT   TCTCAGAACA   TGCTTAGAGG   TGAAGATATG
4021   TCTTTCCTTG   AGAAGGATGC   ACCTTACATG   GTAGGTGATG   TTATCACTAG   TGGTGATATC
4081   ACTTGTGTTG   TAATACCCTC   CAAAAAGGCT   GGTGGCACTA   CTGAGATGCT   CTCAAGAGCT
4141   TTGAAGAAAG   TGCCAGTTGA   TGAGTATATA   ACCACGTACC   CTGGACAAGG   ATGTGCTGGT
4201   TATACACTTG   AGGAAGCTAA   GACTGCTCTT   AAGAAATGCA   AATCTGCATT   TTATGTACTA
4261   CCTTCAGAAG   CACCTAATGC   TAAGGAAGAG   ATTCTAGGAA   CTGTATCCTG   GAATTTGAGA
4321   GAAATGCTTG   CTCATGCTGA   AGAGACAAGA   AAATTAATGC   CTATATGCAT   GGATGTTAGA
4381   GCCATAATGG   CAACCATCCA   ACGTAAGTAT   AAAGGAATTA   AAATTCAAGA   GGGCATCGTT
4441   GACTATGGTG   TCCGATTCTT   CTTTTATACT   AGTAAAGAGC   CTGTAGCTTC   TATTATTACG
4501   AAGCTGAACT   CTCTAAATGA   GCCGCTTGTC   ACAATGCCAA   TTGGTTATGT   GACACATGGT
4561   TTTAATCTTG   AAGAGGCTGC   GCGCTGTATG   CGTTCTCTTA   AAGCTCCTGC   CGTAGTGTCA
4621   GTATCATCAC   CAGATGCTGT   TACTACATAT   AATGGATACC   TCACTTCGTC   ATCAAAGACA
4681   TCTGAGGAGC   ACTTTGTAGA   AACAGTTTCT   TTGGCTGGCT   CTTACAGAGA   TTGGTCCTAT
4741   TCAGGACAGC   GTACAGAGTT   AGGTGTTGAA   TTTCTTAAGC   GTGGTGACAA   AATTGTGTAC
4801   CACACTCTGG   AGAGCCCCGT   CGAGTTTCAT   CTTGACGGTG   AGGTTCTTTC   ACTTGACAAA
4861   CTAAAGAGTC   TCTTATCCCT   GCGGGAGGTT   AAGACTATAA   AAGTGTTCAC   AACTGTGGAC
4921   AACACTAATC   TCCACACACA   GCTTGTGGAT   ATGTCTATGA   CATATGGACA   GCAGTTTGGT
4981   CCAACATACT   TGGATGGTGC   TGATGTTACA   AAAATTAAAC   CTCATGTAAA   TCATGAGGGT
5041   AAGACTTTCT   TTGTACTACC   TAGTGATGAC   ACACTACGTA   GTGAAGCTTT   CGAGTACTAC
5101   CATACTCTTG   ATGAGAGTTT   TCTTGGTAGG   TACATGTCTG   CTTTAAACCA   CACAAAGAAA
5161   TGGAAATTTC   CTCAAGTTGG   TGGTTTAACT   TCAATTAAAT   GGGCTGATAA   CAATTGTTAT
5221   TTGTCTAGTG   TTTTATTAGC   ACTTCAACAG   CTTGAAGTCA   AATTCAATGC   ACCAGCACTT
5281   CAAGAGGCTT   ATTATAGAGC   CCGTGCTGGT   GATGCTGCTA   ACTTTTGTGC   ACTCATACTC
5341   GCTTACAGTA   ATAAAACTGT   TGGCGAGCTT   GGTGATGTCA   GAGAAACTAT   GACCCATCTT
5401   CTACAGCATG   CTAATTTGGA   ATCTGCAAAG   CGAGTTCTTA   ATGTGGTGTG   TAAACATTGT
5461   GGTCAGAAAA   CTACTACCTT   AACGGGTGTA   GAAGCTGTGA   TGTATATGGG   TACTCTATCT
5521   TATGATAATC   TTAAGACAGG   TGTTTCCATT   CCATGTGTGT   GTGGTCGTGA   TGCTACACAA
5581   TATCTAGTAC   AACAAGAGTC   TTCTTTTGTT   ATGATGTCTG   CACCACCTGC   TGAGTATAAA
5641   TTACAGCAAG   GTACATTCTT   ATGTGCGAAT   GAGTACACTG   GTAACTATCA   GTGTGGTCAT
5701   TACACTCATA   TAACTGCTAA   GGAGACCCTC   TATCGTATTG   ACGGAGCTCA   CCTTACAAAG
5761   ATGTCAGAGT   ACAAAGGACC   AGTGACTGAT   GTTTTCTACA   AGGAAACATC   TTACACTACA
5821   ACCATCAAGC   CTGTGTCGTA   TAAACTCGAT   GGAGTTACTT   ACACAGAGAT   TGAACCAAAA
5881   TTGGATGGGT   ATTATAAAAA   GGATAATGCT   TACTATACAG   AGCAGCCTAT   AGACCTTGTA
5941   CCAACTCAAC   CATTACCAAA   TGCGAGTTTT   GATAATTTCA   AACTCACATG   TTCTAACACA
6001   AAATTTGCTG   ATGATTTAAA   TCAAATGACA   GGCTTCACAA   AGCCAGCTTC   ACGAGAGCTA
6061   TCTGTCACAT   TCTTCCCAGA   CTTGAATGGC   GATGTAGTGG   CTATTGACTA   TAGACACTAT
6121   TCAGCGAGTT   TCAAGAAAGG   TGCTAAATTA   CTGCATAAGC   CAATTGTTTG   GCACATTAAC
6181   CAGGCTACAA   CCAAGACAAC   GTTCAAACCA   AACACTTGGT   GTTTACGTTG   TCTTTGGAGT
6241   ACAAAGCCAG   TAGATACTTC   AAATTCATTT   GAAGTTCTGG   CAGTAGAAGA   CACACAAGGA
6301   ATGGACAATC   TTGCTTGTGA   AAGTCAACAA   CCCACCTCTG   AAGAAGTAGT   GGAAAATCCT
6361   ACCATACAGA   AGGAAGTCAT   AGAGTGTGAC   GTGAAAACTA   CCGAAGTTGT   AGGCAATGTC
6421   ATACTTAAAC   CATCAGATGA   AGGTGTTAAA   GTAACACAAG   AGTTAGGTCA   TGAGGATCTT
6481   ATGGCTGCTT   ATGTGGAAAA   CACAAGCATT   ACCATTAAGA   AACCTAATGA   GCTTTCACTA
6541   GCCTTAGGTT   TAAAAACAAT   TGCCACTCAT   GGTATTGCTG   CAATTAATAG   TGTTCCTTGG
6601   AGTAAAATTT   TGGCTTATGT   CAAACCATTC   TTAGGACAAG   CAGCAATTAC   AACATCAAAT
6661   TGCGCTAAGA   GATTAGCACA   ACGTGTGTTT   AACAATTATA   TGCCTTATGT   GTTTACATTA
6721   TTGTTCCAAT   TGTGTACTTT   TACTAAAAGT   ACCAATTCTA   GAATTAGAGC   TTCACTACCT
6781   ACAACTATTG   CTAAAAATAG   TGTTAAGAGT   GTTGCTAAAT   TATGTTTGGA   TGCCGGCATT
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Figure 6-C

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6841  AATTATGTGA  AGTCACCCAA  ATTTTCTAAA  TTGTTCACAA  TCGCTATGTG  GCTATTGTTG
6901  TTAAGTATTT  GCTTAGGTTC  TCTAATCTGT  GTAACTGCTG  CTTTTGGTGT  ACTCTTATCT
6961  AATTTTGGTG  CTCCTTCTTA  TTGTAATGGC  GTTAGAGAAT  TGTATCTTAA  TTCGTCTAAC
7021  GTTACTACTA  TGGATTTCTG  TGAAGGTTCT  TTTCCTTGCA  GCATTTGTTT  AAGTGGATTA
7081  GACTCCCTTG  ATTCTTATCC  AGCTCTTGAA  ACCATTCAGG  TGACGATTTC  ATCGTACAAG
7141  CTAGACTTGA  CAATTTTAGG  TCTGGCCGCT  GAGTGGGTTT  TGGCATATAT  GTTGTTCACA
7201  AAATTCTTTT  ATTTATTAGG  TCTTTCAGCT  ATAATGCAGG  TGTTCTTTGG  CTATTTTGCT
7261  AGTCATTTCA  TCAGCAATTC  TTGGCTCATG  TGGTTTATCA  TTAGTATTGT  ACAAATGGCA
7321  CCCGTTTCTG  CAATGGTTAG  GATGTACATC  TTCTTTGCTT  CTTTCTACTA  CATATGGAAG
7381  AGCTATGTTC  ATATCATGGA  TGGTTGCACC  TCTTCGACTT  GCATGATGTG  CTATAAGCGC
7441  AATCGTGCCA  CACGCGTTGA  GTGTACAACT  ATTGTTAATG  GCATGAAGAG  ATCTTTCTAT
7501  GTCTATGCAA  ATGGAGGCCG  TGGCTTCTGC  AAGACTCACA  ATTGGAATTG  TCTCAATTGT
7561  GACACATTTT  GCACTGGTAG  TACATTCATT  AGTGATGAAG  TTGCTCGTGA  TTTGTCACTC
7621  CAGTTTAAAA  GACCAATCAA  CCCTACTGAC  CAGTCATCGT  ATATTGTTGA  TAGTGTTGCT
7681  GTGAAAAATG  GCGCGCTTCA  CCTCTACTTT  GACAAGGCTG  GTCAAAAGAC  CTATGAGAGA
7741  CATCCGCTCT  CCCATTTTGT  CAATTTAGAC  AATTTGAGAG  CTAACAACAC  TAAAGGTTCA
7801  CTGCCTATTA  ATGTCATAGT  TTTTGATGGC  AAGTCCAAAT  GCGACGAGTC  TGCTTCTAAG
7861  TCTGCTTCTG  TGTACTACAG  TCAGCTGATG  TGCCAACCTA  TTCTGTTGCT  TGACCAAGCT
7921  CTTGTATCAA  ACGTTGGAGA  TAGTACTGAA  GTTTCCGTTA  AGATGTTTGA  TGCTTATGTC
7981  GACACCTTTT  CAGCAACTTT  TAGTGTTCCT  ATGGAAAAAC  TTAAGGCACT  TGTTGCTACA
8041  GCTCACAGCG  AGTTAGCAAA  GGGTGTAGCT  TTAGATGGTG  TCCTTTCTAC  ATTCGTGTCA
8101  GCTGCCCGAC  AAGGTGTTGT  TGATACCGAT  GTTGACACAA  AGGATGTTAT  TGAATGTCTC
8161  AAACTTTCAC  ATCACTCTGA  CTTAGAAGTG  ACAGGTGACA  GTTGTAACAA  TTTCATGCTC
8221  ACCTATAATA  AGGTTGAAAA  CATGACGCCC  AGAGATCTTG  GCGCATGTAT  TGACTGTAAT
8281  GCAAGGCATA  TCAATGCCCA  AGTAGCAAAA  AGTCACAATG  TTTCACTCAT  CTGGAATGTA
8341  AAAGACTACA  TGTCTTTATC  TGAACAGCTG  CGTAAACAAA  TTCGTACTGC  TGCCAAGAAG
8401  AACAACATAC  CTTTTACACT  AACTTGTGCT  ACAACTAGAC  AGGTTGTCAA  TGTCATAACT
8461  ACTAAAATCT  CACTCAAGGG  TGGTAAGATT  GTTAGTACTT  GTTTTAAACT  TATGCTTAAG
8521  GCCACATTAT  TGTGCGTTCT  TGCTGCATTG  GTTTGTTATA  TCGTTATGCC  AGTACATACA
8581  TTGTCAATCC  ATGATGGTTA  CACAAATGAA  ATCATTGGTT  ACAAAGCCAT  TCAGGATGGT
8641  GTCACTCGTG  ACATCATTTC  TACTGATGAT  TGTTTTGCAA  ATAAACATGC  TGGTTTTGAC
8701  GCATGGTTTA  GCCAGCGTGG  TGGTTCATAC  AAAAATGACA  AAAGCTGCCC  TGTAGTAGCT
8761  GCTATCATTA  CAAGAGAGAT  TGGTTTCATA  GTGCCTGGCT  TACCGGGTAC  TGTGCTGAGA
8821  GCAATCAATG  GTGACTTCTT  GCATTTTCTA  CCTCGTGTTT  TTAGTGCTGT  TGGCAACATT
8881  TGCTACACAC  CTTCCAAACT  CATTGAGTAT  AGTGATTTTG  CTACCTCTGC  TTGCGTTCTT
8941  GCTGCTGAGT  GTACAATTTT  TAAGGATGCT  ATGGGCAAAC  CTGTGCCATA  TTGTTATGAC
9001  ACTAATTTGC  TAGAGGGTTC  TATTTCTTAT  AGTGAGCTTC  GTCCAGACAC  TCGTTATGTG
9061  CTTATGGATG  GTTCCATCAT  ACAGTTTCCT  AACACTTACC  TGGAGGGTTC  TGTTAGAGTA
9121  GTAACAACTT  TTGATGCTGA  GTACTGTAGA  CATGGTACAT  GCGAAAGGTC  AGAAGTAGGT
9181  ATTTGCCTAT  CTACCAGTGG  TAGATGGGTT  CTTAATAATG  AGCATTACAG  AGCTCTATCA
9241  GGAGTTTTCT  GTGGTGTTGA  TGCGATGAAT  CTCATAGCTA  ACATCTTTAC  TCCTCTTGTG
9301  CAACCTGTGG  GTGCTTTAGA  TGTGTCTGCT  TCAGTAGTGG  CTGGTGGTAT  TATTGCCATA
9361  TTGGTGACTT  GTGCTGCCTA  CTACTTTATG  AAATTCAGAC  GTGTTTTTGG  TGAGTACAAC
9421  CATGTTGTTG  CTGCTAATGC  ACTTTTGTTT  TTGATGTCTT  TCACTATACT  CTGTCTGGTA
9481  CCAGCTTACA  GCTTTCTGCC  GGGAGTCTAC  TCAGTCTTTT  ACTTGTACTT  GACATTCTAT
9541  TTCACCAATG  ATGTTTCATT  CTTGGCTCAC  CTTCAATGGT  TTGCCATGTT  TTCTCCTATT
9601  GTGCCTTTTT  GGATAACAGC  AATCTATGTA  TTCTGTATTT  CTCTGAAGCA  CTGCCATTGG
9661  TTCTTTAACA  ACTATCTTAG  GAAAAGAGTC  ATGTTTAATG  GAGTTACATT  TAGTACCTTC
9721  GAGGAGGCTG  CTTTGTGTAC  CTTTTTGCTC  AACAAGGAAA  TGTACCTAAA  ATTGCGTAGC
9781  GAGACACTGT  TGCCACTTAC  ACAGTATAAC  AGGTATCTTG  CTCTATATAA  CAAGTACAAG
9841  TATTTCAGTG  GAGCCTTAGA  TACTACCAGC  TATCGTGAAG  CAGCTTGCTG  CCACTTAGCA
9901  AAGGCTCTAA  ATGACTTTAG  CAACTCAGGT  GCTGATGTTC  TCTACCAACC  ACCACAGACA
9961  TCAATCACTT  CTGCTGTTCT  GCAGAGTGGT  TTTAGGAAAA  TGGCATTCCC  GTCAGGCAAA
10021 GTTGAAGGGT  GCATGGTACA  AGTAACCTGT  GGAACTACAA  CTCTTAATGG  ATTGTGGTTG
10081 GATGACACAG  TATACTGTCC  AAGACATGTC  ATTTGCACAG  CAGAAGACAT  GCTTAATCCT
10141 AACTATGAAG  ATCTGCTCAT  TCGCAAATCC  AACCATAGCT  TTCTTGTTCA  GGCTGGCAAT
10201 GTTCAACTTC  GTGTTATTGG  CCATTCTATG  CAAAATTGTC  TGCTTAGGCT  TAAAGTTGAT
10261 ACTTCTAACC  CTAAGACACC  CAAGTATAAA  TTTGTCCGTA  TCCAACCTGG  TCAAACATTT
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Figure 6-D

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10321 TCAGTTCTAG  CATGCTACAA  TGGTTCACCA  TCTGGTGTTT  ATCAGTGTGC  CATGAGACCT
10381 AATCATACCA  TTAAAGGTTC  TTTCCTTAAT  GGATCATGTG  GTAGTGTTGG  TTTTAACATT
10441 GATTATGATT  GCGTGTCTTT  CTGCTATATG  CATCATATGG  AGCTTCCAAC  AGGAGTACAC
10501 GCTGGTACTG  ACTTAGAAGG  TAAATTCTAT  GGTCCATTTG  TTGACAGACA  AACTGCACAG
10561 GCTGCAGGTA  CAGACACAAC  CATAACATTA  AATGTTTTGG  CATGGCTGTA  TGCTGCTGTT
10621 ATCAATGGTG  ATAGGTGGTT  TCTTAATAGA  TTCACCACTA  CTTTGAATGA  CTTTAACCTT
10681 GTGGCAATGA  AGTACAACTA  TGAACCTTTG  ACACAAGATC  ATGTTGACAT  ATTGGGACCT
10741 CTTTCTGCTC  AAACAGGAAT  TGCCGTCTTA  GATATGTGTG  CTGCTTTGAA  AGAGCTGCTG
10801 CAGAATGGTA  TGAATGGTCG  TACTATCCTT  GGTAGCACTA  TTTTAGAAGA  TGAGTTTACA
10861 CCATTTGATG  TTGTTAGACA  ATGCTCTGGT  GTTACCTTCC  AAGGTAAGTT  CAAGAAAATT
10921 GTTAAGGGCA  CTCATCATTG  GATGCTTTTA  ACTTTCTTGA  CATCACTATT  GATTCTTGTT
10981 CAAAGTACAC  AGTGGTCACT  GTTTTTCTTT  GTTTACGAGA  ATGCTTTCTT  GCCATTTACT
11041 CTTGGTATTA  TGGCAATTGC  TGCATGTGCT  ATGCTGCTTG  TTAAGCATAA  GCACGCATTC
11101 TTGTGCTTGT  TTCTGTTACC  TTCTCTTGCA  ACAGTTGCTT  ACTTTAATAT  GGTCTACATG
11161 CCTGCTAGCT  GGGTGATGCG  TATCATGACA  TGGCTTGAAT  TGGCTGACAC  TAGCTTGTCT
11221 GGTTATAGGC  TTAAGGATTG  TGTTATGTAT  GCTTCAGCTT  TAGTTTTGCT  TATTCTCATG
11281 ACAGCTCGCA  CTGTTTATGA  TGATGCTGCT  AGACGTGTTT  GGACACTGAT  GAATGTCATT
11341 ACACTTGTTT  ACAAAGTCTA  CTATGGTAAT  GCTTTAGATC  AAGCTATTTC  CATGTGGGCC
11401 TTAGTTATTT  CTGTAACCTC  TAACTATTCT  GGTGTCGTTA  CGACTATCAT  GTTTTTAGCT
11461 AGAGCTATAG  TGTTTGTGTG  TGTTGAGTAT  TACCCATTGT  TATTTATTAC  TGGCAACACC
11521 TTACAGTGTA  TCATGCTTGT  TTATTGTTTC  TTAGGCTATT  GTTGCTGCTG  CTACTTTGGC
11581 CTTTTCTGTT  TACTCAACCG  TTACTTCAGG  CTTACTCTTG  GTGTTTATGA  CTACTTGGTC
11641 TCTACACAAG  AATTTAGGTA  TATGAACTCC  CAGGGGCTTT  TGCCTCCTAA  GAGTAGTATT
11701 GATGCTTTCA  AGCTTAACAT  TAAGTTGTTG  GGTATTGGAG  GTAAACCATG  TATCAAGGTT
11761 GCTACTGTAC  AGTCTAAAAT  GTCTGACGTA  AAGTGCACAT  CTGTGGTACT  GCTCTCGGTT
11821 CTTCAACAAC  TTAGAGTAGA  GTCATCTTCT  AAATTGTGGG  CACAATGTGT  ACAACTCCAC
11881 AATGATATTC  TTCTTGCAAA  AGACACAACT  GAAGCTTTCG  AGAAGATGGT  TTCTCTTTTG
11941 TCTGTTTTGC  TATCCATGCA  GGGTGCTGTA  GACATTAATA  GGTTGTGCGA  GGAAATGCTC
12001 GATAACCGTG  CTACTCTTCA  GGCTATTGCT  TCAGAATTTA  GTTCTTTACC  ATCATATGCC
12061 GCTTATGCCA  CTGCCCAGGA  GGCCTATGAG  CAGGCTGTAG  CTAATGGTGA  TTCTGAAGTC
12121 GTTCTCAAAA  AGTTAAAGAA  ATCTTTGAAT  GTGGCTAAAT  CTGAGTTTGA  CCGTGATGCT
12181 GCCATGCAAC  GCAAGTTGGA  AAAGATGGCA  GATCAGGCTA  TGACCCAAAT  GTACAAACAG
12241 GCAAGATCTG  AGGACAAGAG  GGCAAAAGTA  ACTAGTGCTA  TGCAAACAAT  GCTCTTCACT
12301 ATGCTTAGGA  AGCTTGATAA  TGATGCACTT  AACAACATTA  TCAACAATGC  GCGTGATGGT
12361 TGTGTTCCAC  TCAACATCAT  ACCATTGACT  ACAGCAGCCA  AACTCATGGT  TGTTGTCCCT
12421 GATTATGGTA  CCTACAAGAA  CACTTGTGAT  GGTAACACCT  TTACATATGC  ATCTGCACTC
12481 TGGGAAATCC  AGCAAGTTGT  TGATGCGGAT  AGCAAGATTG  TTCAACTTAG  TGAAATTAAC
12541 ATGGACAATT  CACCAAATTT  GGCTTGGCCT  CTTATTGTTA  CAGCTCTAAG  AGCCAACTCA
12601 GCTGTTAAAC  TACAGAATAA  TGAACTGAGT  CCAGTAGCAC  TACGACAGAT  GTCCTGTGCG
12661 GCTGGTACCA  CACAAACAGC  TTGTACTGAT  GACAATGCAC  TTGCCTACTA  TAACAATTCG
12721 AAGGGAGGTA  GGTTTGTGCT  GGCATTACTA  TCAGACCACC  AAGATCTCAA  ATGGGCTAGA
12781 TTCCCTAAGA  GTGATGGTAC  AGGTACAATT  TACACAGAAC  TGGAACCACC  TTGTAGGTTT
12641 GTTACAGACA  CACCAAAAGG  GCCTAAAGTG  AAATACTTGT  ACTTCATCAA  AGGCTTAAAC
12901 AACCTAAATA  GAGGTATGGT  GCTGGGCAGT  TTAGCTGCTA  CAGTACGTCT  TCAGGCTGGA
12961 AATGCTACAG  AAGTACCTGC  CAATTCAACT  GTGCTTTCCT  TCTGTGCTTT  TGCAGTAGAC
13021 CCTGCTAAAG  CATATAAGGA  TTACCTAGCA  AGTGGAGGAC  AACCAATCAC  CAACTGTGTG
13081 AAGATGTTGT  GTACACACAC  TGGTACAGGA  CAGGCAATTA  CTGTAACACC  AGAAGCTAAC
13141 ATGGACCAAG  AGTCCTTTGG  TGGTGCTTCA  TGTTGTCTGT  ATTGTAGATG  CCACATTGAC
13201 CATCCAAATC  CTAAAGGATT  CTGTGACTTG  AAAGGTAAGT  ACGTCCAAAT  ACCTACCACT
13261 TGTGCTAATG  ACCCAGTGGG  TTTTACACTT  AGAAACACAG  TCTGTACCGT  CTGCGGAATG
13321 TGGAAAGGTT  ATGGCTGTAG  TTGTGACCAA  CTCCGCGAAC  CCTTGATGCA  GTCTGCGGAT
13381 GCATCAACGT  TTTTAAACGG  GTTTGCGGTG  TAAGTGCAGC  CCGTCTTACA  CCGTGCGGCA
13441 CAGGCACTAG  TACTGATGTC  GTCTACAGGG  CTTTTGATAT  TTACAACGAA  AAAAGTGCTG
13501 GTTTTGCAAA  GTTCCTAAAA  ACTAATTGCT  GTCGCTTCCA  GGAGAAGGAT  GAGGAAGGCA
13561 ATTTATTAGA  CTCTTACTTT  GTAGTTAAGA  GGCATACTAT  GTCTAACTAC  CAACATGAAG
13621 AGACTATTTA  TAACTTGGTT  AAAGATTGTC  CAGCGGTTGC  TGTCCATGAC  TTTTTCAAGT
13681 TTAGAGTAGA  TGGTGACATG  GTACCACATA  TATCACGTCA  GCGTCTAACT  AAATACACAA
13741 TGGCTGATTT  AGTCTATGCT  CTACGTCATT  TTGATGAGGG  TAATTGTGAT  ACATTAAAAG
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Figure 6-E

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13801 AAATACTCGT CACATACAAT TGCTGTGATG ATGATTATTT CAATAAGAAG GATTGGTATG
13861 ACTTCGTAGA GAATCCTGAC ATCTTACGCG TATATGCTAA CTTAGGTGAG CGTGTACGCC
13921 AATCATTATT AAAGACTGTA CAATTCTGCG ATGCTATGCG TGATGCAGGC ATTGTAGGCG
13981 TACTGACATT AGATAATCAG GATCTTAATG GGAACTGGTA CGATTTCGGT GATTTCGTAC
14041 AAGTAGGACC AGGCTGCGGA GTTCCTATTG TGGATTCATA TTACTCATTG CTGATGCCCA
14101 TCCTCACTTT GACTAGGGCA TTGGCTGCTG AGTCCCATAT GGATGCTGAT CTCGCAAAAC
14161 CACTTATTAA GTGGGATTTG CTGAAATATG ATTTTACGGA AGAGAGACTT TGTCTCTTCG
14221 ACCGTTATTT TAAATATTGG GACCAGACAT ACCATCCCAA TTGTATTAAC TGTTTGGATG
14281 ATAGGTGTAT CCTTCATTGT GCAAACTTTA ATGTGTTATT TTCTACTGTG TTTCCACCTA
14341 CAAGTTTTGG ACCACTAGTA AGAAAAATAT TTGTAGATGG TGTTCCTTTT GTTGTTTCAA
14401 CTGGATACCA TTTTCGTGAG TTAGGAGTCG TACATAATCA GGATGTAAAC TTACATAGCT
14461 CGCGTCTCAG TTTCAAGGAA CTTTTAGTGT ATGCTGCTGA TCCAGCTATG CATGCAGCTT
14521 CTGGCAATTT ATTGCTAGAT AAACGCACTA CATGCTTTTC AGTAGCTGCA CTAACAAACA
14581 ATGTTGCTTT TCAAACTGTC AAACCCGGTA ATTTTAATAA AGACTTTTAT GACTTTGCTG
14641 TGTCTAAAGG TTTCTTTAAG GAAGGAAGTT CTGTTGAACT AAAACACTTC TTCTTTGCTC
14701 AGGATGGCAA CGCTGCTATC AGTGATTATG ACTATTATCG TTATAATCTG CCAACAATGT
14761 GTGATATCAG ACAACTCCTA TTCGTAGTTG AAGTTGTTGA TAAATACTTT GATTGTTACG
14821 ATGGTGGCTG TATTAATGCC AACCAAGTAA TCGTTAACAA TCTGGATAAA TCAGCTGGTT
14861 TCCCATTTAA TAAATGGGGT AAGGCTAGAC TTTATTATGA CTCAATGAGT TATGAGGATC
14941 AAGATGCACT TTTCGCGTAT ACTAAGCGTA ATGTCATCCC TACTATAACT CAAATGAATC
15001 TTAAGTATGC CATTAGTGCA AAGAATAGAG CTCGCACCGT AGCTGGTGTC TCTATCTGTA
15061 GTACTATGAC AAATAGACAG TTTCATCAGA AATTATTGAA GTCAATAGCC GCCACTAGAG
15121 GAGCTACTGT GGTAATTGGA ACAAGCAAGT TTTACGGTGG CTGGCATAAT ATGTTAAAAA
15181 CTGTTTACAG TGATGTAGAA ACTCCACACC TTATGGGTTG GGATTATCCA AAATGTGACA
15241 GAGCCATGCC TAACATGCTT AGGATAATGG CCTCTCTTGT TCTTGCTCGC AAACATAACA
15301 CTTGCTGTAA CTTATCACAC CGTTTCTACA GGTTAGCTAA CGAGTGTGCG CAAGTATTAA
15361 GTGAGATGGT CATGTGTGGC GGCTCACTAT ATGTTAAACC AGGTGGAACA TCATCCGGTG
15421 ATGCTACAAC TGCTTATGCT AATAGTGTCT TTAACATTTG TCAAGCTGTT ACAGCCAATG
15481 TAAATGCACT TCTTTCAACT GATGGTAATA AGATAGCTGA CAAGTATGTC CGCAATCTAC
15541 AACACAGGCT CTATGAGTGT CTCTATAGAA ATAGGGATGT TGATCATGAA TTCGTGGATG
15601 AGTTTTACGC TTACCTGCGT AAACATTTCT CCATGATGAT TCTTTCTGAT GATGCCGTTG
15661 TGTGCTATAA CAGTAACTAT GCGGCTCAAG GTTTAGTAGC TAGCATTAAG AACTTTAAGG
15721 CAGTTCTTTA TTATCAAAAT AATGTGTTCA TGTCTGAGGC AAAATGTTGG ACTGAGACTG
15781 ACCTTACTAA AGGACCTCAC GAATTTTGCT CACAGCATAC AATGCTAGTT AAACAAGGAG
15841 ATGATTACGT GTACCTGCCT TACCCAGATC CATCAAGAAT ATTAGGCGCA GGCTGTTTTG
15901 TCGATGATAT TGTCAAAACA GATGGTACAC TTATGATTGA AAGGTTCGTG TCACTGGCTA
15961 TTGATGCTTA CCCACTTACA AAACATCCTA ATCAGGAGTA TGCTGATGTC TTTCACTTGT
16021 ATTTACAATA CATTAGAAAG TTACATGATG AGCTTACTGG CCACATGTTG GACATGTATT
16081 CCGTAATGCT AACTAATGAT AACACCTCAC GGTACTGGGA ACCTGAGTTT TATGAGGCTA
16141 TGTACACACC ACATACAGTC TTGCAGGCTG TAGGTGCTTG TGTATTGTGC AATTCACAGA
16201 CTTCACTTCG TTGCGGTGCC TGTATTAGGA GACCATTCCT ATGTTGCAAG TGCTGCTATG
16261 ACCATGTCAT TTCAACATCA CACAAATTAG TGTTGTCTGT TAATCCCTAT GTTTGCAATG
16321 CCCCAGGTTG TGATGTCACT GATGTGACAC AACTGTATCT AGGAGGTATG AGCTATTATT
16381 GCAAGTCACA TAAGCCTCCC ATTAGTTTTC CATTATGTGC TAATGGTCAG GTTTTTGGTT
16441 TATACAAAAA CACATGTGTA GGCAGTGACA ATGTCACTGA CTTCAATGCG ATAGCAACAT
16501 GTGATTGGAC TAATGCTGGC GATTACATAC TTGCCAACAC TTGTACTGAG AGACTCAAGC
16561 TTTTCGCAGC AGAAACGCTC AAAGCCACTG AGGAAACATT TAAGCTGTCA TATGGTATTG
16621 CCACTGTACG CGAAGTACTC TCTGACAGAG AATTGCATCT TTCATGGGAG GTTGGAAAAC
16661 CTAGACCACC ATTGAACAGA AACTATGTCT TTACTGGTTA CCGTGTAACT AAAAATAGTA
16741 AAGTACAGAT TGGAGAGTAC ACCTTTGAAA AAGGTGACTA TGGTGATGCT GTTGTGTACA
16801 GAGGTACTAC GACATACAAG TTGAATGTTG GTGATTACTT TGTGTTGACA TCTCACACTG
16861 TAATGCCACT TAGTGCACCT ACTCTAGTGC CACAAGAGCA CTATGTGAGA ATTACTGGCT
16921 TGTACCCAAC ACTCAACATC TCAGATGAGT TTTCTAGCAA TGTTGCAAAT TATCAAAAGG
16981 TCGGCATGCA AAAGTACTCT ACACTCCAAG GACCACCTGG TACTGGTAAG AGTCATTTTG
17041 CCATCGGACT TGCTCTCTAT TACCCATCTG CTCGCATAGT GTATACGGCA TGCTCTCATG
17101 CAGCTGTTGA TGCCCTATGT GAAAAGGCAT TAAAATATTT GCCCATAGAT AAATGTAGTA
17161 GAATCATACC TGCGCGTGCG CGCGTAGAGT GTTTTGATAA ATTCAAAGTG AATTCAACAC
17221 TAGAACAGTA TGTTTTCTGC ACTGTAAATG CATTGCCAGA AACAACTGCT GACATTGTAG
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Figure 6-F

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17281 TCTTTGATGA  AATCTCTATG  GCTACTAATT  ATGACTTGAG  TGTTGTCAAT  GCTAGACTTC
17341 GTGCAAAACA  CTACGTCTAT  ATTGGCGATC  CTGCTCAATT  ACCAGCCCCC  CGCACATTGC
17401 TGACTAAAGG  CACACTAGAA  CCAGAATATT  TTAATTCAGT  GTGCAGACTT  ATGAAAACAA
17461 TAGGTCCAGA  CATGTTCCTT  GGAACTTGTC  GCCGTTGTCC  TGCTGAAATT  GTTGACACTG
17521 TGAGTGCTTT  AGTTTATGAC  AATAAGCTAA  AAGCACACAA  GGATAAGTCA  GCTCAATGCT
17561 TCAAAATGTT  CTACAAAGGT  GTTATTACAC  ATGATGTTTC  ATCTGCAATC  AACAGACCTC
17641 AAATAGGCGT  TGTAAGAGAA  TTTCTTACAC  GCAATCCTGC  TTGGAGAAAA  GCTGTTTTTA
17701 TCTCACCTTA  TAATTCACAG  AACGCTGTAG  CTTCAAAAAT  CTTAGGATTG  CCTACGCAGA
17761 CTGTTGATTC  ATCACAGGGT  TCTGAATATG  ACTATGTCAT  ATTCACACAA  ACTACTGAAA
17821 CAGCACACTC  TTGTAATGTC  AACCGCTTCA  ATGTGGCTAT  CACAAGGGCA  AAAATTGGCA
17881 TTTTGTGCAT  AATGTCTGAT  AGAGATCTTT  ATGACAAACT  GCAATTTACA  AGTCTAGAAA
17941 TACCACGTCG  CAATGTGGCT  ACATTACAAG  CAGAAAATGT  AACTGGACTT  TTTAAGGACT
18001 GTAGTAAGAT  CATTACTGGT  CTTCATCCTA  CACAGGCACC  TACACACCTC  AGCGTTGATA
18061 TAAAATTCAA  GACTGAAGGA  TTATGTGTTG  ACATACCAGG  CATACCAAAG  GACATGACCT
18121 ACCGTAGACT  CATCTCTATG  ATGGGTTTCA  AAATGAATTA  CCAAGTCAAT  GGTTACCCTA
18181 ATATGTTTAT  CACCCGCGAA  GAAGCTATTC  GTCACGTTCG  TGCGTGGATT  GGCTTTGATG
18241 TAGAGGGCTG  TCATGCAACT  AGAGATGCTG  TGGGTACTAA  CCTACCTCTC  CAGCTAGGAT
18301 TTTCTACAGG  TGTTAACTTA  GTAGCTGTAC  CGACTGGTTA  TGTTGACACT  GAAAATAACA
18361 CAGAATTCAC  CAGAGTTAAT  GCAAAACCTC  CACCAGGTGA  CCAGTTTAAA  CATCTTATAC
18421 CACTCATGTA  TAAAGGCTTG  CCCTGGAATG  TAGTGCGTAT  TAAGATAGTA  CAAATGCTCA
18481 GTGATACACT  GAAAGGATTG  TCAGACAGAG  TCGTGTTCGT  CCTTTGGGCG  CATGGCTTTG
18541 AGCTTACATC  AATGAAGTAC  TTTGTCAAGA  TTGGACCTGA  AAGAACGTGT  TGTCTGTGTG
18601 ACAAACGTGC  AACTTGCTTT  TCTACTTCAT  CAGATACTTA  TGCCTGCTGG  AATCATTCTG
18651 TGGGTTTTGA  CTATGTCTAT  AACCCATTTA  TGATTGATGT  TCAGCAGTGG  GGCTTTACGG
18721 GTAACCTTCA  GAGTAACCAT  GACCAACATT  GCCAGGTACA  TGGAAATGCA  CATGTGGCTA
18781 GTTGTGATGC  TATCATGACT  AGATGTTTAG  CAGTCCATGA  GTGCTTTGTT  AAGCGCGTTG
18841 ATTGGTCTGT  TGAATACCCT  ATTATAGGAG  ATGAACTGAG  GGTTAATTCT  GCTTGCAGAA
18901 AAGTACAACA  CATGGTTGTG  AAGTCTGCAT  TGCTTGCTGA  TAAGTTTCCA  GTTCTTCATG
18961 ACATTGGAAA  TCCAAAGGCT  ATCAAGTGTG  TGCCTCAGGC  TGAAGTAGAA  TGGAAGTTCT
19021 ACGATGCTCA  GCCATGTAGT  GACAAAGCTT  ACAAAATAGA  GGAACTCTTC  TATTCTTATG
19081 CTACACATCA  CGATAAATTC  ACTGATGGTG  TTTGTTTGTT  TTGGAATTGT  AACGTTGATC
19141 GTTACCCAGC  CAATGCAATT  GTGTGTAGGT  TTGACACAAG  AGTCTTGTCA  AACTTGAACT
19201 TACCAGGCTG  TGATGGTGGT  AGTTTGTATG  TGAATAAGCA  TGCATTCCAC  ACTCCAGCTT
19261 TCGATAAAAG  TGCATTTACT  AATTTAAAGC  AATTGCCTTT  CTTTTACTAT  TCTGATAGTC
19321 CTTGTGAGTC  TCATGGCAAA  CAAGTAGTGT  CGGATATTGA  TTATGTTCCA  CTCAAATCTG
19381 CTACGTGTAT  TACACGATGC  AATTTAGGTG  GTGCTGTTTG  CAGACACCAT  GCAAATGAGT
19441 ACCGACAGTA  CTTGGATGCA  TATAATATGA  TGATTTCTGC  TGGATTTAGC  CTATGGATTT
19501 ACAAACAATT  TGATACTTAT  AACCTGTGGA  ATACATTTAC  CAGGTTACAG  AGTTTAGAAA
19561 ATGTGGCTTA  TAATGTTGTT  AATAAAGGAC  ACTTTGATGG  ACACGCCGGC  GAAGCACCTG
19621 TTTCCATCAT  TAATAATGCT  GTTTACACAA  AGGTAGATGG  TATTGATGTG  GAGATCTTTG
19681 AAAATAAGAC  AACACTTCCT  GTTAATGTTG  CATTTGAGCT  TTGGGCTAAG  CGTAACATTA
19741 AACCAGTGCC  AGAGATTAAG  ATACTCAATA  ATTTGGGTGT  TGATATCGCT  GCTAATACTG
19801 TAATCTGGGA  CTACAAAAGA  GAAGCCCCAG  CACATGTATC  TACAATAGGT  GTCTGCACAA
19861 TGACTGACAT  TGCCAAGAAA  CCTACTGAGA  GTGCTTGTTC  TTCACTTACT  GTCTTGTTTG
19921 ATGGTAGAGT  GGAAGGACAG  GTAGACCTTT  TTAGAAACGC  CCGTAATGGT  GTTTTAATAA
19931 CAGAAGGTTC  AGTCAAAGGT  CTAACACCTT  CAAAGGGACC  AGCACAAGCT  AGCGTCAATG
20041 GAGTCACATT  AATTGGAGAA  TCAGTAAAAA  CACAGTTTAA  CTACTTTAAG  AAAGTAGACG
20101 GCATTATTCA  ACAGTTGCCT  GAAACCTACT  TTACTCAGAG  CAGAGACTTA  GAGGATTTTA
20161 AGCCCAGATC  ACAAATGGAA  ACTGACTTTC  TCGAGCTCGC  TATGGATGAA  TTCATACAGC
20221 GATATAAGCT  CGAGGGCTAT  GCCTTCGAAC  ACATCGTTTA  TGGAGATTTC  AGTCATGGAC
20281 AACTTGGCGG  TCTTCATTTA  ATGATAGGCT  TAGCCAAGCG  CTCACAAGAT  TCACCACTTA
20341 AATTAGAGGA  TTTTATCCCT  ATGGACAGCA  CAGTGAAAAA  TTACTTCATA  ACAGATGCGC
20401 AAACAGGTTC  ATCAAAATGT  GTGTGTTCTG  TGATTGATCT  TTTACTTGAT  GACTTTGTCG
20461 AGATAATAAA  GTCACAAGAT  TTGTCAGTGA  TTTCAAAAGT  GGTCAAGGTT  ACAATTGACT
20521 ATGCTGAAAT  TTCATTCATG  CTTTGGTGTA  AGGATGGACA  TGTTGAAACC  TTCTACCCAA
20581 AACTACAAGC  AAGTCAAGCG  TGGCAACCAG  GTGTTGCGAT  GCCTAACTTG  TACAAGATGC
20641 AAAGAATGCT  TCTTGAAAAG  TGTGACCTTC  AGAATTATGG  TGAAAATGCT  GTTATACCAA
20701 AAGGAATAAT  GATGAATGTC  GCAAAGTATA  CTCAACTGTG  TCAATACTTA  AATACACTTA
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Figure 6-G

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20761 CTTTAGCTGT  ACCCTACAAC  ATGAGAGTTA  TTCACTTTGG  TGCTGGCTCT  GATAAAGGAG
20821 TTGCACCAGG  TACAGCTGTG  CTCAGACAAT  GGTTGCCAAC  TGGCACACTA  CTTGTCGATT
20881 CAGATCTTAA  TGACTTCGTC  TCCGACGCAG  ATTCTACTTT  AATTGGAGAC  TGTGCAACAG
20941 TACATACGGC  TAATAAATGG  GACCTTATTA  TTAGCGATAT  GTATGACCCT  AGGACCAAAC
21001 ATGTGACAAA  AGAGAATGAC  TCTAAAGAAG  GGTTTTTCAC  TTATCTGTGT  GGATTTATAA
21061 AGCAAAAACT  AGCCCTGGGT  GGTTCTATAG  CTGTAAAGAT  AACAGAGCAT  TCTTGGAATG
21121 CTGACCTTTA  CAAGCTTATG  GGCCATTTCT  CATGGTGGAC  AGCTTTTGTT  ACAAATGTAA
21181 ATGCATCATC  ATCGGAAGCA  TTTTTAATTG  GGGCTAACTA  TCTTGGCAAG  CCGAAGGAAC
21241 AAATTGATGG  CTATACCATG  CATGCTAACT  ACATTTTCTG  GAGGAACACA  AATCCTATCC
21301 AGTTGTCTTC  CTATTCACTC  TTTGACATGA  GCAAATTTCC  TCTTAAATTA  AGAGGAACTG
21361 CTGTAATGTC  TCTTAAGGAG  AATCAAATCA  ATGATATGAT  TTATTCTCTT  CTGGAAAAAG
21421 GTAGGCTTAT  CATTAGAGAA  AACAACAGAG  TTGTGGTTTC  AAGTGATATT  CTTGTTAACA
21481 ACTAAACGAA  CATGTTTATT  TTCTTATTAT  TTCTTACTCT  CACTAGTGGT  AGTGACCTTG
21541 ACCGGTGCAC  CACTTTTGAT  GATGTTCAAG  CTCCTAATTA  CACTCAACAT  ACTTCATCTA
21601 TGAGGGGGGT  TTACTATCCT  GATGAAATTT  TTAGATCAGA  CACTCTTTAT  TTAACTCAGG
21661 ATTTATTTCT  TCCATTTTAT  TCTAATGTTA  CAGGGTTTCA  TACTATTAAT  CATACGTTTG
21721 GCAACCCTGT  CATACCTTTT  AAGGATGGTA  TTTATTTTGC  TGCCACAGAG  AAATCAAATG
21781 TTGTCCGTGG  TTGGGTTTTT  GGTTCTACCA  TGAACAACAA  GTCACAGTCG  GTGATTATTA
21841 TTAACAATTC  TACTAATGTT  GTTATACGAG  CATGTAACTT  TGAATTGTGT  GACAACCCTT
21901 TCTTTGCTGT  TTCTAAACCC  ATGGGTACAC  AGACACATAC  TATGATATTC  GATAATGCAT
21951 TTAATTGCAC  TTTCGAGTAC  ATATCTGATG  CCTTTTCGCT  TGATGTTTCA  GAAAAGTCAG
22021 GTAATTTTAA  ACACTTACGA  GAGTTTGTGT  TTAAAAATAA  AGATGGGTTT  CTCTATGTTT
22081 ATAAGGGCTA  TCAACCTATA  GATGTAGTTC  GTGATCTACC  TTCTGGTTTT  AACACTTTGA
22141 AACCTATTTT  TAAGTTGCCT  CTTGGTATTA  ACATTACAAA  TTTTAGAGCC  ATTCTTACAG
22201 CCTTTTCACC  TGCTCAAGAC  ATTTGGGGCA  CGTCAGCTGC  AGCCTATTTT  GTTGGCTATT
22261 TAAAGCCAAC  TACATTTATG  CTCAAGTATG  ATGAAAATGG  TACAATCACA  GATGCTGTTG
22321 ATTGTTCTCA  AAATCCACTT  GCTGAACTCA  AATGCTCTGT  TAAGAGCTTT  GAGATTGACA
22381 AAGGAATTTA  CCAGACCTCT  AATTTCAGGG  TTGTTCCCTC  AGGAGATGTT  GTGAGATTCC
22441 CTAATATTAC  AAACTTGTGT  CCTTTTGGAG  AGGTTTTTAA  TCCTACTAAA  TTCCCTTCTG
22501 TCTATGCATG  GGAGAGAAAA  AAAATTTCTA  ATTGTGTTGC  TGATTACTCT  GTGCTCTACA
22561 ACTCAACATT  TTTTTCAACC  TTTAAGTGCT  ATGGCGTTTC  TGCCACTAAG  TTGAATGATC
22621 TTTGCTTCTC  CAATGTCTAT  GCAGATTCTT  TTGTAGTCAA  GGGAGATGAT  GTAAGACAAA
22681 TAGCGCCAGG  ACAAACTGGT  GTTATTGCTG  ATTATAATTA  TAAATTGCCA  GATGATTTCA
22741 TGGGTTGTGT  CCTTGCTTGG  AATACTAGGA  ACATTGATGC  TACTTCAACT  GGTAATTATA
22801 ATTATAAATA  TAGGTATCTT  AGACATGGCA  AGCTTAGGCC  CTTTGAGAGA  GACATATCTA
22861 ATGTGCCTTT  CTCCCCTGAT  GGCAAACCTT  GCACCCCACC  TGCTCTTAAT  TGTTATTGGC
22921 CATTAAATGA  TTATGGTTTT  TACACCACTA  CTGGCATTGG  CTACCAACCT  TACAGAGTTG
22981 TAGTACTTTC  TTTTGAACTT  TTAAATGCAC  CGGCCACGGT  TTGTGGACCA  AAATTATCCA
23041 CTGACCTTAT  TAAGAACCAG  TGTGTCAATT  TTAATTTTAA  TGGACTCACT  GGTACTGGTG
23101 TGTTAACTCC  TTCTTCAAAG  AGATTTCAAC  CATTTCAACA  ATTTGGCCGT  GATGTTTCTG
23161 ATTTCACTGA  TTCCGTTCGA  GATCCTAAAA  CATCTGAAAT  ATTAGACATT  TCACCTTGCT
23221 CTTTTGGGGG  TGTAAGTGTA  ATTACACCTG  GAACAAATGC  TTCATCTGAA  GTTGCTGTTC
23281 TATATCAAGA  TGTTAACTGC  ACTGATGTTT  CTACAGCAAT  TCATGCAGAT  CAACTCACAC
23341 CAGCTTGGCG  CATATATTCT  ACTGGAAACA  ATGTATTCCA  GACTCAAGCA  GGCTGTCTTA
23401 TAGGAGCTGA  GCATGTCGAC  ACTTCTTATG  AGTGCGACAT  TCCTATTGGA  GCTGGCATTT
23461 GTGCTAGTTA  CCATACAGTT  TCTTTATTAC  GTAGTACTAG  CCAAAAATCT  ATTGTGGCTT
23521 ATACTATGTC  TTTAGGTGCT  GATAGTTCAA  TTGCTTACTC  TAATAACACC  ATTGCTATAC
23581 CTACTAACTT  TTCAATTAGC  ATTACTACAG  AAGTAATGCC  TGTTTCTATG  GCTAAAACCT
23641 CCGTAGATTG  TAATATGTAC  ATCTGCGGAG  ATTCTACTGA  ATGTGCTAAT  TTGCTTCTCC
23701 AATATGGTAG  CTTTTGCACA  CAACTAAATC  GTGCACTCTC  AGGTATTGCT  GCTGAACAGG
23761 ATCGCAACAC  ACGTGAAGTG  TTCGCTCAAG  TCAAACAAAT  GTACAAAACC  CCAACTTTGA
23821 AATATTTTGG  TGGTTTTAAT  TTTTCACAAA  TATTACCTGA  CCCTCTAAAG  CCAACTAAGA
23881 GGTCTTTTAT  TGAGGACTTG  CTCTTTAATA  AGGTGACACT  CGCTGATGCT  GGCTTCATGA
23941 AGCAATATGG  CGAATGCCTA  GGTGATATTA  ATGCTAGAGA  TCTCATTTGT  GCGCAGAAGT
23001 TCAATGGACT  TACAGTGTTG  CCACCTCTGC  TCACTGATGA  TATGATTGCT  GCCTACACTG
24061 CTGCTCTAGT  TAGTGGTACT  GCCACTGCTG  GATGGACATT  TGGTGCTGGC  GCTGCTCTTC
24121 AAATACCTTT  TGCTATGCAA  ATGGCATATA  GGTTCAATGG  CATTGGAGTT  ACCCAAAATG
24181 TTCTCTATGA  GAACCAAAAA  CAAATCGCCA  ACCAATTTAA  CAAGGCGATT  AGTCAAATTC
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Figure 6-H

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24241 AAGAATCACT  TACAACAACA  TCAACTGCAT  TGGGCAAGCT  GCAAGACGTT  GTTAACCAGA
24301 ATGCTCAAGC  ATTAAACACA  CTTGTTAAAC  AACTTAGCTC  TAATTTTGGT  GCAATTTCAA
24361 GTGTGCTAAA  TGATATCCTT  TCGCGACTTG  ATAAAGTCGA  GGCGGAGGTA  CAAATTGACA
24421 GGTTAATTAC  AGGCAGACTT  CAAAGCCTTC  AAACCTATGT  AACACAACAA  CTAATCAGGG
24481 CTGCTGAAAT  CAGGGCTTCT  GCTAATCTTG  CTGCTACTAA  AATGTCTGAG  TGTGTTCTTG
24541 GACAATCAAA  AAGAGTTGAC  TTTTGTGGAA  AGGGCTACCA  CCTTATGTCC  TTCCCACAAG
24601 CAGCCCCGCA  TGGTGTTGTC  TTCCTACATG  TCACGTATGT  GCCATCCCAG  GAGAGGAACT
24661 TCACCACAGC  GCCAGCAATT  TGTCATGAAG  GCAAAGCATA  CTTCCCTCGT  GAAGGTGTTT
24721 TTGTGTTTAA  TGGCACTTCT  TGGTTTATTA  CACAGAGGAA  CTTCTTTTCT  CCACAAATAA
24781 TTACTACAGA  CAATACATTT  GTCTCAGGAA  ATTGTGATGT  CGTTATTGGC  ATCATTAACA
24841 ACACAGTTTA  TGATCCTCTG  CAACCTGAGC  TTGACTCATT  CAAAGAAGAG  CTGGACAAGT
24901 ACTTCAAAAA  TCATACATCA  CCAGATGTTG  ATCTTGGCGA  CATTTCAGGC  ATTAACGCTT
24961 CTGTCGTCAA  CATTCAAAAA  GAAATTGACC  GCCTCAATGA  GGTCGCTAAA  AATTTAAATG
25021 AATCACTCAT  TGACCTTCAA  GAATTGGGAA  AATATGAGCA  ATATATTAAA  TGGCCTTGGT
25081 ATGTTTGGCT  CGGCTTCATT  GCTGGACTAA  TTGCCATCGT  CATGGTTACA  ATCTTGCTTT
25141 GTTGCATGAC  TAGTTGTTGC  AGTTGCCTCA  AGGGTGCATG  CTCTTGTGGT  TCTTGCTGCA
25201 AGTTTGATGA  GGATGACTCT  GAGCCAGTTC  TCAAGGGTGT  CAAATTACAT  TACACATAAA
25261 CGAACTTATG  GATTTGTTTA  TGAGATTTTT  TACTCTTGGA  TCAATTACTG  CACAGCCAGT
25321 AAAAATTGAC  AATGCTTCTC  CTGCAAGTAC  TGTTCATGCT  ACAGCAACGA  TACCGCTACA
253B1 AGCCTCACTC  CCTTTCGGAT  GGCTTGTTAT  TGGCGTTGCA  TTTCTTGCTG  TTTTTCAGAG
25441 CGCTACCAAA  ATAATTGCGC  TCAATAAAAG  ATGGCAGCTA  GCCCTTTATA  AGGGCTTCCA
25501 GTTCATTTGC  AATTTACTGC  TGCTATTTGT  TACCATCTAT  TCACATCTTT  TGCTTGTCGC
25561 TGCAGGTAAG  GAGGCGCAAT  TTTTGTACCT  CTATGCCTTG  ATATATTTTC  TACAATGCAT
25621 CAACGCATGT  AGAATTATTA  TGAGATGTTG  GCTTTGTTGG  AAGTGCAAAT  CCAAGAACCC
25661 ATTACTTTAT  GATGCCAACT  ACTTTGTTTG  CTGGCACACA  CATAACTATG  ACTACTGTAT
25741 ACCATATAAC  AGTGTCACAG  ATACAATTGT  CGTTACTGAA  GGiGACGGCA  TTTCAACACC
25801 AAAACTCAAA  GAAGACTACC  AAATTGGTGG  TTATTCTGAG  GATAGGCACT  CAGGTGTTAA
25861 AGACTATGTC  GTTGTACATG  GCTATTTCAC  CGAAGTTTAC  TACCAGCTTG  AGTCTACACA
25921 AATTACTACA  GACACTGGTA  TTGAAAATGC  TACATTCTTC  ATCTTTAACA  AGCTTGTTAA
25981 AGACCCACCG  AATGTGCAAA  TACACACAAT  CGACGGCTCT  TCAGGAGTTG  CTAATCCAGC
26041 AATGGATCCA  ATTTATGATG  AGCCGACGAC  GACTACTAGC  GTGCCTTTGT  AAGCACAAGA
26101 AAGTGAGTAC  GAACTTATGT  ACTCATTCGT  TTCGGAAGAA  ACAGGTACGT  TAATAGTTAA
26161 TAGCGTACTT  CTTTTTCTTG  CTTTCGTGGT  ATTCTTGCTA  GTCACACTAG  CCATCCTTAC
26221 TGCGCTTCGA  TTGTGTGCGT  ACTGCTGCAA  TATTGTTAAC  GTGAGTTTAG  TAAAACCAAC
26281 GGTTTACGTC  TACTCGCGTG  TTAAAAATCT  GAACTCTTCT  GAAGGAGTTC  CTGATCTTCT
26341 GGTCTAAACG  AACTAACTAT  TATTATTATT  CTGTTTGGAA  CTTTAACATT  GCTTATCATG
26401 GCAGACAACG  GTACTATTAC  CGTTGAGGAG  CTTAAACAAC  TCCTGGAACA  ATGGAACCTA
26461 GTAATAGGTT  TCCTATTCCT  AGCCTGGATT  ATGTTACTAC  AATTTGCCTA  TTCTAATCGG
26521 AACAGGTTTT  TGTACATAAT  AAAGCTTGTT  TTCCTCTGGC  TCTTGTGGCC  AGTAACACTT
26581 GCTTGTTTTG  TGCTTGCTGT  TGTCTACAGA  ATTAATTGGG  TGACTGGCGG  GATTGCGATT
26641 GCAATGGCTT  GTATTGTAGG  CTTGATGTGG  CTTAGCTACT  TCGTTGCTTC  CTTCAGGCTG
26701 TTTGCTCGTA  CCCGCTCAAT  GTGGTCATTC  AACCCAGAAA  CAAACATTCT  TCTCAATGTG
26761 CCTCTCCGGG  GGACAATTGT  GACCAGACCG  CTCATGGAAA  GTGAACTTGT  CATTGGTGCT
26821 GTGATCATTC  GTGGTCACTT  GCGAATGGCC  GGACACTCCC  TAGGGCGCTG  TGACATTAAG
26681 GACCTGCCAA  AAGAGATCAC  TGTGGCTACA  TCACGAACGC  TTTCTTATTA  CAAATTAGGA
26941 GCGTCGCAGC  GTGTAGGCAC  TGATTCAGGT  TTTGCTGCAT  ACAACCGCTA  CCGTATTGGA
27001 AACTATAAAT  TAAATACAGA  CCACGCCGGT  AGCAACGACA  ATATTGCTTT  GCTAGTACAG
27061 TAAGTGACAA  CAGATGTTTC  ATCTTGTTGA  CTTCCAGGTT  ACAATAGCAG  AGATATTGAT
27121 TATCATTATG  AGGACTTTCA  GGATTGCTAT  TTGGAATCTT  GACGTTATAA  TAAGTTCAAT
27181 AGTGAGACAA  TTATTTAAGC  CTCTAACTAA  GAAGAATTAT  TCGGAGTTAG  ATGATGAAGA
27241 ACCTATGGAG  TTAGATTATC  CATAAAACGA  ACATGAAAAT  TATTCTCTTC  CTGACATTGA
27301 TTGTATTTAC  ATCTTGCGAG  CTATATCACT  ATCAGGAGTG  TGTTAGAGGT  ACGACTGTAC
27361 TACTAAAAGA  ACCTTGCCCA  TCAGGAACAT  ACGAGGGCAA  TTCACCATTT  CACCCTCTTG
27421 CTGACAATAA  ATTTGCACTA  ACTTGCACTA  GCACACACTT  TGCTTTTGCT  TGTGCTGACG
27461 GTACTCGACA  TACCTATCAG  CTGCGTGCAA  GATCAGTTTC  ACCAAAACTT  TTCATCAGAC
27541 AAGAGGAGGT  TCAACAAGAG  CTCTACTCGC  CACTTTTTCT  CATTGTTGCT  GCTCTAGTAT
27601 TTTTAATACT  TTGCTTCACC  ATTAAGAGAA  AGACAGAATG  AATGAGCTCA  CTTTAATTGA
27661 CTTCTATTTG  TGCTTTTTAG  CCTTTCTGCT  ATTCCTTGTT  TTAATAATGC  TTATTATATT
```

Figure 6-I

```
27721 TTGGTTTTCA  CTCGAAATCC  AGGATCTAGA  AGAACCTTGT  ACCAAAGTCT  AAACGAACAT
27781 GAAACTTCTC  ATTGTTTTGA  CTTGTATTTC  TCTATGCAGT  TGCATATGCA  CTGTAGTACA
27B41 GCGCTGTGCA  TCTAATAAAC  CTCATGTGCT  TGAAGATCCT  TGTAAGGTAC  AACACTAGGG
27901 GTAATACTTA  TAGCACTGCT  TGGCTTTGTG  CTCTAGGAAA  GGTTTTACCT  TTTCATAGAT
27961 GGCACACTAT  GGTTCAAACA  TGCACACCTA  ATGTTACTAT  CAACTGTCAA  GATCCAGCTG
28021 GTGGTGCGCT  TATAGCTAGG  TGTTGGTACC  TTCATGAAGG  TCACCAAACT  GCTGCATTTA
26081 GAGACGTACT  TGTTGTTTTA  AATAAACGAA  CAAATTAAAA  TGTCTGATAA  TGGACCCCAA
28141 TCAAACCAAC  GTAGTGCCCC  CCGCATTACA  TTTGGTGGAC  CCACAGATTC  AACTGACAAT
28201 AACCAGAATG  GAGGACGCAA  TGGGGCAAGG  CCAAAACAGC  GCCGACCCCA  AGGTTTACCC
28261 AATAATACTG  CGTCTTGGTT  CACAGCTCTC  ACTCAGCATG  GCAAGGAGGA  ACTTAGATTC
28321 CCTCGAGGCC  AGGGCGTTCC  AATCAACACC  AATAGTGGTC  CAGATGACCA  AATTGGCTAC
28381 TACCGAAGAG  CTACCCGACG  AGTTCGTGGT  GGTGACGGCA  AAATGAAAGA  GCTCAGCCCC
28441 AGATGGTACT  TCTATTACCT  AGGAACTGGC  CCAGAAGCTT  CACTTCCCTA  CGGCGCTAAC
28501 AAAGAAGGCA  TCGTATGGGT  TGCAACTGAG  GGAGCCTTGA  ATACACCCAA  AGACCACATT
28561 GGCACCCGCA  ATCCTAATAA  CAATGCTGCC  ACCGTGCTAC  AACTTCCTCA  AGGAACAACA
28621 TTGCCAAAAG  GCTTCTACGC  AGAGGGAAGC  AGAGGCGGCA  GTCAAGCCTC  TTCTCGCTCC
28681 TCATCACGTA  GTCGCGGTAA  TTCAAGAAAT  TCAACTCCTG  GCAGCAGTAG  GGGAAATTCT
28741 CCTGCTCGAA  TGGCTAGCGG  AGGTGGTGAA  ACTGCCCTCG  CGCTATTGCT  GCTAGACAGA
28601 TTGAACCAGC  TTGAGAGCAA  AGTTTCTGGT  AAAGGCCAAC  AACAACAAGG  CCAAACTGTC
28861 ACTAAGAAAT  CTGCTGCTGA  GGCATCTAAA  AAGCCTCGCC  AAAAACGTAC  TGCCACAAAA
28921 CAGTACAACG  TCACTCAAGC  ATTTGGGAGA  CGTGGTCCAG  AACAAACCCA  AGGAAATTTC
28981 GGGGACCAAG  ACCTAATCAG  ACAAGGAACT  GATTACAAAC  ATTGGCCGCA  AATTGCACAA
29041 TTTGCTCCAA  GTGCCTCTGC  ATTCTTTGGA  ATGTCACGCA  TTGGCATGGA  AGTCACACCT
29101 TCGGGAACAT  GGCTGACTTA  TCATGGAGCC  ATTAAATTGG  ATGACAAAGA  TCCACAATTC
29161 AAAGACAACG  TCATACTGCT  GAACAAGCAC  ATTGACGCAT  ACAAAACATT  CCCACCAACA
29221 GAGCCTAAAA  AGGACAAAAA  GAAAAAGACT  GATGAAGCTC  AGCCTTTGCC  GCAGAGACAA
29281 AAGAAGCAGC  CCACTGTGAC  TCTTCTTCCT  GCGGCTGACA  TGGATGATTT  CTCCAGACAA
29341 CTTCAAAATT  CCATGAGTGG  AGCTTCTGCT  GATTCAACTC  AGGCATAAAC  ACTCATGATG
29401 ACCACACAAG  GCAGATGGGC  TATGTAAACG  TTTTCGCAAT  TCCGTTTACG  ATACATAGTC
29461 TACTCTTGTG  CAGAATGAAT  TCTCGTAACT  AAACAGCACA  AGTAGGTTTA  GTTAACTTTA
29521 ATCTCACATA  GCAATCTTTA  ATCAATGTGT  AACATTAGGG  AGGACTTGAA  AGAGCCACCA
29581 CATTTTCATC  GAGGCCACGC  GGAGTACGAT  CGAGGGTACA  GTGAATAATG  CTAGGGAGAG
29641 CTGCCTATAT  GGAAGAGCCC  TAATGTGTAA  AATTAATTTT  AGTAGTGCTA  TCCCCATGTG
29701 ATTTTAATAG  CTTCTTAGGA  GAATGACAAA   AAAAAAAAAA  AA
```

Figure 7-A

```
pCV8

                                                       HpyCH4III
                                                   HpaII       |
                                                    NciI       |
                                                   ScrFI       |
                                                  PfoI |       |
                                                StyD4I |       |
                                                BsmAI| |       |
                                                BsmBI| |       |
                                                AluI|| |       |
                                               CviJI|| |       |
                                            Fnu4HI ||| |       |
                                          HpyCH4V| ||| |       |
                                           NlaIII| ||| |       |
                                             NspI| ||| |       |                     BstF5I
                                             TseI| ||| |       |                       NciI
        BstUI                              MnlI || ||| |  MaeIII                      ScrFI
         HhaI                            FatI | || ||| |  Tsp45I       SfaNI         HpaII|          DrdI
      BstUI |               HphI     HphI   | | || ||| | BbvI  |   AluI    |       StyD4I||          HgaI
     HinP1I |       HpyCH4III  |  Hpy188I   | | || ||| | BslI  |  CviJI    |   AciI     |||   FokI CviJI|
          | |               |  |        |   | | || ||| |    |  |      |    |      |     |||      |     ||
        tcgcgcgtttcggtgatgacggtgaaaacctctgacacatgcagctcccggagacggtcacagcttgtctgtaagcggatgccgggagcagacaagcccg
      1 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 100
        agcgcgcaaagccactactgccacttttggagactgtgtacgtcgagggcctctgccagtgtcgaacagacattcgcctacggccctcgtctgttcgggc

a       S  R  V  S  V  M  T  V  K  T  S  D  T  C  S  S  R  R  R  S  Q  L  V  C  K  R  M  P  G  A  D  K  P  V -
b        R  A  F  R  *  *  R  *  K  P  L  T  H  A  A  P  G  D  G  H  S  L  S  V  S  G  C  R  E  Q  T  S  P   -
c         A  R  F  G  D  D  G  E  N  L  *  H  M  Q  L  P  E  T  V  T  A  C  L  *  A  D  A  G  S  R  Q  A  R  -

                                                                                            AciI
                                                                                      HpyF10VI |
                                                                                       BstAPI| |
                                                                                         MwoI| |
                                                                 BspCNI                 NdeI|| |
                                                                BseMII|          Bme1580I  ||| |
                                                                 SfaNI|           BsiHKAI  ||| |
           BstUI                              MseI         Hpy188I   ||    DdeI  Bsp1286I  ||| |
            HhaI     FauI                  CviJI |       TauI    |   ||  RsaI |   Hpy8I |  ||| |
           FauI|  AciI  |                Cac8I | |   Fnu4HI |    |   ||Csp6I| | HpyCH4V |  ||| |
        HinP1I||MspA1I  |   AciI       CviJI | | |    AciI| |    |   ||TatI|| | ApaLI | |  ||| |     SfaNI
             |||     |  |      |           | | |       || |    |   |||| | |     | | |  ||| |         |
        tcagggcgcgtcagcgggtgttggcgggtgtcggggctggcttaactatgcggcatcagagcagattgtactgagagtgcaccatatgcggtgtgaaata
    101 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 200
        agtcccgcgcagtcgcccacaaccgcccacagccccgaccgaattgatacgccgtagtctcgtctaacatgactctcacgtggtatacgccacactttat

a         R  A  R  Q  R  V  L  A  G  V  G  A  G  L  T  M  R  H  Q  S  R  L  Y  *  E  C  T  I  C  G  V  K  Y  -
b       S  G  R  V  S  G  C  W  R  V  S  G  L  A  *  L  C  G  I  R  A  D  C  T  E  S  A  P  Y  A  V  *  N  T -
c        Q  G  A  S  A  G  V  G  G  C  R  G  W  L  N  Y  A  A  S  E  Q  I  V  L  R  V  H  H  M  R  C  E  I   -
```

Figure 7-B

```
                                            HpyF10VI
                                               MwoI|
                                               BbvI||
                                          BbeI  |||                                           CviJI
                                         HaeII  |||                                          HaeIII
                                          HhaI| |||                                          Cac8I |
                                         SfaNI| |||           HpyCH4III                     Sau96I |
                                        NlaIV|| |||              HhaI   |                     AciI | |
                                         SfoI|| |||               FspI| |                   MboII| | |
                                        BsaHI||| |||           HinP1I|| |                HpyF10VI|| | |
                                       HinP1I||| |||          Fnu4HI ||| |                   MwoI||| | |
                                     HpyF10VI||| |||           CviJI| ||| |               BsiEI |||| | |
                                         NarI||| |||            TseI| ||| |              BstKTI |||| | |
                                        BanI|||| |||    HpyF10VI || ||| |                 PvuI |||| | |
                                        KasI|||| |||         BglI| || ||| |               DpnI| |||| | |
      AciI                 AciI        MwoI|||| |||         MwoI| || ||| |               FauI|| |||| | |       MnlI
        |                         |       |||||  |||       || || |||   |           |||| ||||  | |       EarI |
        ccgcacagatgcgtaaggagaaaataccgcatcaggcgccattcgccattcaggctgcgcaactgttgggaagggcgatcggtgcgggcctcttcgctat
    201 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 300
        ggcgtgtctacgcattcctcttttatggcgtagtccgcggtaagcggtaagtccgacgcgttgacaacccttcccgctagccacgcccggagaagcgata

a        R  T  D  A  *  G  E  N  T  A  S  G  A  I  R  H  S  G  C  A  T  V  G  K  G  D  R  C  G  P  L  R  Y  -
b         A  Q  M  R  K  E  K  I  P  H  Q  A  P  F  A  I  Q  A  A  Q  L  L  G  R  A  I  G  A  G  L  F  A  I  -
c        P  H  R  C  V  R  R  K  Y  R  I  R  R  H  S  P  F  R  L  R  N  C  W  E  G  R  S  V  R  A  S  S  L  L -

                                                                                   TaiI
             Cac8I                                             BstNI             Hpy99I|
             AluI |                                            ScrFI          HpyCH4IV ||        BsrI
            CviJI |            HpyCH4V                        BsaJI|      Hpy188III  | ||       CviJI|
           MspA1I |           Fnu4HI |                       PspGI||      MaeIII  |  | ||      HaeIII|
            PvuII |          BstF5I| |                      StyD4I||      Tsp45I  |  | ||     Hpy99I|| HindIII
          Cac8I | |BbvI          TseI| |FokI MseI  MaeIII      |||BmrI  BsrI |  |  | ||      EaeI||| TspRI|
              | | |    |            || |   |    |         |    |||    |      | |  |    | ||          ||||      ||
        tacgccagctggcgaaagggggatgtgctgcaaggcgattaagttgggtaacgccagggttttcccagtcacgacgttgtaaaacgacggccagtgccaa
    301 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 400
        atgcggtcgaccgctttccccctacacgacgttccgctaattcaacccattgcggtcccaaaagggtcagtgctgcaacattttgctgccggtcacggtt

a       Y  A  S  W  R  K  G  D  V  L  Q  G  D  *  V  G  *  R  Q  G  F  P  S  H  D  V  V  K  R  R  P  V  P  S -
b        T  P  A  G  E  R  G  M  C  C  K  A  I  K  L  G  N  A  R  V  F  P  V  T  T  L  *  N  D  G  Q  C  Q  -
c         R  Q  L  A  K  G  G  C  A  A  R  R  L  S  W  V  T  P  G  F  S  Q  S  R  R  C  K  T  T  A  S  A  K  -
```

Figure 7 C

```
                                                      BstF5I           BslI
        BceAI                                          RsaI|     Tsp509I  |
       AluI |          BsmFI                         Csp6I||   FokI    |  |               HpyCH4III
      CviJI |    Tsp509I   |                   BslI  TatI|||MseI  |    |  |          BceAI        | CviJI
          | |          |   |                      |     ||||   |  |    |  |              |        |     |
          gcttgaaagagataaattgaacaagtatggtcgtcccctgttgggatgtactattaaacctaaattggggttatctgctaaaaactacggtagagccgtt
      401 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 500
          cgaactttctctatttaacttgttcataccagcaggggacaaccctacatgataatttggatttaaccccaatagacgatttttgatgccatctcggcaa

a           L  K  E  I  N  *  T  S  M  V  V  P  C  W  D  V  L  L  N  L  N  W  G  Y  L  L  K  T  T  V  E  P  F  -
b         A  *  K  R  *  I  E  Q  V  W  S  S  P  V  G  M  Y  Y  *  T  *  I  G  V  I  C  *  K  L  R  *  S  R  L -
c          L  E  R  D  K  L  N  K  Y  G  R  P  L  L  G  C  T  I  K  P  K  L  G  L  S  A  K  N  Y  G  R  A  V   -

                        Hpy8I                             MmeI
                     TspDTI |                           Hpy8I|             PpiI      BstKTI
       BbsI         AciI  | |                           TaiI||            XcmI|       DpnI|
      MboII   XmnI BstUI  | |              PpiI  HpyCH4IV  |||         BsaXI ||     MboI ||          BsaXI
          |      |     |  | |                 |         |  |||             | ||        | ||              |
          tatgaatgtcttcgcggtggacttgattttactaaagatgatgagaacgtgaactcacaaccatttatgcgttggagagatcgtttcttattttgtgccg
      501 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 600
          atacttacagaagcgccacctgaactaaaatgatttctactactcttgcacttgagtgttggtaaatacgcaacctctctagcaaagaataaaacacggc

a          M  N  V  F  A  V  D  L  I  L  L  K  M  M  R  T  *  T  H  N  H  L  C  V  G  E  I  V  S  Y  F  V  P   -
b           *  M  S  S  R  W  T  *  F  Y  *  R  *  *  E  R  E  L  T  T  I  Y  A  L  E  R  S  F  L  I  L  C  R  -
c         Y  E  C  L  R  G  G  L  D  F  T  K  D  D  E  N  V  N  S  Q  P  F  M  R  W  R  D  R  F  L  F  C  A  E -

                                                                             NlaIII
                                                                           FatI    |
                                                                          RsaI|    |
                                                                        Csp6I||    |        MboII
                                                                       PstI |||    |     BstKTI |
                                                                  HpyCH4V | |||    |      DpnI| |     HpyF10VI
                                                                   SfcI | | |||    |    BclI || |  AluI      |
                PsiI      CviJI                 HphI       BspMI BsmI | | | |||NspI     MboI || | CviJI  MwoI|
                   |          |                    |           |    | | | | |||    |       | || |     |     ||
          aagcactttataaagcacaggctgaaacaggtgaaatcaaagggcattacttgaatgctactgcaggtacatgcgaagaaatgatcaaaagagctgtatt
      601 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 700
          ttcgtgaaatatttcgtgtccgactttgtccactttagtttcccgtaatgaacttacgatgacgtccatgtacgcttctttactagttttctcgacataa

a         K  H  F  I  K  H  R  L  K  Q  V  K  S  K  G  I  T  *  M  L  L  Q  V  H  A  K  K  *  S  K  E  L  Y  L -
b          S  T  L  *  S  T  G  *  N  R  *  N  Q  R  A  L  L  E  C  Y  C  R  Y  M  R  R  N  D  Q  K  S  C  I   -
c           A  L  Y  K  A  Q  A  E  T  G  E  I  K  G  H  Y  L  N  A  T  A  G  T  C  E  E  M  I  K  R  A  V  F  -
```

Figure 7-D

```
                       BsiEI
                      BstKTI     NlaIII
                        PvuI     NsiI |                                                          Hpy8I
          BcgI         DpnI|  BfrBI | |       HphI                   AluI                        AccI|
     Tsp509I |    Hpy188I ||   FatI | |     BcgI |HinfI             CviJI                      FokI ||
   BfaI    | |       MboI ||HpyCH4V | |  MseI  | | TfiI  AciI     BfaI  |CviJI                MboII ||
      |    | |          | ||      | | |     |  | |    |     |        |  |    |                    | ||
    tgctagagaattgggcgttccgatcgtaatgcatgactacttaacggggggattcaccgcaaatactagcttggctcattattgccgagataatggtcta
701 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 800
    acgatctcttaacccgcaaggctagcattacgtactgatgaattgcccccctaagtggcgtttatgatcgaaccgagtaataacggctctattaccagat

a     L  E  N  W  A  F  R  S  *  C  M  T  T  *  R  G  D  S  P  Q  I  L  A  W  L  I  I  A  E  I  M  V  Y  -
b   C  *  R  I  G  R  S  D  R  N  A  *  L  L  N  G  G  I  H  R  K  Y  *  L  G  S  L  L  P  R  *  W  S  T -
c    A  R  E  L  G  V  P  I  V  M  H  D  Y  L  T  G  G  F  T  A  N  T  S  L  A  H  Y  C  R  D  N  G  L   -

                            AciI
                          NlaIII
                            NspI
                            SphI
                         BsrDI |
                         Cac8I |
                      HpyF10VI |
                          NsiI |
                       BstAPI| |
                         MwoI| |
                       BfrBI|| |                                  BciVI
                        FatI|| |                        MboII      NciI                   TaiI
                     HpyCH4V|| |                     NlaIII |     ScrFI                BsaAI |
                HpyCH4V    ||| |                   FatI   | |     BslI|                SnaBI |
           HpyCH4III  |    ||| |               HinfI  |   | |    HpaII|            HpyCH4IV| |
      BstF5I       |  |    ||| |                TfiI  |   | |  StyD4I||          MaeIII   || |
           |       |  |    ||| |                   |  |   | |       |||               |   || |
    cttcttcacatccaccgtgcaatgcatgcggttattgatagacagaagaatcatggtatccacttccgggtattagcaaaagcgttacgtatgtctggtg
801 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 900
    gaagaagtgtaggtggcacgttacgtacgccaataactatctgtcttcttagtaccataggtgaaggcccataatcgttttcgcaatgcatacagaccac

a    F  F  T  S  T  V  Q  C  M  R  L  L  I  D  R  R  I  M  V  S  T  S  G  Y  *  Q  K  R  Y  V  C  L  V   -
b     S  S  H  P  P  C  N  A  C  G  Y  *  *  T  E  E  S  W  Y  P  L  P  G  I  S  K  S  V  T  Y  V  W  W  -
c   L  L  H  I  H  R  A  M  H  A  V  I  D  R  Q  K  N  H  G  I  H  F  R  V  L  A  K  A  L  R  M  S  G  G -
```

Figure 7-E

```
                       HpyCH4III
                           KpnI|
                        NlaIV ||
        BstKTI           RsaI ||
         DpnI|         Csp6I| ||
       BaeI ||       Acc65I|| ||        BaeI    BaeI
       MboI || BaeI    BanI|| ||     Hpy8I |   BsmAI       HphI     CviJI
          | ||    |       ||| ||         | |       |          |         |
         gagatcatattcactctggtaccgtagtaggtaaacttgaaggtgaaagagacataactttgggctttgttgatttactgcgtgatgattttgttgaaca
     901 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 1000
         ctctagtataagtgagaccatggcatcatccatttgaacttccactttctctgtattgaaacccgaaacaactaaatgacgcactactaaaacaacttgt

a        E  I  I  F  T  L  V  P  *  *  V  N  L  K  V  K  E  T  *  L  W  A  L  L  I  Y  C  V  M  I  L  L  N  K-
b         R  S  Y  S  L  W  Y  R  S  R  *  T  *  R  *  K  R  H  N  F  G  L  C  *  F  T  A  *  *  F  C  *  T   -
c          D  H  I  H  S  G  T  V  V  G  K  L  E  G  E  R  D  I  T  L  G  F  V  D  L  L  R  D  D  F  V  E  Q  -

                                                           Hin4I
                                                      Eco57I   |
                                                     Eco57MI   |
                                                    BstNI  |   |
                                                    ScrFI  |   |
                                                  PspGI |  |   |
       BstKTI                                     SexAI |  |   |      Hpy188III
         TaqI    AciI        Hpy188III           StyD4I |  |   |     CviJI   |
        DpnI|   BpuEI           SmlI |          BsaI  | |  |   |BsaJI     |  |            TaiI
      MboI ||   BstUI      Hin4I   | |         BsmAI  | |  |   |  BtgI MnlI  |    HpyCH4IV  |   NdeI Cac8I
         | ||       |          |   | |             |  | |  |   |    |     |  |           |  |      |    |
         agatcgaagtcgcggtatttatttcactcaagattgggtctctttaccaggtgttctacccgtggcttcaggaggtattcacgtttggcatatgcctgct
    1001 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 1100
         tctagcttcagcgccataaataaagtgagttctaacccagagaaatggtccacaagatgggcaccgaagtcctccataagtgcaaaccgtatacggacga

a          I  E  V  A  V  F  I  S  L  K  I  G  S  L  Y  Q  V  F  Y  P  W  L  Q  E  V  F  T  F  G  I  C  L  L  -
b        R  S  K  S  R  Y  L  F  H  S  R  L  G  L  F  T  R  C  S  T  R  G  F  R  R  Y  S  R  L  A  Y  A  C  S-
c         D  R  S  R  G  I  Y  F  T  Q  D  W  V  S  L  P  G  V  L  P  V  A  S  G  G  I  H  V  W  H  M  P  A   -
```

Figure 7-F

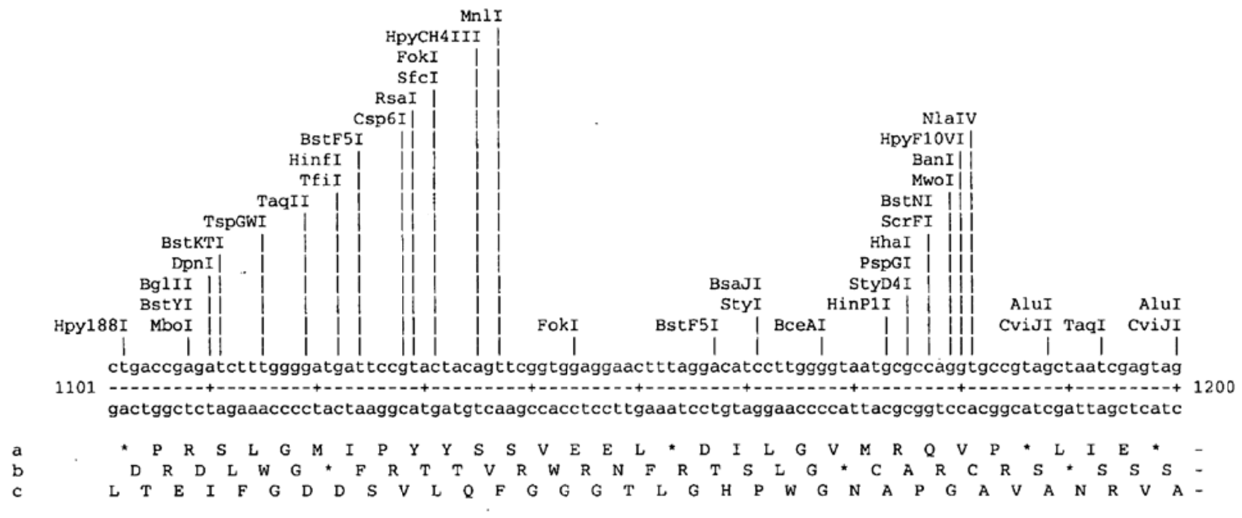

MnlI
HpyCH4III
FokI
SfcI
RsaI
Csp6I
BstF5I
HinfI
TfiI
TaqII
TspGWI
BstKTI
DpnI
BglII
BstYI
Hpy188I
MboI
FokI
BsaJI
StyI
BstF5I
BceAI
NlaIV
HpyF10VI
BanI
MwoI
BstNI
ScrFI
HhaI
PspGI
StyD4I
HinP1I
AluI
CviJI
TaqI
AluI
CviJI
ctgaccgagatctttggggatgattccgtactacagttcggtggaggaactttaggacatccttggggtaatgcgccaggtgccgtagctaatcgagtag
1101
1200
gactggctctagaaacccctactaaggcatgatgtcaagccacctccttgaaatcctgtaggaaccccattacgcggtccacggcatcgattagctcatc
a * P R S L G M I P Y Y S S V E E L * D I L G V M R Q V P * L I E * -
b D R D L W G * F R T T V R W R N F R T S L G * C A R C R S * S S S -
c L T E I F G D D S V L Q F G G G T L G H P W G N A P G A V A N R V A -

Figure 7-G

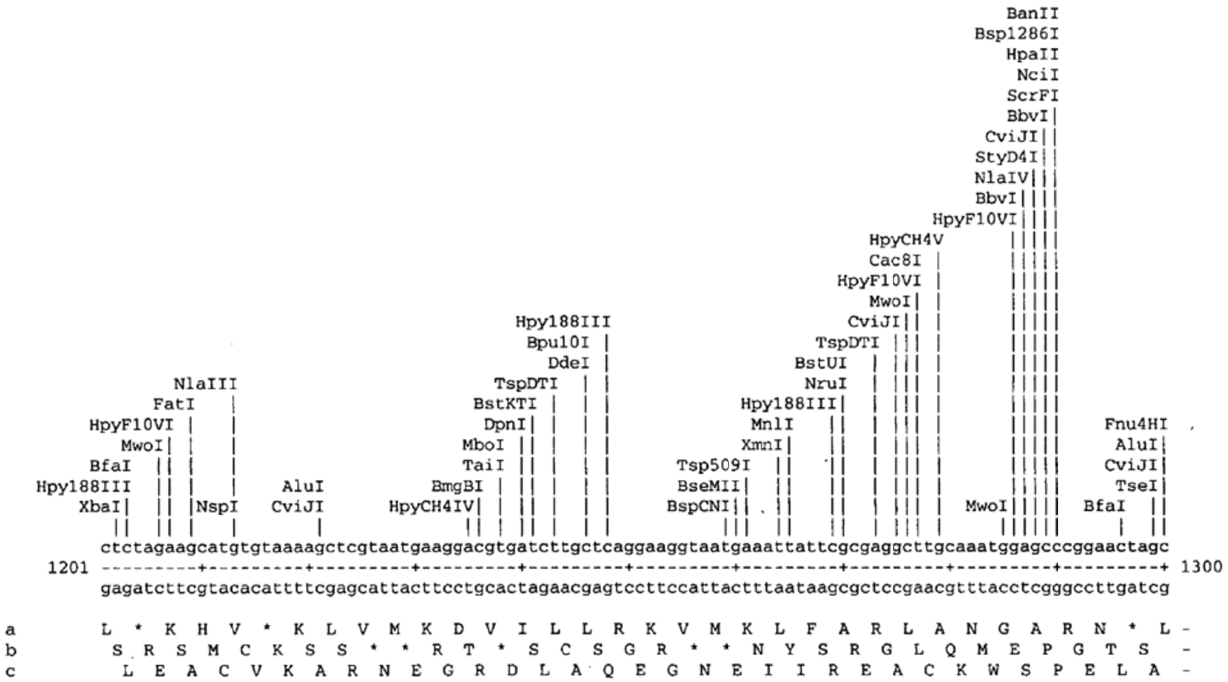

NlaIII
FatI
HpyF10VI
MwoI
BfaI
Hpy188III
XbaI
NspI
AluI
CviJI
Hpy188III
Bpu10I
DdeI
TspDTI
BstKTI
DpnI
MboI
TaiI
BmgBI
HpyCH4IV
Hpy188III
MnlI
XmnI
Tsp509I
BseMII
BspCNI
BstUI
NruI
TspDTI
CviJI
MwoI
HpyF10VI
Cac8I
HpyCH4V
BanII
Bsp1286I
HpaII
NciI
ScrFI
BbvI
CviJI
StyD4I
NlaIV
BbvI
HpyF10VI
MwoI
Fnu4HI
AluI
CviJI
TseI
BfaI
ctctagaagcatgtgtaaaagctcgtaatgaaggacgtgatcttgctcaggaaggtaatgaaattattcgcgaggcttgcaaatggagcccggaactagc
1201 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 1300
gagatcttcgtacacattttcgagcattacttcctgcactagaacgagtccttccattactttaataagcgctccgaacgtttacctcgggccttgatcg
a L * K H V * K L V M K D V I L L R K V M K L F A R L A N G A R N * L -
b S R S M C K S S * * R T * S C S G R * * N Y S R G L Q M E P G T S -
c L E A C V K A R N E G R D L A Q E G N E I I R E A C K W S P E L A -

Figure 7-G

```
                                                              TaiI
                                                             BbvI|
                                                Fnu4HI     BtsI ||
                                 BstKTI       HpyCH4V| HpyCH4IV ||                Hpy8I
         Fnu4HI                   DpnI|Tsp509I      ||    TspRI ||                AccI|
          TseI|                 MboI ||  MseI|   TseI|  Hpy8I | ||         HpyCH4III ||        Tsp509I
             ||                    | ||     ||      ||      | | ||                 | ||             |
            tgctgcttgtgaagtatggaaagagatcgtatttaattttgcagcagtggacgttttggataagtaaaaacagtagacattagcagataaattagcagga
       1301 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 1400
            acgacgaacacttcatacctttctctagcataaattaaaacgtcgtcacctgcaaaacctattcattttgtcatctgtaatcgtctatttaatcgtcct

   a           L  L  V  K  Y  G  K  R  S  Y  L  I  L  Q  Q  W  T  F  W  I  S  K  N  S  R  H  *  Q  I  N  *  Q  E -
   b         C  C  L  *  S  M  E  R  D  R  I  *  F  C  S  S  G  R  F  G  *  V  K  T  V  D  I  S  R  *  I  S  R  K-
   c          A  A  C  E  V  W  K  E  I  V  F  N  F  A  A  V  D  V  L  D  K  *  K  Q  *  T  L  A  D  K  L  A  G  -

                                                                          MseI
                                                                  Tsp509I   |
                                                                  HpyCH4V|  |
                                                            Tsp509I     ||  |    CviJI
                                     Tsp509I            Tsp509I    |    ||  |   HaeIII
                  BpuEI           SmlI     |              MseI|    |    ||  |  Sau96I|                     CviJI
                      |              |     |                 ||    |    ||  |       ||                         |
            aataaagaaggataaggagaaagaactcaagtaattatccttcgttctcttaattgaattgcaattaaactcggcccaatcttttactaaaggattgag
       1401 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 1500
            ttatttcttcctattcctctttcttgagttcattaataggaagcaagagaattaacttaacgttaatttgagccgggttagaaaatgattttcctaactc

   a          I  K  K  D  K  E  K  E  L  K  *  L  S  F  V  L  L  I  E  L  Q  L  N  S  A  Q  S  F  T  K  R  I  E  -
   b           *  R  R  I  R  R  K  N  S  S  N  Y  P  S  F  S  *  L  N  C  N  *  T  R  P  N  L  L  L  K  G  L  S -
   c         N  K  E  G  *  G  E  R  T  Q  V  I  I  L  R  S  L  N  *  I  A  I  K  L  G  P  I  F  Y  *  K  D  *  A-

                                                                                      BfaI
                      HinfI                                                          Hpy188III              MlyI
                       TfiI  HpyCH4V         DdeI            BfaI                        XbaI|              PleI
                          |        |            |               |                           ||                 |
            ccgaatacaacaaagattctattgcatatatttgactaagtatatacttacctagatatacaagatttgaaatacaaaatctagaaactaaatcaaaa
       1501 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 1600
            ggcttatgttgtttctaagataacgtatataaactgattcatatatgaatggatctatatgttctaaactttatgttttagatctttgatttagtttt

   a         P  N  T  T  K  I  L  L  H  I  F  *  L  S  I  Y  L  P  R  Y  T  R  F  E  I  Q  N  L  E  N  *  I  K  I-
   b          R  I  Q  Q  R  F  Y  C  I  Y  F  D  *  V  Y  T  Y  L  D  I  Q  D  L  K  Y  K  I  *  K  T  K  S  K  -
   c           E  Y  N  K  D  S  I  A  Y  I  L  T  K  Y  I  L  T  *  I  Y  K  I  *  N  T  K  S  R  K  L  N  Q  N -
```

Figure 7-H

```
                                                             HincII
                                                              Hpy8I
                                                              AccI|
                                                              TaqI|
                                                             SalI||
                                                            PstI|||
                                                       HpyCH4V ||||
                                                       Cac8I | ||||
                                                        SfcI | ||||
                                                    NlaIII | | ||||
                                                      NspI | | ||||
                                                      SphI | | ||||
                                                   Cac8I | | | ||||
                                                  FatI | | | | ||||
                                               HpyCH4V | | | | ||||
                                               Cac8I | | | | | ||||
                                              AluI | | | | | | ||||
                                             CviJI | | | | | | ||||
                                            AlwI | | | | | | | ||||
                                          TaqI | | | | | | | | ||||
                                     BstKTI  | | | | | | | | | ||||                               RsaI
         HinfI                        DpnI|  | | | | | | | | | ||||                             Csp6I|
      DdeI   |                      MboI ||  | | | | | | | | | |||| HpyCH4III    Hpy188I        TatI||
         |   |                         | ||  | | | | | | | | | ||||         |          |           |||
        tctaagactcaaatctttctattgttgtcttggatcatcgagcttgcatgcctgcagtcgactttcacagtttccattctgaaatgttctctgtactata
   1601 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 1700
        agattctgagtttagaaagataacaacagaacctagtagctcgaacgtacggacgtcagctgaaagtgtcaaaggtaagactttacaagagacatgatat

a         *  D  S  N  L  S  I  V  V  L  D  H  R  A  C  M  P  A  V  D  F  H  S  F  H  S  E  M  F  S  V  L  *  -
b       S  K  T  Q  I  F  L  L  L  S  W  I  I  E  L  A  C  L  Q  S  T  F  T  V  S  I  L  K  C  S  L  Y  Y  N -
c        L  R  L  K  S  F  Y  C  C  L  G  S  S  S  L  H  A  C  S  R  L  S  Q  F  P  F  *  N  V  L  C  T  I    -

                                             Hpy8I            MnlI
                 HinfI                       MboII        EarI  |
                  TfiI             Tsp509I   AccI|      Hpy188I  |      CviJI                     HpyCH4V
                     |                   |      ||            |  |        |                           |
        ataaatagtaagtgaatcaacttactactaaaaaaattagtagacttcctcttcggaatagaaatagcctatttctacatagggaaagtcgtgtgcaatg
   1701 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 1800
        tatttatcattcacttagttgaatgatgatttttttaatcatctgaaggagaagccttatctttatcggataaagatgtatccctttcagcacacgttac

a        *  I  V  S  E  S  T  Y  Y  *  K  N  *  *  T  S  S  S  E  *  K  *  P  I  S  T  *  G  K  S  C  A  M    -
b         K  *  *  V  N  Q  L  T  T  K  K  I  S  R  L  P  L  R  N  R  N  S  L  F  L  H  R  E  S  R  V  Q  *  -
c       I  N  S  K  *  I  N  L  L  L  K  K  L  V  D  F  L  F  G  I  E  I  A  Y  F  Y  I  G  K  V  V  C  N  E -
```

Figure 7-I

```
                                                                                                    MlyI
                                                                                                   PleI|
                                                                                                 MmeI ||
                                                                                                 NciI ||
                                                                                                ScrFI ||
                                                                                                 SmaI ||
                                                                                    NciI       HpaII| ||
                                                                                   ScrFI        NciI| ||
                                                                                  HpaII|       ScrFI| ||
                                                                                StyD4I||       AvaI|| ||
                                                                             BsmFI   |||      BsaJI|| ||
                                                                             BccI|   |||     StyD4I|| ||
               TspDTI                                                        BfaI|   |||       XmaI|| ||
            Cac8I   |                                                       SpeI||   |||    StyD4I||| ||
        HpyCH4V |   |                                 Tsp509I          Hpy188I |||   |||  HinfI  |||| ||
     BsrDI    | |   | MnlI                 MaeIII       FokI|      BstF5I    | |||   ||| TaqI |  |||| ||
         |    | |   |    |                      |          ||           |    | |||   |||    | |  |||| ||
        aaaaatgcaagcacgatttggggagaggttttttctctattgtaacaaggaataattatctactccatccgactagttccgggttcgagtcccgggcaac
   1801 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 1900
        tttttacgttcgtgctaaacccctctccaaaaaagagataacattgttccttattaatagatgaggtaggctgatcaaggcccaagctcagggcccgttg

a       K  N  A  S  T  I  W  G  E  V  F  S  L  L  *  Q  G  I  I  I  Y  S  I  R  L  V  P  G  S  S  P  G  Q  P -
b        K  M  Q  A  R  F  G  E  R  F  F  L  Y  C  N  K  E  *  L  S  T  P  S  D  *  F  R  V  R  V  P  G  N   -
c         K  C  K  H  D  L  G  R  G  F  F  S  I  V  T  R  N  N  Y  L  L  H  P  T  S  S  G  F  E  S  R  A  T  -

                     BspCNI
                    BseMII|  Hpy188I                            ApoI             ApoI
       NdeI     BfaI     ||    DdeI|      TspDTI             Tsp509I          Tsp509I
          |        |     ||       ||           |                   |                |
        ccatatggaaactagaaaggagcaatctgagttttgatttttcactcacttcatttacaaaattttttggtttggtaaattttgttgtatggatatacaa
   1901 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 2000
        ggtatacctttgatctttcctcgttagactcaaaactaaaaagtgagtgaagtaaatgttttaaaaaaccaaaccatttaaaacaacatacctatatgtt

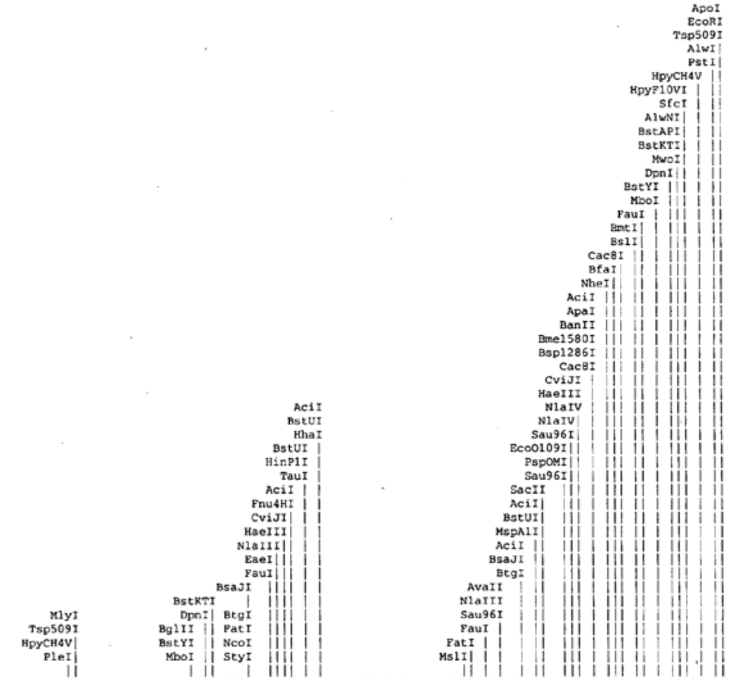
a         I  W  K  L  E  R  S  N  L  S  F  D  F  S  L  T  S  F  T  K  F  F  G  L  V  N  F  V  V  W  I  Y  N  -
b       P  Y  G  N  *  K  G  A  I  *  V  L  I  F  H  S  L  H  L  Q  N  F  L  V  W  *  I  L  L  Y  G  Y  T  T -
c        H  M  E  T  R  K  E  Q  S  E  F  *  F  F  T  H  F  I  Y  K  I  F  W  F  G  K  F  C  C  M  D  I  Q   -
```

Figure 7-J

```
                                                                                                TaiI
                                                                                             BsaAI |
                                                                                           AflIII| |
                   CviJI                                                                 HpyCH4IV| |
                Cac8I  | HincII                         MseI                            MseI    || |
  HpyCH4III   CviJI  | |  Hpy8I                   HpyCH4III |      CviJI            BfaI   |    || |    HinfI
            |      | | |      |                           | |          |               |   |    || |        |
           ctgtcggggctggcttggttgacattggtatatagtctatattatactgttaaataacaagccttctattatctttctagttaatacgtgtgcttgggag
      2001 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 2100
           gacagccccgaccgaaccaactgtaaccatatatcagatataatatgacaatttattgttcggaagataatagaaagatcaattatgcacacgaaccctc

a           C  R  G  W  L  G  *  H  W  Y  I  V  Y  I  I  L  L  N  N  K  P  S  I  I  F  L  V  N  T  C  A  W  E   -
b            V  G  A  G  L  V  D  I  G  I  *  S  I  L  Y  C  *  I  T  S  L  L  L  S  F  *  L  I  R  V  L  G  S -
c          L  S  G  L  A  W  L  T  L  V  Y  S  L  Y  Y  T  V  K  *  Q  A  F  Y  Y  L  S  S  *  Y  V  C  L  G  V-
```

Figure 7-K



```
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2101 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 2200
     aggaacgttaaacttatttggttctagaatggtaccggcgcgccccaagagtagtagtagtagtaccaggcgcccccgggcgatcgtcctagacgtctta

a     S  L  Q  F  E  *  T  K  I  L  P  W  P  R  G  V  L  I  I  I  I  M  V  R  G  G  P  L  A  G  S  A  E  F -
b      P  C  N  L  N  K  P  R  S  Y  H  G  R  A  G  F  S  S  S  S  S  W  S  A  G  A  R  *  Q  D  L  Q  N  -
c       L  A  I  *  I  N  Q  D  L  T  M  A  A  R  G  S  H  H  H  H  H  G  P  R  G  P  A  S  R  I  C  R  I -
```

Figure 7-L

```
                     AlwI
                   NlaIII
                BsaJI   |
                 BtgI   |
                 FatI   |
                 NcoI   |
                 StyI   |
              BstKTI|   |
               DpnI||   |                                      BstNI                                    BstNI
              NlaIV||   |                                      ScrFI                                    ScrFI
            BamHI |||   |                                     PfoI |                                  CviJI |
            BstYI |||   |        RsaI                MseI    PspGI |                                  PspGI |
        CviJI   | |||   |      Csp6I|HpyCH4III     AluI |   StyD4I |           BfaI                  StyD4I |
        AlwI|MboI |||   | HpyCH4III||  MnlI  |    CviJI |   BseRI| |       NlaIV  |                  BfaI | |
           ||   | |||   |         |||     |  |        | |       || |           |  |                    |  | |
         tcggcttGGATCCATGgcagacaacggtactattaccgttgaggagcttaaacaactcctggaacaatggaacctagtaataggtttcctattcctagcc
    2201 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 2300
         agccgaaCCTAGGTACcgtctgttgccatgataatggcaactcctcgaatttgttgaggaccttgttaccttggatcattatccaaaggataaggatcgg

a          G  L  D  P  W  Q  T  T  V  L  L  P  L  R  S  L  N  N  S  W  N  N  G  T  *  *  *  V  S  Y  S  *  P  -
b        S  A  W  I  H  G  R  Q  R  Y  Y  Y  R  *  G  A  *  T  T  P  G  T  M  E  P  S  N  R  F  P  I  P  S  L -
c         R  L  G  S  M  A  D  N  G  T  I  T  V  E  E  L  K  Q  L  L  E  Q  W  N  L  V  I  G  F  L  F  L  A   -

                                                                                          MaeIII
                                                                                          BsrI |
                                                                                        CviJI| |
                                                                                       HaeIII| |
                                                                                         MscI| |
                                                                                       EaeI || |
                                                      RsaI                         HpyF10VI || |
                                                    Csp6I|       AluI                 MwoI| || |
                                                   BsrGI||      CviJI               MnlI || || |
           MaeIII Tsp509I            Hpy188I        TatI||  HindIII |          CviJI   | || || |
                |       |                  |           |||        | |              |   | || || |
         tggattatgttactacaatttgcctattctaatcggaacaggtttttgtacataataaagcttgttttcctctggctcttgtggccagtaacacttgctt
    2301 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 2400
         acctaatacaatgatgttaaacggataagattagccttgtccaaaaacatgtattatttcgaacaaaaggagaccgagaacaccggtcattgtgaacgaa

a         G  L  C  Y  Y  N  L  P  I  L  I  G  T  G  F  C  T  *  *  S  L  F  S  S  G  S  C  G  Q  *  H  L  L   -
b          D  Y  V  T  T  I  C  L  F  *  S  E  Q  V  F  V  H  N  K  A  C  F  P  L  A  L  V  A  S  N  T  C  L  -
c        W  I  M  L  L  Q  F  A  Y  S  N  R  N  R  F  L  Y  I  I  K  L  V  F  L  W  L  L  W  P  V  T  L  A  C -
```

Figure 7-M

```
                               Tsp509I
                                 AseI|                                                         Eco57I
                                 MseI|                                                        Eco57MI
                           Tsp509I  ||                                                          AluI|
                           TaqII |  ||                                                         CviJI|
                        Hpy8I  | |  ||   FauI       HphI                                    BlpI   ||
                         SfcI  | |  ||MaeIII|    BsrI  |            BsrDI                   DdeI   ||
              Cac8I     AccI|  | |  ||Tsp45I|   AciI|  |   HpyCH4V CviJI|       CviJI     CviJI|   ||
                  |        ||  | |  ||     ||      ||  |         |     ||           |         ||   ||
         gttttgtgcttgctgttgtctacagaattaattgggtgactggcgggattgcgattgcaatggcttgtattgtaggcttgatgtggcttagctacttcgt
    2401 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 2500
         caaaacacgaacgacaacagatgtcttaattaacccactgaccgccctaacgctaacgttaccgaacataacatccgaactacaccgaatcgatgaagca

a        V  L  C  L  L  L  S  T  E  L  I  G  *  L  A  G  L  R  L  Q  W  L  V  L  *  A  *  C  G  L  A  T  S  L -
b         F  C  A  C  C  C  L  Q  N  *  L  G  D  W  R  D  C  D  C  N  G  L  Y  C  R  L  D  V  A  *  L  L  R   -
c          F  V  L  A  V  V  Y  R  I  N  W  V  T  G  G  I  A  I  A  M  A  C  I  V  G  L  M  W  L  S  Y  F  V  -

                                                                                        BslI
                                                                                        NciI     MaeIII
                                  BsrBI                                                ScrFI     Tsp45I
                                 AciI |                                               BsaJI|   MfeI   |
                              RsaI  | |                                               HpaII|Tsp509I   |
                 CviJI      Csp6I|  | | FauI                MboII                   StyD4I||MnlI  |   | BsmFI
                     |          ||  | |    |                    |                        |||   |  |   |     |
         tgcttccttcaggctgtttgctcgtacccgctcaatgtggtcattcaacccagaaacaaacattcttctcaatgtgcctctccgggggacaattgtgacc
    2501 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 2600
         acgaaggaagtccgacaaacgagcatgggcgagttacaccagtaagttgggtctttgtttgtaagaagagttacacggagaggccccctgttaacactgg
                  <-- ML523
a          L  P  S  G  C  L  L  V  P  A  Q  C  G  H  S  T  Q  K  Q  T  F  F  S  M  C  L  S  G  G  Q  L  *  P  -
b        C  F  L  Q  A  V  C  S  Y  P  L  N  V  V  I  Q  P  R  N  K  H  S  S  Q  C  A  S  P  G  D  N  C  D  Q -
c         A  S  F  R  L  F  A  R  T  R  S  M  W  S  F  N  P  E  T  N  I  L  L  N  V  P  L  R  G  T  I  V  T   -
```

Figure 7-N

```
                                                                                       MaeIII
                                                                                       Tsp45I
                                                                                       HaeII|
                                                                                       HhaI||
              NlaIII                                                               HinP1I |||      AvaII
            FatI   |                       BstKTI                   HpaII       BfaI    | |||   EcoO109I
         BsrBI |   |                        DpnI|                  CviJI|     AvrII|    | |||      PpuMI
          XcmI |   |                       BclI||  MaeIII         HaeIII|     BsaJI|    | |||     Sau96I
        AciI | |   |  Hpy8I                MboI||  Tsp45I          EaeI||      StyI|    | |||    MseI  |
           | | |   |      |                   |||       |             |||         ||    | |||       |  |
        agaccgctcatggaaagtgaacttgtcattggtgctgtgatcattcgtggtcacttgcgaatggccggacactccctagggcgctgtgacattaaggacc
   2601 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 2700
        tctggcgagtacctttcacttgaacagtaaccacgacactagtaagcaccagtgaacgcttaccggcctgtgagggatcccgcgacactgtaattcctgg

a        D  R  S  W  K  V  N  L  S  L  V  L  *  S  F  V  V  T  C  E  W  P  D  T  P  *  G  A  V  T  L  R  T    -
b         T  A  H  G  K  *  T  C  H  W  C  C  D  H  S  W  S  L  A  N  G  R  T  L  P  R  A  L  *  H  *  G  P  -
c       R  P  L  M  E  S  E  L  V  I  G  A  V  I  I  R  G  H  L  R  M  A  G  H  S  L  G  R  C  D  I  K  D  L-

                           Hpy188III
                        CviJI      |
                       TspRI|      |
                HpyCH4III  ||      |                                               TspRI
               BstKTI   |  ||      |                                             HinfI |
                DpnI|   |  ||      |                             Fnu4HI           TfiI |      HpyCH4V
              MboI ||   |  ||      |             Tsp509I        Hpy99I|          BbvI| |     Fnu4HI |
          BspMI  | ||   |  ||      |   XmnI       HgaI |          TseI|       BbvI  || |      TseI| |
              |  | ||   |  ||      |      |          | |             ||          |  || |         || |
        tgccaaaagagatcactgtggctacatcacgaacgctttcttattacaaattaggagcgtcgcagcgtgtaggcactgattcaggttttgctgcatacaa
   2701 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 2800
        acggttttctctagtgacaccgatgtagtgcttgcgaaagaataatgtttaatcctcgcagcgtcgcacatccgtgactaagtccaaaacgacgtatgtt

a       C  Q  K  R  S  L  W  L  H  H  E  R  F  L  I  T  N  *  E  R  R  S  V  *  A  L  I  Q  V  L  L  H  T  T -
b        A  K  R  D  H  C  G  Y  I  T  N  A  F  L  L  Q  I  R  S  V  A  A  C  R  H  *  F  R  F  C  C  I  Q   -
c         P  K  E  I  T  V  A  T  S  R  T  L  S  Y  Y  K  L  G  A  S  Q  R  V  G  T  D  S  G  F  A  A  Y  N  -
```

Figure 7-O

```
                                                                                ApoI
                                                                               EcoRI
                                                                             Tsp509I
                                                                          BcgI     |
                                                                     HpyCH4III     |         BceAI
                                                                       RsaI   |    |      ApoI    |
                                        HpaII                        Csp6I |  |    |     EcoRI    |
   HpyCH4III             MseI           BcgI |                       TatI ||  |    |   Tsp509I    |
 AciI       |      Tsp509I   |         BsrFI |           SspI     BfaI   |||  |    |   CviJI  |   |
     |      |             |  |              ||                |        | |||  |    |        | |   |
     ccgctaccgtattggaaactataaattaaatacagaccacgccggtagcaacgacaatattgctttgctagtacagtaaGAATTCaagccgaattccagc
2801 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 2900
     ggcgatggcataacctttgatatttaatttatgtctggtgcggccatcgttgctgttataacgaaacgatcatgtcattCTTAAGttcggcttaaggtcg

a       A  T  V  L  E  T  I  N  *  I  Q  T  T  P  V  A  T  T  I  L  L  C  *  Y  S  K  N  S  S  R  I  P  A  -
b     P  L  P  Y  W  K  L  *  I  K  Y  R  P  R  R  *  Q  R  Q  Y  C  F  A  S  T  V  R  I  Q  A  E  F  Q  H -
c      R  Y  R  I  G  N  Y  K  L  N  T  D  H  A  G  S  N  D  N  I  A  L  L  V  Q  *  E  F  K  P  N  S  S  -

                                          MseI
                                          PacI
                                  Tsp509I    |
                                      AseI|  |
                                      MseI|  |
                  AlwI          Tsp509I  ||  |
                  BfaI           BanII|  ||  |
                 SpeI|        BsiHKAI |  ||  |
              Hin4I ||       Bsp1286I |  ||  |
           MaeIII | ||           SacI |  ||  |
           BsiEI| | ||         AluI | |  ||  |
          CviJI|| | ||         AlwI | |  ||  |
         HaeIII|| | ||        CviJI | |  ||  |
           TauI|| | ||      EcoICRI | |  ||  |
         BsrI ||| | ||   Hpy188I  | | |  ||  |
         EaeI ||| | ||  BstKTI |  | | |  ||  |
         EagI ||| | ||   DpnI| |  | | |  ||  |
       Fnu4HI ||| | ||  NlaIV| |  | | |  ||  |                                          BfaI
        TspRI ||| | ||BamHI || |  | | |  ||  |                                          AluI|
        AciI| ||| | ||BstYI || |  | | |  ||  |CviJI                                    CviJI|
   BstXI   || ||| | || MboI || |  | | |  ||  |Hin4I             Tsp509I                MboII|
       |   |||||| | ||    | || |  | | |  ||  |    |                    |                   ||
     acactggcggccgttactagtggatccgagctctaattaattaaggcttttctgctaacatatagcaatttttgaagaaaggaaagctagaaatacccaa
2901 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 3000
     tgtgaccgccggcaatgatcacctaggctcgagattaattaattccgaaaagacgattgtatatcgttaaaaacttctttcctttcgatctttatgggtt

a      H  W  R  P  L  L  V  D  P  S  S  N  *  L  R  L  F  C  *  H  I  A  I  F  E  E  R  K  A  R  N  T  Q  -
b       T  G  G  R  Y  *  W  I  R  A  L  I  N  *  G  F  S  A  N  I  *  Q  F  L  K  K  G  K  L  E  I  P  N -
c     T  L  A  A  V  T  S  G  S  E  L  *  L  I  K  A  F  L  L  T  Y  S  N  F  *  R  K  E  S  *  K  Y  P  I -
```

Figure 7-P

```
                                                                            Hin4I
                                                                    ApoI   HincII
                                                                   EcoRI     HpaI                     HpyCH4V
                                 Eco57I             HinfI        Tsp509I    Hpy8I                     BciVI|
                                Eco57MI              TfiI       Hpy188I|    MseI| Hpy99I         TspDTI   ||
                                      |                 |             ||       ||      |              |   ||
          tatcttgctgaagcaagatattgggtatttctttttttttttattttgaatctttctattctgaattcagttaacgacgagatttagtatcctttcttgca
     3001 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 3100
          atagaacgacttcgttctataacccataaagaaaaaaaaaataaaacttagaaagataagacttaagtcaattgctgctctaaatcataggaaagaacgt

a         Y  L  A  E  A  R  Y  W  V  F  L  F  F  L  F  *  I  F  L  F  *  I  Q  L  T  T  R  F  S  I  L  S  C  T -
b          I  L  L  K  Q  D  I  G  Y  F  F  F  F  Y  F  E  S  F  Y  S  E  F  S  *  R  R  D  L  V  S  F  L  A   -
c           S  C  *  S  K  I  L  G  I  S  F  F  F  I  L  N  L  S  I  L  N  S  V  N  D  E  I  *  Y  P  F  L  H  -

                                       ApoI
                                      EcoRI
                                    Tsp509I
             Hpy188III              RsaI  |                     BslI
        Hin4I  BssSI |            Csp6I|  |  Tsp509I         EcoNI |
            |      | |                ||  |        |             | |
          ctttcataactcgtgaaatgccgagttggtacgaattcccccaatttgcgacctaccataggatttgttatgtaaataggtatatgttcctttccattat
     3101 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 3200
          gaaagtattgagcactttacggctcaaccatgcttaagggggttaaacgctggatggtatcctaaacaatacatttatccatatacaaggaaaggtaata

a           F  I  T  R  E  M  P  S  W  Y  E  F  P  Q  F  A  T  Y  H  R  I  C  Y  V  N  R  Y  M  F  L  S  I  M  -
b         L  S  *  L  V  K  C  R  V  G  T  N  S  P  N  L  R  P  T  I  G  F  V  M  *  I  G  I  C  S  F  P  L  * -
c          F  H  N  S  *  N  A  E  L  V  R  I  P  P  I  C  D  L  P  *  D  L  L  C  K  *  V  Y  V  P  F  H  Y   -
```

Figure 7-Q

```
                                                               TaiI
                                                           MaeIII |
                                                       HpyCH4IV|  |
                                                          NlaIV  || |
                                                         AvaII|  || |
                                                        Sau96I|  || |
                                                          NciI || || |
                                                         ScrFI || || |
                                                          SmaI || || |
                                                         HpaII| || || |
                                                          NciI| || || |
                                                         ScrFI| || || |
                             BsrDI                        AvaI|| || || |
                           FauI |                        BsaJI|| || || |
            BstUI      CviJI  | |                       StyD4I|| || || |
             NruI     HaeIII  | |                         XmaI|| || || |
       Hpy188III|       MscI  | |                       StyD4I||| || || |                             AluI
       HinfI   ||      EaeI | | |      SfaNI    BsmI    |||| || || | BseRI                          CviJI
        TfiI   ||  TspDTI|  | | | AciI    |    BfaI|    |||| || || |BsmFI |TspDTI            MnlI    |
           |   ||       ||  | | |   |     |      ||    |||| || || |    |  |    |              |     |
       gaatcgcgattgtatggccaaccattgcgggtagaatgctagatgcccgggaccacgttactattgtttctttctcctccttcatattgagcttttctat
  3201 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 3300
       cttagcgctaacataccggttggtaacgcccatcttacgatctacgggccctggtgcaatgataacaaagaaagaggaggaagtataactcgaaaagata

a       N  R  D  C  M  A  N  H  C  G  *  N  A  R  C  P  G  P  R  Y  Y  C  F  F  L  L  L  H  I  E  L  F  Y  -
b      · I  A  I  V  W  P  T  I  A  G  R  M  L  D  A  R  D  H  V  T  I  V  S  F  S  S  F  I  L  S  F  S  I  -
c      E  S  R  L  Y  G  Q  P  L  R  V  E  C  *  M  P  G  T  T  L  L  L  F  L  S  P  P  S  Y  *  A  F  L  F -

                                      BsiEI
                                     BstKTI
                                      Hin4I
                                       PvuI
                      KpnI             TaqI
                    NlaIV |            DpnI|
                      RsaI |           FauI||
                    Csp6I| |          MboI|||                                 TaiI                      BpmI
              BccI  Acc65I|| |      MnlI  ||||                              BmgBI |                  Eco57MI
        Hin4I  |     BanI|| |   AciI  |   ||||        MnlI      CviJI     HpyCH4IV| |              CviJI    |
            |  |        ||| |     |   |   ||||          |         |              || |                  |    |
       ttttgccaataaatgatggtacctccccccgccacgatcgaacgggaatggataagaggcttgtgggattgacgtgatagggtagggttggctatactgc
  3301 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 3400
       aaaacggttatttactaccatggaggggggcggtgctagcttgcccttacctattctccgaacaccctaactgcactatcccatcccaaccgatatgacg

a      F  C  Q  *  M  M  V  P  P  P  A  T  I  E  R  E  W  I  R  G  L  W  D  *  R  D  R  V  G  L  A  I  L  L -
b       F  A  N  K  *  W  Y  L  P  P  P  R  S  N  G  N  G  *  E  A  C  G  I  D  V  I  G  *  G  W  L  Y  C  -
c        L  P  I  N  D  G  T  S  P  R  H  D  R  T  G  M  D  K  R  L  V  G  L  T  *  *  G  R  V  G  Y  T  A  -
```

Figure 7-R

```
                                                     BstKTI
                                                      DpnI|               HpyF10VI
                                                     NlaIV|            AciI      |
                                                   BamHI ||      HpyF10VI |      |
                 CviJI            HaeII            BstYI ||         MwoI| |      |
              BstNI  |            HhaI|       Eco57I   | || Hpy188III  || |      |        HinfI
              ScrFI  |           AfeI||      Eco57MI   | ||   BssSI |  || |      |       TaqI |
            PspGI |  |        HinP1I|||        AlwI|   | ||  CviJI| |  || |      |   MlyI   | |
           StyD4I |  |   Hpy188I   ||||   MnlI   ||MboI || AlwI || |  || |  MwoI|   PleI   | |  MnlI
                | |  |         |   ||||       |   ||   | ||    | || |  || |     ||      |   | |     |
     tggtggcgaactccaggctaataatctgaagcgcttggaagttgtagggaggatcctatggctcgtgaagcggttatcgccgaagtatcgactcaactat
3401 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 3500
     accaccgcttgaggtccgattattagacttcgcgaaccttcaacatccctcctaggataccgagcacttcgccaatagcggcttcatagctgagttgata

a      V  A  N  S  R  L  I  I  *  S  A  W  K  L  *  G  G  S  Y  G  S  *  S  G  Y  R  R  S  I  D  S  T  I  -
b    W  W  R  T  P  G  *  *  S  E  A  L  G  S  C  R  E  D  P  M  A  R  E  A  V  I  A  E  V  S  T  Q  L  S -
c     G  G  E  L  Q  A  N  N  L  K  R  L  E  V  V  G  R  I  L  W  L  V  K  R  L  S  P  K  Y  R  L  N  Y   -

                                                     RsaI
                                                   Csp6I|
                                                CviJI  ||
                                               HaeIII  ||
                                              Cac8I |  ||
                                           TaiI   | |  ||
                                        Hpy99I|   | |  ||
                                    HpyCH4IV ||   | |  ||                         CviJI
                                   BccI    | ||   | |  ||                        HaeIII
                                 BceAI|    | ||   | |  ||                          TauI
                                TaqI ||    | ||   | |  ||             BccI     BstF5I |
                          Hpy188III| ||    | ||   | |  ||           AciI |     Fnu4HI |
                          HaeII   || ||    | ||   | |  ||        NlaIV | |      AciI| |        DraIII
                          HhaI|   || ||    | ||   | |  ||       CviJI| | |   BceAI || |     HpyCH4III
   HgaI               HinP1I ||   || ||    | ||   | |  ||    RsaI   || | |   BtsI| || |  CviJI      |
Hpy188I      BsaHI  TaqI   | ||   || ||    | ||EaeI |  ||  Csp6I|   || | |  TspRI| || | FokI |      |
      |         |     |   | ||   || ||    | ||   | |  ||      ||   || | |      || || |    | |      |
     cagaggtagttggcgtcatcgagcgccatctcgaaccgacgttgctggccgtacatttgtacggctccgcagtggatggcggcctgaagccacacagtga
3501 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 3600
     gtctccatcaaccgcagtagctcgcggtagagcttggctgcaacgaccggcatgtaaacatgccgaggcgtcacctaccgccggacttcggtgtgtcact

a     R  G  S  W  R  H  R  A  P  S  R  T  D  V  A  G  R  T  F  V  R  L  R  S  G  W  R  P  E  A  T  Q  *   -
b      E  V  V  G  V  I  E  R  H  L  E  P  T  L  L  A  V  H  L  Y  G  S  A  V  D  G  G  L  K  P  H  S  D  -
c    Q  R  *  L  A  S  S  S  A  I  S  N  R  R  C  W  P  Y  I  C  T  A  P  Q  W  M  A  A  *  S  H  T  V  I -
```

Figure 7-S

```
                                                         AluI
                                                       CviJI|
                                                      Cac8I |
                        HpyCH4III                    TspDTI |                                BstNI
                     BstEII     |                    TauI | |                                ScrFI
                  HpyCH4III     |                Fnu4HI | | | BstKTI                       BsaJI |
       Eco57I        MaeIII     |                 AciI| | | |  DpnI|                       PspGI |
      Eco57MI        Tsp45I     | CviJI          BstUI| | | |BclI ||                      StyD4I |
    TspRI   |  MaeIII     |     |  HphI      Hin4I   || | | |MboI ||         Hin4I    CviJI    | |
        |   |       |     |     |     |          |   || | | |   | ||             |        |    | |
        tattgatttgctggttacggtgaccgtaaggcttgatgaaacaacgcggcgagctttgatcaacgaccttttggaaacttcggcttcccctggagagagc
   3601 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 3700
        ataactaaacgaccaatgccactggcattccgaactactttgttgcgccgctcgaaactagttgctggaaaacctttgaagccgaaggggacctctctcg

a       Y  *  F  A  G  Y  G  D  R  K  A  *  *  N  N  A  A  S  F  D  Q  R  P  F  G  N  F  G  F  P  W  R  E  R -
b        I  D  L  L  V  T  V  T  V  R  L  D  E  T  T  R  R  A  L  I  N  D  L  L  E  T  S  A  S  P  G  E  S   -
c         L  I  C  W  L  R  *  P  *  G  L  M  K  Q  R  G  E  L  *  S  T  T  F  W  K  L  R  L  P  L  E  R  A  -

                                                                                   Tsp509I
                                            Hpy99I                                HpyCH4V|
                   HphI                    TspGWI |                            HpyF10VI ||
                  SfcI|               Bme1580I  | |                          BstUI    | ||
                 HhaI||                BsiHKAI  | |                           HhaI    | ||
               BpmI |||               Bsp1286I  | |                       HinP1I |    | ||
              BstUI |||                Hpy8I |  | |                    BlpI    | |    | ||
            Eco57MI |||              HpyCH4V |  | |                    DdeI    | |    | ||           HinP1I
      HinfI  HinP1I |||MaeIII        ApaLI | |  | |    BsaJI           AluI|   | |    | ||         Fnu4HI |
       TfiI  AciI | |||Tsp45I       MslI | | |  | |     BtgI          CviJI|   | |MwoI| ||          TseI| |
          |     | | |||     |         |  | | |  | |        |              ||   | |   || ||             || |
        gagattctccgcgctgtagaagtcaccattgttgtgcacgacgacatcattccgtggcgttatccagctaagcgcgaactgcaatttggagaatggcagc
   3701 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 3800
        ctctaagaggcgcgacatcttcagtggtaacaacacgtgctgctgtagtaaggcaccgcaataggtcgattcgcgcttgacgttaaacctcttaccgtcg

a         D  S  P  R  C  R  S  H  H  C  C  A  R  R  H  H  S  V  A  L  S  S  *  A  R  T  A  I  W  R  M  A  A  -
b       E  I  L  R  A  V  E  V  T  I  V  V  H  D  D  I  I  P  W  R  Y  P  A  K  R  E  L  Q  F  G  E  W  Q  R -
c        R  F  S  A  L  *  K  S  P  L  L  C  T  T  T  S  F  R  G  V  I  Q  L  S  A  N  C  N  L  E  N  G  S   -
```

Figure 7-T

```
                                             BsiEI
                                            BstKTI
              BbvI                    CviJI   PvuI         CviJI
             BsrDI                  Cac8I |   TaqI    BstKTI   |
           BspMI |HpyCH4V         CviJI | |  DpnI|     DpnI|   |                                BsaJI   AvaII
       HhaI    | | MboII|      TaqI   | | |MboI ||   MboI ||   |                                 StyI  Sau96I
          |    | |     ||         |   | | |   | ||      | ||   |                                    |       |
          gcaatgacattcttgcaggtatcttcgagccagccacgatcgacattgatctggctatcttgctgacaaaagcaagagaacatagcgttgccttggtagg
     3801 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 3900
          cgttactgtaagaacgtccatagaagctcggtcggtgctagctgtaactagaccgatagaacgactgttttcgttctcttgtatcgcaacggaaccatcc

a          Q  *  H  S  C  R  Y  L  R  A  S  H  D  R  H  *  S  G  Y  L  A  D  K  S  K  R  T  *  R  C  L  G  R   -
b           N  D  I  L  A  G  I  F  E  P  A  T  I  D  I  D  L  A  I  L  L  T  K  A  R  E  H  S  V  A  L  V  G  -
c         A  M  T  F  L  Q  V  S  S  S  Q  P  R  S  T  L  I  W  L  S  C  *  Q  K  Q  E  N  I  A  L  P  W  *  V-

                                 Hpy188III
                                   NlaIV |
              AciI             HpaII   | |
              TauI            BsaWI|   | |     BstKTI
          Fnu4HI |           BstKTI|   | |       MnlI        HaeII
           AciI| |            DpnI||   | |      DpnI|        HhaI|                            TauI       Cac8I
         MspA1I| |           EciI|||   | |   BstYI ||    HinP1I ||                          AciI |      BsrI |
          MnlI|| |     AlwI MboI||||   | |    MboI || AlwI    | ||        MseI TspDTI     Fnu4HI |     CviJI |
             ||| |        |    |||||   | ||      | ||    |    | ||           |      |          | |         | |
          tccagcggcggaggaactctttgatccggttcctgaacaggatctatttgaggcgctaaatgaaaccttaacgctatggaactcgccgcccgactgggct
     3901 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 4000
          aggtcgccgcctccttgagaaactaggccaaggacttgtcctagataaactccgcgatttactttggaattgcgataccttgagcggcgggctgacccga

a         S  S  G  G  G  T  L  *  S  G  S  *  T  G  S  I  *  G  A  K  *  N  L  N  A  M  E  L  A  A  R  L  G  W-
b          P  A  A  E  E  L  F  D  P  V  P  E  Q  D  L  F  E  A  L  N  E  T  L  T  L  W  N  S  P  P  D  W  A   -
c           Q  R  R  R  N  S  L  I  R  F  L  N  R  I  Y  L  R  R  *  M  K  P  *  R  Y  G  T  R  R  P  T  G  L  -
```

Figure 7-U

```
                                                        HpaII
                                                       BsrFI|
                                                  MaeIII    ||
                                                  HhaI |    ||
                                              HinP1I | |    ||                                  BsrI
                                               RsaI  | | |  ||          BbvI              HpyF10VI |
                                            Csp6I|   | | |  ||          HhaI       Fnu4HI    BglI| |
                         TaiI              FauI ||   | | |  ||         BstUI |       TseI|    MwoI| |
    BmrI       BsmFI  HpyCH4IV | AciI BslI | ||   | | |  ||        HinP1I |     BstF5I|| FokI  || | BmrI
       |           |         | |     |    | | ||   | | |  ||             | |          |||    |  || |    |
     ggcgatgagcgaaatgtagtgcttacgttgtcccgcatttggtacagcgcagtaaccggcaaaatcgcgccgaaggatgtcgctgccgactgggcaatgg
4001 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 4100
     ccgctactcgctttacatcacgaatgcaacagggcgtaaaccatgtcgcgtcattggccgttttagcgcggcttcctacagcgacggctgacccgttacc

a     R  *  A  K  C  S  A  Y  V  V  P  H  L  V  Q  R  S  N  R  Q  N  R  A  E  G  C  R  C  R  L  G  N  G  -
b    G  D  E  R  N  V  V  L  T  L  S  R  I  W  Y  S  A  V  T  G  K  I  A  P  K  D  V  A  A  D  W  A  M  E -
c     A  M  S  E  M  *  C  L  R  C  P  A  F  G  T  A  Q  *  P  A  K  S  R  R  R  M  S  L  P  T  G  Q  W  -

                                                                                               BstKTI
                                                                                                 DpnI|
                                                                                               MboI ||
                                                                                               MnlI ||
                                                                                             HhaI | ||
                                                                                          BstUI | | ||
                                                                                          Cac8I | | ||
                                                                                            HhaI| | ||
                                                                                         HinP1I | | ||
                                                                                       HpyF10VI | | ||
                                                                                           MwoI|| | ||
                                                                                         BssHII|| | ||
                                                                                          BstUI|| | ||
                                                                                         HinP1I|| | ||
         BsrI                                                                        CviJI   ||| | | ||
       CviJI |                                                                       HaeIII  ||| | | ||
      HaeIII |                                                                       MboII   ||| | | ||
      Sau96I| |                                                                       MmeI | ||| | | ||
      Cac8I|| |                                                                     MboII| | ||| | | ||
       NaeI|| |                                                                   BstKTI || | ||| | | ||
     HpaII||| |                                                                     DpnI|| | ||| | | ||
     BmrI|||| |                                                                   MboI ||| | ||| | | ||
    BsrFI|||| |                                               CviJI               |||| | ||| | | ||
   NgoMIV|||| |                                          HpyF10VI |               |||| | ||| | | ||
  Cac8I |||||  |                                            BfaI | |               |||| | ||| | | ||
  HaeII| |||||  |                                           AluI|  | |             |||| | ||| | | ||
  HhaI|| |||||  |                                          CviJI| MwoI| |          |||| | ||| | | ||
HinP1I ||| |||||  |                                            || || |             | || || | ||| | | ||
BsrDI| ||| |||||  |            CviJI                          || || |             | || || | ||| | | ||
    || ||| |||||  |               |                           || || |             | || || | ||| | | ||
     agcgcctgccggcccagtatcagcccgtcatacttgaagctagacaggcttatcttggacaagaagaagatcgcttggcctcgcgcgcagatcagttgga
4101 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 4200
     tcgcggacggccgggtcatagtcgggcagtatgaacttcgatctgtccgaatagaacctgttcttcttctagcgaaccggagcgcgcgtctagtcaacct

a     A  P  A  G  P  V  S  A  R  H  T  *  S  *  T  G  L  S  W  T  R  R  R  S  L  G  L  A  R  R  S  V  G  -
b      R  L  P  A  Q  Y  Q  P  V  I  L  E  A  R  Q  A  Y  L  G  Q  E  E  D  R  L  A  S  R  A  D  Q  L  E -
c    S  A  C  R  P  S  I  S  P  S  Y  L  K  L  D  R  L  I  L  D  K  K  K  I  A  W  P  R  A  Q  I  S  W  K -
```

Figure 7-V

```
                   TaiI                            Hpy188III
                BsaAI |            BcgI                TaqI|
               DraIII |           DdeI|                AvaI||
            HpyCH4IV| |    BstKTI    ||               SmlI||
   ApoI   MboII    || |       DpnI|  ||               XhoI||         Tsp509I
Tsp509I   Hpy8I|   || |     MboI ||  ||           BsmAI  ||| DdeI    BcgI  |                       EarI
      |       ||   || |        | ||  ||               |  |||    |       |  |                          |
     agaatttgtccactacgtgaaaggcgagatcactaaggtagttggcaaataactcgagactaagtggataaaattagatagaaaaaaggtctaaataaaa
4201 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 4300
     tcttaaacaggtgatgcactttccgctctagtgattccatcaaccgtttattgagctctgattcacctattttaatctatcttttttccagatttatttt

a    R  I  C  P  L  R  E  R  R  D  H  *  G  S  W  Q  I  T  R  D  *  V  D  K  I  R  *  K  K  G  L  N  K  K -
b     E  F  V  H  Y  V  K  G  E  I  T  K  V  V  G  K  *  L  E  T  K  W  I  K  L  D  R  K  K  V  *  I  K   -
c      N  L  S  T  T  *  K  A  R  S  L  R  *  L  A  N  N  S  R  L  S  G  *  N  *  I  E  K  R  S  K  *  K  -

                   BstKTI              Tsp509I
                    DpnI|              Hin4I |                                 MseI         Hpy188I
                  MboI ||           HpyCH4V |                           Tsp509I |        BsmAI   |
         Hin4I MboII | ||     MaeIII   MboII | MboII          Tsp509I   HpyCH4V| |        BsmBI   |
             |     | | ||        |           |   |     |            |         || |            |   |
     aagaagagaaatagaaagatcaaaaatcagttacgaaaatgcagtaattcttcttttttcttctaattgattgcaattaaactcgtctcaatctgaaaaa
4301 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 4400
     ttcttctctttatctttctagtttttagtcaatgcttttacgtcattaagaagaaaaaagaagattaactaacgttaatttgagcagagttagactttttt

a      E  E  K  *  K  D  Q  K  S  V  T  K  M  Q  *  F  F  F  F  L  L  I  D  C  N  *  T  R  L  N  L  K  K  -
b    K  K  R  N  R  K  I  K  N  Q  L  R  K  C  S  N  S  S  F  F  F  *  L  I  A  I  K  L  V  S  I  *  K  K -
c     R  R  E  I  E  R  S  K  I  S  Y  E  N  A  V  I  L  L  F  S  S  N  *  L  Q  L  N  S  S  Q  S  E  K   -

                                      NlaIII
                               Hpy188III   |
                                   BspHI|  |
                                  BstKTI|  |
                                    FatI|  |
                                   DpnI||  |            HinfI
                 DraI            BsmAI|||  |             TfiI
         CviJI  MseI|            MboI||||  |  Hpy188III     |          MnlI                MboII
            |      ||               |||||  |             |  |             |                    |
     agattgagccgagtttaaatagattttgatacgatcatgagacttgacaaatcgggattcctctattctatatatttagaagatataaaggtataataca
4401 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 4500
     tctaactcggctcaaatttatctaaaactatgctagtactctgaactgtttagccctaaggagataagatatataaatcttctatatttccatattatgt

a     D  *  A  E  F  K  *  I  L  I  R  S  *  D  L  T  N  R  D  S  S  I  L  Y  I  *  K  I  *  R  Y  N  T   -
b      I  E  P  S  L  N  R  F  *  Y  D  H  E  T  *  Q  I  G  I  P  L  F  Y  I  F  R  R  Y  K  G  I  I  Q  -
c    R  L  S  R  V  *  I  D  F  D  T  I  M  R  L  D  K  S  G  F  L  Y  S  I  Y  L  E  D  I  K  V  *  Y  N -
```

Figure 7-W

```
                                     Bsu36I
                              TaqI     DdeI
                      BfaI   AlwI| BstKTI |
                 Hpy188III  AluI||  DpnI| |                                          HinfI
                     XbaI| CviJI||MboI || |                       SfcI                TfiI  CviJI       FokI
                        ||     |||   | || |                          |                   |      |          |
          ataaataaatacaatctagaagctcgatgatccttaggattggtatattcttttctatcctgtagtttgtagtttccctgaatcaagccaagtatcacac
     4501 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 4600
          tatttatttatgttagatcttcgagctactaggaatcctaaccatataagaaaagataggacatcaaacatcaaagggacttagttcggttcatagtgtg

a         I  N  K  Y  N  L  E  A  R  *  S  L  G  L  V  Y  S  F  L  S  C  S  L  *  F  P  *  I  K  P  S  I  T  P -
b          *  I  N  T  I  *  K  L  D  D  P  *  D  W  Y  I  L  F  Y  P  V  V  C  S  F  P  E  S  S  Q  V  S  H   -
c           K  *  I  Q  S  R  S  S  M  I  L  R  I  G  I  F  F  S  I  L  *  F  V  V  S  L  N  Q  A  K  Y  H  T  -

               BstF5I                                                                 ApoI
               BsmFI|                                      Tsp509I                 Tsp509I
                MnlI|    BccI TspGWI                         MseI|                  MseI |
                   ||       |      |                            ||                     | |
          ctctttctacccatcctgtatattgtcccctttgttccgtgttgaaatagaaccttaatttattacttatttttttattaaattttagatttgttagtga
     4601 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 4700
          gagaaagatgggtaggacatataacaggggaaacaaggcacaactttatcttggaattaaataatgaataaaaaaataatttaaaatctaaacaatcact

a           L  S  T  H  P  V  Y  C  P  L  C  S  V  L  K  *  N  L  N  L  L  L  I  F  L  L  N  F  R  F  V  S  D  -
b         L  F  L  P  I  L  Y  I  V  P  F  V  P  C  *  N  R  T  L  I  Y  Y  L  F  F  Y  *  I  L  D  L  L  V  I -
c          S  F  Y  P  S  C  I  L  S  P  L  F  R  V  E  I  E  P  *  F  I  T  Y  F  F  I  K  F  *  I  C  *  *   -

                                                                                            ApoI
                                                                                         Tsp509I
                                                            MnlI                         Hin4I |
                                     Tsp509I             Hin4I |            SfaNI    TaqI    | |
                                           |                 | |                |       |    | |
          ttagatattagtattagacgagattttacgaaacaattatttttttatttctttataggagaggacaaatctcttttttcgatgcgaatttgacacgaca
     4701 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 4800
          aatctataatcataatctgctctaaaatgctttgttaataaaaaaataaagaaatatcctctcctgtttagagaaaaaagctacgcttaaactgtgctgt

a          *  I  L  V  L  D  E  I  L  R  N  N  Y  F  F  I  S  L  *  E  R  T  N  L  F  F  R  C  E  F  D  T  T   -
b           R  Y  *  Y  *  T  R  F  Y  E  T  I  I  F  L  F  L  Y  R  R  G  Q  I  S  F  F  D  A  N  L  T  R  H  -
c         L  D  I  S  I  R  R  D  F  T  K  Q  L  F  F  Y  F  F  I  G  E  D  K  S  L  F  S  M  R  I  *  H  D  I -
```

Figure 7-X

```
             TauI
           AciI |                                                                              Hpy188I
         Fnu4HI |     Tsp509I          DraI                         AseI                     HinfI   |
         CviJI| |    MseI   |  FalI   MseI|             NlaIV       MseI           MmeI      TfiI    |
             || |       |   |     |      ||                 |         |               |         |    |
     taggagaagccgccctttattaaaaattatattattttaaataatataaagggggttccaacatattaatatatagtgaagtgttcccccagattcagaa
4801 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 4900
     atcctcttcggcgggaaataatttttaatataataaaatttattatatttcccccaaggttgtataattatatatcacttcacaagggggtctaagtctt

a    *  E  K  P  P  F  I  K  N  Y  I  I  L  N  N  I  K  G  V  P  T  Y  *  Y  I  V  K  C  S  P  R  F  R  T -
b     R  R  S  R  P  L  L  K  I  I  L  F  *  I  I  *  R  G  F  Q  H  I  N  I  *  *  S  V  P  P  D  S  E   -
c      G  E  A  A  L  Y  *  K  L  Y  Y  F  K  *  Y  K  G  G  S  N  I  L  I  Y  S  E  V  F  P  Q  I  Q  N  -

                                                                 Hpy188I
                                MseI     BfaI                DdeI       |                    Tsp509I
                                   |        |                   |       |                         |
     ctttttttcaatactcacaatccttattagttaataatcctagtgattggatttctatgcttagtctgataggaaataagatattcaaataaataatttt
4901 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 5000
     gaaaaaaagttatgagtgttaggaataatcaattattaggatcactaacctaaagatacgaatcagactatcctttattctataagtttatttattaaaa

a      F  F  Q  Y  S  Q  S  L  L  V  N  N  P  S  D  W  I  S  M  L  S  L  I  G  N  K  I  F  K  *  I  I  L  -
b    L  F  F  N  T  H  N  P  Y  *  L  I  I  L  V  I  G  F  L  C  L  V  *  *  E  I  R  Y  S  N  K  *  F  Y -
c     F  F  S  I  L  T  I  L  I  S  *  *  S  *  *  L  D  F  Y  A  *  S  D  R  K  *  D  I  Q  I  N  N  F   -

                                 HpyCH4V
                                  NlaIII                                                            AarI
    TspDTI                       Hin4I |                                  Tsp509I                  BspMI
 Hin4I   |         TspDTI       FatI | |                     BccI           MseI|TaqI      MseI    XmnI|
     |   |              |          | | |                        |              ||   |         |       ||
     atagcgaatgactattcatctattgtattttcatgcaaatagggggcaagaaaactctatggaaagatggtggtttaattcgatgttgtttaagaaggag
5001 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 5100
     tatcgcttactgataagtagataacataaaagtacgtttatcccccgttcttttgagatacctttctaccaccaaattaagctacaacaaattcttcctc

a     *  R  M  T  I  H  L  L  Y  F  H  A  N  R  G  Q  E  N  S  M  E  R  W  W  F  N  S  M  L  F  K  K  E   -
b      S  E  *  L  F  I  Y  C  I  F  M  Q  I  G  G  K  K  T  L  W  K  D  G  G  L  I  R  C  C  L  R  R  S  -
c    I  A  N  D  Y  S  S  I  V  F  S  C  K  *  G  A  R  K  L  Y  G  K  M  V  V  *  F  D  V  V  *  E  G  V -
```

Figure 7-Y

```
                                                                       BsaBI     TspDTI
                                                                    BstKTI |    MmeI  |
                                                                     DpnI| |TspDTI |  |
  BstBI                                    AvaII                  BstYI || |MboII| |  |        MnlI
   TaqI           CviJI                   Sau96I              AlwI MboI || |TaqI|| |  |     BsaXI |
      |               |                        |                 |    | || |   ||| |  |         | |
     ttcgaacgcaggtgtgggctaaataaatcaatgggcagtcttggtcctattgaaaataccaatgaagatccaaatcgaaaagtgaaaaacattcatagtt
5101 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 5200
     aagcttgcgtccacacccgatttatttagttacccgtcagaaccaggataacttttatggttacttctaggtttagcttttcactttttgtaagtatcaa

a    F  E  R  R  C  G  L  N  K  S  M  G  S  L  G  P  I  E  N  T  N  E  D  P  N  R  K  V  K  N  I  H  S  W -
b     S  N  A  G  V  G  *  I  N  Q  W  A  V  L  V  L  L  K  I  P  M  K  I  Q  I  E  K  *  K  T  F  I  V   -
c      R  T  Q  V  W  A  K  *  I  N  G  Q  S  W  S  Y  *  K  Y  Q  *  R  S  K  S  K  S  E  K  H  S  *  L  -

            Tsp509I
     Hpy188III    |
        MaeIII    |                                               ApoI
        Tsp45I    |    HpyCH4V                                 Tsp509I
     HinfI   |    |    BsaXI |                                Hpy188I|
      TfiI   |    | BfaI   | |                       MseI TspDTI    ||     Hpy188I
         |   |    |    |   | |                          |      |    ||           |
     ggaggaatcgtgacaattctagttgcagtaatgttgattatttattcggcgttaaagacattcggaatttcatctctgatgacacttttttagttagtga
5201 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 5300
     cctccttagcactgttaagatcaacgtcattacaactaataaataagccgcaatttctgtaagccttaaagtagagactactgtgaaaaaatcaatcact

a      R  N  R  D  N  S  S  C  S  N  V  D  Y  L  F  G  V  K  D  I  R  N  F  I  S  D  D  T  F  L  V  S  D  -
b    G  G  I  V  T  I  L  V  A  V  M  L  I  I  Y  S  A  L  K  T  F  G  I  S  S  L  M  T  L  F  *  L  V  I -
c     E  E  S  *  Q  F  *  L  Q  *  C  *  L  F  I  R  R  *  R  H  S  E  F  H  L  *  *  H  F  F  S  *  *   -

                                                                     BspCNI
                                                                    BseMII|
                                                                   BstKTI||
                                                                    DpnI||| Hpy188I     BfaI
    BsmAI  HpyCH4III           BccI                              MboI  ||||    DdeI|Hpy8I  |
        |          |              |                                  | ||||       ||    |  |
     taggaatggagacagttattccatctattttgatattgaaaatcatatttttgagattgacaacgatcattcttttctgagtgaactagaaagttctttt
5301 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 5400
     atccttacctctgtcaataaggtagataaaactataacttttagtataaaaactctaactgttgctagtaagaaaagactcacttgatctttcaagaaaa

a     R  N  G  D  S  Y  S  I  Y  F  D  I  E  N  H  I  F  E  I  D  N  D  H  S  F  L  S  E  L  E  S  S  F   -
b      G  M  E  T  V  I  P  S  I  L  I  L  K  I  I  F  L  R  L  T  T  I  I  L  F  *  V  N  *  K  V  L  F  -
c    *  E  W  R  Q  L  F  H  L  F  *  Y  *  K  S  Y  F  *  D  *  Q  R  S  F  F  S  E  *  T  R  K  F  F  L -
```

Figure 7-Z

```
                                                                            NlaIII
                                                                              NspI
                                                       BstKTI               MmeI |
                                                        DpnI|           AflIII | |
                     Tsp509I                         BstYI ||  Tsp509I    FatI | |
               TaqI   TaqI | Hpy188I             AlwI MboI ||  MboII |    PciI | |
                  |      | |       |                |    | ||       | |       | | |
          tatagttatcgaaactcgaattatcggaataatggatttaggggcgaagatccctactataattcttacatgtatgatactcaatatagttggaataatc
     5401 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 5500
          atatcaatagctttgagcttaatagccttattacctaaatccccgcttctagggatgatattaagaatgtacatactatgagttatatcaaccttattag

a         Y  S  Y  R  N  S  N  Y  R  N  N  G  F  R  G  E  D  P  Y  Y  N  S  Y  M  Y  D  T  Q  Y  S  W  N  N  H -
b          I  V  I  E  T  R  I  I  G  I  M  D  L  G  A  K  I  P  T  I  I  L  T  C  M  I  L  N  I  V  G  I  I   -
c           *  L  S  K  L  E  L  S  E  *  W  I  *  G  R  R  S  L  L  *  F  L  H  V  *  Y  S  I  *  L  E  *  S  -

                                                                                            BceAI
                                                                                        HpyCH4III
                                                                                           MaeIII
                HpyCH4V                                                           HpyCH4III     |
          AseI  Eco57I|    BsaBI                                                     MaeIII     |
          MseI Eco57MI|MboII   |          BsmAI                   PsiI       Tsp509I Tsp45I     |  HphI Sau96I
             |       ||    |   |              |                      |             |      |     |     |      |
          acattaatagttgcattgatagttatcttcagtctcaaatctgtatagatacttccattataagtggtagtgagaattacggtgacagttacatttatag
     5501 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 5600
          tgtaattatcaacgtaactatcaatagaagtcagagtttagacatatctatgaaggtaatattcaccatcactcttaatgccactgtcaatgtaaatatc

a           I  N  S  C  I  D  S  Y  L  Q  S  Q  I  C  I  D  T  S  I  I  S  G  S  E  N  Y  G  D  S  Y  I  Y  R  -
b         T  L  I  V  A  L  I  V  I  F  S  L  K  S  V  *  I  L  P  L  *  V  V  V  R  I  T  V  T  V  T  F  I  G -
c          H  *  *  L  H  *  *  L  S  S  V  S  N  L  Y  R  Y  F  H  Y  K  W  *  *  E  L  R  *  Q  L  H  L  *   -

                                                          Hpy8I                   MseI
       CviJI                    HphI                  BsrI    |         HpyF10VI     BtsI|
      HaeIII                TaqI   |    MnlI       NlaIV |AccI|            MwoI|    TspRI|
           |                   |   |       |           | |   ||               ||        ||
          ggccgtttgtggtggtgaaagtcgaaatagtagtgaaaacgagggttccagtagacgaactcgcacgaagggcagtgatttaactataagagaaagttct
     5601 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 5700
          ccggcaaacaccaccactttcagctttatcatcacttttgctcccaaggtcatctgcttgagcgtgcttcccgtcactaaattgatattctctttcaaga

a          A  V  C  G  G  E  S  R  N  S  S  E  N  E  G  S  S  R  R  T  R  T  K  G  S  D  L  T  I  R  E  S  S   -
b           P  F  V  V  V  K  V  E  I  V  V  K  T  R  V  P  V  D  E  L  A  R  R  A  V  I  *  L  *  E  K  V  L  -
c         G  R  L  W  W  *  K  S  K  *  *  *  K  R  G  F  Q  *  T  N  S  H  E  G  Q  *  F  N  Y  K  R  K  F  * -
```

Figure 7-AA

```
           MaeIII
        TaqI    |
       AvaI|    |
  Hpy188III|    |
       SmlI|    |
       XhoI|    |
    BstKTI||    |
     DpnI|||    |                                                            ApoI
   MboI ||||    |                                               Tsp509I   Tsp509I
  MnlI  ||||    |                                Tsp509I         MseI | PsiI    |                   SspI
       |||||    |                                      |            | |    |    |                       |
     aatgatctcgaggtaactcaaaaatacaggcatttgtgggttcaatgcgaaaattgttatggattaaattataagaaatttttgaatcaaaaatgaata
5701 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 5800
     ttactagagctccattgagtttttatgtccgtaaacacccaagttacgcttttaacaatacctaatttaatattctttaaaaactttagtttttacttat

a     N  D  L  E  V  T  Q  K  Y  R  H  L  W  V  Q  C  E  N  C  Y  G  L  N  Y  K  K  F  L  K  S  K  M  N  I -
b      M  I  S  R  *  L  K  N  T  G  I  C  G  F  N  A  K  I  V  M  D  *  I  I  R  N  F  *  N  Q  K  *  I  -
c       *  S  R  G  N  S  K  I  Q  A  F  V  G  S  M  R  K  L  L  W  I  K  L  *  E  I  F  E  I  K  N  E  Y -

                                               ApoI
                                              EcoRI                                               Tsp509I
        TspDTI                              Tsp509I        NlaIII   AluI                      BsrBI     |
      Hpy8I  |    EcoRV                Hpy188I    |      FatI   |  CviJI        Tsp509I       AciI |    |
          |  |        |                      |    |         |   |      |              |          | |    |
     tttgtgaacaatgtggatatcatttgaaaatgagtagttcagatagaattcgtaatcatggtcatagctgtttcctgtgtgaaattgttatccgctcaca
5801 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 5900
     aaacacttgttacacctatagtaaacttttactcatcaagtctatcttaagcattagtaccagtatcgacaaaggacacactttaacaataggcgagtgt

a      C  E  Q  C  G  Y  H  L  K  M  S  S  S  D  R  I  R  N  H  G  H  S  C  F  L  C  E  I  V  I  R  S  Q  -
b     F  V  N  N  V  D  I  I  *  K  *  V  V  Q  I  E  F  V  I  M  V  I  A  V  S  C  V  K  L  L  S  A  H  N -
c      L  *  T  M  W  I  S  F  E  N  E  *  F  R  *  N  S  *  S  W  S  *  L  F  P  V  *  N  C  Y  P  L  T  -

                                                NlaIV                                          AciI
                                             HpyF10VI|                                         Cac8I
                                         BstNI      ||                                         TspRI
                                         ScrFI      ||                                 HpyF10VI     |
                                         BsaJI|     ||                                    MwoI |    |
                                         CviJI||    ||                   Tsp509I         BtsI ||    |
                    HpaII                PspGI||BanI||          AluI      AseI |       HhaI  |||    |
                    CviJI|              StyD4I||MwoI||         CviJI      MseI |   HinP1I  | |||    |
                        ||                   |||   |||             |          ||         | | |||    |
     attccacacaacatacgagccggaagcataaagtgtaaagcctggggtgcctaatgagtgagctaactcacattaattgcgttgcgctcactgcccgctt
5901 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 6000
     taaggtgtgttgtatgctcggccttcgtatttcacatttcggaccccacggattactcactcgattgagtgtaattaacgcaacgcgagtgacgggcgaa

a      F  H  T  T  Y  E  P  E  A  *  S  V  K  P  G  V  P  N  E  *  A  N  S  H  *  L  R  C  A  H  C  P  L  -
b       S  T  Q  H  T  S  R  K  H  K  V  *  S  L  G  C  L  M  S  E  L  T  H  I  N  C  V  A  L  T  A  R  F -
c     I  P  H  N  I  R  A  G  S  I  K  C  K  A  W  G  A  *  *  V  S  *  L  T  L  I  A  L  R  S  L  P  A  F -
```

Figure 7-BB

```
                                                       AciI
                                                      BstUI
                                                       HhaI
                                                       MnlI
                                                      BslI|
                                    AseI            TspDTI|
                                    MseI            BstUI||
                              HpyCH4V  |           HinP1I||
                             Fnu4HI |  |          BsaXI |||                        HaeII
                              AluI| |  |        FauI  | |||                        HhaI|
                             CviJI| |  |      CviJI|  | |||                     BsaXI ||
                            MspA1I| |  |     HaeIII|  | |||                    HinP1I ||
      Hpy188III              PvuII| |  |     EaeI ||  | |||                HpyF10VI | ||  EarI      MlyI
      BsrI    |               TseI| |  |HinfI   | ||  | |||                   MwoI| | ||  SapI      PleI
      FauI    |  BbvI      Cac8I || |  | TfiI   | ||  | |||      AciI       MboII|| | || AciI|    BbvI |
         |    |     |          || |  |    |   | ||  | |||         |           ||| | ||    ||       | |
        tccagtcgggaaacctgtcgtgccagctgcattaatgaatcggccaacgcgcggggagaggcggtttgcgtattgggcgctcttccgcttcctcgctcac
   6001 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 6100
        aggtcagccctttggacagcacggtcgacgtaattacttagccggttgcgcgcccctctccgccaaacgcataacccgcgagaaggcgaaggagcgagtg

a       S  S  R  E  T  C  R  A  S  C  I  N  E  S  A  N  A  R  G  E  A  V  C  V  L  G  A  L  P  L  P  R  S  L -
b        P  V  G  K  P  V  V  P  A  A  L  M  N  R  P  T  R  G  E  R  R  F  A  Y  W  A  L  F  R  F  L  A  H   -
c         Q  S  G  N  L  S  C  Q  L  H  *  *  I  G  Q  R  A  G  R  G  G  L  R  I  G  R  S  S  A  S  S  L  T  -

                                               AluI
                                              CviJI
                                         HpyF10VI |
                BbvI                  AciI      | |
                HhaI                 BsrBI      | |
            HinP1I |               Cac8I |      | |
          Fnu4HI | |              TauI | |      | |
           TseI| | |          Fnu4HI | | |      | |
       TaqII  || | |           AciI| | | |      | |
       TspRI  || | |       Fnu4HI || | | |      | |
     HinfI |  || | |       CviJI| || | | |      | |                             HinfI
     MnlI| |  || | | BsiEI  TseI| || | | |  MwoI| |         AciI HpyCH4III       TfiI
        || |  || | |     |     || || | | |     || |            |         |          |
        tgactcgctgcgctcggtcgttcggctgcggcgagcggtatcagctcactcaaaggcggtaatacggttatccacagaatcaggggataacgcaggaaag
   6101 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 6200
        actgagcgacgcgagccagcaagccgacgccgctcgccatagtcgagtgagtttccgccattatgccaataggtgtcttagtcccctattgcgtcctttc

a         T  R  C  A  R  S  F  G  C  G  E  R  Y  Q  L  T  Q  R  R  *  Y  G  Y  P  Q  N  Q  G  I  T  Q  E  R  -
b       *  L  A  A  L  G  R  S  A  A  A  S  G  I  S  S  L  K  G  G  N  T  V  I  H  R  I  R  G  *  R  R  K  E -
c        D  S  L  R  S  V  V  R  L  R  R  A  V  S  A  H  S  K  A  V  I  R  L  S  T  E  S  G  D  N  A  G  K   -
```

## Figure 7-CC

```
                                     HpyCH4III              Cac8I
                                      NlaIV  |           HpyF10VI
                                  BstNI   |  |       BstUI      |
                                  ScrFI   |  |        TauI      |
         NlaIII                 CviJI |   |  |        AciI      |
           NspI                HaeIII |   |  |      Fnu4HI      |
     AflIII   |        Cac8I    PspGI |   |  |     CviJI |      |               AciI
       FatI   |      CviJI |   StyD4I |   |  |   HaeIII| |      |             NlaIV|
       PciI   |     HaeIII | BslI   | |   |  | BslI   || |  MwoI|    EciI    CviJI||             BpuEI SfaNI
          |   |          | |    |   | |   |  |    |   || |     ||       |        |||                 |     |
         aacatgtgagcaaaaggccagcaaaaggccaggaaccgtaaaaaggccgcgttgctggcgttttccataggctccgcccccctgacgagcatcacaaaa
    6201 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 6300
         ttgtacactcgttttccggtcgttttccggtccttggcatttttccggcgcaacgaccgcaaaaggtatccgaggcggggggactgctcgtagtgtttt

a         T  C  E  Q  K  A  S  K  R  P  G  T  V  K  R  P  R  C  W  R  F  S  I  G  S  A  P  L  T  S  I  T  K   -
b          H  V  S  K  R  P  A  K  G  Q  E  P  *  K  G  R  V  A  G  V  F  P  *  A  P  P  P  *  R  A  S  Q  K  -
c        N  M  *  A  K  G  Q  Q  K  A  R  N  R  K  K  A  A  L  L  A  F  F  H  R  L  R  P  P  D  E  H  H  K  N-

                  Hpy188I
                  HgaI  |                                                                MnlI
               DrdI  |  |                                           BstNI              HhaI |
               MnlI  |  |                              BstNI        ScrFI          HinP1I | |
             SmlI |  |  |                              ScrFI      BsaJI |      BssSI    | | |
          Hpy99I| |  |  |                            PspGI |      PspGI |  AluI    |    | | |
       TaqI    || |  |  |                           StyD4I |     StyD4I | CviJI    |    | | |   Hpy188I
          |    || |  |  |                                | |          | |     |    |    | | |         |
         atcgacgctcaagtcagaggtggcgaaacccgacaggactataaagataccaggcgtttccccctggaagctccctcgtgcgctctcctgttccgaccct
    6301 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 6400
         tagctgcgagttcagtctccaccgctttgggctgtcctgatatttctatggtccgcaaagggggaccttcgagggagcacgcgagaggacaaggctggga

a        I  D  A  Q  V  R  G  G  E  T  R  Q  D  Y  K  D  T  R  R  F  P  L  E  A  P  S  C  A  L  L  F  R  P  C -
b         S  T  L  K  S  E  V  A  K  P  D  R  T  I  K  I  P  G  V  S  P  W  K  L  P  R  A  L  S  C  S  D  P   -
c          R  R  S  S  Q  R  W  R  N  P  T  G  L  *  R  Y  Q  A  F  P  P  G  S  S  L  V  R  S  P  V  P  T  L  -
```

Figure 7-DD

```
           EciI
         HpaII|
        BsaWI||
         BslI||
     BciVI  |||
     TauI|  |||                                   HaeII
   AciI ||  |||       AciI                        HhaI|      AluI                         BseMII
 Fnu4HI ||  |||   MmeI   |      Hpy188III     HinP1I ||     CviJI   SfcI      DdeI       BspCNI|
      | ||  |||      |   |              |          | ||         |      |         |            ||
     gccgcttaccggatacctgtccgcctttctcccttcgggaagcgtggcgctttctcatagctcacgctgtaggtatctcagttcggtgtaggtcgttcgc
6401 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 6500
     cggcgaatggcctatggacaggcggaaagagggaagcccttcgcaccgcgaaagagtatcgagtgcgacatccatagagtcaagccacatccagcaagcg

a      R  L  P  D  T  C  P  P  F  S  L  R  E  A  W  R  F  L  I  A  H  A  V  G  I  S  V  R  C  R  S  F  A  -
b    A  A  Y  R  I  P  V  R  L  S  P  F  G  K  R  G  A  F  S  *  L  T  L  *  V  S  Q  F  G  V  G  R  S  L -
c     P  L  T  G  Y  L  S  A  F  L  P  S  G  S  V  A  L  S  H  S  S  R  C  R  Y  L  S  S  V  *  V  V  R   -

                                                  HhaI
                 Bme1580I                     HinP1I |                            HpaII
                   BsiHKAI                  Fnu4HI | |                             MlyI
           CviJI Bsp1286I                  MspA1I| | |                             NciI
       AluI    |  Hpy8I |                    TseI| | |   MaeIII          HinfI    ScrFI
      BseYI    |HpyCH4V |           CviJI  AciI || | | HpaII |   Hpy188III  |    PleI|
      CviJI    |ApaLI | |       BbvI    | BsiEI || | | BsaWI| |       SmlI  | StyD4I||    BpuEI
          |    |    | | |          |    |     | || | |     || |           |  |      |||        |
     tccaagctgggctgtgtgcacgaaccccccgttcagcccgaccgctgcgccttatccggtaactatcgtcttgagtccaacccggtaagacacgacttat
6501 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 6600
     aggttcgacccgacacacgtgcttggggggcaagtcgggctggcgacgcggaataggccattgatagcagaactcaggttgggccattctgtgctgaata

a     P  S  W  A  V  C  T  N  P  P  F  S  P  T  A  A  P  Y  P  V  T  I  V  L  S  P  T  R  *  D  T  T  Y   -
b      Q  A  G  L  C  A  R  T  P  R  S  A  R  P  L  R  L  I  R  *  L  S  S  *  V  Q  P  G  K  T  R  L  I  -
c    S  K  L  G  C  V  H  E  P  P  V  Q  P  D  R  C  A  L  S  G  N  Y  R  L  E  S  N  P  V  R  H  D  L  S -
```

Figure 7-EE

```
                              BbvI
                             BsrI|
                            TspRI|
                           BbvI ||
                         MaeIII ||
                       AlwNI  | ||
                    CviJI  |  | ||
                 Fnu4HI |  |  | ||
                  TseI| |  |  | ||
                BsrI || |  |  | ||
              Fnu4HI || |  |  | ||
               TspRI || |  |  | ||                                                   CviJI     CviJI
       MmeI    TseI| || |  |  | ||      MnlI              AciI  SfcI Hpy188III      HaeIII   BslI   |  BfaI
          |       || || |  |  | ||         |                 |     |         |           |      |   |     |
          cgccactggcagcagccactggtaacaggattagcagagcgaggtatgtaggcggtgctacagagttcttgaagtggtggcctaactacggctacactag
     6601 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 6700
          gcggtgaccgtcgtcggtgaccattgtcctaatcgtctcgctccatacatccgccacgatgtctcaagaacttcaccaccggattgatgccgatgtgatc

a         R  H  W  Q  Q  P  L  V  T  G  L  A  E  R  G  M  *  A  V  L  Q  S  S  *  S  G  G  L  T  T  A  T  L  E -
b          A  T  G  S  S  H  W  *  Q  D  *  Q  S  E  V  C  R  R  C  Y  R  V  L  E  V  V  A  *  L  R  L  H  *    -
c           P  L  A  A  A  T  G  N  R  I  S  R  A  R  Y  V  G  G  A  T  E  F  L  K  W  W  P  N  Y  G  Y  T  R  -

                                                                             HpaII
                                                                            BstKTI|
                                                                            DpnI ||
                                                                          MboI  |||
                                                                   Hpy188III  | |||
                                         MaeIII       Eco57I         AluI   | | |||
        HpyCH4III            HhaI        BsrI  |     Eco57MI         AlwI   | | |||          MspA1I
         BceAI   |       HinP1I  |     CviJI | |  Hpy188I   |       CviJI   | | |||          AciI  |  AciI
              |  |             | |          || |         |  |            |  | | |||              | |      |
          aaggacagtatttggtatctgcgctctgctgaagccagttaccttcggaaaaagagttggtagctcttgatccggcaaacaaaccaccgctggtagcggt
     6701 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 6800
          ttcctgtcataaaccatagacgcgagacgacttcggtcaatggaagcctttttctcaaccatcgagaactaggccgtttgtttggtggcgaccatcgcca

a           G  Q  Y  L  V  S  A  L  C  *  S  Q  L  P  S  E  K  E  L  V  A  L  D  P  A  N  K  P  P  L  V  A  V  -
b         K  D  S  I  W  Y  L  R  S  A  E  A  S  Y  L  R  K  K  S  W  *  L  L  I  R  Q  T  N  H  R  W  *  R  W -
c          R  T  V  F  G  I  C  A  L  L  K  P  V  T  F  G  K  R  V  G  S  S  *  S  G  K  Q  T  T  A  G  S  G    -
```

Figure 7-FF

```
                                                       BstKTI
                                                         DpnI|
                                                      BstYI ||
                                                       MboI ||
                                                    AlwI  | ||
                                BpuEI             AlwI |  | ||
                                 HhaI        Hpy188III |  | ||
                               BbvI |           SmlI | |  | ||
                  Fnu4HI      BstUI |        BstKTI| | |  | ||  BstKTI                             BseMII
                   TseI|     HinP1I |         DpnI|| | |  | ||   DpnI|                 DdeI       BspCNI|
                Cac8I || HpyF10VI | |      BstYI ||| | |  | ||  MboII|                PpiI|   TspRI    ||
            HpyCH4V | ||    MwoI| | |       MboI ||| | |  | || MboI ||         Hpy188I   || HgaI  |    ||
                  | | ||       || | |          | ||| | |  | ||    | ||               |   ||    |  |    ||
     ggtttttttgtttgcaagcagcagattacgcgcagaaaaaaaggatctcaagaagatcctttgatcttttctacggggtctgacgctcagtggaacgaaa
6801 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 6900
     ccaaaaaaacaaacgttcgtcgtctaatgcgcgtctttttttcctagagttcttctaggaaactagaaaagatgccccagactgcgagtcaccttgcttt

a     V  F  L  F  A  S  S  R  L  R  A  E  K  K  D  L  K  K  I  L  *  S  F  L  R  G  L  T  L  S  G  T  K   -
b      F  F  C  L  Q  A  A  D  Y  A  Q  K  K  R  I  S  R  R  S  F  D  L  F  Y  G  V  *  R  S  V  E  R  K  -
c    G  F  F  V  C  K  Q  Q  I  T  R  R  K  K  G  S  Q  E  D  P  L  I  F  S  T  G  S  D  A  Q  W  N  E  N -

                                                      BstKTI
                                          BstKTI       DpnI|
                                           DpnI|    BstYI ||
                         NlaIII         BstYI ||     MboI ||      MseI
         MseI      Hpy188III  |          MboI ||   BfaI | ||Tsp509I  |
         TaiI         BspHI|  |        HphI | || AlwI | | ||  DraI|  |           DraI
  HpyCH4IV  |     PpiI FatI|  |    MboII  | | ||AlwI| | | || MseI||  |          MseI|TspDTI
         |  |        |    ||  |        |  | | ||   || | | ||    |||  |             ||     |
     actcacgttaagggattttggtcatgagattatcaaaaaggatcttcacctagatccttttaaattaaaaatgaagttttaaatcaatctaaagtatata
6901 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 7000
     tgagtgcaattccctaaaaccagtactctaatagtttttcctagaagtggatctaggaaaatttaatttttacttcaaaatttagttagatttcatatat

a    T  H  V  K  G  F  W  S  *  D  Y  Q  K  G  S  S  P  R  S  F  *  I  K  N  E  V  L  N  Q  S  K  V  Y  M -
b     L  T  L  R  D  F  G  H  E  I  I  K  K  D  L  H  L  D  P  F  K  L  K  M  K  F  *  I  N  L  K  Y  I   -
c      S  R  *  G  I  L  V  M  R  L  S  K  R  I  F  T  *  I  L  L  N  *  K  *  S  F  K  S  I  *  S  I  Y  -
```

Figure 7-GG

```
                                                                    BseMII
                                                                   BspCNI|
                                                                 TspDTI ||
                                                                 FokI | ||
                   HpyCH4III                    NlaIV         BstKTI| | ||              MlyI
                      MaeIII          MnlI     BanI |          DpnI|| | ||              PleI
         Hpy8I   Hpy188I   |        MseI |    TspRI |   DdeI MboI ||| | ||  BstF5I  Hin4I  | HinfI AhdI
             |         |   |           | |        | |      |    | ||| | ||       |      |  |     |    |
        tgagtaaacttggtctgacagttaccaatgcttaatcagtgaggcacctatctcagcgatctgtctatttcgttcatccatagttgcctgactccccgtc
   7001 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 7100
        actcatttgaaccagactgtcaatggttacgaattagtcactccgtggatagagtcgctagacagataaagcaagtaggtatcaacggactgaggggcag

a         S  K  L  G  L  T  V  T  N  A  *  S  V  R  H  L  S  Q  R  S  V  Y  F  V  H  P  *  L  P  D  S  P  S  -
b       *  V  N  L  V  *  Q  L  P  M  L  N  Q  *  G  T  Y  L  S  D  L  S  I  S  F  I  H  S  C  L  T  P  R  R -
c        E  *  T  W  S  D  S  Y  Q  C  L  I  S  E  A  P  I  S  A  I  C  L  F  R  S  S  I  V  A  *  L  P  V    -

                                             BsrI                    BpmI
                                           BccI |                 Eco57MI
                                          NlaIV |              BstUI    |
                                         CviJI| |             AciI |    |        Hpy188III
                                        HaeIII| | HpyCH4V   BsaI | |    |          NlaIV |
                                       Sau96I|| |  TspRI|  BsmAI | |    |         CviJI| |
                   MnlI                BmrI ||| |Fnu4HI||  BsrDI | |    |      HpaII  || |
   Hpy99I       Hin4I |      CviJI   BbvI | ||| | TseI||| Hin4I| | | HphI     BsrFI|  || |Hin4I
        |           | |          |      | | ||| |    ||||     || | |    |         ||  || |    |
        gtgtagataactacgatacgggagggcttaccatctggccccagtgctgcaatgataccgcgagacccacgctcaccggctccagatttatcagcaataa
   7101 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 7200
        cacatctattgatgctatgccctcccgaatggtagaccggggtcacgacgttactatggcgctctgggtgcgagtggccgaggtctaaatagtcgttatt

a        C  R  *  L  R  Y  G  R  A  Y  H  L  A  P  V  L  Q  *  Y  R  E  T  H  A  H  R  L  Q  I  Y  Q  Q  *   -
b         V  D  N  Y  D  T  G  G  L  T  I  W  P  Q  C  C  N  D  T  A  R  P  T  L  T  G  S  R  F  I  S  N  K  -
c       V  *  I  T  T  I  R  E  G  L  P  S  G  P  S  A  A  M  I  P  R  D  P  R  S  P  A  P  D  L  S  A  I  N -
```

Figure 7-HH

```
                               HhaI
                           HinP1I |
                       CviJI    | |
                      HaeIII    | |
                  HpyF10VI |    | |
               HpaII     | |    | |             FokI                   Tsp509I      NciI
              CviJI|Sau96I |    | |       HpyCH4V  |                 BccI    |     ScrFI   BfaI
            Cac8I || BglI| |    | |   AvaII     |  |       BstF5I   MnlI|AseI|    HpaII|  AluI|
          CviJI | || MwoI| |    | |  Sau96I EciI|  |   AciI     |BsrI  ||MseI|  StyD4I|| CviJI|
              | | ||    || |    | |       |    ||  |      |     |   |  ||   ||       |||     ||
          accagccagccggaagggccgagcgcagaagtggtcctgcaactttatccgcctccatccagtctattaattgttgccgggaagctagagtaagtagttc
     7201 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 7300
          tggtcggtcggccttcccggctcgcgtcttcaccaggacgttgaaataggcggaggtaggtcagataattaacaacggcccttcgatctcattcatcaag

a         T  S  Q  P  E  G  P  S  A  E  V  V  L  Q  L  Y  P  P  P  S  S  L  L  I  V  A  G  K  L  E  *  V  V  R  -
b          P  A  S  R  K  G  R  A  Q  K  W  S  C  N  F  I  R  L  H  P  V  Y  *  L  L  P  G  S  *  S  K  *  F    -
c           Q  P  A  G  R  A  E  R  R  S  G  P  A  T  L  S  A  S  I  Q  S  I  N  C  C  R  E  A  R  V  S  S  S   -

                              TaiI
                           AclI  |                                                              NlaIV
                       HpyCH4IV  |                     MaeIII                               HpaII   |
                        HhaI  |  |                      SfaNI                              BsaWI|   |
            MseI       FspI|  |  |                     Tsp45I         TspDTI              AluI ||   |     DpnI
        BsrI   |    HinP1I||  |  | BsrDI  SfcI       MslI   |       Hpy99I |   CviJI     CviJI ||   |   MboI |
           |   |         |||  |  |     |     |          |   |            | |       |         | ||   |      | |
          gccagttaatagtttgcgcaacgttgttgccattgctacaggcatcgtggtgtcacgctcgtcgtttggtatggcttcattcagctccggttcccaacga
     7301 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 7400
          cggtcaattatcaaacgcgttgcaacaacggtaacgatgtccgtagcaccacagtgcgagcagcaaaccataccgaagtaagtcgaggccaagggttgct

a           Q  L  I  V  C  A  T  L  L  P  L  L  Q  A  S  W  C  H  A  R  R  L  V  W  L  H  S  A  P  V  P  N  D   -
b         A  S  *  *  F  A  Q  R  C  C  H  C  Y  R  H  R  G  V  T  L  V  V  W  Y  G  F  I  Q  L  R  F  P  T  I  -
c          P  V  N  S  L  R  N  V  V  A  I  A  T  G  I  V  V  S  R  S  S  F  G  M  A  S  F  S  S  G  S  Q  R    -
```

Figure 7-II

```
                                                                           Hpy188I
                                                                         MnlI    |
                      BstKTI                                         BsiEI  |    |
                       DpnI|                                        BstKTI  |    |           TauI
                    NlaIII||                                          PvuI  |    |         AciI |
                     MboI|||                        AluI             DpnI|  |    |       Fnu4HI |
                  FatI  ||||      HpyCH4V          CviJI        Hpy188I ||  |    |       CviJI| |
               AlwI  |  ||||  NlaIII    |      TaqII   |   AvaII      | ||  |    |      HaeIII| |   BtsI
    BstKTI MaeIII |  |  ||||FatI   |    |    AciI  |   |  Sau96I   MboI ||  |    |      EaeI || |  TspRI
         |       ||  |  ||||   |   |    |       |  |   |       |      | ||  |    |         | || |      |
         tcaaggcgagttacatgatcccccatgttgtgcaaaaaagcggttagctccttcggtcctccgatcgttgtcagaagtaagttggccgcagtgttatcac
    7401 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 7500
         agttccgctcaatgtactagggggtacaacacgttttttcgccaatcgaggaagccaggaggctagcaacagtcttcattcaaccggcgtcacaatagtg

a         Q  G  E  L  H  D  P  P  C  C  A  K  K  R  L  A  P  S  V  L  R  S  L  S  E  V  S  W  P  Q  C  Y  H   -
b          K  A  S  Y  M  I  P  H  V  V  Q  K  S  G  *  L  L  R  S  S  D  R  C  Q  K  *  V  G  R  S  V  I  T  -
c        S  R  R  V  T  *  S  P  M  L  C  K  K  A  V  S  S  F  G  P  P  I  V  V  R  S  K  L  A  A  V  L  S  L-

                             BbvI            BstF5I
                         Tsp509I|             SfaNI
                          TspRI||           NlaIII|                             RsaI
                      HpyCH4V |||         FatI   ||                             ScaI
           MslI     BtsI    | |||  HpyCH4III |   ||                           Csp6I|   BspCNI
        NlaIII| Fnu4HI |    | |||     TspGWI |   ||              MaeIII       TatI||  BseMII|  Hpy188I
      FatI   ||  TseI| |    | ||| FokI     | |   ||    BccI      Tsp45I     BsrI |||  HphI ||    DdeI|   BcgI
         |   ||     || |    | |||    |     | |   ||       |           |        | |||     | ||       ||      |
         tcatggttatggcagcactgcataattctcttactgtcatgccatccgtaagatgcttttctgtgactggtgagtactcaaccaagtcattctgagaata
    7501 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 7600
         agtaccaataccgtcgtgacgtattaagagaatgacagtacggtaggcattctacgaaaagacactgaccactcatgagttggttcagtaagactcttat

a        S  W  L  W  Q  H  C  I  I  L  L  L  S  C  H  P  *  D  A  F  L  *  L  V  S  T  Q  P  S  H  S  E  N  S-
b         H  G  Y  G  S  T  A  *  F  S  Y  C  H  A  I  R  K  M  L  F  C  D  W  *  V  L  N  Q  V  I  L  R  I   -
c          M  V  M  A  A  L  H  N  S  L  T  V  M  P  S  V  R  C  F  S  V  T  G  E  Y  S  T  K  S  F  *  E  *  -
```

Figure 7-JJ

```
                                   BcgI
                                BsaHI |
                             HpaII  | |                                                             BpuEI
                              NciI  | |                                                           TaiI  |
              BsiEI          ScrFI  | |                 HhaI                                   AclI  |  |
           TauI   |         TaqII|  | |              BstUI |                               HpyCH4IV  |  |
       Fnu4HI |   |       StyD4I||  | |             HinP1I |              DraI BsiHKAI         XmnI  |  |
        AciI| |   |   HgaI     |||  | |             AciI | |            MseI| Bsp1286I    MboII   |  |  |
           || |   |      |     |||  | |                | | |               ||        |        |   |  |  |
     gtgtatgcggcgaccgagttgctcttgcccggcgtcaatacgggataataccgcgccacatagcagaactttaaaagtgctcatcattggaaaacgttct
7601 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 7700
     cacatacgccgctggctcaacgagaacgggccgcagttatgccctattatggcgcggtgtatcgtcttgaaattttcacgagtagtaaccttttgcaaga

a      V  C  G  D  R  V  A  L  A  R  R  Q  Y  G  I  I  P  R  H  I  A  E  L  *  K  C  S  S  L  E  N  V  L  -
b    V  Y  A  A  T  E  L  L  L  P  G  V  N  T  G  *  Y  R  A  T  *  Q  N  F  K  S  A  H  H  W  K  T  F  F -
c     C  M  R  R  P  S  C  S  C  P  A  S  I  R  D  N  T  A  P  H  S  R  T  L  K  V  L  I  I  G  K  R  S   -

                                                                    MboII
                                                               Bme1580I |
                                                                BsiHKAI |
                                                               Bsp1286I |
                                                                Hpy8I | |
                                                              HpyCH4V | |
                                 AlwI     BsrI                ApaLI | | |
                      BstKTI MspA1I |  BstKTI|               Eco57I | | |
                       DpnI| AciI | |   DpnI||              Eco57MI | | |  BstKTI
                    BstYI || AlwI | |BstYI |||   MaeIII    BssSI  | | | |   DpnI|          SfaNI
                SmlI MboI ||PpiI| | | MboI ||| TaqI   |     PpiI  | | | | MboI ||TaqII  HphI   |  TaqII
                   |    | ||   || | |    | |||    |   |        |  | | | |    | ||    |     |   |      |
     tcggggcgaaaactctcaaggatcttaccgctgttgagatccagttcgatgtaacccactcgtgcacccaactgatcttcagcatcttttactttcacca
7701 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 7800
     agccccgcttttgagagttcctagaatggcgacaactctaggtcaagctacattgggtgagcacgtgggttgactagaagtcgtagaaaatgaaagtggt

a     R  G  E  N  S  Q  G  S  Y  R  C  *  D  P  V  R  C  N  P  L  V  H  P  T  D  L  Q  H  L  L  L  S  P   -
b      G  A  K  T  L  K  D  L  T  A  V  E  I  Q  F  D  V  T  H  S  C  T  Q  L  I  F  S  I  F  Y  F  H  Q  -
c    S  G  R  K  L  S  R  I  L  P  L  L  R  S  S  S  M  *  P  T  R  A  P  N  *  S  S  A  S  F  T  F  T  S -

                                        TauI
                                      AciI |                                 MboII
                       HphI         Fnu4HI |                       MslI     TspGWI         EarI     SspI
                          |              | |                         |           |            |        |
     gcgtttctgggtgagcaaaaacaggaaggcaaaatgccgcaaaaaagggaataagggcgacacggaaatgttgaatactcatactcttcctttttcaata
7801 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 7900
     cgcaaagacccactcgtttttgtccttccgttttacggcgttttttcccttattcccgctgtgcctttacaacttatgagtatgagaaggaaaaagttat

a    A  F  L  G  E  Q  K  Q  E  G  K  M  P  Q  K  R  E  *  G  R  H  G  N  V  E  Y  S  Y  S  S  F  F  N  I -
b     R  F  W  V  S  K  N  R  K  A  K  C  R  K  K  G  N  K  G  D  T  E  M  L  N  T  H  T  L  P  F  S  I   -
c      V  S  G  *  A  K  T  G  R  Q  N  A  A  K  K  G  I  R  A  T  R  K  C  *  I  L  I  L  F  L  F  Q  Y  -
```

Figure 7-KK

```
                                             AciI
                                            BsrBI
                                         NlaIII |
                                        BciVI | |                                               HhaI
                                        BsmAI | |                                            BstUI |
                                   Hpy188III| | |                                           HinP1I |
                                      BspHI|| | |                                           AciI | |
                                       FatI|| | |                                        NlaIV | | |
                                          ||| | |                                            | | | |
             ttattgaagcatttatcagggttattgtctcatgagcggatacatatttgaatgtatttagaaaaataaacaaataggggttccgcgcacatttccccga
        7901 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 8000
             aataacttcgtaaatagtcccaataacagagtactcgcctatgtataaacttacataaatctttttatttgtttatccccaaggcgcgtgtaaaggggct

    a          I  E  A  F  I  R  V  I  V  S  *  A  D  T  Y  L  N  V  F  R  K  I  N  K  *  G  F  R  A  H  F  P  E -
    b        L  L  K  H  L  S  G  L  L  S  H  E  R  I  H  I  *  M  Y  L  E  K  *  T  N  R  G  S  A  H  I  S  P  K-
    c         Y  *  S  I  Y  Q  G  Y  C  L  M  S  G  Y  I  F  E  C  I  *  K  N  K  Q  I  G  V  P  R  T  F  P  R  -

                                                                                CviJI
                           DdeI                                                HaeIII
                         AatII|                                             EcoO109I|
                          TaiI|               NlaIII                          Sau96I|
                        ZraI ||         Hpy188III  |                       BssSI   ||
                      BsaHI| ||            BspHI|  |                  Hpy188III    ||
                   HpyCH4IV| ||             FatI|  |MseI               MnlI    |   ||
                          || ||                ||  |   |                   |   |   ||
             aaagtgccacctgacgtctaagaaaccattattatcatgacattaacctataaaaataggcgtatcacgaggccctttcgtc
        8001 ---------+---------+---------+---------+---------+---------+---------+---------+-- 8082
             tttcacggtggactgcagattctttggtaataatagtactgtaattggatatttttatccgcatagtgctccgggaaagcag

    a         K  C  H  L  T  S  K  K  P  L  L  S  *  H  *  P  I  K  I  G  V  S  R  G  P  F  V   -
    b          S  A  T  *  R  L  R  N  H  Y  Y  H  D  I  N  L  *  K  *  A  Y  H  E  A  L  S     -
    c        K  V  P  P  D  V  *  E  T  I  I  I  M  T  L  T  Y  K  N  R  R  I  T  R  P  F  R    -
```

Figure 7-LL

```
 Enzymes that do cut and were not excluded:

AarI     AatII     AccI   Acc65I     AciI     AclI     AfeI   AflIII     AhdI     AluI     AlwI    AlwNI     ApaI
ApaLI     ApoI     AseI     AvaI    AvaII    AvrII     BaeI    BamHI     BanI    BanII     BbeI     BbsI     BbvI
BccI     BceAI     BcgI    BciVI     BclI     BfaI    BfrBI     BglI    BglII     BlpI Bme1580I    BmgBI     BmrI
BmtI      BpmI   Bpu10I    BpuEI     BsaI    BsaAI    BsaBI    BsaHI    BsaJI    BsaWI    BsaXI   BseMII    BseRI
BseYI    BsiEI  BsiHKAI     BslI     BsmI    BsmAI    BsmBI    BsmFI Bsp1286I  BspCNI    BspHI    BspMI     BsrI
BsrBI    BsrDI    BsrFI    BsrGI   BssHII    BssSI   BstAPI    BstBI   BstEII   BstF5I   BstKTI    BstNI    BstUI
BstXI    BstYI   Bsu36I     BtgI     BtsI    Cac8I    Csp6I    CviJI     DdeI     DpnI     DraI   DraIII     DrdI
EaeI      EagI     EarI     EciI   Eco57I  EcoICRI  Eco57MI    EcoNI Eco0109I    EcoRI    EcoRV     FalI     FatI
FauI    Fnu4HI     FokI     FspI    HaeII   HaeIII     HgaI     HhaI    Hin4I   HinP1I   HincII  HindIII    HinfI
HpaI     HpaII     HphI    Hpy8I   Hpy99I  Hpy188I Hpy188III HpyCH4III HpyCH4IV HpyCH4V HpyF10VI     KasI     KpnI
MaeIII    MboI    MboII     MfeI     MlyI     MmeI     MnlI     MscI     MseI     MslI   MspA1I     MwoI     NaeI
NarI      NciI     NcoI     NdeI   NgoMIV     NheI   NlaIII    NlaIV     NruI     NsiI     NspI     PacI     PciI
PfoI      PleI     PpiI    PpuMI     PsiI    PspGI   PspOMI     PstI     PvuI    PvuII     RsaI     SacI    SacII
SalI      SapI   Sau96I     ScaI    ScrFI    SexAI    SfaNI     SfcI     SfoI     SmaI     SmlI    SnaBI     SpeI
SphI      SspI     StyI   StyD4I     TaiI     TaqI    TaqII     TatI     TauI     TfiI     TseI   Tsp45I  Tsp509I
TspDTI  TspGWI    TspRI     XbaI     XcmI     XhoI     XmaI     XmnI     ZraI

 Enzymes that do not cut:

AflII     AgeI     AleI     AloI     AscI    AsiSI    BbvCI     BplI     BsgI    BsiWI    BspEI  BstZ17I     ClaI
FseI     FspAI     MluI     NotI    PflMI     PmeI     PmlI    PshAI     PsrI    RsrII    SanDI     SbfI     SfiI
SgrAI     SrfI     StuI     SwaI  Tth111I

 Enzymes excluded; MinCuts: 1  MaxCuts: 100000

 NONE
```

Figure 8-A

```
tcgcgcgttt cggtgatgac ggtgaaaacc tctgacacat gcagctcccg gagacggtca 60
cagcttgtct gtaagcggat gccgggagca gacaagcccg tcagggcgcg tcagcgggtg 120
ttggcgggtg tcggggctgg cttaactatg cggcatcaga gcagattgta ctgagagtgc 180
accatatgcg gtgtgaaata ccgcacagat gcgtaaggag aaaataccgc atcaggcgcc 240
attcgccatt caggctgcgc aactgttggg aagggcgatc ggtgcgggcc tcttcgctat 300
tacgccagct ggcgaaaggg ggatgtgctg caaggcgatt aagttgggta acgccagggt 360
tttcccagtc acgacgttgt aaaacgacgg ccagtgccaa gcttgaaaga gataaattga 420
acaagtatgg tcgtcccctg ttgggatgta ctattaaacc taaattgggg ttatctgcta 480
aaaactacgg tagagccgtt tatgaatgtc ttcgcggtgg acttgatttt actaaagatg 540
atgagaacgt gaactcacaa ccatttatgc gttggagaga tcgtttctta ttttgtgccg 600
aagcacttta taaagcacag gctgaaacag gtgaaatcaa agggcattac ttgaatgcta 660
ctgcaggtac atgcgaagaa atgatcaaaa gagctgtatt tgctagagaa ttgggcgttc 720
cgatcgtaat gcatgactac ttaacggggg gattcaccgc aaatactagc ttggctcatt 780
attgccgaga taatggtcta cttcttcaca tccaccgtgc aatgcatgcg gttattgata 840
gacagaagaa tcatggtatc cacttccggg tattagcaaa agcgttacgt atgtctggtg 900
gagatcatat tcactctggt accgtagtag gtaaacttga aggtgaaaga gacataactt 960
tgggctttgt tgatttactg cgtgatgatt ttgttgaaca agatcgaagt cgcggtattt 1020
atttcactca agattgggtc tctttaccag gtgttctacc cgtggcttca ggaggtattc 1080
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```

Figure 8-B

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Figure 8-C

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Figure 8-D

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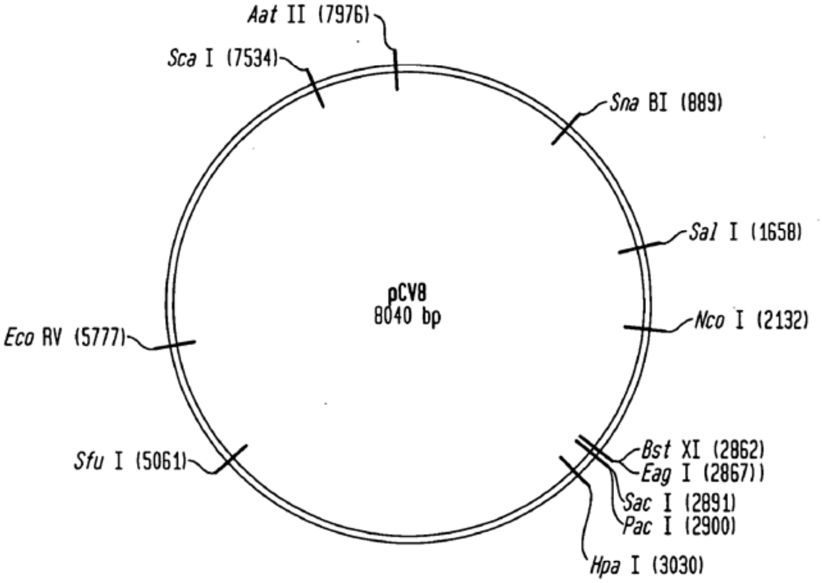
FIG. 9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Sca I (7534)
Sna BI (889)
Sal I (1658)
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8040 bp
Nco I (2132)
Eco RV (5777)
Bst XI (2862)
Eag I (2867))
Sfu I (5061)
Sac I (2891)
Pac I (2900)
Hpa I (3030)

FIG. 10

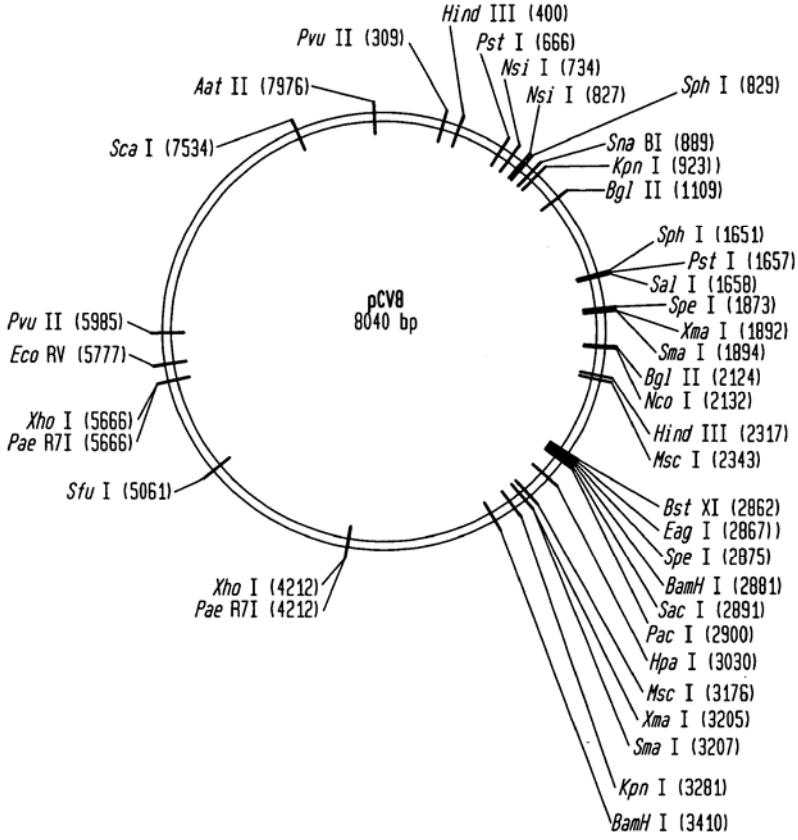
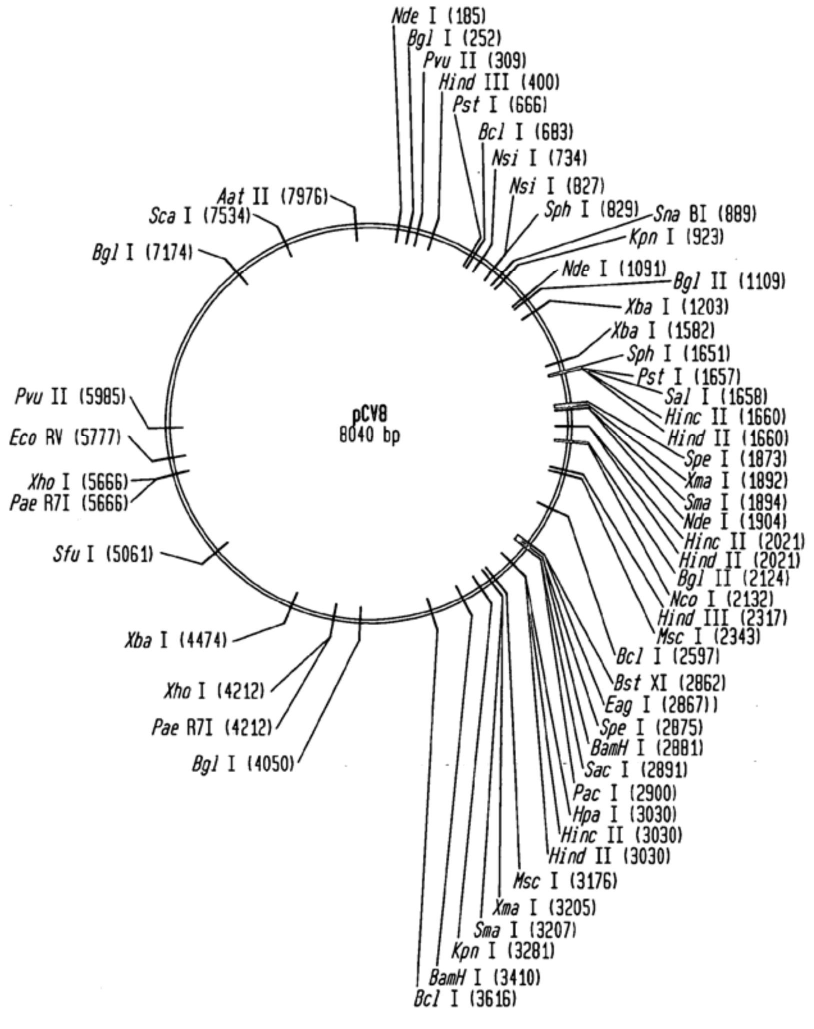

pCV8
8040 bp
Hind III (400)
Pvu II (309)
Pst I (666)
Nsi I (734)
Nsi I (827)
Sph I (829)
Aat II (7976)
Sca I (7534)
Sna BI (889)
Kpn I (923)
Bgl II (1109)
Sph I (1651)
Pst I (1657)
Sal I (1658)
Spe I (1873)
Xma I (1892)
Sma I (1894)
Bgl II (2124)
Nco I (2132)
Hind III (2317)
Msc I (2343)
Pvu II (5985)
Eco RV (5777)
Xho I (5666)
Pae R7I (5666)
Sfu I (5061)
Bst XI (2862)
Eag I (2867)
Spe I (2875)
BamH I (2881)
Sac I (2891)
Pac I (2900)
Hpa I (3030)
Msc I (3176)
Xma I (3205)
Sma I (3207)
Kpn I (3281)
BamH I (3410)
Xho I (4212)
Pae R7I (4212)

FIG. 11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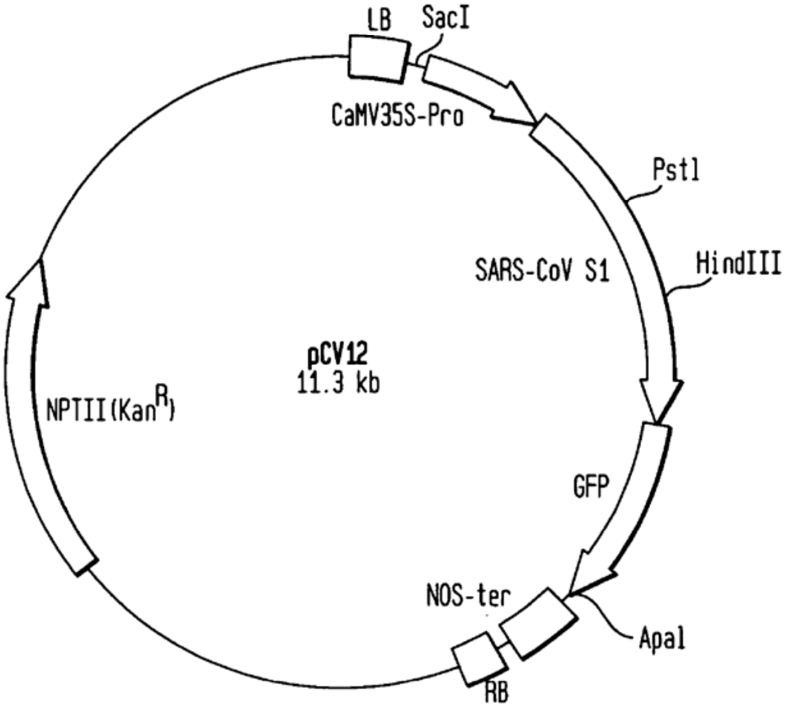
8040 bp
Nde I (185)
Bgl I (252)
Pvu II (309)
Hind III (400)
Pst I (666)
Bcl I (683)
Nsi I (734)
Nsi I (827)
Sph I (829)
Sna BI (889)
Kpn I (923)
Nde I (1091)
Bgl II (1109)
Xba I (1203)
Xba I (1582)
Sph I (1651)
Pst I (1657)
Sal I (1658)
Hinc II (1660)
Hind II (1660)
Spe I (1873)
Xma I (1892)
Sma I (1894)
Nde I (1904)
Hinc II (2021)
Hind II (2021)
Bgl II (2124)
Nco I (2132)
Hind III (2317)
Msc I (2343)
Bcl I (2597)
Bst XI (2862)
Eag I (2867))
Spe I (2875)
BamH I (2881)
Sac I (2891)
Pac I (2900)
Hpa I (3030)
Hinc II (3030)
Hind II (3030)
Msc I (3176)
Xma I (3205)
Sma I (3207)
Kpn I (3281)
BamH I (3410)
Bcl I (3616)
Bgl I (4050)
Pae R7I (4212)
Xho I (4212)
Xba I (4474)
Sfu I (5061)
Pae R7I (5666)
Xho I (5666)
Eco RV (5777)
Pvu II (5985)
Bgl I (7174)
Sca I (7534)
Aat II (7976)

FIG. 12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SacI
CaMV35S-Pro
Pstl
SARS-CoV S1
HindIII
pCV12
11.3 kb
NPTII(Kan$^R$)
GFP
NOS-ter
Apal
RB

Figure 13-A

```
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cagtaa                                                            666
```

Figure 13-B

```
  1 MADNGTITVE ELKQLLEQWN LVIGFLFLAW IMLLQFAYSN RNRFLYIIKL VFLWLLWPVT
 61 LACFVLAAVY RINWVTGGIA IAMACIVGLM WLSYFVASFR LFARTRSMWS FNPETNILLN
121 VPLRGTIVTR PLMESELVIG AVIIRGHLRM AGHSLGRCDI KDLPKEITVA TSRTLSYYKL
181 GASQRVGTDS GFAAYNRYRI GNYKLNTDHA GSNDNIALLV Q
```

Figure 14-A

```
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aagttgcctc ttggtattaa cattacaaat tttagagcca ttcttacagc cttttcacct 720
gctcaagaca tttggggcac gtcagctgca gcctattttg ttggctattt aaagccaact 780
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cagacctcta atttcagggt tgttccctca ggagatgttg tgagattccc taatattaca 960
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Figure 14-B

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ggcagacttc aaagccttca aacctatgta acacaacaac taatcagggc tgctgaaatc 3000
agggcttctg ctaatcttgc tgctactaaa atgtctgagt gtgttcttgg acaatcaaaa 3060
agagttgact tttgtggaaa gggctaccac cttatgtcct tcccacaagc agccccgcat 3120
ggtgttgtct tcctacatgt cacgtatgtg ccatcccagg agaggaactt caccacagcg 3180
ccagcaattt gtcatgaagg caaagcatac ttccctcgtg aaggtgtttt tgtgtttaat 3240
ggcacttctt ggtttattac acagaggaac ttcttttctc cacaaataat tactacagac 3300
aatacatttg tctcaggaaa ttgtgatgtc gttattggca tcattaacaa cacagtttat 3360
gatcctctgc aacctgagct tgactcattc aaagaagagc tggacaagta cttcaaaaat 3420
catacatcac cagatgttga tcttggcgac atttcaggca ttaacgcttc tgtcgtcaac 3480
attcaaaaag aaattgaccg cctcaatgag gtcgctaaaa atttaaatga atcactcatt 3540
gaccttcaag aattgggaaa atatgagcaa tatattaaat ggccttggta tgtttggctc 3600
ggcttcattg ctggactaat tgccatcgtc atggttacaa tcttgctttg ttgcatgact 3660
agttgttgca gttgcctcaa gggtgcatgc tcttgtggtt cttgctgcaa gtttgatgag 3720
gatgactctg agccagttct caagggtgtc aaattacatt acacataa             3768
```

Figure 15

```
   1 MFIFLLFLTL TSGSDLDRCT TFDDVQAPNY TQHTSSMRGV YYPDEIFRSD TLYLTQDLFL
  61 PFYSNVTGFH TINHTFGNPV IPFKDGIYFA ATEKSNVVRG WVFGSTMNNK SQSVIIINNS
 121 TNVVIRACNF ELCDNPFFAV SKPMGTQTHT MIFDNAFNCT FEYISDAFSL DVSEKSGNFK
 181 HLREFVFKNK DGFLYVYKGY QPIDVVRDLP SGFNTLKPIF KLPLGINITN FRAILTAFSP
 241 AQDIWGTSAA AYFVGYLKPT TFMLKYDENG TITDAVDCSQ NPLAELKCSV KSFEIDKGIY
 301 QTSNFRVVPS GDVVRFPNIT NLCPFGEVFN ATKFPSVYAW ERKKISNCVA DYSVLYNSTF
 361 FSTFKCYGVS ATKLNDLCFS NVYADSFVVK GDDVRQIAPG QTGVIADYNY KLPDDFMGCV
 421 LAWNTRNIDA TSTGNYNYKY RYLRHGKLRP FERDISNVPF SPDGKPCTPP ALNCYWPLND
 481 YGFYTTTGIG YQPYRVVVLS FELLNAPATV CGPKLSTDLI KNQCVNFNFN GLTGTGVLTP
 541 SSKRFQPFQQ FGRDVSDFTD SVRDPKTSEI LDISPCSFGG VSVITPGTNA SSEVAVLYQD
 601 VNCTDVSTAI HADQLTPAWR IYSTGNNVFQ TQAGCLIGAE HVDTSYECDI PIGAGICASY
 661 HTVSLLRSTS QKSIVAYTMS LGADSSIAYS NNTIAIPTNF SISITTEVMP VSMAKTSVDC
 721 NMYICGDSTE CANLLLQYGS FCTQLNRALS GIAAEQDRNT REVFAQVKQM YKTPTLKYFG
 781 GFNFSQILPD PLKPTKRSFI EDLLFNKVTL ADAGFMKQYG ECLGDINARD LICAQKFNGL
 841 TVLPPLLTDD MIAAYTAALV SGTATAGWTF GAGAALQIPF AMQMAYRFNG IGVTQNVLYE
 901 NQKQIANQFN KAISQIQESL TTTSTALGKL QDVVNQNAQA LNTLVKQLSS NFGAISSVLN
 961 DILSRLDKVE AEVQIDRLIT GRLQSLQTYV TQQLIRAAEI RASANLAATK MSECVLGQSK
1021 RVDFCGKGYH LMSFPQAAPH GVVFLHVTYV PSQERNFTTA PAICHEGKAY FPREGVFVFN
1081 GTSWFITQRN FFSPQIITTD NTFVSGNCDV VIGIINNTVY DPLQPELDSF KEELDKYFKN
1141 HTSPDVDLGD ISGINASVVN IQKEIDRLNE VAKNLNESLI DLQELGKYEQ YIKWPWYVWL
1201 GFIAGLIAIV MVTILLCCMT SCCSCLKGAC SCGSCCKFDE DDSEPVLKGV KLHYT
```

Figure 16-A

```
  1 - ATATTAGGTTTTACCTACCCAGGAAAAGCCAACCAACCTCGATCTCTTGTAGATCTGTT - 60
    - I  L  G  F  Y  L  P  R  K  S  Q  P  T  S  I  S  C  R  S  V
    -  Y  *  V  F  T  Y  P  G  K  A  N  Q  P  R  S  L  V  D  L  F
    -   I  R  F  L  P  T  Q  E  K  P  T  N  L  D  L  L  *  I  C  S
 61 - CTCTAAACGAACTTTAAAATCTGTGTAGCTGTCGCTCGGCTGCATGCCTAGTGCACCTAC - 120
    - L  *  T  N  F  K  I  C  V  A  V  A  R  L  H  A  *  C  T  Y
    -  S  K  R  T  L  K  S  V  *  L  S  L  G  C  M  P  S  A  P  T
    -   L  N  E  L  *  N  L  C  S  C  R  S  A  A  C  L  V  H  L  R
121 - GCAGTATAAACAATAATAAATTTTACTGTCGTTGACAAGAAACGAGTAACTCGTCCCTCT - 180
    - A  V  *  T  I  I  N  F  T  V  V  D  K  K  R  V  T  R  P  S
    -  Q  Y  K  Q  *  *  I  L  L  S  L  T  R  N  E  *  L  V  P  L
    -   S  I  N  N  N  K  F  Y  C  R  *  Q  E  T  S  N  S  S  L  F
181 - TCTGCAGACTGCTTACGGTTTCGTCCGTGTTGCAGTCGATCATCAGCATACCTAGGTTTC - 240
    - S  A  D  C  L  R  F  R  P  C  C  S  R  S  S  A  Y  L  G  F
    -  L  Q  T  A  Y  G  F  V  R  V  A  V  D  H  Q  H  T  *  V  S
    -   C  R  L  L  T  V  S  S  V  L  Q  S  I  I  S  I  P  R  F  R
241 - GTCCGGGTGTGACCGAAAGGTAAGATGGAGAGCCTTGTTCTTGGTGTCAACGAGAAAACA - 300
    - V  R  V  *  P  K  G  K  M  E  S  L  V  L  G  V  N  E  K  T
    -  S  G  C  D  R  K  V  R  W  R  A  L  F  L  V  S  T  R  K  H
    -   P  G  V  T  E  R  *  D  G  E  P  C  S  W  C  Q  R  E  N  T
301 - CACGTCCAACTCAGTTTGCCTGTCCTTCAGGTTAGAGACGTGCTAGTGCGTGGCTTCGGG - 360
    - H  V  Q  L  S  L  P  V  L  Q  V  R  D  V  L  V  R  G  F  G
    -  T  S  N  S  V  C  L  S  F  R  L  E  T  C  *  C  V  A  S  G
    -   R  P  T  Q  F  A  C  P  S  G  *  R  R  A  S  A  W  L  R  G
361 - GACTCTGTGGAAGAGGCCCTATCGGAGGCACGTGAACACCTCAAAAATGGCACTTGTGGT - 420
    - D  S  V  E  E  A  L  S  E  A  R  E  H  L  K  N  G  T  C  G
    -  T  L  W  K  R  P  Y  R  R  H  V  N  T  S  K  M  A  L  V  V
    -   L  C  G  R  G  P  I  G  G  T  *  T  P  Q  K  W  H  L  W  S
421 - CTAGTAGAGCTGGAAAAAGGCGTACTGCCCCAGCTTGAACAGCCCTATGTGTTCATTAAA - 480
    - L  V  E  L  E  K  G  V  L  P  Q  L  E  Q  P  Y  V  F  I  K
    -  *  *  S  W  K  K  A  Y  C  P  S  L  N  S  P  M  C  S  L  N
    -   S  R  A  G  K  R  R  T  A  P  A  *  T  A  L  C  V  H  *  T
481 - CGTTCTGATGCCTTAAGCACCAATCACGGCCACAAGGTCGTTGAGCTGGTTGCAGAAATG - 540
    - R  S  D  A  L  S  T  N  H  G  H  K  V  V  E  L  V  A  E  M
    -  V  L  M  P  *  A  P  I  T  A  T  R  S  L  S  W  L  Q  K  W
    -   F  *  C  L  K  H  Q  S  R  P  Q  G  R  *  A  G  C  R  N  G
541 - GACGGCATTCAGTACGGTCGTAGCGGTATAACACTGGGAGTACTCGTGCCACATGTGGGC - 600
    - D  G  I  Q  Y  G  R  S  G  I  T  L  G  V  L  V  P  H  V  G
    -  T  A  F  S  T  V  V  A  V  *  H  W  E  Y  S  C  H  M  W  A
    -   R  H  S  V  R  S  *  R  Y  N  T  G  S  T  R  A  T  C  G  R
601 - GAAACCCCAATTGCATACCGCAATGTTCTTCTTCGTAAGAACGGTAATAAGGGAGCCGGT - 660
    - E  T  P  I  A  Y  R  N  V  L  L  R  K  N  G  N  K  G  A  G
    -  K  P  Q  L  H  T  A  M  F  F  F  V  R  T  V  I  R  E  P  V
    -   N  P  N  C  I  P  Q  C  S  S  S  *  E  R  *  *  G  S  R  W
661 - GGTCATAGCTATGGCATCGATCTAAAGTCTTATGACTTAGGTGACGAGCTTGGCACTGAT - 720
    - G  H  S  Y  G  I  D  L  K  S  Y  D  L  G  D  E  L  G  T  D
    -  V  I  A  M  A  S  I  *  S  L  M  T  *  V  T  S  L  A  L  I
    -   S  *  L  W  H  R  S  K  V  L  *  L  R  *  R  A  W  H  *  S
```

Figure 16-B

```
 721 - CCCATTGAAGATTATGAACAAAACTGGAACACTAAGCATGGCAGTGGTGCACTCCGTGAA - 780
     - P  I  E  D  Y  E  Q  N  W  N  T  K  H  G  S  G  A  L  R  E
     -  P  L  K  I  M  N  K  T  G  T  L  S  M  A  V  V  H  S  V  N
     -   H  *  R  L  *  T  K  L  E  H  *  A  W  Q  W  C  T  P  *  T
 781 - CTCACTCGTGAGCTCAATGGAGGTGCAGTCACTCGCTATGTCGACAACAATTTCTGTGGC - 840
     - L  T  R  E  L  N  G  G  A  V  T  R  Y  V  D  N  N  F  C  G
     -  S  L  V  S  S  M  E  V  Q  S  L  A  M  S  T  T  I  S  V  A
     -   H  S  *  A  Q  W  R  C  S  H  S  L  C  R  Q  Q  F  L  W  P
 841 - CCAGATGGGTACCCTCTTGATTGCATCAAAGATTTTCTCGCACGCGCGGGCAAGTCAATG - 900
     - P  D  G  Y  P  L  D  C  I  K  D  F  L  A  R  A  G  K  S  M
     -  Q  M  G  T  L  L  I  A  S  K  I  F  S  H  A  R  A  S  Q  C
     -   R  W  V  P  S  *  L  H  Q  R  F  S  R  T  R  G  Q  V  N  V
 901 - TGCACTCTTTCCGAACAACTTGATTACATCGAGTCGAAGAGAGGTGTCTACTGCTGCCGT - 960
     - C  T  L  S  E  Q  L  D  Y  I  E  S  K  R  G  V  Y  C  C  R
     -  A  L  F  P  N  N  L  I  T  S  S  R  R  E  V  S  T  A  A  V
     -   H  S  F  R  T  T  *  L  H  R  V  E  E  R  C  L  L  L  P  *
 961 - GACCATGAGCATGAAATTGCCTGGTTCACTGAGCGCTCTGATAAGAGCTACGAGCACCAG - 1020
     - D  H  E  H  E  I  A  W  F  T  E  R  S  D  K  S  Y  E  H  Q
     -  T  M  S  M  K  L  P  G  S  L  S  A  L  I  R  A  T  S  T  R
     -   P  *  A  *  N  C  L  V  H  *  A  L  *  *  E  L  R  A  P  D
1021 - ACACCCTTCGAAATTAAGAGTGCCAAGAAATTTGACACTTTCAAAGGGGAATGCCCAAAG - 1080
     - T  P  F  E  I  K  S  A  K  K  F  D  T  F  K  G  E  C  P  K
     -  H  P  S  K  L  R  V  P  R  N  L  T  L  S  K  G  N  A  Q  S
     -   T  L  R  N  *  E  C  Q  E  I  *  H  F  Q  R  G  M  P  K  V
1081 - TTTGTGTTTCCTCTTAACTCAAAAGTCAAAGTCATTCAACCACGTGTTGAAAAGAAAAAG - 1140
     - F  V  F  P  L  N  S  K  V  K  V  I  Q  P  R  V  E  K  K  K
     -  L  C  F  L  L  T  Q  K  S  K  S  F  N  H  V  L  K  R  K  R
     -   C  V  S  S  *  L  K  S  Q  S  H  S  T  T  C  *  K  E  K  D
1141 - ACTGAGGGTTTCATGGGGCGTATACGCTCTGTGTACCCTGTTGCATCTCCACAGGAGTGT - 1200
     - T  E  G  F  M  G  R  I  R  S  V  Y  P  V  A  S  P  Q  E  C
     -  L  R  V  S  W  G  V  Y  A  L  C  T  L  L  H  L  H  R  S  V
     -   *  G  F  H  G  A  Y  T  L  C  V  P  C  C  I  S  T  G  V  *
1201 - AACAATATGCACTTGTCTACCTTGATGAAATGTAATCATTGCGATGAAGTTTCATGGCAG - 1260
     - N  N  M  H  L  S  T  L  M  K  C  N  H  C  D  E  V  S  W  Q
     -  T  I  C  T  C  L  P  *  *  N  V  I  I  A  M  K  F  H  G  R
     -   Q  Y  A  L  V  Y  L  D  E  M  *  S  L  R  *  S  F  M  A  D
1261 - ACGTGCGACTTTCTGAAAGCCACTTGTGAACATTGTGGCACTGAAAATTTAGTTATTGAA - 1320
     - T  C  D  F  L  K  A  T  C  E  H  C  G  T  E  N  L  V  I  E
     -  R  A  T  F  *  K  P  L  V  N  I  V  A  L  K  I  *  L  L  K
     -   V  R  L  S  E  S  H  L  *  T  L  W  H  *  K  F  S  Y  *  R
1321 - GGACCTACTACATGTGGGTACCTACCTACTAATGCTGTAGTGAAAATGCCATGTCCTGCC - 1380
     - G  P  T  T  C  G  Y  L  P  T  N  A  V  V  K  M  P  C  P  A
     -  D  L  L  H  V  G  T  Y  L  L  M  L  *  *  K  C  H  V  L  P
     -   T  Y  Y  M  W  V  P  T  Y  *  C  C  S  E  N  A  M  S  C  L
1381 - TGTCAAGACCCAGAGATTGGACCTGAGCATAGTGTTGCAGATTATCACAACCACTCAAAC - 1440
     - C  Q  D  P  E  I  G  P  E  H  S  V  A  D  Y  H  N  H  S  N
     -  V  K  T  Q  R  L  D  L  S  I  V  L  Q  I  I  T  T  T  Q  T
     -   S  R  P  R  D  W  T  *  A  *  C  C  R  L  S  Q  P  L  K  H
1441 - ATTGAAACTCGACTCCGCAAGGGAGGTAGGACTAGATGTTTTGGAGGCTGTGTGTTTGCC - 1500
     - I  E  T  R  L  R  K  G  G  R  T  R  C  F  G  G  C  V  F  A
     -  L  K  L  D  S  A  R  E  V  G  L  D  V  L  E  A  V  C  L  P
     -   *  N  S  T  P  Q  G  R  *  D  *  M  F  W  R  L  C  V  C  L
```

Figure 16-C

```
1501 - TATGTTGGCTGCTATAATAAGCGTGCCTACTGGGTTCCTCGTGCTAGTGCTGATATTGGC - 1560
     - Y  V  G  C  Y  N  K  R  A  Y  W  V  P  R  A  S  A  D  I  G
     -  M  L  A  A  I  I  S  V  P  T  G  F  L  V  L  V  L  I  L  A
     -   C  W  L  L  *  *  A  C  L  L  G  S  S  C  *  C  *  Y  W  L
1561 - TCAGGCCATACTGGCATTACTGGTGACAATGTGGAGACCTTGAATGAGGATCTCCTTGAG - 1620
     - S  G  H  T  G  I  T  G  D  N  V  E  T  L  N  E  D  L  L  E
     -  Q  A  I  L  A  L  L  V  T  M  W  R  P  *  M  R  I  S  L  R
     -   R  P  Y  W  H  Y  W  *  Q  C  G  D  L  E  *  G  S  P  *  D
1621 - ATACTGAGTCGTGAACGTGTTAACATTAACATTGTTGGCGATTTTCATTTGAATGAAGAG - 1680
     - I  L  S  R  E  R  V  N  I  N  I  V  G  D  F  H  L  N  E  E
     -  Y  *  V  V  N  V  L  T  L  T  L  L  A  I  F  I  *  M  K  R
     -   T  E  S  *  T  C  *  H  *  H  C  W  R  F  S  F  E  *  R  G
1681 - GTTGCCATCATTTTGGCATCTTTCTCTGCTTCTACAAGTGCCTTTATTGACACTATAAAG - 1740
     - V  A  I  I  L  A  S  F  S  A  S  T  S  A  F  I  D  T  I  K
     -  L  P  S  F  W  H  L  S  L  L  L  Q  V  P  L  L  T  L  *  R
     -   C  H  H  F  G  I  F  L  C  F  Y  K  C  L  Y  *  H  Y  K  E
1741 - AGTCTTGATTACAAGTCTTTCAAAACCATTGTTGAGTCCTGCGGTAACTATAAAGTTACC - 1800
     - S  L  D  Y  K  S  F  K  T  I  V  E  S  C  G  N  Y  K  V  T
     -  V  L  I  T  S  L  S  K  P  L  L  S  P  A  V  T  I  K  L  P
     -   S  *  L  Q  V  F  Q  N  H  C  *  V  L  R  *  L  *  S  Y  Q
1801 - AAGGGAAAGCCCGTAAAAGGTGCTTGGAACATTGGACAACAGAGATCAGTTTTAACACCA - 1860
     - K  G  K  P  V  K  G  A  W  N  I  G  Q  Q  R  S  V  L  T  P
     -  R  E  S  P  *  K  V  L  G  T  L  D  N  R  D  Q  F  *  H  H
     -   G  K  A  R  K  R  C  L  E  H  W  T  T  E  I  S  F  N  T  T
1861 - CTGTGTGGTTTTCCCTCACAGGCTGCTGGTGTTATCAGATCAATTTTTGCGCGCACACTT - 1920
     - L  C  G  F  P  S  Q  A  A  G  V  I  R  S  I  F  A  R  T  L
     -  C  V  V  F  P  H  R  L  L  V  L  S  D  Q  F  L  R  A  H  L
     -   V  W  F  S  L  T  G  C  W  C  Y  Q  I  N  F  C  A  H  T  *
1921 - GATGCAGCAAACCACTCAATTCCTGATTTGCAAAGAGCAGCTGTCACCATACTTGATGGT - 1980
     - D  A  A  N  H  S  I  P  D  L  Q  R  A  A  V  T  I  L  D  G
     -  M  Q  Q  T  T  Q  F  L  I  C  K  E  Q  L  S  P  Y  L  M  V
     -   C  S  K  P  L  N  S  *  F  A  K  S  S  C  H  H  T  *  W  Y
1981 - ATTTCTGAACAGTCATTACGTCTTGTCGACGCCATGGTTTATACTTCAGACCTGCTCACC - 2040
     - I  S  E  Q  S  L  R  L  V  D  A  M  V  Y  T  S  D  L  L  T
     -  F  L  N  S  H  Y  V  L  S  T  P  W  F  I  L  Q  T  C  S  P
     -   F  *  T  V  I  T  S  C  R  R  H  G  L  Y  F  R  P  A  H  Q
2041 - AACAGTGTCATTATTATGGCATATGTAACTGGTGGTCTTGTACAACAGACTTCTCAGTGG - 2100
     - N  S  V  I  I  M  A  Y  V  T  G  G  L  V  Q  Q  T  S  Q  W
     -  T  V  S  L  L  W  H  M  *  L  V  V  L  Y  N  R  L  L  S  G
     -   Q  C  H  Y  Y  G  I  C  N  W  W  S  C  T  T  D  F  S  V  V
2101 - TTGTCTAATCTTTTGGGCACTACTGTTGAAAAACTCAGGCCTATCTTTGAATGGATTGAG - 2160
     - L  S  N  L  L  G  T  T  V  E  K  L  R  P  I  F  E  W  I  E
     -  C  L  I  F  W  A  L  L  L  K  N  S  G  L  S  L  N  G  L  R
     -   V  *  S  F  G  H  Y  C  *  K  T  Q  A  Y  L  *  M  D  *  G
2161 - GCGAAACTTAGTGCAGGAGTTGAATTTCTCAAGGATGCTTGGGAGATTCTCAAATTTCTC - 2220
     - A  K  L  S  A  G  V  E  F  L  K  D  A  W  E  I  L  K  F  L
     -  R  N  L  V  Q  E  L  N  F  S  R  M  L  G  R  F  S  N  F  S
     -   E  T  *  C  R  S  *  I  S  Q  G  C  L  G  D  S  Q  I  S  H
2221 - ATTACAGGTGTTTTTGACATCGTCAAGGGTCAAATACAGGTTGCTTCAGATAACATCAAG - 2280
     - I  T  G  V  F  D  I  V  K  G  Q  I  Q  V  A  S  D  N  I  K
     -  L  Q  V  F  L  T  S  S  R  V  K  Y  R  L  L  Q  I  T  S  R
     -   Y  R  C  F  *  H  R  Q  G  S  N  T  G  C  F  R  *  H  Q  G
```

Figure 16-D

```
2281 - GATTGTGTAAAATGCTTCATTGATGTTGTTAACAAGGCACTCGAAATGTGCATTGATCAA - 2340
     - D  C  V  K  C  F  I  D  V  V  N  K  A  L  E  M  C  I  D  Q
     -  I  V  *  N  A  S  L  M  L  L  T  R  H  S  K  C  A  L  I  K
     -   L  C  K  M  L  H  *  C  C  *  Q  G  T  R  N  V  H  *  S  S
2341 - GTCACTATCGCTGGCGCAAAGTTGCGATCACTCAACTTAGGTGAAGTCTTCATCGCTCAA - 2400
     - V  T  I  A  G  A  K  L  R  S  L  N  L  G  E  V  F  I  A  Q
     -  S  L  S  L  A  Q  S  C  D  H  S  T  *  V  K  S  S  S  L  K
     -   H  Y  R  W  R  K  V  A  I  T  Q  L  R  *  S  L  H  R  S  K
2401 - AGCAAGGGACTTTACCGTCAGTGTATACGTGGCAAGGAGCAGCTGCAACTACTCATGCCT - 2460
     - S  K  G  L  Y  R  Q  C  I  R  G  K  E  Q  L  Q  L  L  M  P
     -  A  R  D  F  T  V  S  V  Y  V  A  R  S  S  C  N  Y  S  C  L
     -   Q  G  T  L  P  S  V  Y  T  W  Q  G  A  A  A  T  T  H  A  S
2461 - CTTAAGGCACCAAAAGAAGTAACCTTTCTTGAAGGTGATTCACATGACACAGTACTTACC - 2520
     - L  K  A  P  K  E  V  T  F  L  E  G  D  S  H  D  T  V  L  T
     -  L  R  H  Q  K  K  *  P  F  L  K  V  I  H  M  T  Q  Y  L  P
     -   *  G  T  K  R  S  N  L  S  *  R  *  F  T  *  H  S  T  Y  L
2521 - TCTGAGGAGGTTGTTCTCAAGAACGGTGAACTCGAAGCACTCGAGACGCCCGTTGATAGC - 2580
     - S  E  E  V  V  L  K  N  G  E  L  E  A  L  E  T  P  V  D  S
     -  L  R  R  L  F  S  R  T  V  N  S  K  H  S  R  R  P  L  I  A
     -   *  G  G  C  S  Q  E  R  *  T  R  S  T  R  D  A  R  *  *  L
2581 - TTCACAAATGGAGCTATCGTCGGCACACCAGTCTGTGTAAATGGCCTCATGCTCTTAGAG - 2640
     - F  T  N  G  A  I  V  G  T  P  V  C  V  N  G  L  M  L  L  E
     -  S  Q  M  E  L  S  S  A  H  Q  S  V  *  M  A  S  C  S  *  R
     -   H  K  W  S  Y  R  R  H  T  S  L  C  K  W  P  H  A  L  R  D
2641 - ATTAAGGACAAAGAACAATACTGCGCATTGTCTCCTGGTTTACTGGCTACAAACAATGTC - 2700
     - I  K  D  K  E  Q  Y  C  A  L  S  P  G  L  L  A  T  N  N  V
     -  L  R  T  K  N  N  T  A  H  C  L  L  V  Y  W  L  Q  T  M  S
     -   *  G  Q  R  T  I  L  R  I  V  S  W  F  T  G  Y  K  Q  C  L
2701 - TTTCGCTTAAAAGGGGGTGCACCAATTAAAGGTGTAACCTTTGGAGAAGATACTGTTTGG - 2760
     - F  R  L  K  G  G  A  P  I  K  G  V  T  F  G  E  D  T  V  W
     -  F  A  *  K  G  V  H  Q  L  K  V  *  P  L  E  K  I  L  F  G
     -   S  L  K  R  G  C  T  N  *  R  C  N  L  W  R  R  Y  C  L  G
2761 - GAAGTTCAAGGTTACAAGAATGTGAGAATCACATTTGAGCTTGATGAACGTGTTGACAAA - 2820
     - E  V  Q  G  Y  K  N  V  R  I  T  F  E  L  D  E  R  V  D  K
     -  K  F  K  V  T  R  M  *  E  S  H  L  S  L  M  N  V  L  T  K
     -   S  S  R  L  Q  E  C  E  N  H  I  *  A  *  *  T  C  *  Q  S
2821 - GTGCTTAATGAAAAGTGCTCTGTCTACACTGTTGAATCCGGTACCGAAGTTACTGAGTTT - 2880
     - V  L  N  E  K  C  S  V  Y  T  V  E  S  G  T  E  V  T  E  F
     -  C  L  M  K  S  A  L  S  T  L  L  N  P  V  P  K  L  L  S  L
     -   A  *  *  K  V  L  C  L  H  C  *  I  R  Y  R  S  Y  *  V  C
2881 - GCATGTGTTGTAGCAGAGGCTGTTGTGAAGACTTTACAACCAGTTTCTGATCTCCTTACC - 2940
     - A  C  V  V  A  E  A  V  V  K  T  L  Q  P  V  S  D  L  L  T
     -  H  V  L  *  Q  R  L  L  *  R  L  Y  N  Q  F  L  I  S  L  P
     -   M  C  C  S  R  G  C  C  E  D  F  T  T  S  F  *  S  P  Y  Q
2941 - AACATGGGTATTGATCTTGATGAGTGGAGTGTAGCTACATTCTACTTATTTGATGATGCT - 3000
     - N  M  G  I  D  L  D  E  W  S  V  A  T  F  Y  L  F  D  D  A
     -  T  W  V  L  I  L  M  S  G  V  *  L  H  S  T  Y  L  M  M  L
     -   H  G  Y  *  S  *  *  V  E  C  S  Y  I  L  L  I  *  *  C  W
3001 - GGTGAAGAAAACTTTTCATCACGTATGTATTGTTCCTTTTACCCTCCAGATGAGGAAGAA - 3060
     - G  E  E  N  F  S  S  R  M  Y  C  S  F  Y  P  P  D  E  E  E
     -  V  K  K  T  F  H  H  V  C  I  V  P  F  T  L  Q  M  R  K  K
     -   *  R  K  L  F  I  T  Y  V  L  F  L  L  P  S  R  *  G  R  R
```

Figure 16-E

```
3061 - GAGGACGATGCAGAGTGTGAGGAAGAAGAAATTGATGAAACCTGTGAACATGAGTACGGT - 3120
     - E  D  D  A  E  C  E  E  E  E  I  D  E  T  C  E  H  E  Y  G
     -  R  T  M  Q  S  V  R  K  K  K  L  M  K  P  V  N  M  S  T  V
     -   G  R  C  R  V  *  G  R  R  N  *  *  N  L  *  T  *  V  R  Y
3121 - ACAGAGGATGATTATCAAGGTCTCCCTCTGGAATTTGGTGCCTCAGCTGAAACAGTTCGA - 3180
     - T  E  D  D  Y  Q  G  L  P  L  E  F  G  A  S  A  E  T  V  R
     -  Q  R  M  I  I  K  V  S  L  W  N  L  V  P  Q  L  K  Q  F  E
     -   R  G  *  L  S  R  S  P  S  G  I  W  C  L  S  *  N  S  S  S
3181 - GTTGAGGAAGAAGAAGAGGAAGACTGGCTGGATGATACTACTGAGCAATCAGAGATTGAG - 3240
     - V  E  E  E  E  E  E  D  W  L  D  D  T  T  E  Q  S  E  I  E
     -  L  R  K  K  K  R  K  T  G  W  M  I  L  L  S  N  Q  R  L  S
     -   *  G  R  R  R  G  R  L  A  G  *  Y  Y  *  A  I  R  D  *  A
3241 - CCAGAACCAGAACCTACACCTGAAGAACCAGTTAATCAGTTTACTGGTTATTTAAAACTT - 3300
     - P  E  P  E  P  T  P  E  E  P  V  N  Q  F  T  G  Y  L  K  L
     -  Q  N  Q  N  L  H  L  K  N  Q  L  I  S  L  L  V  I  *  N  L
     -   R  T  R  T  Y  T  *  R  T  S  *  S  V  Y  W  L  F  K  T  Y
3301 - ACTGACAATGTTGCCATTAAATGTGTTGACATCGTTAAGGAGGCACAAAGTGCTAATCCT - 3360
     - T  D  N  V  A  I  K  C  V  D  I  V  K  E  A  Q  S  A  N  P
     -  L  T  M  L  P  L  N  V  L  T  S  L  R  R  H  K  V  L  I  L
     -   *  Q  C  C  H  *  M  C  *  H  R  *  G  G  T  K  C  *  S  Y
3361 - ATGGTGATTGTAAATGCTGCTAACATACACCTGAAACATGGTGGTGGTGTAGCAGGTGCA - 3420
     - M  V  I  V  N  A  A  N  I  H  L  K  H  G  G  G  V  A  G  A
     -  W  *  L  *  M  L  L  T  Y  T  *  N  M  V  V  V  *  Q  V  H
     -   G  D  C  K  C  C  *  H  T  P  E  T  W  W  W  C  S  R  C  T
3421 - CTCAACAAGGCAACCAATGGTGCCATGCAAAAGGAGAGTGATGATTACATTAAGCTAAAT - 3480
     - L  N  K  A  T  N  G  A  M  Q  K  E  S  D  D  Y  I  K  L  N
     -  S  T  R  Q  P  M  V  P  C  K  R  R  V  M  I  T  L  S  *  M
     -   Q  Q  G  N  Q  W  C  H  A  K  G  E  *  *  L  H  *  A  K  W
3481 - GGCCCTCTTACAGTAGGAGGGTCTTGTTTGCTTTCTGGACATAATCTTGCTAAGAAGTGT - 3540
     - G  P  L  T  V  G  G  S  C  L  L  S  G  H  N  L  A  K  K  C
     -  A  L  L  Q  *  E  G  L  V  C  F  L  D  I  I  L  L  R  S  V
     -   P  S  Y  S  R  R  V  L  F  A  F  W  T  *  S  C  *  E  V  S
3541 - CTGCATGTTGTTGGACCTAACCTAAATGCAGGTGAGGACATCCAGCTTCTTAAGGCAGCA - 3600
     - L  H  V  V  G  P  N  L  N  A  G  E  D  I  Q  L  L  K  A  A
     -  C  M  L  L  D  L  T  *  M  Q  V  R  T  S  S  F  L  R  Q  H
     -   A  C  C  W  T  *  P  K  C  R  *  G  H  P  A  S  *  G  S  I
3601 - TATGAAAATTTCAATTCACAGGACATCTTACTTGCACCATTGTTGTCAGCAGGCATATTT - 3660
     - Y  E  N  F  N  S  Q  D  I  L  L  A  P  L  L  S  A  G  I  F
     -  M  K  I  S  I  H  R  T  S  Y  L  H  H  C  C  Q  Q  A  Y  L
     -   *  K  F  Q  F  T  G  H  L  T  C  T  I  V  V  S  R  H  I  W
3661 - GGTGCTAAACCACTTCAGTCTTTACAAGTGTGCGTGCAGACGGTTCGTACACAGGTTTAT - 3720
     - G  A  K  P  L  Q  S  L  Q  V  C  V  Q  T  V  R  T  Q  V  Y
     -  V  L  N  H  F  S  L  Y  K  C  A  C  R  R  F  V  H  R  F  I
     -   C  *  T  T  S  V  F  T  S  V  R  A  D  G  S  Y  T  G  L  Y
3721 - ATTGCAGTCAATGACAAAGCTCTTTATGAGCAGGTTGTCATGGATTATCTTGATAACCTG - 3780
     - I  A  V  N  D  K  A  L  Y  E  Q  V  V  M  D  Y  L  D  N  L
     -  L  Q  S  M  T  K  L  F  M  S  R  L  S  W  I  I  L  I  T  *
     -   C  S  Q  *  Q  S  S  L  *  A  G  C  H  G  L  S  *  *  P  E
3781 - AAGCCTAGAGTGGAAGCACCTAAACAAGAGGAGCCACCAAACACAGAAGATTCCAAAACT - 3840
     - K  P  R  V  E  A  P  K  Q  E  E  P  P  N  T  E  D  S  K  T
     -  S  L  E  W  K  H  L  N  K  R  S  H  Q  T  Q  K  I  P  K  L
     -   A  *  S  G  S  T  *  T  R  G  A  T  K  H  R  R  F  Q  N  *
```

Figure 16-F

```
3841 - GAGGAGAAATCTGTCGTACAGAAGCCTGTCGATGTGAAGCCAAAAATTAAGGCCTGCATT - 3900
     - E  E  K  S  V  V  Q  K  P  V  D  V  K  P  K  I  K  A  C  I
     -  R  R  N  L  S  Y  R  S  L  S  M  *  S  Q  K  L  R  P  A  L
     -   G  E  I  C  R  T  E  A  C  R  C  E  A  K  N  *  G  L  H  *
3901 - GATGAGGTTACCACAACACTGGAAGAAACTAAGTTTCTTACCAATAAGTTACTCTTGTTT - 3960
     - D  E  V  T  T  T  L  E  E  T  K  F  L  T  N  K  L  L  L  F
     -  M  R  L  P  Q  H  W  K  K  L  S  F  L  P  I  S  Y  S  C  L
     -   *  G  Y  H  N  T  G  R  N  *  V  S  Y  Q  *  V  T  L  V  C
3961 - GCTGATATCAATGGTAAGCTTTACCATGATTCTCAGAACATGCTTAGAGGTGAAGATATG - 4020
     - A  D  I  N  G  K  L  Y  H  D  S  Q  N  M  L  R  G  E  D  M
     -  L  I  S  M  V  S  F  T  M  I  L  R  T  C  L  E  V  K  I  C
     -   *  Y  Q  W  *  A  L  P  *  F  S  E  H  A  *  R  *  R  Y  V
4021 - TCTTTCCTTGAGAAGGATGCACCTTACATGGTAGGTGATGTTATCACTAGTGGTGATATC - 4080
     - S  F  L  E  K  D  A  P  Y  M  V  G  D  V  I  T  S  G  D  I
     -  L  S  L  R  R  M  H  L  T  W  *  V  M  L  S  L  V  V  I  S
     -   F  P  *  E  G  C  T  L  H  G  R  *  C  Y  H  *  W  *  Y  H
4081 - ACTTGTGTTGTAATACCCTCCAAAAAGGCTGGTGGCACTACTGAGATGCTCTCAAGAGCT - 4140
     - T  C  V  V  I  P  S  K  K  A  G  G  T  T  E  M  L  S  R  A
     -  L  V  L  *  Y  P  P  K  R  L  V  A  L  L  R  C  S  Q  E  L
     -   L  C  C  N  T  L  Q  K  G  W  W  H  Y  *  D  A  L  K  S  F
4141 - TTGAAGAAAGTGCCAGTTGATGAGTATATAACCACGTACCCTGGACAAGGATGTGCTGGT - 4200
     - L  K  K  V  P  V  D  E  Y  I  T  T  Y  P  G  Q  G  C  A  G
     -  *  R  K  C  Q  L  M  S  I  *  P  R  T  L  D  K  D  V  L  V
     -   E  E  S  A  S  *  *  V  Y  N  H  V  P  W  T  R  M  C  W  L
4201 - TATACACTTGAGGAAGCTAAGACTGCTCTTAAGAAATGCAAATCTGCATTTTATGTACTA - 4260
     - Y  T  L  E  E  A  K  T  A  L  K  K  C  K  S  A  F  Y  V  L
     -  I  H  L  R  K  L  R  L  L  L  R  N  A  N  L  H  F  M  Y  Y
     -   Y  T  *  G  S  *  D  C  S  *  E  M  Q  I  C  I  L  C  T  T
4261 - CCTTCAGAAGCACCTAATGCTAAGGAAGAGATTCTAGGAACTGTATCCTGGAATTTGAGA - 4320
     - P  S  E  A  P  N  A  K  E  E  I  L  G  T  V  S  W  N  L  R
     -  L  Q  K  H  L  M  L  R  K  R  F  *  E  L  Y  P  G  I  *  E
     -   F  R  S  T  *  C  *  G  R  D  S  R  N  C  I  L  E  F  E  R
4321 - GAAATGCTTGCTCATGCTGAAGAGACAAGAAAATTAATGCCTATATGCATGGATGTTAGA - 4380
     - E  M  L  A  H  A  E  E  T  R  K  L  M  P  I  C  M  D  V  R
     -  K  C  L  L  M  L  K  R  Q  E  N  *  C  L  Y  A  W  M  L  E
     -   N  A  C  S  C  *  R  D  K  K  I  N  A  Y  M  H  G  C  *  S
4381 - GCCATAATGGCAACCATCCAACGTAAGTATAAAGGAATTAAAATTCAAGAGGGCATCGTT - 4440
     - A  I  M  A  T  I  Q  R  K  Y  K  G  I  K  I  Q  E  G  I  V
     -  P  *  W  Q  P  S  N  V  S  I  K  E  L  K  F  K  R  A  S  L
     -   H  N  G  N  H  P  T  *  V  *  R  N  *  N  S  R  G  H  R  *
4441 - GACTATGGTGTCCGATTCTTCTTTTATACTAGTAAAGAGCCTGTAGCTTCTATTATTACG - 4500
     - D  Y  G  V  R  F  F  F  Y  T  S  K  E  P  V  A  S  I  I  T
     -  T  M  V  S  D  S  S  F  I  L  V  K  S  L  *  L  L  L  L  R
     -   L  W  C  P  I  L  L  L  Y  *  *  R  A  C  S  F  Y  Y  Y  E
4501 - AAGCTGAACTCTCTAAATGAGCCGCTTGTCACAATGCCAATTGGTTATGTGACACATGGT - 4560
     - K  L  N  S  L  N  E  P  L  V  T  M  P  I  G  Y  V  T  H  G
     -  S  *  T  L  *  M  S  R  L  S  Q  C  Q  L  V  M  *  H  M  V
     -   A  E  L  S  K  *  A  A  C  H  N  A  N  W  L  C  D  T  W  F
```

Figure 16-G

```
4561 - TTTAATCTTGAAGAGGCTGCGCGCTGTATGCGTTCTCTTAAAGCTCCTGCCGTAGTGTCA - 4620
     -F  N  L  E  E  A  A  R  C  M  R  S  L  K  A  P  A  V  V  S
     - L  I  L  K  R  L  R  A  V  C  V  L  L  K  L  L  P  *  C  Q
     -  *  S  *  R  G  C  A  L  Y  A  F  S  *  S  S  C  R  S  V  S
4621 - GTATCATCACCAGATGCTGTTACTACATATAATGGATACCTCACTTCGTCATCAAAGACA - 4680
     -V  S  S  P  D  A  V  T  T  Y  N  G  Y  L  T  S  S  S  K  T
     - Y  H  H  Q  M  L  L  L  H  I  M  D  T  S  L  R  H  Q  R  H
     -  I  I  T  R  C  C  Y  Y  I  *  W  I  P  H  F  V  I  K  D  I
4681 - TCTGAGGAGCACTTTGTAGAAACAGTTTCTTTGGCTGGCTCTTACAGAGATTGGTCCTAT - 4740
     -S  E  E  H  F  V  E  T  V  S  L  A  G  S  Y  R  D  W  S  Y
     - L  R  S  T  L  *  K  Q  F  L  W  L  A  L  T  E  I  G  P  I
     -  *  G  A  L  C  R  N  S  F  F  G  W  L  L  Q  R  L  V  L  F
4741 - TCAGGACAGCGTACAGAGTTAGGTGTTGAATTTCTTAAGCGTGGTGACAAAATTGTGTAC - 4800
     -S  G  Q  R  T  E  L  G  V  E  F  L  K  R  G  D  K  I  V  Y
     - Q  D  S  V  Q  S  *  V  L  N  F  L  S  V  V  T  K  L  C  T
     -  R  T  A  Y  R  V  R  C  *  I  S  *  A  W  *  Q  N  C  V  P
4801 - CACACTCTGGAGAGCCCCGTCGAGTTTCATCTTGACGGTGAGGTTCTTTCACTTGACAAA - 4860
     -H  T  L  E  S  P  V  E  F  H  L  D  G  E  V  L  S  L  D  K
     - T  L  W  R  A  P  S  S  F  I  L  T  V  R  F  F  H  L  T  N
     -  H  S  G  E  P  R  R  V  S  S  *  R  *  G  S  F  T  *  Q  T
4861 - CTAAAGAGTCTCTTATCCCTGCGGGAGGTTAAGACTATAAAAGTGTTCACAACTGTGGAC - 4920
     -L  K  S  L  L  S  L  R  E  V  K  T  I  K  V  F  T  T  V  D
     - *  R  V  S  Y  P  C  G  R  L  R  L  *  K  C  S  Q  L  W  T
     -  K  E  S  L  I  P  A  G  G  *  D  Y  K  S  V  H  N  C  G  Q
4921 - AACACTAATCTCCACACACAGCTTGTGGATATGTCTATGACATATGGACAGCAGTTTGGT - 4980
     -N  T  N  L  H  T  Q  L  V  D  M  S  M  T  Y  G  Q  Q  F  G
     - T  L  I  S  T  H  S  L  W  I  C  L  *  H  M  D  S  S  L  V
     -  H  *  S  P  H  T  A  C  G  Y  V  Y  D  I  W  T  A  V  W  S
4981 - CCAACATACTTGGATGGTGCTGATGTTACAAAAATTAAACCTCATGTAAATCATGAGGGT - 5040
     -P  T  Y  L  D  G  A  D  V  T  K  I  K  P  H  V  N  H  E  G
     - Q  H  T  W  M  V  L  M  L  Q  K  L  N  L  M  *  I  M  R  V
     -  N  I  L  G  W  C  *  C  Y  K  N  *  T  S  C  K  S  *  G  *
5041 - AAGACTTTCTTTGTACTACCTAGTGATGACACACTACGTAGTGAAGCTTTCGAGTACTAC - 5100
     -K  T  F  F  V  L  P  S  D  D  T  L  R  S  E  A  F  E  Y  Y
     - R  L  S  L  Y  Y  L  V  M  T  H  Y  V  V  K  L  S  S  T  T
     -  D  F  L  C  T  T  *  *  *  H  T  T  *  *  S  F  R  V  L  P
5101 - CATACTCTTGATGAGAGTTTTCTTGGTAGGTACATGTCTGCTTTAAACCACACAAAGAAA - 5160
     -H  T  L  D  E  S  F  L  G  R  Y  M  S  A  L  N  H  T  K  K
     - I  L  L  M  R  V  F  L  V  G  T  C  L  L  *  T  T  Q  R  N
     -  Y  S  *  *  E  F  S  W  *  V  H  V  C  F  K  P  H  K  E  M
5161 - TGGAAATTTCCTCAAGTTGGTGGTTTAACTTCAATTAAATGGGCTGATAACAATTGTTAT - 5220
     -W  K  F  P  Q  V  G  G  L  T  S  I  K  W  A  D  N  N  C  Y
     - G  N  F  L  K  L  V  V  *  L  Q  L  N  G  L  I  T  I  V  I
     -  E  I  S  S  S  W  W  F  N  F  N  *  M  G  *  *  Q  L  L  F
5221 - TTGTCTAGTGTTTTATTAGCACTTCAACAGCTTGAAGTCAAATTCAATGCACCAGCACTT - 5280
     -L  S  S  V  L  L  A  L  Q  Q  L  E  V  K  F  N  A  P  A  L
     - C  L  V  F  Y  *  H  F  N  S  L  K  S  N  S  M  H  Q  H  F
     -  V  *  C  F  I  S  T  S  T  A  *  S  Q  I  Q  C  T  S  T  S
5281 - CAAGAGGCTTATTATAGAGCCCGTGCTGGTGATGCTGCTAACTTTTGTGCACTCATACTC - 5340
     -Q  E  A  Y  Y  R  A  R  A  G  D  A  A  N  F  C  A  L  I  L
     - K  R  L  I  I  E  P  V  L  V  M  L  L  T  F  V  H  S  Y  S
     -  R  G  L  L  *  S  P  C  W  *  C  C  *  L  L  C  T  H  T  R
```

Figure 16-H

```
5341 - GCTTACAGTAATAAAACTGTTGGCGAGCTTGGTGATGTCAGAGAAACTATGACCCATCTT - 5400
     - A  Y  S  N  K  T  V  G  E  L  G  D  V  R  E  T  M  T  H  L
     -  L  T  V  I  K  L  L  A  S  L  V  M  S  E  K  L  *  P  I  F
     -   L  Q  *  *  N  C  W  R  A  W  *  C  Q  R  N  Y  D  P  S  S
5401 - CTACAGCATGCTAATTTGGAATCTGCAAAGCGAGTTCTTAATGTGGTGTGTAAACATTGT - 5460
     - L  Q  H  A  N  L  E  S  A  K  R  V  L  N  V  V  C  K  H  C
     -  Y  S  M  L  I  W  N  L  Q  S  E  F  L  M  W  C  V  N  I  V
     -   T  A  C  *  F  G  I  C  K  A  S  S  *  C  G  V  *  T  L  W
5461 - GGTCAGAAAACTACTACCTTAACGGGTGTAGAAGCTGTGATGTATATGGGTACTCTATCT - 5520
     - G  Q  K  T  T  T  L  T  G  V  E  A  V  M  Y  M  G  T  L  S
     -  V  R  K  L  L  P  *  R  V  *  K  L  *  C  I  W  V  L  Y  L
     -   S  E  N  Y  Y  L  N  G  C  R  S  C  D  V  Y  G  Y  S  I  L
5521 - TATGATAATCTTAAGACAGGTGTTTCCATTCCATGTGTGTGTGGTCGTGATGCTACACAA - 5580
     - Y  D  N  L  K  T  G  V  S  I  P  C  V  C  G  R  D  A  T  Q
     -  M  I  I  L  R  Q  V  F  P  F  H  V  C  V  V  V  M  L  H  N
     -   *  *  S  *  D  R  C  F  H  S  M  C  V  W  S  *  C  Y  T  I
5581 - TATCTAGTACAACAAGAGTCTTCTTTTGTTATGATGTCTGCACCACCTGCTGAGTATAAA - 5640
     - Y  L  V  Q  Q  E  S  S  F  V  M  M  S  A  P  P  A  E  Y  K
     -  I  *  Y  N  K  S  L  L  L  L  *  C  L  H  H  L  L  S  I  N
     -   S  S  T  T  R  V  F  F  C  Y  D  V  C  T  T  C  *  V  *  I
5641 - TTACAGCAAGGTACATTCTTATGTGCGAATGAGTACACTGGTAACTATCAGTGTGGTCAT - 5700
     - L  Q  Q  G  T  F  L  C  A  N  E  Y  T  G  N  Y  Q  C  G  H
     -  Y  S  K  V  H  S  Y  V  R  M  S  T  L  V  T  I  S  V  V  I
     -   T  A  R  Y  I  L  M  C  E  *  V  H  W  *  L  S  V  W  S  L
5701 - TACACTCATATAACTGCTAAGGAGACCCTCTATCGTATTGACGGAGCTCACCTTACAAAG - 5760
     - Y  T  H  I  T  A  K  E  T  L  Y  R  I  D  G  A  H  L  T  K
     -  T  L  I  *  L  L  R  R  P  S  I  V  L  T  E  L  T  L  Q  R
     -   H  S  Y  N  C  *  G  D  P  L  S  Y  *  R  S  S  P  Y  K  D
5761 - ATGTCAGAGTACAAAGGACCAGTGACTGATGTTTTCTACAAGGAAACATCTTACACTACA - 5820
     - M  S  E  Y  K  G  P  V  T  D  V  F  Y  K  E  T  S  Y  T  T
     -  C  Q  S  T  K  D  Q  *  L  M  F  S  T  R  K  H  L  T  L  Q
     -   V  R  V  Q  R  T  S  D  *  C  F  L  Q  G  N  I  L  H  Y  N
5821 - ACCATCAAGCCTGTGTCGTATAAACTCGATGGAGTTACTTACACAGAGATTGAACCAAAA - 5880
     - T  I  K  P  V  S  Y  K  L  D  G  V  T  Y  T  E  I  E  P  K
     -  P  S  S  L  C  R  I  N  S  M  E  L  L  T  Q  R  L  N  Q  N
     -   H  Q  A  C  V  V  *  T  R  W  S  Y  L  H  R  D  *  T  K  I
5881 - TTGGATGGGTATTATAAAAAGGATAATGCTTACTATACAGAGCAGCCTATAGACCTTGTA - 5940
     - L  D  G  Y  Y  K  K  D  N  A  Y  Y  T  E  Q  P  I  D  L  V
     -  W  M  G  I  I  K  R  I  M  L  T  I  Q  S  S  L  *  T  L  Y
     -   G  W  V  L  *  K  G  *  C  L  L  Y  R  A  A  Y  R  P  C  T
5941 - CCAACTCAACCATTACCAAATGCGAGTTTTGATAATTTCAAACTCACATGTTCTAACACA - 6000
     - P  T  Q  P  L  P  N  A  S  F  D  N  F  K  L  T  C  S  N  T
     -  Q  L  N  H  Y  Q  M  R  V  L  I  I  S  N  S  H  V  L  T  Q
     -   N  S  T  I  T  K  C  E  F  *  *  F  Q  T  H  M  F  *  H  K
6001 - AAATTTGCTGATGATTTAAATCAAATGACAGGCTTCACAAAGCCAGCTTCACGAGAGCTA - 6060
     - K  F  A  D  D  L  N  Q  M  T  G  F  T  K  P  A  S  R  E  L
     -  N  L  L  M  I  *  I  K  *  Q  A  S  Q  S  Q  L  H  E  S  Y
     -   I  C  *  *  F  K  S  N  D  R  L  H  K  A  S  F  T  R  A  I
6061 - TCTGTCACATTCTTCCCAGACTTGAATGGCGATGTAGTGGCTATTGACTATAGACACTAT - 6120
     - S  V  T  F  F  P  D  L  N  G  D  V  V  A  I  D  Y  R  H  Y
     -  L  S  H  S  S  Q  T  *  M  A  M  *  W  L  L  T  I  D  T  I
     -   C  H  I  L  P  R  L  E  W  R  C  S  G  Y  *  L  *  T  L  F
```

Figure 16-I

```
6121 - TCAGCGAGTTTCAAGAAAGGTGCTAAATTACTGCATAAGCCAATTGTTTGGCACATTAAC - 6180
     - S  A  S  F  K  K  G  A  K  L  L  H  K  P  I  V  W  H  I  N
     -  Q  R  V  S  R  K  V  L  N  Y  C  I  S  Q  L  F  G  T  L  T
     -   S  E  F  Q  E  R  C  *  I  T  A  *  A  N  C  L  A  H  *  P
6181 - CAGGCTACAACCAAGACAACGTTCAAACCAAACACTTGGTGTTTACGTTGTCTTTGGAGT - 6240
     - Q  A  T  T  K  T  T  F  K  P  N  T  W  C  L  R  C  L  W  S
     -  R  L  Q  P  R  Q  R  S  N  Q  T  L  G  V  Y  V  V  F  G  V
     -   G  Y  N  Q  D  N  V  Q  T  K  H  L  V  F  T  L  S  L  E  Y
6241 - ACAAAGCCAGTAGATACTTCAAATTCATTTGAAGTTCTGGCAGTAGAAGACACACAAGGA - 6300
     - T  K  P  V  D  T  S  N  S  F  E  V  L  A  V  E  D  T  Q  G
     -  Q  S  Q  *  I  L  Q  I  H  L  K  F  W  Q  *  K  T  H  K  E
     -   K  A  S  R  Y  F  K  F  I  *  S  S  G  S  R  R  H  T  R  N
6301 - ATGGACAATCTTGCTTGTGAAAGTCAACAACCCACCTCTGAAGAAGTAGTGGAAAATCCT - 6360
     - M  D  N  L  A  C  E  S  Q  Q  P  T  S  E  E  V  V  E  N  P
     -  W  T  I  L  L  V  K  V  N  N  P  P  L  K  K  *  W  K  I  L
     -   G  Q  S  C  L  *  K  S  T  T  H  L  *  R  S  S  G  K  S  Y
6361 - ACCATACAGAAGGAAGTCATAGAGTGTGACGTGAAAACTACCGAAGTTGTAGGCAATGTC - 6420
     - T  I  Q  K  E  V  I  E  C  D  V  K  T  T  E  V  V  G  N  V
     -  P  Y  R  R  K  S  *  S  V  T  *  K  L  P  K  L  *  A  M  S
     -   H  T  E  G  S  H  R  V  *  R  E  N  Y  R  S  C  R  Q  C  H
6421 - ATACTTAAACCATCAGATGAAGGTGTTAAAGTAACACAAGAGTTAGGTCATGAGGATCTT - 6480
     - I  L  K  P  S  D  E  G  V  K  V  T  Q  E  L  G  H  E  D  L
     -  Y  L  N  H  Q  M  K  V  L  K  *  H  K  S  *  V  M  R  I  L
     -   T  *  T  I  R  *  R  C  *  S  N  T  R  V  R  S  *  G  S  Y
6481 - ATGGCTGCTTATGTGGAAAACACAAGCATTACCATTAAGAAACCTAATGAGCTTTCACTA - 6540
     - M  A  A  Y  V  E  N  T  S  I  T  I  K  K  P  N  E  L  S  L
     -  W  L  L  M  W  K  T  Q  A  L  P  L  R  N  L  M  S  F  H  *
     -   G  C  L  C  G  K  H  K  H  Y  H  *  E  T  *  *  A  F  T  S
6541 - GCCTTAGGTTTAAAAACAATTGCCACTCATGGTATTGCTGCAATTAATAGTGTTCCTTGG - 6600
     - A  L  G  L  K  T  I  A  T  H  G  I  A  A  I  N  S  V  P  W
     -  P  *  V  *  K  Q  L  P  L  M  V  L  L  Q  L  I  V  F  L  G
     -   L  R  F  K  N  N  C  H  S  W  Y  C  C  N  *  *  C  S  L  E
6601 - AGTAAAATTTTGGCTTATGTCAAACCATTCTTAGGACAAGCAGCAATTACAACATCAAAT - 6660
     - S  K  I  L  A  Y  V  K  P  F  L  G  Q  A  A  I  T  T  S  N
     -  V  K  F  W  L  M  S  N  H  S  *  D  K  Q  Q  L  Q  H  Q  I
     -   *  N  F  G  L  C  Q  T  I  L  R  T  S  S  N  Y  N  I  K  L
6661 - TGCGCTAAGAGATTAGCACAACGTGTGTTTAACAATTATATGCCTTATGTGTTTACATTA - 6720
     - C  A  K  R  L  A  Q  R  V  F  N  N  Y  M  P  Y  V  F  T  L
     -  A  L  R  D  *  H  N  V  C  L  T  I  I  C  L  M  C  L  H  Y
     -   R  *  E  I  S  T  T  C  V  *  Q  L  Y  A  L  C  V  Y  I  I
6721 - TTGTTCCAATTGTGTACTTTTACTAAAAGTACCAATTCTAGAATTAGAGCTTCACTACCT - 6780
     - L  F  Q  L  C  T  F  T  K  S  T  N  S  R  I  R  A  S  L  P
     -  C  S  N  C  V  L  L  L  K  V  P  I  L  E  L  E  L  H  Y  L
     -   V  P  I  V  Y  F  Y  *  K  Y  Q  F  *  N  *  S  F  T  T  Y
6781 - ACAACTATTGCTAAAAATAGTGTTAAGAGTGTTGCTAAATTATGTTTGGATGCCGGCATT - 6840
     - T  T  I  A  K  N  S  V  K  S  V  A  K  L  C  L  D  A  G  I
     -  Q  L  L  L  K  I  V  L  R  V  L  L  N  Y  V  W  M  P  A  L
     -   N  Y  C  *  K  *  C  *  E  C  C  *  I  M  F  G  C  R  H  *
6841 - AATTATGTGAAGTCACCCAAATTTTCTAAATTGTTCACAATCGCTATGTGGCTATTGTTG - 6900
     - N  Y  V  K  S  P  K  F  S  K  L  F  T  I  A  M  W  L  L  L
     -  I  M  *  S  H  P  N  F  L  N  C  S  Q  S  L  C  G  Y  C  C
     -   L  C  E  V  T  Q  I  F  *  I  V  H  N  R  Y  V  A  I  V  V
```

Figure 16-J

```
6901 - TTAAGTATTTGCTTAGGTTCTCTAATCTGTGTAACTGCTGCTTTTGGTGTACTCTTATCT - 6960
     - L  S  I  C  L  G  S  L  I  C  V  T  A  A  F  G  V  L  L  S
     -  *  V  F  A  *  V  L  *  S  V  *  L  L  L  L  V  Y  S  Y  L
     -   K  Y  L  L  R  F  S  N  L  C  N  C  C  F  W  C  T  L  I  *
6961 - AATTTGGTGCTCCTTCTTATTGTAATGGCGTTAGAGAATTGTATCTTAATTCGTCTAAC - 7020
     - N  F  G  A  P  S  Y  C  N  G  V  R  E  L  Y  L  N  S  S  N
     -  I  L  V  L  L  L  I  V  M  A  L  E  N  C  I  L  I  R  L  T
     -   F  W  C  S  F  L  L  *  W  R  *  R  I  V  S  *  F  V  *  R
7021 - GTTACTACTATGGATTTCTGTGAAGGTTCTTTTCCTTGCAGCATTTGTTTAAGTGGATTA - 7080
     - V  T  T  M  D  F  C  E  G  S  F  P  C  S  I  C  L  S  G  L
     -  L  L  L  W  I  S  V  K  V  L  F  L  A  A  F  V  *  V  D  *
     -   Y  Y  Y  G  F  L  *  R  F  F  S  L  Q  H  L  F  K  W  I  R
7081 - GACTCCCTTGATTCTTATCCAGCTCTTGAAACCATTCAGGTGACGATTTCATCGTACAAG - 7140
     - D  S  L  D  S  Y  P  A  L  E  T  I  Q  V  T  I  S  S  Y  K
     -  T  P  L  I  L  I  Q  L  L  K  P  F  R  *  R  F  H  R  T  S
     -   L  P  *  F  L  S  S  S  *  N  H  S  G  D  D  F  I  V  Q  A
7141 - CTAGACTTGACAATTTTAGGTCTGGCCGCTGAGTGGGTTTTGGCATATATGTTGTTCACA - 7200
     - L  D  L  T  I  L  G  L  A  A  E  W  V  L  A  Y  M  L  F  T
     -  *  T  *  Q  F  *  V  W  P  L  S  G  F  W  H  I  C  C  S  Q
     -   R  L  D  N  F  R  S  G  R  *  V  G  F  G  I  Y  V  V  H  K
7201 - AAATTCTTTTATTTATTAGGTCTTTCAGCTATAATGCAGGTGTTCTTTGGCTATTTTGCT - 7260
     - K  F  F  Y  L  L  G  L  S  A  I  M  Q  V  F  F  G  Y  F  A
     -  N  S  F  I  Y  *  V  F  Q  L  *  C  R  C  S  L  A  I  L  L
     -   I  L  L  F  I  R  S  F  S  Y  N  A  G  V  L  W  L  F  C  *
7261 - AGTCATTTCATCAGCAATTCTTGGCTCATGTGGTTTATCATTAGTATTGTACAAATGGCA - 7320
     - S  H  F  I  S  N  S  W  L  M  W  F  I  I  S  I  V  Q  M  A
     -  V  I  S  S  A  I  L  G  S  C  G  L  S  L  V  L  Y  K  W  H
     -   S  F  H  Q  Q  F  L  A  H  V  V  Y  H  *  Y  C  T  N  G  T
7321 - CCCGTTTCTGCAATGGTTAGGATGTACATCTTCTTTGCTTCTTTCTACTACATATGGAAG - 7380
     - P  V  S  A  M  V  R  M  Y  I  F  F  A  S  F  Y  Y  I  W  K
     -  P  F  L  Q  W  L  G  C  T  S  S  L  L  L  S  T  T  Y  G  R
     -   R  F  C  N  G  *  D  V  H  L  L  C  F  F  L  L  H  M  E  E
7381 - AGCTATGTTCATATCATGGATGGTTGCACCTCTTCGACTTGCATGATGTGCTATAAGCGC - 7440
     - S  Y  V  H  I  M  D  G  C  T  S  S  T  C  M  M  C  Y  K  R
     -  A  M  F  I  S  W  M  V  A  P  L  R  L  A  *  C  A  I  S  A
     -   L  C  S  Y  H  G  W  L  H  L  F  D  L  H  D  V  L  *  A  Q
7441 - AATCGTGCCACACGCGTTGAGTGTACAACTATTGTTAATGGCATGAAGAGATCTTTCTAT - 7500
     - N  R  A  T  R  V  E  C  T  T  I  V  N  G  M  K  R  S  F  Y
     -  I  V  P  H  A  L  S  V  Q  L  L  L  M  A  *  R  D  L  S  M
     -   S  C  H  T  R  *  V  Y  N  Y  C  *  W  H  E  E  I  F  L  C
7501 - GTCTATGCAAATGGAGGCCGTGGCTTCTGCAAGACTCACAATTGGAATTGTCTCAATTGT - 7560
     - V  Y  A  N  G  G  R  G  F  C  K  T  H  N  W  N  C  L  N  C
     -  S  M  Q  M  E  A  V  A  S  A  R  L  T  I  G  I  V  S  I  V
     -   L  C  K  W  R  P  W  L  L  Q  D  S  Q  L  E  L  S  Q  L  *
7561 - GACACATTTTGCACTGGTAGTACATTCATTAGTGATGAAGTTGCTCGTGATTTGTCACTC - 7620
     - D  T  F  C  T  G  S  T  F  I  S  D  E  V  A  R  D  L  S  L
     -  T  H  F  A  L  V  V  H  S  L  V  M  K  L  L  V  I  C  H  S
     -   H  I  L  H  W  *  Y  I  H  *  *  *  S  C  S  *  F  V  T  P
7621 - CAGTTTAAAAGACCAATCAACCCTACTGACCAGTCATCGTATATTGTTGATAGTGTTGCT - 7680
     - Q  F  K  R  P  I  N  P  T  D  Q  S  S  Y  I  V  D  S  V  A
     -  S  L  K  D  Q  S  T  L  L  T  S  H  R  I  L  L  I  V  L  L
     -   V  *  K  T  N  Q  P  Y  *  P  V  I  V  Y  C  *  *  C  C  C
```

Figure 16-K

```
7681 - GTGAAAAATGGCGCGCTTCACCTCTACTTTGACAAGGCTGGTCAAAAGACCTATGAGAGA - 7740
     - V  K  N  G  A  L  H  L  Y  F  D  K  A  G  Q  K  T  Y  E  R
     -  *  K  M  A  R  F  T  S  T  L  T  R  L  V  K  R  P  M  R  D
     -   E  K  W  R  A  S  P  L  L  *  Q  G  W  S  K  D  L  *  E  T
7741 - CATCCGCTCTCCCATTTTGTCAATTTAGACAATTTGAGAGCTAACAACACTAAAGGTTCA - 7800
     - H  P  L  S  H  F  V  N  L  D  N  L  R  A  N  N  T  K  G  S
     -  I  R  S  P  I  L  S  I  *  T  I  *  E  L  T  T  L  K  V  H
     -   S  A  L  P  F  C  Q  F  R  Q  F  E  S  *  Q  H  *  R  F  T
7801 - CTGCCTATTAATGTCATAGTTTTTGATGGCAAGTCCAAATGCGACGAGTCTGCTTCTAAG - 7860
     - L  P  I  N  V  I  V  F  D  G  K  S  K  C  D  E  S  A  S  K
     -  C  L  L  M  S  *  F  L  M  A  S  P  N  A  T  S  L  L  L  S
     -   A  Y  *  C  H  S  F  *  W  Q  V  Q  M  R  R  V  C  F  *  V
7861 - TCTGCTTCTGTGTACTACAGTCAGCTGATGTGCCAACCTATTCTGTTGCTTGACCAAGCT - 7920
     - S  A  S  V  Y  Y  S  Q  L  M  C  Q  P  I  L  L  L  D  Q  A
     -  L  L  L  C  T  T  V  S  *  C  A  N  L  F  C  C  L  T  K  L
     -   C  F  C  V  L  Q  S  A  D  V  P  T  Y  S  V  A  *  P  S  S
7921 - CTTGTATCAAACGTTGGAGATAGTACTGAAGTTTCCGTTAAGATGTTTGATGCTTATGTC - 7980
     - L  V  S  N  V  G  D  S  T  E  V  S  V  K  M  F  D  A  Y  V
     -  L  Y  Q  T  L  E  I  V  L  K  F  P  L  R  C  L  M  L  M  S
     -   C  I  K  R  W  R  *  Y  *  S  F  R  *  D  V  *  C  L  C  R
7981 - GACACCTTTTCAGCAACTTTTAGTGTTCCTATGGAAAAACTTAAGGCACTTGTTGCTACA - 8040
     - D  T  F  S  A  T  F  S  V  P  M  E  K  L  K  A  L  V  A  T
     -  T  P  F  Q  Q  L  L  V  F  L  W  K  N  L  R  H  L  L  L  Q
     -   H  L  F  S  N  F  *  C  S  Y  G  K  T  *  G  T  C  C  Y  S
8041 - GCTCACAGCGAGTTAGCAAAGGGTGTAGCTTTAGATGGTGTCCTTTCTACATTCGTGTCA - 8100
     - A  H  S  E  L  A  K  G  V  A  L  D  G  V  L  S  T  F  V  S
     -  L  T  A  S  *  Q  R  V  *  L  *  M  V  S  F  L  H  S  C  Q
     -   S  Q  R  V  S  K  G  C  S  F  R  W  C  P  F  Y  I  R  V  S
8101 - GCTGCCCGACAAGGTGTTGTTGATACCGATGTTGACACAAAGGATGTTATTGAATGTCTC - 8160
     - A  A  R  Q  G  V  V  D  T  D  V  D  T  K  D  V  I  E  C  L
     -  L  P  D  K  V  L  L  I  P  M  L  T  Q  R  M  L  L  N  V  S
     -   C  P  T  R  C  C  *  Y  R  C  *  H  K  G  C  Y  *  M  S  Q
8161 - AAACTTTCACATCACTCTGACTTAGAAGTGACAGGTGACAGTTGTAACAATTTCATGCTC - 8220
     - K  L  S  H  H  S  D  L  E  V  T  G  D  S  C  N  N  F  M  L
     -  N  F  H  I  T  L  T  *  K  *  Q  V  T  V  V  T  I  S  C  S
     -   T  F  T  S  L  *  L  R  S  D  R  *  Q  L  *  Q  F  H  A  H
8221 - ACCTATAATAAGGTTGAAAACATGACGCCCAGAGATCTTGGCGCATGTATTGACTGTAAT - 8280
     - T  Y  N  K  V  E  N  M  T  P  R  D  L  G  A  C  I  D  C  N
     -  P  I  I  R  L  K  T  *  R  P  E  I  L  A  H  V  L  T  V  M
     -   L  *  *  G  *  K  H  D  A  Q  R  S  W  R  M  Y  *  L  *  C
8281 - GCAAGGCATATCAATGCCCAAGTAGCAAAAAGTCACAATGTTTCACTCATCTGGAATGTA - 8340
     - A  R  H  I  N  A  Q  V  A  K  S  H  N  V  S  L  I  W  N  V
     -  Q  G  I  S  M  P  K  *  Q  K  V  T  M  F  H  S  S  G  M  *
     -   K  A  Y  Q  C  P  S  S  K  K  S  Q  C  F  T  H  L  E  C  K
8341 - AAAGACTACATGTCTTTATCTGAACAGCTGCGTAAACAAATTCGTACTGCTGCCAAGAAG - 8400
     - K  D  Y  M  S  L  S  E  Q  L  R  K  Q  I  R  T  A  A  K  K
     -  K  T  T  C  L  Y  L  N  S  C  V  N  K  F  V  L  L  P  R  R
     -   R  L  H  V  F  I  *  T  A  A  *  T  N  S  Y  C  C  Q  E  E
8401 - AACAACATACCTTTTACACTAACTTGTGCTACAACTAGACAGGTTGTCAATGTCATAACT - 8460
     - N  N  I  P  F  T  L  T  C  A  T  T  R  Q  V  V  N  V  I  T
     -  T  T  Y  L  L  H  *  L  V  L  Q  L  D  R  L  S  M  S  *  L
     -   Q  H  T  F  Y  T  N  L  C  Y  N  *  T  G  C  Q  C  H  N  Y
```

Figure 16-L

```
8461 - ACTAAAATCTCACTCAAGGGTGGTAAGATTGTTAGTACTTGTTTTAAACTTATGCTTAAG - 8520
     - T  K  I  S  L  K  G  G  K  I  V  S  T  C  F  K  L  M  L  K
     -  L  K  S  H  S  R  V  V  R  L  L  V  L  V  L  N  L  C  L  R
     -   *  N  L  T  Q  G  W  *  D  C  *  Y  L  F  *  T  Y  A  *  G
8521 - GCCACATTATTGTGCGTTCTTGCTGCATTGGTTTGTTATATCGTTATGCCAGTACATACA - 8580
     - A  T  L  L  C  V  L  A  A  L  V  C  Y  I  V  M  P  V  H  T
     -  P  H  Y  C  A  F  L  L  H  W  F  V  I  S  L  C  Q  Y  I  H
     -   H  I  I  V  R  S  C  C  I  G  L  L  Y  R  Y  A  S  T  Y  I
8581 - TTGTCAATCCATGATGGTTACACAAATGAAATCATTGGTTACAAAGCCATTCAGGATGGT - 8640
     - L  S  I  H  D  G  Y  T  N  E  I  I  G  Y  K  A  I  Q  D  G
     -  C  Q  S  M  M  V  T  Q  M  K  S  L  V  T  K  P  F  R  M  V
     -   V  N  P  *  W  L  H  K  *  N  H  W  L  Q  S  H  S  G  W  C
8641 - GTCACTCGTGACATCATTTCTACTGATGATTGTTTTGCAAATAAACATGCTGGTTTTGAC - 8700
     - V  T  R  D  I  I  S  T  D  D  C  F  A  N  K  H  A  G  F  D
     -  S  L  V  T  S  F  L  L  M  I  V  L  Q  I  N  M  L  V  L  T
     -   H  S  *  H  H  F  Y  *  *  L  F  C  K  *  T  C  W  F  *  R
8701 - GCATGGTTTAGCCAGCGTGGTGGTTCATACAAAAATGACAAAAGCTGCCCTGTAGTAGCT - 8760
     - A  W  F  S  Q  R  G  G  S  Y  K  N  D  K  S  C  P  V  V  A
     -  H  G  L  A  S  V  V  V  H  T  K  M  T  K  A  A  L  *  *  L
     -   M  V  *  P  A  W  W  F  I  Q  K  *  Q  K  L  P  C  S  S  C
8761 - GCTATCATTACAAGAGAGATTGGTTTCATAGTGCCTGGCTTACCGGGTACTGTGCTGAGA - 8820
     - A  I  I  T  R  E  I  G  F  I  V  P  G  L  P  G  T  V  L  R
     -  L  S  L  Q  E  R  L  V  S  *  C  L  A  Y  R  V  L  C  *  E
     -   Y  H  Y  K  R  D  W  F  H  S  A  W  L  T  G  Y  C  A  E  S
8821 - GCAATCAATGGTGACTTCTTGCATTTTCTACCTCGTGTTTTTAGTGCTGTTGGCAACATT - 8880
     - A  I  N  G  D  F  L  H  F  L  P  R  V  F  S  A  V  G  N  I
     -  Q  S  M  V  T  S  C  I  F  Y  L  V  F  L  V  L  L  A  T  F
     -   N  Q  W  *  L  L  A  F  S  T  S  C  F  *  C  C  W  Q  H  L
8881 - TGCTACACACCTTCCAAACTCATTGAGTATAGTGATTTGCTACCTCTGCTTGCGTTCTT - 8940
     - C  Y  T  P  S  K  L  I  E  Y  S  D  F  A  T  S  A  C  V  L
     -  A  T  H  L  P  N  S  L  S  I  V  I  L  L  P  L  L  A  F  L
     -   L  H  T  F  Q  T  H  *  V  *  *  F  C  Y  L  C  L  R  S  C
8941 - GCTGCTGAGTGTACAATTTTTAAGGATGCTATGGGCAAACCTGTGCCATATTGTTATGAC - 9000
     - A  A  E  C  T  I  F  K  D  A  M  G  K  P  V  P  Y  C  Y  D
     -  L  L  S  V  Q  F  L  R  M  L  W  A  N  L  C  H  I  V  M  T
     -   C  *  V  Y  N  F  *  G  C  Y  G  Q  T  C  A  I  L  L  *  H
9001 - ACTAATTTGCTAGAGGGTTCTATTTCTTATAGTGAGCTTCGTCCAGACACTCGTTATGTG - 9060
     - T  N  L  L  E  G  S  I  S  Y  S  E  L  R  P  D  T  R  Y  V
     -  L  I  C  *  R  V  L  F  L  I  V  S  F  V  Q  T  L  V  M  C
     -   *  F  A  R  G  F  Y  F  L  *  *  A  S  S  R  H  S  L  C  A
9061 - CTTATGGATGGTTCCATCATACAGTTTCCTAACACTTACCTGGAGGGTTCTGTTAGAGTA - 9120
     - L  M  D  G  S  I  I  Q  F  P  N  T  Y  L  E  G  S  V  R  V
     -  L  W  M  V  P  S  Y  S  F  L  T  L  T  W  R  V  L  L  E  *
     -   Y  G  W  F  H  H  T  V  S  *  H  L  P  G  G  F  C  *  S  S
9121 - GTAACAACTTTTGATGCTGAGTACTGTAGACATGGTACATGCGAAAGGTCAGAAGTAGGT - 9180
     - V  T  T  F  D  A  E  Y  C  R  H  G  T  C  E  R  S  E  V  G
     -  *  Q  L  L  M  L  S  T  V  D  M  V  H  A  K  G  Q  K  *  V
     -   N  N  F  *  C  *  V  L  *  T  W  Y  M  R  K  V  R  S  R  Y
9181 - ATTTGCCTATCTACCAGTGGTAGATGGGTTCTTAATAATGAGCATTACAGAGCTCTATCA - 9240
     - I  C  L  S  T  S  G  R  W  V  L  N  N  E  H  Y  R  A  L  S
     -  F  A  Y  L  P  V  V  D  G  F  L  I  M  S  I  T  E  L  Y  Q
     -   L  P  I  Y  Q  W  *  M  G  S  *  *  *  A  L  Q  S  S  I  R
```

Figure 16-M

```
9241 - GGAGTTTTCTGTGGTGTTGATGCGATGAATCTCATAGCTAACATCTTTACTCCTCTTGTG - 9300
     - G  V  F  C  G  V  D  A  M  N  L  I  A  N  I  F  T  P  L  V
     -  E  F  S  V  V  L  M  R  *  I  S  *  L  T  S  L  L  L  L  C
     -   S  F  L  W  C  *  C  D  E  S  H  S  *  H  L  Y  S  S  C  A
9301 - CAACCTGTGGGTGCTTTAGATGTGTCTGCTTCAGTAGTGGCTGGTGGTATTATTGCCATA - 9360
     - Q  P  V  G  A  L  D  V  S  A  S  V  V  A  G  G  I  I  A  I
     -  N  L  W  V  L  *  M  C  L  L  Q  *  W  L  V  V  L  L  P  Y
     -   T  C  G  C  F  R  C  V  C  F  S  S  G  W  W  Y  Y  C  H  I
9361 - TTGGTGACTTGTGCTGCCTACTACTTTATGAAATTCAGACGTGTTTTTGGTGAGTACAAC - 9420
     - L  V  T  C  A  A  Y  Y  F  M  K  F  R  R  V  F  G  E  Y  N
     -  W  *  L  V  L  P  T  T  L  *  N  S  D  V  F  L  V  S  T  T
     -   G  D  L  C  C  L  L  L  Y  E  I  Q  T  C  F  W  *  V  Q  P
9421 - CATGTTGTTGCTGCTAATGCACTTTTGTTTTTGATGTCTTTCACTATACTCTGTCTGGTA - 9480
     - H  V  V  A  A  N  A  L  L  F  L  M  S  F  T  I  L  C  L  V
     -  M  L  L  L  L  M  H  F  C  F  *  C  L  S  L  Y  S  V  W  Y
     -   C  C  C  C  *  C  T  F  V  F  D  V  F  H  Y  T  L  S  G  T
9481 - CCAGCTTACAGCTTTCTGCCGGGAGTCTACTCAGTCTTTTACTTGTACTTGACATTCTAT - 9540
     - P  A  Y  S  F  L  P  G  V  Y  S  V  F  Y  L  Y  L  T  F  Y
     -  Q  L  T  A  F  C  R  E  S  T  Q  S  F  T  C  T  *  H  S  I
     -   S  L  Q  L  S  A  G  S  L  L  S  L  L  L  V  L  D  I  L  F
9541 - TTCACCAATGATGTTTCATTCTTGGCTCACCTTCAATGGTTTGCCATGTTTTCTCCTATT - 9600
     - F  T  N  D  V  S  F  L  A  H  L  Q  W  F  A  M  F  S  P  I
     -  S  P  M  M  F  H  S  W  L  T  F  N  G  L  P  C  F  L  L  L
     -   H  Q  *  C  F  I  L  G  S  P  S  M  V  C  H  V  F  S  Y  C
9601 - GTGCCTTTTTGGATAACAGCAATCTATGTATTCTGTATTTCTCTGAAGCACTGCCATTGG - 9660
     - V  P  F  W  I  T  A  I  Y  V  F  C  I  S  L  K  H  C  H  W
     -  C  L  F  G  *  Q  Q  S  M  Y  S  V  F  L  *  S  T  A  I  G
     -   A  F  L  D  N  S  N  L  C  I  L  Y  F  S  E  A  L  P  L  V
9661 - TTCTTTAACAACTATCTTAGGAAAAGAGTCATGTTTAATGGAGTTACATTTAGTACCTTC - 9720
     - F  F  N  N  Y  L  R  K  R  V  M  F  N  G  V  T  F  S  T  F
     -  S  L  T  T  I  L  G  K  E  S  C  L  M  E  L  H  L  V  P  S
     -   L  *  Q  L  S  *  E  K  S  H  V  *  W  S  Y  I  *  Y  L  R
9721 - GAGGAGGCTGCTTTGTGTACCTTTTTGCTCAACAAGGAAATGTACCTAAAATTGCGTAGC - 9780
     - E  E  A  A  L  C  T  F  L  L  N  K  E  M  Y  L  K  L  R  S
     -  R  R  L  L  C  V  P  F  C  S  T  R  K  C  T  *  N  C  V  A
     -   G  G  C  F  V  Y  L  F  A  Q  Q  G  N  V  P  K  I  A  *  R
9781 - GAGACACTGTTGCCACTTACACAGTATAACAGGTATCTTGCTCTATATAACAAGTACAAG - 9840
     - E  T  L  L  P  L  T  Q  Y  N  R  Y  L  A  L  Y  N  K  Y  K
     -  R  H  C  C  H  L  H  S  I  T  G  I  L  L  Y  I  T  S  T  S
     -   D  T  V  A  T  Y  T  V  *  Q  V  S  C  S  I  *  Q  V  Q  V
9841 - TATTTCAGTGGAGCCTTAGATACTACCAGCTATCGTGAAGCAGCTTGCTGCCACTTAGCA - 9900
     - Y  F  S  G  A  L  D  T  T  S  Y  R  E  A  A  C  C  H  L  A
     -  I  S  V  E  P  *  I  L  P  A  I  V  K  Q  L  A  A  T  *  Q
     -   F  Q  W  S  L  R  Y  Y  Q  L  S  *  S  S  L  L  P  L  S  K
9901 - AAGGCTCTAAATGACTTTAGCAACTCAGGTGCTGATGTTCTCTACCAACCACCACAGACA - 9960
     - K  A  L  N  D  F  S  N  S  G  A  D  V  L  Y  Q  P  P  Q  T
     -  R  L  *  M  T  L  A  T  Q  V  L  M  F  S  T  N  H  H  R  H
     -   G  S  K  *  L  *  Q  L  R  C  *  C  S  L  P  T  T  T  D  I
```

Figure 16-N

```
 9961 - TCAATCACTTCTGCTGTTCTGCAGAGTGGTTTTAGGAAAATGGCATTCCCGTCAGGCAAA - 10020
      - S  I  T  S  A  V  L  Q  S  G  F  R  K  M  A  F  P  S  G  K
      -  Q  S  L  L  L  F  C  R  V  V  L  G  K  W  H  S  R  Q  A  K
      -   N  H  F  C  C  S  A  E  W  F  *  E  N  G  I  P  V  R  Q  S
10021 - GTTGAAGGGTGCATGGTACAAGTAACCTGTGGAACTACAACTCTTAATGGATTGTGGTTG - 10080
      - V  E  G  C  M  V  Q  V  T  C  G  T  T  T  L  N  G  L  W  L
      -  L  K  G  A  W  Y  K  *  P  V  E  L  Q  L  L  M  D  C  G  W
      -   *  R  V  H  G  T  S  N  L  W  N  Y  N  S  *  W  I  V  V  G
10081 - GATGACACAGTATACTGTCCAAGACATGTCATTTGCACAGCAGAAGACATGCTTAATCCT - 10140
      - D  D  T  V  Y  C  P  R  H  V  I  C  T  A  E  D  M  L  N  P
      -  M  T  Q  Y  T  V  Q  D  M  S  F  A  Q  Q  K  T  C  L  I  L
      -   *  H  S  I  L  S  K  T  C  H  L  H  S  R  R  H  A  *  S  *
10141 - AACTATGAAGATCTGCTCATTCGCAAATCCAACCATAGCTTTCTTGTTCAGGCTGGCAAT - 10200
      - N  Y  E  D  L  L  I  R  K  S  N  H  S  F  L  V  Q  A  G  N
      -  T  M  K  I  C  S  F  A  N  P  T  I  A  F  L  F  R  L  A  M
      -   L  *  R  S  A  H  S  Q  I  Q  P  *  L  S  C  S  G  W  Q  C
10201 - GTTCAACTTCGTGTTATTGGCCATTCTATGCAAAATTGTCTGCTTAGGCTTAAAGTTGAT - 10260
      - V  Q  L  R  V  I  G  H  S  M  Q  N  C  L  L  R  L  K  V  D
      -  F  N  F  V  L  L  A  I  L  C  K  I  V  C  L  G  L  K  L  I
      -   S  T  S  C  Y  W  P  F  Y  A  K  L  S  A  *  A  *  S  *  Y
10261 - ACTTCTAACCCTAAGACACCCAAGTATAAATTTGTCCGTATCCAACCTGGTCAAACATTT - 10320
      - T  S  N  P  K  T  P  K  Y  K  F  V  R  I  Q  P  G  Q  T  F
      -  L  L  T  L  R  H  P  S  I  N  L  S  V  S  N  L  V  K  H  F
      -   F  *  P  *  D  T  Q  V  *  I  C  P  Y  P  T  W  S  N  I  F
10321 - TCAGTTCTAGCATGCTACAATGGTTCACCATCTGGTGTTTATCAGTGTGCCATGAGACCT - 10380
      - S  V  L  A  C  Y  N  G  S  P  S  G  V  Y  Q  C  A  M  R  P
      -  Q  F  *  H  A  T  M  V  H  H  L  V  F  I  S  V  P  *  D  L
      -   S  S  S  M  L  Q  W  F  T  I  W  C  L  S  V  C  H  E  T  *
10381 - AATCATACCATTAAAGGTTCTTTCCTTAATGGATCATGTGGTAGTGTTGGTTTTAACATT - 10440
      - N  H  T  I  K  G  S  F  L  N  G  S  C  G  S  V  G  F  N  I
      -  I  I  P  L  K  V  L  S  L  M  D  H  V  V  V  L  V  L  T  L
      -   S  Y  H  *  R  F  F  P  *  W  I  M  W  *  C  W  F  *  H  *
10441 - GATTATGATTGCGTGTCTTTCTGCTATATGCATCATATGGAGCTTCCAACAGGAGTACAC - 10500
      - D  Y  D  C  V  S  F  C  Y  M  H  H  M  E  L  P  T  G  V  H
      -  I  M  I  A  C  L  S  A  I  C  I  I  W  S  F  Q  Q  E  Y  T
      -   L  *  L  R  V  F  L  L  Y  A  S  Y  G  A  S  N  R  S  T  R
10501 - GCTGGTACTGACTTAGAAGGTAAATTCTATGGTCCATTTGTTGACAGACAAACTGCACAG - 10560
      - A  G  T  D  L  E  G  K  F  Y  G  P  F  V  D  R  Q  T  A  Q
      -  L  V  L  T  *  K  V  N  S  M  V  H  L  L  T  D  K  L  H  R
      -   W  Y  *  L  R  R  *  I  L  W  S  I  C  *  Q  T  N  C  T  G
10561 - GCTGCAGGTACAGACACAACCATAACATTAAATGTTTTGGCATGGCTGTATGCTGCTGTT - 10620
      - A  A  G  T  D  T  T  I  T  L  N  V  L  A  W  L  Y  A  A  V
      -  L  Q  V  Q  T  Q  P  *  H  *  M  F  W  H  G  C  M  L  L  L
      -   C  R  Y  R  H  N  H  N  I  K  C  F  G  M  A  V  C  C  C  Y
10621 - ATCAATGGTGATAGGTGGTTTCTTAATAGATTCACCACTACTTTGAATGACTTTAACCTT - 10680
      - I  N  G  D  R  W  F  L  N  R  F  T  T  T  L  N  D  F  N  L
      -  S  M  V  I  G  G  F  L  I  D  S  P  L  L  *  M  T  L  T  L
      -   Q  W  *  *  V  V  S  *  *  I  H  H  Y  F  E  *  L  *  P  C
```

Figure 16-O

```
10681 - GTGGCAATGAAGTACAACTATGAACCTTTGACACAAGATCATGTTGACATATTGGGACCT - 10740
      - V  A  M  K  Y  N  Y  E  P  L  T  Q  D  H  V  D  I  L  G  P
      -  W  Q  *  S  T  T  M  N  L  *  H  K  I  M  L  T  Y  W  D  L
      -   G  N  E  V  Q  L  *  T  F  D  T  R  S  C  *  H  I  G  T  S
10741 - CTTTCTGCTCAAACAGGAATTGCCGTCTTAGATATGTGTGCTGCTTTGAAAGAGCTGCTG - 10800
      - L  S  A  Q  T  G  I  A  V  L  D  M  C  A  A  L  K  E  L  L
      -  F  L  L  K  Q  E  L  P  S  *  I  C  V  L  L  *  K  S  C  C
      -   F  C  S  N  R  N  C  R  L  R  Y  V  C  C  F  E  R  A  A  A
10801 - CAGAATGGTATGAATGGTCGTACTATCCTTGGTAGCACTATTTAGAAGATGAGTTTACA - 10860
      - Q  N  G  M  N  G  R  T  I  L  G  S  T  I  L  E  D  E  F  T
      -  R  M  V  *  M  V  V  L  S  L  V  A  L  F  *  K  M  S  L  H
      -   E  W  Y  E  W  S  Y  Y  P  W  *  H  Y  F  R  R  *  V  Y  T
10861 - CCATTTGATGTTGTTAGACAATGCTCTGGTGTTACCTTCCAAGGTAAGTTCAAGAAAATT - 10920
      - P  F  D  V  V  R  Q  C  S  G  V  T  F  Q  G  K  F  K  K  I
      -  H  L  M  L  L  D  N  A  L  V  L  P  S  K  V  S  S  R  K  L
      -   I  *  C  C  *  T  M  L  W  C  Y  L  P  R  *  V  Q  E  N  C
10921 - GTTAAGGGCACTCATCATTGGATGCTTTTAACTTTCTTGACATCACTATTGATTCTTGTT - 10980
      - V  K  G  T  H  H  W  M  L  L  T  F  L  T  S  L  L  I  L  V
      -  L  R  A  L  I  I  G  C  F  *  L  S  *  H  H  Y  *  F  L  F
      -   *  G  H  S  S  L  D  A  F  N  F  L  D  I  T  I  D  S  C  S
10981 - CAAAGTACACAGTGGTCACTGTTTTTCTTTGTTTACGAGAATGCTTTCTTGCCATTTACT - 11040
      - Q  S  T  Q  W  S  L  F  F  F  V  Y  E  N  A  F  L  P  F  T
      -  K  V  H  S  G  H  C  F  S  L  F  T  R  M  L  S  C  H  L  L
      -   K  Y  T  V  V  T  V  F  L  C  L  R  E  C  F  L  A  I  Y  S
11041 - CTTGGTATTATGGCAATTGCTGCATGTGCTATGCTGCTTGTTAAGCATAAGCACGCATTC - 11100
      - L  G  I  M  A  I  A  A  C  A  M  L  L  V  K  H  K  H  A  F
      -  L  V  L  W  Q  L  L  H  V  L  C  C  L  L  S  I  S  T  H  S
      -   W  Y  Y  G  N  C  C  M  C  Y  A  A  C  *  A  *  A  R  I  L
11101 - TTGTGCTTGTTTCTGTTACCTTCTCTTGCAACAGTTGCTTACTTTAATATGGTCTACATG - 11160
      - L  C  L  F  L  L  P  S  L  A  T  V  A  Y  F  N  M  V  Y  M
      -  C  A  C  F  C  Y  L  L  L  Q  Q  L  L  T  L  I  W  S  T  C
      -   V  L  V  S  V  T  F  S  C  N  S  C  L  L  *  Y  G  L  H  A
11161 - CCTGCTAGCTGGGTGATGCGTATCATGACATGGCTTGAATTGGCTGACACTAGCTTGTCT - 11220
      - P  A  S  W  V  M  R  I  M  T  W  L  E  L  A  D  T  S  L  S
      -  L  L  A  G  *  C  V  S  *  H  G  L  N  W  L  T  L  A  C  L
      -   C  *  L  G  D  A  Y  H  D  M  A  *  I  G  *  H  *  L  V  W
11221 - GGTTATAGGCTTAAGGATTGTGTTATGTATGCTTCAGCTTTAGTTTTGCTTATTCTCATG - 11280
      - G  Y  R  L  K  D  C  V  M  Y  A  S  A  L  V  L  L  I  L  M
      -  V  I  G  L  R  I  V  L  C  M  L  Q  L  *  F  C  L  F  S  *
      -   L  *  A  *  G  L  C  Y  V  C  F  S  F  S  F  A  Y  S  H  D
11281 - ACAGCTCGCACTGTTTATGATGATGCTGCTAGACGTGTTTGGACACTGATGAATGTCATT - 11340
      - T  A  R  T  V  Y  D  D  A  A  R  R  V  W  T  L  M  N  V  I
      -  Q  L  A  L  F  M  M  M  L  L  D  V  F  G  H  *  *  M  S  L
      -   S  S  H  C  L  *  *  C  C  *  T  C  L  D  T  D  E  C  H  Y
11341 - ACACTTGTTTACAAAGTCTACTATGGTAATGCTTTAGATCAAGCTATTTCCATGTGGGCC - 11400
      - T  L  V  Y  K  V  Y  Y  G  N  A  L  D  Q  A  I  S  M  W  A
      -  H  L  F  T  K  S  T  M  V  M  L  *  I  K  L  F  P  C  G  P
      -   T  C  L  Q  S  L  L  W  *  C  F  R  S  S  Y  F  H  V  G  L
```

Figure 16-P

```
11401 - TTAGTTATTTCTGTAACCTCTAACTATTCTGGTGTCGTTACGACTATCATGTTTTTAGCT - 11460
       -L  V  I  S  V  T  S  N  Y  S  G  V  V  T  T  I  M  F  L  A
      -  *  L  F  L  *  P  L  T  I  L  V  S  L  R  L  S  C  F  *  L
      -   S  Y  F  C  N  L  *  L  F  W  C  R  Y  D  Y  H  V  F  S  *
11461 - AGAGCTATAGTGTTTGTGTGTGTTGAGTATTACCCATTGTTATTTATTACTGGCAACACC - 11520
       -R  A  I  V  F  V  C  V  E  Y  Y  P  L  L  F  I  T  G  N  T
      -  E  L  *  C  L  C  V  L  S  I  T  H  C  Y  L  L  L  A  T  P
      -   S  Y  S  V  C  V  C  *  V  L  P  I  V  I  Y  Y  W  Q  H  L
11521 - TTACAGTGTATCATGCTTGTTTATTGTTTCTTAGGCTATTGTTGCTGCTGCTACTTTGGC - 11580
       -L  Q  C  I  M  L  V  Y  C  F  L  G  Y  C  C  C  C  Y  F  G
      -  Y  S  V  S  C  L  F  I  V  S  *  A  I  V  A  A  A  T  L  A
      -   T  V  Y  H  A  C  L  L  F  L  R  L  L  L  L  L  L  L  W  P
11581 - CTTTTCTGTTTACTCAACCGTTACTTCAGGCTTACTCTTGGTGTTTATGACTACTTGGTC - 11640
       -L  F  C  L  L  N  R  Y  F  R  L  T  L  G  V  Y  D  Y  L  V
      -  F  S  V  Y  S  T  V  T  S  G  L  L  L  V  F  M  T  T  W  S
      -   F  L  F  T  Q  P  L  L  Q  A  Y  S  W  C  L  *  L  L  G  L
11641 - TCTACACAAGAATTTAGGTATATGAACTCCCAGGGGCTTTTGCCTCCTAAGAGTAGTATT - 11700
       -S  T  Q  E  F  R  Y  M  N  S  Q  G  L  L  P  P  K  S  S  I
      -  L  H  K  N  L  G  I  *  T  P  R  G  F  C  L  L  R  V  V  L
      -   Y  T  R  I  *  V  Y  E  L  P  G  A  F  A  S  *  E  *  Y  *
11701 - GATGCTTTCAAGCTTAACATTAAGTTGTTGGGTATTGGAGGTAAACCATGTATCAAGGTT - 11760
       -D  A  F  K  L  N  I  K  L  L  G  I  G  G  K  P  C  I  K  V
      -  M  L  S  S  L  T  L  S  C  W  V  L  E  V  N  H  V  S  R  L
      -   C  F  Q  A  *  H  *  V  V  G  Y  W  R  *  T  M  Y  Q  G  C
11761 - GCTACTGTACAGTCTAAAATGTCTGACGTAAAGTGCACATCTGTGGTACTGCTCTCGGTT - 11820
       -A  T  V  Q  S  K  M  S  D  V  K  C  T  S  V  V  L  L  S  V
      -  L  L  Y  S  L  K  C  L  T  *  S  A  H  L  W  Y  C  S  R  F
      -   Y  C  T  V  *  N  V  *  R  K  V  H  I  C  G  T  A  L  G  S
11821 - CTTCAACAACTTAGAGTAGAGTCATCTTCTAAATTGTGGGCACAATGTGTACAACTCCAC - 11880
       -L  Q  Q  L  R  V  E  S  S  S  K  L  W  A  Q  C  V  Q  L  H
      -  F  N  N  L  E  *  S  H  L  L  N  C  G  H  N  V  Y  N  S  T
      -   S  T  T  *  S  R  V  I  F  *  I  V  G  T  M  C  T  T  P  Q
11881 - AATGATATTCTTCTTGCAAAAGACACAACTGAAGCTTTCGAGAAGATGGTTTCTCTTTTG - 11940
       -N  D  I  L  L  A  K  D  T  T  E  A  F  E  K  M  V  S  L  L
      -  M  I  F  F  L  Q  K  T  Q  L  K  L  S  R  R  W  F  L  F  C
      -   *  Y  S  S  C  K  R  H  N  *  S  F  R  E  D  G  F  S  F  V
11941 - TCTGTTTTGCTATCCATGCAGGGTGCTGTAGACATTAATAGGTTGTGCGAGGAAATGCTC - 12000
       -S  V  L  L  S  M  Q  G  A  V  D  I  N  R  L  C  E  E  M  L
      -  L  F  C  Y  P  C  R  V  L  *  T  L  I  G  C  A  R  K  C  S
      -   C  F  A  I  H  A  G  C  C  R  H  *  *  V  V  R  G  N  A  R
12001 - GATAACCGTGCTACTCTTCAGGCTATTGCTTCAGAATTTAGTTCTTTACCATCATATGCC - 12060
       -D  N  R  A  T  L  Q  A  I  A  S  E  F  S  S  L  P  S  Y  A
      -  I  T  V  L  L  F  R  L  L  L  Q  N  L  V  L  Y  H  H  M  P
      -   *  P  C  Y  S  S  G  Y  C  F  R  I  *  F  F  T  I  I  C  R
12061 - GCTTATGCCACTGCCCAGGAGGCCTATGAGCAGGCTGTAGCTAATGGTGATTCTGAAGTC - 12120
       -A  Y  A  T  A  Q  E  A  Y  E  Q  A  V  A  N  G  D  S  E  V
      -  L  M  P  L  P  R  R  P  M  S  R  L  *  L  M  V  I  L  K  S
      -   L  C  H  C  P  G  G  L  *  A  G  C  S  *  W  *  F  *  S  R
```

Figure 16-Q

```
12121 - GTTCTCAAAAAGTTAAAGAAATCTTTGAATGTGGCTAAATCTGAGTTTGACCGTGATGCT - 12180
      -V  L  K  K  L  K  K  S  L  N  V  A  K  S  E  F  D  R  D  A
      -  F  S  K  S  *  R  N  L  *  M  W  L  N  L  S  L  T  V  M  L
      -   S  Q  K  V  K  E  I  F  E  C  G  *  I  *  V  *  P  *  C  C
12181 - GCCATGCAACGCAAGTTGGAAAAGATGGCAGATCAGGCTATGACCCAAATGTACAAACAG - 12240
      -A  M  Q  R  K  L  E  K  M  A  D  Q  A  M  T  Q  M  Y  K  Q
      -  P  C  N  A  S  W  K  R  W  Q  I  R  L  *  P  K  C  T  N  R
      -   H  A  T  Q  V  G  K  D  G  R  S  G  Y  D  P  N  V  Q  T  G
12241 - GCAAGATCTGAGGACAAGAGGGCAAAAGTAACTAGTGCTATGCAAACAATGCTCTTCACT - 12300
      -A  R  S  E  D  K  R  A  K  V  T  S  A  M  Q  T  M  L  F  T
      -  Q  D  L  R  T  R  G  Q  K  *  L  V  L  C  K  Q  C  S  S  L
      -   K  I  *  G  Q  E  G  K  S  N  *  C  Y  A  N  N  A  L  H  Y
12301 - ATGCTTAGGAAGCTTGATAATGATGCACTTAACAACATTATCAACAATGCGCGTGATGGT - 12360
      -M  L  R  K  L  D  N  D  A  L  N  N  I  I  N  N  A  R  D  G
      -  C  L  G  S  L  I  M  M  H  L  T  T  L  S  T  M  R  V  M  V
      -   A  *  E  A  *  *  *  C  T  *  Q  H  Y  Q  Q  C  A  *  W  L
12361 - TGTGTTCCACTCAACATCATACCATTGACTACAGCAGCCAAACTCATGGTTGTTGTCCCT - 12420
      -C  V  P  L  N  I  I  P  L  T  T  A  A  K  L  M  V  V  V  P
      -  V  F  H  S  T  S  Y  H  *  L  Q  Q  P  N  S  W  L  L  S  L
      -   C  S  T  Q  H  H  T  I  D  Y  S  S  Q  T  H  G  C  C  P  *
12421 - GATTATGGTACCTACAAGAACACTTGTGATGGTAACACCTTTACATATGCATCTGCACTC - 12480
      -D  Y  G  T  Y  K  N  T  C  D  G  N  T  F  T  Y  A  S  A  L
      -  I  M  V  P  T  R  T  L  V  M  V  T  P  L  H  M  H  L  H  S
      -   L  W  Y  L  Q  E  H  L  *  W  *  H  L  Y  I  C  I  C  T  L
12481 - TGGGAAATCCAGCAAGTTGTTGATGCGGATAGCAAGATTGTTCAACTTAGTGAAATTAAC - 12540
      -W  E  I  Q  Q  V  V  D  A  D  S  K  I  V  Q  L  S  E  I  N
      -  G  K  S  S  K  L  L  M  R  I  A  R  L  F  N  L  V  K  L  T
      -   G  N  P  A  S  C  *  C  G  *  Q  D  C  S  T  *  *  N  *  H
12541 - ATGGACAATTCACCAAATTTGGCTTGGCCTCTTATTGTTACAGCTCTAAGAGCCAACTCA - 12600
      -M  D  N  S  P  N  L  A  W  P  L  I  V  T  A  L  R  A  N  S
      -  W  T  I  H  Q  I  W  L  G  L  L  L  L  Q  L  *  E  P  T  Q
      -   G  Q  F  T  K  F  G  L  A  S  Y  C  Y  S  S  K  S  Q  L  S
12601 - GCTGTTAAACTACAGAATAATGAACTGAGTCCAGTAGCACTACGACAGATGTCCTGTGCG - 12660
      -A  V  K  L  Q  N  N  E  L  S  P  V  A  L  R  Q  M  S  C  A
      -  L  L  N  Y  R  I  M  N  *  V  Q  *  H  Y  D  R  C  P  V  R
      -   C  *  T  T  E  *  *  T  E  S  S  S  T  T  T  D  V  L  C  G
12661 - GCTGGTACCACACAAACAGCTTGTACTGATGACAATGCACTTGCCTACTATAACAATTCG - 12720
      -A  G  T  T  Q  T  A  C  T  D  D  N  A  L  A  Y  Y  N  N  S
      -  L  V  P  H  K  Q  L  V  L  M  T  M  H  L  P  T  I  T  I  R
      -   W  Y  H  T  N  S  L  Y  *  *  Q  C  T  C  L  L  *  Q  F  E
12721 - AAGGGAGGTAGGTTTGTGCTGGCATTACTATCAGACCACCAAGATCTCAAATGGGCTAGA - 12780
      -K  G  G  R  F  V  L  A  L  L  S  D  H  Q  D  L  K  W  A  R
      -  R  E  V  G  L  C  W  H  Y  Y  Q  T  T  K  I  S  N  G  L  D
      -   G  R  *  V  C  A  G  I  T  I  R  P  P  R  S  Q  M  G  *  I
12781 - TTCCCTAAGAGTGATGGTACAGGTACAATTTACACAGAACTGGAACCACCTTGTAGGTTT - 12840
      -F  P  K  S  D  G  T  G  T  I  Y  T  E  L  E  P  P  C  R  F
      -  S  L  R  V  M  V  Q  V  Q  F  T  Q  N  W  N  H  L  V  G  L
      -   P  *  E  *  W  Y  R  Y  N  L  H  R  T  G  T  T  L  *  V  C
12841 - GTTACAGACACACCAAAAGGGCCTAAAGTGAAATACTTGTACTTCATCAAAGGCTTAAAC - 12900
      -V  T  D  T  P  K  G  P  K  V  K  Y  L  Y  F  I  K  G  L  N
      -  L  Q  T  H  Q  K  G  L  K  *  N  T  C  T  S  S  K  A  *  T
      -   Y  R  H  T  K  R  A  *  S  E  I  L  V  L  H  Q  R  L  K  Q
```

Figure 16-R

```
12901 - AACCTAAATAGAGGTATGGTGCTGGGCAGTTTAGCTGCTACAGTACGTCTTCAGGCTGGA - 12960
      - N  L  N  R  G  M  V  L  G  S  L  A  A  T  V  R  L  Q  A  G
      -  T  *  I  E  V  W  C  W  A  V  *  L  L  Q  Y  V  F  R  L  E
      -   P  K  *  R  Y  G  A  G  Q  F  S  C  Y  S  T  S  S  G  W  K
12961 - AATGCTACAGAAGTACCTGCCAATTCAACTGTGCTTTCCTTCTGTGCTTTTGCAGTAGAC - 13020
      - N  A  T  E  V  P  A  N  S  T  V  L  S  F  C  A  F  A  V  D
      -  M  L  Q  K  Y  L  P  I  Q  L  C  F  P  S  V  L  L  Q  *  T
      -   C  Y  R  S  T  C  Q  F  N  C  A  F  L  L  C  F  C  S  R  P
13021 - CCTGCTAAAGCATATAAGGATTACCTAGCAAGTGGAGGACAACCAATCACCAACTGTGTG - 13080
      - P  A  K  A  Y  K  D  Y  L  A  S  G  G  Q  P  I  T  N  C  V
      -  L  L  K  H  I  R  I  T  *  Q  V  E  D  N  Q  S  P  T  V  *
      -   C  *  S  I  *  G  L  P  S  K  W  R  T  T  N  H  Q  L  C  E
13081 - AAGATGTTGTGTACACACACTGGTACAGGACAGGCAATTACTGTAACACCAGAAGCTAAC - 13140
      - K  M  L  C  T  H  T  G  T  G  Q  A  I  T  V  T  P  E  A  N
      -  R  C  C  V  H  T  L  V  Q  D  R  Q  L  L  *  H  Q  K  L  T
      -   D  V  V  Y  T  H  W  Y  R  T  G  N  Y  C  N  T  R  S  *  H
13141 - ATGGACCAAGAGTCCTTTGGTGGTGCTTCATGTTGTCTGTATTGTAGATGCCACATTGAC - 13200
      - M  D  Q  E  S  F  G  G  A  S  C  C  L  Y  C  R  C  H  I  D
      -  W  T  K  S  P  L  V  V  L  H  V  V  C  I  V  D  A  T  L  T
      -   G  P  R  V  L  W  W  C  F  M  L  S  V  L  *  M  P  H  *  P
13201 - CATCCAAATCCTAAAGGATTCTGTGACTTGAAAGGTAAGTACGTCCAAATACCTACCACT - 13260
      - H  P  N  P  K  G  F  C  D  L  K  G  K  Y  V  Q  I  P  T  T
      -  I  Q  I  L  K  D  S  V  T  *  K  V  S  T  S  K  Y  L  P  L
      -   S  K  S  *  R  I  L  *  L  E  R  *  V  R  P  N  T  Y  H  L
13261 - TGTGCTAATGACCCAGTGGGTTTTACACTTAGAAACACAGTCTGTACCGTCTGCGGAATG - 13320
      - C  A  N  D  P  V  G  F  T  L  R  N  T  V  C  T  V  C  G  M
      -  V  L  M  T  Q  W  V  L  H  L  E  T  Q  S  V  P  S  A  E  C
      -   C  *  *  P  S  G  F  Y  T  *  K  H  S  L  Y  R  L  R  N  V
13321 - TGGAAAGGTTATGGCTGTAGTTGTGACCAACTCCGCGAACCCTTGATGCAGTCTGCGGAT - 13380
      - W  K  G  Y  G  C  S  C  D  Q  L  R  E  P  L  M  Q  S  A  D
      -  G  K  V  M  A  V  V  V  T  N  S  A  N  P  *  C  S  L  R  M
      -   E  R  L  W  L  *  L  *  P  T  P  R  T  L  D  A  V  C  G  C
13381 - GCATCAACGTTTTTAAACGGGTTTGCGGTGTAAGTGCAGCCCGTCTTACACCGTGCGGCA - 13440
      - A  S  T  F  L  N  G  F  A  V  *  V  Q  P  V  L  H  R  A  A
      -  H  Q  R  F  *  T  G  L  R  C  K  C  S  P  S  Y  T  V  R  H
      -   I  N  V  F  K  R  V  C  G  V  S  A  A  R  L  T  P  C  G  T
13441 - CAGGCACTAGTACTGATGTCGTCTACAGGGCTTTTGATATTTACAACGAAAAAAGTGCTG - 13500
      - Q  A  L  V  L  M  S  S  T  G  L  L  I  F  T  T  K  K  V  L
      -  R  H  *  Y  *  C  R  L  Q  G  F  *  Y  L  Q  R  K  K  C  W
      -   G  T  S  T  D  V  V  Y  R  A  F  D  I  Y  N  E  K  S  A  G
13501 - GTTTTGCAAAGTTCCTAAAAACTAATTGCTGTCGCTTCCAGGAGAAGGATGAGGAAGGCA - 13560
      - V  L  Q  S  S  *  K  L  I  A  V  A  S  R  R  R  M  R  K  A
      -  F  C  K  V  P  K  N  *  L  L  S  L  P  G  E  G  *  G  R  Q
      -   F  A  K  F  L  K  T  N  C  C  R  F  Q  E  K  D  E  E  G  N
13561 - ATTTATTAGACTCTTACTTTGTAGTTAAGAGGCATACTATGTCTAACTACCAACATGAAG - 13620
      - I  Y  *  T  L  T  L  *  L  R  G  I  L  C  L  T  T  N  M  K
      -  F  I  R  L  L  L  C  S  *  E  A  Y  Y  V  *  L  P  T  *  R
      -   L  L  D  S  Y  F  V  V  K  R  H  T  M  S  N  Y  Q  H  E  E
13621 - AGACTATTTATAACTTGGTTAAAGATTGTCCAGCGGTTGCTGTCCATGACTTTTTCAAGT - 13680
      - R  L  F  I  T  W  L  K  I  V  Q  R  L  L  S  M  T  F  S  S
      -  D  Y  L  *  L  G  *  R  L  S  S  G  C  C  P  *  L  F  Q  V
      -   T  I  Y  N  L  V  K  D  C  P  A  V  A  V  H  D  F  F  K  F
```

Figure 16-S

```
13681 - TTAGAGTAGATGGTGACATGGTACCACATATATCACGTCAGCGTCTAACTAAATACACAA - 13740
      - L  E  *  M  V  T  W  Y  H  I  Y  H  V  S  V  *  L  N  T  Q
      -  *  S  R  W  *  H  G  T  T  Y  I  T  S  A  S  N  *  I  H  N
      -   R  V  D  G  D  M  V  P  H  I  S  R  Q  R  L  T  K  Y  T  M
13741 - TGGCTGATTTAGTCTATGCTCTACGTCATTTTGATGAGGGTAATTGTGATACATTAAAAG - 13800
      - W  L  I  *  S  M  L  Y  V  I  L  M  R  V  I  V  I  H  *  K
      -  G  *  F  S  L  C  S  T  S  F  *  *  G  *  L  *  Y  I  K  R
      -   A  D  L  V  Y  A  L  R  H  F  D  E  G  N  C  D  T  L  K  E
13801 - AAATACTCGTCACATACAATTGCTGTGATGATGATTATTTCAATAAGAAGGATTGGTATG - 13860
      - K  Y  S  S  H  T  I  A  V  M  M  I  I  S  I  R  R  I  G  M
      -  N  T  R  H  I  Q  L  L  *  *  *  L  F  Q  *  E  G  L  V  *
      -   I  L  V  T  Y  N  C  C  D  D  D  Y  F  N  K  K  D  W  Y  D
13861 - ACTTCGTAGAGAATCCTGACATCTTACGCGTATATGCTAACTTAGGTGAGCGTGTACGCC - 13920
      - T  S  *  R  I  L  T  S  Y  A  Y  M  L  T  *  V  S  V  Y  A
      -  L  R  R  E  S  *  H  L  T  R  I  C  *  L  R  *  A  C  T  P
      -   F  V  E  N  P  D  I  L  R  V  Y  A  N  L  G  E  R  V  R  Q
13921 - AATCATTATTAAAGACTGTACAATTCTGCGATGCTATGCGTGATGCAGGCATTGTAGGCG - 13980
      - N  H  Y  *  R  L  Y  N  S  A  M  L  C  V  M  Q  A  L  *  A
      -  I  I  I  K  D  C  T  I  L  R  C  Y  A  *  C  R  H  C  R  R
      -   S  L  L  K  T  V  Q  F  C  D  A  M  R  D  A  G  I  V  G  V
13981 - TACTGACATTAGATAATCAGGATCTTAATGGGAACTGGTACGATTTCGGTGATTTCGTAC - 14040
      - Y  *  H  *  I  I  R  I  L  M  G  T  G  T  I  S  V  I  S  Y
      -  T  D  I  R  *  S  G  S  *  W  E  L  V  R  F  R  *  F  R  T
      -   L  T  L  D  N  Q  D  L  N  G  N  W  Y  D  F  G  D  F  V  Q
14041 - AAGTAGCACCAGGCTGCGGAGTTCCTATTGTGGATTCATATTACTCATTGCTGATGCCCA - 14100
      - K  *  H  Q  A  A  E  F  L  L  W  I  H  I  T  H  C  *  C  P
      -  S  S  T  R  L  R  S  S  Y  C  G  F  I  L  L  I  A  D  A  H
      -   V  A  P  G  C  G  V  P  I  V  D  S  Y  Y  S  L  L  M  P  I
14101 - TCCTCACTTTGACTAGGGCATTGGCTGCTGAGTCCCATATGGATGCTGATCTCGCAAAAC - 14160
      - S  S  L  *  L  G  H  W  L  L  S  P  I  W  M  L  I  S  Q  N
      -  P  H  F  D  *  G  I  G  C  *  V  P  Y  G  C  *  S  R  K  T
      -   L  T  L  T  R  A  L  A  A  E  S  H  M  D  A  D  L  A  K  P
14161 - CACTTATTAAGTGGGATTTGCTGAAATATGATTTTACGGAAGAGAGACTTTGTCTCTTCG - 14220
      - H  L  L  S  G  I  C  *  N  M  I  L  R  K  R  D  F  V  S  S
      -  T  Y  *  V  G  F  A  E  I  *  F  Y  G  R  E  T  L  S  L  R
      -   L  I  K  W  D  L  L  K  Y  D  F  T  E  E  R  L  C  L  F  D
14221 - ACCGTTATTTTAAATATTGGGACCAGACATACCATCCCAATTGTATTAACTGTTTGGATG - 14280
      - T  V  I  L  N  I  G  T  R  H  T  I  P  I  V  L  T  V  W  M
      -  P  L  F  *  I  L  G  P  D  I  P  S  Q  L  Y  *  L  F  G  *
      -   R  Y  F  K  Y  W  D  Q  T  Y  H  P  N  C  I  N  C  L  D  D
14281 - ATAGGTGTATCCTTCATTGTGCAAACTTTAATGTGTTATTTTCTACTGTGTTTCCACCTA - 14340
      - I  G  V  S  F  I  V  Q  T  L  M  C  Y  F  L  L  C  F  H  L
      -  *  V  Y  P  S  L  C  K  L  *  C  V  I  F  Y  C  V  S  T  Y
      -   R  C  I  L  H  C  A  N  F  N  V  L  F  S  T  V  F  P  P  T
14341 - CAAGTTTTGGACCACTAGTAAGAAAAATATTTGTAGATGGTGTTCCTTTTGTTGTTTCAA - 14400
      - Q  V  L  D  H  *  *  E  K  Y  L  *  M  V  F  L  L  L  F  Q
      -  K  F  W  T  T  S  K  K  N  I  C  R  W  C  S  F  C  C  F  N
      -   S  F  G  P  L  V  R  K  I  F  V  D  G  V  P  F  V  V  S  T
14401 - CTGGATACCATTTTCGTGAGTTAGGAGTCGTACATAATCAGGATGTAAACTTACATAGCT - 14460
      - L  D  T  I  F  V  S  *  E  S  Y  I  I  R  M  *  T  Y  I  A
      -  W  I  P  F  S  *  V  R  S  R  T  *  S  G  C  K  L  T  *  L
      -   G  Y  H  F  R  E  L  G  V  V  H  N  Q  D  V  N  L  H  S  S
```

Figure 16-T

```
14461 - CGCGTCTCAGTTTCAAGGAACTTTTAGTGTATGCTGCTGATCCAGCTATGCATGCAGCTT - 14520
      - R  V  S  V  S  R  N  F  *  C  M  L  L  I  Q  L  C  M  Q  L
      -  A  S  Q  F  Q  G  T  F  S  V  C  C  *  S  S  Y  A  C  S  F
      -   R  L  S  F  K  E  L  L  V  Y  A  A  D  P  A  M  H  A  A  S
14521 - CTGGCAATTTATTGCTAGATAAACGCACTACATGCTTTTCAGTAGCTGCACTAACAAACA - 14580
      - L  A  I  Y  C  *  I  N  A  L  H  A  F  Q  *  L  H  *  Q  T
      -  W  Q  F  I  A  R  *  T  H  Y  M  L  F  S  S  C  T  N  K  Q
      -   G  N  L  L  L  D  K  R  T  T  C  F  S  V  A  A  L  T  N  N
14581 - ATGTTGCTTTTCAAACTGTCAAACCCGGTAATTTTAATAAAGACTTTTATGACTTTGCTG - 14640
      - M  L  L  F  K  L  S  N  P  V  I  L  I  K  T  F  M  T  L  L
      -  C  C  F  S  N  C  Q  T  R  *  F  *  *  R  L  L  *  L  C  C
      -   V  A  F  Q  T  V  K  P  G  N  F  N  K  D  F  Y  D  F  A  V
14641 - TGTCTAAAGGTTTCTTTAAGGAAGGAAGTTCTGTTGAACTAAAACACTTCTTCTTTGCTC - 14700
      - C  L  K  V  S  L  R  K  E  V  L  L  N  *  N  T  S  S  L  L
      -  V  *  R  F  L  *  G  R  K  F  C  *  T  K  T  L  L  L  C  S
      -   S  K  G  F  F  K  E  G  S  S  V  E  L  K  H  F  F  F  A  Q
14701 - AGGATGGCAACGCTGCTATCAGTGATTATGACTATTATCGTTATAATCTGCCAACAATGT - 14760
      - R  M  A  T  L  L  S  V  I  M  T  I  I  V  I  I  C  Q  Q  C
      -  G  W  Q  R  C  Y  Q  *  L  *  L  L  S  L  *  S  A  N  N  V
      -   D  G  N  A  A  I  S  D  Y  D  Y  Y  R  Y  N  L  P  T  M  C
14761 - GTGATATCAGACAACTCCTATTCGTAGTTGAAGTTGTTGATAAATACTTTGATTGTTACG - 14820
      - V  I  S  D  N  S  Y  S  *  L  K  L  L  I  N  T  L  I  V  T
      -  *  Y  Q  T  T  P  I  R  S  *  S  C  *  *  I  L  *  L  L  R
      -   D  I  R  Q  L  L  F  V  V  E  V  V  D  K  Y  F  D  C  Y  D
14821 - ATGGTGGCTGTATTAATGCCAACCAAGTAATCGTTAACAATCTGGATAAATCAGCTGGTT - 14880
      - M  V  A  V  L  M  P  T  K  *  S  L  T  I  W  I  N  Q  L  V
      -  W  W  L  Y  *  C  Q  P  S  N  R  *  Q  S  G  *  I  S  W  F
      -   G  G  C  I  N  A  N  Q  V  I  V  N  N  L  D  K  S  A  G  F
14881 - TCCCATTTAATAAATGGGGTAAGGCTAGACTTTATTATGACTCAATGAGTTATGAGGATC - 14940
      - S  H  L  I  N  G  V  R  L  D  F  I  M  T  Q  *  V  M  R  I
      -  P  I  *  *  M  G  *  G  *  T  L  L  *  L  N  E  L  *  G  S
      -   P  F  N  K  W  G  K  A  R  L  Y  Y  D  S  M  S  Y  E  D  Q
14941 - AAGATGCACTTTTCGCGTATACTAAGCGTAATGTCATCCCTACTATAACTCAAATGAATC - 15000
      - K  M  H  F  S  R  I  L  S  V  M  S  S  L  L  *  L  K  *  I
      -  R  C  T  F  R  V  Y  *  A  *  C  H  P  Y  Y  N  S  N  E  S
      -   D  A  L  F  A  Y  T  K  R  N  V  I  P  T  I  T  Q  M  N  L
15001 - TTAAGTATGCCATTAGTGCAAAGAATAGAGCTCGCACCGTAGCTGGTGTCTCTATCTGTA - 15060
      - L  S  M  P  L  V  Q  R  I  E  L  A  P  *  L  V  S  L  S  V
      -  *  V  C  H  *  C  K  E  *  S  S  H  R  S  W  C  L  Y  L  *
      -   K  Y  A  I  S  A  K  N  R  A  R  T  V  A  G  V  S  I  C  S
15061 - GTACTATGACAAATAGACAGTTTCATCAGAAATTATTGAAGTCAATAGCCGCCACTAGAG - 15120
      - V  L  *  Q  I  D  S  F  I  R  N  Y  *  S  Q  *  P  P  L  E
      -  Y  Y  D  K  *  T  V  S  S  E  I  I  E  V  N  S  R  H  *  R
      -   T  M  T  N  R  Q  F  H  Q  K  L  L  K  S  I  A  A  T  R  G
15121 - GAGCTACTGTGGTAATTGGAACAAGCAAGTTTTACGGTGGCTGGCATAATATGTTAAAAA - 15180
      - E  L  L  W  *  L  E  Q  A  S  F  T  V  A  G  I  I  C  *  K
      -  S  Y  C  G  N  W  N  K  Q  V  L  R  W  L  A  *  Y  V  K  N
      -   A  T  V  V  I  G  T  S  K  F  Y  G  G  W  H  N  M  L  K  T
```

Figure 16-U

```
15181 - CTGTTTACAGTGATGTAGAAACTCCACACCTTATGGGTTGGGATTATCCAAAATGTGACA - 15240
      - L  F  T  V  M  *  K  L  H  T  L  W  V  G  I  I  Q  N  V  T
      -  C  L  Q  *  C  R  N  S  T  P  Y  G  L  G  L  S  K  M  *  Q
      -   V  Y  S  D  V  E  T  P  H  L  M  G  W  D  Y  P  K  C  D  R
15241 - GAGCCATGCCTAACATGCTTAGGATAATGGCCTCTCTTGTTCTTGCTCGCAAACATAACA - 15300
      - E  P  C  L  T  C  L  G  *  W  P  L  L  F  L  L  A  N  I  T
      -  S  H  A  *  H  A  *  D  N  G  L  S  C  S  C  S  Q  T  *  H
      -   A  M  P  N  M  L  R  I  M  A  S  L  V  L  A  R  K  H  N  T
15301 - CTTGCTGTAACTTATCACACCGTTTCTACAGGTTAGCTAACGAGTGTGCGCAAGTATTAA - 15360
      - L  A  V  T  Y  H  T  V  S  T  G  *  L  T  S  V  R  K  Y  *
      -  L  L  *  L  I  T  P  F  L  Q  V  S  *  R  V  C  A  S  I  K
      -   C  C  N  L  S  H  R  F  Y  R  L  A  N  E  C  A  Q  V  L  S
15361 - GTGAGATGGTCATGTGTGGCGGCTCACTATATGTTAAACCAGGTGGAACATCATCCGGTG - 15420
      - V  R  W  S  C  V  A  A  H  Y  M  L  N  Q  V  E  H  H  P  V
      -  *  D  G  H  V  W  R  L  T  I  C  *  T  R  W  N  I  I  R  *
      -   E  M  V  M  C  G  G  S  L  Y  V  K  P  G  G  T  S  S  G  D
15421 - ATGCTACAACTGCTTATGCTAATAGTGTCTTTAACATTTGTCAAGCTGTTACAGCCAATG - 15480
      - M  L  Q  L  L  M  L  I  V  S  L  T  F  V  K  L  L  Q  P  M
      -  C  Y  N  C  L  C  *  *  C  L  *  H  L  S  S  C  Y  S  Q  C
      -   A  T  T  A  Y  A  N  S  V  F  N  I  C  Q  A  V  T  A  N  V
15481 - TAAATGCACTTCTTTCAACTGATGGTAATAAGATAGCTGACAAGTATGTCCGCAATCTAC - 15540
      - *  M  H  F  F  Q  L  M  V  I  R  *  L  T  S  M  S  A  I  Y
      -  K  C  T  S  F  N  *  W  *  *  D  S  *  Q  V  C  P  Q  S  T
      -   N  A  L  L  S  T  D  G  N  K  I  A  D  K  Y  V  R  N  L  Q
15541 - AACACAGGCTCTATGAGTGTCTCTATAGAAATAGGGATGTTGATCATGAATTCGTGGATG - 15600
      - N  T  G  S  M  S  V  S  I  E  I  G  M  L  I  M  N  S  W  M
      -  T  Q  A  L  *  V  S  L  *  K  *  G  C  *  S  *  I  R  G  *
      -   H  R  L  Y  E  C  L  Y  R  N  R  D  V  D  H  E  F  V  D  E
15601 - AGTTTACGCTTACCTGCGTAAACATTTCTCCATGATGATTCTTTCTGATGATGCCGTTG - 15660
      - S  F  T  L  T  C  V  N  I  S  P  *  *  F  F  L  M  M  P  L
      -  V  L  R  L  P  A  *  T  F  L  H  D  D  S  F  *  *  C  R  C
      -   F  Y  A  Y  L  R  K  H  F  S  M  M  I  L  S  D  D  A  V  V
15661 - TGTGCTATAACAGTAACTATGCGGCTCAAGGTTTAGTAGCTAGCATTAAGAACTTTAAGG - 15720
      - C  A  I  T  V  T  M  R  L  K  V  *  *  L  A  L  R  T  L  R
      -  V  L  *  Q  *  L  C  G  S  R  F  S  S  *  H  *  E  L  *  G
      -   C  Y  N  S  N  Y  A  A  Q  G  L  V  A  S  I  K  N  F  K  A
15721 - CAGTTCTTTATTATCAAAATAATGTGTTCATGTCTGAGGCAAAATGTTGGACTGAGACTG - 15780
      - Q  F  F  I  I  K  I  M  C  S  C  L  R  Q  N  V  G  L  R  L
      -  S  S  L  L  S  K  *  C  V  H  V  *  G  K  M  L  D  *  D  *
      -   V  L  Y  Y  Q  N  N  V  F  M  S  E  A  K  C  W  T  E  T  D
15781 - ACCTTACTAAAGGACCTCACGAATTTTGCTCACAGCATACAATGCTAGTTAAACAAGGAG - 15840
      - T  L  L  K  D  L  T  N  F  A  H  S  I  Q  C  *  L  N  K  E
      -  P  Y  *  R  T  S  R  I  L  L  T  A  Y  N  A  S  *  T  R  R
      -   L  T  K  G  P  H  E  F  C  S  Q  H  T  M  L  V  K  Q  G  D
15841 - ATGATTACGTGTACCTGCCTTACCCAGATCCATCAAGAATATTAGGCGCAGGCTGTTTTG - 15900
      - M  I  T  C  T  C  L  T  Q  I  H  Q  E  Y  *  A  Q  A  V  L
      -  *  L  R  V  P  A  L  P  R  S  I  K  N  I  R  R  R  L  F  C
      -   D  Y  V  Y  L  P  Y  P  D  P  S  R  I  L  G  A  G  C  F  V
15901 - TCGATGATATTGTCAAAACAGATGGTACACTTATGATTGAAAGGTTCGTGTCACTGGCTA - 15960
      - S  M  I  L  S  K  Q  M  V  H  L  *  L  K  G  S  C  H  W  L
      -  R  *  Y  C  Q  N  R  W  Y  T  Y  D  *  K  V  R  V  T  G  Y
      -   D  D  I  V  K  T  D  G  T  L  M  I  E  R  F  V  S  L  A  I
```

Figure 16-V

```
15961 - TTGATGCTTACCCACTTACAAAACATCCTAATCAGGAGTATGCTGATGTCTTTCACTTGT - 16020
      - L  M  L  T  H  L  Q  N  I  L  I  R  S  M  L  M  S  F  T  C
      -  *  C  L  P  T  Y  K  T  S  *  S  G  V  C  *  C  L  S  L  V
      -   D  A  Y  P  L  T  K  H  P  N  Q  E  Y  A  D  V  F  H  L  Y
16021 - ATTTACAATACATTAGAAAGTTACATGATGAGCTTACTGGCCACATGTTGGACATGTATT - 16080
      - I  Y  N  T  L  E  S  Y  M  M  S  L  L  A  T  C  W  T  C  I
      -  F  T  I  H  *  K  V  T  *  *  A  Y  W  P  H  V  G  H  V  F
      -   L  Q  Y  I  R  K  L  H  D  E  L  T  G  H  M  L  D  M  Y  S
16081 - CCGTAATGCTAACTAATGATAACACCTCACGGTACTGGGAACCTGAGTTTTATGAGGCTA - 16140
      - P  *  C  *  L  M  I  T  P  H  G  T  G  N  L  S  F  M  R  L
      -  R  N  A  N  *  *  *  H  L  T  V  L  G  T  *  V  L  *  G  Y
      -   V  M  L  T  N  D  N  T  S  R  Y  W  E  P  E  F  Y  E  A  M
16141 - TGTACACACCACATACAGTCTTGCAGGCTGTAGGTGCTTGTGTATTGTGCAATTCACAGA - 16200
      - C  T  H  H  I  Q  S  C  R  L  *  V  L  V  Y  C  A  I  H  R
      -  V  H  T  T  Y  S  L  A  G  C  R  C  L  C  I  V  Q  F  T  D
      -   Y  T  P  H  T  V  L  Q  A  V  G  A  C  V  L  C  N  S  Q  T
16201 - CTTCACTTCGTTGCGGTGCCTGTATTAGGAGACCATTCCTATGTTGCAAGTGCTGCTATG - 16260
      - L  H  F  V  A  V  P  V  L  G  D  H  S  Y  V  A  S  A  A  M
      -  F  T  S  L  R  C  L  Y  *  E  T  I  P  M  L  Q  V  L  L  *
      -   S  L  R  C  G  A  C  I  R  R  P  F  L  C  C  K  C  C  Y  D
16261 - ACCATGTCATTTCAACATCACACAAATTAGTGTTGTCTGTTAATCCCTATGTTTGCAATG - 16320
      - T  M  S  F  Q  H  H  T  N  *  C  C  L  L  I  P  M  F  A  M
      -  P  C  H  F  N  I  T  Q  I  S  V  V  C  *  S  L  C  L  Q  C
      -   H  V  I  S  T  S  H  K  L  V  L  S  V  N  P  Y  V  C  N  A
16321 - CCCCAGGTTGTGATGTCACTGATGTGACACAACTGTATCTAGGAGGTATGAGCTATTATT - 16380
      - P  Q  V  V  M  S  L  M  *  H  N  C  I  *  E  V  *  A  I  I
      -  P  R  L  *  C  H  *  C  D  T  T  V  S  R  R  Y  E  L  L  L
      -   P  G  C  D  V  T  D  V  T  Q  L  Y  L  G  G  M  S  Y  Y  C
16381 - GCAAGTCACATAAGCCTCCCATTAGTTTTCCATTATGTGCTAATGGTCAGGTTTTTGGTT - 16440
      - A  S  H  I  S  L  P  L  V  F  H  Y  V  L  M  V  R  F  L  V
      -  Q  V  T  *  A  S  H  *  F  S  I  M  C  *  W  S  G  F  W  F
      -   K  S  H  K  P  P  I  S  F  P  L  C  A  N  G  Q  V  F  G  L
16441 - TATACAAAAACACATGTGTAGGCAGTGACAATGTCACTGACTTCAATGCGATAGCAACAT - 16500
      - Y  T  K  T  H  V  *  A  V  T  M  S  L  T  S  M  R  *  Q  H
      -  I  Q  K  H  M  C  R  Q  *  Q  C  H  *  L  Q  C  D  S  N  M
      -   Y  K  N  T  C  V  G  S  D  N  V  T  D  F  N  A  I  A  T  C
16501 - GTGATTGGACTAATGCTGGCGATTACATACTTGCCAACACTTGTACTGAGAGACTCAAGC - 16560
      - V  I  G  L  M  L  A  I  T  Y  L  P  T  L  V  L  R  D  S  S
      -  *  L  D  *  C  W  R  L  H  T  C  Q  H  L  Y  *  E  T  Q  A
      -   D  W  T  N  A  G  D  Y  I  L  A  N  T  C  T  E  R  L  K  L
16561 - TTTTCGCAGCAGAAACGCTCAAAGCCACTGAGGAAACATTTAAGCTGTCATATGGTATTG - 16620
      - F  S  Q  Q  K  R  S  K  P  L  R  K  H  L  S  C  H  M  V  L
      -  F  R  S  R  N  A  Q  S  H  *  G  N  I  *  A  V  I  W  Y  C
      -   F  A  A  E  T  L  K  A  T  E  E  T  F  K  L  S  Y  G  I  A
16621 - CCACTGTACGCGAAGTACTCTCTGACAGAGAATTGCATCTTTCATGGGAGGTTGGAAAAC - 16680
      - P  L  Y  A  K  Y  S  L  T  E  N  C  I  F  H  G  R  L  E  N
      -  H  C  T  R  S  T  L  *  Q  R  I  A  S  F  M  G  G  W  K  T
      -   T  V  R  E  V  L  S  D  R  E  L  H  L  S  W  E  V  G  K  P
```

Figure 16-W

```
16681 - CTAGACCACCATTGAACAGAAACTATGTCTTTACTGGTTACCGTGTAACTAAAAATAGTA - 16740
      - L  D  H  H  *  T  E  T  M  S  L  L  V  T  V  *  L  K  I  V
      -  *  T  T  I  E  Q  K  L  C  L  Y  W  L  P  C  N  *  K  *  *
      -   R  P  P  L  N  R  N  Y  V  F  T  G  Y  R  V  T  K  N  S  K
16741 - AAGTACAGATTGGAGAGTACACCTTTGAAAAAGGTGACTATGGTGATGCTGTTGTGTACA - 16800
      - K  Y  R  L  E  S  T  P  L  K  K  V  T  M  V  M  L  L  C  T
      -  S  T  D  W  R  V  H  L  *  K  R  *  L  W  *  C  C  C  V  Q
      -   V  Q  I  G  E  Y  T  F  E  K  G  D  Y  G  D  A  V  V  Y  R
16801 - GAGGTACTACGACATACAAGTTGAATGTTGGTGATTACTTTGTGTTGACATCTCACACTG - 16860
      - E  V  L  R  H  T  S  *  M  L  V  I  T  L  C  *  H  L  T  L
      -  R  Y  Y  D  I  Q  V  E  C  W  *  L  L  C  V  D  I  S  H  C
      -   G  T  T  T  Y  K  L  N  V  G  D  Y  F  V  L  T  S  H  T  V
16861 - TAATGCCACTTAGTGCACCTACTCTAGTGCCACAAGAGCACTATGTGAGAATTACTGGCT - 16920
      - *  C  H  L  V  H  L  L  *  C  H  K  S  T  M  *  E  L  L  A
      -  N  A  T  *  C  T  Y  S  S  A  T  R  A  L  C  E  N  Y  W  L
      -   M  P  L  S  A  P  T  L  V  P  Q  E  H  Y  V  R  I  T  G  L
16921 - TGTACCCAACACTCAACATCTCAGATGAGTTTTCTAGCAATGTTGCAAATTATCAAAAGG - 16980
      - C  T  Q  H  S  T  S  Q  M  S  F  L  A  M  L  Q  I  I  K  R
      -  V  P  N  T  Q  H  L  R  *  V  F  *  Q  C  C  K  L  S  K  G
      -   Y  P  T  L  N  I  S  D  E  F  S  S  N  V  A  N  Y  Q  K  V
16981 - TCGGCATGCAAAAGTACTCTACACTCCAAGGACCACCTGGTACTGGTAAGAGTCATTTTG - 17040
      - S  A  C  K  S  T  L  H  S  K  D  H  L  V  L  V  R  V  I  L
      -  R  H  A  K  V  L  Y  T  P  R  T  T  W  Y  W  *  E  S  F  C
      -   G  M  Q  K  Y  S  T  L  Q  G  P  P  G  T  G  K  S  H  F  A
17041 - CCATCGGACTTGCTCTCTATTACCCATCTGCTCGCATAGTGTATACGGCATGCTCTCATG - 17100
      - P  S  D  L  L  S  I  T  H  L  L  A  *  C  I  R  H  A  L  M
      -  H  R  T  C  S  L  L  P  I  C  S  H  S  V  Y  G  M  L  S  C
      -   I  G  L  A  L  Y  Y  P  S  A  R  I  V  Y  T  A  C  S  H  A
17101 - CAGCTGTTGATGCCCTATGTGAAAAGGCATTAAAATATTTGCCCATAGATAAATGTAGTA - 17160
      - Q  L  L  M  P  Y  V  K  R  H  *  N  I  C  P  *  I  N  V  V
      -  S  C  *  C  P  M  *  K  G  I  K  I  F  A  H  R  *  M  *  *
      -   A  V  D  A  L  C  E  K  A  L  K  Y  L  P  I  D  K  C  S  R
17161 - GAATCATACCTGCGCGTGCGCGCGTAGAGTGTTTTGATAAATTCAAAGTGAATTCAACAC - 17220
      - E  S  Y  L  R  V  R  A  *  S  V  L  I  N  S  K  *  I  Q  H
      -  N  H  T  C  A  C  A  R  R  V  F  *  *  I  Q  S  E  F  N  T
      -   I  I  P  A  R  A  R  V  E  C  F  D  K  F  K  V  N  S  T  L
17221 - TAGAACAGTATGTTTTCTGCACTGTAAATGCATTGCCAGAAACAACTGCTGACATTGTAG - 17280
      - *  N  S  M  F  S  A  L  *  M  H  C  Q  K  Q  L  L  T  L  *
      -  R  T  V  C  F  L  H  C  K  C  I  A  R  N  N  C  *  H  C  S
      -   E  Q  Y  V  F  C  T  V  N  A  L  P  E  T  T  A  D  I  V  V
17281 - TCTTTGATGAAATCTCTATGGCTACTAATTATGACTTGAGTGTTGTCAATGCTAGACTTC - 17340
      - S  L  M  K  S  L  W  L  L  I  M  T  *  V  L  S  M  L  D  F
      -  L  *  *  N  L  Y  G  Y  *  L  *  L  E  C  C  Q  C  *  T  S
      -   F  D  E  I  S  M  A  T  N  Y  D  L  S  V  V  N  A  R  L  R
17341 - GTGCAAAACACTACGTCTATATTGGCGATCCTGCTCAATTACCAGCCCCCCGCACATTGC - 17400
      - V  Q  N  T  T  S  I  L  A  I  L  L  N  Y  Q  P  P  A  H  C
      -  C  K  T  L  R  L  Y  W  R  S  C  S  I  T  S  P  P  H  I  A
      -   A  K  H  Y  V  Y  I  G  D  P  A  Q  L  P  A  P  R  T  L  L
17401 - TGACTAAAGGCACACTAGAACCAGAATATTTTAATTCAGTGTGCAGACTTATGAAAACAA - 17460
      - *  L  K  A  H  *  N  Q  N  I  L  I  Q  C  A  D  L  *  K  Q
      -  D  *  R  H  T  R  T  R  I  F  *  F  S  V  Q  T  Y  E  N  N
      -   T  K  G  T  L  E  P  E  Y  F  N  S  V  C  R  L  M  K  T  I
```

Figure 16-X

```
17461 - TAGGTCCAGACATGTTCCTTGGAACTTGTCGCCGTTGTCCTGCTGAAATTGTTGACACTG - 17520
      - *  V  Q  T  C  S  L  E  L  V  A  V  V  L  L  K  L  L  T  L
      -  R  S  R  H  V  P  W  N  L  S  P  L  S  C  *  N  C  *  H  C
      -   G  P  D  M  F  L  G  T  C  R  R  C  P  A  E  I  V  D  T  V
17521 - TGAGTGCTTTAGTTTATGACAATAAGCTAAAAGCACACAAGGATAAGTCAGCTCAATGCT - 17580
      - *  V  L  *  F  M  T  I  S  *  K  H  T  R  I  S  Q  L  N  A
      -  E  C  F  S  L  *  Q  *  A  K  S  T  Q  G  *  V  S  S  M  L
      -   S  A  L  V  Y  D  N  K  L  K  A  H  K  D  K  S  A  Q  C  F
17581 - TCAAAATGTTCTACAAAGGTGTTATTACACATGATGTTTCATCTGCAATCAACAGACCTC - 17640
      - S  K  C  S  T  K  V  L  L  H  M  M  F  H  L  Q  S  T  D  L
      -  Q  N  V  L  Q  R  C  Y  Y  T  *  C  F  I  C  N  Q  Q  T  S
      -   K  M  F  Y  K  G  V  I  T  H  D  V  S  S  A  I  N  R  P  Q
17641 - AAATAGGCGTTGTAAGAGAATTTCTTACACGCAATCCTGCTTGGAGAAAAGCTGTTTTTA - 17700
      - K  *  A  L  *  E  N  F  L  H  A  I  L  L  G  E  K  L  F  L
      -  N  R  R  C  K  R  I  S  Y  T  Q  S  C  L  E  K  S  C  F  Y
      -   I  G  V  V  R  E  F  L  T  R  N  P  A  W  R  K  A  V  F  I
17701 - TCTCACCTTATAATTCACAGAACGCTGTAGCTTCAAAAATCTTAGGATTGCCTACGCAGA - 17760
      - S  H  L  I  I  H  R  T  L  *  L  Q  K  S  *  D  C  L  R  R
      -  L  T  L  *  F  T  E  R  C  S  F  K  N  L  R  I  A  Y  A  D
      -   S  P  Y  N  S  Q  N  A  V  A  S  K  I  L  G  L  P  T  Q  T
17761 - CTGTTGATTCATCACAGGGTTCTGAATATGACTATGTCATATTCACACAAACTACTGAAA - 17820
      - L  L  I  H  H  R  V  L  N  M  T  M  S  Y  S  H  K  L  L  K
      -  C  *  F  I  T  G  F  *  I  *  L  C  H  I  H  T  N  Y  *  N
      -   V  D  S  S  Q  G  S  E  Y  D  Y  V  I  F  T  Q  T  T  E  T
17821 - CAGCACACTCTTGTAATGTCAACCGCTTCAATGTGGCTATCACAAGGGCAAAAATTGGCA - 17880
      - Q  H  T  L  V  M  S  T  A  S  M  W  L  S  Q  G  Q  K  L  A
      -  S  T  L  L  *  C  Q  P  L  Q  C  G  Y  H  K  G  K  N  W  H
      -   A  H  S  C  N  V  N  R  F  N  V  A  I  T  R  A  K  I  G  I
17881 - TTTTGTGCATAATGTCTGATAGAGATCTTTATGACAAACTGCAATTTACAAGTCTAGAAA - 17940
      - F  C  A  *  C  L  I  E  I  F  M  T  N  C  N  L  Q  V  *  K
      -  F  V  H  N  V  *  *  R  S  L  *  Q  T  A  I  Y  K  S  R  N
      -   L  C  I  M  S  D  R  D  L  Y  D  K  L  Q  F  T  S  L  E  I
17941 - TACCACGTCGCAATGTGGCTACATTACAAGCAGAAAATGTAACTGGACTTTTTAAGGACT - 18000
      - Y  H  V  A  M  W  L  H  Y  K  Q  K  M  *  L  D  F  L  R  T
      -  T  T  S  Q  C  G  Y  I  T  S  R  K  C  N  W  T  F  *  G  L
      -   P  R  R  N  V  A  T  L  Q  A  E  N  V  T  G  L  F  K  D  C
18001 - GTAGTAAGATCATTACTGGTCTTCATCCTACACAGGCACCTACACACCTCAGCGTTGATA - 18060
      - V  V  R  S  L  L  V  F  I  L  H  R  H  L  H  T  S  A  L  I
      -  *  *  D  H  Y  W  S  S  S  Y  T  G  T  Y  T  P  Q  R  *  Y
      -   S  K  I  I  T  G  L  H  P  T  Q  A  P  T  H  L  S  V  D  I
18061 - TAAAATTCAAGACTGAAGGATTATGTGTTGACATACCAGGCATACCAAAGGACATGACCT - 18120
      - *  N  S  R  L  K  D  Y  V  L  T  Y  Q  A  Y  Q  R  T  *  P
      -  K  I  Q  D  *  R  I  M  C  *  H  T  R  H  T  K  G  H  D  L
      -   K  F  K  T  E  G  L  C  V  D  I  P  G  I  P  K  D  M  T  Y
18121 - ACCGTAGACTCATCTCTATGATGGGTTTCAAAATGAATTACCAAGTCAATGGTTACCCTA - 18180
      - T  V  D  S  S  L  *  W  V  S  K  *  I  T  K  S  M  V  T  L
      -  P  *  T  H  L  Y  D  G  F  Q  N  E  L  P  S  Q  W  L  P  *
      -   R  R  L  I  S  M  M  G  F  K  M  N  Y  Q  V  N  G  Y  P  N
```

Figure 16-Y

```
                18181 -
ATATGTTTATCACCCGCGAAGAAGCTATTCGTCACGTTCGTGCGTGGATTGGCTTTGATG - 18240
      - I  C  L  S  P  A  K  K  L  F  V  T  F  V  R  G  L  A  L  M
      -  Y  V  Y  H  P  R  R  S  Y  S  S  R  S  C  V  D  W  L  *  C
      -   M  F  I  T  R  E  E  A  I  R  H  V  R  A  W  I  G  F  D  V
18241 - TAGAGGGCTGTCATGCAACTAGAGATGCTGTGGGTACTAACCTACCTCTCCAGCTAGGAT - 18300
      - *  R  A  V  M  Q  L  E  M  L  W  V  L  T  Y  L  S  S  *  D
      -  R  G  L  S  C  N  *  R  C  C  G  Y  *  P  T  S  P  A  R  I
      -   E  G  C  H  A  T  R  D  A  V  G  T  N  L  P  L  Q  L  G  F
18301 - TTTCTACAGGTGTTAACTTAGTAGCTGTACCGACTGGTTATGTTGACACTGAAAATAACA - 18360
      - F  L  Q  V  L  T  *  *  L  Y  R  L  V  M  L  T  L  K  I  T
      -  F  Y  R  C  *  L  S  S  C  T  D  W  L  C  *  H  *  K  *  H
      -   S  T  G  V  N  L  V  A  V  P  T  G  Y  V  D  T  E  N  N  T
18361 - CAGAATTCACCAGAGTTAATGCAAAACCTCCACCAGGTGACCAGTTTAAACATCTTATAC - 18420
      - Q  N  S  P  E  L  M  Q  N  L  H  Q  V  T  S  L  N  I  L  Y
      -  R  I  H  Q  S  *  C  K  T  S  T  R  *  P  V  *  T  S  Y  T
      -   E  F  T  R  V  N  A  K  P  P  P  G  D  Q  F  K  H  L  I  P
18421 - CACTCATGTATAAAGGCTTGCCCTGGAATGTAGTGCGTATTAAGATAGTACAAATGCTCA - 18480
      - H  S  C  I  K  A  C  P  G  M  *  C  V  L  R  *  Y  K  C  S
      -  T  H  V  *  R  L  A  L  E  C  S  A  Y  *  D  S  T  N  A  Q
      -   L  M  Y  K  G  L  P  W  N  V  V  R  I  K  I  V  Q  M  L  S
18481 - GTGATACACTGAAAGGATTGTCAGACAGAGTCGTGTTCGTCCTTTGGGCGCATGGCTTTG - 18540
      - V  I  H  *  K  D  C  Q  T  E  S  C  S  S  F  G  R  M  A  L
      -  *  Y  T  E  R  I  V  R  Q  S  R  V  R  P  L  G  A  W  L  *
      -   D  T  L  K  G  L  S  D  R  V  V  F  V  L  W  A  H  G  F  E
18541 - AGCTTACATCAATGAAGTACTTTGTCAAGATTGGACCTGAAAGAACGTGTTGTCTGTGTG - 18600
      - S  L  H  Q  *  S  T  L  S  R  L  D  L  K  E  R  V  V  C  V
      -  A  Y  I  N  E  V  L  C  Q  D  W  T  *  K  N  V  L  S  V  *
      -   L  T  S  M  K  Y  F  V  K  I  G  P  E  R  T  C  C  L  C  D
18601 - ACAAACGTGCAACTTGCTTTTCTACTTCATCAGATACTTATGCCTGCTGGAATCATTCTG - 18660
      - T  N  V  Q  L  A  F  L  L  H  Q  I  L  M  P  A  G  I  I  L
      -  Q  T  C  N  L  L  F  Y  F  I  R  Y  L  C  L  L  E  S  F  C
      -   K  R  A  T  C  F  S  T  S  S  D  T  Y  A  C  W  N  H  S  V
18661 - TGGGTTTTGACTATGTCTATAACCCATTTATGATTGATGTTCAGCAGTGGGGCTTTACGG - 18720
      - W  V  L  T  M  S  I  T  H  L  *  L  M  F  S  S  G  A  L  R
      -  G  F  *  L  C  L  *  P  I  Y  D  *  C  S  A  V  G  L  Y  G
      -   G  F  D  Y  V  Y  N  P  F  M  I  D  V  Q  Q  W  G  F  T  G
18721 - GTAACCTTCAGAGTAACCATGACCAACATTGCCAGGTACATGGAAATGCACATGTGGCTA - 18780
      - V  T  F  R  V  T  M  T  N  I  A  R  Y  M  E  M  H  M  W  L
      -  *  P  S  E  *  P  *  P  T  L  P  G  T  W  K  C  T  C  G  *
      -   N  L  Q  S  N  H  D  Q  H  C  Q  V  H  G  N  A  H  V  A  S
18781 - GTTGTGATGCTATCATGACTAGATGTTTAGCAGTCCATGAGTGCTTTGTTAAGCGCGTTG - 18840
      - V  V  M  L  S  *  L  D  V  *  Q  S  M  S  A  L  L  S  A  L
      -  L  *  C  Y  H  D  *  M  F  S  S  P  *  V  L  C  *  A  R  *
      -   C  D  A  I  M  T  R  C  L  A  V  H  E  C  F  V  K  R  V  D
18841 - ATTGGTCTGTTGAATACCCTATTATAGGAGATGAACTGAGGGTTAATTCTGCTTGCAGAA - 18900
      - I  G  L  L  N  T  L  L  *  E  M  N  *  G  L  I  L  L  A  E
      -  L  V  C  *  I  P  Y  Y  R  R  *  T  E  G  *  F  C  L  Q  K
      -   W  S  V  E  Y  P  I  I  G  D  E  L  R  V  N  S  A  C  R  K
18901 - AAGTACAACACATGGTTGTGAAGTCTGCATTGCTTGCTGATAAGTTTCCAGTTCTTCATG - 18960
      - K  Y  N  T  W  L  *  S  L  H  C  L  L  I  S  F  Q  F  F  M
      -  S  T  T  H  G  C  E  V  C  I  A  C  *  *  V  S  S  S  S  *
      -   V  Q  H  M  V  V  K  S  A  L  L  A  D  K  F  P  V  L  H  D
```

Figure 16-Z

```
18961 - ACATTGGAAATCCAAAGGCTATCAAGTGTGTGCCTCAGGCTGAAGTAGAATGGAAGTTCT - 19020
      - T  L  E  I  Q  R  L  S  S  V  C  L  R  L  K  *  N  G  S  S
      -  H  W  K  S  K  G  Y  Q  V  C  A  S  G  *  S  R  M  E  V  L
      -   I  G  N  P  K  A  I  K  C  V  P  Q  A  E  V  E  W  K  F  Y
19021 - ACGATGCTCAGCCATGTAGTGACAAAGCTTACAAAATAGAGGAACTCTTCTATTCTTATG - 19080
      - T  M  L  S  H  V  V  T  K  L  T  K  *  R  N  S  S  I  L  M
      -  R  C  S  A  M  *  *  Q  S  L  Q  N  R  G  T  L  L  F  L  C
      -   D  A  Q  P  C  S  D  K  A  Y  K  I  E  E  L  F  Y  S  Y  A
19081 - CTACACATCACGATAAATTCACTGATGGTGTTTGTTTGTTTTGGAATTGTAACGTTGATC - 19140
      - L  H  I  T  I  N  S  L  M  V  F  V  C  F  G  I  V  T  L  I
      -  Y  T  S  R  *  I  H  *  W  C  L  F  V  L  E  L  *  R  *  S
      -   T  H  H  D  K  F  T  D  G  V  C  L  F  W  N  C  N  V  D  R
19141 - GTTACCCAGCCAATGCAATTGTGTGTAGGTTTGACACAAGAGTCTTGTCAAACTTGAACT - 19200
      - V  T  Q  P  M  Q  L  C  V  G  L  T  Q  E  S  C  Q  T  *  T
      -  L  P  S  Q  C  N  C  V  *  V  *  H  K  S  L  V  K  L  E  L
      -   Y  P  A  N  A  I  V  C  R  F  D  T  R  V  L  S  N  L  N  L
19201 - TACCAGGCTGTGATGGTGGTAGTTTGTATGTGAATAAGCATGCATTCCACACTCCAGCTT - 19260
      - Y  Q  A  V  M  V  V  V  C  M  *  I  S  M  H  S  T  L  Q  L
      -  T  R  L  *  W  W  *  F  V  C  E  *  A  C  I  P  H  S  S  F
      -   P  G  C  D  G  G  S  L  Y  V  N  K  H  A  F  H  T  P  A  F
19261 - TCGATAAAAGTGCATTTACTAATTTAAAGCAATTGCCTTTCTTTTACTATTCTGATAGTC - 19320
      - S  I  K  V  H  L  L  I  *  S  N  C  L  S  F  T  I  L  I  V
      -  R  *  K  C  I  Y  *  F  K  A  I  A  F  L  L  L  F  *  *  S
      -   D  K  S  A  F  T  N  L  K  Q  L  P  F  F  Y  Y  S  D  S  P
19321 - CTTGTGAGTCTCATGGCAAACAAGTAGTGTCGGATATTGATTATGTTCCACTCAAATCTG - 19380
      - L  V  S  L  M  A  N  K  *  C  R  I  L  I  M  F  H  S  N  L
      -  L  *  V  S  W  Q  T  S  S  V  G  Y  *  L  C  S  T  Q  I  C
      -   C  E  S  H  G  K  Q  V  V  S  D  I  D  Y  V  P  L  K  S  A
19381 - CTACGTGTATTACACGATGCAATTTAGGTGGTGCTGTTTGCAGACACCATGCAAATGAGT - 19440
      - L  R  V  L  H  D  A  I  *  V  V  L  F  A  D  T  M  Q  M  S
      -  Y  V  Y  Y  T  M  Q  F  R  W  C  C  L  Q  T  P  C  K  *  V
      -   T  C  I  T  R  C  N  L  G  G  A  V  C  R  H  H  A  N  E  Y
19441 - ACCGACAGTACTTGGATGCATATAATATGATGATTTCTGCTGGATTTAGCCTATGGATTT - 19500
      - T  D  S  T  W  M  H  I  I  *  *  F  L  L  D  L  A  Y  G  F
      -  P  T  V  L  G  C  I  *  Y  D  D  F  C  W  I  *  P  M  D  L
      -   R  Q  Y  L  D  A  Y  N  M  M  I  S  A  G  F  S  L  W  I  Y
19501 - ACAAACAATTTGATACTTATAACCTGTGGAATACATTTACCAGGTTACAGAGTTTAGAAA - 19560
      - T  N  N  L  I  L  I  T  C  G  I  H  L  P  G  Y  R  V  *  K
      -  Q  T  I  *  Y  L  *  P  V  E  Y  I  Y  Q  V  T  E  F  R  K
      -   K  Q  F  D  T  Y  N  L  W  N  T  F  T  R  L  Q  S  L  E  N
19561 - ATGTGGCTTATAATGTTGTTAATAAAGGACACTTTGATGGACACGCCGGCGAAGCACCTG - 19620
      - M  W  L  I  M  L  L  I  K  D  T  L  M  D  T  P  A  K  H  L
      -  C  G  L  *  C  C  *  *  R  T  L  *  W  T  R  R  R  S  T  C
      -   V  A  Y  N  V  V  N  K  G  H  F  D  G  H  A  G  E  A  P  V
19621 - TTTCCATCATTAATAATGCTGTTTACACAAAGGTAGATGGTATTGATGTGGAGATCTTTG - 19680
      - F  P  S  L  I  M  L  F  T  Q  R  *  M  V  L  M  W  R  S  L
      -  F  H  H  *  *  C  C  L  H  K  G  R  W  Y  *  C  G  D  L  *
      -   S  I  I  N  N  A  V  Y  T  K  V  D  G  I  D  V  E  I  F  E
```

Figure 16-AA

```
19681 - AAAATAAGACAACACTTCCTGTTAATGTTGCATTTGAGCTTTGGGCTAAGCGTAACATTA - 19740
      - K  I  R  Q  H  F  L  L  M  L  H  L  S  F  G  L  S  V  T  L
      -  K  *  D  N  T  S  C  *  C  C  I  *  A  L  G  *  A  *  H  *
      -   N  K  T  T  L  P  V  N  V  A  F  E  L  W  A  K  R  N  I  K
19741 - AACCAGTGCCAGAGATTAAGATACTCAATAATTTGGGTGTTGATATCGCTGCTAATACTG - 19800
      - N  Q  C  Q  R  L  R  Y  S  I  I  W  V  L  I  S  L  L  I  L
      -  T  S  A  R  D  *  D  T  Q  *  F  G  C  *  Y  R  C  *  Y  C
      -   P  V  P  E  I  K  I  L  N  N  L  G  V  D  I  A  A  N  T  V
19801 - TAATCTGGGACTACAAAAGAGAAGCCCCAGCACATGTATCTACAATAGGTGTCTGCACAA - 19860
      - *  S  G  T  T  K  E  K  P  Q  H  M  Y  L  Q  *  V  S  A  Q
      -  N  L  G  L  Q  K  R  S  P  S  T  C  I  Y  N  R  C  L  H  N
      -   I  W  D  Y  K  R  E  A  P  A  H  V  S  T  I  G  V  C  T  M
19861 - TGACTGACATTGCCAAGAAACCTACTGAGAGTGCTTGTTCTTCACTTACTGTCTTGTTTG - 19920
      - *  L  T  L  P  R  N  L  L  R  V  L  V  L  H  L  L  S  C  L
      -  D  *  H  C  Q  E  T  Y  *  E  C  L  F  F  T  Y  C  L  V  *
      -   T  D  I  A  K  K  P  T  E  S  A  C  S  S  L  T  V  L  F  D
19921 - ATGGTAGAGTGGAAGGACAGGTAGACCTTTTTAGAAACGCCCGTAATGGTGTTTTAATAA - 19980
      - M  V  E  W  K  D  R  *  T  F  L  E  T  P  V  M  V  F  *  *
      -  W  *  S  G  R  T  G  R  P  F  *  K  R  P  *  W  C  F  N  N
      -   G  R  V  E  G  Q  V  D  L  F  R  N  A  R  N  G  V  L  I  T
19981 - CAGAAGGTTCAGTCAAAGGTCTAACACCTTCAAAGGGACCAGCACAAGCTAGCGTCAATG - 20040
      - Q  K  V  Q  S  K  V  *  H  L  Q  R  D  Q  H  K  L  A  S  M
      -  R  R  F  S  Q  R  S  N  T  F  K  G  T  S  T  S  *  R  Q  W
      -   E  G  S  V  K  G  L  T  P  S  K  G  P  A  Q  A  S  V  N  G
20041 - GAGTCACATTAATTGGAGAATCAGTAAAAACACAGTTTAACTACTTTAAGAAAGTAGACG - 20100
      - E  S  H  *  L  E  N  Q  *  K  H  S  L  T  T  L  R  K  *  T
      -  S  H  I  N  W  R  I  S  K  N  T  V  *  L  L  *  E  S  R  R
      -   V  T  L  I  G  E  S  V  K  T  Q  F  N  Y  F  K  K  V  D  G
20101 - GCATTATTCAACAGTTGCCTGAAACCTACTTTACTCAGAGCAGAGACTTAGAGGATTTTA - 20160
      - A  L  F  N  S  C  L  K  P  T  L  L  R  A  E  T  *  R  I  L
      -  H  Y  S  T  V  A  *  N  L  L  Y  S  E  Q  R  L  R  G  F  *
      -   I  I  Q  Q  L  P  E  T  Y  F  T  Q  S  R  D  L  E  D  F  K
20161 - AGCCCAGATCACAAATGGAAACTGACTTTCTCGAGCTCGCTATGGATGAATTCATACAGC - 20220
      - S  P  D  H  K  W  K  L  T  F  S  S  S  L  W  M  N  S  Y  S
      -  A  Q  I  T  N  G  N  *  L  S  R  A  R  Y  G  *  I  H  T  A
      -   P  R  S  Q  M  E  T  D  F  L  E  L  A  M  D  E  F  I  Q  R
20221 - GATATAAGCTCGAGGGCTATGCCTTCGAACACATCGTTTATGGAGATTTCAGTCATGGAC - 20280
      - D  I  S  S  R  A  M  P  S  N  T  S  F  M  E  I  S  V  M  D
      -  I  *  A  R  G  L  C  L  R  T  H  R  L  W  R  F  Q  S  W  T
      -   Y  K  L  E  G  Y  A  F  E  H  I  V  Y  G  D  F  S  H  G  Q
20281 - AACTTGGCGGTCTTCATTTAATGATAGGCTTAGCCAAGCGCTCACAAGATTCACCACTTA - 20340
      - N  L  A  V  F  I  *  *  *  A  *  P  S  A  H  K  I  H  H  L
      -  T  W  R  S  S  F  N  D  R  L  S  Q  A  L  T  R  F  T  T  *
      -   L  G  G  L  H  L  M  I  G  L  A  K  R  S  Q  D  S  P  L  K
20341 - AATTAGAGGATTTTATCCCTATGGACAGCACAGTGAAAAATTACTTCATAACAGATGCGC - 20400
      - N  *  R  I  L  S  L  W  T  A  Q  *  K  I  T  S  *  Q  M  R
      -  I  R  G  F  Y  P  Y  G  Q  H  S  E  K  L  L  H  N  R  C  A
      -   L  E  D  F  I  P  M  D  S  T  V  K  N  Y  F  I  T  D  A  Q
20401 - AAACAGGTTCATCAAAATGTGTGTGTTCTGTGATTGATCTTTTACTTGATGACTTTGTCG - 20460
      - K  Q  V  H  Q  N  V  C  V  L  *  L  I  F  Y  L  M  T  L  S
      -  N  R  F  I  K  M  C  V  F  C  D  *  S  F  T  *  *  L  C  R
      -   T  G  S  S  K  C  V  C  S  V  I  D  L  L  L  D  D  F  V  E
```

Figure 16-BB

```
20461 - AGATAATAAAGTCACAAGATTTGTCAGTGATTTCAAAAGTGGTCAAGGTTACAATTGACT - 20520
      - R  *  *  S  H  K  I  C  Q  *  F  Q  K  W  S  R  L  Q  L  T
      -  D  N  K  V  T  R  F  V  S  D  F  K  S  G  Q  G  Y  N  *  L
      -   I  I  K  S  Q  D  L  S  V  I  S  K  V  V  K  V  T  I  D  Y
20521 - ATGCTGAAATTTCATTCATGCTTTGGTGTAAGGATGGACATGTTGAAACCTTCTACCCAA - 20580
      - M  L  K  F  H  S  C  F  G  V  R  M  D  M  L  K  P  S  T  Q
      -  C  *  N  F  I  H  A  L  V  *  G  W  T  C  *  N  L  L  P  K
      -   A  E  I  S  F  M  L  W  C  K  D  G  H  V  E  T  F  Y  P  K
20581 - AACTACAAGCAAGTCAAGCGTGGCAACCAGGTGTTGCGATGCCTAACTTGTACAAGATGC - 20640
      - N  Y  K  Q  V  K  R  G  N  Q  V  L  R  C  L  T  C  T  R  C
      -  T  T  S  K  S  S  V  A  T  R  C  C  D  A  *  L  V  Q  D  A
      -   L  Q  A  S  Q  A  W  Q  P  G  V  A  M  P  N  L  Y  K  M  Q
20641 - AAAGAATGCTTCTTGAAAAGTGTGACCTTCAGAATTATGGTGAAAATGCTGTTATACCAA - 20700
      - K  E  C  F  L  K  S  V  T  F  R  I  M  V  K  M  L  L  Y  Q
      -  K  N  A  S  *  K  V  *  P  S  E  L  W  *  K  C  C  Y  T  K
      -   R  M  L  L  E  K  C  D  L  Q  N  Y  G  E  N  A  V  I  P  K
20701 - AAGGAATAATGATGAATGTCGCAAAGTATACTCAACTGTGTCAATACTTAAATACACTTA - 20760
      - K  E  *  *  *  M  S  Q  S  I  L  N  C  V  N  T  *  I  H  L
      -  R  N  N  D  E  C  R  K  V  Y  S  T  V  S  I  L  K  Y  T  Y
      -   G  I  M  M  N  V  A  K  Y  T  Q  L  C  Q  Y  L  N  T  L  T
20761 - CTTTAGCTGTACCCTACAACATGAGAGTTATTCACTTTGGTGCTGGCTCTGATAAAGGAG - 20820
      - L  *  L  Y  P  T  T  *  E  L  F  T  L  V  L  A  L  I  K  E
      -  F  S  C  T  L  Q  H  E  S  Y  S  L  W  C  W  L  *  *  R  S
      -   L  A  V  P  Y  N  M  R  V  I  H  F  G  A  G  S  D  K  G  V
20821 - TTGCACCAGGTACAGCTGTGCTCAGACAATGGTTGCCAACTGGCACACTACTTGTCGATT - 20880
      - L  H  Q  V  Q  L  C  S  D  N  G  C  Q  L  A  H  Y  L  S  I
      -  C  T  R  Y  S  C  A  Q  T  M  V  A  N  W  H  T  T  C  R  F
      -   A  P  G  T  A  V  L  R  Q  W  L  P  T  G  T  L  L  V  D  S
20881 - CAGATCTTAATGACTTCGTCTCCGACGCAGATTCTACTTTAATTGGAGACTGTGCAACAG - 20940
      - Q  I  L  M  T  S  S  P  T  Q  I  L  L  *  L  E  T  V  Q  Q
      -  R  S  *  *  L  R  L  R  R  R  F  Y  F  N  W  R  L  C  N  S
      -   D  L  N  D  F  V  S  D  A  D  S  T  L  I  G  D  C  A  T  V
20941 - TACATACGGCTAATAAATGGGACCTTATTATTAGCGATATGTATGACCCTAGGACCAAAC - 21000
      - Y  I  R  L  I  N  G  T  L  L  L  A  I  C  M  T  L  G  P  N
      -  T  Y  G  *  *  M  G  P  Y  Y  *  R  Y  V  *  P  *  D  Q  T
      -   H  T  A  N  K  W  D  L  I  I  S  D  M  Y  D  P  R  T  K  H
21001 - ATGTGACAAAAGAGAATGACTCTAAAGAAGGGTTTTTCACTTATCTGTGTGGATTTATAA - 21060
      - M  *  Q  K  R  M  T  L  K  K  G  F  S  L  I  C  V  D  L  *
      -  C  D  K  R  E  *  L  *  R  R  V  F  H  L  S  V  W  I  Y  K
      -   V  T  K  E  N  D  S  K  E  G  F  F  T  Y  L  C  G  F  I  K
21061 - AGCAAAAACTAGCCCTGGGTGGTTCTATAGCTGTAAAGATAACAGAGCATTCTTGGAATG - 21120
      - S  K  N  *  P  W  V  V  L  *  L  *  R  *  Q  S  I  L  G  M
      -  A  K  T  S  P  G  W  F  Y  S  C  K  D  N  R  A  F  L  E  C
      -   Q  K  L  A  L  G  G  S  I  A  V  K  I  T  E  H  S  W  N  A
21121 - CTGACCTTTACAAGCTTATGGGCCATTTCTCATGGTGGACAGCTTTTGTTACAAATGTAA - 21180
      - L  T  F  T  S  L  W  A  I  S  H  G  G  Q  L  L  L  Q  M  *
      -  *  P  L  Q  A  Y  G  P  F  L  M  V  D  S  F  C  Y  K  C  K
      -   D  L  Y  K  L  M  G  H  F  S  W  W  T  A  F  V  T  N  V  N
```

Figure 16-CC

```
21181 - ATGCATCATCATCGGAAGCATTTTTAATTGGGGCTAACTATCTTGGCAAGCCGAAGGAAC - 21240
      - M  H  H  H  R  K  H  F  *  L  G  L  T  I  L  A  S  R  R  N
      -  C  I  I  I  G  S  I  F  N  W  G  *  L  S  W  Q  A  E  G  T
      -   A  S  S  S  E  A  F  L  I  G  A  N  Y  L  G  K  P  K  E  Q
21241 - AAATTGATGGCTATACCATGCATGCTAACTACATTTTCTGGAGGAACACAAATCCTATCC - 21300
      - K  L  M  A  I  P  C  M  L  T  T  F  S  G  G  T  Q  I  L  S
      -  N  *  W  L  Y  H  A  C  *  L  H  F  L  E  E  H  K  S  Y  P
      -   I  D  G  Y  T  M  H  A  N  Y  I  F  W  R  N  T  N  P  I  Q
21301 - AGTTGTCTTCCTATTCACTCTTTGACATGAGCAAATTTCCTCTTAAATTAAGAGGAACTG - 21360
      - S  C  L  P  I  H  S  L  T  *  A  N  F  L  L  N  *  E  E  L
      -  V  V  F  L  F  T  L  *  H  E  Q  I  S  S  *  I  K  R  N  C
      -   L  S  S  Y  S  L  F  D  M  S  K  F  P  L  K  L  R  G  T  A
21361 - CTGTAATGTCTCTTAAGGAGAATCAAATCAATGATATGATTTATTCTCTTCTGGAAAAAG - 21420
      - L  *  C  L  L  R  R  I  K  S  M  I  *  F  I  L  F  W  K  K
      -  C  N  V  S  *  G  E  S  N  Q  *  Y  D  L  F  S  S  G  K  R
      -   V  M  S  L  K  E  N  Q  I  N  D  M  I  Y  S  L  L  E  K  G
21421 - GTAGGCTTATCATTAGAGAAAACAACAGAGTTGTGGTTTCAAGTGATATTCTTGTTAACA - 21480
      - V  G  L  S  L  E  K  T  T  E  L  W  F  Q  V  I  F  L  L  T
      -  *  A  Y  H  *  R  K  Q  Q  S  C  G  F  K  *  Y  S  C  *  Q
      -   R  L  I  I  R  E  N  N  R  V  V  V  S  S  D  I  L  V  N  N
21481 - ACTAAACGAACATGTTTATTTTCTTATTATTTCTTACTCTCACTAGTGGTAGTGACCTTG - 21540
      - T  K  R  T  C  L  F  S  Y  Y  F  L  L  S  L  V  V  V  T  L
      -  L  N  E  H  V  Y  F  L  I  I  S  Y  S  H  *  W  *  *  P  *
      -   *  T  N  M  F  I  F  L  L  F  L  T  L  T  S  G  S  D  L  D
21541 - ACCGGTGCACCACTTTTGATGATGTTCAAGCTCCTAATTACACTCAACATACTTCATCTA - 21600
      - T  G  A  P  L  L  M  M  F  K  L  L  I  T  L  N  I  L  H  L
      -  P  V  H  H  F  *  *  C  S  S  S  *  L  H  S  T  Y  F  I  Y
      -   R  C  T  T  F  D  D  V  Q  A  P  N  Y  T  Q  H  T  S  S  M
21601 - TGAGGGGGGTTTACTATCCTGATGAAATTTTTAGATCAGACACTCTTTATTTAACTCAGG - 21660
      - *  G  G  F  T  I  L  M  K  F  L  D  Q  T  L  F  I  *  L  R
      -  E  G  G  L  L  S  *  *  N  F  *  I  R  H  S  L  F  N  S  G
      -   R  G  V  Y  Y  P  D  E  I  F  R  S  D  T  L  Y  L  T  Q  D
21661 - ATTTATTTCTTCCATTTTATTCTAATGTTACAGGGTTTCATACTATTAATCATACGTTTG - 21720
      - I  Y  F  F  H  F  I  L  M  L  Q  G  F  I  L  L  I  I  R  L
      -  F  I  S  S  I  L  F  *  C  Y  R  V  S  Y  Y  *  S  Y  V  W
      -   L  F  L  P  F  Y  S  N  V  T  G  F  H  T  I  N  H  T  F  G
21721 - GCAACCCTGTCATACCTTTTAAGGATGGTATTTATTTTGCTGCCACAGAGAAATCAAATG - 21780
      - A  T  L  S  Y  L  L  R  M  V  F  I  L  L  P  Q  R  N  Q  M
      -  Q  P  C  H  T  F  *  G  W  Y  L  F  C  C  H  R  E  I  K  C
      -   N  P  V  I  P  F  K  D  G  I  Y  F  A  A  T  E  K  S  N  V
21781 - TTGTCCGTGGTTGGGTTTTTGGTTCTACCATGAACAACAAGTCACAGTCGGTGATTATTA - 21840
      - L  S  V  V  G  F  L  V  L  P  *  T  T  S  H  S  R  *  L  L
      -  C  P  W  L  G  F  W  F  Y  H  E  Q  Q  V  T  V  G  D  Y  Y
      -   V  R  G  W  V  F  G  S  T  M  N  N  K  S  Q  S  V  I  I  I
21841 - TTAACAATTCTACTAATGTTGTTATACGAGCATGTAACTTTGAATTGTGTGACAACCCTT - 21900
      - L  T  I  L  L  M  L  L  Y  E  H  V  T  L  N  C  V  T  T  L
      -  *  Q  F  Y  *  C  C  Y  T  S  M  *  L  *  I  V  *  Q  P  F
      -   N  N  S  T  N  V  V  I  R  A  C  N  F  E  L  C  D  N  P  F
```

Figure 16-DD

```
21901 - TCTTTGCTGTTTCTAAACCCATGGGTACACAGACACATACTATGATATTCGATAATGCAT - 21960
      - S  L  L  F  L  N  P  W  V  H  R  H  I  L  *  Y  S  I  M  H
      -  L  C  C  F  *  T  H  G  Y  T  D  T  Y  Y  D  I  R  *  C  I
      -   F  A  V  S  K  P  M  G  T  Q  T  H  T  M  I  F  D  N  A  F
21961 - TTAATTGCACTTTCGAGTACATATCTGATGCCTTTTCGCTTGATGTTTCAGAAAAGTCAG - 22020
      - L  I  A  L  S  S  T  Y  L  M  P  F  R  L  M  F  Q  K  S  Q
      -  *  L  H  F  R  V  H  I  *  C  L  F  A  *  C  F  R  K  V  R
      -   N  C  T  F  E  Y  I  S  D  A  F  S  L  D  V  S  E  K  S  G
22021 - GTAATTTTAAACACTTACGAGAGTTTGTGTTTAAAAATAAAGATGGGTTTCTCTATGTTT - 22080
      - V  I  L  N  T  Y  E  S  L  C  L  K  I  K  M  G  F  S  M  F
      -  *  F  *  T  L  T  R  V  C  V  *  K  *  R  W  V  S  L  C  L
      -   N  F  K  H  L  R  E  F  V  F  K  N  K  D  G  F  L  Y  V  Y
22081 - ATAAGGGCTATCAACCTATAGATGTAGTTCGTGATCTACCTTCTGGTTTTAACACTTTGA - 22140
      - I  R  A  I  N  L  *  M  *  F  V  I  Y  L  L  V  L  T  L  *
      -  *  G  L  S  T  Y  R  C  S  S  *  S  T  F  W  F  *  H  F  E
      -   K  G  Y  Q  P  I  D  V  V  R  D  L  P  S  G  F  N  T  L  K
22141 - AACCTATTTTTAAGTTGCCTCTTGGTATTAACATTACAAATTTTAGAGCCATTCTTACAG - 22200
      - N  L  F  L  S  C  L  L  V  L  T  L  Q  I  L  E  P  F  L  Q
      -  T  Y  F  *  V  A  S  W  Y  *  H  Y  K  F  *  S  H  S  Y  S
      -   P  I  F  K  L  P  L  G  I  N  I  T  N  F  R  A  I  L  T  A
22201 - CCTTTTCACCTGCTCAAGACATTTGGGGCACGTCAGCTGCAGCCTATTTTGTTGGCTATT - 22260
      - P  F  H  L  L  K  T  F  G  A  R  Q  L  Q  P  I  L  L  A  I
      -  L  F  T  C  S  R  H  L  G  H  V  S  C  S  L  F  C  W  L  F
      -   F  S  P  A  Q  D  I  W  G  T  S  A  A  A  Y  F  V  G  Y  L
22261 - TAAAGCCAACTACATTTATGCTCAAGTATGATGAAAATGGTACAATCACAGATGCTGTTG - 22320
      - *  S  Q  L  H  L  C  S  S  M  M  K  M  V  Q  S  Q  M  L  L
      -  K  A  N  Y  I  Y  A  Q  V  *  *  K  W  Y  N  H  R  C  C  *
      -   K  P  T  T  F  M  L  K  Y  D  E  N  G  T  I  T  D  A  V  D
22321 - ATTGTTCTCAAAATCCACTTGCTGAACTCAAATGCTCTGTTAAGAGCTTTGAGATTGACA - 22380
      - I  V  L  K  I  H  L  L  N  S  N  A  L  L  R  A  L  R  L  T
      -  L  F  S  K  S  T  C  *  T  Q  M  L  C  *  E  L  *  D  *  Q
      -   C  S  Q  N  P  L  A  E  L  K  C  S  V  K  S  F  E  I  D  K
22381 - AAGGAATTTACCAGACCTCTAATTTCAGGGTTGTTCCCTCAGGAGATGTTGTGAGATTCC - 22440
      - K  E  F  T  R  P  L  I  S  G  L  F  P  Q  E  M  L  *  D  S
      -  R  N  L  P  D  L  *  F  Q  G  C  S  L  R  R  C  C  E  I  P
      -   G  I  Y  Q  T  S  N  F  R  V  V  P  S  G  D  V  V  R  F  P
22441 - CTAATATTACAAACTTGTGTCCTTTTGGAGAGGTTTTTAATGCTACTAAATTCCCTTCTG - 22500
      - L  I  L  Q  T  C  V  L  L  E  R  F  L  M  L  L  N  S  L  L
      -  *  Y  Y  K  L  V  S  F  W  R  G  F  *  C  Y  *  I  P  F  C
      -   N  I  T  N  L  C  P  F  G  E  V  F  N  A  T  K  F  P  S  V
22501 - TCTATGCATGGGAGAGAAAAAAAATTTCTAATTGTGTTGCTGATTACTCTGTGCTCTACA - 22560
      - S  M  H  G  R  E  K  K  F  L  I  V  L  L  I  T  L  C  S  T
      -  L  C  M  G  E  K  K  N  F  *  L  C  C  *  L  L  C  A  L  Q
      -   Y  A  W  E  R  K  K  I  S  N  C  V  A  D  Y  S  V  L  Y  N
22561 - ACTCAACATTTTTTTCAACCTTTAAGTGCTATGGCGTTTCTGCCACTAAGTTGAATGATC - 22620
      - T  Q  H  F  F  Q  P  L  S  A  M  A  F  L  P  L  S  *  M  I
      -  L  N  I  F  F  N  L  *  V  L  W  R  F  C  H  *  V  E  *  S
      -   S  T  F  F  S  T  F  K  C  Y  G  V  S  A  T  K  L  N  D  L
```

Figure 16-EE

```
22621 - TTTGCTTCTCCAATGTCTATGCAGATTCTTTTGTAGTCAAGGGAGATGATGTAAGACAAA - 22680
      - F  A  S  P  M  S  M  Q  I  L  L  *  S  R  E  M  M  *  D  K
      -  L  L  L  Q  C  L  C  R  F  F  C  S  Q  G  R  *  C  K  T  N
      -   C  F  S  N  V  Y  A  D  S  F  V  V  K  G  D  D  V  R  Q  I
22681 - TAGCGCCAGGACAAACTGGTGTTATTGCTGATTATAATTATAAATTGCCAGATGATTTCA - 22740
      - *  R  Q  D  K  L  V  L  L  L  I  I  I  I  N  C  Q  M  I  S
      -  S  A  R  T  N  W  C  Y  C  *  L  *  L  *  I  A  R  *  F  H
      -   A  P  G  Q  T  G  V  I  A  D  Y  N  Y  K  L  P  D  D  F  M
22741 - TGGGTTGTGTCCTTGCTTGGAATACTAGGAACATTGATGCTACTTCAACTGGTAATTATA - 22800
      - W  V  V  S  L  L  G  I  L  G  T  L  M  L  L  Q  L  V  I  I
      -  G  L  C  P  C  L  E  Y  *  E  H  *  C  Y  F  N  W  *  L  *
      -   G  C  V  L  A  W  N  T  R  N  I  D  A  T  S  T  G  N  Y  N
22801 - ATTATAAATATAGGTATCTTAGACATGGCAAGCTTAGGCCCTTTGAGAGAGACATATCTA - 22860
      - I  I  N  I  G  I  L  D  M  A  S  L  G  P  L  R  E  T  Y  L
      -  L  *  I  *  V  S  *  T  W  Q  A  *  A  L  *  E  R  H  I  *
      -   Y  K  Y  R  Y  L  R  H  G  K  L  R  P  F  E  R  D  I  S  N
22861 - ATGTGCCTTTCTCCCCTGATGGCAAACCTTGCACCCCACCTGCTCTTAATTGTTATTGGC - 22920
      - M  C  L  S  P  L  M  A  N  L  A  P  H  L  L  L  I  V  I  G
      -  C  A  F  L  P  *  W  Q  T  L  H  P  T  C  S  *  L  L  L  A
      -   V  P  F  S  P  D  G  K  P  C  T  P  P  A  L  N  C  Y  W  P
22921 - CATTAAATGATTATGGTTTTTACACCACTACTGGCATTGGCTACCAACCTTACAGAGTTG - 22980
      - H  *  M  I  M  V  F  T  P  L  L  A  L  A  T  N  L  T  E  L
      -  I  K  *  L  W  F  L  H  H  Y  W  H  W  L  P  T  L  Q  S  C
      -   L  N  D  Y  G  F  Y  T  T  T  G  I  G  Y  Q  P  Y  R  V  V
22981 - TAGTACTTTCTTTTGAACTTTTAAATGCACCGGCCACGGTTTGTGGACCAAAATTATCCA - 23040
      - *  Y  F  L  L  N  F  *  M  H  R  P  R  F  V  D  Q  N  Y  P
      -  S  T  F  F  *  T  F  K  C  T  G  H  G  L  W  T  K  I  I  H
      -   V  L  S  F  E  L  L  N  A  P  A  T  V  C  G  P  K  L  S  T
23041 - CTGACCTTATTAAGAACCAGTGTGTCAATTTTAATTTTAATGGACTCACTGGTACTGGTG - 23100
      - L  T  L  L  R  T  S  V  S  I  L  I  L  M  D  S  L  V  L  V
      -  *  P  Y  *  E  P  V  C  Q  F  *  F  *  W  T  H  W  Y  W  C
      -   D  L  I  K  N  Q  C  V  N  F  N  F  N  G  L  T  G  T  G  V
23101 - TGTTAACTCCTTCTTCAAAGAGATTTCAACCATTTCAACAATTTGGCCGTGATGTTTCTG - 23160
      - C  *  L  L  L  Q  R  D  F  N  H  F  N  N  L  A  V  M  F  L
      -  V  N  S  F  F  K  E  I  S  T  I  S  T  I  W  P  *  C  F  *
      -   L  T  P  S  S  K  R  F  Q  P  F  Q  Q  F  G  R  D  V  S  D
23161 - ATTTCACTGATTCCGTTCGAGATCCTAAAACATCTGAAATATTAGACATTTCACCTTGCT - 23220
      - I  S  L  I  P  F  E  I  L  K  H  L  K  Y  *  T  F  H  L  A
      -  F  H  *  F  R  S  R  S  *  N  I  *  N  I  R  H  F  T  L  L
      -   F  T  D  S  V  R  D  P  K  T  S  E  I  L  D  I  S  P  C  S
23221 - CTTTTGGGGGTGTAAGTGTAATTACACCTGGAACAAATGCTTCATCTGAAGTTGCTGTTC - 23280
      - L  L  G  V  *  V  *  L  H  L  E  Q  M  L  H  L  K  L  L  F
      -  F  W  G  C  K  C  N  Y  T  W  N  K  C  F  I  *  S  C  C  S
      -   F  G  G  V  S  V  I  T  P  G  T  N  A  S  S  E  V  A  V  L
23281 - TATATCAAGATGTTAACTGCACTGATGTTTCTACAGCAATTCATGCAGATCAACTCACAC - 23340
      - Y  I  K  M  L  T  A  L  M  F  L  Q  Q  F  M  Q  I  N  S  H
      -  I  S  R  C  *  L  H  *  C  F  Y  S  N  S  C  R  S  T  H  T
      -   Y  Q  D  V  N  C  T  D  V  S  T  A  I  H  A  D  Q  L  T  P
```

Figure 16-FF

```
23341 - CAGCTTGGCGCATATATTCTACTGGAAACAATGTATTCCAGACTCAAGCAGGCTGTCTTA - 23400
      - Q  L  G  A  Y  I  L  L  E  T  M  Y  S  R  L  K  Q  A  V  L
      -  S  L  A  H  I  F  Y  W  K  Q  C  I  P  D  S  S  R  L  S  Y
      -   A  W  R  I  Y  S  T  G  N  N  V  F  Q  T  Q  A  G  C  L  I
23401 - TAGGAGCTGAGCATGTCGACACTTCTTATGAGTGCGACATTCCTATTGGAGCTGGCATTT - 23460
      - *  E  L  S  M  S  T  L  L  M  S  A  T  F  L  L  E  L  A  F
      -  R  S  *  A  C  R  H  F  L  *  V  R  H  S  Y  W  S  W  H  L
      -   G  A  E  H  V  D  T  S  Y  E  C  D  I  P  I  G  A  G  I  C
23461 - GTGCTAGTTACCATACAGTTTCTTTATTACGTAGTACTAGCCAAAAATCTATTGTGGCTT - 23520
      - V  L  V  T  I  Q  F  L  Y  Y  V  V  L  A  K  N  L  L  W  L
      -  C  *  L  P  Y  S  F  F  I  T  *  Y  *  P  K  I  Y  C  G  L
      -   A  S  Y  H  T  V  S  L  L  R  S  T  S  Q  K  S  I  V  A  Y
23521 - ATACTATGTCTTTAGGTGCTGATAGTTCAATTGCTTACTCTAATAACACCATTGCTATAC - 23580
      - I  L  C  L  *  V  L  I  V  Q  L  L  T  L  I  T  P  L  L  Y
      -  Y  Y  V  F  R  C  *  *  F  N  C  L  L  *  *  H  H  C  Y  T
      -   T  M  S  L  G  A  D  S  S  I  A  Y  S  N  N  T  I  A  I  P
23581 - CTACTAACTTTTCAATTAGCATTACTACAGAAGTAATGCCTGTTTCTATGGCTAAAACCT - 23640
      - L  L  T  F  Q  L  A  L  L  Q  K  *  C  L  F  L  W  L  K  P
      -  Y  *  L  F  N  *  H  Y  Y  R  S  N  A  C  F  Y  G  *  N  L
      -   T  N  F  S  I  S  I  T  T  E  V  M  P  V  S  M  A  K  T  S
23641 - CCGTAGATTGTAATATGTACATCTGCGGAGATTCTACTGAATGTGCTAATTTGCTTCTCC - 23700
      - P  *  I  V  I  C  T  S  A  E  I  L  L  N  V  L  I  C  F  S
      -  R  R  L  *  Y  V  H  L  R  R  F  Y  *  M  C  *  F  A  S  P
      -   V  D  C  N  M  Y  I  C  G  D  S  T  E  C  A  N  L  L  L  Q
23701 - AATATGGTAGCTTTTGCACACAACTAAATCGTGCACTCTCAGGTATTGCTGCTGAACAGG - 23760
      - N  M  V  A  F  A  H  N  *  I  V  H  S  Q  V  L  L  L  N  R
      -  I  W  *  L  L  H  T  T  K  S  C  T  L  R  Y  C  C  *  T  G
      -   Y  G  S  F  C  T  Q  L  N  R  A  L  S  G  I  A  A  E  Q  D
23761 - ATCGCAACACACGTGAAGTGTTCGCTCAAGTCAAACAAATGTACAAAACCCCAACTTTGA - 23820
      - I  A  T  H  V  K  C  S  L  K  S  N  K  C  T  K  P  Q  L  *
      -  S  Q  H  T  *  S  V  R  S  S  Q  T  N  V  Q  N  P  N  F  E
      -   R  N  T  R  E  V  F  A  Q  V  K  Q  M  Y  K  T  P  T  L  K
23821 - AATATTTTGGTGGTTTTAATTTTTCACAAATATTACCTGACCCTCTAAAGCCAACTAAGA - 23880
      - N  I  L  V  V  L  I  F  H  K  Y  Y  L  T  L  *  S  Q  L  R
      -  I  F  W  W  F  *  F  F  T  N  I  T  *  P  S  K  A  N  *  E
      -   Y  F  G  G  F  N  F  S  Q  I  L  P  D  P  L  K  P  T  K  R
23881 - GGTCTTTTATTGAGGACTTGCTCTTTAATAAGGTGACACTCGCTGATGCTGGCTTCATGA - 23940
      - G  L  L  L  R  T  C  S  L  I  R  *  H  S  L  M  L  A  S  *
      -  V  F  Y  *  G  L  A  L  *  *  G  D  T  R  *  C  W  L  H  E
      -   S  F  I  E  D  L  L  F  N  K  V  T  L  A  D  A  G  F  M  K
23941 - AGCAATATGGCGAATGCCTAGGTGATATTAATGCTAGAGATCTCATTTGTGCGCAGAAGT - 24000
      - S  N  M  A  N  A  *  V  I  L  M  L  E  I  S  F  V  R  R  S
      -  A  I  W  R  M  P  R  *  Y  *  C  *  R  S  H  L  C  A  E  V
      -   Q  Y  G  E  C  L  G  D  I  N  A  R  D  L  I  C  A  Q  K  F
24001 - TCAATGGACTTACAGTGTTGCCACCTCTGCTCACTGATGATATGATTGCTGCCTACACTG - 24060
      - S  M  D  L  Q  C  C  H  L  C  S  L  M  I  *  L  L  P  T  L
      -  Q  W  T  Y  S  V  A  T  S  A  H  *  *  Y  D  C  C  L  H  C
      -   N  G  L  T  V  L  P  P  L  L  T  D  D  M  I  A  A  Y  T  A
```

Figure 16-GG

```
24061 - CTGCTCTAGTTAGTGGTACTGCCACTGCTGGATGGACATTTGGTGCTGGCGCTGCTCTTC - 24120
      -L  L  *  L  V  V  L  P  L  L  D  G  H  L  V  L  A  L  L  F
      - C  S  S  *  W  Y  C  H  C  W  M  D  I  W  C  W  R  C  S  S
      -  A  L  V  S  G  T  A  T  A  G  W  T  F  G  A  G  A  A  L  Q
24121 - AAATACCTTTTGCTATGCAAATGGCATATAGGTTCAATGGCATTGGAGTTACCCAAAATG - 24180
      -K  Y  L  L  L  C  K  W  H  I  G  S  M  A  L  E  L  P  K  M
      - N  T  F  C  Y  A  N  G  I  *  V  Q  W  H  W  S  Y  P  K  C
      -  I  P  F  A  M  Q  M  A  Y  R  F  N  G  I  G  V  T  Q  N  V
24181 - TTCTCTATGAGAACCAAAAACAAATCGCCAACCAATTTAACAAGGCGATTAGTCAAATTC - 24240
      -F  S  M  R  T  K  N  K  S  P  T  N  L  T  R  R  L  V  K  F
      - S  L  *  E  P  K  T  N  R  Q  P  I  *  Q  G  D  *  S  N  S
      -  L  Y  E  N  Q  K  Q  I  A  N  Q  F  N  K  A  I  S  Q  I  Q
24241 - AAGAATCACTTACAACAACATCAACTGCATTGGGCAAGCTGCAAGACGTTGTTAACCAGA - 24300
      -K  N  H  L  Q  Q  H  Q  L  H  W  A  S  C  K  T  L  L  T  R
      - R  I  T  Y  N  N  I  N  C  I  G  Q  A  A  R  R  C  *  P  E
      -  E  S  L  T  T  T  S  T  A  L  G  K  L  Q  D  V  V  N  Q  N
24301 - ATGCTCAAGCATTAAACACACTTGTTAAACAACTTAGCTCTAATTTTGGTGCAATTTCAA - 24360
      -M  L  K  H  *  T  H  L  L  N  N  L  A  L  I  L  V  Q  F  Q
      - C  S  S  I  K  H  T  C  *  T  T  *  L  *  F  W  C  N  F  K
      -  A  Q  A  L  N  T  L  V  K  Q  L  S  S  N  F  G  A  I  S  S
24361 - GTGTGCTAAATGATATCCTTTCGCGACTTGATAAAGTCGAGGCGGAGGTACAAATTGACA - 24420
      -V  C  *  M  I  S  F  R  D  L  I  K  S  R  R  R  Y  K  L  T
      - C  A  K  *  Y  P  F  A  T  *  *  S  R  G  G  G  T  N  *  Q
      -  V  L  N  D  I  L  S  R  L  D  K  V  E  A  E  V  Q  I  D  R
24421 - GGTTAATTACAGGCAGACTTCAAAGCCTTCAAACCTATGTAACACAACAACTAATCAGGG - 24480
      -G  *  L  Q  A  D  F  K  A  F  K  P  M  *  H  N  N  *  S  G
      - V  N  Y  R  Q  T  S  K  P  S  N  L  C  N  T  T  T  N  Q  G
      -  L  I  T  G  R  L  Q  S  L  Q  T  Y  V  T  Q  Q  L  I  R  A
24481 - CTGCTGAAATCAGGGCTTCTGCTAATCTTGCTGCTACTAAAATGTCTGAGTGTGTTCTTG - 24540
      -L  L  K  S  G  L  L  L  I  L  L  L  L  K  C  L  S  V  F  L
      - C  *  N  Q  G  F  C  *  S  C  C  Y  *  N  V  *  V  C  S  W
      -  A  E  I  R  A  S  A  N  L  A  A  T  K  M  S  E  C  V  L  G
24541 - GACAATCAAAAAGAGTTGACTTTTGTGGAAAGGGCTACCACCTTATGTCCTTCCCACAAG - 24600
      -D  N  Q  K  E  L  T  F  V  E  R  A  T  T  L  C  P  S  H  K
      - T  I  K  K  S  *  L  L  W  K  G  L  P  P  Y  V  L  P  T  S
      -  Q  S  K  R  V  D  F  C  G  K  G  Y  H  L  M  S  F  P  Q  A
24601 - CAGCCCCGCATGGTGTTGTCTTCCTACATGTCACGTATGTGCCATCCCAGGAGAGGAACT - 24660
      -Q  P  R  M  V  L  S  S  Y  M  S  R  M  C  H  P  R  R  G  T
      - S  P  A  W  C  C  L  P  T  C  H  V  C  A  I  P  G  E  E  L
      -  A  P  H  G  V  V  F  L  H  V  T  Y  V  P  S  Q  E  R  N  F
24661 - TCACCACAGCGCCAGCAATTTGTCATGAAGGCAAAGCATACTTCCCTCGTGAAGGTGTTT - 24720
      -S  P  Q  R  Q  Q  F  V  M  K  A  K  H  T  S  L  V  K  V  F
      - H  H  S  A  S  N  L  S  *  R  Q  S  I  L  P  S  *  R  C  F
      -  T  T  A  P  A  I  C  H  E  G  K  A  Y  F  P  R  E  G  V  F
24721 - TTGTGTTTAATGGCACTTCTTGGTTTATTACACAGAGGAACTTCTTTTCTCCACAAATAA - 24780
      -L  C  L  M  A  L  L  G  L  L  H  R  G  T  S  F  L  H  K  *
      - C  V  *  W  H  F  L  V  Y  Y  T  E  E  L  L  F  S  T  N  N
      -  V  F  N  G  T  S  W  F  I  T  Q  R  N  F  F  S  P  Q  I  I
24781 - TTACTACAGACAATACATTTGTCTCAGGAAATTGTGATGTCGTTATTGGCATCATTAACA - 24840
      -L  L  Q  T  I  H  L  S  Q  E  I  V  M  S  L  L  A  S  L  T
      - Y  Y  R  Q  Y  I  C  L  R  K  L  *  C  R  Y  W  H  H  *  Q
      -  T  T  D  N  T  F  V  S  G  N  C  D  V  V  I  G  I  I  N  N
```

Figure 16-HH

```
24841 - ACACAGTTTATGATCCTCTGCAACCTGAGCTTGACTCATTCAAAGAAGAGCTGGACAAGT - 24900
      - T  Q  F  M  I  L  C  N  L  S  L  T  H  S  K  K  S  W  T  S
      -  H  S  L  *  S  S  A  T  *  A  *  L  I  Q  R  R  A  G  Q  V
      -   T  V  Y  D  P  L  Q  P  E  L  D  S  F  K  E  E  L  D  K  Y
24901 - ACTTCAAAAATCATACATCACCAGATGTTGATCTTGGCGACATTTCAGGCATTAACGCTT - 24960
      - T  S  K  I  I  H  H  Q  M  L  I  L  A  T  F  Q  A  L  T  L
      -  L  Q  K  S  Y  I  T  R  C  *  S  W  R  H  F  R  H  *  R  F
      -   F  K  N  H  T  S  P  D  V  D  L  G  D  I  S  G  I  N  A  S
24961 - CTGTCGTCAACATTCAAAAAGAAATTGACCGCCTCAATGAGGTCGCTAAAAATTTAAATG - 25020
      - L  S  S  T  F  K  K  K  L  T  A  S  M  R  S  L  K  I  *  M
      -  C  R  Q  H  S  K  R  N  *  P  P  Q  *  G  R  *  K  F  K  *
      -   V  V  N  I  Q  K  E  I  D  R  L  N  E  V  A  K  N  L  N  E
25021 - AATCACTCATTGACCTTCAAGAATTGGGAAAATATGAGCAATATATTAAATGGCCTTGGT - 25080
      - N  H  S  L  T  F  K  N  W  E  N  M  S  N  I  L  N  G  L  G
      -  I  T  H  *  P  S  R  I  G  K  I  *  A  I  Y  *  M  A  L  V
      -   S  L  I  D  L  Q  E  L  G  K  Y  E  Q  Y  I  K  W  P  W  Y
25081 - ATGTTTGGCTCGGCTTCATTGCTGGACTAATTGCCATCGTCATGGTTACAATCTTGCTTT - 25140
      - M  F  G  S  A  S  L  L  D  *  L  P  S  S  W  L  Q  S  C  F
      -  C  L  A  R  L  H  C  W  T  N  C  H  R  H  G  Y  N  L  A  L
      -   V  W  L  G  F  I  A  G  L  I  A  I  V  M  V  T  I  L  L  C
25141 - GTTGCATGACTAGTTGTTGCAGTTGCCTCAAGGGTGCATGCTCTTGTGGTTCTTGCTGCA - 25200
      - V  A  *  L  V  V  A  V  A  S  R  V  H  A  L  V  V  L  A  A
      -  L  H  D  *  L  L  Q  L  P  Q  G  C  M  L  L  W  F  L  L  Q
      -   C  M  T  S  C  C  S  C  L  K  G  A  C  S  C  G  S  C  C  K
25201 - AGTTTGATGAGGATGACTCTGAGCCAGTTCTCAAGGGTGTCAAATTACATTACACATAAA - 25260
      - S  L  M  R  M  T  L  S  Q  F  S  R  V  S  N  Y  I  T  H  K
      -  V  *  *  G  *  L  *  A  S  S  Q  G  C  Q  I  T  L  H  I  N
      -   F  D  E  D  D  S  E  P  V  L  K  G  V  K  L  H  Y  T  *  T
25261 - CGAACTTATGGATTTGTTTATGAGATTTTTACTCTTGGATCAATTACTGCACAGCCAGT - 25320
      - R  T  Y  G  F  V  Y  E  I  F  Y  S  W  I  N  Y  C  T  A  S
      -  E  L  M  D  L  F  M  R  F  F  T  L  G  S  I  T  A  Q  P  V
      -   N  L  W  I  C  L  *  D  F  L  L  L  D  Q  L  L  H  S  Q  *
25321 - AAAAATTGACAATGCTTCTCCTGCAAGTACTGTTCATGCTACAGCAACGATACCGCTACA - 25380
      - K  N  *  Q  C  F  S  C  K  Y  C  S  C  Y  S  N  D  T  A  T
      -  K  I  D  N  A  S  P  A  S  T  V  H  A  T  A  T  I  P  L  Q
      -   K  L  T  M  L  L  L  Q  V  L  F  M  L  Q  Q  R  Y  R  Y  K
25381 - AGCCTCACTCCCTTTCGGATGGCTTGTTATTGGCGTTGCATTTCTTGCTGTTTTTCAGAG - 25440
      - S  L  T  P  F  R  M  A  C  Y  W  R  C  I  S  C  C  F  S  E
      -  A  S  L  P  F  G  W  L  V  I  G  V  A  F  L  A  V  F  Q  S
      -   P  H  S  L  S  D  G  L  L  L  A  L  H  F  L  L  F  F  R  A
25441 - CGCTACCAAAATAATTGCGCTCAATAAAAGATGGCAGCTAGCCCTTTATAAGGGCTTCCA - 25500
      - R  Y  Q  N  N  C  A  Q  *  K  M  A  A  S  P  L  *  G  L  P
      -  A  T  K  I  I  A  L  N  K  R  W  Q  L  A  L  Y  K  G  F  Q
      -   L  P  K  *  L  R  S  I  K  D  G  S  *  P  F  I  R  A  S  S
25501 - GTTCATTTGCAATTTACTGCTGCTATTTGTTACCATCTATTCACATCTTTTGCTTGTCGC - 25560
      - V  H  L  Q  F  T  A  A  I  C  Y  H  L  F  T  S  F  A  C  R
      -  F  I  C  N  L  L  L  L  F  V  T  I  Y  S  H  L  L  L  V  A
      -   S  F  A  I  Y  C  C  Y  L  L  P  S  I  H  I  F  C  L  S  L
```

Figure 16-II

```
25561 - TGCAGGTAAGGAGGCGCAATTTTTGTACCTCTATGCCTTGATATATTTTCTACAATGCAT - 25620
      - C  R  *  G  G  A  I  F  V  P  L  C  L  D  I  F  S  T  M  H
      -  A  G  K  E  A  Q  F  L  Y  L  Y  A  L  I  Y  F  L  Q  C  I
      -   Q  V  R  R  R  N  F  C  T  S  M  P  *  Y  I  F  Y  N  A  S
25621 - CAACGCATGTAGAATTATTATGAGATGTTGGCTTTGTTGGAAGTGCAAATCCAAGAACCC - 25680
      - Q  R  M  *  N  Y  Y  E  M  L  A  L  L  E  V  Q  I  Q  E  P
      -  N  A  C  R  I  I  M  R  C  W  L  C  W  K  C  K  S  K  N  P
      -   T  H  V  E  L  L  *  D  V  G  F  V  G  S  A  N  P  R  T  H
25681 - ATTACTTTATGATGCCAACTACTTTGTTTGCTGGCACACACATAACTATGACTACTGTAT - 25740
      - I  T  L  *  C  Q  L  L  C  L  L  A  H  T  *  L  *  L  L  Y
      -  L  L  Y  D  A  N  Y  F  V  C  W  H  T  H  N  Y  D  Y  C  I
      -   Y  F  M  M  P  T  T  L  F  A  G  T  H  I  T  M  T  T  V  Y
25741 - ACCATATAACAGTGTCACAGATACAATTGTCGTTACTGAAGGTGACGGCATTTCAACACC - 25800
      - T  I  *  Q  C  H  R  Y  N  C  R  Y  *  R  *  R  H  F  N  T
      -  P  Y  N  S  V  T  D  T  I  V  V  T  E  G  D  G  I  S  T  P
      -   H  I  T  V  S  Q  I  Q  L  S  L  L  K  V  T  A  F  Q  H  Q
25801 - AAAACTCAAAGAAGACTACCAAATTGGTGGTTATTCTGAGGATAGGCACTCAGGTGTTAA - 25860
      - K  T  Q  R  R  L  P  N  W  W  L  F  *  G  *  A  L  R  C  *
      -  K  L  K  E  D  Y  Q  I  G  G  Y  S  E  D  R  H  S  G  V  K
      -   N  S  K  K  T  T  K  L  V  V  I  L  R  I  G  T  Q  V  L  K
25861 - AGACTATGTCGTTGTACATGGCTATTTCACCGAAGTTTACTACCAGCTTGAGTCTACACA - 25920
      - R  L  C  R  C  T  W  L  F  H  R  S  L  L  P  A  *  V  Y  T
      -  D  Y  V  V  V  H  G  Y  F  T  E  V  Y  Y  Q  L  E  S  T  Q
      -   T  M  S  L  Y  M  A  I  S  P  K  F  T  T  S  L  S  L  H  K
25921 - AATTACTACAGACACTGGTATTGAAAATGCTACATTCTTCATCTTTAACAAGCTTGTTAA - 25980
      - N  Y  Y  R  H  W  Y  *  K  C  Y  I  L  H  L  *  Q  A  C  *
      -  I  T  T  D  T  G  I  E  N  A  T  F  F  I  F  N  K  L  V  K
      -   L  L  Q  T  L  V  L  K  M  L  H  S  S  S  L  T  S  L  L  K
25981 - AGACCCACCGAATGTGCAAATACACACAATCGACGGCTCTTCAGGAGTTGCTAATCCAGC - 26040
      - R  P  T  E  C  A  N  T  H  N  R  R  L  F  R  S  C  *  S  S
      -  D  P  P  N  V  Q  I  H  T  I  D  G  S  S  G  V  A  N  P  A
      -   T  H  R  M  C  K  Y  T  Q  S  T  A  L  Q  E  L  L  I  Q  Q
26041 - AATGGATCCAATTTATGATGAGCCGACGACGACTACTAGCGTGCCTTTGTAAGCACAAGA - 26100
      - N  G  S  N  L  *  *  A  D  D  D  Y  *  R  A  F  V  S  T  R
      -  M  D  P  I  Y  D  E  P  T  T  T  T  S  V  P  L  *  A  Q  E
      -   W  I  Q  F  M  M  S  R  R  R  L  L  A  C  L  C  K  H  K  K
26101 - AAGTGAGTACGAACTTATGTACTCATTCGTTTCGGAAGAAACAGGTACGTTAATAGTTAA - 26160
      - K  *  V  R  T  Y  V  L  I  R  F  G  R  N  R  Y  V  N  S  *
      -  S  E  Y  E  L  M  Y  S  F  V  S  E  E  T  G  T  L  I  V  N
      -   V  S  T  N  L  C  T  H  S  F  R  K  K  Q  V  R  *  *  L  I
26161 - TAGCGTACTTCTTTTTCTTGCTTTCGTGGTATTCTTGCTAGTCACACTAGCCATCCTTAC - 26220
      - *  R  T  S  F  S  C  F  R  G  I  L  A  S  H  T  S  H  P  Y
      -  S  V  L  L  F  L  A  F  V  V  F  L  L  V  T  L  A  I  L  T
      -   A  Y  F  F  F  L  L  S  W  Y  S  C  *  S  H  *  P  S  L  L
26221 - TGCGCTTCGATTGTGTGCGTACTGCTGCAATATTGTTAACGTGAGTTTAGTAAAACCAAC - 26280
      - C  A  S  I  V  C  V  L  L  Q  Y  C  *  R  E  F  S  K  T  N
      -  A  L  R  L  C  A  Y  C  C  N  I  V  N  V  S  L  V  K  P  T
      -   R  F  D  C  V  R  T  A  A  I  L  L  T  *  V  *  *  N  Q  R
26281 - GGTTTACGTCTACTCGCGTGTTAAAAATCTGAACTCTTCTGAAGGAGTTCCTGATCTTCT - 26340
      - G  L  R  L  L  A  C  *  K  S  E  L  F  *  R  S  S  *  S  S
      -  V  Y  V  Y  S  R  V  K  N  L  N  S  S  E  G  V  P  D  L  L
      -   F  T  S  T  R  V  L  K  I  *  T  L  L  K  E  F  L  I  F  W
```

Figure 16-JJ

```
26341 - GGTCTAAACGAACTAACTATTATTATTATTCTGTTTGGAACTTTAACATTGCTTATCATG - 26400
      - G  L  N  E  L  T  I  I  I  I  L  F  G  T  L  T  L  L  I  M
      -  V  *  T  N  *  L  L  L  L  F  C  L  E  L  *  H  C  L  S  W
      -   S  K  R  T  N  Y  Y  Y  Y  S  V  W  N  F  N  I  A  Y  H  G
26401 - GCAGACAACGGTACTATTACCGTTGAGGAGCTTAAACAACTCCTGGAACAATGGAACCTA - 26460
      - A  D  N  G  T  I  T  V  E  E  L  K  Q  L  L  E  Q  W  N  L
      -  Q  T  T  V  L  L  P  L  R  S  L  N  N  S  W  N  N  G  T  *
      -   R  Q  R  Y  Y  Y  R  *  G  A  *  T  T  P  G  T  M  E  P  S
26461 - GTAATAGGTTTCCTATTCCTAGCCTGGATTATGTTACTACAATTTGCCTATTCTAATCGG - 26520
      - V  I  G  F  L  F  L  A  W  I  M  L  L  Q  F  A  Y  S  N  R
      -  *  *  V  S  Y  S  *  P  G  L  C  Y  Y  N  L  P  I  L  I  G
      -   N  R  F  P  I  P  S  L  D  Y  V  T  T  I  C  L  F  *  S  E
26521 - AACAGGTTTTTGTACATAATAAAGCTTGTTTTCCTCTGGCTCTTGTGGCCAGTAACACTT - 26580
      - N  R  F  L  Y  I  I  K  L  V  F  L  W  L  L  W  P  V  T  L
      -  T  G  F  C  T  *  *  S  L  F  S  S  G  S  C  G  Q  *  H  L
      -   Q  V  F  V  H  N  K  A  C  F  P  L  A  L  V  A  S  N  T  C
26581 - GCTTGTTTTGTGCTTGCTGTTGTCTACAGAATTAATTGGGTGACTGGCGGGATTGCGATT - 26640
      - A  C  F  V  L  A  V  V  Y  R  I  N  W  V  T  G  G  I  A  I
      -  L  V  L  C  L  L  L  S  T  E  L  I  G  *  L  A  G  L  R  L
      -   L  F  C  A  C  C  C  L  Q  N  *  L  G  D  W  R  D  C  D  C
26641 - GCAATGGCTTGTATTGTAGGCTTGATGTGGCTTAGCTACTTCGTTGCTTCCTTCAGGCTG - 26700
      - A  M  A  C  I  V  G  L  M  W  L  S  Y  F  V  A  S  F  R  L
      -  Q  W  L  V  L  *  A  *  C  G  L  A  T  S  L  L  P  S  G  C
      -   N  G  L  Y  C  R  L  D  V  A  *  L  L  R  C  F  L  Q  A  V
26701 - TTTGCTCGTACCCGCTCAATGTGGTCATTCAACCCAGAAACAAACATTCTTCTCAATGTG - 26760
      - F  A  R  T  R  S  M  W  S  F  N  P  E  T  N  I  L  L  N  V
      -  L  L  V  P  A  Q  C  G  H  S  T  Q  K  Q  T  F  F  S  M  C
      -   C  S  Y  P  L  N  V  V  I  Q  P  R  N  K  H  S  S  Q  C  A
26761 - CCTCTCCGGGGGACAATTGTGACCAGACCGCTCATGGAAAGTGAACTTGTCATTGGTGCT - 26820
      - P  L  R  G  T  I  V  T  R  P  L  M  E  S  E  L  V  I  G  A
      -  L  S  G  G  Q  L  *  P  D  R  S  W  K  V  N  L  S  L  V  L
      -   S  P  G  D  N  C  D  Q  T  A  H  G  K  *  T  C  H  W  C  C
26821 - GTGATCATTCGTGGTCACTTGCGAATGGCCGGACACTCCCTAGGGCGCTGTGACATTAAG - 26880
      - V  I  I  R  G  H  L  R  M  A  G  H  S  L  G  R  C  D  I  K
      -  *  S  F  V  V  T  C  E  W  P  D  T  P  *  G  A  V  T  L  R
      -   D  H  S  W  S  L  A  N  G  R  T  L  P  R  A  L  *  H  *  G
26881 - GACCTGCCAAAAGAGATCACTGTGGCTACATCACGAACGCTTTCTTATTACAAATTAGGA - 26940
      - D  L  P  K  E  I  T  V  A  T  S  R  T  L  S  Y  Y  K  L  G
      -  T  C  Q  K  R  S  L  W  L  H  H  E  R  F  L  I  T  N  *  E
      -   P  A  K  R  D  H  C  G  Y  I  T  N  A  F  L  L  Q  I  R  S
26941 - GCGTCGCAGCGTGTAGGCACTGATTCAGGTTTTGCTGCATACAACCGCTACCGTATTGGA - 27000
      - A  S  Q  R  V  G  T  D  S  G  F  A  A  Y  N  R  Y  R  I  G
      -  R  R  S  V  *  A  L  I  Q  V  L  L  H  T  T  A  T  V  L  E
      -   V  A  A  C  R  H  *  F  R  F  C  C  I  Q  P  L  P  Y  W  K
27001 - AACTATAAATTAAATACAGACCACGCCGGTAGCAACGACAATATTGCTTTGCTAGTACAG - 27060
      - N  Y  K  L  N  T  D  H  A  G  S  N  D  N  I  A  L  L  V  Q
      -  T  I  N  *  I  Q  T  T  P  V  A  T  T  I  L  L  C  *  Y  S
      -   L  *  I  K  Y  R  P  R  R  *  Q  R  Q  Y  C  F  A  S  T  V
```

Figure 16-KK

```
27061 - TAAGTGACAACAGATGTTTCATCTTGTTGACTTCCAGGTTACAATAGCAGAGATATTGAT - 27120
      - *  V  T  T  D  V  S  S  C  *  L  P  G  Y  N  S  R  D  I  D
      -  K  *  Q  Q  M  F  H  L  V  D  F  Q  V  T  I  A  E  I  L  I
      -   S  D  N  R  C  F  I  L  L  T  S  R  L  Q  *  Q  R  Y  *  L
27121 - TATCATTATGAGGACTTTCAGGATTGCTATTTGGAATCTTGACGTTATAATAAGTTCAAT - 27180
      - Y  H  Y  E  D  F  Q  D  C  Y  L  E  S  *  R  Y  N  K  F  N
      -  I  I  M  R  T  F  R  I  A  I  W  N  L  D  V  I  I  S  S  I
      -   S  L  *  G  L  S  G  L  L  F  G  I  L  T  L  *  *  V  Q  *
27181 - AGTGAGACAATTATTTAAGCCTCTAACTAAGAAGAATTATTCGGAGTTAGATGATGAAGA - 27240
      - S  E  T  I  I  *  A  S  N  *  E  E  L  F  G  V  R  *  *  R
      -  V  R  Q  L  F  K  P  L  T  K  K  N  Y  S  E  L  D  D  E  E
      -   *  D  N  Y  L  S  L  *  L  R  R  I  I  R  S  *  M  M  K  N
27241 - ACCTATGGAGTTAGATTATCCATAAAACGAACATGAAAATTATTCTCTTCCTGACATTGA - 27300
      - T  Y  G  V  R  L  S  I  K  R  T  *  K  L  F  S  S  *  H  *
      -  P  M  E  L  D  Y  P  *  N  E  H  E  N  Y  S  L  P  D  I  D
      -   L  W  S  *  I  I  H  K  T  N  M  K  I  I  L  F  L  T  L  I
27301 - TTGTATTTACATCTTGCGAGCTATATCACTATCAGGAGTGTGTTAGAGGTACGACTGTAC - 27360
      - L  Y  L  H  L  A  S  Y  I  T  I  R  S  V  L  E  V  R  L  Y
      -  C  I  Y  I  L  R  A  I  S  L  S  G  V  C  *  R  Y  D  C  T
      -   V  F  T  S  C  E  L  Y  H  Y  Q  E  C  V  R  G  T  T  V  L
27361 - TACTAAAAGAACCTTGCCCATCAGGAACATACGAGGGCAATTCACCATTTCACCCTCTTG - 27420
      - Y  *  K  N  L  A  H  Q  E  H  T  R  A  I  H  H  F  T  L  L
      -  T  K  R  T  L  P  I  R  N  I  R  G  Q  F  T  I  S  P  S  C
      -   L  K  E  P  C  P  S  G  T  Y  E  G  N  S  P  F  H  P  L  A
27421 - CTGACAATAAATTTGCACTAACTTGCACTAGCACACACTTTGCTTTTGCTTGTGCTGACG - 27480
      - L  T  I  N  L  H  *  L  A  L  A  H  T  L  L  L  L  V  L  T
      -  *  Q  *  I  C  T  N  L  H  *  H  T  L  C  F  C  L  C  *  R
      -   D  N  K  F  A  L  T  C  T  S  T  H  F  A  F  A  C  A  D  G
27481 - GTACTCGACATACCTATCAGCTGCGTGCAAGATCAGTTTCACCAAAACTTTTCATCAGAC - 27540
      - V  L  D  I  P  I  S  C  V  Q  D  Q  F  H  Q  N  F  S  S  D
      -  Y  S  T  Y  L  S  A  A  C  K  I  S  F  T  K  T  F  H  Q  T
      -   T  R  H  T  Y  Q  L  R  A  R  S  V  S  P  K  L  F  I  R  Q
27541 - AAGAGGAGGTTCAACAAGAGCTCTACTCGCCACTTTTTCTCATTGTTGCTGCTCTAGTAT - 27600
      - K  R  R  F  N  K  S  S  T  R  H  F  F  S  L  L  L  L  *  Y
      -  R  G  G  S  T  R  A  L  L  A  T  F  S  H  C  C  C  S  S  I
      -   E  E  V  Q  Q  E  L  Y  S  P  L  F  L  I  V  A  A  L  V  F
27601 - TTTTAATACTTTGCTTCACCATTAAGAGAAAGACAGAATGAATGAGCTCACTTTAATTGA - 27660
      - F  *  Y  F  A  S  P  L  R  E  R  Q  N  E  *  A  H  F  N  *
      -  F  N  T  L  L  H  H  *  E  K  D  R  M  N  E  L  T  L  I  D
      -   L  I  L  C  F  T  I  K  R  K  T  E  *  M  S  S  L  *  L  T
27661 - CTTCTATTTGTGCTTTTTAGCCTTTCTGCTATTCCTTGTTTTAATAATGCTTATTATATT - 27720
      - L  L  F  V  L  F  S  L  S  A  I  P  C  F  N  N  A  Y  Y  I
      -  F  Y  L  C  F  L  A  F  L  L  F  L  V  L  I  M  L  I  I  F
      -   S  I  C  A  F  *  P  F  C  Y  S  L  F  *  *  C  L  L  Y  F
27721 - TTGGTTTTCACTCGAAATCCAGGATCTAGAAGAACCTTGTACCAAAGTCTAAACGAACAT - 27780
      - L  V  F  T  R  N  P  G  S  R  R  T  L  Y  Q  S  L  N  E  H
      -  W  F  S  L  E  I  Q  D  L  E  E  P  C  T  K  V  *  T  N  M
      -   G  F  H  S  K  S  R  I  *  K  N  L  V  P  K  S  K  R  T  *
```

Figure 16-LL

```
27781 - GAAACTTCTCATTGTTTTGACTTGTATTTCTCTATGCAGTTGCATATGCACTGTAGTACA - 27840
      - E  T  S  H  C  F  D  L  Y  F  S  M  Q  L  H  M  H  C  S  T
      -  K  L  L  I  V  L  T  C  I  S  L  C  S  C  I  C  T  V  V  Q
      -   N  F  S  L  F  *  L  V  F  L  Y  A  V  A  Y  A  L  *  Y  S
27841 - GCGCTGTGCATCTAATAAACCTCATGTGCTTGAAGATCCTTGTAAGGTACAACACTAGGG - 27900
      - A  L  C  I  *  *  T  S  C  A  *  R  S  L  *  G  T  T  L  G
      -  R  C  A  S  N  K  P  H  V  L  E  D  P  C  K  V  Q  H  *  G
      -   A  V  H  L  I  N  L  M  C  L  K  I  L  V  R  Y  N  T  R  G
27901 - GTAATACTTATAGCACTGCTTGGCTTTGTGCTCTAGGAAAGGTTTTACCTTTTCATAGAT - 27960
      - V  I  L  I  A  L  L  G  F  V  L  *  E  R  F  Y  L  F  I  D
      -  *  Y  L  *  H  C  L  A  L  C  S  R  K  G  F  T  F  S  *  M
      -   N  T  Y  S  T  A  W  L  C  A  L  G  K  V  L  P  F  H  R  W
27961 - GGCACACTATGGTTCAAACATGCACACCTAATGTTACTATCAACTGTCAAGATCCAGCTG - 28020
      - G  T  L  W  F  K  H  A  H  L  M  L  L  S  T  V  K  I  Q  L
      -  A  H  Y  G  S  N  M  H  T  *  C  Y  Y  Q  L  S  R  S  S  W
      -   H  T  M  V  Q  T  C  T  P  N  V  T  I  N  C  Q  D  P  A  G
28021 - GTGGTGCGCTTATAGCTAGGTGTTGGTACCTTCATGAAGGTCACCAAACTGCTGCATTTA - 28080
      - V  V  R  L  *  L  G  V  G  T  F  M  K  V  T  K  L  L  H  L
      -  W  C  A  Y  S  *  V  L  V  P  S  *  R  S  P  N  C  C  I  *
      -   G  A  L  I  A  R  C  W  Y  L  H  E  G  H  Q  T  A  A  F  R
28081 - GAGACGTACTTGTTGTTTTAAATAAACGAACAAATTAAAATGTCTGATAATGGACCCCAA - 28140
      - E  T  Y  L  L  F  *  I  N  E  Q  I  K  M  S  D  N  G  P  Q
      -  R  R  T  C  C  F  K  *  T  N  K  L  K  C  L  I  M  D  P  N
      -   D  V  L  V  V  L  N  K  R  T  N  *  N  V  *  *  W  T  P  I
28141 - TCAAACCAACGTAGTGCCCCCCGCATTACATTTGGTGGACCCACAGATTCAACTGACAAT - 28200
      - S  N  Q  R  S  A  P  R  I  T  F  G  G  P  T  D  S  T  D  N
      -  Q  T  N  V  V  P  P  A  L  H  L  V  D  P  Q  I  Q  L  T  I
      -   K  P  T  *  C  P  P  H  Y  I  W  W  T  H  R  F  N  *  Q  *
28201 - AACCAGAATGGAGGACGCAATGGGGCAAGGCCAAAACAGCGCCGACCCCAAGGTTTACCC - 28260
      - N  Q  N  G  G  R  N  G  A  R  P  K  Q  R  R  P  Q  G  L  P
      -  T  R  M  E  D  A  M  G  Q  G  Q  N  S  A  D  P  K  V  Y  P
      -   P  E  W  R  T  Q  W  G  K  A  K  T  A  P  T  P  R  F  T  Q
28261 - AATAATACTGCGTCTTGGTTCACAGCTCTCACTCAGCATGGCAAGGAGGAACTTAGATTC - 28320
      - N  N  T  A  S  W  F  T  A  L  T  Q  H  G  K  E  E  L  R  F
      -  I  I  L  R  L  G  S  Q  L  S  L  S  M  A  R  R  N  L  D  S
      -   *  Y  C  V  L  V  H  S  S  H  S  A  W  Q  G  G  T  *  I  P
28321 - CCTCGAGGCCAGGGCGTTCCAATCAACACCAATAGTGGTCCAGATGACCAAATTGGCTAC - 28380
      - P  R  G  Q  G  V  P  I  N  T  N  S  G  P  D  D  Q  I  G  Y
      -  L  E  A  R  A  F  Q  S  T  P  I  V  V  Q  M  T  K  L  A  T
      -   S  R  P  G  R  S  N  Q  H  Q  *  W  S  R  *  P  N  W  L  L
28381 - TACCGAAGAGCTACCCGACGAGTTCGTGGTGGTGACGGCAAAATGAAAGAGCTCAGCCCC - 28440
      - Y  R  R  A  T  R  R  V  R  G  G  D  G  K  M  K  E  L  S  P
      -  T  E  E  L  P  D  E  F  V  V  V  T  A  K  *  K  S  S  A  P
      -   P  K  S  Y  P  T  S  S  W  W  *  R  Q  N  E  R  A  Q  P  Q
28441 - AGATGGTACTTCTATTACCTAGGAACTGGCCCAGAAGCTTCACTTCCCTACGGCGCTAAC - 28500
      - R  W  Y  F  Y  Y  L  G  T  G  P  E  A  S  L  P  Y  G  A  N
      -  D  G  T  S  I  T  *  E  L  A  Q  K  L  H  F  P  T  A  L  T
      -   M  V  L  L  L  P  R  N  W  P  R  S  F  T  S  L  R  R  *  Q
```

Figure 16-MM

```
28501 - AAAGAAGGCATCGTATGGGTTGCAACTGAGGGAGCCTTGAATACACCCAAAGACCACATT - 28560
      - K  E  G  I  V  W  V  A  T  E  G  A  L  N  T  P  K  D  H  I
      -  K  K  A  S  Y  G  L  Q  L  R  E  P  *  I  H  P  K  T  T  L
      -   R  R  H  R  M  G  C  N  *  G  S  L  E  Y  T  Q  R  P  H  W
28561 - GGCACCCGCAATCCTAATAACAATGCTGCCACCGTGCTACAACTTCCTCAAGGAACAACA - 28620
      - G  T  R  N  P  N  N  N  A  A  T  V  L  Q  L  P  Q  G  T  T
      -  A  P  A  I  L  I  T  M  L  P  P  C  Y  N  F  L  K  E  Q  H
      -   H  P  Q  S  *  *  Q  C  C  H  R  A  T  T  S  S  R  N  N  I
28621 - TTGCCAAAAGGCTTCTACGCAGAGGGAAGCAGAGGCGGCAGTCAAGCCTCTTCTCGCTCC - 28680
      - L  P  K  G  F  Y  A  E  G  S  R  G  G  S  Q  A  S  S  R  S
      -  C  Q  K  A  S  T  Q  R  E  A  E  A  A  V  K  P  L  L  A  P
      -   A  K  R  L  L  R  R  G  K  Q  R  R  Q  S  S  L  F  S  L  L
28681 - TCATCACGTAGTCGCGGTAATTCAAGAAATTCAACTCCTGGCAGCAGTAGGGGAAATTCT - 28740
      - S  S  R  S  R  G  N  S  R  N  S  T  P  G  S  S  R  G  N  S
      -  H  H  V  V  A  V  I  Q  E  I  Q  L  L  A  A  V  G  E  I  L
      -   I  T  *  S  R  *  F  K  K  F  N  S  W  Q  Q  *  G  K  F  S
28741 - CCTGCTCGAATGGCTAGCGGAGGTGGTGAAACTGCCCTCGCGCTATTGCTGCTAGACAGA - 28800
      - P  A  R  M  A  S  G  G  G  E  T  A  L  A  L  L  L  L  D  R
      -  L  L  E  W  L  A  E  V  V  K  L  P  S  R  Y  C  C  *  T  D
      -   C  S  N  G  *  R  R  W  *  N  C  P  R  A  I  A  A  R  Q  I
28801 - TTGAACCAGCTTGAGAGCAAAGTTTCTGGTAAAGGCCAACAACAACAAGGCCAAACTGTC - 28860
      - L  N  Q  L  E  S  K  V  S  G  K  G  Q  Q  Q  Q  G  Q  T  V
      -  *  T  S  L  R  A  K  F  L  V  K  A  N  N  N  K  A  K  L  S
      -   E  P  A  *  E  Q  S  F  W  *  R  P  T  T  T  R  P  N  C  H
28861 - ACTAAGAAATCTGCTGCTGAGGCATCTAAAAAGCCTCGCCAAAAACGTACTGCCACAAAA - 28920
      - T  K  K  S  A  A  E  A  S  K  K  P  R  Q  K  R  T  A  T  K
      -  L  R  N  L  L  L  R  H  L  K  S  L  A  K  N  V  L  P  Q  N
      -   *  E  I  C  C  *  G  I  *  K  A  S  P  K  T  Y  C  H  K  T
28921 - CAGTACAACGTCACTCAAGCATTTGGGAGACGTGGTCCAGAACAAACCCAAGGAAATTTC - 28980
      - Q  Y  N  V  T  Q  A  F  G  R  R  G  P  E  Q  T  Q  G  N  F
      -  S  T  T  S  L  K  H  L  G  D  V  V  Q  N  K  P  K  E  I  S
      -   V  Q  R  H  S  S  I  W  E  T  W  S  R  T  N  P  R  K  F  R
28981 - GGGGACCAAGACCTAATCAGACAAGGAACTGATTACAAACATTGGCCGCAAATTGCACAA - 29040
      - G  D  Q  D  L  I  R  Q  G  T  D  Y  K  H  W  P  Q  I  A  Q
      -  G  T  K  T  *  S  D  K  E  L  I  T  N  I  G  R  K  L  H  N
      -   G  P  R  P  N  Q  T  R  N  *  L  Q  T  L  A  A  N  C  T  I
29041 - TTTGCTCCAAGTGCCTCTGCATTCTTTGGAATGTCACGCATTGGCATGGAAGTCACACCT - 29100
      - F  A  P  S  A  S  A  F  F  G  M  S  R  I  G  M  E  V  T  P
      -  L  L  Q  V  P  L  H  S  L  E  C  H  A  L  A  W  K  S  H  L
      -   C  S  K  C  L  C  I  L  W  N  V  T  H  W  H  G  S  H  T  F
29101 - TCGGGAACATGGCTGACTTATCATGGAGCCATTAAATTGGATGACAAAGATCCACAATTC - 29160
      - S  G  T  W  L  T  Y  H  G  A  I  K  L  D  D  K  D  P  Q  F
      -  R  E  H  G  *  L  I  M  E  P  L  N  W  M  T  K  I  H  N  S
      -   G  N  M  A  D  L  S  W  S  H  *  I  G  *  Q  R  S  T  I  Q
29161 - AAAGACAACGTCATACTGCTGAACAAGCACATTGACGCATACAAAACATTCCCACCAACA - 29220
      - K  D  N  V  I  L  L  N  K  H  I  D  A  Y  K  T  F  P  P  T
      -  K  T  T  S  Y  C  *  T  S  T  L  T  H  T  K  H  S  H  Q  Q
      -   R  Q  R  H  T  A  E  Q  A  H  *  R  I  Q  N  I  P  T  N  R
29221 - GAGCCTAAAAAGGACAAAAAGAAAAAGACTGATGAAGCTCAGCCTTTGCCGCAGAGACAA - 29280
      - E  P  K  K  D  K  K  K  K  T  D  E  A  Q  P  L  P  Q  R  Q
      -  S  L  K  R  T  K  R  K  R  L  M  K  L  S  L  C  R  R  D  K
      -   A  *  K  G  Q  K  E  K  D  *  *  S  S  A  F  A  A  E  T  K
```

Figure 16-NN

```
29281 - AAGAAGCAGCCCACTGTGACTCTTCTTCCTGCGGCTGACATGGATGATTTCTCCAGACAA - 29340
      - K  K  Q  P  T  V  T  L  L  P  A  A  D  M  D  D  F  S  R  Q
      -  R  S  S  P  L  *  L  F  F  L  R  L  T  W  M  I  S  P  D  N
      -   E  A  A  H  C  D  S  S  S  C  G  *  H  G  *  F  L  Q  T  T
29341 - CTTCAAAATTCCATGAGTGGAGCTTCTGCTGATTCAACTCAGGCATAAACACTCATGATG - 29400
      - L  Q  N  S  M  S  G  A  S  A  D  S  T  Q  A  *  T  L  M  M
      -  F  K  I  P  *  V  E  L  L  L  I  Q  L  R  H  K  H  S  *  *
      -   S  K  F  H  E  W  S  F  C  *  F  N  S  G  I  N  T  H  D  D
29401 - ACCACACAAGGCAGATGGGCTATGTAAACGTTTTCGCAATTCCGTTTACGATACATAGTC - 29460
      - T  T  Q  G  R  W  A  M  *  T  F  S  Q  F  R  L  R  Y  I  V
      -  P  H  K  A  D  G  L  C  K  R  F  R  N  S  V  Y  D  T  *  S
      -   H  T  R  Q  M  G  Y  V  N  V  F  A  I  P  F  T  I  H  S  L
29461 - TACTCTTGTGCAGAATGAATTCTCGTAACTAAACAGCACAAGTAGGTTTAGTTAACTTTA - 29520
      - Y  S  C  A  E  *  I  L  V  T  K  Q  H  K  *  V  *  L  T  L
      -  T  L  V  Q  N  E  F  S  *  L  N  S  T  S  R  F  S  *  L  *
      -   L  L  C  R  M  N  S  R  N  *  T  A  Q  V  G  L  V  N  F  N
29521 - ATCTCACATAGCAATCTTTAATCAATGTGTAACATTAGGGAGGACTTGAAAGAGCCACCA - 29580
      - I  S  H  S  N  L  *  S  M  C  N  I  R  E  D  L  K  E  P  P
      -  S  H  I  A  I  F  N  Q  C  V  T  L  G  R  T  *  K  S  H  H
      -   L  T  *  Q  S  L  I  N  V  *  H  *  G  G  L  E  R  A  T  T
29581 - CATTTTCATCGAGGCCACGCGGAGTACGATCGAGGGTACAGTGAATAATGCTAGGGAGAG - 29640
      - H  F  H  R  G  H  A  E  Y  D  R  G  Y  S  E  *  C  *  G  E
      -  I  F  I  E  A  T  R  S  T  I  E  G  T  V  N  N  A  R  E  S
      -   F  S  S  R  P  R  G  V  R  S  R  V  Q  *  I  M  L  G  R  A
29641 - CTGCCTATATGGAAGAGCCCTAATGTGTAAAATTAATTTAGTAGTGCTATCCCCATGTG - 29700
      - L  P  I  W  K  S  P  N  V  *  N  *  F  *  *  C  Y  P  H  V
      -  C  L  Y  G  R  A  L  M  C  K  I  N  F  S  S  A  I  P  M  *
      -   A  Y  M  E  E  P  *  C  V  K  L  I  L  V  V  L  S  P  C  D
29701 - ATTTAATAGCTTCTTAGGAGAATGACAAAAAAAAAAAAAAAA - 29742
      - I  L  I  A  S  *  E  N  D  K  K  K  K  K  X
      -  F  *  *  L  L  R  R  M  T  K  K  K  K  X
      -   F  N  S  F  L  G  E  *  Q  K  K  K  K  X
```

Figure 17-A

```
  1 - TTTTTTTTTTTTTTTGTCATTCTCCTAAGAAGCTATTAAAATCACATGGGGATAGCACTA - 60
    - F  F  F  F  F  V  I  L  L  R  S  Y  *  N  H  M  G  I  A  L
    -  F  F  F  F  L  S  F  S  *  E  A  I  K  I  T  W  G  *  H  Y
    -   F  F  F  F  C  H  S  P  K  K  L  L  K  S  H  G  D  S  T  T
 61 - CTAAAATTAATTTTACACATTAGGGCTCTTCCATATAGGCAGCTCTCCCTAGCATTATTC - 120
    - L  K  L  I  L  H  I  R  A  L  P  Y  R  Q  L  S  L  A  L  F
    -  *  N  *  F  Y  T  L  G  L  F  H  I  G  S  S  P  *  H  Y  S
    -   K  I  N  F  T  H  *  G  S  S  I  *  A  A  L  P  S  I  I  H
121 - ACTGTACCCTCGATCGTACTCCGCGTGGCCTCGATGAAAATGTGGTGGCTCTTTCAAGTC - 180
    - T  V  P  S  I  V  L  R  V  A  S  M  K  M  W  W  L  F  Q  V
    -  L  Y  P  R  S  Y  S  A  W  P  R  *  K  C  G  G  S  F  K  S
    -   C  T  L  D  R  T  P  R  G  L  D  E  N  V  V  A  L  S  S  P
181 - CTCCCTAATGTTACACATTGATTAAAGATTGCTATGTGAGATTAAAGTTAACTAAACCTA - 240
    - L  P  N  V  T  H  *  L  K  I  A  M  *  D  *  S  *  L  N  L
    -  S  L  M  L  H  I  D  *  R  L  L  C  E  I  K  V  N  *  T  Y
    -   P  *  C  Y  T  L  I  K  D  C  Y  V  R  L  K  L  T  K  P  T
241 - CTTGTGCTGTTTAGTTACGAGAATTCATTCTGCACAAGAGTAGACTATGTATCGTAAACG - 300
    - L  V  L  F  S  Y  E  N  S  F  C  T  R  V  D  Y  V  S  *  T
    -  L  C  C  L  V  T  R  I  H  S  A  Q  E  *  T  M  Y  R  K  R
    -   C  A  V  *  L  R  E  F  I  L  H  K  S  R  L  C  I  V  N  G
301 - GAATTGCGAAAACGTTTACATAGCCCATCTGCCTTGTGTGGTCATCATGAGTGTTTATGC - 360
    - E  L  R  K  R  L  H  S  P  S  A  L  C  G  H  H  E  C  L  C
    -  N  C  E  N  V  Y  I  A  H  L  P  C  V  V  I  M  S  V  Y  A
    -   I  A  K  T  F  T  *  P  I  C  L  V  W  S  S  *  V  F  M  P
361 - CTGAGTTGAATCAGCAGAAGCTCCACTCATGGAATTTTGAAGTTGTCTGGAGAAATCATC - 420
    - L  S  *  I  S  R  S  S  T  H  G  I  L  K  L  S  G  E  I  I
    -  *  V  E  S  A  E  A  P  L  M  E  F  *  S  C  L  E  K  S  S
    -   E  L  N  Q  Q  K  L  H  S  W  N  F  E  V  V  W  R  N  H  P
421 - CATGTCAGCCGCAGGAAGAAGAGTCACAGTGGGCTGCTTCTTTTGTCTCTGCGGCAAAGG - 480
    - H  V  S  R  R  K  K  S  H  S  G  L  L  L  L  S  L  R  Q  R
    -  M  S  A  A  G  R  R  V  T  V  G  C  F  F  C  L  C  G  K  G
    -   C  Q  P  Q  E  E  E  S  Q  W  A  A  S  F  V  S  A  A  K  A
481 - CTGAGCTTCATCAGTCTTTTTCTTTTTGTCCTTTTTAGGCTCTGTTGGTGGGAATGTTTT - 540
    - L  S  F  I  S  L  F  L  F  V  L  F  R  L  C  W  W  E  C  F
    -  *  A  S  S  V  F  F  F  L  S  F  L  G  S  V  G  G  N  V  L
    -   E  L  H  Q  S  F  S  F  C  P  F  *  A  L  L  V  G  M  F  C
541 - GTATGCGTCAATGTGCTTGTTCAGCAGTATGACGTTGTCTTTGAATTGTGGATCTTTGTC - 600
    - V  C  V  N  V  L  V  Q  Q  Y  D  V  V  F  E  L  W  I  F  V
    -  Y  A  S  M  C  L  F  S  S  M  T  L  S  L  N  C  G  S  L  S
    -   M  R  Q  C  A  C  S  A  V  *  R  C  L  *  I  V  D  L  C  H
601 - ATCCAATTTAATGGCTCCATGATAAGTCAGCCATGTTCCCGAAGGTGTGACTTCCATGCC - 660
    - I  Q  F  N  G  S  M  I  S  Q  P  C  S  R  R  C  D  F  H  A
    -  S  N  L  M  A  P  *  *  V  S  H  V  P  E  G  V  T  S  M  P
    -   P  I  *  W  L  H  D  K  S  A  M  F  P  K  V  *  L  P  C  Q
661 - AATGCGTGACATTCCAAAGAATGCAGAGGCACTTGGAGCAAATTGTGCAATTTGCGGCCA - 720
    - N  A  *  H  S  K  E  C  R  G  T  W  S  K  L  C  N  L  R  P
    -  M  R  D  I  P  K  N  A  E  A  L  G  A  N  C  A  I  C  G  Q
    -   C  V  T  F  Q  R  M  Q  R  H  L  E  Q  I  V  Q  F  A  A  N
```

Figure 17-B

```
 721 - ATGTTTGTAATCAGTTCCTTGTCTGATTAGGTCTTGGTCCCCGAAATTTCCTTGGGTTTG - 780
     - M  F  V  I  S  S  L  S  D  *  V  L  V  P  E  I  S  L  G  L
     -  C  L  *  S  V  P  C  L  I  R  S  W  S  P  K  F  P  W  V  C
     -   V  C  N  Q  F  L  V  *  L  G  L  G  P  R  N  F  L  G  F  V
 781 - TTCTGGACCACGTCTCCCAAATGCTTGAGTGACGTTGTACTGTTTTGTGGCAGTACGTTT - 840
     - F  W  T  T  S  P  K  C  L  S  D  V  V  L  F  C  G  S  T  F
     -  S  G  P  R  L  P  N  A  *  V  T  L  Y  C  F  V  A  V  R  F
     -   L  D  H  V  S  Q  M  L  E  *  R  C  T  V  L  W  Q  Y  V  F
 841 - TTGGCGAGGCTTTTTAGATGCCTCAGCAGCAGATTTCTTAGTGACAGTTTGGCCTTGTTG - 900
     - L  A  R  L  F  R  C  L  S  S  R  F  L  S  D  S  L  A  L  L
     -  W  R  G  F  L  D  A  S  A  A  D  F  L  V  T  V  W  P  C  C
     -   G  E  A  F  *  M  P  Q  Q  Q  I  S  *  *  Q  F  G  L  V  V
 901 - TTGTTGGCCTTTACCAGAAACTTTGCTCTCAAGCTGGTTCAATCTGTCTAGCAGCAATAG - 960
     - L  L  A  F  T  R  N  F  A  L  K  L  V  Q  S  V  *  Q  Q  *
     -  C  W  P  L  P  E  T  L  L  S  S  W  F  N  L  S  S  S  N  S
     -   V  G  L  Y  Q  K  L  C  S  Q  A  G  S  I  C  L  A  A  I  A
 961 - CGCGAGGGCAGTTTCACCACCTCCGCTAGCCATTCGAGCAGGAGAATTTCCCCTACTGCT - 1020
     - R  E  G  S  F  T  T  S  A  S  H  S  S  R  R  I  S  P  T  A
     -  A  R  A  V  S  P  P  P  L  A  I  R  A  G  E  F  P  L  L  L
     -   R  G  Q  F  H  H  L  R  *  P  F  E  Q  E  N  F  P  Y  C  C
1021 - GCCAGGAGTTGAATTTCTTGAATTACCGCGACTACGTGATGAGGAGCGAGAAGAGGCTTG - 1080
     - A  R  S  *  I  S  *  I  T  A  T  T  *  *  G  A  R  R  G  L
     -  P  G  V  E  F  L  E  L  P  R  L  R  D  E  E  R  E  E  A  *
     -   Q  E  L  N  F  L  N  Y  R  D  Y  V  M  R  S  E  K  R  L  D
1081 - ACTGCCGCCTCTGCTTCCCTCTGCGTAGAAGCCTTTTGGCAATGTTGTTCCTTGAGGAAG - 1140
     - T  A  A  S  A  S  L  C  V  E  A  F  W  Q  C  C  S  L  R  K
     -  L  P  P  L  L  P  S  A  *  K  P  F  G  N  V  V  P  *  G  S
     -   C  R  L  C  F  P  L  R  R  S  L  L  A  M  L  F  L  E  E  V
1141 - TTGTAGCACGGTGGCAGCATTGTTATTAGGATTGCGGGTGCCAATGTGGTCTTTGGGTGT - 1200
     - L  *  H  G  G  S  I  V  I  R  I  A  G  A  N  V  V  F  G  C
     -  C  S  T  V  A  A  L  L  L  G  L  R  V  P  M  W  S  L  G  V
     -   V  A  R  W  Q  H  C  Y  *  D  C  G  C  Q  C  G  L  W  V  Y
1201 - ATTCAAGGCTCCCTCAGTTGCAACCCATACGATGCCTTCTTTGTTAGCGCCGTAGGGAAG - 1260
     - I  Q  G  S  L  S  C  N  P  Y  D  A  F  F  V  S  A  V  G  K
     -  F  K  A  P  S  V  A  T  H  T  M  P  S  L  L  A  P  *  G  S
     -   S  R  L  P  Q  L  Q  P  I  R  C  L  L  C  *  R  R  R  E  V
1261 - TGAAGCTTCTGGGCCAGTTCCTAGGTAATAGAAGTACCATCTGGGGCTGAGCTCTTTCAT - 1320
     - *  S  F  W  A  S  S  *  V  I  E  V  P  S  G  A  E  L  F  H
     -  E  A  S  G  P  V  P  R  *  *  K  Y  H  L  G  L  S  S  F  I
     -   K  L  L  G  Q  F  L  G  N  R  S  T  I  W  G  *  A  L  S  F
1321 - TTTGCCGTCACCACCACGAACTCGTCGGGTAGCTCTTCGGTAGTAGCCAATTTGGTCATC - 1380
     - F  A  V  T  T  T  N  S  S  G  S  S  S  V  V  A  N  L  V  I
     -  L  P  S  P  P  R  T  R  R  V  A  L  R  *  *  P  I  W  S  S
     -   C  R  H  H  H  E  L  V  G  *  L  F  G  S  S  Q  F  G  H  L
1381 - TGGACCACTATTGGTGTTGATTGGAACGCCCTGGCCTCGAGGGAATCTAAGTTCCTCCTT - 1440
     - W  T  T  I  G  V  D  W  N  A  L  A  S  R  E  S  K  F  L  L
     -  G  P  L  L  V  L  I  G  T  P  W  P  R  G  N  L  S  S  S  L
     -   D  H  Y  W  C  *  L  E  R  P  G  L  E  G  I  *  V  P  P  C
1441 - GCCATGCTGAGTGAGAGCTGTGAACCAAGACGCAGTATTATTGGGTAAACCTTGGGGTCG - 1500
     - A  M  L  S  E  S  C  E  P  R  R  S  I  I  G  *  T  L  G  S
     -  P  C  *  V  R  A  V  N  Q  D  A  V  L  L  G  K  P  W  G  R
     -   H  A  E  *  E  L  *  T  K  T  Q  Y  Y  W  V  N  L  G  V  G
```

Figure 17-C

```
1501 - GCGCTGTTTTGGCCTTGCCCCATTGCGTCCTCCATTCTGGTTATTGTCAGTTGAATCTGT - 1560
     -A  L  F  W  P  C  P  I  A  S  S  I  L  V  I  V  S  *  I  C
     - R  C  F  G  L  A  P  L  R  P  P  F  W  L  L  S  V  E  S  V
     -  A  V  L  A  L  P  H  C  V  L  H  S  G  Y  C  Q  L  N  L  W
1561 - GGGTCCACCAAATGTAATGCGGGGGGCACTACGTTGGTTTGATTGGGGTCCATTATCAGA - 1620
     -G  S  T  K  C  N  A  G  G  T  T  L  V  *  L  G  S  I  I  R
     - G  P  P  N  V  M  R  G  A  L  R  W  F  D  W  G  P  L  S  D
     -  V  H  Q  M  *  C  G  G  H  Y  V  G  L  I  G  V  H  Y  Q  T
1621 - CATTTTAATTTGTTCGTTTATTTAAAACAACAAGTACGTCTCTAAATGCAGCAGTTTGGT - 1680
     -H  F  N  L  F  V  Y  L  K  Q  Q  V  R  L  *  M  Q  Q  F  G
     - I  L  I  C  S  F  I  *  N  N  K  Y  V  S  K  C  S  S  L  V
     -  F  *  F  V  R  L  F  K  T  T  S  T  S  L  N  A  A  V  W  *
1681 - GACCTTCATGAAGGTACCAACACCTAGCTATAAGCGCACCACCAGCTGGATCTTGACAGT - 1740
     -D  L  H  E  G  T  N  T  *  L  *  A  H  H  Q  L  D  L  D  S
     - T  F  M  K  V  P  T  P  S  Y  K  R  T  T  S  W  I  L  T  V
     -  P  S  *  R  Y  Q  H  L  A  I  S  A  P  P  A  G  S  *  Q  L
1741 - TGATAGTAACATTAGGTGTGCATGTTTGAACCATAGTGTGCCATCTATGAAAAGGTAAAA - 1800
     -*  *  *  H  *  V  C  M  F  E  P  *  C  A  I  Y  E  K  V  K
     - D  S  N  I  R  C  A  C  L  N  H  S  V  P  S  M  K  R  *  N
     -  I  V  T  L  G  V  H  V  *  T  I  V  C  H  L  *  K  G  K  T
1801 - CCTTTCCTAGAGCACAAAGCCAAGCAGTGCTATAAGTATTACCCCTAGTGTTGTACCTTA - 1860
     -P  F  L  E  H  K  A  K  Q  C  Y  K  Y  Y  P  *  C  C  T  L
     - L  S  *  S  T  K  P  S  S  A  I  S  I  T  P  S  V  V  P  Y
     -  F  P  R  A  Q  S  Q  A  V  L  *  V  L  P  L  V  L  Y  L  T
1861 - CAAGGATCTTCAAGCACATGAGGTTTATTAGATGCACAGCGCTGTACTACAGTGCATATG - 1920
     -Q  G  S  S  S  T  *  G  L  L  D  A  Q  R  C  T  T  V  H  M
     - K  D  L  Q  A  H  E  V  Y  *  M  H  S  A  V  L  Q  C  I  C
     -  R  I  F  K  H  M  R  F  I  R  C  T  A  L  Y  Y  S  A  Y  A
1921 - CAACTGCATAGAGAAATACAAGTCAAAACAATGAGAAGTTTCATGTTCGTTTAGACTTTG - 1980
     -Q  L  H  R  E  I  Q  V  K  T  M  R  S  F  M  F  V  *  T  L
     - N  C  I  E  K  Y  K  S  K  Q  *  E  V  S  C  S  F  R  L  W
     -  T  A  *  R  N  T  S  Q  N  N  E  K  F  H  V  R  L  D  F  G
1981 - GTACAAGGTTCTTCTAGATCCTGGATTTCGAGTGAAAACCAAAATATAATAAGCATTATT - 2040
     -V  Q  G  S  S  R  S  W  I  S  S  E  N  Q  N  I  I  S  I  I
     - Y  K  V  L  L  D  P  G  F  R  V  K  T  K  I  *  *  A  L  L
     -  T  R  F  F  *  I  L  D  F  E  *  K  P  K  Y  N  K  H  Y  *
2041 - AAAACAAGGAATAGCAGAAAGGCTAAAAAGCACAAATAGAAGTCAATTAAAGTGAGCTCA - 2100
     -K  T  R  N  S  R  K  A  K  K  H  K  *  K  S  I  K  V  S  S
     - K  Q  G  I  A  E  R  L  K  S  T  N  R  S  Q  L  K  *  A  H
     -  N  K  E  *  Q  K  G  *  K  A  Q  I  E  V  N  *  S  E  L  I
2101 - TTCATTCTGTCTTTCTCTTAATGGTGAAGCAAAGTATTAAAAATACTAGAGCAGCAACAA - 2160
     -F  I  L  S  F  S  *  W  *  S  K  V  L  K  I  L  E  Q  Q  Q
     - S  F  C  L  S  L  N  G  E  A  K  Y  *  K  Y  *  S  S  N  N
     -  H  S  V  F  L  L  M  V  K  Q  S  I  K  N  T  R  A  A  T  M
2161 - TGAGAAAAAGTGGCGAGTAGAGCTCTTGTTGAACCTCCTCTTGTCTGATGAAAAGTTTTG - 2220
     -*  E  K  V  A  S  R  A  L  V  E  P  P  L  V  *  *  K  V  L
     - E  K  K  W  R  V  E  L  L  L  N  L  L  L  S  D  E  K  F  W
     -  R  K  S  G  E  *  S  S  C  *  T  S  S  C  L  M  K  S  F  G
```

Figure 17-D

```
2221 - GTGAAACTGATCTTGCACGCAGCTGATAGGTATGTCGAGTACCGTCAGCACAAGCAAAAG - 2280
     - V  K  L  I  L  H  A  A  D  R  Y  V  E  Y  R  Q  H  K  Q  K
     -  *  N  *  S  C  T  Q  L  I  G  M  S  S  T  V  S  T  S  K  S
     -   E  T  D  L  A  R  S  *  *  V  C  R  V  P  S  A  Q  A  K  A
2281 - CAAAGTGTGTGCTAGTGCAAGTTAGTGCAAATTTATTGTCAGCAAGAGGGTGAAATGGTG - 2340
     - Q  S  V  C  *  C  K  L  V  Q  I  Y  C  Q  Q  E  G  E  M  V
     -  K  V  C  A  S  A  S  *  C  K  F  I  V  S  K  R  V  K  W  *
     -   K  C  V  L  V  Q  V  S  A  N  L  L  S  A  R  G  *  N  G  E
2341 - AATTGCCCTCGTATGTTCCTGATGGGCAAGGTTCTTTTAGTAGTACAGTCGTACCTCTAA - 2400
     - N  C  P  R  M  F  L  M  G  K  V  L  L  V  V  Q  S  Y  L  *
     -  I  A  L  V  C  S  *  W  A  R  F  F  *  *  Y  S  R  T  S  N
     -   L  P  S  Y  V  P  D  G  Q  G  S  F  S  S  T  V  V  P  L  T
2401 - CACACTCCTGATAGTGATATAGCTCGCAAGATGTAAATACAATCAATGTCAGGAAGAGAA - 2460
     - H  T  P  D  S  D  I  A  R  K  M  *  I  Q  S  M  S  G  R  E
     -  T  L  L  I  V  I  *  L  A  R  C  K  Y  N  Q  C  Q  E  E  N
     -   H  S  *  *  *  Y  S  S  Q  D  V  N  T  I  N  V  R  K  R  I
2461 - TAATTTTCATGTTCGTTTTATGGATAATCTAACTCCATAGGTTCTTCATCATCTAACTCC - 2520
     - *  F  S  C  S  F  Y  G  *  S  N  S  I  G  S  S  S  S  N  S
     -  N  F  H  V  R  F  M  D  N  L  T  P  *  V  L  H  H  L  T  P
     -   I  F  M  F  V  L  W  I  I  *  L  H  R  F  F  I  I  *  L  R
2521 - GAATAATTCTTCTTAGTTAGAGGCTTAAATAATTGTCTCACTATTGAACTTATTATAACG - 2580
     - E  *  F  F  L  V  R  G  L  N  N  C  L  T  I  E  L  I  I  T
     -  N  N  S  S  *  L  E  A  *  I  I  V  S  L  L  N  L  L  *  R
     -   I  I  L  L  S  *  R  L  K  *  L  S  H  Y  *  T  Y  Y  N  V
2581 - TCAAGATTCCAAATAGCAATCCTGAAAGTCCTCATAATGATAATCAATATCTCTGCTATT - 2640
     - S  R  F  Q  I  A  I  L  K  V  L  I  M  I  I  N  I  S  A  I
     -  Q  D  S  K  *  Q  S  *  K  S  S  *  *  *  S  I  S  L  L  L
     -   K  I  P  N  S  N  P  E  S  P  H  N  D  N  Q  Y  L  C  Y  C
2641 - GTAACCTGGAAGTCAACAAGATGAAACATCTGTTGTCACTTACTGTACTAGCAAAGCAAT - 2700
     - V  T  W  K  S  T  R  *  N  I  C  C  H  L  L  Y  *  Q  S  N
     -  *  P  G  S  Q  Q  D  E  T  S  V  V  T  Y  C  T  S  K  A  I
     -   N  L  E  V  N  K  M  K  H  L  L  S  L  T  V  L  A  K  Q  Y
2701 - ATTGTCGTTGCTACCGGCGTGGTCTGTATTTAATTTATAGTTTCCAATACGGTAGCGGTT - 2760
     - I  V  V  A  T  G  V  V  C  I  *  F  I  V  S  N  T  V  A  V
     -  L  S  L  L  P  A  W  S  V  F  N  L  *  F  P  I  R  *  R  L
     -   C  R  C  Y  R  R  G  L  Y  L  I  Y  S  F  Q  Y  G  S  G  C
2761 - GTATGCAGCAAAACCTGAATCAGTGCCTACACGCTGCGACGCTCCTAATTTGTAATAAGA - 2820
     - V  C  S  K  T  *  I  S  A  Y  T  L  R  R  S  *  F  V  I  R
     -  Y  A  A  K  P  E  S  V  P  T  R  C  D  A  P  N  L  *  *  E
     -   M  Q  Q  N  L  N  Q  C  L  H  A  A  T  L  L  I  C  N  K  K
2821 - AAGCGTTCGTGATGTAGCCACAGTGATCTCTTTTGGCAGGTCCTTAATGTCACAGCGCCC - 2880
     - K  R  S  *  C  S  H  S  D  L  F  W  Q  V  L  N  V  T  A  P
     -  S  V  R  D  V  A  T  V  I  S  F  G  R  S  L  M  S  Q  R  P
     -   A  F  V  M  *  P  Q  *  S  L  L  A  G  P  *  C  H  S  A  L
2881 - TAGGGAGTGTCCGGCCATTCGCAAGTGACCACGAATGATCACAGCACCAATGACAAGTTC - 2940
     - *  G  V  S  G  H  S  Q  V  T  T  N  D  H  S  T  N  D  K  F
     -  R  E  C  P  A  I  R  K  *  P  R  M  I  T  A  P  M  T  S  S
     -   G  S  V  R  P  F  A  S  D  H  E  *  S  Q  H  Q  *  Q  V  H
2941 - ACTTTCCATGAGCGGTCTGGTCACAATTGTCCCCCGGAGAGGCACATTGAGAAGAATGTT - 3000
     - T  F  H  E  R  S  G  H  N  C  P  P  E  R  H  I  E  K  N  V
     -  L  S  M  S  G  L  V  T  I  V  P  R  R  G  T  L  R  R  M  F
     -   F  P  *  A  V  W  S  Q  L  S  P  G  E  A  H  *  E  E  C  L
```

Figure 17-E

```
3001 - TGTTTCTGGGTTGAATGACCACATTGAGCGGGTACGAGCAAACAGCCTGAAGGAAGCAAC - 3060
     - C  F  W  V  E  *  P  H  *  A  G  T  S  K  Q  P  E  G  S  N
     -  V  S  G  L  N  D  H  I  E  R  V  R  A  N  S  L  K  E  A  T
     -   F  L  G  *  M  T  T  L  S  G  Y  E  Q  T  A  *  R  K  Q  R
3061 - GAAGTAGCTAAGCCACATCAAGCCTACAATACAAGCCATTGCAATCGCAATCCCGCCAGT - 3120
     - E  V  A  K  P  H  Q  A  Y  N  T  S  H  C  N  R  N  P  A  S
     -  K  *  L  S  H  I  K  P  T  I  Q  A  I  A  I  A  I  P  P  V
     -   S  S  *  A  T  S  S  L  Q  Y  K  P  L  Q  S  Q  S  R  Q  S
3121 - CACCCAATTAATTCTGTAGACAACAGCAAGCACAAAACAAGCAAGTGTTACTGGCCACAA - 3180
     - H  P  I  N  S  V  D  N  S  K  H  K  T  S  K  C  Y  W  P  Q
     -  T  Q  L  I  L  *  T  T  A  S  T  K  Q  A  S  V  T  G  H  K
     -   P  N  *  F  C  R  Q  Q  Q  A  Q  N  K  Q  V  L  L  A  T  R
3181 - GAGCCAGAGGAAAACAAGCTTTATTATGTACAAAAACCTGTTCCGATTAGAATAGGCAAA - 3240
     - E  P  E  E  N  K  L  Y  Y  V  Q  K  P  V  P  I  R  I  G  K
     -  S  Q  R  K  T  S  F  I  M  Y  K  N  L  F  R  L  E  *  A  N
     -   A  R  G  K  Q  A  L  L  C  T  K  T  C  S  D  *  N  R  Q  I
3241 - TTGTAGTAACATAATCCAGGCTAGGAATAGGAAACCTATTACTAGGTTCCATTGTTCCAG - 3300
     - L  *  *  H  N  P  G  *  E  *  E  T  Y  Y  *  V  P  L  F  Q
     -  C  S  N  I  I  Q  A  R  N  R  K  P  I  T  R  F  H  C  S  R
     -   V  V  T  *  S  R  L  G  I  G  N  L  L  L  G  S  I  V  P  G
3301 - GAGTTGTTTAAGCTCCTCAACGGTAATAGTACCGTTGTCTGCCATGATAAGCAATGTTAA - 3360
     - E  L  F  K  L  L  N  G  N  S  T  V  V  C  H  D  K  Q  C  *
     -  S  C  L  S  S  S  T  V  I  V  P  L  S  A  M  I  S  N  V  K
     -   V  V  *  A  P  Q  R  *  *  Y  R  C  L  P  *  *  A  M  L  K
3361 - AGTTCCAAACAGAATAATAATAATAGTTAGTTCGTTTAGACCAGAAGATCAGGAACTCCT - 3420
     - S  S  K  Q  N  N  N  N  S  *  F  V  *  T  R  R  S  G  T  P
     -  V  P  N  R  I  I  I  I  V  S  S  F  R  P  E  D  Q  E  L  L
     -   F  Q  T  E  *  *  *  *  L  V  R  L  D  Q  K  I  R  N  S  F
3421 - TCAGAAGAGTTCAGATTTTTAACACGCGAGTAGACGTAAACCGTTGGTTTTACTAAACTC - 3480
     - S  E  E  F  R  F  L  T  R  E  *  T  *  T  V  G  F  T  K  L
     -  Q  K  S  S  D  F  *  H  A  S  R  R  K  P  L  V  L  L  N  S
     -   R  R  V  Q  I  F  N  T  R  V  D  V  N  R  W  F  Y  *  T  H
3481 - ACGTTAACAATATTGCAGCAGTACGCACACAATCGAAGCGCAGTAAGGATGGCTAGTGTG - 3540
     - T  L  T  I  L  Q  Q  Y  A  H  N  R  S  A  V  R  M  A  S  V
     -  R  *  Q  Y  C  S  S  T  H  T  I  E  A  Q  *  G  W  L  V  *
     -   V  N  N  I  A  A  V  R  T  Q  S  K  R  S  K  D  G  *  C  D
3541 - ACTAGCAAGAATACCACGAAAGCAAGAAAAAGAAGTACGCTATTAACTATTAACGTACCT - 3600
     - T  S  K  N  T  T  K  A  R  K  R  S  T  L  L  T  I  N  V  P
     -  L  A  R  I  P  R  K  Q  E  K  E  V  R  Y  *  L  L  T  Y  L
     -   *  Q  E  Y  H  E  S  K  K  K  K  Y  A  I  N  Y  *  R  T  C
3601 - GTTTCTTCCGAAACGAATGAGTACATAAGTTCGTACTCACTTTCTTGTGCTTACAAAGGC - 3660
     - V  S  S  E  T  N  E  Y  I  S  S  Y  S  L  S  C  A  Y  K  G
     -  F  L  P  K  R  M  S  T  *  V  R  T  H  F  L  V  L  T  K  A
     -   F  F  R  N  E  *  V  H  K  F  V  L  T  F  L  C  L  Q  R  H
3661 - ACGCTAGTAGTCGTCGTCGGCTCATCATAAATTGGATCCATTGCTGGATTAGCAACTCCT - 3720
     - T  L  V  V  V  V  G  S  S  *  I  G  S  I  A  G  L  A  T  P
     -  R  *  *  S  S  S  A  H  H  K  L  D  P  L  L  D  *  Q  L  L
     -   A  S  S  R  R  R  L  I  I  N  W  I  H  C  W  I  S  N  S  *
```

Figure 17-F

```
3721 - GAAGAGCCGTCGATTGTGTGTATTTGCACATTCGGTGGGTCTTTAACAAGCTTGTTAAAG - 3780
     - E  E  P  S  I  V  C  I  C  T  F  G  G  S  L  T  S  L  L  K
     -  K  S  R  R  L  C  V  F  A  H  S  V  G  L  *  Q  A  C  *  R
     -   R  A  V  D  C  V  Y  L  H  I  R  W  V  F  N  K  L  V  K  D
3781 - ATGAAGAATGTAGCATTTTCAATACCAGTGTCTGTAGTAATTTGTGTAGACTCAAGCTGG - 3840
     - M  K  N  V  A  F  S  I  P  V  S  V  V  I  C  V  D  S  S  W
     -  *  R  M  *  H  F  Q  Y  Q  C  L  *  *  F  V  *  T  Q  A  G
     -   E  E  C  S  I  F  N  T  S  V  C  S  N  L  C  R  L  K  L  V
3841 - TAGTAAACTTCGGTGAAATAGCCATGTACAACGACATAGTCTTTAACACCTGAGTGCCTA - 3900
     - *  *  T  S  V  K  *  P  C  T  T  T  *  S  L  T  P  E  C  L
     -  S  K  L  R  *  N  S  H  V  Q  R  H  S  L  *  H  L  S  A  Y
     -   V  N  F  G  E  I  A  M  Y  N  D  I  V  F  N  T  *  V  P  I
3901 - TCCTCAGAATAACCACCAATTTGGTAGTCTTCTTTGAGTTTTGGTGTTGAAATGCCGTCA - 3960
     - S  S  E  *  P  P  I  W  *  S  S  L  S  F  G  V  E  M  P  S
     -  P  Q  N  N  H  Q  F  G  S  L  L  *  V  L  V  L  K  C  R  H
     -   L  R  I  T  T  N  L  V  V  F  F  E  F  W  C  *  N  A  V  T
3961 - CCTTCAGTAACGACAATTGTATCTGTGACACTGTTATATGGTATACAGTAGTCATAGTTA - 4020
     - P  S  V  T  T  I  V  S  V  T  L  L  Y  G  I  Q  *  S  *  L
     -  L  Q  *  R  Q  L  Y  L  *  H  C  Y  M  V  Y  S  S  H  S  Y
     -   F  S  N  D  N  C  I  C  D  T  V  I  W  Y  T  V  V  I  V  M
4021 - TGTGTGTGCCAGCAAACAAAGTAGTTGGCATCATAAAGTAATGGGTTCTTGGATTTGCAC - 4080
     - C  V  C  Q  Q  T  K  *  L  A  S  *  S  N  G  F  L  D  L  H
     -  V  C  A  S  K  Q  S  S  W  H  H  K  V  M  G  S  W  I  C  T
     -   C  V  P  A  N  K  V  V  G  I  I  K  *  W  V  L  G  F  A  L
4081 - TTCCAACAAAGCCAACATCTCATAATAATTCTACATGCGTTGATGCATTGTAGAAAATAT - 4140
     - F  Q  Q  S  Q  H  L  I  I  I  L  H  A  L  M  H  C  R  K  Y
     -  S  N  K  A  N  I  S  *  *  F  Y  M  R  *  C  I  V  E  N  I
     -   P  T  K  P  T  S  H  N  N  S  T  C  V  D  A  L  *  K  I  Y
4141 - ATCAAGGCATAGAGGTACAAAAATTGCGCCTCCTTACCTGCAGCGACAAGCAAAAGATGT - 4200
     - I  K  A  *  R  Y  K  N  C  A  S  L  P  A  A  T  S  K  R  C
     -  S  R  H  R  G  T  K  I  A  P  P  Y  L  Q  R  Q  A  K  D  V
     -   Q  G  I  E  V  Q  K  L  R  L  L  T  C  S  D  K  Q  K  M  *
4201 - GAATAGATGGTAACAAATAGCAGCAGTAAATTGCAAATGAACTGGAAGCCCTTATAAAGG - 4260
     - E  *  M  V  T  N  S  S  S  K  L  Q  M  N  W  K  P  L  *  R
     -  N  R  W  *  Q  I  A  A  V  N  C  K  *  T  G  S  P  Y  K  G
     -   I  D  G  N  K  *  Q  Q  *  I  A  N  E  L  E  A  L  I  K  G
4261 - GCTAGCTGCCATCTTTTATTGAGCGCAATTATTTTGGTAGCGCTCTGAAAAACAGCAAGA - 4320
     - A  S  C  H  L  L  L  S  A  I  I  L  V  A  L  *  K  T  A  R
     -  L  A  A  I  F  Y  *  A  Q  L  F  W  *  R  S  E  K  Q  Q  E
     -   *  L  P  S  F  I  E  R  N  Y  F  G  S  A  L  K  N  S  K  K
4321 - AATGCAACGCCAATAACAAGCCATCCGAAAGGGAGTGAGGCTTGTAGCGGTATCGTTGCT - 4380
     - N  A  T  P  I  T  S  H  P  K  G  S  E  A  C  S  G  I  V  A
     -  M  Q  R  Q  *  Q  A  I  R  K  G  V  R  L  V  A  V  S  L  L
     -   C  N  A  N  N  K  P  S  E  R  E  *  G  L  *  R  Y  R  C  C
4381 - GTAGCATGAACAGTACTTGCAGGAGAAGCATTGTCAATTTTTACTGGCTGTGCAGTAATT - 4440
     - V  A  *  T  V  L  A  G  E  A  L  S  I  F  T  G  C  A  V  I
     -  *  H  E  Q  Y  L  Q  E  K  H  C  Q  F  L  L  A  V  Q  *  L
     -   S  M  N  S  T  C  R  R  S  I  V  N  F  Y  W  L  C  S  N  *
4441 - GATCCAAGAGTAAAAAATCTCATAAACAAATCCATAAGTTCGTTTATGTGTAATGTAATT - 4500
     - D  P  R  V  K  N  L  I  N  K  S  I  S  S  F  M  C  N  V  I
     -  I  Q  E  *  K  I  S  *  T  N  P  *  V  R  L  C  V  M  *  F
     -   S  K  S  K  K  S  H  K  Q  I  H  K  F  V  Y  V  *  C  N  L
```

Figure 17-G

```
4501 - TGACACCCTTGAGAACTGGCTCAGAGTCATCCTCATCAAACTTGCAGCAAGAACCACAAG - 4560
     - *  H  P  *  E  L  A  Q  S  H  P  H  Q  T  C  S  K  N  H  K
     -  D  T  L  E  N  W  L  R  V  I  L  I  K  L  A  A  R  T  T  R
     -   T  P  L  R  T  G  S  E  S  S  S  S  N  L  Q  Q  E  P  Q  E
4561 - AGCATGCACCCTTGAGGCAACTGCAACAACTAGTCATGCAACAAAGCAAGATTGTAACCA - 4620
     - S  M  H  P  *  G  N  C  N  N  *  S  C  N  K  A  R  L  *  P
     -  A  C  T  L  E  A  T  A  T  T  S  H  A  T  K  Q  D  C  N  H
     -   H  A  P  L  R  Q  L  Q  Q  L  V  M  Q  Q  S  K  I  V  T  M
4621 - TGACGATGGCAATTAGTCCAGCAATGAAGCCGAGCCAAACATACCAAGGCCATTTAATAT - 4680
     - *  R  W  Q  L  V  Q  Q  *  S  R  A  K  H  T  K  A  I  *  Y
     -  D  D  G  N  *  S  S  N  E  A  E  P  N  I  P  R  P  F  N  I
     -   T  M  A  I  S  P  A  M  K  P  S  Q  T  Y  Q  G  H  L  I  Y
4681 - ATTGCTCATATTTTCCCAATTCTTGAAGGTCAATGAGTGATTCATTTAAATTTTTAGCGA - 4740
     - I  A  H  I  F  P  I  L  E  G  Q  *  V  I  H  L  N  F  *  R
     -  L  L  I  F  S  Q  F  L  K  V  N  E  *  F  I  *  I  F  S  D
     -   C  S  Y  F  P  N  S  *  R  S  M  S  D  S  F  K  F  L  A  T
4741 - CCTCATTGAGGCGGTCAATTTCTTTTTGAATGTTGACGACAGAAGCGTTAATGCCTGAAA - 4800
     - P  H  *  G  G  Q  F  L  F  E  C  *  R  Q  K  R  *  C  L  K
     -  L  I  E  A  V  N  F  F  L  N  V  D  D  R  S  V  N  A  *  N
     -   S  L  R  R  S  I  S  F  *  M  L  T  T  E  A  L  M  P  E  M
4801 - TGTCGCCAAGATCAACATCTGGTGATGTATGATTTTTGAAGTACTTGTCCAGCTCTTCTT - 4860
     - C  R  Q  D  Q  H  L  V  M  Y  D  F  *  S  T  C  P  A  L  L
     -  V  A  K  I  N  I  W  *  C  M  I  F  E  V  L  V  Q  L  F  F
     -   S  P  R  S  T  S  G  D  V  *  F  L  K  Y  L  S  S  S  S  L
4861 - TGAATGAGTCAAGCTCAGGTTGCAGAGGATCATAAACTGTGTTGTTAATGATGCCAATAA - 4920
     - *  M  S  Q  A  Q  V  A  E  D  H  K  L  C  C  *  *  C  Q  *
     -  E  *  V  K  L  R  L  Q  R  I  I  N  C  V  V  N  D  A  N  N
     -   N  E  S  S  S  G  C  R  G  S  *  T  V  L  L  M  M  P  I  T
4921 - CGACATCACAATTTCCTGAGACAAATGTATTGTCTGTAGTAATTATTTGTGGAGAAAAGA - 4980
     - R  H  H  N  F  L  R  Q  M  Y  C  L  *  *  L  F  V  E  K  R
     -  D  I  T  I  S  *  D  K  C  I  V  C  S  N  Y  L  W  R  K  E
     -   T  S  Q  F  P  E  T  N  V  L  S  V  V  I  I  C  G  E  K  K
4981 - AGTTCCTCTGTGTAATAAACCAAGAAGTGCCATTAAACACAAAAACACCTTCACGAGGGA - 5040
     - S  S  S  V  *  *  T  K  K  C  H  *  T  Q  K  H  L  H  E  G
     -  V  P  L  C  N  K  P  R  S  A  I  K  H  K  N  T  F  T  R  E
     -   F  L  C  V  I  N  Q  E  V  P  L  N  T  K  T  P  S  R  G  K
5041 - AGTATGCTTTGCCTTCATGACAAATTGCTGGCGCTGTGGTGAAGTTCCTCTCCTGGGATG - 5100
     - S  M  L  C  L  H  D  K  L  L  A  L  W  *  S  S  S  P  G  M
     -  V  C  F  A  F  M  T  N  C  W  R  C  G  E  V  P  L  L  G  W
     -   Y  A  L  P  S  *  Q  I  A  G  A  V  V  K  F  L  S  W  D  G
5101 - GCACATACGTGACATGTAGGAAGACAACACCATGCGGGGCTGCTTGTGGGAAGGACATAA - 5160
     - A  H  T  *  H  V  G  R  Q  H  H  A  G  L  L  V  G  R  T  *
     -  H  I  R  D  M  *  E  D  N  T  M  R  G  C  L  W  E  G  H  K
     -   T  Y  V  T  C  R  K  T  T  P  C  G  A  A  C  G  K  D  I  R
5161 - GGTGGTAGCCCTTTCCACAAAAGTCAACTCTTTTTGATTGTCCAAGAACACACTCAGACA - 5220
     - G  G  S  P  F  H  K  S  Q  L  F  L  I  V  Q  E  H  T  Q  T
     -  V  V  A  L  S  T  K  V  N  S  F  *  L  S  K  N  T  L  R  H
     -   W  *  P  F  P  Q  K  S  T  L  F  D  C  P  R  T  H  S  D  I
```

Figure 17-H

```
5221 - TTTTAGTAGCAGCAAGATTAGCAGAAGCCCTGATTTCAGCAGCCCTGATTAGTTGTTGTG - 5280
     - F  *  *  Q  Q  D  *  Q  K  P  *  F  Q  Q  P  *  L  V  V  V
     -  F  S  S  S  K  I  S  R  S  P  D  F  S  S  P  D  *  L  L  C
     -   L  V  A  A  R  L  A  E  A  L  I  S  A  A  L  I  S  C  C  V
5281 - TTACATAGGTTTGAAGGCTTTGAAGTCTGCCTGTAATTAACCTGTCAATTTGTACCTCCG - 5340
     - L  H  R  F  E  G  F  E  V  C  L  *  L  T  C  Q  F  V  P  P
     -  Y  I  G  L  K  A  L  K  S  A  C  N  *  P  V  N  L  Y  L  R
     -   T  *  V  *  R  L  *  S  L  P  V  I  N  L  S  I  C  T  S  A
5341 - CCTCGACTTTATCAAGTCGCGAAAGGATATCATTTAGCACACTTGAAATTGCACCAAAAT - 5400
     - P  R  L  Y  Q  V  A  K  G  Y  H  L  A  H  L  K  L  H  Q  N
     -  L  D  F  I  K  S  R  K  D  I  I  *  H  T  *  N  C  T  K  I
     -   S  T  L  S  S  R  E  R  I  S  F  S  T  L  E  I  A  P  K  L
5401 - TAGAGCTAAGTTGTTTAACAAGTGTGTTTAATGCTTGAGCATTCTGGTTAACAACGTCTT - 5460
     - *  S  *  V  V  *  Q  V  C  L  M  L  E  H  S  G  *  Q  R  L
     -  R  A  K  L  F  N  K  C  V  *  C  L  S  I  L  V  N  N  V  L
     -   E  L  S  C  L  T  S  V  F  N  A  *  A  F  W  L  T  T  S  C
5461 - GCAGCTTGCCCAATGCAGTTGATGTTGTTGTAAGTGATTCTTGAATTTGACTAATCGCCT - 5520
     - A  A  C  P  M  Q  L  M  L  L  *  V  I  L  E  F  D  *  S  P
     -  Q  L  A  Q  C  S  *  C  C  C  K  *  F  L  N  L  T  N  R  L
     -   S  L  P  N  A  V  D  V  V  V  S  D  S  *  I  *  L  I  A  L
5521 - TGTTAAATTGGTTGGCGATTTGTTTTTGGTTCTCATAGAGAACATTTTGGGTAACTCCAA - 5580
     - C  *  I  G  W  R  F  V  F  G  S  H  R  E  H  F  G  *  L  Q
     -  V  K  L  V  G  D  L  F  L  V  L  I  E  N  I  L  G  N  S  N
     -   L  N  W  L  A  I  C  F  W  F  S  *  R  T  F  W  V  T  P  M
5581 - TGCCATTGAACCTATATGCCATTTGCATAGCAAAAGGTATTTGAAGAGCAGCGCCAGCAC - 5640
     - C  H  *  T  Y  M  P  F  A  *  Q  K  V  F  E  E  Q  R  Q  H
     -  A  I  E  P  I  C  H  L  H  S  K  R  Y  L  K  S  S  A  S  T
     -   P  L  N  L  Y  A  I  C  I  A  K  G  I  *  R  A  A  P  A  P
5641 - CAAATGTCCATCCAGCAGTGGCAGTACCACTAACTAGAGCAGCAGTGTAGGCAGCAATCA - 5700
     - Q  M  S  I  Q  Q  W  Q  Y  H  *  L  E  Q  Q  C  R  Q  Q  S
     -  K  C  P  S  S  S  G  S  T  T  N  *  S  S  S  V  G  S  N  H
     -   N  V  H  P  A  V  A  V  P  L  T  R  A  A  V  *  A  A  I  I
5701 - TATCATCAGTGAGCAGAGGTGGCAACACTGTAAGTCCATTGAACTTCTGCGCACAAATGA - 5760
     - Y  H  Q  *  A  E  V  A  T  L  *  V  H  *  T  S  A  H  K  *
     -  I  I  S  E  Q  R  W  Q  H  C  K  S  I  E  L  L  R  T  N  E
     -   S  S  V  S  R  G  G  N  T  V  S  P  L  N  F  C  A  Q  M  R
5761 - GATCTCTAGCATTAATATCACCTAGGCATTCGCCATATTGCTTCATGAAGCCAGCATCAG - 5820
     - D  L  *  H  *  Y  H  L  G  I  R  H  I  A  S  *  S  Q  H  Q
     -  I  S  S  I  N  I  T  *  A  F  A  I  L  L  H  E  A  S  I  S
     -   S  L  A  L  I  S  P  R  H  S  P  Y  C  F  M  K  P  A  S  A
5821 - CGAGTGTCACCTTATTAAAGAGCAAGTCCTCAATAAAAGACCTCTTAGTTGGCTTTAGAG - 5880
     - R  V  S  P  Y  *  R  A  S  P  Q  *  K  T  S  *  L  A  L  E
     -  E  C  H  L  I  K  E  Q  V  L  N  K  R  P  L  S  W  L  *  R
     -   S  V  T  L  L  K  S  K  S  S  I  K  D  L  L  V  G  F  R  G
5881 - GGTCAGGTAATATTTGTGAAAAATTAAAACCACCAAAATATTTCAAAGTTGGGGTTTTGT - 5940
     - G  Q  V  I  F  V  K  N  *  N  H  Q  N  I  S  K  L  G  F  C
     -  V  R  *  Y  L  *  K  I  K  T  T  K  I  F  Q  S  W  G  F  V
     -   S  G  N  I  C  E  K  L  K  P  P  K  Y  F  K  V  G  V  L  Y
5941 - ACATTTGTTTGACTTGAGCGAACACTTCACGTGTGTTGCGATCCTGTTCAGCAGCAATAC - 6000
     - T  F  V  *  L  E  R  T  L  H  V  C  C  D  P  V  Q  Q  Q  Y
     -  H  L  F  D  L  S  E  H  F  T  C  V  A  I  L  F  S  S  N  T
     -   I  C  L  T  *  A  N  T  S  R  V  L  R  S  C  S  A  A  I  P
```

Figure 17-I

```
6001 - CTGAGAGTGCACGATTTAGTTGTGTGCAAAAGCTACCATATTGGAGAAGCAAATTAGCAC - 6060
     - L  R  V  H  D  L  V  V  C  K  S  Y  H  I  G  E  A  N  *  H
     -  *  E  C  T  I  *  L  C  A  K  A  T  I  L  E  K  Q  I  S  T
     -   E  S  A  R  F  S  C  V  Q  K  L  P  Y  W  R  S  K  L  A  H
6061 - ATTCAGTAGAATCTCCGCAGATGTACATATTACAATCTACGGAGGTTTTAGCCATAGAAA - 6120
     - I  Q  *  N  L  R  R  C  T  Y  Y  N  L  R  R  F  *  P  *  K
     -  F  S  R  I  S  A  D  V  H  I  T  I  Y  G  G  F  S  H  R  N
     -   S  V  E  S  P  Q  M  Y  I  L  Q  S  T  E  V  L  A  I  E  T
6121 - CAGGCATTACTTCTGTAGTAATGCTAATTGAAAAGTTAGTAGGTATAGCAATGGTGTTAT - 6180
     - Q  A  L  L  L  *  *  C  *  L  K  S  *  *  V  *  Q  W  C  Y
     -  R  H  Y  F  C  S  N  A  N  *  K  V  S  R  Y  S  N  G  V  I
     -   G  I  T  S  V  V  M  L  I  E  K  L  V  G  I  A  M  V  L  L
6181 - TAGAGTAAGCAATTGAACTATCAGCACCTAAAGACATAGTATAAGCCACAATAGATTTTT - 6240
     - *  S  K  Q  L  N  Y  Q  H  L  K  T  *  Y  K  P  Q  *  I  F
     -  R  V  S  N  *  T  I  S  T  *  R  H  S  I  S  H  N  R  F  L
     -   E  *  A  I  E  L  S  A  P  K  D  I  V  *  A  T  I  D  F  W
6241 - GGCTAGTACTACGTAATAAAGAAACTGTATGGTAACTAGCACAAATGCCAGCTCCAATAG - 6300
     - G  *  Y  Y  V  I  K  K  L  Y  G  N  *  H  K  C  Q  L  Q  *
     -  A  S  T  T  *  *  R  N  C  M  V  T  S  T  N  A  S  S  N  R
     -   L  V  L  R  N  K  E  T  V  W  *  L  A  Q  M  P  A  P  I  G
6301 - GAATGTCGCACTCATAAGAAGTGTCGACATGCTCAGCTCCTATAAGACAGCCTGCTTGAG - 6360
     - E  C  R  T  H  K  K  C  R  H  A  Q  L  L  *  D  S  L  L  E
     -  N  V  A  L  I  R  S  V  D  M  L  S  S  Y  K  T  A  C  L  S
     -   M  S  H  S  *  E  V  S  T  C  S  A  P  I  R  Q  P  A  *  V
6361 - TCTGGAATACATTGTTTCCAGTAGAATATATGCGCCAAGCTGGTGTGAGTTGATCTGCAT - 6420
     - S  G  I  H  C  F  Q  *  N  I  C  A  K  L  V  *  V  D  L  H
     -  L  E  Y  I  V  S  S  R  I  Y  A  P  S  W  C  E  L  I  C  M
     -   W  N  T  L  F  P  V  E  Y  M  R  Q  A  G  V  S  *  S  A  *
6421 - GAATTGCTGTAGAAACATCAGTGCAGTTAACATCTTGATATAGAACAGCAACTTCAGATG - 6480
     - E  L  L  *  K  H  Q  C  S  *  H  L  D  I  E  Q  Q  L  Q  M
     -  N  C  C  R  N  I  S  A  V  N  I  L  I  *  N  S  N  F  R  *
     -   I  A  V  E  T  S  V  Q  L  T  S  *  Y  R  T  A  T  S  D  E
6481 - AAGCATTTGTTCCAGGTGTAATTACACTTACACCCCCAAAAGAGCAAGGTGAAATGTCTA - 6540
     - K  H  L  F  Q  V  *  L  H  L  H  P  Q  K  S  K  V  K  C  L
     -  S  I  C  S  R  C  N  Y  T  Y  T  P  K  R  A  R  *  N  V  *
     -   A  F  V  P  G  V  I  T  L  T  P  P  K  E  Q  G  E  M  S  N
6541 - ATATTTCAGATGTTTTAGGATCTCGAACGGAATCAGTGAAATCAGAAACATCACGGCCAA - 6600
     - I  F  Q  M  F  *  D  L  E  R  N  Q  *  N  Q  K  H  H  G  Q
     -  Y  F  R  C  F  R  I  S  N  G  I  S  E  I  R  N  I  T  A  K
     -   I  S  D  V  L  G  S  R  T  E  S  V  K  S  E  T  S  R  P  N
6601 - ATTGTTGAAATGGTTGAAATCTCTTTGAAGAAGGAGTTAACACACCAGTACCAGTGAGTC - 6660
     - I  V  E  M  V  E  I  S  L  K  K  E  L  T  H  Q  Y  Q  *  V
     -  L  L  K  W  L  K  S  L  *  R  R  S  *  H  T  S  T  S  E  S
     -   C  *  N  G  *  N  L  F  E  E  G  V  N  T  P  V  P  V  S  P
6661 - CATTAAAATTAAAATTGACACACTGGTTCTTAATAAGGTCAGTGGATAATTTTGGTCCAC - 6720
     - H  *  N  *  N  *  H  T  G  S  *  *  G  Q  W  I  I  L  V  H
     -  I  K  I  K  I  D  T  L  V  L  N  K  V  S  G  *  F  W  S  T
     -   L  K  L  K  L  T  H  W  F  L  I  R  S  V  D  N  F  G  P  Q
```

Figure 17-J

```
6721 - AAACCGTGGCCGGTGCATTTAAAAGTTCAAAAGAAAGTACTACAACTCTGTAAGGTTGGT - 6780
     - K  P  W  P  V  H  L  K  V  Q  K  K  V  L  Q  L  C  K  V  G
     -  N  R  G  R  C  I  *  K  F  K  R  K  Y  Y  N  S  V  R  L  V
     -   T  V  A  G  A  F  K  S  S  K  E  S  T  T  T  L  *  G  W  *
6781 - AGCCAATGCCAGTAGTGGTGTAAAAACCATAATCATTTAATGGCCAATAACAATTAAGAG - 6840
     - S  Q  C  Q  *  W  C  K  N  H  N  H  L  M  A  N  N  N  *  E
     -  A  N  A  S  S  G  V  K  T  I  I  I  *  W  P  I  T  I  K  S
     -   P  M  P  V  V  V  *  K  P  *  S  F  N  G  Q  *  Q  L  R  A
6841 - CAGGTGGGGTGCAAGGTTTGCCATCAGGGGAGAAAGGCACATTAGATATGTCTCTCTCAA - 6900
     - Q  V  G  C  K  V  C  H  Q  G  R  K  A  H  *  I  C  L  S  Q
     -  R  W  G  A  R  F  A  I  R  G  E  R  H  I  R  Y  V  S  L  K
     -   G  G  V  Q  G  L  P  S  G  E  K  G  T  L  D  M  S  L  S  K
6901 - AGGGCCTAAGCTTGCCATGTCTAAGATACCTATATTTATAATTATAATTACCAGTTGAAG - 6960
     - R  A  *  A  C  H  V  *  D  T  Y  I  Y  N  Y  N  Y  Q  L  K
     -  G  P  K  L  A  M  S  K  I  P  I  F  I  I  I  I  T  S  *  S
     -   G  L  S  L  P  C  L  R  Y  L  Y  L  *  L  *  L  P  V  E  V
6961 - TAGCATCAATGTTCCTAGTATTCCAAGCAAGGACACAACCCATGAAATCATCTGGCAATT - 7020
     - *  H  Q  C  S  *  Y  S  K  Q  G  H  N  P  *  N  H  L  A  I
     -  S  I  N  V  P  S  I  P  S  K  D  T  T  H  E  I  I  W  Q  F
     -   A  S  M  F  L  V  F  Q  A  R  T  Q  P  M  K  S  S  G  N  L
7021 - TATAATTATAATCAGCAATAACACCAGTTTGTCCTGGCGCTATTTGTCTTACATCATCTC - 7080
     - Y  N  Y  N  Q  Q  *  H  Q  F  V  L  A  L  F  V  L  H  H  L
     -  I  I  I  I  S  N  N  T  S  L  S  W  R  Y  L  S  Y  I  I  S
     -   *  L  *  S  A  I  T  P  V  C  P  G  A  I  C  L  T  S  S  P
7081 - CCTTGACTACAAAAGAATCTGCATAGACATTGGAGAAGCAAAGATCATTCAACTTAGTGG - 7140
     - P  *  L  Q  K  N  L  H  R  H  W  R  S  K  D  H  S  T  *  W
     -  L  D  Y  K  R  I  C  I  D  I  G  E  A  K  I  I  Q  L  S  G
     -   L  T  T  K  E  S  A  *  T  L  E  K  Q  R  S  F  N  L  V  A
7141 - CAGAAACGCCATAGCACTTAAAGGTTGAAAAAAATGTTGAGTTGTAGAGCACAGAGTAAT - 7200
     - Q  K  R  H  S  T  *  R  L  K  K  M  L  S  C  R  A  Q  S  N
     -  R  N  A  I  A  L  K  G  *  K  K  C  *  V  V  E  H  R  V  I
     -   E  T  P  *  H  L  K  V  E  K  N  V  E  L  *  S  T  E  *  S
7201 - CAGCAACACAATTAGAAATTTTTTTTCTCTCCCATGCATAGACAGAAGGGAATTTAGTAG - 7260
     - Q  Q  H  N  *  K  F  F  F  S  P  M  H  R  Q  K  G  I  *  *
     -  S  N  T  I  R  N  F  F  S  L  P  C  I  D  R  R  E  F  S  S
     -   A  T  Q  L  E  I  F  F  L  S  H  A  *  T  E  G  N  L  V  A
7261 - CATTAAAAACCTCTCCAAAAGGACACAAGTTTGTAATATTAGGGAATCTCACAACATCTC - 7320
     - H  *  K  P  L  Q  K  D  T  S  L  *  Y  *  G  I  S  Q  H  L
     -  I  K  N  L  S  K  R  T  Q  V  C  N  I  R  E  S  H  N  I  S
     -   L  K  T  S  P  K  G  H  K  F  V  I  L  G  N  L  T  T  S  P
7321 - CTGAGGGAACAACCCTGAAATTAGAGGTCTGGTAAATTCCTTTGTCAATCTCAAAGCTCT - 7380
     - L  R  E  Q  P  *  N  *  R  S  G  K  F  L  C  Q  S  Q  S  S
     -  *  G  N  N  P  E  I  R  G  L  V  N  S  F  V  N  L  K  A  L
     -   E  G  T  T  L  K  L  E  V  W  *  I  P  L  S  I  S  K  L  L
7381 - TAACAGAGCATTTGAGTTCAGCAAGTGGATTTTGAGAACAATCAACAGCATCTGTGATTG - 7440
     - *  Q  S  I  *  V  Q  Q  V  D  F  E  N  N  Q  Q  H  L  *  L
     -  N  R  A  F  E  F  S  K  W  I  L  R  T  I  N  S  I  C  D  C
     -   T  E  H  L  S  S  A  S  G  F  *  E  Q  S  T  A  S  V  I  V
7441 - TACCATTTTCATCATACTTGAGCATAAATGTAGTTGGCTTTAAATAGCCAACAAAATAGG - 7500
     - Y  H  F  H  H  T  *  A  *  M  *  L  A  L  N  S  Q  Q  N  R
     -  T  I  F  I  I  L  E  H  K  C  S  W  L  *  I  A  N  K  I  G
     -   P  F  S  S  Y  L  S  I  N  V  V  G  F  K  *  P  T  K  *  A
```

Figure 17-K

```
7501 - CTGCAGCTGACGTGCCCCAAATGTCTTGAGCAGGTGAAAAGGCTGTAAGAATGGCTCTAA - 7560
     - L  Q  L  T  C  P  K  C  L  E  Q  V  K  R  L  *  E  W  L  *
     -  C  S  *  R  A  P  N  V  L  S  R  *  K  G  C  K  N  G  S  K
     -   A  A  D  V  P  Q  M  S  *  A  G  E  K  A  V  R  M  A  L  K
7561 - AATTTGTAATGTTAATACCAAGAGGCAACTTAAAAATAGGTTTCAAAGTGTTAAAACCAG - 7620
     - N  L  *  C  *  Y  Q  E  A  T  *  K  *  V  S  K  C  *  N  Q
     -  I  C  N  V  N  T  K  R  Q  L  K  N  R  F  Q  S  V  K  T  R
     -   F  V  M  L  I  P  R  G  N  L  K  I  G  F  K  V  L  K  P  E
7621 - AAGGTAGATCACGAACTACATCTATAGGTTGATAGCCCTTATAAACATAGAGAAACCCAT - 7680
     - K  V  D  H  E  L  H  L  *  V  D  S  P  Y  K  H  R  E  T  H
     -  R  *  I  T  N  Y  I  Y  R  L  I  A  L  I  N  I  E  K  P  I
     -   G  R  S  R  T  T  S  I  G  *  *  P  L  *  T  *  R  N  P  S
7681 - CTTTATTTTTAAACACAAACTCTCGTAAGTGTTTAAAATTACCTGACTTTTCTGAAACAT - 7740
     - L  Y  F  *  T  Q  T  L  V  S  V  *  N  Y  L  T  F  L  K  H
     -  F  I  F  K  H  K  L  S  *  V  F  K  I  T  *  L  F  *  N  I
     -   L  F  L  N  T  N  S  R  K  C  L  K  L  P  D  F  S  E  T  S
7741 - CAAGCGAAAAGGCATCAGATATGTACTCGAAAGTGCAATTAAATGCATTATCGAATATCA - 7800
     - Q  A  K  R  H  Q  I  C  T  R  K  C  N  *  M  H  Y  R  I  S
     -  K  R  K  G  I  R  Y  V  L  E  S  A  I  K  C  I  I  E  Y  H
     -   S  E  K  A  S  D  M  Y  S  K  V  Q  L  N  A  L  S  N  I  I
7801 - TAGTATGTGTCTGTGTACCCATGGGTTTAGAAACAGCAAAGAAAGGGTTGTCACACAATT - 7860
     - *  Y  V  S  V  Y  P  W  V  *  K  Q  Q  R  K  G  C  H  T  I
     -  S  M  C  L  C  T  H  G  F  R  N  S  K  E  R  V  V  T  Q  F
     -   V  C  V  C  V  P  M  G  L  E  T  A  K  K  G  L  S  H  N  S
7861 - CAAAGTTACATGCTCGTATAACAACATTAGTAGAATTGTTAATAATAATCACCGACTGTG - 7920
     - Q  S  Y  M  L  V  *  Q  H  *  *  N  C  *  *  *  S  P  T  V
     -  K  V  T  C  S  Y  N  N  I  S  R  I  V  N  N  N  H  R  L  *
     -   K  L  H  A  R  I  T  T  L  V  E  L  L  I  I  I  T  D  C  D
7921 - ACTTGTTGTTCATGGTAGAACCAAAAACCCAACCACGGACAACATTTGATTTCTCTGTGG - 7980
     - T  C  C  S  W  *  N  Q  K  P  N  H  G  Q  H  L  I  S  L  W
     -  L  V  V  H  G  R  T  K  N  P  T  T  D  N  I  *  F  L  C  G
     -   L  L  F  M  V  E  P  K  T  Q  P  R  T  T  F  D  F  S  V  A
7981 - CAGCAAAATAAATACCATCCTTAAAAGGTATGACAGGGTTGCCAAACGTATGATTAATAG - 8040
     - Q  Q  N  K  Y  H  P  *  K  V  *  Q  G  C  Q  T  Y  D  *  *
     -  S  K  I  N  T  I  L  K  R  Y  D  R  V  A  K  R  M  I  N  S
     -   A  K  *  I  P  S  L  K  G  M  T  G  L  P  N  V  *  L  I  V
8041 - TATGAAACCCTGTAACATTAGAATAAAATGGAAGAAATAAATCCTGAGTTAAATAAAGAG - 8100
     - Y  E  T  L  *  H  *  N  K  M  E  E  I  N  P  E  L  N  K  E
     -  M  K  P  C  N  I  R  I  K  W  K  K  *  I  L  S  *  I  K  S
     -   *  N  P  V  T  L  E  *  N  G  R  N  K  S  *  V  K  *  R  V
8101 - TGTCTGATCTAAAAATTTCATCAGGATAGTAAACCCCCCTCATAGATGAAGTATGTTGAG - 8160
     - C  L  I  *  K  F  H  Q  D  S  K  P  P  S  *  M  K  Y  V  E
     -  V  *  S  K  N  F  I  R  I  V  N  P  P  H  R  *  S  M  L  S
     -   S  D  L  K  I  S  S  G  *  *  T  P  L  I  D  E  V  C  *  V
8161 - TGTAATTAGGAGCTTGAACATCATCAAAAGTGGTGCACCGGTCAAGGTCACTACCACTAG - 8220
     - C  N  *  E  L  E  H  H  Q  K  W  C  T  G  Q  G  H  Y  H  *
     -  V  I  R  S  L  N  I  I  K  S  G  A  P  V  K  V  T  T  T  S
     -   *  L  G  A  *  T  S  S  K  V  V  H  R  S  R  S  L  P  L  V
```

Figure 17-L

```
8221 - TGAGAGTAAGAAATAATAAGAAAATAAACATGTTCGTTTAGTTGTTAACAAGAATATCAC - 8280
     -*  E  *  E  I  I  R  K  *  T  C  S  F  S  C  *  Q  E  Y  H
     -  E  S  K  K  *  *  E  N  K  H  V  R  L  V  V  N  K  N  I  T
     -   R  V  R  N  N  K  K  I  N  M  F  V  *  L  L  T  R  I  S  L
8281 - TTGAAACCACAACTCTGTTGTTTTCTCTAATGATAAGCCTACCTTTTTCCAGAAGAGAAT - 8340
     -L  K  P  Q  L  C  C  F  L  *  *  *  A  Y  L  F  P  E  E  N
     -  *  N  H  N  S  V  V  F  S  N  D  K  P  T  F  F  Q  K  R  I
     -   E  T  T  T  L  L  F  S  L  M  I  S  L  P  F  S  R  R  E  *
8341 - AAATCATATCATTGATTTGATTCTCCTTAAGAGACATTACAGCAGTTCCTCTTAATTTAA - 8400
     -K  S  Y  H  *  F  D  S  P  *  E  T  L  Q  Q  F  L  L  I  *
     -  N  H  I  I  D  L  I  L  L  K  R  H  Y  S  S  S  S  *  F  K
     -   I  I  S  L  I  *  F  S  L  R  D  I  T  A  V  P  L  N  L  R
8401 - GAGGAAATTTGCTCATGTCAAAGAGTGAATAGGAAGACAACTGGATAGGATTTGTGTTCC - 8460
     -E  E  I  C  S  C  Q  R  V  N  R  K  T  T  G  *  D  L  C  S
     -  R  K  F  A  H  V  K  E  *  I  G  R  Q  L  D  R  I  C  V  P
     -   G  N  L  L  M  S  K  S  E  *  E  D  N  W  I  G  F  V  F  L
8461 - TCCAGAAAATGTAGTTAGCATGCATGGTATAGCCATCAATTTGTTCCTTCGGCTTGCCAA - 8520
     -S  R  K  C  S  *  H  A  W  Y  S  H  Q  F  V  P  S  A  C  Q
     -  P  E  N  V  V  S  M  H  G  I  A  I  N  L  F  L  R  L  A  K
     -   Q  K  M  *  L  A  C  M  V  *  P  S  I  C  S  F  G  L  P  R
8521 - GATAGTTAGCCCCAATTAAAAATGCTTCCGATGATGATGCATTTACATTTGTAACAAAAG - 8580
     -D  S  *  P  Q  L  K  M  L  P  M  M  M  H  L  H  L  *  Q  K
     -  I  V  S  P  N  *  K  C  F  R  *  *  C  I  Y  I  C  N  K  S
     -   *  L  A  P  I  K  N  A  S  D  D  D  A  F  T  F  V  T  K  A
8581 - CTGTCCACCATGAGAAATGGCCCATAAGCTTGTAAAGGTCAGCATTCCAAGAATGCTCTG - 8640
     -L  S  T  M  R  N  G  P  *  A  C  K  G  Q  H  S  K  N  A  L
     -  C  P  P  *  E  M  A  H  K  L  V  K  V  S  I  P  R  M  L  C
     -   V  H  H  E  K  W  P  I  S  L  *  R  S  A  F  Q  E  C  S  V
8641 - TTATCTTTACAGCTATAGAACCACCCAGGGCTAGTTTTTGCTTTATAAATCCACACAGAT - 8700
     -L  S  L  Q  L  *  N  H  P  G  L  V  F  A  L  *  I  H  T  D
     -  Y  L  Y  S  Y  R  T  T  Q  G  *  F  L  L  Y  K  S  T  Q  I
     -   I  F  T  A  I  E  P  P  R  A  S  F  C  F  I  N  P  H  R  *
8701 - AAGTGAAAAACCCTTCTTTAGAGTCATTCTCTTTTGTCACATGTTTGGTCCTAGGGTCAT - 8760
     -K  *  K  T  L  L  *  S  H  S  L  L  S  H  V  W  S  *  G  H
     -  S  E  K  P  F  F  R  V  I  L  F  C  H  M  F  G  P  R  V  I
     -   V  K  N  P  S  L  E  S  F  S  F  V  T  C  L  V  L  G  S  Y
8761 - ACATATCGCTAATAATAAGGTCCCATTTATTAGCCGTATGTACTGTTGCACAGTCTCCAA - 8820
     -T  Y  R  *  *  *  G  P  I  Y  *  P  Y  V  L  L  H  S  L  Q
     -  H  I  A  N  N  K  V  P  F  I  S  R  M  Y  C  C  T  V  S  N
     -   I  S  L  I  I  R  S  H  L  L  A  V  C  T  V  A  Q  S  P  I
8821 - TTAAAGTAGAATCTGCGTCGGAGACGAAGTCATTAAGATCTGAATCGACAAGTAGTGTGC - 8880
     -L  K  *  N  L  R  R  R  R  S  H  *  D  L  N  R  Q  V  V  C
     -  *  S  R  I  C  V  G  D  E  V  I  K  I  *  I  D  K  *  C  A
     -   K  V  E  S  A  S  E  T  K  S  L  R  S  E  S  T  S  S  V  P
8881 - CAGTTGGCAACCATTGTCTGAGCACAGCTGTACCTGGTGCAACTCCTTTATCAGAGCCAG - 8940
     -Q  L  A  T  I  V  *  A  Q  L  Y  L  V  Q  L  L  Y  Q  S  Q
     -  S  W  Q  P  L  S  E  H  S  C  T  W  C  N  S  F  I  R  A  S
     -   V  G  N  H  C  L  S  T  A  V  P  G  A  T  P  L  S  E  P  A
8941 - CACCAAAGTGAATAACTCTCATGTTGTAGGGTACAGCTAAAGTAAGTGTATTTAAGTATT - 9000
     -H  Q  S  E  *  L  S  C  C  R  V  Q  L  K  *  V  Y  L  S  I
     -  T  K  V  N  N  S  H  V  V  G  Y  S  *  S  K  C  I  *  V  L
     -   P  K  *  I  T  L  M  L  *  G  T  A  K  V  S  V  F  K  Y  *
```

Figure 17-M

```
9001 - GACACAGTTGAGTATACTTTGCGACATTCATCATTATTCCTTTTGGTATAACAGCATTTT - 9060
     - D  T  V  E  Y  T  L  R  H  S  S  L  F  L  L  V  *  Q  H  F
     -  T  Q  L  S  I  L  C  D  I  H  H  Y  S  F  W  Y  N  S  I  F
     -   H  S  *  V  Y  F  A  T  F  I  I  I  P  F  G  I  T  A  F  S
9061 - CACCATAATTCTGAAGGTCACACTTTTCAAGAAGCATTCTTTGCATCTTGTACAAGTTAG - 9120
     - H  H  N  S  E  G  H  T  F  Q  E  A  F  F  A  S  C  T  S  *
     -  T  I  I  L  K  V  T  L  F  K  K  H  S  L  H  L  V  Q  V  R
     -   P  *  F  *  R  S  H  F  S  R  S  I  L  C  I  L  Y  K  L  G
9121 - GCATCGCAACACCTGGTTGCCACGCTTGACTTGCTTGTAGTTTTGGGTAGAAGGTTTCAA - 9180
     - A  S  Q  H  L  V  A  T  L  D  L  L  V  V  L  G  R  R  F  Q
     -  H  R  N  T  W  L  P  R  L  T  C  L  *  F  W  V  E  G  F  N
     -   I  A  T  P  G  C  H  A  *  L  A  C  S  F  G  *  K  V  S  T
9181 - CATGTCCATCCTTACACCAAAGCATGAATGAAATTTCAGCATAGTCAATTGTAACCTTGA - 9240
     - H  V  H  P  Y  T  K  A  *  M  K  F  Q  H  S  Q  L  *  P  *
     -  M  S  I  L  T  P  K  H  E  *  N  F  S  I  V  N  C  N  L  D
     -   C  P  S  L  H  Q  S  M  N  E  I  S  A  *  S  I  V  T  L  T
9241 - CCACTTTTGAAATCACTGACAAATCTTGTGACTTTATTATCTCGACAAAGTCATCAAGTA - 9300
     - P  L  L  K  S  L  T  N  L  V  T  L  L  S  R  Q  S  H  Q  V
     -  H  F  *  N  H  *  Q  I  L  *  L  Y  Y  L  D  K  V  I  K  *
     -   T  F  E  I  T  D  K  S  C  D  F  I  I  S  T  K  S  S  S  K
9301 - AAAGATCAATCACAGAACACACACATTTTGATGAACCTGTTTGCGCATCTGTTATGAAGT - 9360
     - K  D  Q  S  Q  N  T  H  I  L  M  N  L  F  A  H  L  L  *  S
     -  K  I  N  H  R  T  H  T  F  *  *  T  C  L  R  I  C  Y  E  V
     -   R  S  I  T  E  H  T  H  F  D  E  P  V  C  A  S  V  M  K  *
9361 - AATTTTTCACTGTGCTGTCCATAGGGATAAAATCCTCTAATTTAAGTGGTGAATCTTGTG - 9420
     - N  F  S  L  C  C  P  *  G  *  N  P  L  I  *  V  V  N  L  V
     -  I  F  H  C  A  V  H  R  D  K  I  L  *  F  K  W  *  I  L  *
     -   F  F  T  V  L  S  I  G  I  K  S  S  N  L  S  G  E  S  C  E
9421 - AGCGCTTGGCTAAGCCTATCATTAAATGAAGACCGCCAAGTTGTCCATGACTGAAATCTC - 9480
     - S  A  W  L  S  L  S  L  N  E  D  R  Q  V  V  H  D  *  N  L
     -  A  L  G  *  A  Y  H  *  M  K  T  A  K  L  S  M  T  E  I  S
     -   R  L  A  K  P  I  I  K  *  R  P  P  S  C  P  *  L  K  S  P
9481 - CATAAACGATGTGTTCGAAGGCATAGCCCTCGAGCTTATATCGCTGTATGAATTCATCCA - 9540
     - H  K  R  C  V  R  R  H  S  P  R  A  Y  I  A  V  *  I  H  P
     -  I  N  D  V  F  E  G  I  A  L  E  L  I  S  L  Y  E  F  I  H
     -   *  T  M  C  S  K  A  *  P  S  S  L  Y  R  C  M  N  S  S  I
9541 - TAGCGAGCTCGAGAAAGTCAGTTTCCATTTGTGATCTGGGCTTAAAATCCTCTAAGTCTC - 9600
     - *  R  A  R  E  S  Q  F  P  F  V  I  W  A  *  N  P  L  S  L
     -  S  E  L  E  K  V  S  F  H  L  *  S  G  L  K  I  L  *  V  S
     -   A  S  S  R  K  S  V  S  I  C  D  L  G  L  K  S  S  K  S  L
9601 - TGCTCTGAGTAAAGTAGGTTTCAGGCAACTGTTGAATAATGCCGTCTACTTTCTTAAAGT - 9660
     - C  S  E  *  S  R  F  Q  A  T  V  E  *  C  R  L  L  S  *  S
     -  A  L  S  K  V  G  F  R  Q  L  L  N  N  A  V  Y  F  L  K  V
     -   L  *  V  K  *  V  S  G  N  C  *  I  M  P  S  T  F  L  K  *
9661 - AGTTAAACTGTGTTTTTACTGATTCTCCAATTAATGTGACTCCATTGACGCTAGCTTGTG - 9720
     - S  *  T  V  F  L  L  I  L  Q  L  M  *  L  H  *  R  *  L  V
     -  V  K  L  C  F  Y  *  F  S  N  *  C  D  S  I  D  A  S  L  C
     -   L  N  C  V  F  T  D  S  P  I  N  V  T  P  L  T  L  A  C  A
9721 - CTGGTCCCTTTGAAGGTGTTAGACCTTTGACTGAACCTTCTGTTATTAAAACACCATTAC - 9780
     - L  V  P  L  K  V  L  D  L  *  L  N  L  L  L  L  K  H  H  Y
     -  W  S  L  *  R  C  *  T  F  D  *  T  F  C  Y  *  N  T  I  T
     -   G  P  F  E  G  V  R  P  L  T  E  P  S  V  I  K  T  P  L  R
```

Figure 17-N

```
 9781 - GGGCGTTTCTAAAAAGGTCTACCTGTCCTTCCACTCTACCATCAAACAAGACAGTAAGTG - 9840
      - G  R  F  *  K  G  L  P  V  L  P  L  Y  H  Q  T  R  Q  *  V
      -  G  V  S  K  K  V  Y  L  S  F  H  S  T  I  K  Q  D  S  K  *
      -   A  F  L  K  R  S  T  C  P  S  T  L  P  S  N  K  T  V  S  E
 9841 - AAGAACAAGCACTCTCAGTAGGTTTCTTGGCAATGTCAGTCATTGTGCAGACACCTATTG - 9900
      - K  N  K  H  S  Q  *  V  S  W  Q  C  Q  S  L  C  R  H  L  L
      -  R  T  S  T  L  S  R  F  L  G  N  V  S  H  C  A  D  T  Y  C
      -   E  Q  A  L  S  V  G  F  L  A  M  S  V  I  V  Q  T  P  I  V
 9901 - TAGATACATGTGCTGGGGCTTCTCTTTTGTAGTCCCAGATTACAGTATTAGCAGCGATAT - 9960
      - *  I  H  V  L  G  L  L  F  C  S  P  R  L  Q  Y  *  Q  R  Y
      -  R  Y  M  C  W  G  F  S  F  V  V  P  D  Y  S  I  S  S  D  I
      -   D  T  C  A  G  A  S  L  L  *  S  Q  I  T  V  L  A  A  I  S
 9961 - CAACACCCAAATTATTGAGTATCTTAATCTCTGGCACTGGTTTAATGTTACGCTTAGCCC - 10020
      - Q  H  P  N  Y  *  V  S  *  S  L  A  L  V  *  C  Y  A  *  P
      -  N  T  Q  I  I  E  Y  L  N  L  W  H  W  F  N  V  T  L  S  P
      -   T  P  K  L  L  S  I  L  I  S  G  T  G  L  M  L  R  L  A  Q
10021 - AAAGCTCAAATGCAACATTAACAGGAAGTGTTGTCTTATTTTCAAAGATCTCCACATCAA - 10080
      - K  A  Q  M  Q  H  *  Q  E  V  L  S  Y  F  Q  R  S  P  H  Q
      -  K  L  K  C  N  I  N  R  K  C  C  L  I  F  K  D  L  H  I  N
      -   S  S  N  A  T  L  T  G  S  V  V  L  F  S  K  I  S  T  S  I
10081 - TACCATCTACCTTTGTGTAAACAGCATTATTAATGATGGAAACAGGTGCTTCGCCGGCGT - 10140
      - Y  H  L  P  L  C  K  Q  H  Y  *  *  W  K  Q  V  L  R  R  R
      -  T  I  Y  L  C  V  N  S  I  I  N  D  G  N  R  C  F  A  G  V
      -   P  S  T  F  V  *  T  A  L  L  M  M  E  T  G  A  S  P  A  C
10141 - GTCCATCAAAGTGTCCTTTATTAACAACATTATAAGCCACATTTTCTAAACTCTGTAACC - 10200
      - V  H  Q  S  V  L  Y  *  Q  H  Y  K  P  H  F  L  N  S  V  T
      -  S  I  K  V  S  F  I  N  N  I  I  S  H  I  F  *  T  L  *  P
      -   P  S  K  C  P  L  L  T  T  L  *  A  T  F  S  K  L  C  N  L
10201 - TGGTAAATGTATTCCACAGGTTATAAGTATCAAATTGTTTGTAAATCCATAGGCTAAATC - 10260
      - W  *  M  Y  S  T  G  Y  K  Y  Q  I  V  C  K  S  I  G  *  I
      -  G  K  C  I  P  Q  V  I  S  I  K  L  F  V  N  P  *  A  K  S
      -   V  N  V  F  H  R  L  *  V  S  N  C  L  *  I  H  R  L  N  P
10261 - CAGCAGAAATCATCATATTATATGCATCCAAGTACTGTCGGTACTCATTTGCATGGTGTC - 10320
      - Q  Q  K  S  S  Y  Y  M  H  P  S  T  V  G  T  H  L  H  G  V
      -  S  R  N  H  H  I  I  C  I  Q  V  L  S  V  L  I  C  M  V  S
      -   A  E  I  I  I  L  Y  A  S  K  Y  C  R  Y  S  F  A  W  C  L
10321 - TGCAAACAGCACCACCTAAATTGCATCGTGTAATACACGTAGCAGATTTGAGTGGAACAT - 10380
      - C  K  Q  H  H  L  N  C  I  V  *  Y  T  *  Q  I  *  V  E  H
      -  A  N  S  T  T  *  I  A  S  C  N  T  R  S  R  F  E  W  N  I
      -   Q  T  A  P  P  K  L  H  R  V  I  H  V  A  D  L  S  G  T  *
10381 - AATCAATATCCGACACTACTTGTTTGCCATGAGACTCACAAGGACTATCAGAATAGTAAA - 10440
      - N  Q  Y  P  T  L  L  V  C  H  E  T  H  K  D  Y  Q  N  S  K
      -  I  N  I  R  H  Y  L  F  A  M  R  L  T  R  T  I  R  I  V  K
      -   S  I  S  D  T  T  C  L  P  *  D  S  Q  G  L  S  E  *  *  K
10441 - AGAAAGGCAATTGCTTTAAATTAGTAAATGCACTTTTATCGAAAGCTGGAGTGTGGAATG - 10500
      - R  K  A  I  A  L  N  *  *  M  H  F  Y  R  K  L  E  C  G  M
      -  E  R  Q  L  L  *  I  S  K  C  T  F  I  E  S  W  S  V  E  C
      -   K  G  N  C  F  K  L  V  N  A  L  L  S  K  A  G  V  W  N  A
10501 - CATGCTTATTCACATACAAACTACCACCATCACAGCCTGGTAAGTTCAAGTTTGACAAGA - 10560
      - H  A  Y  S  H  T  N  Y  H  H  H  S  L  V  S  S  S  L  T  R
      -  M  L  I  H  I  Q  T  T  T  I  T  A  W  *  V  Q  V  *  Q  D
      -   C  L  F  T  Y  K  L  P  P  S  Q  P  G  K  F  K  F  D  K  T
```

Figure 17-O

```
10561 - CTCTTGTGTCAAACCTACACACAATTGCATTGGCTGGGTAACGATCAACGTTACAATTCC - 10620
      - L  L  C  Q  T  Y  T  Q  L  H  W  L  G  N  D  Q  R  Y  N  S
      -  S  C  V  K  P  T  H  N  C  I  G  W  V  T  I  N  V  T  I  P
      -   L  V  S  N  L  H  T  I  A  L  A  G  *  R  S  T  L  Q  F  Q
10621 - AAAACAAACAAACACCATCAGTGAATTTATCGTGATGTGTAGCATAAGAATAGAAGAGTT - 10680
      - K  T  N  K  H  H  Q  *  I  Y  R  D  V  *  H  K  N  R  R  V
      -  K  Q  T  N  T  I  S  E  F  I  V  M  C  S  I  R  I  E  E  F
      -   N  K  Q  T  P  S  V  N  L  S  *  C  V  A  *  E  *  K  S  S
10681 - CCTCTATTTTGTAAGCTTTGTCACTACATGGCTGAGCATCGTAGAACTTCCATTCTACTT - 10740
      - P  L  F  C  K  L  C  H  Y  M  A  E  H  R  R  T  S  I  L  L
      -  L  Y  F  V  S  F  V  T  T  W  L  S  I  V  E  L  P  F  Y  F
      -   S  I  L  *  A  L  S  L  H  G  *  A  S  *  N  F  H  S  T  S
10741 - CAGCCTGAGGCACACACTTGATAGCCTTTGGATTTCCAATGTCATGAAGAACTGGAAACT - 10800
      - Q  P  E  A  H  T  *  *  P  L  D  F  Q  C  H  E  E  L  E  T
      -  S  L  R  H  T  L  D  S  L  W  I  S  N  V  M  K  N  W  K  L
      -   A  *  G  T  H  L  I  A  F  G  F  P  M  S  *  R  T  G  N  L
10801 - TATCAGCAAGCAATGCAGACTTCACAACCATGTGTTGTACTTTTCTGCAAGCAGAATTAA - 10860
      - Y  Q  Q  A  M  Q  T  S  Q  P  C  V  V  L  F  C  K  Q  N  *
      -  I  S  K  Q  C  R  L  H  N  H  V  L  Y  F  S  A  S  R  I  N
      -   S  A  S  N  A  D  F  T  T  M  C  C  T  F  L  Q  A  E  L  T
10861 - CCCTCAGTTCATCTCCTATAATAGGGTATTCAACAGACCAATCAACGCGCTTAACAAAGC - 10920
      - P  S  V  H  L  L  *  *  G  I  Q  Q  T  N  Q  R  A  *  Q  S
      -  P  Q  F  I  S  Y  N  R  V  F  N  R  P  I  N  A  L  N  K  A
      -   L  S  S  S  P  I  I  G  Y  S  T  D  Q  S  T  R  L  T  K  H
10921 - ACTCATGGACTGCTAAACATCTAGTCATGATAGCATCACAACTAGCCACATGTGCATTTC - 10980
      - T  H  G  L  L  N  I  *  S  *  *  H  H  N  *  P  H  V  H  F
      -  L  M  D  C  *  T  S  S  H  D  S  I  T  T  S  H  M  C  I  S
      -   S  W  T  A  K  H  L  V  M  I  A  S  Q  L  A  T  C  A  F  P
10981 - CATGTACCTGGCAATGTTGGTCATGGTTACTCTGAAGGTTACCCGTAAAGCCCCACTGCT - 11040
      - H  V  P  G  N  V  G  H  G  Y  S  E  G  Y  P  *  S  P  T  A
      -  M  Y  L  A  M  L  V  M  V  T  L  K  V  T  R  K  A  P  L  L
      -   C  T  W  Q  C  W  S  W  L  L  *  R  L  P  V  K  P  H  C  *
11041 - GAACATCAATCATAAATGGGTTATAGACATAGTCAAAACCCACAGAATGATTCCAGCAGG - 11100
      - E  H  Q  S  *  M  G  Y  R  H  S  Q  N  P  Q  N  D  S  S  R
      -  N  I  N  H  K  W  V  I  D  I  V  K  T  H  R  M  I  P  A  G
      -   T  S  I  I  N  G  L  *  T  *  S  K  P  T  E  *  F  Q  Q  A
11101 - CATAAGTATCTGATGAAGTAGAAAAGCAAGTTGCACGTTTGTCACACAGACAACACGTTC - 11160
      - H  K  Y  L  M  K  *  K  S  K  L  H  V  C  H  T  D  N  T  F
      -  I  S  I  *  *  S  R  K  A  S  C  T  F  V  T  Q  T  T  R  S
      -   *  V  S  D  E  V  E  K  Q  V  A  R  L  S  H  R  Q  H  V  L
11161 - TTTCAGGTCCAATCTTGACAAAGTACTTCATTGATGTAAGCTCAAAGCCATGCGCCCAAA - 11220
      - F  Q  V  Q  S  *  Q  S  T  S  L  M  *  A  Q  S  H  A  P  K
      -  F  R  S  N  L  D  K  V  L  H  *  C  K  L  K  A  M  R  P  K
      -   S  G  P  I  L  T  K  Y  F  I  D  V  S  S  K  P  C  A  Q  R
11221 - GGACGAACACGACTCTGTCTGACAATCCTTTCAGTGTATCACTGAGCATTTGTACTATCT - 11280
      - G  R  T  R  L  C  L  T  I  L  S  V  Y  H  *  A  F  V  L  S
      -  D  E  H  D  S  V  *  Q  S  F  Q  C  I  T  E  H  L  Y  Y  L
      -   T  N  T  T  L  S  D  N  P  F  S  V  S  L  S  I  C  T  I  L
```

Figure 17-P

```
11281 - TAATACGCACTACATTCCAGGGCAAGCCTTTATACATGAGTGGTATAAGATGTTTAAACT - 11340
      - *  Y  A  L  H  S  R  A  S  L  Y  T  *  V  V  *  D  V  *  T
      -  N  T  H  Y  I  P  G  Q  A  F  I  H  E  W  Y  K  M  F  K  L
      -   I  R  T  T  F  Q  G  K  P  L  Y  M  S  G  I  R  C  L  N  W
11341 - GGTCACCTGGTGGAGGTTTTGCATTAACTCTGGTGAATTCTGTGTTATTTTCAGTGTCAA - 11400
      - G  H  L  V  E  V  L  H  *  L  W  *  I  L  C  Y  F  Q  C  Q
      -  V  T  W  W  R  F  C  I  N  S  G  E  F  C  V  I  F  S  V  N
      -   S  P  G  G  G  F  A  L  T  L  V  N  S  V  L  F  S  V  S  T
11401 - CATAACCAGTCGGTACAGCTACTAAGTTAACACCTGTAGAAAATCCTAGCTGGAGAGGTA - 11460
      - H  N  Q  S  V  Q  L  L  S  *  H  L  *  K  I  L  A  G  E  V
      -  I  T  S  R  Y  S  Y  *  V  N  T  C  R  K  S  *  L  E  R  *
      -   *  P  V  G  T  A  T  K  L  T  P  V  E  N  P  S  W  R  G  R
11461 - GGTTAGTACCCACAGCATCTCTAGTTGCATGACAGCCCTCTACATCAAAGCCAATCCACG - 11520
      - G  *  Y  P  Q  H  L  *  L  H  D  S  P  L  H  Q  S  Q  S  T
      -  V  S  T  H  S  I  S  S  C  M  T  A  L  Y  I  K  A  N  P  R
      -   L  V  P  T  A  S  L  V  A  *  Q  P  S  T  S  K  P  I  H  A
11521 - CACGAACGTGACGAATAGCTTCTTCGCGGGTGATAAACATATTAGGGTAACCATTGACTT - 11580
      - H  E  R  D  E  *  L  L  R  G  *  *  T  Y  *  G  N  H  *  L
      -  T  N  V  T  N  S  F  F  A  G  D  K  H  I  R  V  T  I  D  L
      -   R  T  *  R  I  A  S  S  R  V  I  N  I  L  G  *  P  L  T  W
11581 - GGTAATTCATTTTGAAACCCATCATAGAGATGAGTCTACGGTAGGTCATGTCCTTTGGTA - 11640
      - G  N  S  F  *  N  P  S  *  R  *  V  Y  G  R  S  C  P  L  V
      -  V  I  H  F  E  T  H  H  R  D  E  S  T  V  G  H  V  L  W  Y
      -   *  F  I  L  K  P  I  I  E  M  S  L  R  *  V  M  S  F  G  M
11641 - TGCCTGGTATGTCAACACATAATCCTTCAGTCTTGAATTTTATATCAACGCTGAGGTGTG - 11700
      - C  L  V  C  Q  H  I  I  L  Q  S  *  I  L  Y  Q  R  *  G  V
      -  A  W  Y  V  N  T  *  S  F  S  L  E  F  Y  I  N  A  E  V  C
      -   P  G  M  S  T  H  N  P  S  V  L  N  F  I  S  T  L  R  C  V
11701 - TAGGTGCCTGTGTAGGATGAAGACCAGTAATGATCTTACTACAGTCCTTAAAAAGTCCAG - 11760
      - *  V  P  V  *  D  E  D  Q  *  *  S  Y  Y  S  P  *  K  V  Q
      -  R  C  L  C  R  M  K  T  S  N  D  L  T  T  V  L  K  K  S  S
      -   G  A  C  V  G  *  R  P  V  M  I  L  L  Q  S  L  K  S  P  V
11761 - TTACATTTTCTGCTTGTAATGTAGCCACATTGCGACGTGGTATTTCTAGACTTGTAAATT - 11820
      - L  H  F  L  L  V  M  *  P  H  C  D  V  V  F  L  D  L  *  I
      -  Y  I  F  C  L  *  C  S  H  I  A  T  W  Y  F  *  T  C  K  L
      -   T  F  S  A  C  N  V  A  T  L  R  R  G  I  S  R  L  V  N  C
11821 - GCAGTTTGTCATAAAGATCTCTATCAGACATTATGCACAAAATGCCAATTTTTGCCCTTG - 11880
      - A  V  C  H  K  D  L  Y  Q  T  L  C  T  K  C  Q  F  L  P  L
      -  Q  F  V  I  K  I  S  I  R  H  Y  A  Q  N  A  N  F  C  P  C
      -   S  L  S  *  R  S  L  S  D  I  M  H  K  M  P  I  F  A  L  V
11881 - TGATAGCCACATTGAAGCGGTTGACATTACAAGAGTGTGCTGTTTCAGTAGTTTGTGTGA - 11940
      - *  *  P  H  *  S  G  *  H  Y  K  S  V  L  F  Q  *  F  V  *
      -  D  S  H  I  E  A  V  D  I  T  R  V  C  C  F  S  S  L  C  E
      -   I  A  T  L  K  R  L  T  L  Q  E  C  A  V  S  V  V  C  V  N
11941 - ATATGACATAGTCATATTCAGAACCCTGTGATGAATCAACAGTCTGCGTAGGCAATCCTA - 12000
      - I  *  H  S  H  I  Q  N  P  V  M  N  Q  Q  S  A  *  A  I  L
      -  Y  D  I  V  I  F  R  T  L  *  *  I  N  S  L  R  R  Q  S  *
      -   M  T  *  S  Y  S  E  P  C  D  E  S  T  V  C  V  G  N  P  K
```

Figure 17-Q

```
12001 - AGATTTTTGAAGCTACAGCGTTCTGTGAATTATAAGGTGAGATAAAAACAGCTTTTCTCC - 12060
      - R  F  L  K  L  Q  R  S  V  N  Y  K  V  R  *  K  Q  L  F  S
      -  D  F  *  S  Y  S  V  L  *  I  I  R  *  D  K  N  S  F  S  P
      -   I  F  E  A  T  A  F  C  E  L  *  G  E  I  K  T  A  F  L  Q
12061 - AAGCAGGATTGCGTGTAAGAAATTCTCTTACAACGCCTATTTGAGGTCTGTTGATTGCAG - 12120
      - K  Q  D  C  V  *  E  I  L  L  Q  R  L  F  E  V  C  *  L  Q
      -  S  R  I  A  C  K  K  F  S  Y  N  A  Y  L  R  S  V  D  C  R
      -   A  G  L  R  V  R  N  S  L  T  T  P  I  *  G  L  L  I  A  D
12121 - ATGAAACATCATGTGTAATAACACCTTTGTAGAACATTTTGAAGCATTGAGCTGACTTAT - 12180
      - M  K  H  H  V  *  *  H  L  C  R  T  F  *  S  I  E  L  T  Y
      -  *  N  I  M  C  N  N  T  F  V  E  H  F  E  A  L  S  *  L  I
      -   E  T  S  C  V  I  T  P  L  *  N  I  L  K  H  *  A  D  L  S
12181 - CCTTGTGTGCTTTTAGCTTATTGTCATAAACTAAAGCACTCACAGTGTCAACAATTTCAG - 12240
      - P  C  V  L  L  A  Y  C  H  K  L  K  H  S  Q  C  Q  Q  F  Q
      -  L  V  C  F  *  L  I  V  I  N  *  S  T  H  S  V  N  N  F  S
      -   L  C  A  F  S  L  L  S  *  T  K  A  L  T  V  S  T  I  S  A
12241 - CAGGACAACGGCGACAAGTTCCAAGGAACATGTCTGGACCTATTGTTTTCATAAGTCTGC - 12300
      - Q  D  N  G  D  K  F  Q  G  T  C  L  D  L  L  F  S  *  V  C
      -  R  T  T  A  T  S  S  K  E  H  V  W  T  Y  C  F  H  K  S  A
      -   G  Q  R  R  Q  V  P  R  N  M  S  G  P  I  V  F  I  S  L  H
12301 - ACACTGAATTAAAATATTCTGGTTCTAGTGTGCCTTTAGTCAGCAATGTGCGGGGGGCTG - 12360
      - T  L  N  *  N  I  L  V  L  V  C  L  *  S  A  M  C  G  G  L
      -  H  *  I  K  I  F  W  F  *  C  A  F  S  Q  Q  C  A  G  G  W
      -   T  E  L  K  Y  S  G  S  S  V  P  L  V  S  N  V  R  G  A  G
12361 - GTAATTGAGCAGGATCGCCAATATAGACGTAGTGTTTTGCACGAAGTCTAGCATTGACAA - 12420
      - V  I  E  Q  D  R  Q  Y  R  R  S  V  L  H  E  V  *  H  *  Q
      -  *  L  S  R  I  A  N  I  D  V  V  F  C  T  K  S  S  I  D  N
      -   N  *  A  G  S  P  I  *  T  *  C  F  A  R  S  L  A  L  T  T
12421 - CACTCAAGTCATAATTAGTAGCCATAGAGATTTCATCAAAGACTACAATGTCAGCAGTTG - 12480
      - H  S  S  H  N  *  *  P  *  R  F  H  Q  R  L  Q  C  Q  Q  L
      -  T  Q  V  I  I  S  S  H  R  D  F  I  K  D  Y  N  V  S  S  C
      -   L  K  S  *  L  V  A  I  E  I  S  S  K  T  T  M  S  A  V  V
12481 - TTTCTGGCAATGCATTTACAGTGCAGAAAACATACTGTTCTAGTGTTGAATTCACTTTGA - 12540
      - F  L  A  M  H  L  Q  C  R  K  H  T  V  L  V  L  N  S  L  *
      -  F  W  Q  C  I  Y  S  A  E  N  I  L  F  *  C  *  I  H  F  E
      -   S  G  N  A  F  T  V  Q  K  T  Y  C  S  S  V  E  F  T  L  N
12541 - ATTTATCAAAACACTCTACGCGCGCACGCGCAGGTATGATTCTACTACATTTATCTATGG - 12600
      - I  Y  Q  N  T  L  R  A  H  A  Q  V  *  F  Y  Y  I  Y  L  W
      -  F  I  K  T  L  Y  A  R  T  R  R  Y  D  S  T  T  F  I  Y  G
      -   L  S  K  H  S  T  R  A  R  A  G  M  I  L  L  H  L  S  M  G
12601 - GCAAATATTTTAATGCCTTTTCACATAGGGCATCAACAGCTGCATGAGAGCATGCCGTAT - 12660
      - A  N  I  L  M  P  F  H  I  G  H  Q  Q  L  H  E  S  M  P  Y
      -  Q  I  F  *  C  L  F  T  *  G  I  N  S  C  M  R  A  C  R  I
      -   K  Y  F  N  A  F  S  H  R  A  S  T  A  A  *  E  H  A  V  Y
12661 - ACACTATGCGAGCAGATGGGTAATAGAGAGCAAGTCCGATGGCAAAATGACTCTTACCAG - 12720
      - T  L  C  E  Q  M  G  N  R  E  Q  V  R  W  Q  N  D  S  Y  Q
      -  H  Y  A  S  R  W  V  I  E  S  K  S  D  G  K  M  T  L  T  S
      -   T  M  R  A  D  G  *  *  R  A  S  P  M  A  K  *  L  L  P  V
```

Figure 17-R

```
12721 - TACCAGGTGGTCCTTGGAGTGTAGAGTACTTTTGCATGCCGACCTTTTGATAATTTGCAA - 12780
      - Y  Q  V  V  L  G  V  *  S  T  F  A  C  R  P  F  D  N  L  Q
      -  T  R  W  S  L  E  C  R  V  L  L  H  A  D  L  L  I  I  C  N
      -   P  G  G  P  W  S  V  E  Y  F  C  M  P  T  F  *  *  F  A  T
12781 - CATTGCTAGAAAACTCATCTGAGATGTTGAGTGTTGGGTACAAGCCAGTAATTCTCACAT - 12840
      - H  C  *  K  T  H  L  R  C  *  V  L  G  T  S  Q  *  F  S  H
      -  I  A  R  K  L  I  *  D  V  E  C  W  V  Q  A  S  N  S  H  I
      -   L  L  E  N  S  S  E  M  L  S  V  G  Y  K  P  V  I  L  T  *
12841 - AGTGCTCTTGTGGCACTAGAGTAGGTGCACTAAGTGGCATTACAGTGTGAGATGTCAACA - 12900
      - S  A  L  V  A  L  E  *  V  H  *  V  A  L  Q  C  E  M  S  T
      -  V  L  L  W  H  *  S  R  C  T  K  W  H  Y  S  V  R  C  Q  H
      -   C  S  C  G  T  R  V  G  A  L  S  G  I  T  V  *  D  V  N  T
12901 - CAAAGTAATCACCAACATTCAACTTGTATGTCGTAGTACCTCTGTACACAACAGCATCAC - 12960
      - Q  S  N  H  Q  H  S  T  C  M  S  *  Y  L  C  T  Q  Q  H  H
      -  K  V  I  T  N  I  Q  L  V  C  R  S  T  S  V  H  N  S  I  T
      -   K  *  S  P  T  F  N  L  Y  V  V  V  P  L  Y  T  T  A  S  P
12961 - CATAGTCACCTTTTTCAAAGGTGTACTCTCCAATCTGTACTTTACTATTTTTAGTTACAC - 13020
      - H  S  H  L  F  Q  R  C  T  L  Q  S  V  L  Y  Y  F  *  L  H
      -  I  V  T  F  F  K  G  V  L  S  N  L  Y  F  T  I  F  S  Y  T
      -   *  S  P  F  S  K  V  Y  S  P  I  C  T  L  L  F  L  V  T  R
13021 - GGTAACCAGTAAAGACATAGTTTCTGTTCAATGGTGGTCTAGGTTTTCCAACCTCCCATG - 13080
      - G  N  Q  *  R  H  S  F  C  S  M  V  V  *  V  F  Q  P  P  M
      -  V  T  S  K  D  I  V  S  V  Q  W  W  S  R  F  S  N  L  P  *
      -   *  P  V  K  T  *  F  L  F  N  G  G  L  G  F  P  T  S  H  E
13081 - AAAGATGCAATTCTCTGTCAGAGAGTACTTCGCGTACAGTGGCAATACCATATGACAGCT - 13140
      - K  D  A  I  L  C  Q  R  V  L  R  V  Q  W  Q  Y  H  M  T  A
      -  K  M  Q  F  S  V  R  E  Y  F  A  Y  S  G  N  T  I  *  Q  L
      -   R  C  N  S  L  S  E  S  T  S  R  T  V  A  I  P  Y  D  S  L
13141 - TAAATGTTTCCTCAGTGGCTTTGAGCGTTTCTGCTGCGAAAAGCTTGAGTCTCTCAGTAC - 13200
      - *  M  F  P  Q  W  L  *  A  F  L  L  R  K  A  *  V  S  Q  Y
      -  K  C  F  L  S  G  F  E  R  F  C  C  E  K  L  E  S  L  S  T
      -   N  V  S  S  V  A  L  S  V  S  A  A  K  S  L  S  L  S  V  Q
13201 - AAGTGTTGGCAAGTATGTAATCGCCAGCATTAGTCCAATCACATGTTGCTATCGCATTGA - 13260
      - K  C  W  Q  V  C  N  R  Q  H  *  S  N  H  M  L  L  S  H  *
      -  S  V  G  K  Y  V  I  A  S  I  S  P  I  T  C  C  Y  R  I  E
      -   V  L  A  S  M  *  S  P  A  L  V  Q  S  H  V  A  I  A  L  K
13261 - AGTCAGTGACATTGTCACTGCCTACACATGTGTTTTTGTATAAACCAAAAACCTGACCAT - 13320
      - S  Q  *  H  C  H  C  L  H  M  C  F  C  I  N  Q  K  P  D  H
      -  V  S  D  I  V  T  A  Y  T  C  V  F  V  *  T  K  N  L  T  I
      -   S  V  T  L  S  L  P  T  H  V  F  L  Y  K  P  K  T  *  P  L
13321 - TAGCACATAATGGAAAACTAATGGGAGGCTTATGTGACTTGCAATAATAGCTCATACCTC - 13380
      - *  H  I  M  E  N  *  W  E  A  Y  V  T  C  N  N  S  S  Y  L
      -  S  T  *  W  K  T  N  G  R  L  M  *  L  A  I  I  A  H  T  S
      -   A  H  N  G  K  L  M  G  G  L  C  D  L  Q  *  *  L  I  P  P
13381 - CTAGATACAGTTGTGTCACATCAGTGACATCACAACCTGGGGCATTGCAAACATAGGGAT - 13440
      - L  D  T  V  V  S  H  Q  *  H  H  N  L  G  H  C  K  H  R  D
      -  *  I  Q  L  C  H  I  S  D  I  T  T  W  G  I  A  N  I  G  I
      -   R  Y  S  C  V  T  S  V  T  S  Q  P  G  A  L  Q  T  *  G  L
```

Figure 17-S

```
13441 - TAACAGACAACACTAATTTGTGTGATGTTGAAATGACATGGTCATAGCAGCACTTGCAAC - 13500
      -*  Q  T  T  L  I  C  V  M  L  K  *  H  G  H  S  S  T  C  N
      - N  R  Q  H  *  F  V  *  C  *  N  D  M  V  I  A  A  L  A  T
      -  T  D  N  T  N  L  C  D  V  E  M  T  W  S  *  Q  H  L  Q  H
13501 - ATAGGAATGGTCTCCTAATACAGGCACCGCAACGAAGTGAAGTCTGTGAATTGCACAATA - 13560
      -I  G  M  V  S  *  Y  R  H  R  N  E  V  K  S  V  N  C  T  I
      - *  E  W  S  P  N  T  G  T  A  T  K  *  S  L  *  I  A  Q  Y
      -  R  N  G  L  L  I  Q  A  P  Q  R  S  E  V  C  E  L  H  N  T
13561 - CACAAGCACCTACAGCCTGCAAGACTGTATGTGGTGTGTACATAGCCTCATAAAACTCAG - 13620
      -H  K  H  L  Q  P  A  R  L  Y  V  V  C  T  *  P  H  K  T  Q
      - T  S  T  Y  S  L  Q  D  C  M  W  C  V  H  S  L  I  K  L  R
      -  Q  A  P  T  A  C  K  T  V  C  G  V  Y  I  A  S  *  N  S  G
13621 - GTTCCCAGTACCGTGAGGTGTTATCATTAGTTAGCATTACGGAATACATGTCCAACATGT - 13680
      -V  P  S  T  V  R  C  Y  H  *  L  A  L  R  N  T  C  P  T  C
      - F  P  V  P  *  G  V  I  I  S  *  H  Y  G  I  H  V  Q  H  V
      -  S  Q  Y  R  E  V  L  S  L  V  S  I  T  E  Y  M  S  N  M  W
13681 - GGCCAGTAAGCTCATCATGTAACTTTCTAATGTATTGTAAATACAAGTGAAAGACATCAG - 13740
      -G  Q  *  A  H  H  V  T  F  *  C  I  V  N  T  S  E  R  H  Q
      - A  S  K  L  I  M  *  L  S  N  V  L  *  I  Q  V  K  D  I  S
      -  P  V  S  S  S  C  N  F  L  M  Y  C  K  Y  K  *  K  T  S  A
13741 - CATACTCCTGATTAGGATGTTTTGTAAGTGGGTAAGCATCAATAGCCAGTGACACGAACC - 13800
      -H  T  P  D  *  D  V  L  *  V  G  K  H  Q  *  P  V  T  R  T
      - I  L  L  I  R  M  F  C  K  W  V  S  I  N  S  Q  *  H  E  P
      -  Y  S  *  L  G  C  F  V  S  G  *  A  S  I  A  S  D  T  N  L
13801 - TTTCAATCATAAGTGTACCATCTGTTTTGACAATATCATCGACAAAACAGCCTGCGCCTA - 13860
      -F  Q  S  *  V  Y  H  L  F  *  Q  Y  H  R  Q  N  S  L  R  L
      - F  N  H  K  C  T  I  C  F  D  N  I  I  D  K  T  A  C  A  *
      -  S  I  I  S  V  P  S  V  L  T  I  S  S  T  K  Q  P  A  P  N
13861 - ATATTCTTGATGGATCTGGGTAAGGCAGGTACACGTAATCATCTCCTTGTTTAACTAGCA - 13920
      -I  F  L  M  D  L  G  K  A  G  T  R  N  H  L  L  V  *  L  A
      - Y  S  *  W  I  W  V  R  Q  V  H  V  I  I  S  L  F  N  *  H
      -  I  L  D  G  S  G  *  G  R  Y  T  *  S  S  P  C  L  T  S  I
13921 - TTGTATGCTGTGAGCAAAATTCGTGAGGTCCTTTAGTAAGGTCAGTCTCAGTCCAACATT - 13980
      -L  Y  A  V  S  K  I  R  E  V  L  *  *  G  Q  S  Q  S  N  I
      - C  M  L  *  A  K  F  V  R  S  F  S  K  V  S  L  S  P  T  F
      -  V  C  C  E  Q  N  S  *  G  P  L  V  R  S  V  S  V  Q  H  F
13981 - TTGCCTCAGACATGAACACATTATTTGATAATAAAGAACTGCCTTAAAGTTCTTAATGC - 14040
      -L  P  Q  T  *  T  H  Y  F  D  N  K  E  L  P  *  S  S  *  C
      - C  L  R  H  E  H  I  I  L  I  I  K  N  C  L  K  V  L  N  A
      -  A  S  D  M  N  T  L  F  *  *  *  R  T  A  L  K  F  L  M  L
14041 - TAGCTACTAAACCTTGAGCCGCATAGTTACTGTTATAGCACACAACGGCATCATCAGAAA - 14100
      -*  L  L  N  L  E  P  H  S  Y  C  Y  S  T  Q  R  H  H  Q  K
      - S  Y  *  T  L  S  R  I  V  T  V  I  A  H  N  G  I  I  R  K
      -  A  T  K  P  *  A  A  *  L  L  L  *  H  T  T  A  S  S  E  R
14101 - GAATCATCATGGAGAAATGTTTACGCAGGTAAGCGTAAAACTCATCCACGAATTCATGAT - 14160
      -E  S  S  W  R  N  V  Y  A  G  K  R  K  T  H  P  R  I  H  D
      - N  H  H  G  E  M  F  T  Q  V  S  V  K  L  I  H  E  F  M  I
      -  I  I  M  E  K  C  L  R  R  *  A  *  N  S  S  T  N  S  *  S
14161 - CAACATCCCTATTTCTATAGAGACACTCATAGAGCCTGTGTTGTAGATTGCGGACATACT - 14220
      -Q  H  P  Y  F  Y  R  D  T  H  R  A  C  V  V  D  C  G  H  T
      - N  I  P  I  S  I  E  T  L  I  E  P  V  L  *  I  A  D  I  L
      -  T  S  L  F  L  *  R  H  S  *  S  L  C  C  R  L  R  T  Y  L
```

Figure 17-T

```
14221 - TGTCAGCTATCTTATTACCATCAGTTGAAAGAAGTGCATTTACATTGGCTGTAACAGCTT - 14280
      - C  Q  L  S  Y  Y  H  Q  L  K  E  V  H  L  H  W  L  *  Q  L
      -  V  S  Y  L  I  T  I  S  *  K  K  C  I  Y  I  G  C  N  S  L
      -   S  A  I  L  L  P  S  V  E  R  S  A  F  T  L  A  V  T  A  *
14281 - GACAAATGTTAAAGACACTATTAGCATAAGCAGTTGTAGCATCACCGGATGATGTTCCAC - 14340
      - D  K  C  *  R  H  Y  *  H  K  Q  L  *  H  H  R  M  M  F  H
      -  T  N  V  K  D  T  I  S  I  S  S  C  S  I  T  G  *  C  S  T
      -   Q  M  L  K  T  L  L  A  *  A  V  V  A  S  P  D  D  V  P  P
14341 - CTGGTTTAACATATAGTGAGCCGCCACACATGACCATCTCACTTAATACTTGCGCACACT - 14400
      - L  V  *  H  I  V  S  R  H  T  *  P  S  H  L  I  L  A  H  T
      -  W  F  N  I  *  *  A  A  T  H  D  H  L  T  *  Y  L  R  T  L
      -   G  L  T  Y  S  E  P  P  H  M  T  I  S  L  N  T  C  A  H  S
14401 - CGTTAGCTAACCTGTAGAAACGGTGTGATAAGTTACAGCAAGTGTTATGTTTGCGAGCAA - 14460
      - R  *  L  T  C  R  N  G  V  I  S  Y  S  K  C  Y  V  C  E  Q
      -  V  S  *  P  V  E  T  V  *  *  V  T  A  S  V  M  F  A  S  K
      -   L  A  N  L  *  K  R  C  D  K  L  Q  Q  V  L  C  L  R  A  R
14461 - GAACAAGAGAGGCCATTATCCTAAGCATGTTAGGCATGGCTCTGTCACATTTTGGATAAT - 14520
      - E  Q  E  R  P  L  S  *  A  C  *  A  W  L  C  H  I  L  D  N
      -  N  K  R  G  H  Y  P  K  H  V  R  H  G  S  V  T  F  W  I  I
      -   T  R  E  A  I  I  L  S  M  L  G  M  A  L  S  H  F  G  *  S
14521 - CCCAACCCATAAGGTGTGGAGTTTCTACATCACTGTAAACAGTTTTTAACATATTATGCC - 14580
      - P  N  P  *  G  V  E  F  L  H  H  C  K  Q  F  L  T  Y  Y  A
      -  P  T  H  K  V  W  S  F  Y  I  T  V  N  S  F  *  H  I  M  P
      -   Q  P  I  R  C  G  V  S  T  S  L  *  T  V  F  N  I  L  C  Q
14581 - AGCCACCGTAAAACTTGCTTGTTCCAATTACCACAGTAGCTCCTCTAGTGGCGGCTATTG - 14640
      - S  H  R  K  T  C  L  F  Q  L  P  Q  *  L  L  *  W  R  L  L
      -  A  T  V  K  L  A  C  S  N  Y  H  S  S  S  S  S  G  G  Y  *
      -   P  P  *  N  L  L  V  P  I  T  T  V  A  P  L  V  A  A  I  D
14641 - ACTTCAATAATTTCTGATGAAACTGTCTATTTGTCATAGTACTACAGATAGAGACACCAG - 14700
      - T  S  I  I  S  D  E  T  V  Y  L  S  *  Y  Y  R  *  R  H  Q
      -  L  Q  *  F  L  M  K  L  S  I  C  H  S  T  T  D  R  D  T  S
      -   F  N  N  F  *  *  N  C  L  F  V  I  V  L  Q  I  E  T  P  A
14701 - CTACGGTGCGAGCTCTATTCTTTGCACTAATGGCATACTTAAGATTCATTTGAGTTATAG - 14760
      - L  R  C  E  L  Y  S  L  H  *  W  H  T  *  D  S  F  E  L  *
      -  Y  G  A  S  S  I  L  C  T  N  G  I  L  K  I  H  L  S  Y  S
      -   T  V  R  A  L  F  F  A  L  M  A  Y  L  R  F  I  *  V  I  V
14761 - TAGGGATGACATTACGCTTAGTATACGCGAAAAGTGCATCTTGATCCTCATAACTCATTG - 14820
      - *  G  *  H  Y  A  *  Y  T  R  K  V  H  L  D  P  H  N  S  L
      -  R  D  D  I  T  L  S  I  R  E  K  C  I  L  I  L  I  T  H  *
      -   G  M  T  L  R  L  V  Y  A  K  S  A  S  *  S  S  *  L  I  E
14821 - AGTCATAATAAAGTCTAGCCTTACCCCATTTATTAAATGGGAAACCAGCTGATTTATCCA - 14880
      - S  H  N  K  V  *  P  Y  P  I  Y  *  M  G  N  Q  L  I  Y  P
      -  V  I  I  K  S  S  L  T  P  F  I  K  W  E  T  S  *  F  I  Q
      -   S  *  *  S  L  A  L  P  H  L  L  N  G  K  P  A  D  L  S  R
14881 - GATTGTTAACGATTACTTGGTTGGCATTAATACAGCCACCATCGTAACAATCAAAGTATT - 14940
      - D  C  *  R  L  L  G  W  H  *  Y  S  H  H  R  N  N  Q  S  I
      -  I  V  N  D  Y  L  V  G  I  N  T  A  T  I  V  T  I  K  V  F
      -   L  L  T  I  T  W  L  A  L  I  Q  P  P  S  *  Q  S  K  Y  L
```

Figure 17-U

```
14941 - TATCAACAACTTCAACTACGAATAGGAGTTGTCTGATATCACACATTGTTGGCAGATTAT - 15000
      - Y  Q  Q  L  Q  L  R  I  G  V  V  *  Y  H  T  L  L  A  D  Y
      -  I  N  N  F  N  Y  E  *  E  L  S  D  I  T  H  C  W  Q  I  I
      -   S  T  T  S  T  T  N  R  S  C  L  I  S  H  I  V  G  R  L  *
15001 - AACGATAATAGTCATAATCACTGATAGCAGCGTTGCCATCCTGAGCAAAGAAGAAGTGTT - 15060
      - N  D  N  S  H  N  H  *  *  Q  R  C  H  P  E  Q  R  R  S  V
      -  T  I  I  V  I  I  T  D  S  S  V  A  I  L  S  K  E  E  V  F
      -   R  *  *  S  *  S  L  I  A  A  L  P  S  *  A  K  K  K  C  F
15061 - TTAGTTCAACAGAACTTCCTTCCTTAAAGAAACCTTTAGACACAGCAAAGTCATAAAAGT - 15120
      - L  V  Q  Q  N  F  L  P  *  R  N  L  *  T  Q  Q  S  H  K  S
      -  *  F  N  R  T  S  F  L  K  E  T  F  R  H  S  K  V  I  K  V
      -   S  S  T  E  L  P  S  L  K  K  P  L  D  T  A  K  S  *  K  S
15121 - CTTTATTAAAATTACCGGGTTTGACAGTTTGAAAAGCAACATTGTTTGTTAGTGCAGCTA - 15180
      - L  Y  *  N  Y  R  V  *  Q  F  E  K  Q  H  C  L  L  V  Q  L
      -  F  I  K  I  T  G  F  D  S  L  K  S  N  I  V  C  *  C  S  Y
      -   L  L  K  L  P  G  L  T  V  *  K  A  T  L  F  V  S  A  A  T
15181 - CTGAAAAGCATGTAGTGCGTTTATCTAGCAATAAATTGCCAGAAGCTGCATGCATAGCTG - 15240
      - L  K  S  M  *  C  V  Y  L  A  I  N  C  Q  K  L  H  A  *  L
      -  *  K  A  C  S  A  F  I  *  Q  *  I  A  R  S  C  M  H  S  W
      -   E  K  H  V  V  R  L  S  S  N  K  L  P  E  A  A  C  I  A  G
15241 - GATCAGCAGCATACACTAAAAGTTCCTTGAAACTGAGACGCGAGCTATGTAAGTTTACAT - 15300
      - D  Q  Q  H  T  L  K  V  P  *  N  *  D  A  S  Y  V  S  L  H
      -  I  S  S  I  H  *  K  F  L  E  T  E  T  R  A  M  *  V  Y  I
      -   S  A  A  Y  T  K  S  S  L  K  L  R  R  E  L  C  K  F  T  S
15301 - CCTGATTATGTACGACTCCTAACTCACGAAAATGGTATCCAGTTGAAACAACAAAAGGAA - 15360
      - P  D  Y  V  R  L  L  T  H  E  N  G  I  Q  L  K  Q  Q  K  E
      -  L  I  M  Y  D  S  *  L  T  K  M  V  S  S  *  N  N  K  R  N
      -   *  L  C  T  T  P  N  S  R  K  W  Y  P  V  E  T  T  K  G  T
15361 - CACCATCTACAAATATTTTTCTTACTAGTGGTCCAAAACTTGTAGGTGGAAACACAGTAG - 15420
      - H  H  L  Q  I  F  F  L  L  V  V  Q  N  L  *  V  E  T  Q  *
      -  T  I  Y  K  Y  F  S  Y  *  W  S  K  T  C  R  W  K  H  S  R
      -   P  S  T  N  I  F  L  T  S  G  P  K  L  V  G  G  N  T  V  E
15421 - AAAATAACACATTAAAGTTTGCACAATGAAGGATACACCTATCATCCAAACAGTTAATAC - 15480
      - K  I  T  H  *  S  L  H  N  E  G  Y  T  Y  H  P  N  S  *  Y
      -  K  *  H  I  K  V  C  T  M  K  D  T  P  I  I  Q  T  V  N  T
      -   N  N  T  L  K  F  A  Q  *  R  I  H  L  S  S  K  Q  L  I  Q
15481 - AATTGGGATGGTATGTCTGGTCCCAATATTTAAAATAACGGTCGAAGAGACAAAGTCTCT - 15540
      - N  W  D  G  M  S  G  P  N  I  *  N  N  G  R  R  D  K  V  S
      -  I  G  M  V  C  L  V  P  I  F  K  I  T  V  E  E  T  K  S  L
      -   L  G  W  Y  V  W  S  Q  Y  L  K  *  R  S  K  R  Q  S  L  S
15541 - CTTCCGTAAAATCATATTTCAGCAAATCCCACTTAATAAGTGGTTTTGCGAGATCAGCAT - 15600
      - L  P  *  N  H  I  S  A  N  P  T  *  *  V  V  L  R  D  Q  H
      -  F  R  K  I  I  F  Q  Q  I  P  L  N  K  W  F  C  E  I  S  I
      -   S  V  K  S  Y  F  S  K  S  H  L  I  S  G  F  A  R  S  A  S
15601 - CCATATGGGACTCAGCAGCCAATGCCCTAGTCAAAGTGAGGATGGGCATCAGCAATGAGT - 15660
      - P  Y  G  T  Q  Q  P  M  P  *  S  K  *  G  W  A  S  A  M  S
      -  H  M  G  L  S  S  Q  C  P  S  Q  S  E  D  G  H  Q  Q  *  V
      -   I  W  D  S  A  A  N  A  L  V  K  V  R  M  G  I  S  N  E  *
```

Figure 17-V

```
15661 - AATATGAATCCACAATAGGAACTCCGCAGCCTGGTGCTACTTGTACGAAATCACCGAAAT - 15720
      - N  M  N  P  Q  *  E  L  R  S  L  V  L  L  V  R  N  H  R  N
      -  I  *  I  H  N  R  N  S  A  A  W  C  Y  L  Y  E  I  T  E  I
      -   Y  E  S  T  I  G  T  P  Q  P  G  A  T  C  T  K  S  P  K  S
15721 - CGTACCAGTTCCCATTAAGATCCTGATTATCTAATGTCAGTACGCCTACAATGCCTGCAT - 15780
      - R  T  S  S  H  *  D  P  D  Y  L  M  S  V  R  L  Q  C  L  H
      -  V  P  V  P  I  K  I  L  I  I  *  C  Q  Y  A  Y  N  A  C  I
      -   Y  Q  F  P  L  R  S  *  L  S  N  V  S  T  P  T  M  P  A  S
15781 - CACGCATAGCATCGCAGAATTGTACAGTCTTTAATAATGATTGGCGTACACGCTCACCTA - 15840
      - H  A  *  H  R  R  I  V  Q  S  L  I  M  I  G  V  H  A  H  L
      -  T  H  S  I  A  E  L  Y  S  L  *  *  *  L  A  Y  T  L  T  *
      -   R  I  A  S  Q  N  C  T  V  F  N  N  D  W  R  T  R  S  P  K
15841 - AGTTAGCATATACGCGTAAGATGTCAGGATTCTCTACGAAGTCATACCAATCCTTCTTAT - 15900
      - S  *  H  I  R  V  R  C  Q  D  S  L  R  S  H  T  N  P  S  Y
      -  V  S  I  Y  A  *  D  V  R  I  L  Y  E  V  I  P  I  L  L  I
      -   L  A  Y  T  R  K  M  S  G  F  S  T  K  S  Y  Q  S  F  L  L
15901 - TGAAATAATCATCATCACAGCAATTGTATGTGACGAGTATTTCTTTTAATGTATCACAAT - 15960
      - *  N  N  H  H  H  S  N  C  M  *  R  V  F  L  L  M  Y  H  N
      -  E  I  I  I  I  T  A  I  V  C  D  E  Y  F  F  *  C  I  T  I
      -   K  *  S  S  S  Q  Q  L  Y  V  T  S  I  S  F  N  V  S  Q  L
15961 - TACCCTCATCAAAATGACGTAGAGCATAGACTAAATCAGCCATTGTGTATTTAGTTAGAC - 16020
      - Y  P  H  Q  N  D  V  E  H  R  L  N  Q  P  L  C  I  *  L  D
      -  T  L  I  K  M  T  *  S  I  D  *  I  S  H  C  V  F  S  *  T
      -   P  S  S  K  *  R  R  A  *  T  K  S  A  I  V  Y  L  V  R  R
16021 - GCTGACGTGATATATGTGGTACCATGTCACCATCTACTCTAAACTTGAAAAAGTCATGGA - 16080
      - A  D  V  I  Y  V  V  P  C  H  H  L  L  *  T  *  K  S  H  G
      -  L  T  *  Y  M  W  Y  H  V  T  I  Y  S  K  L  E  K  V  M  D
      -   *  R  D  I  C  G  T  M  S  P  S  T  L  N  L  K  K  S  W  T
16081 - CAGCAACCGCTGGACAATCTTTAACCAAGTTATAAATAGTCTCTTCATGTTGGTAGTTAG - 16140
      - Q  Q  P  L  D  N  L  *  P  S  Y  K  *  S  L  H  V  G  S  *
      -  S  N  R  W  T  I  F  N  Q  V  I  N  S  L  F  M  L  V  V  R
      -   A  T  A  G  Q  S  L  T  K  L  *  I  V  S  S  C  W  *  L  D
16141 - ACATAGTATGCCTCTTAACTACAAAGTAAGAGTCTAATAAATTGCCTTCCTCATCCTTCT - 16200
      - T  *  Y  A  S  *  L  Q  S  K  S  L  I  N  C  L  P  H  P  S
      -  H  S  M  P  L  N  Y  K  V  R  V  *  *  I  A  F  L  I  L  L
      -   I  V  C  L  L  T  T  K  *  E  S  N  K  L  P  S  S  S  F  S
16201 - CCTGGAAGCGACAGCAATTAGTTTTTAGGAACTTTGCAAAACCAGCACTTTTTTCGTTGT - 16260
      - P  G  S  D  S  N  *  F  L  G  T  L  Q  N  Q  H  F  F  R  C
      -  L  E  A  T  A  I  S  F  *  E  L  C  K  T  S  T  F  F  V  V
      -   W  K  R  Q  Q  L  V  F  R  N  F  A  K  P  A  L  F  S  L  *
16261 - AAATATCAAAAGCCCTGTAGACGACATCAGTACTAGTGCCTGTGCCGCACGGTGTAAGAC - 16320
      - K  Y  Q  K  P  C  R  R  H  Q  Y  *  C  L  C  R  T  V  *  D
      -  N  I  K  S  P  V  D  D  I  S  T  S  A  C  A  A  R  C  K  T
      -   I  S  K  A  L  *  T  T  S  V  L  V  P  V  P  H  G  V  R  R
16321 - GGGCTGCACTTACACCGCAAACCCGTTTAAAAACGTTGATGCATCCGCAGACTGCATCAA - 16380
      - G  L  H  L  H  R  K  P  V  *  K  R  *  C  I  R  R  L  H  Q
      -  G  C  T  Y  T  A  N  P  F  K  N  V  D  A  S  A  D  C  I  K
      -   A  A  L  T  P  Q  T  R  L  K  T  L  M  H  P  Q  T  A  S  R
```

Figure 17-W

```
16381 - GGGTTCGCGGAGTTGGTCACAACTACAGCCATAACCTTTCCACATTCCGCAGACGGTACA - 16440
       -G  F  A  E  L  V  T  T  T  A  I  T  F  P  H  S  A  D  G  T
      -  G  S  R  S  W  S  Q  L  Q  P  *  P  F  H  I  P  Q  T  V  Q
      -   V  R  G  V  G  H  N  Y  S  H  N  L  S  T  F  R  R  R  Y  R
16441 - GACTGTGTTTCTAAGTGTAAAACCCACTGGGTCATTAGCACAAGTGGTAGGTATTTGGAC - 16500
       -D  C  V  S  K  C  K  T  H  W  V  I  S  T  S  G  R  Y  L  D
      -  T  V  F  L  S  V  K  P  T  G  S  L  A  Q  V  V  G  I  W  T
      -   L  C  F  *  V  *  N  P  L  G  H  *  H  K  W  *  V  F  G  R
16501 - GTACTTACCTTTCAAGTCACAGAATCCTTTAGGATTTGGATGGTCAATGTGGCATCTACA - 16560
       -V  L  T  F  Q  V  T  E  S  F  R  I  W  M  V  N  V  A  S  T
      -  Y  L  P  F  K  S  Q  N  P  L  G  F  G  W  S  M  W  H  L  Q
      -   T  Y  L  S  S  H  R  I  L  *  D  L  D  G  Q  C  G  I  Y  N
16561 - ATACAGACAACATGAAGCACCACCAAAGGACTCTTGGTCCATGTTAGCTTCTGGTGTTAC - 16620
       -I  Q  T  T  *  S  T  T  K  G  L  L  V  H  V  S  F  W  C  Y
      -  Y  R  Q  H  E  A  P  P  K  D  S  W  S  M  L  A  S  G  V  T
      -   T  D  N  M  K  H  H  Q  R  T  L  G  P  C  *  L  L  V  L  Q
16621 - AGTAATTGCCTGTCCTGTACCAGTGTGTGTACACAACATCTTCACACAGTTGGTGATTGG - 16680
       -S  N  C  L  S  C  T  S  V  C  T  Q  H  L  H  T  V  G  D  W
      -  V  I  A  C  P  V  P  V  C  V  H  N  I  F  T  Q  L  V  I  G
      -   *  L  P  V  L  Y  Q  C  V  Y  T  T  S  S  H  S  W  *  L  V
16681 - TTGTCCTCCACTTGCTAGGTAATCCTTATATGCTTTAGCAGGGTCTACTGCAAAAGCACA - 16740
       -L  S  S  T  C  *  V  I  L  I  C  F  S  R  V  Y  C  K  S  T
      -  C  P  P  L  A  R  *  S  L  Y  A  L  A  G  S  T  A  K  A  Q
      -   V  L  H  L  L  G  N  P  Y  M  L  *  Q  G  L  L  Q  K  H  R
16741 - GAAGGAAAGCACAGTTGAATTGGCAGGTACTTCTGTAGCATTTCCAGCCTGAAGACGTAC - 16800
       -E  G  K  H  S  *  I  G  R  Y  F  C  S  I  S  S  L  K  T  Y
      -  K  E  S  T  V  E  L  A  G  T  S  V  A  F  P  A  *  R  R  T
      -   R  K  A  Q  L  N  W  Q  V  L  L  *  H  F  Q  P  E  D  V  L
16801 - TGTAGCAGCTAAACTGCCCAGCACCATACCTCTATTTAGGTTGTTTAAGCCTTTGATGAA - 16860
       -C  S  S  *  T  A  Q  H  H  T  S  I  *  V  V  *  A  F  D  E
      -  V  A  A  K  L  P  S  T  I  P  L  F  R  L  F  K  P  L  M  K
      -   *  Q  L  N  C  P  A  P  Y  L  Y  L  G  C  L  S  L  *  *  S
16861 - GTACAAGTATTTCACTTTAGGCCCTTTTGGTGTGTCTGTAACAAACCTACAAGGTGGTTC - 16920
       -V  Q  V  F  H  F  R  P  F  W  C  V  C  N  K  P  T  R  W  F
      -  Y  K  Y  F  T  L  G  P  F  G  V  S  V  T  N  L  Q  G  G  S
      -   T  S  I  S  L  *  A  L  L  V  C  L  *  Q  T  Y  K  V  V  P
16921 - CAGTTCTGTGTAAATTGTACCTGTACCATCACTCTTAGGGAATCTAGCCCATTTGAGATC - 16980
       -Q  F  C  V  N  C  T  C  T  I  T  L  R  E  S  S  P  F  E  I
      -  S  S  V  *  I  V  P  V  P  S  L  L  G  N  L  A  H  L  R  S
      -   V  L  C  K  L  Y  L  Y  H  H  S  *  G  I  *  P  I  *  D  L
16981 - TTGGTGGTCTGATAGTAATGCCAGCACAAACCTACCTCCCTTCGAATTGTTATAGTAGGC - 17040
       -L  V  V  *  *  *  C  Q  H  K  P  T  S  L  R  I  V  I  V  G
      -  W  W  S  D  S  N  A  S  T  N  L  P  P  F  E  L  L  *  *  A
      -   G  G  L  I  V  M  P  A  Q  T  Y  L  P  S  N  C  Y  S  R  Q
17041 - AAGTGCATTGTCATCAGTACAAGCTGTTTGTGTGGTACCAGCCGCACAGGACATCTGTCG - 17100
       -K  C  I  V  I  S  T  S  C  L  C  G  T  S  R  T  G  H  L  S
      -  S  A  L  S  S  V  Q  A  V  C  V  V  P  A  A  Q  D  I  C  R
      -   V  H  C  H  Q  Y  K  L  F  V  W  Y  Q  P  H  R  T  S  V  V
```

Figure 17-X

```
17101 - TAGTGCTACTGGACTCAGTTCATTATTCTGTAGTTTAACAGCTGAGTTGGCTCTTAGAGC - 17160
      - *  C  Y  W  T  Q  F  I  I  L  *  F  N  S  *  V  G  S  *  S
      -  S  A  T  G  L  S  S  L  F  C  S  L  T  A  E  L  A  L  R  A
      -   V  L  L  D  S  V  H  Y  S  V  V  *  Q  L  S  W  L  L  E  L
17161 - TGTAACAATAAGAGGCCAAGCCAAATTTGGTGAATTGTCCATGTTAATTTCACTAAGTTG - 17220
      - C  N  N  K  R  P  S  Q  I  W  *  I  V  H  V  N  F  T  K  L
      -  V  T  I  R  G  Q  A  K  F  G  E  L  S  M  L  I  S  L  S  *
      -   *  Q  *  E  A  K  P  N  L  V  N  C  P  C  *  F  H  *  V  E
17221 - AACAATCTTGCTATCCGCATCAACAACTTGCTGGATTTCCCAGAGTGCAGATGCATATGT - 17280
      - N  N  L  A  I  R  I  N  N  L  L  D  F  P  E  C  R  C  I  C
      -  T  I  L  L  S  A  S  T  T  C  W  I  S  Q  S  A  D  A  Y  V
      -   Q  S  C  Y  P  H  Q  Q  L  A  G  F  P  R  V  Q  M  H  M  *
17281 - AAAGGTGTTACCATCACAAGTGTTCTTGTAGGTACCATAATCAGGGACAACAACCATGAG - 17340
      - K  G  V  T  I  T  S  V  L  V  G  T  I  I  R  D  N  N  H  E
      -  K  V  L  P  S  Q  V  F  L  *  V  P  *  S  G  T  T  T  M  S
      -   R  C  Y  H  H  K  C  S  C  R  Y  H  N  Q  G  Q  Q  P  *  V
17341 - TTTGGCTGCTGTAGTCAATGGTATGATGTTGAGTGGAACACAACCATCACGCGCATTGTT - 17400
      - F  G  C  C  S  Q  W  Y  D  V  E  W  N  T  T  I  T  R  I  V
      -  L  A  A  V  V  N  G  M  M  L  S  G  T  Q  P  S  R  A  L  L
      -   W  L  L  *  S  M  V  *  C  *  V  E  H  N  H  H  A  H  C  *
17401 - GATAATGTTGTTAAGTGCATCATTATCAAGCTTCCTAAGCATAGTGAAGAGCATTGTTTG - 17460
      - D  N  V  V  K  C  I  I  I  K  L  P  K  H  S  E  E  H  C  L
      -  I  M  L  L  S  A  S  L  S  S  F  L  S  I  V  K  S  I  V  C
      -   *  C  C  *  V  H  H  Y  Q  A  S  *  A  *  *  R  A  L  F  A
17461 - CATAGCACTAGTTACTTTTGCCCTCTTGTCCTCAGATCTTGCCTGTTTGTACATTTGGGT - 17520
      - H  S  T  S  Y  F  C  P  L  V  L  R  S  C  L  F  V  H  L  G
      -  I  A  L  V  T  F  A  L  L  S  S  D  L  A  C  L  Y  I  W  V
      -   *  H  *  L  L  L  P  S  C  P  Q  I  L  P  V  C  T  F  G  S
17521 - CATAGCCTGATCTGCCATCTTTTCCAACTTGCGTTGCATGGCAGCATCACGGTCAAACTC - 17580
      - H  S  L  I  C  H  L  F  Q  L  A  L  H  G  S  I  T  V  K  L
      -  I  A  *  S  A  I  F  S  N  L  R  C  M  A  A  S  R  S  N  S
      -   *  P  D  L  P  S  F  P  T  C  V  A  W  Q  H  H  G  Q  T  Q
17581 - AGATTTAGCCACATTCAAAGATTTCTTTAACTTTTTGAGAACGACTTCAGAATCACCATT - 17640
      - R  F  S  H  I  Q  R  F  L  *  L  F  E  N  D  F  R  I  T  I
      -  D  L  A  T  F  K  D  F  F  N  F  L  R  T  T  S  E  S  P  L
      -   I  *  P  H  S  K  I  S  L  T  F  *  E  R  L  Q  N  H  H  *
17641 - AGCTACAGCCTGCTCATAGGCCTCCTGGGCAGTGGCATAAGCGGCATATGATGGTAAAGA - 17700
      - S  Y  S  L  L  I  G  L  L  G  S  G  I  S  G  I  *  W  *  R
      -  A  T  A  C  S  *  A  S  W  A  V  A  *  A  A  Y  D  G  K  E
      -   L  Q  P  A  H  R  P  P  G  Q  W  H  K  R  H  M  M  V  K  N
17701 - ACTAAATTCTGAAGCAATAGCCTGAAGAGTAGCACGGTTATCGAGCATTTCCTCGCACAA - 17760
      - T  K  F  *  S  N  S  L  K  S  S  T  V  I  E  H  F  L  A  Q
      -  L  N  S  E  A  I  A  *  R  V  A  R  L  S  S  I  S  S  H  N
      -   *  I  L  K  Q  *  P  E  E  *  H  G  Y  R  A  F  P  R  T  T
17761 - CCTATTAATGTCTACAGCACCCTGCATGGATAGCAAAACAGACAAAAGAGAAACCATCTT - 17820
      - P  I  N  V  Y  S  T  L  H  G  *  Q  N  R  Q  K  R  N  H  L
      -  L  L  M  S  T  A  P  C  M  D  S  K  T  D  K  R  E  T  I  F
      -   Y  *  C  L  Q  H  P  A  W  I  A  K  Q  T  K  E  K  P  S  S
17821 - CTCGAAAGCTTCAGTTGTGTCTTTTGCAAGAAGAATATCATTGTGGAGTTGTACACATTG - 17880
      - L  E  S  F  S  C  V  F  C  K  K  N  I  I  V  E  L  Y  T  L
      -  S  K  A  S  V  V  S  F  A  R  R  I  S  L  W  S  C  T  H  C
      -   R  K  L  Q  L  C  L  L  Q  E  E  Y  H  C  G  V  V  H  I  V
```

Figure 17-Y

```
17881 - TGCCCACAATTTAGAAGATGACTCTACTCTAAGTTGTTGAAGAACCGAGAGCAGTACCAC - 17940
      - C  P  Q  F  R  R  *  L  Y  S  K  L  L  K  N  R  E  Q  Y  H
      -  A  H  N  L  E  D  D  S  T  L  S  C  *  R  T  E  S  S  T  T
      -   P  T  I  *  K  M  T  L  L  *  V  V  E  E  P  R  A  V  P  Q
17941 - AGATGTGCACTTTACGTCAGACATTTTAGACTGTACAGTAGCAACCTTGATACATGGTTT - 18000
      - R  C  A  L  Y  V  R  H  F  R  L  Y  S  S  N  L  D  T  W  F
      -  D  V  H  F  T  S  D  I  L  D  C  T  V  A  T  L  I  H  G  L
      -   M  C  T  L  R  Q  T  F  *  T  V  Q  *  Q  P  *  Y  M  V  Y
18001 - ACCTCCAATACCCAACAACTTAATGTTAAGCTTGAAAGCATCAATACTACTCTTAGGAGG - 18060
      - T  S  N  T  Q  Q  L  N  V  K  L  E  S  I  N  T  T  L  R  R
      -  P  P  I  P  N  N  L  M  L  S  L  K  A  S  I  L  L  L  G  G
      -   L  Q  Y  P  T  T  *  C  *  A  *  K  H  Q  Y  Y  S  *  E  A
18061 - CAAAAGCCCCTGGGAGTTCATATACCTAAATTCTTGTGTAGAGACCAAGTAGTCATAAAC - 18120
      - Q  K  P  L  G  V  H  I  P  K  F  L  C  R  D  Q  V  V  I  N
      -  K  S  P  W  E  F  I  Y  L  N  S  C  V  E  T  K  *  S  *  T
      -   K  A  P  G  S  S  Y  T  *  I  L  V  *  R  P  S  S  H  K  H
18121 - ACCAAGAGTAAGCCTGAAGTAACGGTTGAGTAAACAGAAAAGGCCAAAGTAGCAGCAGCA - 18180
      - T  K  S  K  P  E  V  T  V  E  *  T  E  K  A  K  V  A  A  A
      -  P  R  V  S  L  K  *  R  L  S  K  Q  K  R  P  K  *  Q  Q  Q
      -   Q  E  *  A  *  S  N  G  *  V  N  R  K  G  Q  S  S  S  S  N
18181 - ACAATAGCCTAAGAAACAATAAACAAGCATGATACACTGTAAGGTGTTGCCAGTAATAAA - 18240
      - T  I  A  *  E  T  I  N  K  H  D  T  L  *  G  V  A  S  N  K
      -  Q  *  P  K  K  Q  *  T  S  M  I  H  C  K  V  L  P  V  I  N
      -   N  S  L  R  N  N  K  Q  A  *  Y  T  V  R  C  C  Q  *  *  I
18241 - TAACAATGGGTAATACTCAACACACACAAACACTATAGCTCTAGCTAAAAACATGATAGT - 18300
      - *  Q  W  V  I  L  N  T  H  K  H  Y  S  S  S  *  K  H  D  S
      -  N  N  G  *  Y  S  T  H  T  N  T  I  A  L  A  K  N  M  I  V
      -   T  M  G  N  T  Q  H  T  Q  T  L  *  L  *  L  K  T  *  *  S
18301 - CGTAACGACACCAGAATAGTTAGAGGTTACAGAAATAACTAAGGCCCACATGGAAATAGC - 18360
      - R  N  D  T  R  I  V  R  G  Y  R  N  N  *  G  P  H  G  N  S
      -  V  T  T  P  E  *  L  E  V  T  E  I  T  K  A  H  M  E  I  A
      -   *  R  H  Q  N  S  *  R  L  Q  K  *  L  R  P  T  W  K  *  L
18361 - TTGATCTAAAGCATTACCATAGTAGACTTTGTAAACAAGTGTAATGACATTCATCAGTGT - 18420
      - L  I  *  S  I  T  I  V  D  F  V  N  K  C  N  D  I  H  Q  C
      -  *  S  K  A  L  P  *  *  T  L  *  T  S  V  M  T  F  I  S  V
      -   D  L  K  H  Y  H  S  R  L  C  K  Q  V  *  *  H  S  S  V  S
18421 - CCAAACACGTCTAGCAGCATCATCATAAACAGTGCGAGCTGTCATGAGAATAAGCAAAAC - 18480
      - P  N  T  S  S  S  I  I  I  N  S  A  S  C  H  E  N  K  Q  N
      -  Q  T  R  L  A  A  S  S  *  T  V  R  A  V  M  R  I  S  K  T
      -   K  H  V  *  Q  H  H  H  K  Q  C  E  L  S  *  E  *  A  K  L
18481 - TAAAGCTGAAGCATACATAACACAATCCTTAAGCCTATAACCAGACAAGCTAGTGTCAGC - 18540
      - *  S  *  S  I  H  N  T  I  L  K  P  I  T  R  Q  A  S  V  S
      -  K  A  E  A  Y  I  T  Q  S  L  S  L  *  P  D  K  L  V  S  A
      -   K  L  K  H  T  *  H  N  P  *  A  Y  N  Q  T  S  *  C  Q  P
18541 - CAATTCAAGCCATGTCATGATACGCATCACCCAGCTAGCAGGCATGTAGACCATATTAAA - 18600
      - Q  F  K  P  C  H  D  T  H  H  P  A  S  R  H  V  D  H  I  K
      -  N  S  S  H  V  M  I  R  I  T  Q  L  A  G  M  *  T  I  L  K
      -   I  Q  A  M  S  *  Y  A  S  P  S  *  Q  A  C  R  P  Y  *  S
18601 - GTAAGCAACTGTTGCAAGAGAAGGTAACAGAAACAAGCACAAGAATGCGTGCTTATGCTT - 18660
      - V  S  N  C  C  K  R  R  *  Q  K  Q  A  Q  E  C  V  L  M  L
      -  *  A  T  V  A  R  E  G  N  R  N  K  H  K  N  A  C  L  C  L
      -   K  Q  L  L  Q  E  K  V  T  E  T  S  T  R  M  R  A  Y  A  *
```

Figure 17-Z

```
18661 - AACAAGCAGCATAGCACATGCAGCAATTGCCATAATACCAAGAGTAAATGGCAAGAAAGC - 18720
      - N  K  Q  H  S  T  C  S  N  C  H  N  T  K  S  K  W  Q  E  S
      -  T  S  S  I  A  H  A  A  I  A  I  I  P  R  V  N  G  K  K  A
      -   Q  A  A  *  H  M  Q  Q  L  P  *  Y  Q  E  *  M  A  R  K  H
18721 - ATTCTCGTAAACAAAGAAAAACAGTGACCACTGTGTACTTTGAACAAGAATCAATAGTGA - 18780
      - I  L  V  N  K  E  K  Q  *  P  L  C  T  L  N  K  N  Q  *  *
      -  F  S  *  T  K  K  N  S  D  H  C  V  L  *  T  R  I  N  S  D
      -   S  R  K  Q  R  K  T  V  T  T  V  Y  F  E  Q  E  S  I  V  M
18781 - TGTCAAGAAAGTTAAAAGCATCCAATGATGAGTGCCCTTAACAATTTTCTTGAACTTACC - 18840
      - C  Q  E  S  *  K  H  P  M  M  S  A  L  N  N  F  L  E  L  T
      -  V  K  K  V  K  S  I  Q  *  *  V  P  L  T  I  F  L  N  L  P
      -   S  R  K  L  K  A  S  N  D  E  C  P  *  Q  F  S  *  T  Y  L
18841 - TTGGAAGGTAACACCAGAGCATTGTCTAACAACATCAAATGGTGTAAACTCATCTTCTAA - 18900
      - L  E  G  N  T  R  A  L  S  N  N  I  K  W  C  K  L  I  F  *
      -  W  K  V  T  P  E  H  C  L  T  T  S  N  G  V  N  S  S  S  K
      -   G  R  *  H  Q  S  I  V  *  Q  H  Q  M  V  *  T  H  L  L  K
18901 - AATAGTGCTACCAAGGATAGTACGACCATTCATACCATTCTGCAGCAGCTCTTTCAAAGC - 18960
      - N  S  A  T  K  D  S  T  T  I  H  T  I  L  Q  Q  L  F  Q  S
      -  I  V  L  P  R  I  V  R  P  F  I  P  F  C  S  S  S  F  K  A
      -   *  C  Y  Q  G  *  Y  D  H  S  Y  H  S  A  A  A  L  S  K  Q
18961 - AGCACACATATCTAAGACGGCAATTCCTGTTTGAGCAGAAAGAGGTCCCAATATGTCAAC - 19020
      - S  T  H  I  *  D  G  N  S  C  L  S  R  K  R  S  Q  Y  V  N
      -  A  H  I  S  K  T  A  I  P  V  *  A  E  R  G  P  N  M  S  T
      -   H  T  Y  L  R  R  Q  F  L  F  E  Q  K  E  V  P  I  C  Q  H
19021 - ATGATCTTGTGTCAAAGGTTCATAGTTGTACTTCATTGCCACAAGGTTAAAGTCATTCAA - 19080
      - M  I  L  C  Q  R  F  I  V  V  L  H  C  H  K  V  K  V  I  Q
      -  *  S  C  V  K  G  S  *  L  Y  F  I  A  T  R  L  K  S  F  K
      -   D  L  V  S  K  V  H  S  C  T  S  L  P  Q  G  *  S  H  S  K
19081 - AGTAGTGGTGAATCTATTAAGAAACCACCTATCACCATTGATAACAGCAGCATACAGCCA - 19140
      - S  S  G  E  S  I  K  K  P  P  I  T  I  D  N  S  S  I  Q  P
      -  V  V  V  N  L  L  R  N  H  L  S  P  L  I  T  A  A  Y  S  H
      -   *  W  *  I  Y  *  E  T  T  Y  H  H  *  *  Q  Q  H  T  A  M
19141 - TGCCAAAACATTTAATGTTATGGTTGTGTCTGTACCTGCAGCCTGTGCAGTTTGTCTGTC - 19200
      - C  Q  N  I  *  C  Y  G  C  V  C  T  C  S  L  C  S  L  S  V
      -  A  K  T  F  N  V  M  V  V  S  V  P  A  A  C  A  V  C  L  S
      -   P  K  H  L  M  L  W  L  C  L  Y  L  Q  P  V  Q  F  V  C  Q
19201 - AACAAATGGACCATAGAATTTACCTTCTAAGTCAGTACCAGCGTGTACTCCTGTTGGAAG - 19260
      - N  K  W  T  I  E  F  T  F  *  V  S  T  S  V  Y  S  C  W  K
      -  T  N  G  P  *  N  L  P  S  K  S  V  P  A  C  T  P  V  G  S
      -   Q  M  D  H  R  I  Y  L  L  S  Q  Y  Q  R  V  L  L  L  E  A
19261 - CTCCATATGATGCATATAGCAGAAAGACACGCAATCATAATCAATGTTAAAACCAACACT - 19320
      - L  H  M  M  H  I  A  E  R  H  A  I  I  I  N  V  K  T  N  T
      -  S  I  *  C  I  *  Q  K  D  T  Q  S  *  S  M  L  K  P  T  L
      -   P  Y  D  A  Y  S  R  K  T  R  N  H  N  Q  C  *  N  Q  H  Y
19321 - ACCACATGATCCATTAAGGAAAGAACCTTTAATGGTATGATTAGGTCTCATGGCACACTG - 19380
      - T  T  *  S  I  K  E  R  T  F  N  G  M  I  R  S  H  G  T  L
      -  P  H  D  P  L  R  K  E  P  L  M  V  *  L  G  L  M  A  H  *
      -   H  M  I  H  *  G  K  N  L  *  W  Y  D  *  V  S  W  H  T  D
```

Figure 17-AA

```
19381 - ATAAACACCAGATGGTGAACCATTGTAGCATGCTAGAACTGAAAATGTTTGACCAGGTTG - 19440
      - I  N  T  R  W  *  T  I  V  A  C  *  N  *  K  C  L  T  R  L
      -  *  T  P  D  G  E  P  L  *  H  A  R  T  E  N  V  *  P  G  W
      -   K  H  Q  M  V  N  H  C  S  M  L  E  L  K  M  F  D  Q  V  G
19441 - GATACGGACAAATTTATACTTGGGTGTCTTAGGGTTAGAAGTATCAACTTTAAGCCTAAG - 19500
      - D  T  D  K  F  I  L  G  C  L  R  V  R  S  I  N  F  K  P  K
      -  I  R  T  N  L  Y  L  G  V  L  G  L  E  V  S  T  L  S  L  S
      -   Y  G  Q  I  Y  T  W  V  S  *  G  *  K  Y  Q  L  *  A  *  A
19501 - CAGACAATTTTGCATAGAATGGCCAATAACACGAAGTTGAACATTGCCAGCCTGAACAAG - 19560
      - Q  T  I  L  H  R  M  A  N  N  T  K  L  N  I  A  S  L  N  K
      -  R  Q  F  C  I  E  W  P  I  T  R  S  *  T  L  P  A  *  T  R
      -   D  N  F  A  *  N  G  Q  *  H  E  V  E  H  C  Q  P  E  Q  E
19561 - AAAGCTATGGTTGGATTTGCGAATGAGCAGATCTTCATAGTTAGGATTAAGCATGTCTTC - 19620
      - K  A  M  V  G  F  A  N  E  Q  I  F  I  V  R  I  K  H  V  F
      -  K  L  W  L  D  L  R  M  S  R  S  S  *  L  G  L  S  M  S  S
      -   S  Y  G  W  I  C  E  *  A  D  L  H  S  *  D  *  A  C  L  L
19621 - TGCTGTGCAAATGACATGTCTTGGACAGTATACTGTGTCATCCAACCACAATCCATTAAG - 19680
      - C  C  A  N  D  M  S  W  T  V  Y  C  V  I  Q  P  Q  S  I  K
      -  A  V  Q  M  T  C  L  G  Q  Y  T  V  S  S  N  H  N  P  L  R
      -   L  C  K  *  H  V  L  D  S  I  L  C  H  P  T  T  I  H  *  E
19681 - AGTTGTAGTTCCACAGGTTACTTGTACCATGCACCCTTCAACTTTGCCTGACGGGAATGC - 19740
      - S  C  S  S  T  G  Y  L  Y  H  A  P  F  N  F  A  *  R  E  C
      -  V  V  V  P  Q  V  T  C  T  M  H  P  S  T  L  P  D  G  N  A
      -   L  *  F  H  R  L  L  V  P  C  T  L  Q  L  C  L  T  G  M  P
19741 - CATTTTCCTAAAACCACTCTGCAGAACAGCAGAAGTGATTGATGTCTGTGGTGGTTGGTA - 19800
      - H  F  P  K  T  T  L  Q  N  S  R  S  D  *  C  L  W  W  L  V
      -  I  F  L  K  P  L  C  R  T  A  E  V  I  D  V  C  G  G  W  *
      -   F  S  *  N  H  S  A  E  Q  Q  K  *  L  M  S  V  V  V  G  R
19801 - GAGAACATCAGCACCTGAGTTGCTAAAGTCATTTAGAGCCTTTGCTAAGTGGCAGCAAGC - 19860
      - E  N  I  S  T  *  V  A  K  V  I  *  S  L  C  *  V  A  A  S
      -  R  T  S  A  P  E  L  L  K  S  F  R  A  F  A  K  W  Q  Q  A
      -   E  H  Q  H  L  S  C  *  S  H  L  E  P  L  L  S  G  S  K  L
19861 - TGCTTCACGATAGCTGGTAGTATCTAAGGCTCCACTGAAATACTTGTACTTGTTATATAG - 19920
      - C  F  T  I  A  G  S  I  *  G  S  T  E  I  L  V  L  V  I  *
      -  A  S  R  *  L  V  V  S  K  A  P  L  K  Y  L  Y  L  L  Y  R
      -   L  H  D  S  W  *  Y  L  R  L  H  *  N  T  C  T  C  Y  I  E
19921 - AGCAAGATACCTGTTATACTGTGTAAGTGGCAACAGTGTCTCGCTACGCAATTTTAGGTA - 19980
      - S  K  I  P  V  I  L  C  K  W  Q  Q  C  L  A  T  Q  F  *  V
      -  A  R  Y  L  L  Y  C  V  S  G  N  S  V  S  L  R  N  F  R  Y
      -   Q  D  T  C  Y  T  V  *  V  A  T  V  S  R  Y  A  I  L  G  T
19981 - CATTTCCTTGTTGAGCAAAAAGGTACACAAAGCAGCCTCCTCGAAGGTACTAAATGTAAC - 20040
      - H  F  L  V  E  Q  K  G  T  Q  S  S  L  L  E  G  T  K  C  N
      -  I  S  L  L  S  K  K  V  H  K  A  A  S  S  K  V  L  N  V  T
      -   F  P  C  *  A  K  R  Y  T  K  Q  P  P  R  R  Y  *  M  *  L
20041 - TCCATTAAACATGACTCTTTTCCTAAGATAGTTGTTAAAGAACCAATGGCAGTGCTTCAG - 20100
      - S  I  K  H  D  S  F  P  K  I  V  V  K  E  P  M  A  V  L  Q
      -  P  L  N  M  T  L  F  L  R  *  L  L  K  N  Q  W  Q  C  F  R
      -   H  *  T  *  L  F  S  *  D  S  C  *  R  T  N  G  S  A  S  E
```

Figure 17-BB

```
20101 - AGAAATACAGAATACATAGATTGCTGTTATCCAAAAAGGCACAATAGGAGAAAACATGGC - 20160
      - R  N  T  E  Y  I  D  C  C  Y  P  K  R  H  N  R  R  K  H  G
      -  E  I  Q  N  T  *  I  A  V  I  Q  K  G  T  I  G  E  N  M  A
      -   K  Y  R  I  H  R  L  L  L  S  K  K  A  Q  *  E  K  T  W  Q
20161 - AAACCATTGAAGGTGAGCCAAGAATGAAACATCATTGGTGAAATAGAATGTCAAGTACAA - 20220
      - K  P  L  K  V  S  Q  E  *  N  I  I  G  E  I  E  C  Q  V  Q
      -  N  H  *  R  *  A  K  N  E  T  S  L  V  K  *  N  V  K  Y  K
      -   T  I  E  G  E  P  R  M  K  H  H  W  *  N  R  M  S  S  T  S
20221 - GTAAAAGACTGAGTAGACTCCCGGCAGAAAGCTGTAAGCTGGTACCAGACAGAGTATAGT - 20280
      - V  K  D  *  V  D  S  R  Q  K  A  V  S  W  Y  Q  T  E  Y  S
      -  *  K  T  E  *  T  P  G  R  K  L  *  A  G  T  R  Q  S  I  V
      -   K  R  L  S  R  L  P  A  E  S  C  K  L  V  P  D  R  V  *  *
20281 - GAAAGACATCAAAAACAAAAGTGCATTAGCAGCAACAACATGGTTGTACTCACCAAAAAC - 20340
      - E  R  H  Q  K  Q  K  C  I  S  S  N  N  M  V  V  L  T  K  N
      -  K  D  I  K  N  K  S  A  L  A  A  T  T  W  L  Y  S  P  K  T
      -   K  T  S  K  T  K  V  H  *  Q  Q  Q  H  G  C  T  H  Q  K  H
20341 - ACGTCTGAATTTCATAAAGTAGTAGGCAGCACAAGTCACCAATATGGCAATAATACCACC - 20400
      - T  S  E  F  H  K  V  V  G  S  T  S  H  Q  Y  G  N  N  T  T
      -  R  L  N  F  I  K  *  *  A  A  Q  V  T  N  M  A  I  I  P  P
      -   V  *  I  S  *  S  S  R  Q  H  K  S  P  I  W  Q  *  Y  H  Q
20401 - AGCCACTACTGAAGCAGACACATCTAAAGCACCCACAGGTTGCACAAGAGGAGTAAAGAT - 20460
      - S  H  Y  *  S  R  H  I  *  S  T  H  R  L  H  K  R  S  K  D
      -  A  T  T  E  A  D  T  S  K  A  P  T  G  C  T  R  G  V  K  M
      -   P  L  L  K  Q  T  H  L  K  H  P  Q  V  A  Q  E  E  *  R  C
20461 - GTTAGCTATGAGATTCATCGCATCAACACCACAGAAAACTCCTGATAGAGCTCTGTAATG - 20520
      - V  S  Y  E  I  H  R  I  N  T  T  E  N  S  *  *  S  S  V  M
      -  L  A  M  R  F  I  A  S  T  P  Q  K  T  P  D  R  A  L  *  C
      -   *  L  *  D  S  S  H  Q  H  H  R  K  L  L  I  E  L  C  N  A
20521 - CTCATTATTAAGAACCCATCTACCACTGGTAGATAGGCAAATACCTACTTCTGACCTTTC - 20580
      - L  I  I  K  N  P  S  T  T  G  R  *  A  N  T  Y  F  *  P  F
      -  S  L  L  R  T  H  L  P  L  V  D  R  Q  I  P  T  S  D  L  S
      -   H  Y  *  E  P  I  Y  H  W  *  I  G  K  Y  L  L  L  T  F  R
20581 - GCATGTACCATGTCTACAGTACTCAGCATCAAAAGTTGTTACTACTCTAACAGAACCCTC - 20640
      - A  C  T  M  S  T  V  L  S  I  K  S  C  Y  Y  S  N  R  T  L
      -  H  V  P  C  L  Q  Y  S  A  S  K  V  V  T  T  L  T  E  P  S
      -   M  Y  H  V  Y  S  T  Q  H  Q  K  L  L  L  L  *  Q  N  P  P
20641 - CAGGTAAGTGTTAGGAAACTGTATGATGGAACCATCCATAAGCACATAACGAGTGTCTGG - 20700
      - Q  V  S  V  R  K  L  Y  D  G  T  I  H  K  H  I  T  S  V  W
      -  R  *  V  L  G  N  C  M  M  E  P  S  I  S  T  *  R  V  S  G
      -   G  K  C  *  E  T  V  *  W  N  H  P  *  A  H  N  E  C  L  D
20701 - ACGAAGCTCACTATAAGAAATAGAACCCTCTAGCAAATTAGTGTCATAACAATATGGCAC - 20760
      - T  K  L  T  I  R  N  R  T  L  *  Q  I  S  V  I  T  I  W  H
      -  R  S  S  L  *  E  I  E  P  S  S  K  L  V  S  *  Q  Y  G  T
      -   E  A  H  Y  K  K  *  N  P  L  A  N  *  C  H  N  N  M  A  Q
20761 - AGGTTTGCCCATAGCATCCTTAAAAATTGTACACTCAGCAGCAAGAACGCAAGCAGAGGT - 20820
      - R  F  A  H  S  I  L  K  N  C  T  L  S  S  K  N  A  S  R  G
      -  G  L  P  I  A  S  L  K  I  V  H  S  A  A  R  T  Q  A  E  V
      -   V  C  P  *  H  P  *  K  L  Y  T  Q  Q  Q  E  R  K  Q  R  *
```

Figure 17-CC

```
20821 - AGCAAAATCACTATACTCAATGAGTTTGGAAGGTGTGTAGCAAATGTTGCCAACAGCACT - 20880
      - S  K  I  T  I  L  N  E  F  G  R  C  V  A  N  V  A  N  S  T
      -  A  K  S  L  Y  S  M  S  L  E  G  V  *  Q  M  L  P  T  A  L
      -   Q  N  H  Y  T  Q  *  V  W  K  V  C  S  K  C  C  Q  Q  H  *
20881 - AAAAACACGAGGTAGAAAATGCAAGAAGTCACCATTGATTGCTCTCAGCACAGTACCCGG - 20940
      - K  N  T  R  *  K  M  Q  E  V  T  I  D  C  S  Q  H  S  T  R
      -  K  T  R  G  R  K  C  K  K  S  P  L  I  A  L  S  T  V  P  G
      -   K  H  E  V  E  N  A  R  S  H  H  *  L  L  S  A  Q  Y  P  V
20941 - TAAGCCAGGCACTATGAAACCAATCTCTCTTGTAATGATAGCAGCTACTACAGGGCAGCT - 21000
      - *  A  R  H  Y  E  T  N  L  S  C  N  D  S  S  Y  Y  R  A  A
      -  K  P  G  T  M  K  P  I  S  L  V  M  I  A  A  T  T  G  Q  L
      -   S  Q  A  L  *  N  Q  S  L  L  *  *  *  Q  L  L  Q  G  S  F
21001 - TTTGTCATTTTTGTATGAACCACCACGCTGGCTAAACCATGCGTCAAAACCAGCATGTTT - 21060
      - F  V  I  F  V  *  T  T  T  L  A  K  P  C  V  K  T  S  M  F
      -  L  S  F  L  Y  E  P  P  R  W  L  N  H  A  S  K  P  A  C  L
      -   C  H  F  C  M  N  H  H  A  G  *  T  M  R  Q  N  Q  H  V  Y
21061 - ATTTGCAAAACAATCATCAGTAGAAATGATGTCACGAGTGACACCATCCTGAATGGCTTT - 21120
      - I  C  K  T  I  I  S  R  N  D  V  T  S  D  T  I  L  N  G  F
      -  F  A  K  Q  S  S  V  E  M  M  S  R  V  T  P  S  *  M  A  L
      -   L  Q  N  N  H  Q  *  K  *  C  H  E  *  H  H  P  E  W  L  C
21121 - GTAACCAATGATTTCATTTGTGTAACCATCATGGATTGACAATGTATGTACTGGCATAAC - 21180
      - V  T  N  D  F  I  C  V  T  I  M  D  *  Q  C  M  Y  W  H  N
      -  *  P  M  I  S  F  V  *  P  S  W  I  D  N  V  C  T  G  I  T
      -   N  Q  *  F  H  L  C  N  H  H  G  L  T  M  Y  V  L  A  *  R
21181 - GATATAACAAACCAATGCAGCAAGAACGCACAATAATGTGGCCTTAAGCATAAGTTTAAA - 21240
      - D  I  T  N  Q  C  S  K  N  A  Q  *  C  G  L  K  H  K  F  K
      -  I  *  Q  T  N  A  A  R  T  H  N  N  V  A  L  S  I  S  L  K
      -   Y  N  K  P  M  Q  Q  E  R  T  I  M  W  P  *  A  *  V  *  N
21241 - ACAAGTACTAACAATCTTACCACCCTTGAGTGAGATTTTAGTAGTTATGACATTGACAAC - 21300
      - T  S  T  N  N  L  T  T  L  E  *  D  F  S  S  Y  D  I  D  N
      -  Q  V  L  T  I  L  P  P  L  S  E  I  L  V  V  M  T  L  T  T
      -   K  Y  *  Q  S  Y  H  P  *  V  R  F  *  *  L  *  H  *  Q  P
21301 - CTGTCTAGTTGTAGCACAAGTTAGTGTAAAAGGTATGTTGTTCTTCTTGGCAGCAGTACG - 21360
      - L  S  S  C  S  T  S  *  C  K  R  Y  V  V  L  L  G  S  S  T
      -  C  L  V  V  A  Q  V  S  V  K  G  M  L  F  F  L  A  A  V  R
      -   V  *  L  *  H  K  L  V  *  K  V  C  C  S  S  W  Q  Q  Y  E
21361 - AATTTGTTTACGCAGCTGTTCAGATAAAGACATGTAGTCTTTTACATTCCAGATGAGTGA - 21420
      - N  L  F  T  Q  L  F  R  *  R  H  V  V  F  Y  I  P  D  E  *
      -  I  C  L  R  S  C  S  D  K  D  M  *  S  F  T  F  Q  M  S  E
      -   F  V  Y  A  A  V  Q  I  K  T  C  S  L  L  H  S  R  *  V  K
21421 - AACATTGTGACTTTTTGCTACTTGGGCATTGATATGCCTTGCATTACAGTCAATACATGC - 21480
      - N  I  V  T  F  C  Y  L  G  I  D  M  P  C  I  T  V  N  T  C
      -  T  L  *  L  F  A  T  W  A  L  I  C  L  A  L  Q  S  I  H  A
      -   H  C  D  F  L  L  L  G  H  *  Y  A  L  H  Y  S  Q  Y  M  R
21481 - GCCAAGATCTCTGGGCGTCATGTTTTCAACCTTATTATAGGTGAGCATGAAATTGTTACA - 21540
      - A  K  I  S  G  R  H  V  F  N  L  I  I  G  E  H  E  I  V  T
      -  P  R  S  L  G  V  M  F  S  T  L  L  *  V  S  M  K  L  L  Q
      -   Q  D  L  W  A  S  C  F  Q  P  Y  Y  R  *  A  *  N  C  Y  N
```

Figure 17-DD

```
21541 - ACTGTCACCTGTCACTTCTAAGTCAGAGTGATGTGAAAGTTTGAGACATTCAATAACATC - 21600
      - T  V  T  C  H  F  *  V  R  V  M  *  K  F  E  T  F  N  N  I
      -  L  S  P  V  T  S  K  S  E  *  C  E  S  L  R  H  S  I  T  S
      -   C  H  L  S  L  L  S  Q  S  D  V  K  V  *  D  I  Q  *  H  P
21601 - CTTTGTGTCAACATCGGTATCAACAACACCTTGTCGGGCAGCTGACACGAATGTAGAAAG - 21660
      - L  C  V  N  I  G  I  N  N  T  L  S  G  S  *  H  E  C  R  K
      -  F  V  S  T  S  V  S  T  T  P  C  R  A  A  D  T  N  V  E  R
      -   L  C  Q  H  R  Y  Q  Q  H  L  V  G  Q  L  T  R  M  *  K  G
21661 - GACACCATCTAAAGCTACACCCTTTGCTAACTCGCTGTGAGCTGTAGCAACAAGTGCCTT - 21720
      - D  T  I  *  S  Y  T  L  C  *  L  A  V  S  C  S  N  K  C  L
      -  T  P  S  K  A  T  P  F  A  N  S  L  *  A  V  A  T  S  A  L
      -   H  H  L  K  L  H  P  L  L  T  R  C  E  L  *  Q  Q  V  P  *
21721 - AAGTTTTCCATAGGAACACTAAAAGTTGCTGAAAAGGTGTCGACATAAGCATCAAACAT - 21780
      - K  F  F  H  R  N  T  K  S  C  *  K  G  V  D  I  S  I  K  H
      -  S  F  S  I  G  T  L  K  V  A  E  K  V  S  T  *  A  S  N  I
      -   V  F  P  *  E  H  *  K  L  L  K  R  C  R  H  K  H  Q  T  S
21781 - CTTAACGGAAACTTCAGTACTATCTCCAACGTTTGATACAAGAGCTTGGTCAAGCAACAG - 21840
      - L  N  G  N  F  S  T  I  S  N  V  *  Y  K  S  L  V  K  Q  Q
      -  L  T  E  T  S  V  L  S  P  T  F  D  T  R  A  W  S  S  N  R
      -   *  R  K  L  Q  Y  Y  L  Q  R  L  I  Q  E  L  G  Q  A  T  E
21841 - AATAGGTTGGCACATCAGCTGACTGTAGTACACAGAAGCAGACTTAGAAGCAGACTCGTC - 21900
      - N  R  L  A  H  Q  L  T  V  V  H  R  S  R  L  R  S  R  L  V
      -  I  G  W  H  I  S  *  L  *  Y  T  E  A  D  L  E  A  D  S  S
      -   *  V  G  T  S  A  D  C  S  T  Q  K  Q  T  *  K  Q  T  R  R
21901 - GCATTTGGACTTGCCATCAAAAACTATGACATTAATAGGCAGTGAACCTTTAGTGTTGTT - 21960
      - A  F  G  L  A  I  K  N  Y  D  I  N  R  Q  *  T  F  S  V  V
      -  H  L  D  L  P  S  K  T  M  T  L  I  G  S  E  P  L  V  L  L
      -   I  W  T  C  H  Q  K  L  *  H  *  *  A  V  N  L  *  C  C  *
21961 - AGCTCTCAAATTGTCTAAATTGACAAAATGGGAGAGCGGATGTCTCTCATAGGTCTTTTG - 22020
      - S  S  Q  I  V  *  I  D  K  M  G  E  R  M  S  L  I  G  L  L
      -  A  L  K  L  S  K  L  T  K  W  E  S  G  C  L  S  *  V  F  *
      -   L  S  N  C  L  N  *  Q  N  G  R  A  D  V  S  H  R  S  F  D
22021 - ACCAGCCTTGTCAAAGTAGAGGTGAAGCGCGCCATTTTTCACAGCAACACTATCAACAAT - 22080
      - T  S  L  V  K  V  E  V  K  R  A  I  F  H  S  N  T  I  N  N
      -  P  A  L  S  K  *  R  *  S  A  P  F  F  T  A  T  L  S  T  I
      -   Q  P  C  Q  S  R  G  E  A  R  H  F  S  Q  Q  H  Y  Q  Q  Y
22081 - ATACGATGACTGGTCAGTAGGGTTGATTGGTCTTTTAAACTGGAGTGACAAATCACGAGC - 22140
      - I  R  *  L  V  S  R  V  D  W  S  F  K  L  E  *  Q  I  T  S
      -  Y  D  D  W  S  V  G  L  I  G  L  L  N  W  S  D  K  S  R  A
      -   T  M  T  G  Q  *  G  *  L  V  F  *  T  G  V  T  N  H  E  Q
22141 - AACTTCATCACTAATGAATGTACTACCAGTGCAAAATGTGTCACAATTGAGACAATTCCA - 22200
      - N  F  I  T  N  E  C  T  T  S  A  K  C  V  T  I  E  T  I  P
      -  T  S  S  L  M  N  V  L  P  V  Q  N  V  S  Q  L  R  Q  F  Q
      -   L  H  H  *  *  M  Y  Y  Q  C  K  M  C  H  N  *  D  N  S  N
22201 - ATTGTGAGTCTTGCAGAAGCCACGGCCTCCATTTGCATAGACATAGAAAGATCTCTTCAT - 22260
      - I  V  S  L  A  E  A  T  A  S  I  C  I  D  I  E  R  S  L  H
      -  L  *  V  L  Q  K  P  R  P  P  F  A  *  T  *  K  D  L  F  M
      -   C  E  S  C  R  S  H  G  L  H  L  H  R  H  R  K  I  S  S  C
22261 - GCCATTAACAATAGTTGTACACTCAACGCGTGTGGCACGATTGCGCTTATAGCACATCAT - 22320
      - A  I  N  N  S  C  T  L  N  A  C  G  T  I  A  L  I  A  H  H
      -  P  L  T  I  V  V  H  S  T  R  V  A  R  L  R  L  *  H  I  M
      -   H  *  Q  *  L  Y  T  Q  R  V  W  H  D  C  A  Y  S  T  S  C
```

Figure 17-EE

```
22321 - GCAAGTCGAAGAGGTGCAACCATCCATGATATGAACATAGCTCTTCCATATGTAGTAGAA - 22380
      - A  S  R  R  G  A  T  I  H  D  M  N  I  A  L  P  Y  V  V  E
      -  Q  V  E  E  V  Q  P  S  M  I  *  T  *  L  F  H  M  *  *  K
      -   K  S  K  R  C  N  H  P  *  Y  E  H  S  S  S  I  C  S  R  K
22381 - AGAAGCAAAGAAGATGTACATCCTAACCATTGCAGAAACGGGTGCCATTTGTACAATACT - 22440
      - R  S  K  E  D  V  H  P  N  H  C  R  N  G  C  H  L  Y  N  T
      -  E  A  K  K  M  Y  I  L  T  I  A  E  T  G  A  I  C  T  I  L
      -   K  Q  R  R  C  T  S  *  P  L  Q  K  R  V  P  F  V  Q  Y  *
22441 - AATGATAAACCACATGAGCCAAGAATTGCTGATGAAATGACTAGCAAAATAGCCAAAGAA - 22500
      - N  D  K  P  H  E  P  R  I  A  D  E  M  T  S  K  I  A  K  E
      -  M  I  N  H  M  S  Q  E  L  L  M  K  *  L  A  K  *  P  K  N
      -   *  *  T  T  *  A  K  N  C  *  *  N  D  *  Q  N  S  Q  R  T
22501 - CACCTGCATTATAGCTGAAAGACCTAATAAATAAAAGAATTTTGTGAACAACATATATGC - 22560
      - H  L  H  Y  S  *  K  T  *  *  I  K  E  F  C  E  Q  H  I  C
      -  T  C  I  I  A  E  R  P  N  K  *  K  N  F  V  N  N  I  Y  A
      -   P  A  L  *  L  K  D  L  I  N  K  R  I  L  *  T  T  Y  M  P
22561 - CAAAACCCACTCAGCGGCCAGACCTAAAATTGTCAAGTCTAGCTTGTACGATGAAATCGT - 22620
      - Q  N  P  L  S  G  Q  T  *  N  C  Q  V  *  L  V  R  *  N  R
      -  K  T  H  S  A  A  R  P  K  I  V  K  S  S  L  Y  D  E  I  V
      -   K  P  T  Q  R  P  D  L  K  L  S  S  L  A  C  T  M  K  S  S
22621 - CACCTGAATGGTTTCAAGAGCTGGATAAGAATCAAGGGAGTCTAATCCACTTAAACAAAT - 22680
      - H  L  N  G  F  K  S  W  I  R  I  K  G  V  *  S  T  *  T  N
      -  T  *  M  V  S  R  A  G  *  E  S  R  E  S  N  P  L  K  Q  M
      -   P  E  W  F  Q  E  L  D  K  N  Q  G  S  L  I  H  L  N  K  C
22681 - GCTGCAAGGAAAAGAACCTTCACAGAAATCCATAGTAGTAACGTTAGACGAATTAAGATA - 22740
      - A  A  R  K  R  T  F  T  E  I  H  S  S  N  V  R  R  I  K  I
      -  L  Q  G  K  E  P  S  Q  K  S  I  V  V  T  L  D  E  L  R  Y
      -   C  K  E  K  N  L  H  R  N  P  *  *  *  R  *  T  N  *  D  T
22741 - CAATTCTCTAACGCCATTACAATAAGAAGGAGCACCAAAATTAGATAAGAGTACACCAAA - 22800
      - Q  F  S  N  A  I  T  I  R  R  S  T  K  I  R  *  E  Y  T  K
      -  N  S  L  T  P  L  Q  *  E  G  A  P  K  L  D  K  S  T  P  K
      -   I  L  *  R  H  Y  N  K  K  E  H  Q  N  *  I  R  V  H  Q  K
22801 - AGCAGCAGTTACACAGATTAGAGAACCTAAGCAAATACTTAACAACAATAGCCACATAGC - 22860
      - S  S  S  Y  T  D  *  R  T  *  A  N  T  *  Q  Q  *  P  H  S
      -  A  A  V  T  Q  I  R  E  P  K  Q  I  L  N  N  N  S  H  I  A
      -   Q  Q  L  H  R  L  E  N  L  S  K  Y  L  T  T  I  A  T  *  R
22861 - GATTGTGAACAATTTAGAAAATTTGGGTGACTTCACATAATTAATGCCGGCATCCAAACA - 22920
      - D  C  E  Q  F  R  K  F  G  *  L  H  I  I  N  A  G  I  Q  T
      -  I  V  N  N  L  E  N  L  G  D  F  T  *  L  M  P  A  S  K  H
      -   L  *  T  I  *  K  I  W  V  T  S  H  N  *  C  R  H  P  N  I
22921 - TAATTTAGCAACACTCTTAACACTATTTTTAGCAATAGTTGTAGGTAGTGAAGCTCTAAT - 22980
      - *  F  S  N  T  L  N  T  I  F  S  N  S  C  R  *  *  S  S  N
      -  N  L  A  T  L  L  T  L  F  L  A  I  V  V  G  S  E  A  L  I
      -   I  *  Q  H  S  *  H  Y  F  *  Q  *  L  *  V  V  K  L  *  F
22981 - TCTAGAATTGGTACTTTTAGTAAAAGTACACAATTGGAACAATAATGTAAACACATAAGG - 23040
      - S  R  I  G  T  F  S  K  S  T  Q  L  E  Q  *  C  K  H  I  R
      -  L  E  L  V  L  L  V  K  V  H  N  W  N  N  N  V  N  T  *  G
      -   *  N  W  Y  F  *  *  K  Y  T  I  G  T  I  M  *  T  H  K  A
```

Figure 17-FF

```
23041 - CATATAATTGTTAAACACACGTTGTGCTAATCTCTTAGCGCAATTTGATGTTGTAATTGC - 23100
      - H  I  I  V  K  H  T  L  C  *  S  L  S  A  I  *  C  C  N  C
      -  I  *  L  L  N  T  R  C  A  N  L  L  A  Q  F  D  V  V  I  A
      -   Y  N  C  *  T  H  V  V  L  I  S  *  R  N  L  M  L  *  L  L
23101 - TGCTTGTCCTAAGAATGGTTTGACATAAGCCAAAATTTTACTCCAAGGAACACTATTAAT - 23160
      - C  L  S  *  E  W  F  D  I  S  Q  N  F  T  P  R  N  T  I  N
      -  A  C  P  K  N  G  L  T  *  A  K  I  L  L  Q  G  T  L  L  I
      -   L  V  L  R  M  V  *  H  K  P  K  F  Y  S  K  E  H  Y  *  L
23161 - TGCAGCAATACCATGAGTGGCAATTGTTTTTAAACCTAAGGCTAGTGAAAGCTCATTAGG - 23220
      - C  S  N  T  M  S  G  N  C  F  *  T  *  G  *  *  K  L  I  R
      -  A  A  I  P  *  V  A  I  V  F  K  P  K  A  S  E  S  S  L  G
      -   Q  Q  Y  H  E  W  Q  L  F  L  N  L  R  L  V  K  A  H  *  V
23221 - TTTCTTAATGGTAATGCTTGTGTTTTCCACATAAGCAGCCATAAGATCCTCATGACCTAA - 23280
      - F  L  N  G  N  A  C  V  F  H  I  S  S  H  K  I  L  M  T  *
      -  F  L  M  V  M  L  V  F  S  T  *  A  A  I  R  S  S  *  P  N
      -   S  *  W  *  C  L  C  F  P  H  K  Q  P  *  D  P  H  D  L  T
23281 - CTCTTGTGTTACTTTAACACCTTCATCTGATGGTTTAAGTATGACATTGCCTACAACTTC - 23340
      - L  L  C  Y  F  N  T  F  I  *  W  F  K  Y  D  I  A  Y  N  F
      -  S  C  V  T  L  T  P  S  S  D  G  L  S  M  T  L  P  T  T  S
      -   L  V  L  L  *  H  L  H  L  M  V  *  V  *  H  C  L  Q  L  R
23341 - GGTAGTTTTCACGTCACACTCTATGACTTCCTTCTGTATGGTAGGATTTTCCACTACTTC - 23400
      - G  S  F  H  V  T  L  Y  D  F  L  L  Y  G  R  I  F  H  Y  F
      -  V  V  F  T  S  H  S  M  T  S  F  C  M  V  G  F  S  T  T  S
      -   *  F  S  R  H  T  L  *  L  P  S  V  W  *  D  F  P  L  L  L
23401 - TTCAGAGGTGGGTTGTTGACTTTCACAAGCAAGATTGTCCATTCCTTGTGTGTCTTCTAC - 23460
      - F  R  G  G  L  L  T  F  T  S  K  I  V  H  S  L  C  V  F  Y
      -  S  E  V  G  C  *  L  S  Q  A  R  L  S  I  P  C  V  S  S  T
      -   Q  R  W  V  V  D  F  H  K  Q  D  C  P  F  L  V  C  L  L  L
23461 - TGCCAGAACTTCAAATGAATTTGAAGTATCTACTGGCTTTGTACTCCAAAGACAACGTAA - 23520
      - C  Q  N  F  K  *  I  *  S  I  Y  W  L  C  T  P  K  T  T  *
      -  A  R  T  S  N  E  F  E  V  S  T  G  F  V  L  Q  R  Q  R  K
      -   P  E  L  Q  M  N  L  K  Y  L  L  A  L  Y  S  K  D  N  V  N
23521 - ACACCAAGTGTTTGGTTTGAACGTTGTCTTGGTTGTAGCCTGGTTAATGTGCCAAACAAT - 23580
      - T  P  S  V  W  F  E  R  C  L  G  C  S  L  V  N  V  P  N  N
      -  H  Q  V  F  G  L  N  V  V  L  V  V  A  W  L  M  C  Q  T  I
      -   T  K  C  L  V  *  T  L  S  W  L  *  P  G  *  C  A  K  Q  L
23581 - TGGCTTATGCAGTAATTTAGCACCTTTCTTGAAACTCGCTGAATAGTGTCTATAGTCAAT - 23640
      - W  L  M  Q  *  F  S  T  F  L  E  T  R  *  I  V  S  I  V  N
      -  G  L  C  S  N  L  A  P  F  L  K  L  A  E  *  C  L  *  S  I
      -   A  Y  A  V  I  *  H  L  S  *  N  S  L  N  S  V  Y  S  Q  *
23641 - AGCCACTACATCGCCATTCAAGTCTGGGAAGAATGTGACAGATAGCTCTCGTGAAGCTGG - 23700
      - S  H  Y  I  A  I  Q  V  W  E  E  C  D  R  *  L  S  *  S  W
      -  A  T  T  S  P  F  K  S  G  K  N  V  T  D  S  S  R  E  A  G
      -   P  L  H  R  H  S  S  L  G  R  M  *  Q  I  A  L  V  K  L  A
23701 - CTTTGTGAAGCCTGTCATTTGATTTAAATCATCAGCAAATTTTGTGTTAGAACATGTGAG - 23760
      - L  C  E  A  C  H  L  I  *  I  I  S  K  F  C  V  R  T  C  E
      -  F  V  K  P  V  I  *  F  K  S  S  A  N  F  V  L  E  H  V  S
      -   L  *  S  L  S  F  D  L  N  H  Q  Q  I  L  C  *  N  M  *  V
23761 - TTTGAAATTATCAAAACTCGCATTTGGTAATGGTTGAGTTGGTACAAGGTCTATAGGCTG - 23820
      - F  E  I  I  K  T  R  I  W  *  W  L  S  W  Y  K  V  Y  R  L
      -  L  K  L  S  K  L  A  F  G  N  G  *  V  G  T  R  S  I  G  C
      -   *  N  Y  Q  N  S  H  L  V  M  V  E  L  V  Q  G  L  *  A  A
```

Figure 17-GG

```
23821 - CTCTGTATAGTAGCATTATCCTTTTTATAATACCCATCCAATTTTGGTTCAATCTCTGT - 23880
      - L  C  I  V  S  I  I  L  F  I  I  P  I  Q  F  W  F  N  L  C
      -  S  V  *  *  A  L  S  F  L  *  Y  P  S  N  F  G  S  I  S  V
      -   L  Y  S  K  H  Y  P  F  Y  N  T  H  P  I  L  V  Q  S  L  C
23881 - GTAAGTAACTCCATCGAGTTTATACGACACAGGCTTGATGGTTGTAGTGTAAGATGTTTC - 23940
      - V  S  N  S  I  E  F  I  R  H  R  L  D  G  C  S  V  R  C  F
      -  *  V  T  P  S  S  L  Y  D  T  G  L  M  V  V  V  *  D  V  S
      -   K  *  L  H  R  V  Y  T  T  Q  A  *  W  L  *  C  K  M  F  P
23941 - CTTGTAGAAAACATCAGTCACTGGTCCTTTGTACTCTGACATCTTTGTAAGGTGAGCTCC - 24000
      - L  V  E  N  I  S  H  W  S  F  V  L  *  H  L  C  K  V  S  S
      -  L  *  K  T  S  V  T  G  P  L  Y  S  D  I  F  V  R  *  A  P
      -   C  R  K  H  Q  S  L  V  L  C  T  L  T  S  L  *  G  E  L  R
24001 - GTCAATACGATAGAGGGTCTCCTTAGCAGTTATATGAGTGTAATGACCACACTGATAGTT - 24060
      - V  N  T  I  E  G  L  L  S  S  Y  M  S  V  M  T  T  L  I  V
      -  S  I  R  *  R  V  S  L  A  V  I  *  V  *  *  P  H  *  *  L
      -   Q  Y  D  R  G  S  P  *  Q  L  Y  E  C  N  D  H  T  D  S  Y
24061 - ACCAGTGTACTCATTCGCACATAAGAATGTACCTTGCTGTAATTTATACTCAGCAGGTGG - 24120
      - T  S  V  L  I  R  T  *  E  C  T  L  L  *  F  I  L  S  R  W
      -  P  V  Y  S  F  A  H  K  N  V  P  C  C  N  L  Y  S  A  G  G
      -   Q  C  T  H  S  H  I  R  M  Y  L  A  V  I  Y  T  Q  Q  V  V
24121 - TGCAGACATCATAACAAAAGAAGACTCTTGTTGTACTAGATATTGTGTAGCATCACGACC - 24180
      - C  R  H  H  N  K  R  R  L  L  L  Y  *  I  L  C  S  I  T  T
      -  A  D  I  I  T  K  E  D  S  C  C  T  R  Y  C  V  A  S  R  P
      -   Q  T  S  *  Q  K  K  T  L  V  V  L  D  I  V  *  H  H  D  H
24181 - ACACACACATGGAATGGAAACACCTGTCTTAAGATTATCATAAGATAGAGTACCCATATA - 24240
      - T  H  T  W  N  G  N  T  C  L  K  I  I  I  R  *  S  T  H  I
      -  H  T  H  G  M  E  T  P  V  L  R  L  S  *  D  R  V  P  I  Y
      -   T  H  M  E  W  K  H  L  S  *  D  Y  H  K  I  E  Y  P  Y  T
24241 - CATCACAGCTTCTACACCCGTTAAGGTAGTAGTTTTCTGACCACAATGTTTACACACCAC - 24300
      - H  H  S  F  Y  T  R  *  G  S  S  F  L  T  T  M  F  T  H  H
      -  I  T  A  S  T  P  V  K  V  V  V  F  *  P  Q  C  L  H  T  T
      -   S  Q  L  L  H  P  L  R  *  *  F  S  D  H  N  V  Y  T  P  H
24301 - ATTAAGAACTCGCTTTGCAGATTCCAAATTAGCATGCTGTAGAAGATGGGTCATAGTTTC - 24360
      - I  K  N  S  L  C  R  F  Q  I  S  M  L  *  K  M  G  H  S  F
      -  L  R  T  R  F  A  D  S  K  L  A  C  C  R  R  W  V  I  V  S
      -   *  E  L  A  L  Q  I  P  N  *  H  A  V  E  D  G  S  *  F  L
24361 - TCTGACATCACCAAGCTCGCCAACAGTTTTATTACTGTAAGCGAGTATGAGTGCACAAAA - 24420
      - S  D  I  T  K  L  A  N  S  F  I  T  V  S  E  Y  E  C  T  K
      -  L  T  S  P  S  S  P  T  V  L  L  L  *  A  S  M  S  A  Q  K
      -   *  H  H  Q  A  R  Q  Q  F  Y  Y  C  K  R  V  *  V  H  K  S
24421 - GTTAGCAGCATCACCAGCACGGGCTCTATAATAAGCCTCTTGAAGTGCTGGTGCATTGAA - 24480
      - V  S  S  I  T  S  T  G  S  I  I  S  L  L  K  C  W  C  I  E
      -  L  A  A  S  P  A  R  A  L  *  *  A  S  *  S  A  G  A  L  N
      -   *  Q  H  H  Q  H  G  L  Y  N  K  P  L  E  V  L  V  H  *  I
24481 - TTTGACTTCAAGCTGTTGAAGTGCTAATAAAACACTAGACAAATAACAATTGTTATCAGC - 24540
      - F  D  F  K  L  L  K  C  *  *  N  T  R  Q  I  T  I  V  I  S
      -  L  T  S  S  C  *  S  A  N  K  T  L  D  K  *  Q  L  L  S  A
      -   *  L  Q  A  V  E  V  L  I  K  H  *  T  N  N  N  C  Y  Q  P
```

Figure 17-HH

```
24541 - CCATTTAATTGAAGTTAAACCACCAACTTGAGGAAATTTCCATTTCTTTGTGTGGTTTAA - 24600
      - P  F  N  *  S  *  T  T  N  L  R  K  F  P  F  L  C  V  V  *
      -  H  L  I  E  V  K  P  P  T  *  G  N  F  H  F  F  V  W  F  K
      -   I  *  L  K  L  N  H  Q  L  E  E  I  S  I  S  L  C  G  L  K
24601 - AGCAGACATGTACCTACCAAGAAAACTCTCATCAAGAGTATGGTAGTACTCGAAAGCTTC - 24660
      - S  R  H  V  P  T  K  K  T  L  I  K  S  M  V  V  L  E  S  F
      -  A  D  M  Y  L  P  R  K  L  S  S  R  V  W  *  Y  S  K  A  S
      -   Q  T  C  T  Y  Q  E  N  S  H  Q  E  Y  G  S  T  R  K  L  H
24661 - ACTACGTAGTGTGTCATCACTAGGTAGTACAAAGAAAGTCTTACCCTCATGATTTACATG - 24720
      - T  T  *  C  V  I  T  R  *  Y  K  E  S  L  T  L  M  I  Y  M
      -  L  R  S  V  S  S  L  G  S  T  K  K  V  L  P  S  *  F  T  *
      -   Y  V  V  C  H  H  *  V  V  Q  R  K  S  Y  P  H  D  L  H  E
24721 - AGGTTTAATTTTTGTAACATCAGCACCATCCAAGTATGTTGGACCAAACTGCTGTCCATA - 24780
      - R  F  N  F  C  N  I  S  T  I  Q  V  C  W  T  K  L  L  S  I
      -  G  L  I  F  V  T  S  A  P  S  K  Y  V  G  P  N  C  C  P  Y
      -   V  *  F  L  *  H  Q  H  H  P  S  M  L  D  Q  T  A  V  H  M
24781 - TGTCATAGACATATCCACAAGCTGTGTGTGGAGATTAGTGTTGTCCACAGTTGTGAACAC - 24840
      - C  H  R  H  I  H  K  L  C  V  E  I  S  V  V  H  S  C  E  H
      -  V  I  D  I  S  T  S  C  V  W  R  L  V  L  S  T  V  V  N  T
      -   S  *  T  Y  P  Q  A  V  C  G  D  *  C  C  P  Q  L  *  T  L
24841 - TTTTATAGTCTTAACCTCCCGCAGGGATAAGAGACTCTTTAGTTTGTCAAGTGAAAGAAC - 24900
      - F  Y  S  L  N  L  P  Q  G  *  E  T  L  *  F  V  K  *  K  N
      -  F  I  V  L  T  S  R  R  D  K  R  L  F  S  L  S  S  E  R  T
      -   L  *  S  *  P  P  A  G  I  R  D  S  L  V  C  Q  V  K  E  P
24901 - CTCACCGTCAAGATGAAACTCGACGGGGCTCTCCAGAGTGTGGTACACAATTTTGTCACC - 24960
      - L  T  V  K  M  K  L  D  G  A  L  Q  S  V  V  H  N  F  V  T
      -  S  P  S  R  *  N  S  T  G  L  S  R  V  W  Y  T  I  L  S  P
      -   H  R  Q  D  E  T  R  R  G  S  P  E  C  G  T  Q  F  C  H  H
24961 - ACGCTTAAGAAATTCAACACCTAACTCTGTACGCTGTCCTGAATAGGACCAATCTCTGTA - 25020
      - T  L  K  K  F  N  T  *  L  C  T  L  S  *  I  G  P  I  S  V
      -  R  L  R  N  S  T  P  N  S  V  R  C  P  E  *  D  Q  S  L  *
      -   A  *  E  I  Q  H  L  T  L  Y  A  V  L  N  R  T  N  L  C  K
25021 - AGAGCCAGCCAAAGAAACTGTTTCTACAAAGTGCTCCTCAGATGTCTTTGATGACGAAGT - 25080
      - R  A  S  Q  R  N  C  F  Y  K  V  L  L  R  C  L  *  *  R  S
      -  E  P  A  K  E  T  V  S  T  K  C  S  S  D  V  F  D  D  E  V
      -   S  Q  P  K  K  L  F  L  Q  S  A  P  Q  M  S  L  M  T  K  *
25081 - GAGGTATCCATTATATGTAGTAACAGCATCTGGTGATGATACTGACACTACGGCAGGAGC - 25140
      - E  V  S  I  I  C  S  N  S  I  W  *  *  Y  *  H  Y  G  R  S
      -  R  Y  P  L  Y  V  V  T  A  S  G  D  D  T  D  T  T  A  G  A
      -   G  I  H  Y  M  *  *  Q  H  L  V  M  I  L  T  L  R  Q  E  L
25141 - TTTAAGAGAACGCATACAGCGCGCAGCCTCTTCAAGATTAAAACCATGTGTCACATAACC - 25200
      - F  K  R  T  H  T  A  R  S  L  F  K  I  K  T  M  C  H  I  T
      -  L  R  E  R  I  Q  R  A  A  S  S  R  L  K  P  C  V  T  *  P
      -   *  E  N  A  Y  S  A  Q  P  L  Q  D  *  N  H  V  S  H  N  Q
25201 - AATTGGCATTGTGACAAGCGGCTCATTTAGAGAGTTCAGCTTCGTAATAATAGAAGCTAC - 25260
      - N  W  H  C  D  K  R  L  I  *  R  V  Q  L  R  N  N  R  S  Y
      -  I  G  I  V  T  S  G  S  F  R  E  F  S  F  V  I  I  E  A  T
      -   L  A  L  *  Q  A  A  H  L  E  S  S  A  S  *  *  *  K  L  Q
```

Figure 17-II

```
25261 - AGGCTCTTTACTAGTATAAAAGAAGAATCGGACACCATAGTCAACGATGCCCTCTTGAAT - 25320
      - R  L  F  T  S  I  K  E  E  S  D  T  I  V  N  D  A  L  L  N
      -  G  S  L  L  V  *  K  K  N  R  T  P  *  S  T  M  P  S  *  I
      -   A  L  Y  *  Y  K  R  R  I  G  H  H  S  Q  R  C  P  L  E  F
25321 - TTTAATTCCTTTATACTTACGTTGGATGGTTGCCATTATGGCTCTAACATCCATGCATAT - 25380
      - F  N  S  F  I  L  T  L  D  G  C  H  Y  G  S  N  I  H  A  Y
      -  L  I  P  L  Y  L  R  W  M  V  A  I  M  A  L  T  S  M  H  I
      -   *  F  L  Y  T  Y  V  G  W  L  P  L  W  L  *  H  P  C  I  *
25381 - AGGCATTAATTTTCTTGTCTCTTCAGCATGAGCAAGCATTTCTCTCAAATTCCAGGATAC - 25440
      - R  H  *  F  S  C  L  F  S  M  S  K  H  F  S  Q  I  P  G  Y
      -  G  I  N  F  L  V  S  S  A  *  A  S  I  S  L  K  F  Q  D  T
      -   A  L  I  F  L  S  L  Q  H  E  Q  A  F  L  S  N  S  R  I  Q
25441 - AGTTCCTAGAATCTCTTCCTTAGCATTAGGTGCTTCTGAAGGTAGTACATAAAATGCAGA - 25500
      - S  S  *  N  L  F  L  S  I  R  C  F  *  R  *  Y  I  K  C  R
      -  V  P  R  I  S  S  L  A  L  G  A  S  E  G  S  T  *  N  A  D
      -   F  L  E  S  L  P  *  H  *  V  L  L  K  V  V  H  K  M  Q  I
25501 - TTTGCATTTCTTAAGAGCAGTCTTAGCTTCCTCAAGTGTATAACCAGCACATCCTTGTCC - 25560
      - F  A  F  L  K  S  S  L  S  F  L  K  C  I  T  S  T  S  L  S
      -  L  H  F  L  R  A  V  L  A  S  S  S  V  *  P  A  H  P  C  P
      -   C  I  S  *  E  Q  S  *  L  P  Q  V  Y  N  Q  H  I  L  V  Q
25561 - AGGGTACGTGGTTATATACTCATCAACTGGCACTTTCTTCAAAGCTCTTGAGAGCATCTC - 25620
      - R  V  R  G  Y  I  L  I  N  W  H  F  L  Q  S  S  *  E  H  L
      -  G  Y  V  V  I  Y  S  S  T  G  T  F  F  K  A  L  E  S  I  S
      -   G  T  W  L  Y  T  H  Q  L  A  L  S  S  K  L  L  R  A  S  Q
25621 - AGTAGTGCCACCAGCCTTTTTGGAGGGTATTACAACACAAGTGATATCACCACTAGTGAT - 25680
      - S  S  A  T  S  L  F  G  G  Y  Y  N  T  S  D  I  T  T  S  D
      -  V  V  P  P  A  F  L  E  G  I  T  T  Q  V  I  S  P  L  V  I
      -   *  C  H  Q  P  F  W  R  V  L  Q  H  K  *  Y  H  H  *  *  *
25681 - AACATCACCTACCATGTAAGGTGCATCCTTCTCAAGGAAAGACATATCTTCACCTCTAAG - 25740
      - N  I  T  Y  H  V  R  C  I  L  L  K  E  R  H  I  F  T  S  K
      -  T  S  P  T  M  *  G  A  S  F  S  R  K  D  I  S  S  P  L  S
      -   H  H  L  P  C  K  V  H  P  S  Q  G  K  T  Y  L  H  L  *  A
25741 - CATGTTCTGAGAATCATGGTAAAGCTTACCATTGATATCAGCAAACAAGAGTAACTTATT - 25800
      - H  V  L  R  I  M  V  K  L  T  I  D  I  S  K  Q  E  *  L  I
      -  M  F  *  E  S  W  *  S  L  P  L  I  S  A  N  K  S  N  L  L
      -   C  S  E  N  H  G  K  A  Y  H  *  Y  Q  Q  T  R  V  T  Y  W
25801 - GGTAAGAAACTTAGTTTCTTCCAGTGTTGTGGTAACCTCATCAATGCAGGCCTTAATTTT - 25860
      - G  K  K  L  S  F  F  Q  C  C  G  N  L  I  N  A  G  L  N  F
      -  V  R  N  L  V  S  S  S  V  V  V  T  S  S  M  Q  A  L  I  F
      -   *  E  T  *  F  L  P  V  L  W  *  P  H  Q  C  R  P  *  F  L
25861 - TGGCTTCACATCGACAGGCTTCTGTACGACAGATTTCTCCTCAGTTTTGGAATCTTCTGT - 25920
      - W  L  H  I  D  R  L  L  Y  D  R  F  L  L  S  F  G  I  F  C
      -  G  F  T  S  T  G  F  C  T  T  D  F  S  S  V  L  E  S  S  V
      -   A  S  H  R  Q  A  S  V  R  Q  I  S  P  Q  F  W  N  L  L  C
25921 - GTTTGGTGGCTCCTCTTGTTTAGGTGCTTCCACTCTAGGCTTCAGGTTATCAAGATAATC - 25980
      - V  W  W  L  L  L  F  R  C  F  H  S  R  L  Q  V  I  K  I  I
      -  F  G  G  S  S  C  L  G  A  S  T  L  G  F  R  L  S  R  *  S
      -   L  V  A  P  L  V  *  V  L  P  L  *  A  S  G  Y  Q  D  N  P
25981 - CATGACAACCTGCTCATAAAGAGCTTTGTCATTGACTGCAATATAAACCTGTGTACGAAC - 26040
      - H  D  N  L  L  I  K  S  F  V  I  D  C  N  I  N  L  C  T  N
      -  M  T  T  C  S  *  R  A  L  S  L  T  A  I  *  T  C  V  R  T
      -   *  Q  P  A  H  K  E  L  C  H  *  L  Q  Y  K  P  V  Y  E  P
```

Figure 17-JJ

```
26041 - CGTCTGCACGCACACTTGTAAAGACTGAAGTGGTTTAGCACCAAATATGCCTGCTGACAA - 26100
      - R  L  H  A  H  L  *  R  L  K  W  F  S  T  K  Y  A  C  *  Q
      -  V  C  T  H  T  C  K  D  *  S  G  L  A  P  N  M  P  A  D  N
      -   S  A  R  T  L  V  K  T  E  V  V  *  H  Q  I  C  L  L  T  T
26101 - CAATGGTGCAAGTAAGATGTCCTGTGAATTGAAATTTTCATATGCTGCCTTAAGAAGCTG - 26160
      - Q  W  C  K  *  D  V  L  *  I  E  I  F  I  C  C  L  K  K  L
      -  N  G  A  S  K  M  S  C  E  L  K  F  S  Y  A  A  L  R  S  W
      -   M  V  Q  V  R  C  P  V  N  *  N  F  H  M  L  P  *  E  A  G
26161 - GATGTCCTCACCTGCATTTAGGTTAGGTCCAACAACATGCAGACACTTCTTAGCAAGATT - 26220
      - D  V  L  T  C  I  *  V  R  S  N  N  M  Q  T  L  L  S  K  I
      -  M  S  S  P  A  F  R  L  G  P  T  T  C  R  H  F  L  A  R  L
      -   C  P  H  L  H  L  G  *  V  Q  Q  H  A  D  T  S  *  Q  D  Y
26221 - ATGTCCAGAAAGCAAACAAGACCCTCCTACTGTAAGAGGGCCATTTAGCTTAATGTAATC - 26280
      - M  S  R  K  Q  T  R  P  S  Y  C  K  R  A  I  *  L  N  V  I
      -  C  P  E  S  K  Q  D  P  P  T  V  R  G  P  F  S  L  M  *  S
      -   V  Q  K  A  N  K  T  L  L  L  *  E  G  H  L  A  *  C  N  H
26281 - ATCACTCTCCTTTTGCATGGCACCATTGGTTGCCTTGTTGAGTGCACCTGCTACACCACC - 26340
      - I  T  L  L  L  H  G  T  I  G  C  L  V  E  C  T  C  Y  T  T
      -  S  L  S  F  C  M  A  P  L  V  A  L  L  S  A  P  A  T  P  P
      -   H  S  P  F  A  W  H  H  W  L  P  C  *  V  H  L  L  H  H  H
26341 - ACCATGTTTCAGGTGTATGTTAGCAGCATTTACAATCACCATAGGATTAGCACTTTGTGC - 26400
      - T  M  F  Q  V  Y  V  S  S  I  Y  N  H  H  R  I  S  T  L  C
      -  P  C  F  R  C  M  L  A  A  F  T  I  T  I  G  L  A  L  C  A
      -   H  V  S  G  V  C  *  Q  H  L  Q  S  P  *  D  *  H  F  V  P
26401 - CTCCTTAACGATGTCAACACATTTAATGGCAACATTGTCAGTAAGTTTTAAATAACCAGT - 26460
      - L  L  N  D  V  N  T  F  N  G  N  I  V  S  K  F  *  I  T  S
      -  S  L  T  M  S  T  H  L  M  A  T  L  S  V  S  F  K  *  P  V
      -   P  *  R  C  Q  H  I  *  W  Q  H  C  Q  *  V  L  N  N  Q  *
26461 - AAACTGATTAACTGGTTCTTCAGGTGTAGGTTCTGGTTCTGGCTCAATCTCTGATTGCTC - 26520
      - K  L  I  N  W  F  F  R  C  R  F  W  F  W  L  N  L  *  L  L
      -  N  *  L  T  G  S  S  G  V  G  S  G  S  G  S  I  S  D  C  S
      -   T  D  *  L  V  L  Q  V  *  V  L  V  L  A  Q  S  L  I  A  Q
26521 - AGTAGTATCATCCAGCCAGTCTTCCTCTTCTTCTTCCTCAACTCGAACTGTTTCAGCTGA - 26580
      - S  S  I  I  Q  P  V  F  L  F  F  F  L  N  S  N  C  F  S  *
      -  V  V  S  S  S  Q  S  S  S  S  S  S  S  T  R  T  V  S  A  E
      -   *  Y  H  P  A  S  L  P  L  L  L  P  Q  L  E  L  F  Q  L  R
26581 - GGCACCAAATTCCAGAGGGAGACCTTGATAATCATCCTCTGTACCGTACTCATGTTCACA - 26640
      - G  T  K  F  Q  R  E  T  L  I  I  I  L  C  T  V  L  M  F  T
      -  A  P  N  S  R  G  R  P  *  *  S  S  S  V  P  Y  S  C  S  Q
      -   H  Q  I  P  E  G  D  L  D  N  H  P  L  Y  R  T  H  V  H  R
26641 - GGTTTCATCAATTTCTTCTTCCTCACACTCTGCATCGTCCTCTTCTTCCTCATCTGGAGG - 26700
      - G  F  I  N  F  F  F  L  T  L  C  I  V  L  F  F  L  I  W  R
      -  V  S  S  I  S  S  S  S  H  S  A  S  S  S  S  S  S  S  G  G
      -   F  H  Q  F  L  L  P  H  T  L  H  R  P  L  L  P  H  L  E  G
26701 - GTAAAAGGAACAATACATACGTGATGAAAAGTTTTCTTCACCAGCATCATCAAATAAGTA - 26760
      - V  K  G  T  I  H  T  *  *  K  V  F  F  T  S  I  I  K  *  V
      -  *  K  E  Q  Y  I  R  D  E  K  F  S  S  P  A  S  S  N  K  *
      -   K  R  N  N  T  Y  V  M  K  S  F  L  H  Q  H  H  Q  I  S  R
```

Figure 17-KK

```
26761 - GAATGTAGCTACACTCCACTCATCAAGATCAATACCCATGTTGGTAAGGAGATCAGAAAC - 26820
      - E  C  S  Y  T  P  L  I  K  I  N  T  H  V  G  K  E  I  R  N
      -  N  V  A  T  L  H  S  S  R  S  I  P  M  L  V  R  R  S  E  T
      -   M  *  L  H  S  T  H  Q  D  Q  Y  P  C  W  *  G  D  Q  K  L
26821 - TGGTTGTAAAGTCTTCACAACAGCCTCTGCTACAACACATGCAAACTCAGTAACTTCGGT - 26880
      - W  L  *  S  L  H  N  S  L  C  Y  N  T  C  K  L  S  N  F  G
      -  G  C  K  V  F  T  T  A  S  A  T  T  H  A  N  S  V  T  S  V
      -   V  V  K  S  S  Q  Q  P  L  L  Q  H  M  Q  T  Q  *  L  R  Y
26881 - ACCGGATTCAACAGTGTAGACAGAGCACTTTTCATTAAGCACTTTGTCAACACGTTCATC - 26940
      - T  G  F  N  S  V  D  R  A  L  F  I  K  H  F  V  N  T  F  I
      -  P  D  S  T  V  *  T  E  H  F  S  L  S  T  L  S  T  R  S  S
      -   R  I  Q  Q  C  R  Q  S  T  F  H  *  A  L  C  Q  H  V  H  Q
26941 - AAGCTCAAATGTGATTCTCACATTCTTGTAACCTTGAACTTCCCAAACAGTATCTTCTCC - 27000
      - K  L  K  C  D  S  H  I  L  V  T  L  N  F  P  N  S  I  F  S
      -  S  S  N  V  I  L  T  F  L  *  P  *  T  S  Q  T  V  S  S  P
      -   A  Q  M  *  F  S  H  S  C  N  L  E  L  P  K  Q  Y  L  L  Q
27001 - AAAGGTTACACCTTTAATTGGTGCACCCCCTTTTAAGCGAAAGACATTGTTTGTAGCCAG - 27060
      - K  G  Y  T  F  N  W  C  T  P  F  *  A  K  D  I  V  C  S  Q
      -  K  V  T  P  L  I  G  A  P  P  F  K  R  K  T  L  F  V  A  S
      -   R  L  H  L  *  L  V  H  P  L  L  S  E  R  H  C  L  *  P  V
27061 - TAAACCAGGAGACAATGCGCAGTATTGTTCTTTGTCCTTAATCTCTAAGAGCATGAGGCC - 27120
      - *  T  R  R  Q  C  A  V  L  F  F  V  L  N  L  *  E  H  E  A
      -  K  P  G  D  N  A  Q  Y  C  S  L  S  L  I  S  K  S  M  R  P
      -   N  Q  E  T  M  R  S  I  V  L  C  P  *  S  L  R  A  *  G  H
27121 - ATTTACACAGACTGGTGTGCCGACGATAGCTCCATTTGTGAAGCTATCAACGGGCGTCTC - 27180
      - I  Y  T  D  W  C  A  D  D  S  S  I  C  E  A  I  N  G  R  L
      -  F  T  Q  T  G  V  P  T  I  A  P  F  V  K  L  S  T  G  V  S
      -   L  H  R  L  V  C  R  R  *  L  H  L  *  S  Y  Q  R  A  S  R
27181 - GAGTGCTTCGAGTTCACCGTTCTTGAGAACAACCTCCTCAGAGGTAAGTACTGTGTCATG - 27240
      - E  C  F  E  F  T  V  L  E  N  N  L  L  R  G  K  Y  C  V  M
      -  S  A  S  S  S  P  F  L  R  T  T  S  S  E  V  S  T  V  S  C
      -   V  L  R  V  H  R  S  *  E  Q  P  P  Q  R  *  V  L  C  H  V
27241 - TGAATCACCTTCAAGAAAGGTTACTTCTTTTGGTGCCTTAAGAGGCATGAGTAGTTGCAG - 27300
      - *  I  T  F  K  K  G  Y  F  F  W  C  L  K  R  H  E  *  L  Q
      -  E  S  P  S  R  K  V  T  S  F  G  A  L  R  G  M  S  S  C  S
      -   N  H  L  Q  E  R  L  L  L  L  V  P  *  E  A  *  V  V  A  A
27301 - CTGCTCCTTGCCACGTATACACTGACGGTAAAGTCCCTTGCTTTGAGCGATGAAGACTTC - 27360
      - L  L  L  A  T  Y  T  L  T  V  K  S  L  A  L  S  D  E  D  F
      -  C  S  L  P  R  I  H  *  R  *  S  P  L  L  *  A  M  K  T  S
      -   A  P  C  H  V  Y  T  D  G  K  V  P  C  F  E  R  *  R  L  H
27361 - ACCTAAGTTGAGTGATCGCAACTTTGCGCCAGCGATAGTGACTTGATCAATGCACATTTC - 27420
      - T  *  V  E  *  S  Q  L  C  A  S  D  S  D  L  I  N  A  H  F
      -  P  K  L  S  D  R  N  F  A  P  A  I  V  T  *  S  M  H  I  S
      -   L  S  *  V  I  A  T  L  R  Q  R  *  *  L  D  Q  C  T  F  R
27421 - GAGTGCCTTGTTAACAACATCAATGAAGCATTTTACACAATCCTTGATGTTATCTGAAGC - 27480
      - E  C  L  V  N  N  I  N  E  A  F  Y  T  I  L  D  V  I  *  S
      -  S  A  L  L  T  T  S  M  K  H  F  T  Q  S  L  M  L  S  E  A
      -   V  P  C  *  Q  H  Q  *  S  I  L  H  N  P  *  C  Y  L  K  Q
27481 - AACCTGTATTTGACCCTTGACGATGTCAAAAACACCTGTAATGAGAAATTTGAGAATCTC - 27540
      - N  L  Y  L  T  L  D  D  V  K  N  T  C  N  E  K  F  E  N  L
      -  T  C  I  *  P  L  T  M  S  K  T  P  V  M  R  N  L  R  I  S
      -   P  V  F  D  P  *  R  C  Q  K  H  L  *  *  E  I  *  E  S  P
```

Figure 17-LL

```
27541 - CCAAGCATCCTTGAGAAATTCAACTCCTGCACTAAGTTTCGCCTCAATCCATTCAAAGAT - 27600
      - P  S  I  L  E  K  F  N  S  C  T  K  F  R  L  N  P  F  K  D
      -  Q  A  S  L  R  N  S  T  P  A  L  S  F  A  S  I  H  S  K  I
      -   K  H  P  *  E  I  Q  L  L  H  *  V  S  P  Q  S  I  Q  R  *
27601 - AGGCCTGAGTTTTTCAACAGTAGTGCCCAAAAGATTAGACAACCACTGAGAAGTCTGTTG - 27660
      - R  P  E  F  F  N  S  S  A  Q  K  I  R  Q  P  L  R  S  L  L
      -  G  L  S  F  S  T  V  V  P  K  R  L  D  N  H  *  E  V  C  C
      -   A  *  V  F  Q  Q  *  C  P  K  D  *  T  T  T  E  K  S  V  V
27661 - TACAAGACCACCAGTTACATATGCCATAATAATGACACTGTTGGTGAGCAGGTCTGAAGT - 27720
      - Y  K  T  T  S  Y  I  C  H  N  N  D  T  V  G  E  Q  V  *  S
      -  T  R  P  P  V  T  Y  A  I  I  M  T  L  L  V  S  R  S  E  V
      -   Q  D  H  Q  L  H  M  P  *  *  *  H  C  W  *  A  G  L  K  Y
27721 - ATAAACCATGGCGTCGACAAGACGTAATGACTGTTCAGAAATACCATCAAGTATGGTGAC - 27780
      - I  N  H  G  V  D  K  T  *  *  L  F  R  N  T  I  K  Y  G  D
      -  *  T  M  A  S  T  R  R  N  D  C  S  E  I  P  S  S  M  V  T
      -   K  P  W  R  R  Q  D  V  M  T  V  Q  K  Y  H  Q  V  W  *  Q
27781 - AGCTGCTCTTTGCAAATCAGGAATTGAGTGGTTTGCTGCATCAAGTGTGCGCGCAAAAAT - 27840
      - S  C  S  L  Q  I  R  N  *  V  V  C  C  I  K  C  A  R  K  N
      -  A  A  L  C  K  S  G  I  E  W  F  A  A  S  S  V  R  A  K  I
      -   L  L  F  A  N  Q  E  L  S  G  L  L  H  Q  V  C  A  Q  K  L
27841 - TGATCTGATAACACCAGCAGCCTGTGAGGGAAAACCACACAGTGGTGTTAAAACTGATCT - 27900
      - *  S  D  N  T  S  S  L  *  G  K  T  T  Q  W  C  *  N  *  S
      -  D  L  I  T  P  A  A  C  E  G  K  P  H  S  G  V  K  T  D  L
      -   I  *  *  H  Q  Q  P  V  R  E  N  H  T  V  V  L  K  L  I  S
27901 - CTGTTGTCCAATGTTCCAAGCACCTTTTACGGGCTTTCCCTTGGTAACTTTATAGTTACC - 27960
      - L  L  S  N  V  P  S  T  F  Y  G  L  S  L  G  N  F  I  V  T
      -  C  C  P  M  F  Q  A  P  F  T  G  F  P  L  V  T  L  *  L  P
      -   V  V  Q  C  S  K  H  L  L  R  A  F  P  W  *  L  Y  S  Y  R
27961 - GCAGGACTCAACAATGGTTTTGAAAGACTTGTAATCAAGACTCTTTATAGTGTCAATAAA - 28020
      - A  G  L  N  N  G  F  E  R  L  V  I  K  T  L  Y  S  V  N  K
      -  Q  D  S  T  M  V  L  K  D  L  *  S  R  L  F  I  V  S  I  K
      -   R  T  Q  Q  W  F  *  K  T  C  N  Q  D  S  L  *  C  Q  *  R
28021 - GGCACTTGTAGAAGCAGAGAAAGATGCCAAAATGATGGCAACCTCTTCATTCAAATGAAA - 28080
      - G  T  C  R  S  R  E  R  C  Q  N  D  G  N  L  F  I  Q  M  K
      -  A  L  V  E  A  E  K  D  A  K  M  M  A  T  S  S  F  K  *  K
      -   H  L  *  K  Q  R  K  M  P  K  *  W  Q  P  L  H  S  N  E  N
28081 - ATCGCCAACAATGTTAATGTTAACACGTTCACGACTCAGTATCTCAAGGAGATCCTCATT - 28140
      - I  A  N  N  V  N  V  N  T  F  T  T  Q  Y  L  K  E  I  L  I
      -  S  P  T  M  L  M  L  T  R  S  R  L  S  I  S  R  R  S  S  F
      -   R  Q  Q  C  *  C  *  H  V  H  D  S  V  S  Q  G  D  P  H  S
28141 - CAAGGTCTCCACATTGTCACCAGTAATGCCAGTATGGCCTGAGCCAATATCAGCACTAGC - 28200
      - Q  G  L  H  I  V  T  S  N  A  S  M  A  *  A  N  I  S  T  S
      -  K  V  S  T  L  S  P  V  M  P  V  W  P  E  P  I  S  A  L  A
      -   R  S  P  H  C  H  Q  *  C  Q  Y  G  L  S  Q  Y  Q  H  *  H
28201 - ACGAGGAACCCAGTAGGCACGCTTATTATAGCAGCCAACATAGGCAAACACACAGCCTCC - 28260
      - T  R  N  P  V  G  T  L  I  I  A  A  N  I  G  K  H  T  A  S
      -  R  G  T  Q  *  A  R  L  L  *  Q  P  T  *  A  N  T  Q  P  P
      -   E  E  P  S  R  H  A  Y  Y  S  S  Q  H  R  Q  T  H  S  L  Q
```

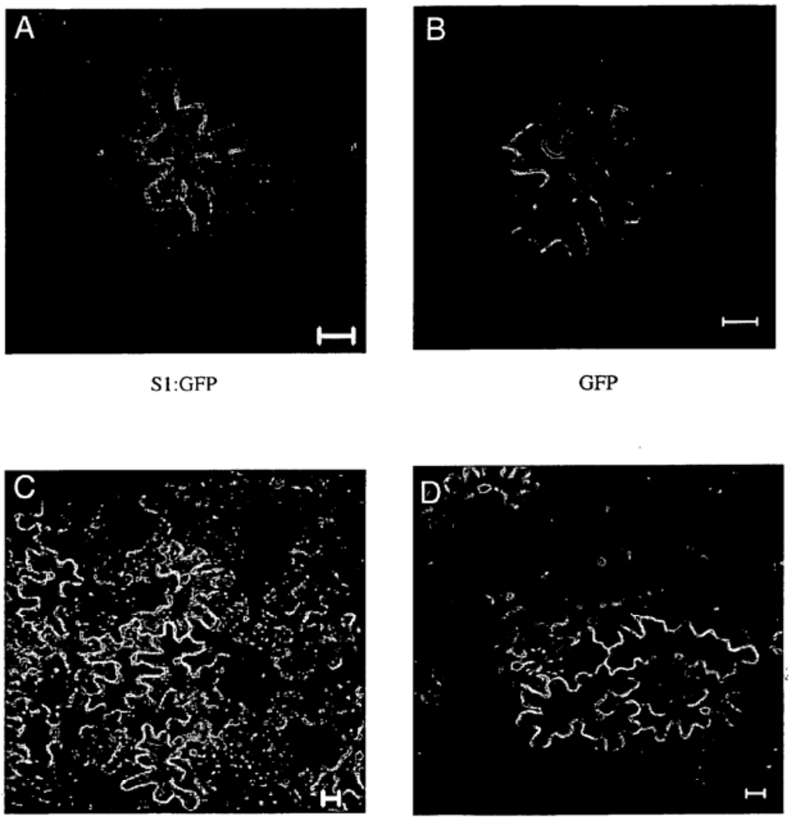
Figure 17-MM

```
28261 - AAAACATCTAGTCCTACCTCCCTTGCGGAGTCGAGTTTCAATGTTTGAGTGGTTGTGATA - 28320
      - K  T  S  S  P  T  S  L  A  E  S  S  F  N  V  *  V  V  V  I
      -  K  H  L  V  L  P  P  L  R  S  R  V  S  M  F  E  W  L  *  *
      -   N  I  *  S  Y  L  P  C  G  V  E  F  Q  C  L  S  G  C  D  N
28321 - ATCTGCAACACTATGCTCAGGTCCAATCTCTGGGTCTTGACAGGCAGGACATGGCATTTT - 28380
      - I  C  N  T  M  L  R  S  N  L  W  V  L  T  G  R  T  W  H  F
      -  S  A  T  L  C  S  G  P  I  S  G  S  *  Q  A  G  H  G  I  F
      -   L  Q  H  Y  A  Q  V  Q  S  L  G  L  D  R  Q  D  M  A  F  S
28381 - CACTACAGCATTAGTAGGTAGGTACCCACATGTAGTAGGTCCTTCAATAACTAAATTTTC - 28440
      - H  Y  S  I  S  R  *  V  P  T  C  S  R  S  F  N  N  *  I  F
      -  T  T  A  L  V  G  R  Y  P  H  V  V  G  P  S  I  T  K  F  S
      -   L  Q  H  *  *  V  G  T  H  M  *  *  V  L  Q  *  L  N  F  Q
28441 - AGTGCCACAATGTTCACAAGTGGCTTTCAGAAAGTCGCACGTCTGCCATGAAACTTCATC - 28500
      - S  A  T  M  F  T  S  G  F  Q  K  V  A  R  L  P  *  N  F  I
      -  V  P  Q  C  S  Q  V  A  F  R  K  S  H  V  C  H  E  T  S  S
      -   C  H  N  V  H  K  W  L  S  E  S  R  T  S  A  M  K  L  H  R
28501 - GCAATGATTACATTTCATCAAGGTAGACAAGTGCATATTGTTACACTCCTGTGGAGATGC - 28560
      - A  M  I  T  F  H  Q  G  R  Q  V  H  I  V  T  L  L  W  R  C
      -  Q  *  L  H  F  I  K  V  D  K  C  I  L  L  H  S  C  G  D  A
      -   N  D  Y  I  S  S  R  *  T  S  A  Y  C  Y  T  P  V  E  M  Q
28561 - AACAGGGTACACAGAGCGTATACGCCCCATGAAACCCTCAGTCTTTTTCTTTTCAACACG - 28620
      - N  R  V  H  R  A  Y  T  P  H  E  T  L  S  L  F  L  F  N  T
      -  T  G  Y  T  E  R  I  R  P  M  K  P  S  V  F  F  F  S  T  R
      -   Q  G  T  Q  S  V  Y  A  P  *  N  P  Q  S  F  S  F  Q  H  V
28621 - TGGTTGAATGACTTTGACTTTTGAGTTAAGAGGAAACACAAACTTTGGGCATTCCCCTTT - 28680
      - W  L  N  D  F  D  F  *  V  K  R  K  H  K  L  W  A  F  P  F
      -  G  *  M  T  L  T  F  E  L  R  G  N  T  N  F  G  H  S  P  L
      -   V  E  *  L  *  L  L  S  *  E  E  T  Q  T  L  G  I  P  L  *
28681 - GAAAGTGTCAAATTTCTTGGCACTCTTAATTTCGAAGGGTGTCTGGTGCTCGTAGCTCTT - 28740
      - E  S  V  K  F  L  G  T  L  N  F  E  G  C  L  V  L  V  A  L
      -  K  V  S  N  F  L  A  L  L  I  S  K  G  V  W  C  S  *  L  L
      -   K  C  Q  I  S  W  H  S  *  F  R  R  V  S  G  A  R  S  S  Y
28741 - ATCAGAGCGCTCAGTGAACCAGGCAATTTCATGCTCATGGTCACGGCAGCAGTAGACACC - 28800
      - I  R  A  L  S  E  P  G  N  F  M  L  M  V  T  A  A  V  D  T
      -  S  E  R  S  V  N  Q  A  I  S  C  S  W  S  R  Q  Q  *  T  P
      -   Q  S  A  Q  *  T  R  Q  F  H  A  H  G  H  G  S  S  R  H  L
28801 - TCTCTTCGACTCGATGTAATCAAGTTGTTCGGAAAGAGTGCACATTGACTTGCCCGCGCG - 28860
      - S  L  R  L  D  V  I  K  L  F  G  K  S  A  H  *  L  A  R  A
      -  L  F  D  S  M  *  S  S  C  S  E  R  V  H  I  D  L  P  A  R
      -   S  S  T  R  C  N  Q  V  V  R  K  E  C  T  L  T  C  P  R  V
28861 - TGCGAGAAAATCTTTGATGCAATCAAGAGGGTACCCATCTGGGCCACAGAAATTGTTGTC - 28920
      - C  E  K  I  F  D  A  I  K  R  V  P  I  W  A  T  E  I  V  V
      -  A  R  K  S  L  M  Q  S  R  G  Y  P  S  G  P  Q  K  L  L  S
      -   R  E  N  L  *  C  N  Q  E  G  T  H  L  G  H  R  N  C  C  R
28921 - GACATAGCGAGTGACTGCACCTCCATTGAGCTCACGAGTGAGTTCACGGAGTGCACCACT - 28980
      - D  I  A  S  D  C  T  S  I  E  L  T  S  E  F  T  E  C  T  T
      -  T  *  R  V  T  A  P  P  L  S  S  R  V  S  S  R  S  A  P  L
      -   H  S  E  *  L  H  L  H  *  A  H  E  *  V  H  G  V  H  H  C
28981 - GCCATGCTTAGTGTTCCAGTTTTGTTCATAATCTTCAATGGGATCAGTGCCAAGCTCGTC - 29040
      - A  M  L  S  V  P  V  L  F  I  I  F  N  G  I  S  A  K  L  V
      -  P  C  L  V  F  Q  F  C  S  *  S  S  M  G  S  V  P  S  S  S
      -   H  A  *  C  S  S  F  V  H  N  L  Q  W  D  Q  C  Q  A  R  H
```

Figure 17-NN

```
29041 - ACCTAAGTCATAAGACTTTAGATCGATGCCATAGCTATGACCACCGGCTCCCTTATTACC - 29100
      - T  *  V  I  R  L  *  I  D  A  I  A  M  T  T  G  S  L  I  T
      -  P  K  S  *  D  F  R  S  M  P  *  L  *  P  P  A  P  L  L  P
      -   L  S  H  K  T  L  D  R  C  H  S  Y  D  H  R  L  P  Y  Y  R
29101 - GTTCTTACGAAGAAGAACATTGCGGTATGCAATTGGGGTTTCGCCCACATGTGGCACGAG - 29160
      - V  L  T  K  K  N  I  A  V  C  N  W  G  F  A  H  M  W  H  E
      -  F  L  R  R  R  T  L  R  Y  A  I  G  V  S  P  T  C  G  T  S
      -   S  Y  E  E  E  H  C  G  M  Q  L  G  F  R  P  H  V  A  R  V
29161 - TACTCCCAGTGTTATACCGCTACGACCGTACTGAATGCCGTCCATTTCTGCAACCAGCTC - 29220
      - Y  S  Q  C  Y  T  A  T  T  V  L  N  A  V  H  F  C  N  Q  L
      -  T  P  S  V  I  P  L  R  P  Y  *  M  P  S  I  S  A  T  S  S
      -   L  P  V  L  Y  R  Y  D  R  T  E  C  R  P  F  L  Q  P  A  Q
29221 - AACGACCTTGTGGCCGTGATTGGTGCTTAAGGCATCAGAACGTTTAATGAACACATAGGG - 29280
      - N  D  L  V  A  V  I  G  A  *  G  I  R  T  F  N  E  H  I  G
      -  T  T  L  W  P  *  L  V  L  K  A  S  E  R  L  M  N  T  *  G
      -   R  P  C  G  R  D  W  C  L  R  H  Q  N  V  *  *  T  H  R  A
29281 - CTGTTCAAGCTGGGGCAGTACGCCTTTTTCCAGCTCTACTAGACCACAAGTGCCATTTTT - 29340
      - L  F  K  L  G  Q  Y  A  F  F  Q  L  Y  *  T  T  S  A  I  F
      -  C  S  S  W  G  S  T  P  F  S  S  S  T  R  P  Q  V  P  F  L
      -   V  Q  A  G  A  V  R  L  F  P  A  L  L  D  H  K  C  H  F  *
29341 - GAGGTGTTCACGTGCCTCCGATAGGGCCTCTTCCACAGAGTCCCCGAAGCCACGCACTAG - 29400
      - E  V  F  T  C  L  R  *  G  L  F  H  R  V  P  E  A  T  H  *
      -  R  C  S  R  A  S  D  R  A  S  S  T  E  S  P  K  P  R  T  S
      -   G  V  H  V  P  P  I  G  P  L  P  Q  S  P  R  S  H  A  L  A
29401 - CACGTCTCTAACCTGAAGGACAGGCAAACTGAGTTGGACGTGTGTTTTCTCGTTGACACC - 29460
      - H  V  S  N  L  K  D  R  Q  T  E  L  D  V  C  F  L  V  D  T
      -  T  S  L  T  *  R  T  G  K  L  S  W  T  C  V  F  S  L  T  P
      -   R  L  *  P  E  G  Q  A  N  *  V  G  R  V  F  S  R  *  H  Q
29461 - AAGAACAAGGCTCTCCATCTTACCTTTCGGTCACACCCGGACGAAACCTAGGTATGCTGA - 29520
      - K  N  K  A  L  H  L  T  F  R  S  H  P  D  E  T  *  V  C  *
      -  R  T  R  L  S  I  L  P  F  G  H  T  R  T  K  P  R  Y  A  D
      -   E  Q  G  S  P  S  Y  L  S  V  T  P  G  R  N  L  G  M  L  M
29521 - TGATCGACTGCAACACGGACGAAACCGTAAGCAGTCTGCAGAAGAGGGACGAGTTACTCG - 29580
      - *  S  T  A  T  R  T  K  P  *  A  V  C  R  R  G  T  S  Y  S
      -  D  R  L  Q  H  G  R  N  R  K  Q  S  A  E  E  G  R  V  T  R
      -   I  D  C  N  T  D  E  T  V  S  S  L  Q  K  R  D  E  L  L  V
29581 - TTTCTTGTCAACGACAGTAAAATTTATTATTGTTTATACTGCGTAGGTGCACTAGGCATG - 29640
      - F  L  V  N  D  S  K  I  Y  Y  C  L  Y  C  V  G  A  L  G  M
      -  F  L  S  T  T  V  K  F  I  I  V  Y  T  A  *  V  H  *  A  C
      -   S  C  Q  R  Q  *  N  L  L  L  F  I  L  R  R  C  T  R  H  A
29641 - CAGCCGAGCGACAGCTACACAGATTTTAAAGTTCGTTTAGAGAACAGATCTACAAGAGAT - 29700
      - Q  P  S  D  S  Y  T  D  F  K  V  R  L  E  N  R  S  T  R  D
      -  S  R  A  T  A  T  Q  I  L  K  F  V  *  R  T  D  L  Q  E  I
      -   A  E  R  Q  L  H  R  F  *  S  S  F  R  E  Q  I  Y  K  R  S
29701 - CGAGGTTGGTTGGCTTTTCCTGGGTAGGTAAAAACCTAATAT - 29742
      - R  G  W  L  A  F  P  G  *  V  K  T  *  Y  X
      -  E  V  G  W  L  F  L  G  R  *  K  P  N  X
      -   R  L  V  G  F  S  W  V  G  K  N  L  I  X
```

Figure 18



S1:GFP

GFP

S1:GFP

GFP

Figure 19-A

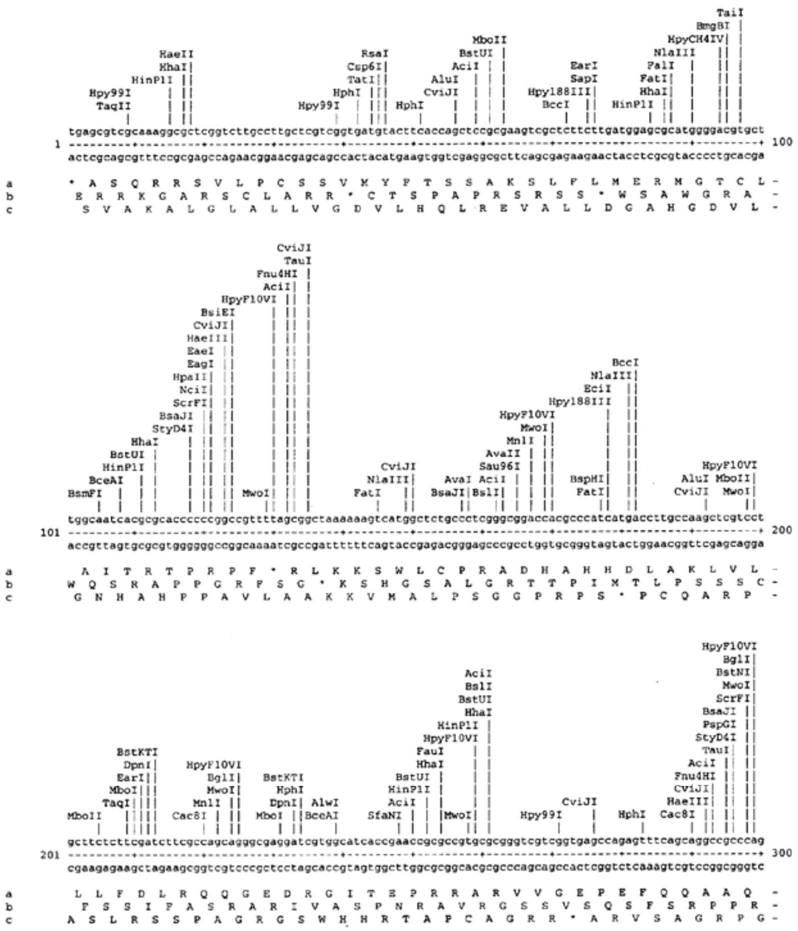

TaiI
BmgBI
HpyCH4IV
MboII
NlaIII
HaeII
RsaI
BstUI
KhaI
Csp6I
AciI
EarI
FalI
HinP1I
TatI
AluI
SapI
FatI
Hpy99I
HphI
CviJI
Hpy188III
HhaI
TaqII
Hpy99I
HphI
BccI
HinP1I
tgagcgtcgcaaaggcgctcggtcttgccttgctcgtcggtgatgtacttcaccagctccgcgaagtcgctcttcttgatggagcgcatggggacgtgct
1
100
actcgcagcgtttccgcgagccagaacggaacgagcagccactacatgaagtggtcgaggcgcttcagcgagaagaactacctcgcgtacccctgcacga
a * A S Q R R S V L P C S S V M Y F T S S A K S L F L M E R M G T C L -
b E R R K G A R S C L A R R * C T S P A P R S R S S * W S A W G R A -
c S V A K A L G L A L L V G D V L H Q L R E V A L L D G A H G D V L -
CviJI
TauI
Fnu4HI
AciI
HpyF10VI
BsiEI
CviJI
HaeIII
EaeI
EagI
HpaII
NciI
ScrFI
BccI
NlaIII
EciI
Hpy188III
BsaJI
StyD4I
HpyF10VI
MwoI
HhaI
MnlI
BstUI
AvaII
HinP1I
CviJI
Sau96I
HpyF10VI
BceAI
NlaIII
AvaI
AciI
BspHI
AluI
MboII
BsmFI
MwoI
FatI
BsaJI
BslI
FatI
CviJI
MwoI
tggcaatcacgcgcacccccggccgttttagcggctaaaaagtcatggctctgccctcgggcggaccacgcccatcatgaccttgccaagctcgtcct
101
200
accgttagtgcgcgtgggggccggcaaaatcgccgatttttcagtaccgagacgggagcccgcctggtgcgggtagtactggaacggttcgagcagga
a A I T R T P R P F * R L K K S W L C P R A D H A H H D L A K L V L -
b W Q S R A P P G R F S G * K S H G S A L G R T T P I M T L P S S S C -
c G N H A H P P A V L A A K K V M A L P S G G P R P S * P C Q A R P -
HpyF10VI
BglI
BstNI
MwoI
ScrFI
BsaJI
PspGI
StyD4I
TauI
AciI
Fnu4HI
CviJI
HaeIII
Cac8I
AciI
BslI
BstUI
HhaI
HinP1I
HpyF10VI
FauI
HhaI
BstUI
HinP1I
AciI
SfaNI
MwoI
BstKTI
DpnI
EarI
MboI
TaqI
MboII
HpyF10VI
BglI
MwoI
MnlI
Cac8I
BstKTI
HphI
DpnI
MboI
AlwI
BceAI
Hpy99I
CviJI
HphI
gcttctcttcgatcttcgccagcagggcgaggatcgtggcatcaccgaaccgcgccgtgcgcgggtcgtcggtgagccagagtttcagcaggccgcccag
201
300
cgaagagaagctagaagcggtcgtcccgctcctagcaccgtagtggcttggcgcggcacgcgcccagcagccactcggtctcaaagtcgtccggcgggtc
a L L F D L R Q Q G E D R G I T E P R R A R V V G E P E F Q Q A A Q -
b F S S I F A S R A R I V A S P N R A V R G S S V S Q S F S R P P R -
c A S L R S S P A G R G S W H H R T A P C A G R R * A R V S A G R P G -

Figure 19-B

```
                                               BsiHKAI
                                              Bsp1286I
                                               TaiI  |
             HpyF10VI                       BmgBI |  |
                MwoI|                   HpyCH4IV| |  |
              SfaNI||                   AciI   || |  |                                       Cac8I
            BstNI |||                  BstUI   || |  |                                     CviJI |
            ScrFI |||                  BslI|   || |  |                                    HaeIII |
          BsaJI | |||                Cac8I||   || |  |                                   Hpy99I| |
          PspGI | |||               AluI |||   || |  |                                    EaeI|| |
         StyD4I | |||              CviJI |||   || |  |                                BspMI  ||| |
         CviJI| | |||            Cac8I | |||   || |  |                              CviJI |  ||| |
        HaeIII| | |||          CviJI | | |||   || |  |                             HaeIII |  ||| |
          TauI| | |||         HaeIII | | |||   || |  |                             EaeI | |  ||| |
       Sau96I|| | |||        Cac8I | | | |||   || |  |                           BstNI| | |  ||| |
      Fnu4HI||| | |||       Sau96I | | | |||   || |  |                           ScrFI| | |  ||| |
    HpyF10VI||| | |||       AciI | | | | |||   || |  |                         BsaJI || | |  ||| |
       AciI|||| | ||| HpyF10VI | | | | | |||   || |  |        Hpy99I           PspGI || | |  ||| |      BceAI
       BglI|||| | |||    MwoI| | | | | | |||   || |  |       BsaHI |          StyD4I || | |  ||| |     CviJI|
       MwoI|||| | |||FauI   || | | | | | |||   || |  |  Hpy8I    | |  HgaI    CviJI| || | |  ||| |    HaeIII|
          ||||| | |||   |   || | | | | | |||   || |  |      |    | |     |        || || | |  ||| |         ||
          gcggcccaggtcgccattgatgcgggccagctcgcggacgtgctcatagtccacgacgcccgtgattttgtagccctggccgacggccagcaggtaggcc
      301 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 400
          cgccgggtccagcggtaactacgcccggtcgagcgcctgcacgagtatcaggtgctgcgggcactaaaacatcgggaccggctgccggtcgtccatccgg

a         A  A  Q  V  A  I  D  A  G  Q  L  A  D  V  L  I  V  H  D  A  R  D  F  V  A  L  A  D  G  Q  Q  V  G  R -
b          R  P  R  S  P  L  M  R  A  S  S  R  T  C  S  *  S  T  T  P  V  I  L  *  P  W  P  T  A  S  R  *  A   -
c           G  P  G  R  H  *  C  G  P  A  R  G  R  A  H  S  P  R  R  P  *  F  C  S  P  G  R  R  P  A  G  R  P  -


                               TauI
                             AciI |
                           Fnu4HI |
                         HpyF10VI |
                            MwoI| |
                            TauI| |
                          AciI || |
                        Fnu4HI || |
                         TauI| || |
                       AciI || || |
                      BsiEI || || |
                     Fnu4HI || || |
                     CviJI| || || |
                    HaeIII| || || |
                   Cac8I || || || |
                    EaeI || || || |
                    EagI || || || |                                                                       FokI
                    NaeI || || || |                                                                    CviJI |
                  HpaII| || || || |                                       BbvI                     TspDTI  | |
                 BsrFI|| || || || |                                   Hpy8I  |                  BstNI   |  | |
                NgoMIV|| || || || |                   Hpy188III       RsaI|  |        Fnu4HI    ScrFI   |  | |
                NlaIII|| || || || |                  EarI     |      Csp6I||  |        CviJI|  PspGI |   |  | |
              FatI   ||| || || || |    MboII    MnlI SapI     |      TatI|||  |         TseI| StyD4I |   |  | |
           CviJI |   ||| || || || |        |       |    |     |        ||||  |            ||      | |   |  | |
               | |   ||| || || || |        |       |    |     |        ||||  |            ||      | |   |  | |
          gacaggctcatgccggccgccgccgccttttcctcaatcgctcttcgttcgtctggaaggcagtacaccttgataggtgggctgcccttcctggttggct
      401 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 500
          ctgtccgagtacggccggcggcggcggaaaaggagttagcgagaagcaagcagaccttccgtcatgtggaactatccacccgacgggaaggaccaaccga

a           Q  A  H  A  G  R  R  R  L  F  L  N  R  S  S  F  V  W  K  A  V  H  L  D  R  W  A  A  L  P  G  W  L   -
b         D  R  L  M  P  A  A  A  A  F  S  S  I  A  L  R  S  S  G  R  Q  Y  T  L  I  G  G  L  P  F  L  V  G  L -
c          T  G  S  C  R  P  P  P  P  F  P  Q  S  L  F  V  R  L  E  G  S  T  P  *  *  V  G  C  P  S  W  L  A    -
```

Figure 19-C

```
                                                           HpyF10VI
                                                              MwoI|
                                                           CviJI ||
                                                         Cac8I | ||
                                              AciI     CviJI | | ||
                                           Cac8I |    HaeIII | | ||
                                            NaeI |   Cac8I | | | ||                         BstNI
                                          HpaII| |    EaeI | | | ||                         ScrFI
                                         BsrFI|| |    NaeI | | | ||                       PspGI |
                                        NgoMIV|| |  HpaII| | | | ||                      StyD4I |
                                         SgrAI|| | BsrFI|| | | | ||      HinfI           AciI | |
               BstF5I   Cac8I          MnlI  ||| | CviJI|| | | | ||       TfiI       BsiHKAI| | |
               CviJI|AciI   |     MaeIII  |  ||| |NgoMIV|| | | | ||    MnlI  |      Bsp1286I| | |
                   ||   |   |          |  |  ||| |     ||| | | | ||       |  |             || | |
        tggtttcatcagccatccgcttgccctcatctgttacgccggcggtagccggccagcctcgcagagcaggattcccgttgagcaccgccaggtgcgaata
    501 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 600
        accaaagtagtcggtaggcgaacgggagtagacaatgcggccgccatcggccggtcggagcgtctcgtcctaagggcaactcgtggcggtccacgcttat

a        G  F  I  S  H  P  L  A  L  I  C  Y  A  G  G  S  R  P  A  S  Q  S  R  I  P  V  E  H  R  Q  V  R  I   -
b         V  S  S  A  I  R  L  P  S  S  V  T  P  A  V  A  G  Q  P  R  R  A  G  F  P  L  S  T  A  R  C  E  *  -
c       W  F  H  Q  P  S  A  C  P  H  L  L  R  R  R  *  P  A  S  L  A  E  Q  D  S  R  *  A  P  P  G  A  N  K -

                                        CviJI
                                       HaeIII
                                        HphI|
                                     Sau96I||
                                  FauI    |||
                                 AciI|    |||                        BciVI
                                 BslI|    |||                      BsaHI |
                                BstUI|    |||                  CviJI   | |
                                BslI||    |||               HpaII  |   | |
                              Cac8I|||    |||                NciI  |   | |
                   BsmFI    BsrBI ||||    |||               ScrFI  |   | |
               TspRI   |   AciI | ||||    |||            StyD4I |  |   | |
             PpiI  |   |  FauI| | ||||    |||         BceAI   | |  |   | |        BsaJI      Hpy8I
      HpyCH4III |  |   | MboII| | ||||    |||PpiI     MmeI|   | |  |   | |  HgaI   StyI      AccI|
              | |  |   |     || | ||||    |||   |        ||   | |  |   | |     |      |         ||
        agggacagtgaagaaggaacacccgctcgcgggtgggcctacttcacctatcctgcccggctgacgccgttggatacaccaaggaaagtctacacgaacc
    601 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 700
        tccctgtcacttcttccttgtgggcgagcgcccacccggatgaagtggataggacgggccgactgcggcaacctatgtggttcctttcagatgtgcttgg

a       R  D  S  E  E  G  T  P  A  R  G  W  A  Y  F  T  Y  P  A  R  L  T  P  L  D  T  P  R  K  V  Y  T  N  P -
b        G  T  V  K  K  E  H  P  L  A  G  G  P  T  S  P  I  L  P  G  *  R  R  W  I  H  Q  G  K  S  T  R  T   -
c         G  Q  *  R  R  N  T  R  S  R  V  G  L  L  H  L  S  C  P  A  D  A  V  G  Y  T  K  E  S  L  H  E  P  -

                                                                                         AciI
                                                                                       MspA1I      HaeII
                                                                                     Fnu4HI |      HhaI|
                                                                             BslI  HpyCH4V| |     BbvI||
                                BccI     BstF5I   FokI                      BslI|     TseI| |  HinP1I|||
                                   |          |      |                         ||        || |       ||||
        ctttggcaaaatcctgtatatcgtgcgaaaaaggatggatataccgaaaaaatcgctataatgaccccgaagcagggttatgcagcggaaaagcgccacg
    701 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 800
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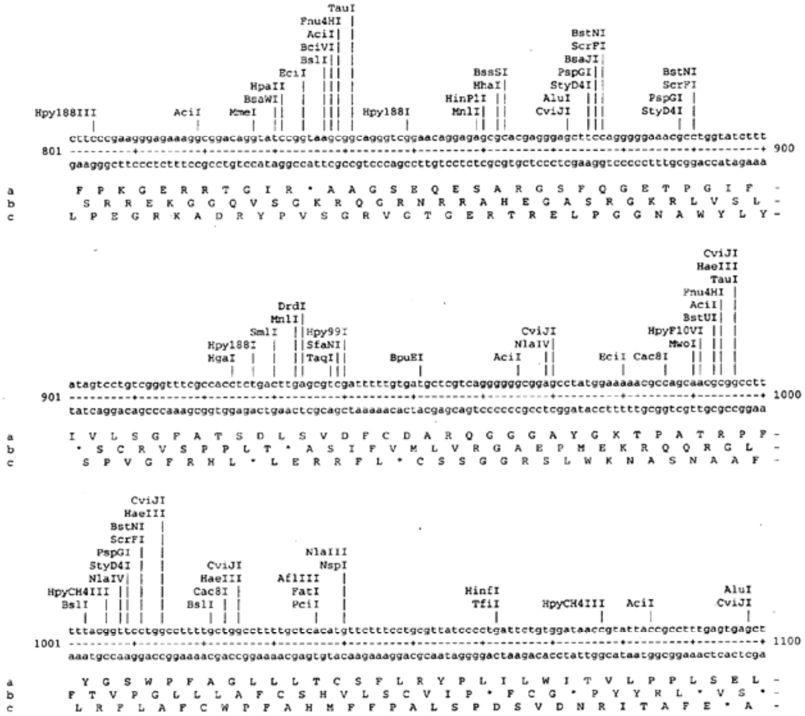
a         L  A  K  S  C  I  S  C  E  K  G  W  I  Y  R  K  N  R  Y  N  D  P  E  A  G  L  C  S  G  K  A  P  R  -
b       L  W  Q  N  P  V  Y  R  A  K  K  D  G  Y  T  E  K  I  A  I  M  T  P  K  Q  G  Y  A  A  E  K  R  H  A -
c        F  G  K  I  L  Y  I  V  R  K  R  M  D  I  P  K  K  S  L  *  *  P  R  S  R  V  M  Q  R  K  S  A  T   -
```

Figure 19-D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AciI
BciVI
BslI
EciI
HpaII
BsaWI
Hpy188III
AciI
MmeI
Hpy188I
BssSI
HhaI
HinP1I
MnlI
BstNI
ScrFI
BsaJI
PspGI
StyD4I
AluI
CviJI
BstNI
ScrFI
PspGI
StyD4I
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900
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a F P K G E R R T G I R * A A G S E Q E S A R G S F Q G E T P G I F -
b S R R E K G G Q V S G K R Q G R N R R A H E G A S R G K R L V S L -
c L P E G R K A D R Y P V S G R V G T G E R T R E L P G G N A W Y L Y -
CviJI
HaeIII
TauI
Fnu4HI
AciI
BstUI
HpyF10VI
MwoI
DrdI
MnlI
SmlI
Hpy99I
SfaNI
Hpy188I
TaqI
HgaI
BpuEI
CviJI
NlaIV
AciI
EciI
Cac8I
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901
1000
tatcaggacagcccaaagcggtggagactgaactcgcagctaaaaacactacgagcagtccccccgcctcggatacctttttgcggtcgttgcgccggaa
a I V L S G F A T S D L S V D F C D A R Q G G G A Y G K T P A T R P F -
b * S C R V S P P L T * A S I F V M L V R G A E P M E K R Q Q R G L -
c S P V G F R H L * L E R R F L * C S S G G R S L W K N A S N A A F -
CviJI
HaeIII
BstNI
ScrFI
PspGI
StyD4I
NlaIV
HpyCH4III
BslI
CviJI
HaeIII
Cac8I
BslI
NlaIII
NspI
AflIII
FatI
PciI
HinfI
TfiI
HpyCH4III
AciI
AluI
CviJI
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1001
1100
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a Y G S W P F A G L L L T C S F L R Y P L I L W I T V L P P L S E L -
b F T V P G L L L A F C S H V L S C V I P * F C G * P Y Y R L * V S * -
c L R F L A F C W P F A H M F F P A L S P D S V D N R I T A F E * A -

Figure 19-E

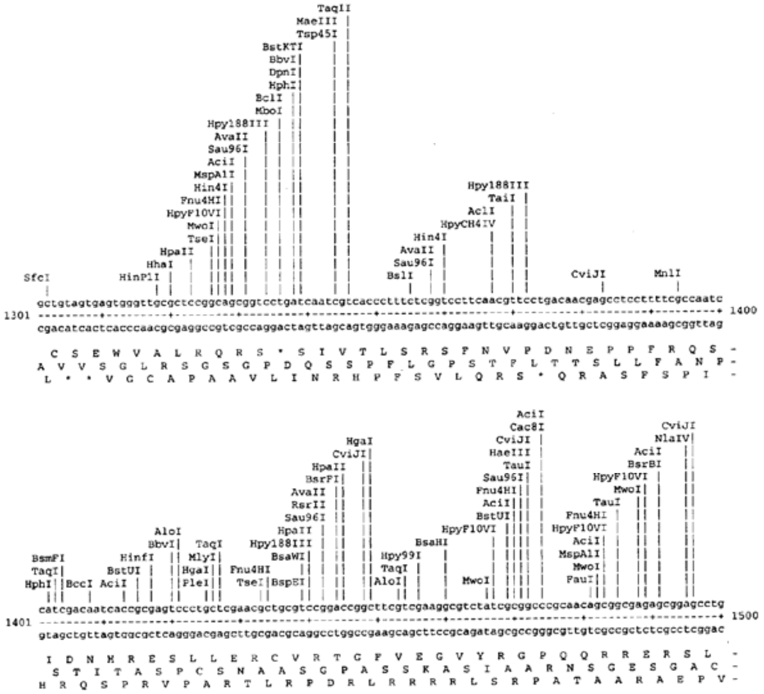
```
                                                                                                     BsiEI
                                                                                                    CviJI|
                                                                                                   HaeIII|
                                                                                                     TauI|
                                                                                                   EaeI ||
                                                                                                   EagI ||
                                                                                                 Fnu4HI ||
                                                                                                   MnlI ||
                                                                                                  AciI| ||
                                                                                                 BstUI| ||
                                                                                                  HhaI| ||
                                                                                              HinPlI || ||
                                                                                          CviJI    | || ||
                                                                                         HaeIII    | || ||
                                                                                     HpyF10VI |    | || ||
                                                    TspRI                               BglI| |    | || ||
                                                    MlyI|                               MwoI| |    | || ||
                      CviJI                        PleI||                            BceAI || |    | || ||
                   Fnu4HI |                       BbvI|||                         TauI   | || |    | || ||
                    TauI| |                     MnlI ||||                        MnlI|   | || |    | || ||
                    TseI| |                  TaqII | ||||                       AciI||   | || |    | || ||
                  AciI || |               HinfI  | | ||||                     Fnu4HI||   | || |    | || ||
                Fnu4HI || |          Fnu4HI   |  | | ||||                     CviJI|||   | || |    | || ||
              Cac8I  | || |           HhaI|   |  | | ||||                    HaeIII|||   | || |    | || ||
            BsrBI |  | || |           TseI|   |  | | ||||                  MboII  ||||   | || |    | || ||
           AciI | |  | || |       HinPlI ||   |  | | ||||    AciI      HaeII   |  ||||   | || |    | || ||
       HpyF10VI | |  | || |     BbvI   | ||   |  | | ||||  EarI |      HhaI|   |  ||||   | || |    | || ||
          MwoI| | |  | || |    BsiEI   | ||   |  | | ||||  SapI |  HinPlI ||   |  ||||   | || |    | || ||
             || | |  | || |        |   | ||   |  | | ||||     | |       | ||   |  ||||   | || |    | || ||
          gataccgctcgccgcagccgaacgaccgagcgcagcgagtcagtgagcgaggaagcggaagagcgccagaaggccgccagagaggccgagcgcggccgtg
     1101 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 1200
          ctatggcgagcggcgtcggcttgctggctcgcgtcgctcagtcactcgctccttcgccttctcgcggtcttccggcggtctctccggctcgcgccggcac

 a         I  P  L  A  A  A  E  R  P  S  A  A  S  Q  *  A  R  K  R  K  S  A  R  R  P  P  E  R  P  S  A  A  V   -
 b          Y  R  S  P  Q  P  N  D  R  A  Q  R  V  S  E  R  G  S  G  R  A  P  E  G  R  Q  R  G  R  A  R  P  *  -
 c        D  T  A  R  R  S  R  T  T  E  R  S  E  S  V  S  E  E  A  E  E  R  Q  K  A  A  R  E  A  E  R  G  R  E-

                                                Fnu4HI                                                BsaXI
                                                CviJI|                                               CviJI|
                                                 TseI|              AciI                           NlaIII||
                                                HgaI||             BstUI                           FokI |||
                                              Cac8I|||        HpyF10VI |                         FatI | |||
                                     CviJI   AciI ||||           MwoI| |   MnlI               Hpy8I | | |||
                              NlaIII  FauI   BslI ||||       Hpy188I|| |  HgaI|               AccI| | | |||
        CviJI     BfaI HgaI FatI   |BbvI | TspDTI ||||    BsaHI    ||| |BsaXI||           BstF5I || | | |||
            |        |    |    |   |   | |      | ||||        |    ||| |    |||                | || | | |||
          aggcttggacgctagggcagggcatgaaaaagcccgtagcgggctgctacgggcgtctgacgcggtggaaagggggaggggatgttgtctacatggctct
     1201 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 1300
          tccgaacctgcgatcccgtcccgtactttttcgggcatcgcccgacgatgcccgcagactgcgccacctttccccctcccctacaacagatgtaccgaga

 a        R  L  G  R  *  G  R  A  *  K  S  P  *  R  A  A  T  G  V  *  R  G  G  K  G  E  G  M  L  S  T  W  L  C -
 b         G  L  D  A  R  A  G  H  E  K  A  R  S  G  L  L  R  A  S  D  A  V  E  R  G  R  G  C  C  L  H  G  S    -
 c          A  W  T  L  G  Q  G  M  K  K  P  V  A  G  C  Y  G  R  L  T  R  W  K  G  G  G  D  V  V  Y  M  A  L  -
```

Figure 19-F


TaqII
MaeIII
Tsp45I
BstKTI
BbvI
DpnI
HphI
BclI
MboI
Hpy188III
AvaII
Sau96I
AciI
MspA1I
Hin4I
Fnu4HI
HpyF10VI
MwoI
TseI
HpaII
HhaI
HinP1I
SfcI
Hpy188III
TaiI
AclI
HpyCH4IV
Hin4I
AvaII
Sau96I
BslI
CviJI
MnlI
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1301
1400
cgacatcactcacccaacgcgaggccgtcgccaggactagttagcagtgggaaagagccaggaagttgcaaggactgttgctcggaggaaagcggttag
a C S E W V A L R Q R S * S I V T L S R S F N V P D N E P P F R Q S -
b A V V S G L R S G S G P D Q S S P F L G P S T F L T T S L L F A N P -
c L * * V G C A P A A V L I N R H P F S V L Q R S * Q R A S F S P I -
AciI
Cac8I
CviJI
HaeIII
TauI
Sau96I
Fnu4HI
AciI
BstUI
HpyF10VI
MwoI
HgaI
CviJI
HpaII
BsrFI
AvaII
RsrII
Sau96I
HpaII
Hpy188III
BsaWI
BspEI
Fnu4HI
TseI
AloI
BbvI
TaqI
HinfI
MlyI
HgaI
PleI
BstUI
AciI
BccI
BsmFI
TaqI
HphI
Hpy99I
TaqI
AloI
BsaHI
CviJI
NlaIV
AciI
BsrBI
HpyF10VI
MwoI
TauI
Fnu4HI
HpyF10VI
AciI
MspA1I
MwoI
FauI
catcgacaatcaccgcgagtccctgctcgaacgctgcgtccggaccggcttcgtcgaaggcgtctatcgcggcccgcaacagcggcgagagcggagcctg
1401
1500
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a I D N H R E S L L E R C V R T G F V E G V Y R G P Q Q R R E R S L -
b S T I T A S P C S N A A S G P A S S K A S I A A R N S G E S G A C -
c H R Q S P R V P A R T L R P D R L R R R R L S R P A T A A R A E P V -

Figure 19-G

```
                          HpyF10VI
                        Cac8I    |
                         NaeI    |
                       HpaII|    |
                      BsrFI||    |
                    NgoMIV|||    |
                    Cac8I |||    |
                 HpyF10VI |||    |
                    MwoI| |||    |
                   HhaI|| |||    |
                BstUI ||| |||    |
               HinP1I ||| |||    |         Cac8I
                 TauI ||| |||    |       CviJI |
                BcgI| ||| |||    |      HaeIII |
               AciI|| ||| |||    |     Cac8I | |
             Fnu4HI|| ||| |||    |      NaeI | |                                                  Tth111I
              TauI||| ||| |||    |    HpaII| | |               HpyCH4III                        HpyF10VI|
            AciI |||| ||| |||    |   BseRI|| | |            NlaIV      |                     HhaI      ||
          Fnu4HI |||| ||| |||    |   BsrFI|| | | HpyF10VI  CviJI|      |     AluI           HgaI|      ||
         NlaIV | |||| ||| |||    | NgoMIV||| | |    MwoI| HaeIII|      |    CviJI         HinP1I|      ||
        BanI | | |||| ||| |||    | SfaNI ||| | |  BcgI ||  MnlI||      |BceAI   |       BsmFI | |      ||
   HpyCH4III | | |||| ||| |||MwoI|BpuEI| ||| | |  SmlI ||Sau96I||      |TspRI   |  BsaBI     || |  MwoI||
           | | | |||| ||| |||   ||    || ||| | |     | ||     |||      |    |   |      |     || |     |||
     ttcaacggtgccgccgcgctcgccggcatcgctgtcgccggcctgctcctcaagcacggccccaacagtgaagtagctgattgtcatcagcgcattgacg
1501 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 1600
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a    F  N  G  A  A  A  L  A  G  I  A  V  A  G  L  L  L  K  H  G  P  N  S  E  V  A  D  C  H  Q  R  I  D  G -
b     S  T  V  P  P  R  S  P  A  S  L  S  P  A  C  S  S  S  T  A  P  T  V  K  *  L  I  V  I  S  A  L  T   -
c      Q  R  C  R  R  A  R  R  H  R  C  R  R  P  A  P  Q  A  R  P  Q  Q  *  S  S  *  L  S  S  A  H  *  R  -

                                                                                                    BstUI
                                                                                                    Cac8I
                                                                                                     HhaI
                                                                                                   HinP1I
                                                                                                 BssHII |
                                                                                                 BstF5I |
                                                                                                  BstUI |
                                                                                                  Cac8I |
                                                                                                   HhaI |
                                                                                                 HinP1I |
                                                                                               BssHII | |
                                                                                               HinP1I | |
                                                                                           NlaIII   | | |
                                                     BsiEI                               FatI   |   | | |
                                                    CviJI|                            Cac8I |   |   | | |
                                                   HaeIII|                             NaeI |   |   | | |
                                                  Hpy99I||                           HpaII| |   |   | | |
              BceAI                           BstUI    |||                          BsrFI|| |   |   | | |
           BsiEI  |                            HhaI    |||                        NgoMIV||| |   |   | | |
          CviJI|  |                        HinP1I |    |||                        SfaNI|||| |   |   | | |
         HaeIII|  |                      Fnu4HI | |    |||                       Cac8I||||| |   |   | | |
         EaeI ||  |                       AluI| | |    |||                      BstUI ||||| |   |   | | |
         EagI ||  |                      CviJI| | |    |||                    BsiEI | ||||| |   |   | | |
     HpyF10VI ||  |                  BceAI   || | |    |||                HpaII   | | ||||| |   |   | | |
       HpaII| ||  |                 HgaI |   || | |    |||                 NciI   | | ||||| |   |   | | |
        MwoI| ||  |            HpyF10VI| |   || | |    |||                ScrFI   | | ||||| |   |   | | |
        NciI| ||  |           BslI    || |   || | |    |||               HhaI |   | | ||||| |   |   | | |
       ScrFI| ||  |          BbvI|    || |   || | |    |||             StyD4I |   | | ||||| |   |   | | |
     BsaJI || ||  |        EcoNI||    || |   || | |    |||           HinP1I | |   | | ||||| |   |   | | |
    StyD4I || ||  |     MnlI   |||MnlI|| |   || | |EaeI|||          BccI  | | |   | | ||||| |   |   | | |
 BsaHI   | || ||  |  AciI  |FauI||MwoI|| |TseI| | |EagI|||        AciI |  | | |   | | ||||| |   |   | | |
     |   | || ||  |     |  |   |||   ||| |   || | |   ||||           | |  | | |   | | ||||| |   |   | | |
     gcgtccccggccgaaaaacccgcctcgcagaggaagcgaagctgcgcgtcggccgtttccatctgcggtgcgcccggtcgcgtgccggcatggatgcgcg
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a      V  P  G  R  K  T  R  L  A  E  E  A  K  L  R  V  G  R  F  H  L  R  C  A  R  S  R  A  G  M  D  A  R  -
b    A  S  P  A  E  K  P  A  S  Q  R  K  R  S  C  A  S  A  V  S  I  C  G  A  P  G  R  V  P  A  W  M  R  A -
c     R  P  R  P  K  N  P  P  R  R  G  S  E  A  A  R  R  P  F  P  S  A  V  R  P  V  A  C  R  H  G  C  A   -
```

Figure 19-H

```
                                                    Hpy188I
                                                   BstKTI |
                                                    DpnI| |
                          Cac8I                   Eco57I| |
                       HpyF10VI                  Eco57MI| |
                         AlwNI|                    Hin4I| |
                        BstAPI|                   MboI || |
                         HaeII|            Hpy188III | || |
                          MwoI|            BsmI    | | || |
                         HhaI||         Cac8I |    | | || |                                         HinfI
                       BbvI |||        AciI | |    | | || |                                      BsmI   |
                     HinPlI |||    Fnu4HI | | |    | | || |                                     EciI|   |
            BccI   HpyF10VI |||     AluI| | | |    | | || |                              HpyF10VI  ||   |
         AciI  |      MwoI| |||    CviJI| | | |    | | || |       BsrI                    BstAPI|  ||   |
        BstUI  |   Fnu4HI|| |||     TseI| | | |    | | || |      HaeII        CviJI   NlaIV    ||  ||   |
      FokI  |  |    TseI||| ||| BbvI   || | | |    | | || |      HhaI|      Hpy99I|  BanI |    ||  ||   |
   HhaI  |  |  | Cac8I |||| ||| FauI   || | | |    | | || |  HinPlI ||   Hpy99I  ||Hin4I| | MwoI|  ||TfiI
      |  |  |  |     | |||| |||    |   || | | |    | | || |       | ||        |  ||    || |    ||  ||   |
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1701 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 1800
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a     A  I  A  V  G  E  Q  R  L  P  E  A  A  G  I  P  D  Q  K  *  A  P  V  V  V  G  S  R  H  R  M  R  M   -
b      P  S  R  *  A  S  S  A  C  L  K  L  R  A  P  P  I  R  N  E  R  Q  S  S  S  A  L  G  T  E  C  V  *  -
c    R  H  R  G  R  R  A  A  P  A  *  S  C  G  H  S  R  S  E  M  S  A  S  R  R  R  L  S  A  P  N  A  Y  D -

                                                                           Fnu4HI
                                                                         HpyF10VI
                                                                           CviJI|
                                                                            MwoI|
                                                                            TseI|
                         BsrI                                            Eco57I||
                       CviJI|               AciI                        Eco57MI||
                      HaeIII|              Cac8I                         Cac8I|||
                      EaeI ||           HpyF10VI                         NaeI||||
                   HgaI  | ||             HaeII|                        HaeII||||
                 CviJI|  | ||              MwoI|                        HpaII||||
               NlaIII||  | ||             HhaI||                       BsrFI|||||
            HpyF10VI|||  | ||         HinPlI |||                        HhaI|||||
               BglI||||  | ||       Fnu4HI | |||                      NgoMIV|||||
               MwoI||||  | ||        TseI| | |||                    HinPlI ||||||
             FatI |||||  | ||    Hpy99I || | |||Hpy188III       HpyF10VI | ||||||
          Cac8I |  |||||  | ||    TaqI | || | |||   FauI |      BbvI    | | ||||||       HpyCH4III   BsrI
       AciI   | |  |||||  | ||  TspRI| | || | ||| BbvI | |     BsrI|MwoI| | ||||||     EciI      |AciI  |
          |   | | |||||  | ||      || | || | |||    | | |        ||   || | ||||||        |      |   |  |
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b     F  S  A  S  M  A  S  A  S  A  S  S  S  A  R  L  F  L  K  C  Q  *  S  A  G  C  *  T  P  N  R  S  A   -
c      S  P  P  A  W  L  R  P  V  R  R  A  A  P  A  C  S  *  S  A  S  K  A  P  A  A  E  P  P  T  V  P  P  -

                                                                           HpyCH4V
                                                                          Fnu4HI |
                                                        TauI              CviJI| |
                                                    Fnu4HI |               TseI| |
                                                BstNI    | |           TspGWI || |
                                                ScrFI    | |        TspRI   | || |
                                               BsaJI|    | |       AlwI  |  | || |
                                              PspGI||    | | HpyCH4III | |  | || |
                       Hpy8I                 StyD4I||    | | BstKTI · || |  | || |
                       AccI|                AvaII |||    | | BbvI|    || |  | || |       NlaIII
               HpyCH4III  ||               Sau96I |||    | | DpnI|    || |  | || |     FatI   |
             Hpy188I    | ||               MnlI | |||AciI| |MboI ||   || |  | || |   Hin4I|   |
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b    S  L  R  V  V  R  P  S  T  P  T  S  F  N  R  S  R  A  A  R  I  T  V  F  G  C  N  F  V  M  L  D  T  L -
c     V  C  V  S  S  D  R  L  R  R  P  R  S  T  G  P  G  R  H  G  S  L  Y  S  A  A  T  L  S  C  L  T  L   -
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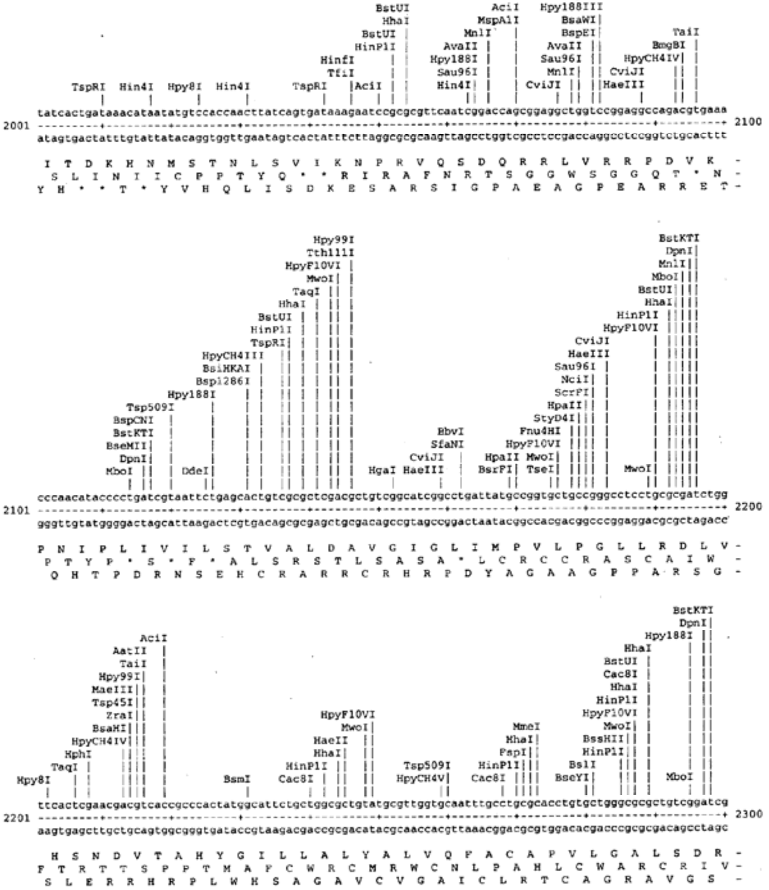
Figure 19-I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BstUI MnlI BspEI TaiI
HinP1I AvaII AvaII BmgBI
HinfI Hpy188I Sau96I HpyCH4IV
TfiI Sau96I MnlI CviJI
TspRI Hin4I Hpy8I Hin4I TspRI AciI Hin4I CviJI HaeIII
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2001 2100
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b S L I N I I C P P T Y Q * * R I R A F N R T S G G W S G G Q T * N -
c Y H * * T * Y V H Q L I S D K E S A R S I G P A E A G P E A R R E T -
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Tth111I
HpyF10VI
MwoI
TaqI
HhaI
BstUI
HinP1I
TspRI
HpyCH4III
BsiHKAI
Bsp1286I
Hpy188I
Tsp509I
BspCNI
BstKTI
BseMII
DpnI
MboI DdeI
BstKTI
DpnI
MnlI
MboI
BstUI
HhaI
HinP1I
HpyF10VI
CviJI
HaeIII
Sau96I
NciI
ScrFI
HpaII
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BbvI Fnu4HI
SfaNI HpyF10VI
CviJI HpaII MwoI
HgaI HaeIII BsrFI TseI MwoI
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2101 2200
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b P T Y P * S * F * A L S R S T L S A S A * L C R C C R A S C A I W -
c Q H T P D R N S E H C R A R R C R H R P D Y A G A A G P P A R S G -
BstKTI
DpnI
AciI Hpy188I
AatII HhaI
TaiI BstUI
Hpy99I Cac8I
MaeIII HhaI
Tsp45I HinP1I
ZraI HpyF10VI HpyF10VI
BsaHI MwoI MmeI MwoI
HpyCH4IV HaeII HhaI BssHII
HphI HhaI FspI HinP1I
TaqI HinP1I Tsp509I HinP1I BslI
Hpy8I BsmI Cac8I HpyCH4V Cac8I BseYI MboI
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2201 2300
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b F T R T T S P P T M A F C W R C M R W C N L P A H L C W A R C R I V -
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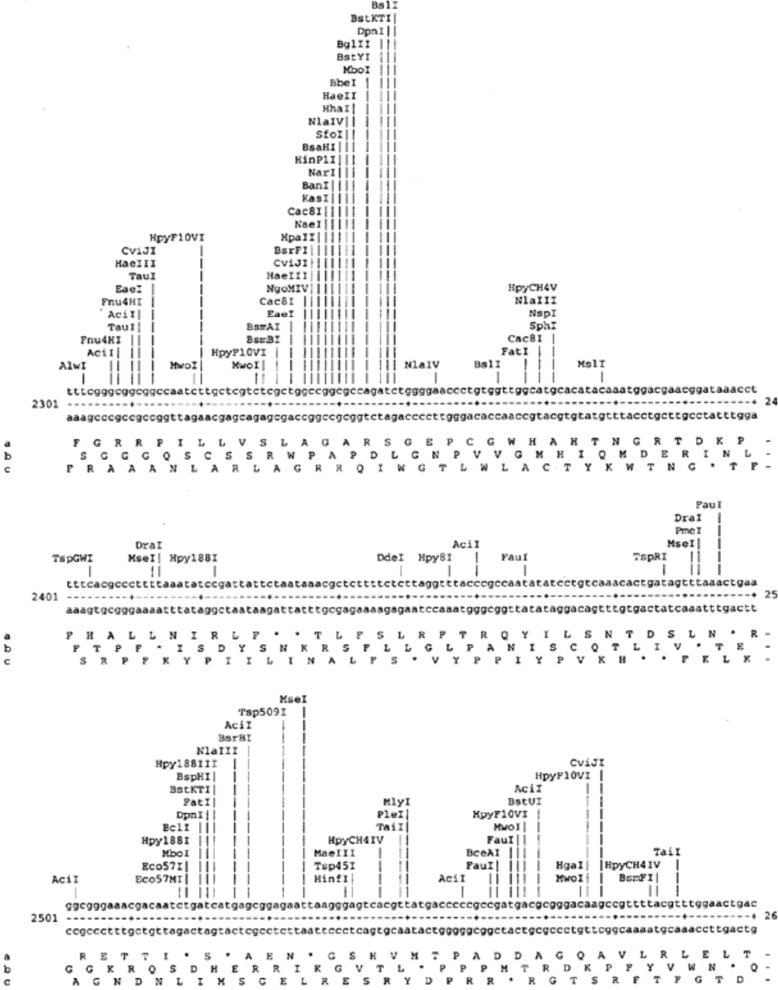
Figure 19-J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HinP1I
NarI
BanI
KasI
Cac8I
NaeI
HpaII
BsrFI
CviJI
HaeIII
NgoMIV
Cac8I
EaeI
BsmAI
BsmBI
HpyF10VI
MwoI
HpyF10VI
CviJI
HaeIII
TauI
EaeI
Fnu4HI
AciI
TauI
Fnu4HI
AciI
AlwI
MwoI
NlaIV
BslI
HpyCH4V
NlaIII
NspI
SphI
Cac8I
FatI
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b S G G G Q S C S S R W P A P D L G N P V V G M H I Q M D E R I N L -
c P R A A A N L A R L A G R R Q I W G T L W L A C T Y K W T N G * T F -
FauI
DraI
PmeI
MseI
TspRI
TspGWI
DraI
MseI
Hpy188I
DdeI
Hpy8I
AciI
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2401
2500
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a F H A L L N I R L F * * T L F S L R F T R Q Y I L S N T D S L N * R -
b F T P F * I S D Y S N K R S F L L G L P A N I S C Q T L I V * T E -
c S R P F K Y P I I L I N A L F S * V Y P P I Y P V K H * * F K L K -
MseI
Tsp509I
AciI
BsrBI
NlaIII
Hpy188III
BspHI
BstKTI
FatI
DpnI
BclI
Hpy188I
MboI
Eco57I
Eco57MI
AciI
HpyCH4IV
MaeIII
Tsp45I
HinfI
MlyI
PleI
TaiI
CviJI
HpyF10VI
AciI
BstUI
HpyF10VI
MwoI
FauI
BceAI
FauI
AciI
HgaI
MwoI
HpyCH4IV
BsmFI
TaiI
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2600
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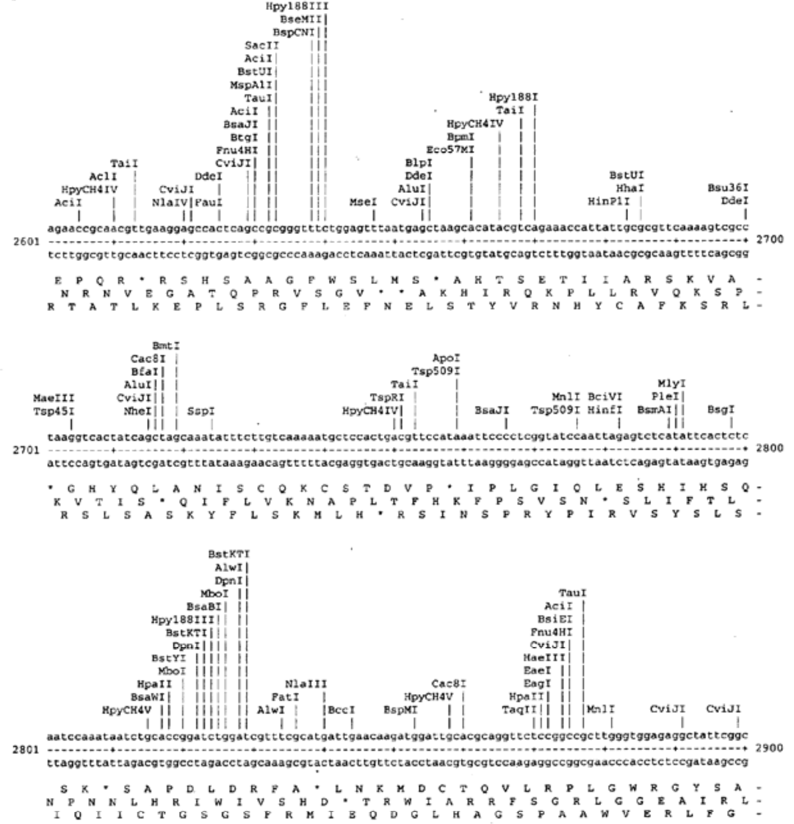
a R E T T I * S * A E N * G S H V M T P A D D A G Q A V L R L E L T -
b G G K R Q S D H E R R I K G V T L * P P P M T R D K P F Y V W N * Q -
c A G N D N L I M S G E L R E S R Y D P R R * R G T S R F T F G T D -

Figure 19-K



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a     E  P  Q  R  *  R  S  H  S  A  A  G  F  W  S  L  M  S  *  A  H  T  S  E  T  I  I  A  R  S  K  V  A  -
b      N  R  N  V  E  G  A  T  Q  P  R  V  S  G  V  *  *  A  K  H  I  R  Q  K  P  L  L  R  V  Q  K  S  P -
c     R  T  A  T  L  K  E  P  L  S  R  G  F  L  E  F  N  E  L  S  T  Y  V  R  N  H  Y  C  A  F  K  S  R  L-

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2701 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 2800
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b     K  V  T  I  S  *  Q  I  F  L  V  K  N  A  P  L  T  F  H  K  F  P  S  V  S  N  *  S  L  I  F  T  L  -
c      R  S  L  S  A  S  K  Y  F  L  S  K  M  L  H  *  R  S  I  N  S  P  R  Y  P  I  R  V  S  Y  S  L  S -

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b     N  P  N  N  L  H  R  I  W  I  V  S  H  D  *  T  R  W  I  A  R  R  F  S  G  R  L  G  G  E  A  I  R  L-
c      I  Q  I  I  C  T  G  S  G  S  F  R  M  I  E  Q  D  G  L  H  A  G  S  P  A  A  W  V  E  R  L  F  G  -
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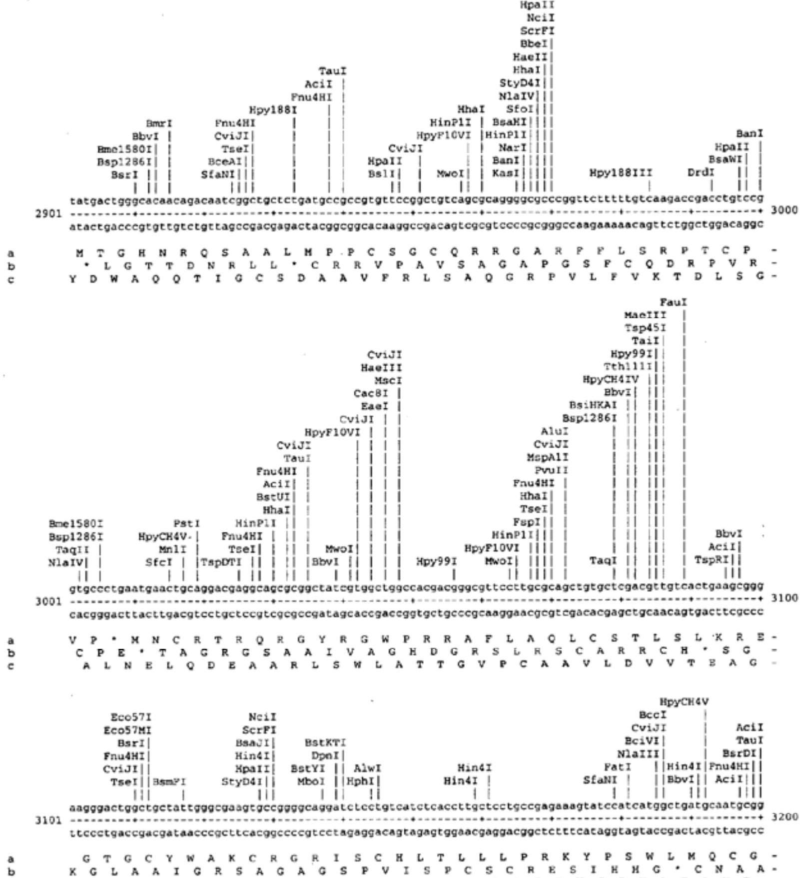
Figure 19-L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BanI
KasI
TauI
AciI
Fnu4HI
Hpy188I
HhaI
HinP1I
HpyF10VI
CviJI
HpaII
BslI
MwoI
BmrI
BbvI
Bme1580I
Bsp1286I
BsrI
Fnu4HI
CviJI
TseI
BceAI
SfaNI
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DrdI
BanI
HpaII
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b * L G T T D N R L L * C R R V P A V S A G A P G S F C Q D R P V R -
c Y D W A Q Q T I G C S D A A V F R L S A Q G R P V L F V K T D L S G -
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MaeIII
Tsp45I
TaiI
Hpy99I
Tth111I
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BbvI
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AluI
CviJI
MspA1I
PvuII
Fnu4HI
HhaI
TseI
FspI
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Eco57MI
BsrI
Fnu4HI
CviJI
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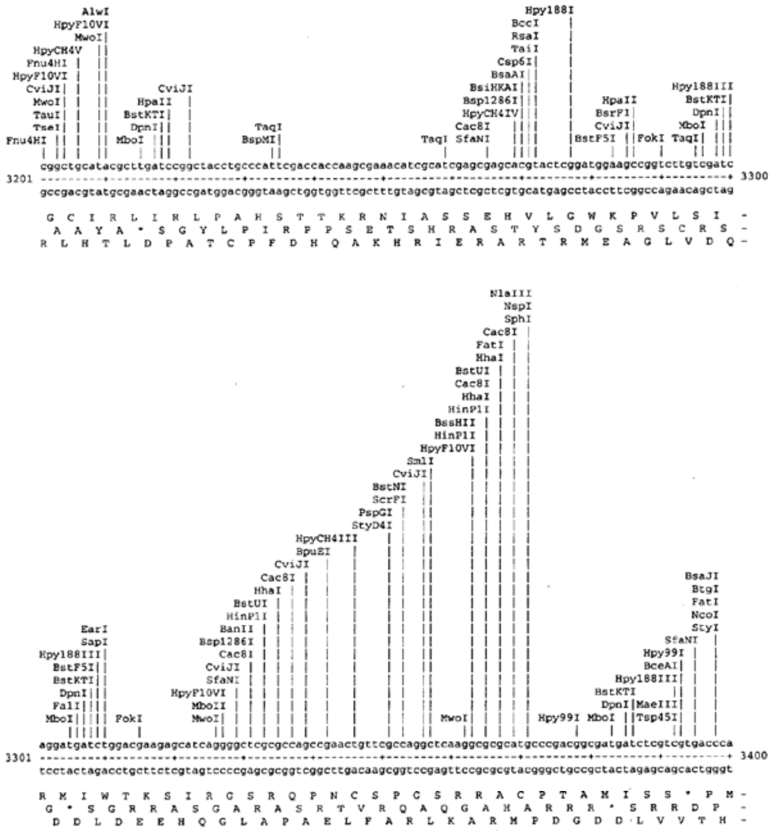
Figure 19-M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BstKTI
DpnI
MboI
TaqI
BspMI
Hpy188I
BccI
RsaI
TaiI
Csp6I
BsaAI
BsiHKAI
Bsp1286I
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Cac8I
TaqI
SfaNI
HpaII
BsrFI
CviJI
BstF5I
FokI
Hpy188III
BstKTI
DpnI
MboI
TaqI
cggctgcatacgcttgatccggctacctgcccattcgaccaccaagcgaaacatcgcatcgagcgagcacgtactcggatggaagccggtcttgtcgatc
3201
3300
gccgacgtatgcgaactaggccgatggacgggtaagctggtggttcgctttgtagcgtagctcgctcgtgcatgagcctaccttcggccagaacagctag
a G C I R L I R L P A H S T T K R N I A S S E H V L G W K P V L S I -
b A A Y A * S G Y L P I R P P S E T S H R A S T Y S D G S R S C R S -
c R L H T L D P A T C P F D H Q A K H R I E R A R T R M E A G L V D Q -
NlaIII
NspI
SphI
Cac8I
FatI
HhaI
BstUI
Cac8I
HhaI
HinP1I
BssHII
HinP1I
HpyF10VI
SmlI
CviJI
BstNI
ScrFI
PspGI
StyD4I
HpyCH4III
BpuEI
CviJI
Cac8I
HhaI
BstUI
HinP1I
BanII
Bsp1286I
Cac8I
CviJI
SfaNI
HpyF10VI
MboII
MwoI
EarI
SapI
Hpy188III
BstF5I
BstKTI
DpnI
FalI
MboI
FokI
MwoI
BsaJI
BtgI
FatI
NcoI
StyI
SfaNI
Hpy99I
BceAI
Hpy188III
BstKTI
DpnI
MaeIII
Hpy99I
MboI
Tsp45I
aggatgatctggacgaagagcatcaggggctcgcgccagccgaactgttcgccaggctcaaggcgcgcatgcccgacggcgatgatctcgtcgtgaccca
3301
3400
tcctactagacctgcttctcgtagtccccgagcgcggtcggcttgacaagcggtccgagttccgcgcgtacgggctgccgctactagagcagcactgggt
a R M I W T K S I R G S R Q P N C S P C S R R A C P T A M I S S * P M -
b G * S G R R A S G A R A S R T V R Q A Q G A H A R R R * S R R D P -
c D D L D E E H Q G L A P A E L F A R L K A R M P D G D D L V V T H -

Figure 19-N

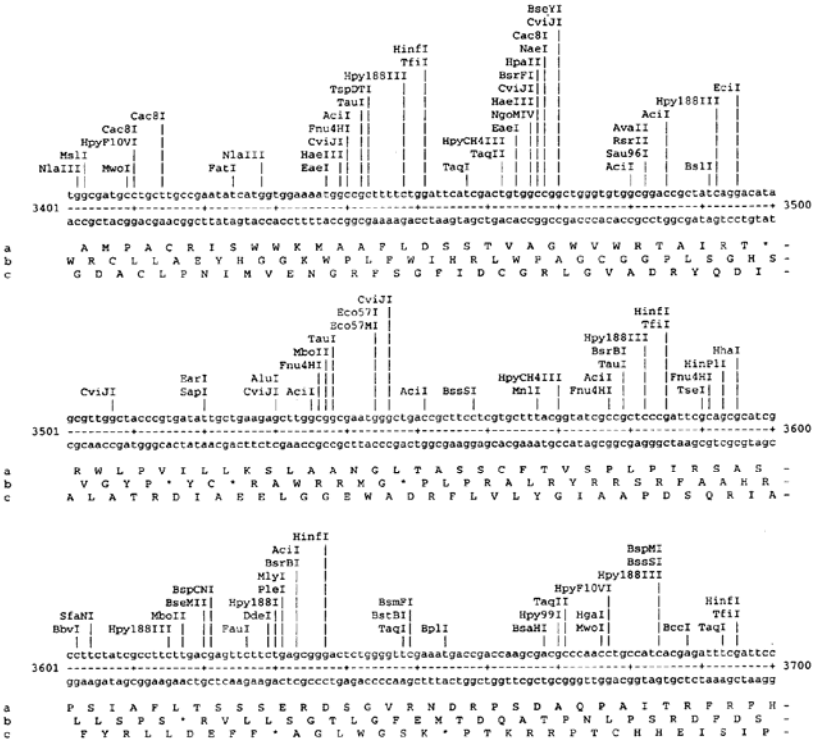

BseYI
CviJI
Cac8I
NaeI
HinfI
TfiI
HpaII
Hpy188III
BsrFI
TspDTI
CviJI
EciI
TauI
HaeIII
Hpy188III
Cac8I
AciI
NgoMIV
AciI
Cac8I
Fnu4HI
EaeI
AvaII
HpyF10VI
CviJI
HpyCH4III
RsrII
MslI
NlaIII
HaeIII
TaqII
Sau96I
NlaIII
MwoI
FatI
EaeI
TaqI
AciI
BslI
tggcgatgcctgcttgccgaatatcatggtggaaaatggccgcttttctggattcatcgactgtggccggctgggtgtggcggaccgctatcaggacata
3401
3500
accgctacggacgaacggcttatagtaccaccttttaccggcgaaaagacctaagtagctgacaccggccgacccacaccgcctggcgatagtcctgtat
a A M P A C R I S W W K M A A F L D S S T V A G W V W R T A I R T * -
b W R C L L A E Y H G G K W P L F W I H R L W P A G C G G P L S G H S -
c G D A C L P N I M V E N G R F S G F I D C G R L G V A D R Y Q D I -
CviJI
Eco57I
Eco57MI
HinfI
TauI
TfiI
MboII
Hpy188III
Fnu4HI
BsrBI
HhaI
TauI
HinPlI
EarI
AluI
HpyCH4III
AciI
Fnu4HI
CviJI
SapI
CviJI
AciI
AciI
BssSI
MnlI
Fnu4HI
TseI
gcgttggctacccgtgatattgctgaagagcttggcggcgaatgggctgaccgcttcctcgtgctttacggtatcgccgctcccgattcgcagcgcatcg
3501
3600
cgcaaccgatgggcactataacgacttctcgaaccgccgcttacccgactggcgaaggagcacgaaatgccatagcggcgagggctaagcgtcgcgtagc
a R W L P V I L L K S L A A N G L T A S S C F T V S P L P I R S A S -
b V G Y P * Y C * R A W R R M G * P L P R A L R Y R R S R F A A H R -
c A L A T R D I A E E L G G E W A D R F L V L Y G I A A P D S Q R I A -
HinfI
AciI
BsrBI
BspMI
MlyI
BssSI
PleI
Hpy188III
BspCNI
HpyF10VI
BseMII
Hpy188I
BsmFI
TaqII
HinfI
SfaNI
MboII
DdeI
BstBI
Hpy99I
HgaI
TfiI
BbvI
Hpy188III
FauI
TaqI
BplI
BsaHI
MwoI
BccI
TaqI
ccttctatcgccttcttgacgagttcttctgagcgggactctggggttcgaaatgaccgaccaagcgacgcccaacctgccatcacgagatttcgattcc
3601
3700
ggaagatagcggaagaactgctcaagaagactcgccctgagaccccaagctttactggctggttcgctgcgggttggacggtagtgctctaaagctaagg
a P S I A F L T S S S E R D S G V R N D R P S D A Q P A I T R F R P H -
b L L S P S * R V L L S G T L G F E M T D Q A T P N L P S R D F D S -
c F Y R L L D E F F * A G L W G S K * P T K R R P T C H H E I S I P -

Figure 19-O

```
                                                                                   MboII
                                                                                  NlaIII
                                                                                   AlwI
                                                                              FatI
                                                                            BstKTI
                                                                             DpnI
                                                                           BstYI
                                                                            MboI
                                                                          MnlI
                                                                        BslI
                                                                       AciI
                                                                      BstUI
                                                                       HhaI
                                                                    FokI
                                                                  HinP1I
                                                                FauI
                                                              BstF5I
                                                              BstKTI
                                                                DpnI
                                                             MboI
                                                           BsmFI
                                                          HgaI
                                                         AlwI
                                                       CviJI
                                                      Cac8I
                                                       NaeI
                                                     HpaII
                                                      BpmI
                                                     BsrFI
                                                   Eco57MI
                                                    NgoMIV
                                                  BsaHI
                                   HinfI        NciI
           TauI                     TfiI       ScrFI
         AciI                    Hpy188I      HpaII
       Fnu4HI                    TspDTI        PfoI                                      BsaJI
     AciI                      CviJI        StyD4I                                        BtgI
     accgccgccttctatgaaaggttgggcttcggaatcgttttccgggacgccggctggatgatcctccagcgcggggatctcatgctggagttcttcgccc
3701 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 3800
     tggcggcggaagatactttccaacccgaagccttagcaaaaggccctgcggccgacctactaggaggtcgcgcccctagagtacgacctcaagaagcggg

a       R  R  L  L  *  K  V  G  L  R  N  R  F  P  G  R  R  L  D  D  P  P  A  R  G  S  H  A  G  V  L  R  P  -
b     T  A  A  F  Y  E  R  L  G  F  G  I  V  F  R  D  A  G  W  M  I  L  Q  R  G  D  L  M  L  E  F  F  A  H -
c      P  P  P  S  M  K  G  W  A  S  E  S  F  S  G  T  P  A  G  *  S  S  S  A  G  I  S  C  W  S  S  S  P  -


                                                                                 Bpu10I
                                                                                   DdeI
                                                                              Hpy188III
                                                                                BstKTI                 Sau96I
      BstKTI                                                                    DpnI                 PspOMI
        BpmI               BsiEI                          BsiEI              MboI                   Sau96I
        DpnI            AciI                            CviJI            BspCNI                   BstKTI
     Eco57MI      HpyF10VI                              HaeIII           BseMII                    DpnI
      BstYI   AciI                  NlaIV                 EaeI            AlwI                      HgaI
       MboI   AlwI    MwoI     TaqI BanI   EcoRV          EagI           BceAI                     MboI
     acgggatctctgcggaacaggcggtcgaaggtgccgatatcattacgacagcaacggccgacaagcacaacgccacgatcctgagcgacaatatgatcgg
3801 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 3900
     tgccctagagacgccttgtccgccagcttccacggctatagtaatgctgtcgttgccggctgttcgtgttgcggtgctaggactcgctgttatactagcc

a      R  D  L  C  G  T  G  G  R  R  C  R  Y  H  Y  D  S  N  G  R  Q  A  Q  R  H  D  P  E  R  Q  Y  D  R  -
b       G  I  S  A  E  Q  A  V  E  G  A  D  I  I  T  T  A  T  A  D  K  H  N  A  T  I  L  S  D  N  M  I  G  -
c     T  G  S  L  R  N  R  R  S  K  V  P  I  S  L  R  Q  Q  R  P  T  S  T  T  P  R  S  *  A  T  I  *  S  G -
```

Figure 19-P

```
                                              SfaNI
                                           BstNI  |
              HgaI                         ScrFI  |
             Hpy8I                       BsaJI |  |
         BsaHI    |                      PspGI |  |
        ApaI  |   |                     StyD4I |  |
       BanII  |   |                   BceAI  | |  |
    Bme1580I  |   |                HpyF10VI  | |  |
    Bsp1286I  |   |                   MwoI|  | |  |
       HpaII  |   |                TauI  ||  | |  |
        NciI  |   |            Fnu4HI |  ||  | |  |                EcoRV
       ScrFI  |   |          HpyF10VI |  ||  | |  |              TaqII  |
     CviJI |  |   |             AciI| |  ||  | |  |            BstUI  | |
    HaeIII |  |   |             MwoI| |  ||  | |  |            AciI | | |
     NlaIV |  |   |          Hpy99I|| |  ||  | |  |           BbvI| | | | Fnu4HI
    StyD4I |  |   |     BsaHI     ||| |  ||  | |  |     HpyCH4V  || | | |  TseI| Hpy188I              AciI
         | |  |   |          |    ||| |  ||  | |  |            | || | | |     ||       |                  |
         gcccggcgtccacatcaacggcgtcggcggcgactgcccaggcaagaccgagatgcaccgcgatatcttgctgcgttcggatattttcgtggagttcccg
    3901 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 4000
         cgggccgcaggtgtagttgccgcagccgccgctgacgggtccgttctggctctacgtggcgctatagaacgacgcaagcctataaaagcacctcaagggc

a        A  R  R  P  H  Q  R  R  R  R  R  L  P  R  Q  D  R  D  A  P  R  Y  L  A  A  F  G  Y  F  R  G  V  P  A-
b         P  G  V  H  I  N  G  V  G  G  D  C  P  G  K  T  E  M  H  R  D  I  L  L  R  S  D  I  F  V  E  F  P  -
c          P  A  S  T  S  T  A  S  A  A  T  A  Q  A  R  P  R  C  T  A  I  S  C  C  V  R  I  F  S  W  S  S  R -


              AlwI
             HpaII          BsiEI
              NciI         BstKTI
             ScrFI  BstF5I   FokI                                             HpyF10VI
          StyD4I |  BstKTI   PvuI                        MseI              HpaII     |
          Hin4I| |   DpnI|  DpnI|                      AflII|   HinfI      BslI|     |
          FauI|| | MboI ||MboI ||         Hin4I         SmlI|    TfiI     BsrFI| MwoI|   BsaBI  Tsp509I
             ||| |    | ||   | ||             |            ||       |         ||    ||       |        |
         ccacagacccggatgatccccgatcgttcaaacatttggcaataaagtttcttaagattgaatcctgttgccggtcttgcgatgattatcatataatttc
    4001 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 4100
         ggtgtctgggcctactaggggctagcaagtttgtaaaccgttatttcaaagaattctaacttaggacaacggccagaacgctactaatagtatattaaag

a          T  D  P  D  D  P  R  S  F  K  H  L  A  I  K  P  L  K  I  E  S  C  C  R  S  C  D  D  Y  H  I  I  S -
b        P  Q  T  R  M  I  P  D  R  S  N  I  W  Q  *  S  F  L  R  L  N  P  V  A  G  L  A  M  I  I  I  *  F  L-
c         H  R  P  G  *  S  P  I  V  Q  T  F  G  N  K  V  S  *  D  *  I  L  L  P  V  L  R  *  L  S  Y  N  F  -


                                                     TaiI
                                             HpyCH4IV   |
                                               NlaIII|  |
                                              NsiI  ||  |
                                            BfrBI | ||  |
                                             FatI | ||  |
                                          HpyCH4V | ||  |
                                      NlaIII    | | ||  |
                                  AflIII   |    | | ||  |
                                    FatI   |    | | ||  |
                                    PciI   |    | | ||  |
                                 MseI  |   |    | | ||  |                                    FauI
                  MseI     Tsp509I  |  |   |    | | ||  |                                MlyI|  |
                  TaiI  NlaIII   |  |  |   |    | | ||  |                                PleI|  |
          HpyCH4IV   |    NspI   |  |  |   |    | | ||  |                             Tsp509I|  |
      Tsp509I     |  |FatI   |   |  |  |NspI    | | ||  |BccI      BsmFI        HinfI AciI  ||  |   MseI
             |    |  |   |   |   |  |  |   |    | | ||  |   |          |            |    |  ||  |      |
         tgttgaattacgttaagcatgtaataattaacatgtaatgcatgacgttatttatgagatgggtttttatgattagagtcccgcaattatacatttaata
    4101 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 4200
         acaacttaatgcaattcgtacattattaattgtacattacgtactgcaataaatactctacccaaaaatactaatctcagggcgttaatatgtaaattat

a         V  E  L  R  *  A  C  N  N  *  H  V  M  H  D  V  I  Y  E  M  G  F  Y  D  *  S  P  A  I  I  H  L  I  -
b          L  N  Y  V  K  H  V  I  I  N  M  *  C  M  T  L  F  M  R  W  V  F  M  I  R  V  P  Q  L  Y  I  *  Y -
c        C  *  I  T  L  S  M  *  *  L  T  C  N  A  *  R  Y  L  *  D  G  F  L  *  L  E  S  R  N  Y  T  F  N  T-
```

Figure 19-Q

```
                                                    AciI                                             CviJI
                                                   BstUI |                                            TauI |
                            HhaI                    HhaI |                                          Fnu4HI |
                           Hin4I |                 BstUI |                    CviJI                 AciI   |
                           BstUI |                 Cac8I |                   HaeIII |               TauI | |
                           Cac8I |                  HhaI |                 Sau96I   |            Fnu4HI  | |
                            HhaI |                HinP1I |               BstKTI   | |            AciI   || |
                          HinP1I |              BssHII   |    MaeIII      DpnI  | | |          Hin4I  | || |
                        BssHII   |   Tsp509I           | |      Hin4I|  MboI   || | |        Cac8I   || || |
   BstUI              HinP1I   | | BfaI      |HinP1I   | | Hin4I     || BfaI | || | |     MnlI     | || || |
         |                   | | |      |    |       | | |       |   ||     || || | |          |   | || || |
        cgcgatagaaaacaaaatatagcgcgcaaactaggataaattatcgcgcgcggtgtcatctatgttactagatcgggcctcctgtcaatgctggcggcgg
   4201 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 4300
        gcgctatcttttgttttatatcgcgcgtttgatcctatttaatagcgcgcgccacagtagatacaatgatctagcccggaggacagttacgaccgccgcc

a       R  D  R  K  Q  N  I  A  R  K  L  G  *  I  I  A  R  G  V  I  Y  V  T  R  S  G  L  L  S  M  L  A  A  A -
b        A  I  E  N  K  I  *  R  A  N  *  D  K  L  S  R  A  V  S  S  M  L  L  D  R  A  S  C  Q  C  W  R  R   -
c         R  *  K  T  K  Y  S  A  Q  T  R  I  N  Y  R  A  R  C  H  L  C  Y  *  I  G  P  P  V  N  A  G  G  G  -

                                                                          Hpy188I
                                                                            DdeI |
                                                                           MnlI ||
                                                                         CviJI |||
                                                                         TauI ||||
                                                                      Fnu4HI |||||
                                                                      MnlI  ||||||
                                                                     AciI | ||||||
                                                                 BspCNI  || ||||||
                                                                BseMII | || ||||||
                                                          Hpy188I     || || ||||||
                                                       MnlI      |    || || ||||||
                                                      AciI |     |    || || ||||||
                                                  BspCNI  ||     |    || || ||||||
                                                 BseMII | ||     |    || || ||||||
                                           Hpy188I     || ||     |    || || ||||||
                                             DdeI |    || ||     |    || || ||||||
                                         CviJI   ||    || ||     |    || || ||||||
                                        MnlI  |  ||    || ||     |    || || ||||||
                                   BspCNI   | |  ||    || ||     |    || || ||||||
                                  BseMII |  | |  ||    || ||     |    || || ||||||
                            Hpy188I     ||  | |  ||    || ||     |    || || ||||||
                              DdeI |    ||  | |  ||    || ||     |    || || ||||||
                           CviJI  ||    ||  | |  ||    || ||     |    || || ||||||
                           TauI | ||    ||  | |  ||    || ||     |    || || ||||||
                       Fnu4HI  || ||    ||  | |  ||    || ||     |    || || ||||||
                        MnlI | || ||    ||  | |  ||    || ||     |    || || ||||||       HpaII
                       AciI || || ||    ||  | |  ||    || ||     |    || || ||||||      BsaWI |
                    BspCNI ||| || ||    ||  | |  ||    || ||     |    || || ||||||     NlaIV ||
                   BseMII |||| || ||    ||  | |  ||    || ||DdeI |    || || ||||||  AciI    |||   CviJI
                         ||||| || ||    ||  | |  ||    || ||    ||    || || ||||||      |   |||        |
        ctctggtggtggttctggtggcggctctgagggtggtggctctgagggtggcggttctgagggtggcggctctgagggaggcggttccggtggtggctct
   4301 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 4400
        gagaccaccaccaagaccaccgccgagactcccaccaccgagactcccaccgccaagactcccaccgccgagactccctccgccaaggccaccaccgaga

a         L  V  V  V  L  V  A  A  L  R  V  V  A  L  R  V  A  V  L  R  V  A  A  L  R  E  A  V  P  V  V  A  L  -
b       L  W  W  W  F  W  W  R  L  *  G  W  W  L  *  G  W  R  F  *  G  W  R  L  *  G  R  R  F  R  W  W  L  W -
c        S  G  G  G  S  G  G  G  S  E  G  G  G  S  E  G  G  G  S  E  G  G  G  S  E  G  G  G  S  G  G  G  S   -

                                                                                      Hpy188I
                                                                                HpyCH4III     |
                                                                                   TspDTI |   |
                                                                                 SfcI     |   |
                                                                                 HhaI |   |   |
      HpaII                                                                     BstUI  |   |   |
     BsaWI  |          BccI                                                 HinP1I   ||   |   |
    NlaIV  ||        HphI   |      TspDTI         CviJI                TaqII       | ||   |   |    HgaI
          |||             | |             |             |                    |     | ||   |   |         |
        ggttccggtgattttgattatgaaaagatggcaaacgctaataagggggctatgaccgaaaatgccgatgaaaacgcgctacagtctgacgctaaaggca
   4401 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 4500
        ccaaggccactaaaactaatacttttctaccgtttgcgattattcccccgatactggcttttacggctacttttgcgcgatgtcagactgcgatttccgt

a        V  P  V  I  L  I  M  K  R  W  Q  T  L  I  R  G  L  *  P  K  M  P  M  K  T  R  Y  S  L  T  L  K  A   -
b         F  R  *  F  *  L  *  K  D  G  K  R  *  *  G  G  Y  D  R  K  C  R  *  K  R  A  T  V  *  R  *  R  Q  -
c       G  S  G  D  F  D  Y  E  K  M  A  N  A  N  K  G  A  M  T  E  N  A  D  E  N  A  L  Q  S  D  A  K  G  K -
```

Figure 19-R

```
                                                                     CviJI
                                           ClaI                     HaeIII
                                           TaqI                      HphI|
                                       TspDTI |                   HpaII ||
                                       BccI | |                 TaiI  | ||
                                   Fnu4HI | | |          HpyCH4IV  |  | ||
           HinfI        FalI        TseI| | | |        MaeIII   |  |  | ||
            TfiI       BbvI|HpyCH4III  || | | |        Tsp45I   |  |  | ||                        BsrI
               |          ||        |  || | | |             |   |  |  | ||                           |
          aacttgattctgtcgctactgattacggtgctgctatcgatggtttcattggtgacgtttccggccttgctaatggtaatggtgctactggtgattttgc
     4501 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 4600
          ttgaactaagacagcgatgactaatgccacgacgatagctaccaaagtaaccactgcaaaggccggaacgattaccattaccacgatgaccactaaaacg

a         N  L  I  L  S  L  L  I  T  V  L  L  S  M  V  S  L  V  T  F  P  A  L  L  M  V  M  V  L  L  V  I  L  L-
b          T  *  F  C  R  Y  *  L  R  C  C  Y  R  W  F  H  W  *  R  F  R  P  C  *  W  *  W  C  Y  W  *  F  C  -
c           L  D  S  V  A  T  D  Y  G  A  A  I  D  G  F  I  G  D  V  S  G  L  A  N  G  N  G  A  T  G  D  F  A -

                                               HphI
          Tsp509I                          Tsp509I|              XmnI
           BpuEI|                         HphI   ||          Tsp509I|
        CviJI  ||                   HpyCH4III|   ||      TspCWI    ||        SspI                    BsaXI
        HphI|  ||          SmlI  MaeIII     ||   ||   MseI  |    ||   TspDTI  |                 MnlI   |
      Cac8I||  ||        CviJI|  Tsp45I     ||   ||  HphI  |  |    ||  BsaXI |  |                BslI|MnlI
          |||  ||            ||       |     ||   ||     |  |  |    ||      | |  |                   ||   |
          tggctctaattcccaaatggctcaagtcggtgacggtgataattcacctttaatgaataatttccgtcaatatttaccttccctccctcaatcggttgaa
     4601 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 4700
          accgagattaagggtttaccgagttcagccactgccactattaagtggaaattacttattaaaggcagttataaatggaagggagggagttagccaactt

a           A  L  I  P  K  W  L  K  S  V  T  V  I  I  H  L  *  *  I  I  S  V  N  I  Y  L  P  S  L  N  R  L  N -
b         W  L  *  F  P  N  G  S  S  R  *  R  *  *  F  T  F  N  E  *  F  P  S  I  F  T  F  P  P  S  I  G  *  M-
c          G  S  N  S  Q  M  A  Q  V  G  D  G  D  N  S  P  L  M  N  N  F  R  Q  Y  L  P  S  L  P  Q  S  V  E  -

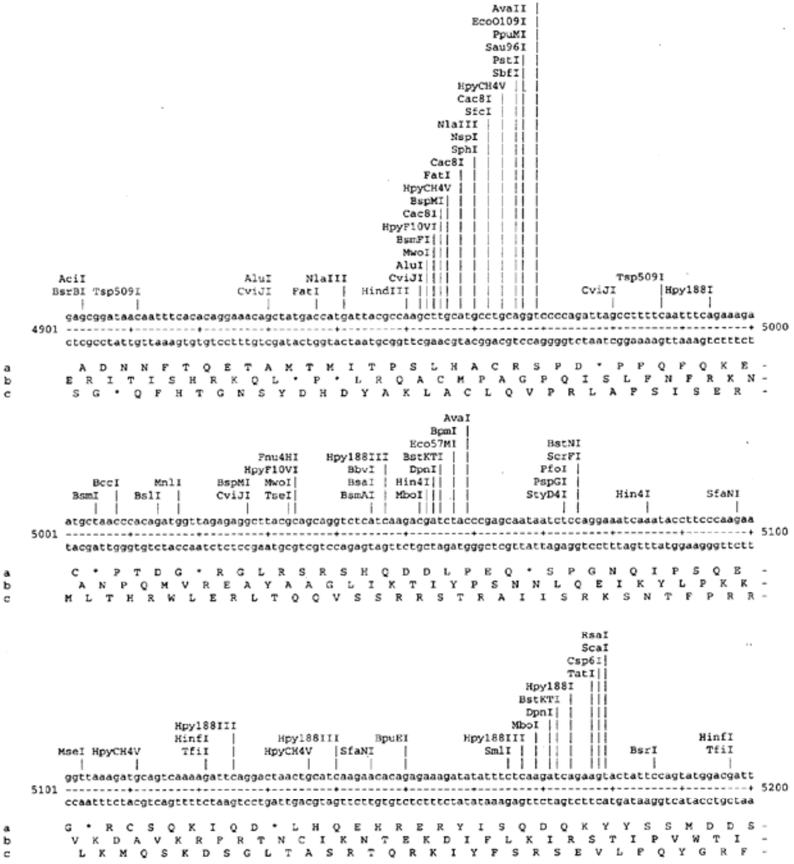
                                                              HinfI
                                                               TfiI
                                                           CviJI  |
                                                          HaeIII  |
                                                          BsaXI|  |
                                                          EaeI||  |
                                                         FauI|||  |           Cac8I
                                                        BslI||||  |          AluI |
                                                     TspDTI|||||  |         CviJI |
                             HpyF10VI                BstUI||||||  |        MspA1I |
                                MwoI|                 HhaI||||||  |         PvuII |
                            BsaXI  ||                MnlI|||||||  |      Fnu4HI | |
                         CviJI  |  ||              BstUI||||||||  |    HpyCH4V| | |                       AciI
                        HaeIII  |  ||             HinP1I||||||||  |  AseI    || | |      Hpy188III     BsrI  |
                       Sau96I|  |  ||   AciI      AciI |||||||||  |  MseI TseI| | |   BbvI       | FauI   |  |
                            ||  |  ||      |         | |||||||||  |     |    || | |      |       |    |   |  |
          tgtcgcccttttgtctttggcccaatacgcaaaccgcctctccccgcgcgttggccgattcattaatgcagctggcacgacaggtttcccgactggaaag
     4701 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 4800
          acagcgggaaaacagaaaccgggttatgcgtttggcggagaggggcgcgcaaccggctaagtaattacgtcgaccgtgctgtccaaagggctgaccttc

a          V  A  L  L  S  L  A  Q  Y  A  N  R  L  S  P  R  V  G  R  F  I  N  A  A  G  T  T  G  F  P  T  G  K  -
b           S  P  F  C  L  W  P  N  T  Q  T  A  S  P  R  A  L  A  D  S  L  M  Q  L  A  R  Q  V  S  R  L  E  S -
c         C  R  P  F  V  F  G  P  I  R  K  P  P  L  P  A  R  W  P  I  H  *  C  S  W  H  D  R  F  P  D  W  K  A-

                                                              CviJI
                            AseI                         HpyF10VI |
                            MseI                           BstNI| |
                      Tsp509I  |                            MwoI| |
                   HhaI     |  |                           ScrFI| |
                 BtsI |     |  |                         BsaJI || |
               HinP1I |     |  |                         PspGI || |
             HpyF10VI |     |  |                        StyD4I || |
                TspRI |     |  |         AluI          NlaIV  | || |                CviJI
       Cac8I    MwoI| |     |  |        CviJI        BanI |  | || |             HpaII  |         Tsp509I
           |       || |     |  |            |           | |  | || |                 |  |               |
          cgggcagtgagcgcaacgcaattaatgtgagttagctcactcattaggcaccccaggctttacactttatgcttccggctcgtatgttgtgtggaattgt
     4801 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 4900
          gcccgtcactcgcgttgcgttaattacactcaatcgagtgagtaatccgtggggtccgaaatgtgaaatacgaaggccgagcatacaacacaccttaaca

a         R  A  V  S  A  T  Q  L  M  *  V  S  S  L  I  R  H  P  R  L  Y  T  L  C  F  R  L  V  C  C  V  E  L  *-
b          G  Q  *  A  Q  R  N  *  C  E  L  A  H  S  L  G  T  P  G  F  T  L  Y  A  S  G  S  Y  V  V  W  N  C  -
c           G  S  E  R  N  A  I  N  V  S  *  L  T  H  *  A  P  Q  A  L  H  F  M  L  P  A  R  M  L  C  G  I  V -
```

Figure 19-S



```
     gagcggataacaatttcacacaggaaacagctatgaccatgattacgccaagcttgcatgcctgcaggtccccagattagccttttcaatttcagaaaga
4901 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 5000
     ctcgcctattgttaaagtgtgtcctttgtcgatactggtactaatgcggttcgaacgtacggacgtccaggggtctaatcggaaaagttaaagtctttct

a      A  D  N  N  F  T  Q  E  T  A  M  T  M  I  T  P  S  L  H  A  C  R  S  P  D  *  P  F  Q  F  Q  K  E  -
b     E  R  I  T  I  S  H  R  K  Q  L  *  P  *  L  R  Q  A  C  M  P  A  G  P  Q  I  S  L  F  N  F  R  K  N -
c      S  G  *  Q  F  H  T  G  N  S  Y  D  H  D  Y  A  K  L  A  C  L  Q  V  P  R  L  A  F  S  I  S  E  R  -

     atgctaacccacagatggttagagaggcttacgcagcaggtctcatcaagacgatctacccgagcaataatctccaggaaatcaaataccttcccaagaa
5001 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 5100
     tacgattgggtgtctaccaatctctccgaatgcgtcgtccagagtagttctgctagatgggctcgttattagaggtcctttagtttatggaagggttctt

a     C  *  P  T  D  G  *  R  G  L  R  S  R  S  H  Q  D  D  L  P  E  Q  *  S  P  G  N  Q  I  P  S  Q  E  -
b      A  N  P  Q  M  V  R  E  A  Y  A  A  G  L  I  K  T  I  Y  P  S  N  N  L  Q  E  I  K  Y  L  P  K  K -
c     M  L  T  H  R  W  L  E  R  L  T  Q  Q  V  S  S  R  R  S  T  R  A  I  I  S  R  K  S  N  T  F  P  R  R -

     ggttaaagatgcagtcaaaagattcaggactaactgcatcaagaacacagagaaagatatatttctcaagatcagaagtactattccagtatggacgatt
5101 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 5200
     ccaatttctacgtcagttttctaagtcctgattgacgtagttcttgtgtctctttctatataaagagttctagtcttcatgataaggtcatacctgctaa

a     G  *  R  C  S  Q  K  I  Q  D  *  L  H  Q  E  H  R  E  R  Y  I  S  Q  D  Q  K  Y  Y  S  S  M  D  D  S  -
b      V  K  D  A  V  K  R  P  R  T  N  C  I  K  N  T  E  K  D  I  F  L  K  I  R  S  T  I  P  V  W  T  I   -
c       L  K  M  Q  S  K  D  S  G  L  T  A  S  R  T  Q  R  K  I  Y  F  S  R  S  E  V  L  F  Q  Y  G  R  F  -
```

Figure 19-T

```
                                                                                  HinfI
                                                                                NlaIII|
                                                                             BsaJI   ||
                                                                              BtgI   ||
                                                                              PatI   ||       MnlI
                                                                              NcoI   ||     MlyI |
                                                   MlyI              TspRI    StyI   ||   HinfI| |
       Cac8I       BsaJI                          PleI|            HinfI |  CviJI|   ||    PleI| |
     CviJI |        StyI  FalI           HinfI  BsmAI||           TfiI | HaeIII|   ||    TfiI| |
         | |           |     |               |      |||                | |      ||   ||       || |
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5201 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 5300
     gttccgaacgaagtgtttggttccgttcattatctctaacctcagagatttttccatcaagggtgacttagtttccggtacctcagtttctaagtttatc

a      R  L  A  S  Q  T  K  A  S  N  R  D  W  S  L  *  K  G  S  S  H  *  I  K  G  H  G  V  K  D  S  N  R  -
b    Q  G  L  L  H  K  P  R  Q  V  I  E  I  G  V  S  K  K  V  V  P  T  E  S  K  A  M  E  S  K  I  Q  I  E -
c     K  A  C  F  T  N  Q  G  K  *  *  R  L  E  S  L  K  R  *  F  P  L  N  Q  R  P  W  S  Q  R  F  K  *    -

                                                                                                  BsiHKAI
                                                                                                 Bsp1286I
                                                          HinfI                                 FalI    |
                                                          PsrI|                            NlaIII  |    |
    BceAI                                                MlyI||                          PatI   |  |    |
   AvaII|                        HpyCH4III              PleI|||                      HincII |   |  |    |
Eco0109I|                        BsrI    |            BsmAI||||                       Hpy8I |   |  |    |
   PpuMI|                   TspDTI  |    |           MlyI |||||                    MboII  | |   |  |    |
  Sau96I|                 PsrI   |  |    |     HinfI PleI |||||        MboII   XmnI    |  | |   |  |    |
       ||                    |   |  |    |         |    | |||||            |      |    |  | |   |  |    |
     aggacctaacagaactcgccgtaaagactggcgaacagttcatacagagtctcttacgactcaatgacaagaagaaaatcttcgtcaacatggtggagca
5301 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 5400
     tcctggattgtcttgagcggcatttctgaccgcttgtcaagtatgtctcagagaatgctgagttactgttcttcttttagaagcagttgtaccacctcgt

a     G  P  N  R  T  R  R  K  D  W  R  T  V  H  T  E  S  L  T  T  Q  *  Q  E  E  N  L  R  Q  H  G  G  A   -
b      D  L  T  E  L  A  V  K  T  G  E  Q  F  I  Q  S  L  L  R  L  N  D  K  K  K  I  F  V  N  M  V  E  H -
c    R  T  *  Q  N  S  P  *  R  L  A  N  S  S  Y  R  V  S  Y  D  S  M  T  R  R  K  S  S  S  T  W  W  S  T-

                                                          MfeI
                                                       Tsp509I
                                                        BsmAI|
                                                        MboII|                         HpaII
                                           BsmAI       Hin4I||                     Hpy188III
             Hpy8I                       Hpy188I     BseMII|||                        BsaWI|
             AccI|                       DdeI  |    BspCNI||||                        BseRI|
         DrdI   ||     Hin4I     HpyCH4III  |  |    BbsI |||||                        BspEI|     BsaJI
            |   ||          |            |  |  |       | |||||                            ||         |
     cgacacacttgtctactccaaaaatatcaaagatacagtctcagaagaccaaagggcaattgagacttttcaacaaagggtaatatccggaaacctcctc
5401 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 5500
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a    R  H  T  C  L  L  Q  K  Y  Q  R  Y  S  L  R  R  P  K  G  N  *  D  F  S  T  K  G  N  I  R  K  P  P  R-
b     D  T  L  V  Y  S  K  N  I  K  D  T  V  S  E  D  Q  R  A  I  E  T  F  Q  Q  R  V  I  S  G  N  L  L   -
c      T  H  L  S  T  P  K  I  S  K  I  Q  S  Q  K  T  K  G  Q  L  R  L  F  N  K  G  *  Y  P  E  T  S  S  -

         MnlI
       BsrDI|
      MnlI ||         MaeIII                                                     BccI
   HinfI | ||     AluI     |                                               HpyF10VI |           SfaNI
    TfiI | ||    CviJI     |                                NlaIV             MwoI| |         CviJI |
Hpy188I| | ||BseYI   |Tsp45I                    MboII      CviJI|          BsrDI || |        HaeIII |
      || | ||    |   |     |                        |          ||              | || |             | |
     ggattccattgcccagctatctgtcactttattgtgaagatagtggaaaaggaaggtggctcctacaaatgccatcattgcgataaaggaaaggccatcg
5501 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 5600
     cctaaggtaacgggtcgatagacagtgaaataacacttctatcaccttttccttccaccgaggatgtttacggtagtaacgctatttcctttccggtagc

a      I  P  L  P  S  Y  L  S  L  Y  C  E  D  S  G  K  G  R  W  L  L  Q  M  P  S  L  R  *  R  K  G  H  R  -
b    G  F  H  C  P  A  I  C  H  F  I  V  K  I  V  E  K  E  G  G  S  Y  K  C  H  H  C  D  K  G  K  A  I  V-
c     D  S  I  A  Q  L  S  V  T  L  L  *  R  *  W  K  R  K  V  A  P  T  N  A  I  I  A  I  K  E  R  P  S   -
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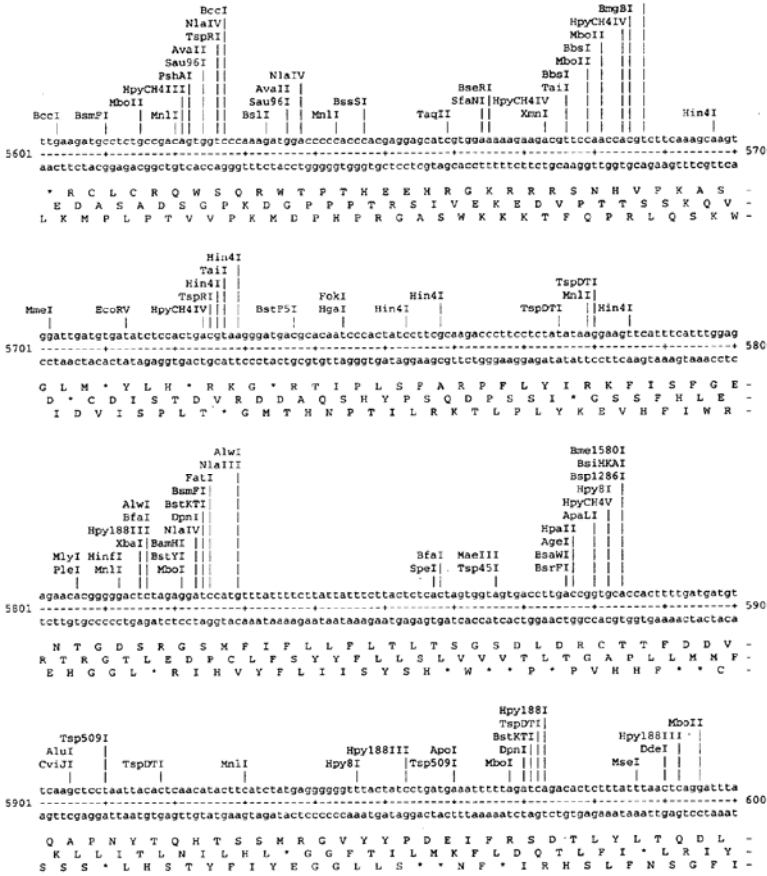
Figure 19-U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BmgBI
NlaIV
HpyCH4IV
TspRI
MboII
AvaII
BbsI
Sau96I
MboII
PshAI
NlaIV
BbsI
HpyCH4III
AvaII
BseRI
TaiI
MboII
Sau96I
BssSI
SfaNI
HpyCH4IV
BccI
BsmFI
MnlI
BslI
MnlI
TaqII
XmnI
Hin4I
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5601
5700
aacttctacggagacggctgtcaccagggtttctacctgggggtgggtgctcctcgtagcaccttttcttctgcaaggttggtgcagaagtttcgttca
a * R C L C R Q W S Q R W T P T H E E H R G K R R R S N H V P K A S -
b E D A S A D S G P K D G P P P T R S I V E K E D V P T T S S K Q V -
c L K M P L P T V V P K M D P H P R G A S W K K K T F Q P R L Q S K W -
Hin4I
TaiI
Hin4I
TspRI
TspDTI
MnlI
FokI
Hin4I
MmeI
EcoRV
HpyCH4IV
BstF5I
HgaI
Hin4I
TspDTI
Hin4I
ggattgatgtgatatctccactgacgtaagggatgacgcacaatcccactatccttcgcaagacccttcctctatataaggaagttcatttcatttggag
5701
5800
cctaactacactatagaggtgactgcattccctactgcgtgttagggtgataggaagcgttctgggaaggagatatattccttcaagtaaagtaaacctc
a G L M * Y L H * R K G * R T I P L S F A R P F L Y I R K F I S F G E -
b D * C D I S T D V R D D A Q S H Y P S Q D P S S I * G S S F H L E -
c I D V I S P L T * G M T H N P T I L R K T L P L Y K E V H F I W R -
AlwI
NlaIII
Bme1580I
BsiHKAI
FatI
Bsp1286I
BsmFI
Hpy8I
AlwI
BstKTI
HpyCH4V
BfaI
DpnI
ApaLI
Hpy188III
NlaIV
HpaII
XbaI
BamHI
AgeI
MlyI
HinfI
BstYI
BfaI
MaeIII
BsaWI
PleI
MnlI
MboI
SpeI
Tsp45I
BsrFI
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5801
5900
tcttgtgcccctgagatctcctaggtacaaataaagaataataaagaatgagagtgatcaccatcactggaactggccacgtggtgaaaactactaca
a N T G D S R G S M F I F L L F L T L T S G S D L D R C T T F D D V -
b R T R G T L E D P C L F S Y Y F L L S L V V V T L T G A P L L M M F -
c E H G G L * R I H V Y F L I I S Y S H * W * * P * P V H H F * * C -
Hpy188I
TspDTI
MboII
Tsp509I
BstKTI
Hpy188III
AluI
Hpy188III
ApoI
DpnI
DdeI
CviJI
TspDTI
MnlI
Hpy8I
Tsp509I
MboI
MseI
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5901
6000
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a Q A P N Y T Q H T S S M R G V Y Y P D E I F R S D T L Y L T Q D L -
b K L L I T L N I L H L * G G F T I L M K F L D Q T L F I * L R I Y -
c S S S * L H S T Y F I Y E G G L L S * * N F * I R H S L F N S G F I -

Figure 19-V

```
                                                     TaiI
                                              HpyCH4IV  |                                    Fnu4HI
   BseMII            TspDTI               AseI       |  |                  MseI    BstF5I     TseI|
  BspCNI|           MaeIII|               MseI       |  |                 BccI|   BbvI  |   FokI ||
       ||                ||                  |       |  |                    ||      |  |      | ||
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6001 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 6100
     aaagaaggtaaaataagattacaatgtcccaaagtatgataattagtatgcaaaccgttgggacagtatggaaaattcctaccataaataaaacgacggt

a    F  L  P  F  Y  S  N  V  T  G  F  H  T  I  N  H  T  F  G  N  P  V  I  P  F  K  D  G  I  Y  F  A  A  T -
b     F  F  H  F  I  L  M  L  Q  G  F  I  L  L  I  I  R  L  A  T  L  S  Y  L  L  R  M  V  F  I  L  L  P  -
c      S  S  I  L  F  *  C  Y  R  V  S  Y  Y  *  S  Y  V  W  Q  P  C  H  T  F  *  G  W  Y  L  F  C  C  H -

                                                         HpyCH4III
                                                           TspDTI|            Tsp509I
                    BsaJI                     NlaIII  MaeIII    ||            HphI  |
        TspGWI       BtgI  BslI             FatI   |  Tsp45I    ||           MseI|  |
             |          |     |                |   |       |    ||              ||  |
     cagagaaatcaaatgttgtccgtggttgggtttttggttctaccatgaacaacaagtcacagtcggtgattattattaacaattctactaatgttgttat
6101 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 6200
     gtctctttagtttacaacaggcaccaacccaaaaaccaagatggtacttgttgttcagtgtcagccactaataataattgttaagatgattacaacaata

a      E  K  S  N  V  V  R  G  W  V  F  G  S  T  M  N  N  K  S  Q  S  V  I  I  I  N  N  S  T  N  V  V  I -
b    Q  R  N  Q  M  L  S  V  V  G  F  L  V  L  P  *  T  T  S  H  S  R  *  L  L  L  T  I  L  L  M  L  L  Y -
c     R  E  I  K  C  C  P  W  L  G  F  W  F  Y  H  E  Q  Q  V  T  V  G  D  Y  Y  *  Q  F  Y  *  C  C  Y  -

                                                             Hpy8I
                                                             RsaI|
                                                           Csp6I||
                                                        NlaIII |||
                                                      BsaJI  | |||                             Tsp509I
        NlaIII                                         BtgI  | |||                               MseI|
          NspI        MaeIII                           FatI  | |||                             NsiI ||
       MaeIII|        Tsp45I                           NcoI  | |||                          BfrBI | ||
      FatI  || Tsp509I     |                           StyI  | |||                  TaqI HpyCH4V  | ||
         |  ||       |     |                              |  | |||                     |       |  | ||
     acgagcatgtaactttgaattgtgtgacaaccctttctttgctgtttctaaacccatgggtacacagacacatactatgatattcgataatgcatttaat
6201 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 6300
     tgctcgtacattgaaacttaacacactgttgggaaagaaacgacaaagatttgggtacccatgtgtctgtgtatgatactataagctattacgtaaatta

a     R  A  C  N  F  E  L  C  D  N  P  F  F  A  V  S  K  P  M  G  T  Q  T  H  T  M  I  F  D  N  A  F  N  -
b      E  H  V  T  L  N  C  V  T  T  L  S  L  L  F  L  N  P  W  V  H  R  H  I  L  *  Y  S  I  M  H  L  I -
c    T  S  M  *  L  *  I  V  *  Q  P  F  L  C  C  F  *  T  H  G  Y  T  D  T  Y  Y  D  I  R  *  C  I  *  L -

              RsaI
            Csp6I|
            SfaNI|
HpyCH4V     TatI||                                              DraI                    DraI
 Hin4I|  TaqI  ||| Hpy188I       Hin4I     Hpy188I     Tsp509I MseI|                   MseI|BccI
     ||     |  |||       |           |           |           |    ||                      ||   |
     tgcactttcgagtacatatctgatgccttttcgcttgatgtttcagaaaagtcaggtaattttaaacacttacgagagtttgtgtttaaaaataaagatg
6301 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 6400
     acgtgaaagctcatgtatagactacggaaaagcgaactacaaagtcttttcagtccattaaaatttgtgaatgctctcaaacacaaatttttatttctac

a    C  T  F  E  Y  I  S  D  A  F  S  L  D  V  S  E  K  S  G  N  F  K  H  L  R  E  F  V  F  K  N  K  D  G -
b     A  L  S  S  T  Y  L  M  P  F  R  L  M  F  Q  K  S  Q  V  I  L  N  T  Y  E  S  L  C  L  K  I  K  M  -
c      H  F  R  V  H  I  *  C  L  F  A  *  C  F  R  K  V  R  *  F  *  T  L  T  R  V  C  V  *  K  *  R  W -

                                                 BstKTI
                                                  DpnI|
                                                MboI ||
                 PsiI CviJI     SfcI     Hpy188III | ||          MseI                 MseI
                    |     |        |             | | ||             |                    |
     ggtttctctatgtttataagggctatcaacctatagatgtagttcgtgatctaccttctggttttaacactttgaaacctatttttaagttgcctcttgg
6401 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 6500
     ccaaagagatacaaatattcccgatagttggatatctacatcaagcactagatggaagaccaaaattgtgaaactttggataaaaattcaacggagaacc

a      F  L  Y  V  Y  K  G  Y  Q  P  I  D  V  V  R  D  L  P  S  G  F  N  T  L  K  P  I  F  K  L  P  L  G -
b    G  F  S  M  F  I  R  A  I  N  L  *  M  *  F  V  I  Y  L  L  V  L  T  L  *  N  L  F  L  S  C  L  L  V -
c     V  S  L  C  L  *  G  L  S  T  Y  R  C  S  S  *  S  T  F  W  F  *  H  F  E  T  Y  F  *  V  A  S  W  -
```

Figure 19-W

```
                                                                               CviJI
                                                                                PstI|
                                                                            Fnu4HI||
                                                                          HpyCH4V|||
                                                                              TseI|||
                                                                           Fnu4HI ||||
                                                                             SfcI ||||
                                                                           AluI|  ||||
                                                                          CviJI|  ||||
                                                                         MspA1I|  ||||
                                                                          PvuII|  ||||
                                                                           TseI|  ||||
                                                                      TaiI   ||  ||||
                                                                  BmgBI |    ||  ||||
                                        AarI               Bme1580I| |    ||  ||||
                         CviJI          BspMI              Bsp1286I| |    ||  ||||                      CviJI
    MnlI     ApoI                BpuEI |   Hpy188III |     HpyCH4IV| |    ||  ||||         CviJI  DraI   |
    MseI  Tsp509I      CviJI      HphI |        SmlI| |  BbvI      || |    ||  ||||   BbvI    | MseI|   |
      |        |           |          ||          |  | |    |       || |    ||  ||||    |      |    ||   |
     tattaacattacaaatttagagccattcttacagccttttcacctgctcaagacatttggggcacgtcagctgcagcctattttgttggctatttaaag
6501 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 6600
     ataattgtaatgtttaaaatctcggtaagaatgtcggaaaagtggacgagttctgtaaaccccgtgcagtcgacgtcggataaaacaaccgataaatttc

a      I  N  I  T  N  F  R  A  I  L  T  A  F  S  P  A  Q  D  I  W  G  T  S  A  A  A  Y  F  V  G  Y  L  K  -
b       L  T  L  Q  I  L  E  P  F  L  Q  P  F  H  L  L  K  T  F  G  A  R  Q  L  Q  P  I  L  L  A  I  *  S  -
c     Y  *  H  Y  K  F  *  S  H  S  Y  S  L  F  T  C  S  R  H  L  G  H  V  S  C  S  L  F  C  W  L  F  K  A -

                                      TspDTI
                                   RsaI  |
                                  SfaNI  |
  BpuEI         SmlI              Csp6I| |    AlwNI                                               MseI
    |              |                  || |       |                                                    |
     ccaactacatttatgctcaagtatgatgaaaatggtacaatcacagatgctgttgattgttctcaaaatccacttgctgaactcaaatgctctgttaaga
6601 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 6700
     ggttgatgtaaatacgagttcatactacttttaccatgttagtgtctacgacaactaacaagagttttaggtgaacgacttgagtttacgagacaattct

a     P  T  T  F  M  L  K  Y  D  E  N  G  T  I  T  D  A  V  D  C  S  Q  N  P  L  A  E  L  K  C  S  V  K  S -
b      Q  L  H  L  C  S  S  M  M  K  M  V  Q  S  Q  M  L  L  I  V  L  K  I  H  L  L  N  S  N  A  L  L  R  -
c       N  Y  I  Y  A  Q  V  *  *  K  W  Y  N  H  R  C  C  *  L  F  S  K  S  T  C  *  T  Q  M  L  C  *  E  -

                                                                          HinfI
                                                       Hpy188III           TfiI
                                                          Bsu36I |      BseMII |
  AluI           ApoI                                       DdeI |    BspCNI| |        SspI
 CviJI        Tsp509I            Tsp509I  MnlI      BsaXI    | |    MnlI  || |      BsaXI|               MnlI
    |              |                   |     |          |    | |      |   || |          ||                  |
     gctttgagattgacaaaggaatttaccagacctctaatttcagggttgttccctcaggagatgttgtgagattccctaatattacaaacttgtgtccttt
6701 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 6800
     cgaaactctaactgtttccttaaatggtctggagattaaagtcccaacaagggagtcctctacaacactctaagggattataatgtttgaacacaggaaa

a       F  E  I  D  K  G  I  Y  Q  T  S  N  F  R  V  V  P  S  G  D  V  V  R  F  P  N  I  T  N  L  C  P  F  -
b     A  L  R  L  T  K  E  F  T  R  P  L  I  S  G  L  F  P  Q  E  M  L  *  D  S  L  I  L  Q  T  C  V  L  L -
c      L  *  D  *  Q  R  N  L  P  D  L  *  F  Q  G  C  S  L  R  R  C  C  E  I  P  *  Y  Y  K  L  V  S  F    -

                                                NlaIII
                                                  NsiI |
                                                 BfrBI | |                 Tsp509I
                         ApoI                     FatI | |            ApoI      |                   BsiHKAI
              MseI    Tsp509I                 HpyCH4V | |         Tsp509I      |                  Bsp1286I
                 |          |                       | | |               |      |                          |
     tggagaggtttttaatgctactaaattcccttctgtctatgcatgggagagaaaaaaaatttctaattgtgttgctgattactctgtgctctacaactca
6801 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 6900
     acctctccaaaaattacgatgatttaagggaagacagatacgtaccctctcttttttttaaagattaacacaacgactaatgagacacgagatgttgagt

a      G  E  V  F  N  A  T  K  F  P  S  V  Y  A  W  E  R  K  K  I  S  N  C  V  A  D  Y  S  V  L  Y  N  S   -
b       E  R  F  L  M  L  L  N  S  L  L  S  M  H  G  R  E  K  K  F  L  I  V  L  L  I  T  L  C  S  T  T  Q  -
c     W  R  G  F  *  C  Y  *  I  P  F  C  L  C  M  G  E  K  K  N  F  *  L  C  C  *  L  L  C  A  L  Q  L  N -
```

Figure 19-X

```
                                                        BstKTI                    HinfI
                                                         DpnI|                     TfiI
                     MseI                    DdeI      MboI ||               HpyCH4V  |     BsaXI
                        |                       |         | ||                     |  |         |
        acatttttttcaacctttaagtgctatggcgtttctgccactaagttgaatgatctttgcttctccaatgtctatgcagattcttttgtagtcaagggag
   6901 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 7000
        tgtaaaaaaagttggaaattcacgataccgcaaagacggtgattcaacttactagaaacgaagaggttacagatacgtctaagaaaacatcagttccctc

a       T  F  F  S  T  F  K  C  Y  G  V  S  A  T  K  L  N  D  L  C  F  S  N  V  Y  A  D  S  F  V  V  K  G  D -
b        H  F  F  Q  P  L  S  A  M  A  F  L  P  L  S  *  M  I  F  A  S  P  M  S  M  Q  I  L  L  *  S  R  E   -
c         I  F  F  N  L  *  V  L  W  R  F  C  H  *  V  E  *  S  L  L  L  Q  C  L  C  R  F  F  C  S  Q  G  R  -

                         BstNI
                         ScrFI
                        HaeII|
                        HhaI||
                       PspGI||                                  TspDTI
                      StyD4I||                            Tsp509I    |
                      BsaXI|||                     Tsp509I      |    |         NlaIII
                    HinP1I||||         BsrI          PsiI| PsiI |    |       FatI   |                   BfaI
                         |||||            |             ||    | |    |          |   |                      |
        atgatgtaagacaaatagcgccaggacaaactggtgttattgctgattataattataaattgccagatgatttcatgggttgtgtccttgcttggaatac
   7001 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 7100
        tactacattctgtttatcgcggtcctgtttgaccacaataacgactaatattaatatttaacggtctactaaagtacccaacacaggaacgaaccttatg

a         D  V  R  Q  I  A  P  G  Q  T  G  V  I  A  D  Y  N  Y  K  L  P  D  D  F  M  G  C  V  L  A  W  N  T  -
b       M  M  *  D  K  *  R  Q  D  K  L  V  L  L  L  I  I  I  I  N  C  Q  M  I  S  W  V  V  S  L  L  G  I  L -
c        *  C  K  T  N  S  A  R  T  N  W  C  Y  C  *  L  *  L  *  I  A  R  *  F  H  G  L  C  P  C  L  E  Y   -

                                                                            CviJI
                                                                           HaeIII
                                                                        Eco0109I|
                                                                          Sau96I|
                                                                      Bpu10I   ||
                                                                        DdeI   ||
                                                                       AluI|   ||
                                                                      CviJI|   ||
                                                                    Cac8I ||   ||
                                   Tsp509I                        HindIII ||   ||
                                BsrI     |                      NlaIII  | ||   ||
    SfaNI                    Tsp509I PsiI| PsiI          DdeI FatI   |  | ||   ||BsmAI
        |                          |    ||    |             |    |   |  | ||   ||   |
        taggaacattgatgctacttcaactggtaattataattataaatataggtatcttagacatggcaagcttaggccctttgagagagacatatctaatgtg
   7101 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 7200
        atccttgtaactacgatgaagttgaccattaatattaatatttatatccatagaatctgtaccgttcgaatccgggaaactctctctgtatagattacac

a        R  N  I  D  A  T  S  T  G  N  Y  N  Y  K  Y  R  Y  L  R  H  G  K  L  R  P  F  E  R  D  I  S  N  V   -
b         G  T  L  M  L  L  Q  L  V  I  I  I  I  N  I  G  I  L  D  M  A  S  L  G  P  L  R  E  T  Y  L  M  C  -
c       *  E  H  *  C  Y  F  N  W  *  L  *  L  *  I  *  V  S  *  T  W  Q  A  *  A  L  *  E  R  H  I  *  C  A -

                           HpyCH4V            AarI       CviJI
                        HpyF10VI |           BspMI      HaeIII
                         BstAPI| |         Tsp509I        MscI                                    CviJI
           BccI            MwoI| |           MseI|      EaeI |MseI                            BsrI    |
              |               || |             ||         | |   |                               |    |
        cctttctcccctgatggcaaaccttgcaccccacctgctcttaattgttattggccattaaatgattatggtttttacaccactactggcattggctacc
   7201 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 7300
        ggaaagaggggactaccgtttggaacgtggggtggacgagaattaacaataaccggtaatttactaataccaaaaatgtggtgatgaccgtaaccgatgg

a       P  F  S  P  D  G  K  P  C  T  P  P  A  L  N  C  Y  W  P  L  N  D  Y  G  F  Y  T  T  T  G  I  G  Y  Q -
b        L  S  P  L  M  A  N  L  A  P  H  L  L  L  I  V  I  G  H  *  M  I  M  V  F  T  P  L  L  A  L  A  T   -
c         F  L  P  *  W  Q  T  L  H  P  T  C  S  *  L  L  L  A  I  K  *  L  W  F  L  H  H  Y  W  H  W  L  P  -
```

Figure 19-Y

```
                                                    HpyCH4III
                                                    BsaJI   |
                                                     BtgI   |
                                                   CviJI|   |
                                                  HaeIII|   |
                                                  EaeI ||   |
                                                HpaII| ||   |
                       RsaI                    BsrFI|: ||   |      Tsp509I
                       ScaI                HpyCH4V ||| ||   |  AvaII     |
                     Csp6I|              DraI    | ||| ||   |  Hpy8I     |
                     TatI||            MseI|     | |||.||   | Sau96I     |         TspRI MseI   BsrI  TspRI
                        |||                ||    | ||||||   |      |     |             |    |      |      |
        aaccttacagagttgtagtactttcttttgaacttttaaatgcaccggccacggtttgtggaccaaaattatccactgaccttattaagaaccagtgtgt
   7301 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 7400
        ttggaatgtctcaacatcatgaaagaaaacttgaaaatttacgtggccggtgccaaacacctggttttaataggtgactggaataattcttggtcacaca

a         P  Y  R  V  V  V  L  S  F  E  L  L  N  A  P  A  T  V  C  G  P  K  L  S  T  D  L  I  K  N  Q  C  V   -
b       N  L  T  E  L  *  Y  F  L  L  N  F  *  M  H  R  P  R  F  V  D  Q  N  Y  P  L  T  L  L  R  T  S  V  S  -
c        T  L  Q  S  C  S  T  F  F  *  T  F  K  C  T  G  H  G  L  W  T  K  I  I  H  *  P  Y  *  E  P  V  C    -

                                         HincII
                                           HpaI
                                BsrI      Hpy8I
                MlyI            RsaI      MboII                                     CviJI
        Tsp509I MseI  BaeI     TspRI      MseI|                                    HaeIII          TspGWI
  Tsp509I MseI| PleI HinfI    Csp6I|  BsrI   ||        BaeI          BceAI Tsp509I EaeI |      Hpy188I  |
        |    ||    |     |        ||     |   ||           |              |       |    | |            |  |
        caattttaattttaatggactcactggtactggtgtgttaactccttcttcaaagagatttcaaccatttcaacaatttggccgtgatgtttctgatttc
   7401 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 7500
        gttaaaattaaaattacctgagtgaccatgaccacacaattgaggaagaagtttctctaaagttggtaaagttgttaaaccggcactacaaagactaaag

a        N  F  N  F  N  G  L  T  G  T  G  V  L  T  P  S  S  K  R  F  Q  P  F  Q  Q  F  C  R  D  V  S  D  F    -
b         I  L  I  L  M  D  S  L  V  L  V  C  *  L  L  L  Q  R  D  F  N  H  F  N  N  L  A  V  M  F  L  I  S   -
c       Q  F  *  F  *  W  T  H  W  Y  W  C  V  N  S  F  F  K  E  I  S  T  I  S  T  I  W  P  *  C  F  *  F  H  -

                    BstKTI
                     DpnI|
                  BstYI ||
                   MboI ||                                                              TspDTI
            Hpy188III | ||                                                            BstNI  |
         TspRI      | | ||                                                            ScrFI  |
       HinfI |  TaqI| | ||                HphI                                      PspGI |  |
        TfiI |AlwI || | ||     Hpy188I SspI  |                             Tsp509I StyD4I |  |
           | |   | || | ||           |    |  |                                   |      | |  |
        actgattccgttcgagatcctaaaacatctgaaatattagacatttcaccttgctcttttgggggtgtaagtgtaattacacctggaacaaatgcttcat
   7501 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 7600
        tgactaaggcaagctctaggattttgtagactttataatctgtaaagtggaacgagaaaacccccacattcacattaatgtggaccttgtttacgaagta

a       T  D  S  V  R  D  P  K  T  S  E  I  L  D  I  S  P  C  S  F  G  G  V  S  V  I  T  P  G  T  N  A  S  S  -
b        L  I  P  F  E  I  L  K  H  L  K  Y  *  T  F  H  L  A  L  L  G  V  *  V  *  L  H  L  E  Q  M  L  H    -
c         *  F  R  S  R  S  *  N  I  *  N  I  R  H  F  T  L  L  F  W  G  C  K  C  N  Y  T  W  N  K  C  F  I   -

                                                                   BstKTI
                                                                    DpnI|
                                                                  MboI ||
                                                             HpyCH4V | ||
                                                              NlaIII | ||
                                                          HpyF10VI | | ||
                                   HpyCH4V                 BstAPI| | | ||
                        Eco57I HincII    |           Tsp509I    || | | ||                HhaI
                       Eco57MI   HpaI    |        SfcI     |    || | | ||            HinP1I |
                    Hpy188III|  Hpy8I    |     TspDTI|     | MwoI| | | ||         AluI    | |
   Hpy188I           BsgI   ||  MseI|    |  TspRI   ||     |FatI|| | | ||        CviJI    | |
         |              |   ||     ||    |      |   ||     |   ||| | | ||            |    | |
        ctgaagttgctgttctatatcaagatgttaactgcactgatgtttctacagcaattcatgcagatcaactcacaccagcttggcgcatatattctactgg
   7601 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 7700
        gacttcaacgacaagatatagttctacaattgacgtgactacaaagatgtcgttaagtacgtctagttgagtgtggtcgaaccgcgtatataagatgacc

a         E  V  A  V  L  Y  Q  D  V  N  C  T  D  V  S  T  A  I  H  A  D  Q  L  T  P  A  W  R  I  Y  S  T  G   -
b       L  K  L  L  F  Y  I  K  M  L  T  A  L  M  F  L  Q  Q  F  M  Q  I  N  S  H  Q  L  G  A  Y  I  L  L  E  -
c        *  S  C  C  S  I  S  R  C  *  L  H  *  C  F  Y  S  N  S  C  R  S  T  H  T  S  L  A  H  I  F  Y  W    -
```

Figure 19-Z

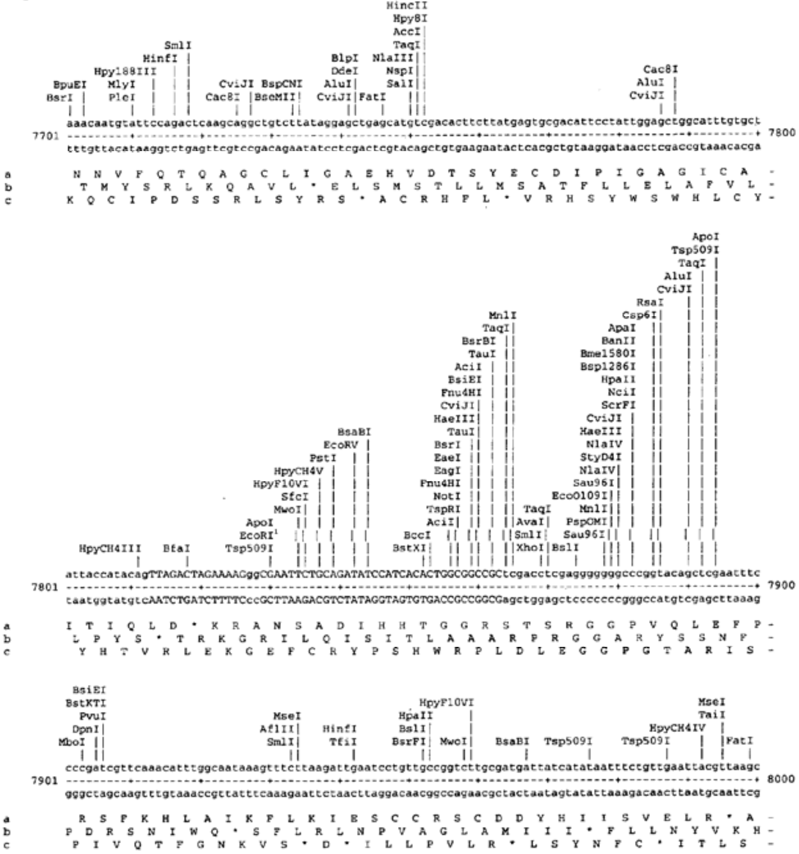

HincII
Hpy8I
AccI
TaqI
SmlI
HinfI
BlpI
NlaIII
Hpy188III
DdeI
NspI
BpuEI
MlyI
CviJI
BspCNI
AluI
SalI
Cac8I
AluI
BsrI
PleI
Cac8I
BseMII
CviJI
FatI
CviJI
aaacaatgtattccagactcaagcaggctgtcttataggagctgagcatgtcgacacttcttatgagtgcgacattcctattggagctggcatttgtgct
7701
7800
tttgttacataaggtctgagttcgtccgacagaatatcctcgactcgtacagctgtgaagaatactcacgctgtaaggataacctcgaccgtaaacacga
a N N V F Q T Q A G C L I G A E H V D T S Y E C D I P I G A G I C A -
b T M Y S R L K Q A V L * E L S M S T L L M S A T F L L E L A F V L -
c K Q C I P D S S R L S Y R S * A C R H P L * V R H S Y W S W H L C Y -
ApoI
Tsp509I
TaqI
AluI
CviJI
RsaI
MnlI
Csp6I
TaqI
ApaI
BsrBI
BanII
TauI
Bme1580I
AciI
Bsp1286I
BsiEI
HpaII
Fnu4HI
NciI
CviJI
ScrFI
HaeIII
CviJI
BsaBI
TauI
HaeIII
EcoRV
BsrI
NlaIV
PstI
EaeI
StyD4I
HpyCH4V
EagI
NlaIV
HpyF10VI
Fnu4HI
Sau96I
SfcI
NotI
Eco0109I
MwoI
TspRI
TaqI
MnlI
ApoI
AciI
AvaI
PspOMI
EcoRI
BccI
SmlI
Sau96I
HpyCH4III
BfaI
Tsp509I
BstXI
XhoI
BslI
attaccatacagTTAGACTAGAAAAGggCGAATTCTGCAGATATCCATCACACTGGCGGCCGCtcgacctcgagggggggcccggtacagctcgaatttc
7801
7900
taatggtatgtcAATCTGATCTTTTCccGCTTAAGACGTCTATAGGTAGTGTGACCGCCGGCGagctggagctcccccccgggccatgtcgagcttaaag
a I T I Q L D * K R A N S A D I H H T G G R S T S R G G P V Q L E F P -
b L P Y S * T R K G R I L Q I S I T L A A A R P R G G A R Y S S N F -
c Y H T V R L E K G E F C R Y P S H W R P L D L E G G P G T A R I S -
BsiEI
BstKTI
HpyF10VI
MseI
PvuI
MseI
HpaII
TaiI
DpnI
AflII
HinfI
BslI
HpyCH4IV
MboI
SmlI
TfiI
BsrFI
MwoI
BsaBI
Tsp509I
Tsp509I
FatI
cccgatcgttcaaacatttggcaataaagtttcttaagattgaatcctgttgccggtcttgcgatgattatcatataatttctgttgaattacgttaagc
7901
8000
gggctagcaagtttgtaaaccgttatttcaaagaattctaacttaggacaacggccagaacgctactaatagtatattaaagacaacttaatgcaattcg
a R S F K H L A I K F L K I E S C C R S C D D Y H I I S V E L R * A -
b P D R S N I W Q * S F L R L N P V A G L A M I I I * F L L N Y V K H -
c P I V Q T F G N K V S * D * I L L P V L R * L S Y N F C * I T L S -

Figure 19-AA

```
                               TaiI
                        HpyCH4IV  |
                         NlaIII|  |
                         NsiI ||  |
                      BfrBI | ||  |
                       FatI | ||  |
                    HpyCH4V | ||  |
                NlaIII    | | ||  |
            AflIII   |    | | ||  |
              FatI   |    | | ||  |
              PciI   |    | | ||  |
           MseI  |   |    | | ||  |                                    FauI
     Tsp509I  |  |   |    | | ||  |                                 MlyI  |
  NlaIII   |  |  |   |    | | ||  |                                PleI|  |
           |  |  |   |    | | ||  |                            Tsp509I||  |
    NspI   |  |  |NspI    | | ||  |BccI      BsmFI        HinfI AciI  ||  |   MseI  BstUI
       |   |  |  |   |    | | ||  |   |           |           |    |  ||  |      |       |
     atgtaataattaacatgtaatgcatgacgttatttatgagatgggtttttatgattagagtcccgcaattatacatttaatacgcgatagaaaacaaaat
8001 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 8100
     tacattattaattgtacattacgtactgcaataaatactctacccaaaaatactaatctcagggcgttaatatgtaaattatgcgctatcttttgtttta

a     C  N  N  *  H  V  M  H  D  V  I  Y  E  M  G  F  Y  D  *  S  P  A  I  I  H  L  I  R  D  R  K  Q  N   -
b      V  I  I  N  M  *  C  M  T  L  F  M  R  W  V  F  M  I  R  V  P  Q  L  Y  I  *  Y  A  I  E  N  K  I  -
c    M  *  *  L  T  C  N  A  *  R  Y  L  *  D  G  F  L  *  L  E  S  R  N  Y  T  F  N  T  R  *  K  T  K  Y -

                                 AciI
                                BstUI                       ApoI
         HhaI                    HhaI                      EcoRI[3]
        Hin4I                 BstUI |                    Tsp509I
      BstUI |                Cac8I  |               Hpy188III  |          Hpy99I       Hpy99I
      Cac8I |                  HhaI |                 BstKTI|  |       BsrI    |   Hpy188III|
       HhaI |                HinP1I |                 BceAI||  |      TspRI    |      MaeIII|
     HinP1I |              BssHII | |                  DpnI||  |     CviJI|    |      Tsp45I|
   BssHII | |     Tsp509I   BstUI | |       MaeIII   MboI |||  |    HaeIII|    |       TaiI||
   HinP1I | | BfaI      |  HinP1I | |   Hin4I    | BfaI | |||  |    EaeI ||    |HpyCH4IV  |||    BsrI
        | | |    |      |       | | |       |    |    | | |||  |       | ||    |       |  |||       |
     atagcgcgcaaactaggataaattatcgcgcgcggtgtcatctatgttactagatcgggaattcactggccgtcgttttacaacgtcgtgactgggaaaa
8101 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 8200
     tatcgcgcgtttgatcctatttaatagcgcgcgccacagtagatacaatgatctagcccttaagtgaccggcagcaaaatgttgcagcactgaccctttt

a    I  A  R  K  L  G  *  I  I  A  R  G  V  I  Y  V  T  R  S  G  I  H  W  P  S  F  Y  N  V  V  T  G  K  T -
b     *  R  A  N  *  D  K  L  S  R  A  V  S  S  M  L  L  D  R  E  F  T  G  R  R  F  T  T  S  *  L  G  K   -
c      S  A  Q  T  R  I  N  Y  R  A  R  C  H  L  C  Y  *  I  G  N  S  L  A  V  V  L  Q  R  R  D  W  E  N  -

                                                                                  BsiEI
                                                                                 BstKTI
                                                                               HpyF10VI
                                                                                   PvuI
                                                                                  DpnI|
                                                                                  MwoI|
                                                                                 FauI||
      MaeIII                                                                    MboI|||
   BstNI   |                                         Cac8I                   MboII ||||
   ScrFI   |                                        AluI |                AciI   | ||||
  BmrI |   |                     BstF5I            CviJI |               Cac8I   | ||||
 BsaJI |   |                Fnu4HI    |           MspA1I |             CviJI |   | ||||
 PspGI |   |          FokI HpyCH4V|   |            PvuII |    MnlI    HaeIII |   | ||||            HinP1I
StyD4I |   |       MseI  |    TseI|   |   BbvI   Cac8I | |   EarI|   Sau96I| |   | ||||     HpyCH4III   |
     | |   |          |  |       ||   |      |       | | |      ||        || |   | ||||             |   |
     ccctggcgttacccaacttaatcgccttgcagcacatccccctttcgccagctggcgtaatagcgaagaggcccgcaccgatcgcccttcccaacagttg
8201 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 8300
     gggaccgcaatgggttgaattagcggaacgtcgtgtagggggaaagcggtcgaccgcattatcgcttctccgggcgtggctagcgggaagggttgtcaac

a       L  A  L  P  N  L  I  A  L  Q  H  I  P  L  S  P  A  G  V  I  A  K  R  P  A  P  I  A  L  P  N  S  C  -
b    P  W  R  Y  P  T  *  S  P  C  S  T  S  P  F  R  Q  L  A  *  *  R  R  G  P  H  R  S  P  F  P  T  V  A -
c     P  G  V  T  Q  L  N  R  L  A  A  H  P  P  F  A  S  W  R  N  S  E  E  A  R  T  D  R  P  S  Q  Q  L   -
```

Figure 19-BB

```
                        HpyF10VI
                   BsrBI       |
                   AciI |      |
                  Cac8I |      |
                  BbeI| |      |
                 HaeII| |      |
                 HhaI|| |      |
               NlaIV||| |      |
                SfoI||| |      |
               BbvI|||| |      |
              BsaHI|||| |      |
             HinP1I|||| |      |                               CviJI
              NarI||||| |      |                           Cac8I   |
              BanI||||| |      |                            NaeI   |
              KasI||||| |      |                            HpaII| |
         HpyF10VI|||||| |      |                           BsrFI|| |
     CviJI      ||||||| |      |                          NgoMIV|| |
  Fnu4HI |      ||||||| |      |                      HpyF10VI ||| |                          BanII
   HhaI| |      ||||||| |  MwoI|                         MwoI| ||| |                       Bsp1286I
  TseI|| | BglI|||||||| | FauI||                        TaiI|| ||| |          AluI           NlaIV|
 FspI||| | MwoI|||||||| |MboII||                 HpyCH4IV   || ||| |          CviJI         CviJI||
     ||| |     |||||||| |    |||                         |  || ||| |              |             |||
     cgcagcctgaatggcgcccgctcctttcgctttcttcccttcctttctcgccacgttcgccggctttccccgtcaagctctaaatcgggggctccctttta
8301 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 8400
     gcgtcggacttaccgcgggcgaggaaagcgaaagaagggaaggaaagagcggtgcaagcggccgaaaggggcagttcgagatttagcccccgagggaaat

a     A  A  *  M  A  F  A  P  P  A  F  F  P  S  F  L  A  T  P  A  G  F  P  R  Q  A  L  N  R  G  L  P  L  -
b      Q  P  E  W  R  P  L  L  S  L  S  S  L  P  F  S  P  R  S  P  A  F  P  V  K  L  *  I  G  G  S  L  *  -
c    R  S  L  N  G  A  R  S  F  R  F  L  P  F  L  S  R  H  V  R  R  L  S  P  S  S  S  K  S  G  A  P  F  R -

                                                                        CviJI
                                                                       HaeIII
                                                                    Sau96I  |
                                                                 DraIII   | |
                                                                   TaiI|  | |
                                                                BsaAI ||  | |
                                        TaqII                    HphI ||  | |
     Hpy188I             NlaIV       BceAI  |               HpyCH4IV| ||  | |         HpyCH4III
    NlaIV  |           BanI  |TaqI    MnlI  |    BccI       Hpy8I  || ||  | |    BccI     MmeI|
        |  |               | |   |       |  |        |           | || ||  | |        |       ||
     gggttccgatttagtgctttacggcacctcgaccccaaaaaacttgatttgggtgatggttcacgtagtgggccatcgccctgatagacggtttttcgcc
8401 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 8500
     cccaaggctaaatcacgaaatgccgtggagctggggttttttgaactaaacccactaccaagtgcatcacccggtagcgggactatctgccaaaaagcgg

a    G  F  R  F  S  A  L  R  H  L  D  P  K  K  L  D  L  G  D  G  S  R  S  G  P  S  P  *  *  T  V  F  R  P -
b     G  S  D  L  V  L  Y  G  T  S  T  P  K  N  L  I  W  V  M  V  H  V  V  G  H  R  P  D  R  R  F  F  A  -
c      V  P  I  *  C  F  T  A  P  R  P  Q  K  T  *  F  G  *  W  F  T  *  W  A  I  A  L  I  D  G  F  S  P  -

                      MlyI
                      TaiI
                     PleI|
               HpyCH4IV ||
                Hpy8I | ||
            HinfI   | | ||          AloI
            DrdI|   | | ||          PpiI
          TaiI ||   | | ||        HinfI|
  HpyCH4IV   | ||   | | ||       BsaXI||                                    CviJI
    AloI  |  | ||   | | ||  MlyI     |||                                BslI    |
   BsaXI  |  | ||   | | ||  PleI     |||                                AvaI|   |
    PpiI  |  | ||   | | ||MseI  |Hpy8I||             BsrI               BslI|   |            PsiI
       |  |  | ||   | | ||   |  |    |||                 |                 ||   |               |
     ctttgacgttggagtccacgttctttaatagtggactcttgttccaaactggaacaacactcaaccctatctcgggctattcttttgatttataagggat
8501 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 8600
     gaaactgcaacctcaggtgcaagaaattatcacctgagaacaaggtttgaccttgttgtgagttgggatagagcccgataagaaaactaaatattcccta

a      L  T  L  E  S  T  F  F  N  S  G  L  L  F  Q  T  G  T  T  L  N  P  I  S  G  Y  S  F  D  L  *  G  I  -
b    L  *  R  W  S  P  R  S  L  I  V  D  S  C  S  K  L  E  Q  H  S  T  L  S  R  A  I  L  L  I  Y  K  G  F -
c     F  D  V  G  V  H  V  L  *  *  W  T  L  V  P  N  W  N  N  T  Q  P  Y  L  G  L  F  F  *  F  I  R  D  -
```

Figure 19-CC

```
                                                                          HpyCH4V                BseMII
                                                                         Fnu4HI |               BspCNI|
                                                                          TseI| |               AciI ||
                                                                       Cac8I || |           BstNI  | ||
                                                                    AciI   | || |           ScrFI  | ||
                                                                HpyF10VI   | || |         CviJI |  | ||
                                                                   MwoI|   | || |        HaeIII |  | ||
                                                                AvaII ||   | || |         PspGI |  | ||
                                                                Hpy8I ||   | || |        StyD4I |  | ||
                   NlaIV                      BseYI           Sau96I  ||   | || |      Sau96I | |  | ||
               Hpy188I |         BccI       Cac8I |          BbvI   | ||   | || |    DdeI   | | |  | ||
                     | |            |           | |             |   | ||   | || |       |   | | |  | ||
         tttgccgatttcggaaccaccatcaaacaggattttcgcctgctggggcaaaccagcgtggaccgcttgctgcaactctctcagggccaggcggtgaagg
    8601 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 8700
         aaacggctaaagccttggtggtagtttgtcctaaaagcggacgaccccgtttggtcgcacctggcgaacgacgttgagagagtcccggtccgccacttcc

a         L  P  I  S  E  P  P  S  N  R  I  F  A  C  W  G  K  P  A  W  T  A  C  C  N  S  L  R  A  R  R  *  R   -
b          C  R  F  R  N  H  H  Q  T  G  F  S  P  A  G  A  N  Q  R  G  P  L  A  A  T  L  S  G  P  G  G  E  G  -
c        F  A  D  F  G  T  T  I  K  Q  D  F  R  L  L  G  Q  T  S  V  D  R  L  L  Q  L  S  Q  G  Q  A  V  K  G -

             AluI
            CviJI                BsrI                 RsaI          AciI
           MspAII               TspRI               Csp6I|         TaiI|           HgaI
            PvuII          BsmAI    |       BmrI    TatI||  HpyCH4IV  ||         MseI |
          HphI  |          BsmBI    |      HphI| BsrI  |||MseI     |  ||  BsrDI     | |   DdeI Tsp509I
             |  |              |    |         ||     | |||   |     |  ||        |   | |      |       |
         gcaatcagctgttgcccgtctcactggtgaaaagaaaaaccaccccagtacattaaaaacgtccgcaatgtgttattaagttgtctaagcgtcaatttgt
    8701 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 8800
         cgttagtcgacaacgggcagagtgaccacttttctttttggtggggtcatgtaatttttgcaggcgttacacaataattcaacagattcgcagttaaaca

a        A  I  S  C  C  P  S  H  W  *  K  E  K  P  P  Q  Y  I  K  N  V  R  N  V  L  L  S  C  L  S  V  N  L  F -
b         Q  S  A  V  A  R  L  T  G  E  K  K  N  H  P  S  T  L  K  T  S  A  M  C  Y  *  V  V  *  A  S  I  C   -
c          N  Q  L  L  P  V  S  L  V  K  R  K  T  T  P  V  H  *  K  R  P  Q  C  V  I  K  L  S  K  R  Q  F  V  -

                                                                                                     NciI
                                                          AluI                                      ScrFI
                                                         CviJI                                      BccI|
                                                      Fnu4HI |                                     HpaII|
                                                       TseI| |                                     BbvI||
                                  CviJI            BsiEI  || |                          CviJI      PfoI||
                                 Cac8I |   AluI    HpaII  || |    BbvI                Fnu4HI |  StyD4I ||
    Hpy8I                     CviJI  | | CviJI    BsrFI|  || | HphI   |       TaqI     TseI| |  HgaI  |||
         |                         | | |      |       ||  || |    |   |          |        || |      | |||
         ttacaccacaatatatcctgccaccagccagccaacagctccccgaccggcagctcggcacaaaatcaccactcgatacaggcagcccatcagtccggga
    8801 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 8900
         aatgtggtgttatataggacggtggtcggtcggttgtcgaggggctggccgtcgagccgtgttttagtggtgagctatgtccgtcgggtagtcaggccct

a          T  P  Q  Y  I  L  P  P  A  S  Q  Q  L  P  D  R  Q  L  G  T  K  S  P  L  D  T  G  S  P  S  V  R  D  -
b        L  H  H  N  I  S  C  H  Q  P  A  N  S  S  P  T  G  S  S  A  Q  N  H  H  S  I  Q  A  A  H  Q  S  G  T -
c         Y  T  T  I  Y  P  A  T  S  Q  P  T  A  P  R  P  A  A  R  H  K  I  T  T  R  Y  R  Q  P  I  S  P  G   -

                                                                                        BceAI
                                                                                         NciI
                                                 NlaIII                                 ScrFI
                                                MaeIII|                                HpaII|
                                              FatI   ||                              StyD4I||
                                              SfaNI  ||                           Fnu4HI  |||
                                      HpyF10VI    |  ||                             AluI| |||
      BsaHI                        TauI       |   |  ||                            CviJI| |||
      BceAI|  BsmFI             Fnu4HI |      |   |  ||                             TseI| |||
       FauI|  AciI | CviJI       AciI| |BstAPI|   |  ||               BbvI     DdeI    || |||
    Tth111I|MspAII |BceAI|   BslI   || |  MwoI|   |  ||        Hpy188I    |   MboII    || |||
          ||     | |    ||      |   || |     ||   |  ||               |   |        |   || |||
         cggcgtcagcgggagagccgttgtaaggcggcagactttgctcatgttaccgatgctattcggaagaacggcaactaagctgccgggtttgaaacacgga
    8901 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 9000
         gccgcagtcgccctctcggcaacattccgccgtctgaaacgagtacaatggctacgataagccttcttgccgttgattcgacggcccaaactttgtgcct

a         G  V  S  G  R  A  V  V  R  R  Q  T  L  L  M  L  P  M  L  F  G  R  T  A  T  K  L  P  G  L  K  H  G   -
b          A  S  A  G  E  P  L  *  G  G  R  L  C  S  C  Y  R  C  Y  S  E  E  R  Q  L  S  C  R  V  *  N  T  D  -
c        R  R  Q  R  E  S  R  C  K  A  A  D  F  A  H  V  T  D  A  I  R  K  N  G  N  *  A  A  G  F  E  T  R  M -
```

Figure 19-DD

```
                FokI                                                                    Tsp509I
              TspGWI                                                                   Hpy188I|
               AciI |                                                                 BstKTI ||
              BstUI |                                                                  DpnI| ||
         BstF5I   | |                                                                  MnlI| ||
         BstKTI   | |                                                                BstYI || ||
           MnlI   | |      NlaIII                     Fnu4HI      BstKTI               MboI || ||
           DpnI|  | |        NspI                     Hin4I|       DpnI|             Hin4I| || ||   CviJI
        MboI ||   | |      FatI  |MaeIII    BbvI       TseI|   BclI ||     AlwI       || || ||  TspDTI|
          |  ||   | |        |   |     |      |         ||     MboI ||       |        || || ||      ||
          tgatctcgcggagggtagcatgttgattgtaacgatgacagagcgttgctgcctgtgatcaaatatcatctccctcgcagagatccgaattatcagcctt
     9001 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 9100
          actagagcgcctcccatcgtacaactaacattgctactgtctcgcaacgacggacactagtttatagtagagggagcgtctctaggcttaatagtcggaa

a         *  S  R  G  G  *  H  V  D  C  N  D  D  R  A  L  L  P  V  I  K  Y  H  L  P  R  R  D  P  N  Y  Q  P  S -
b          D  L  A  E  G  S  M  L  I  V  T  M  T  E  R  C  C  L  *  S  N  I  I  S  L  A  E  I  R  I  I  S  L  -
c           I  S  R  R  V  A  C  *  L  *  R  *  Q  S  V  A  A  C  D  Q  I  S  S  P  S  Q  R  S  E  L  S  A  F -

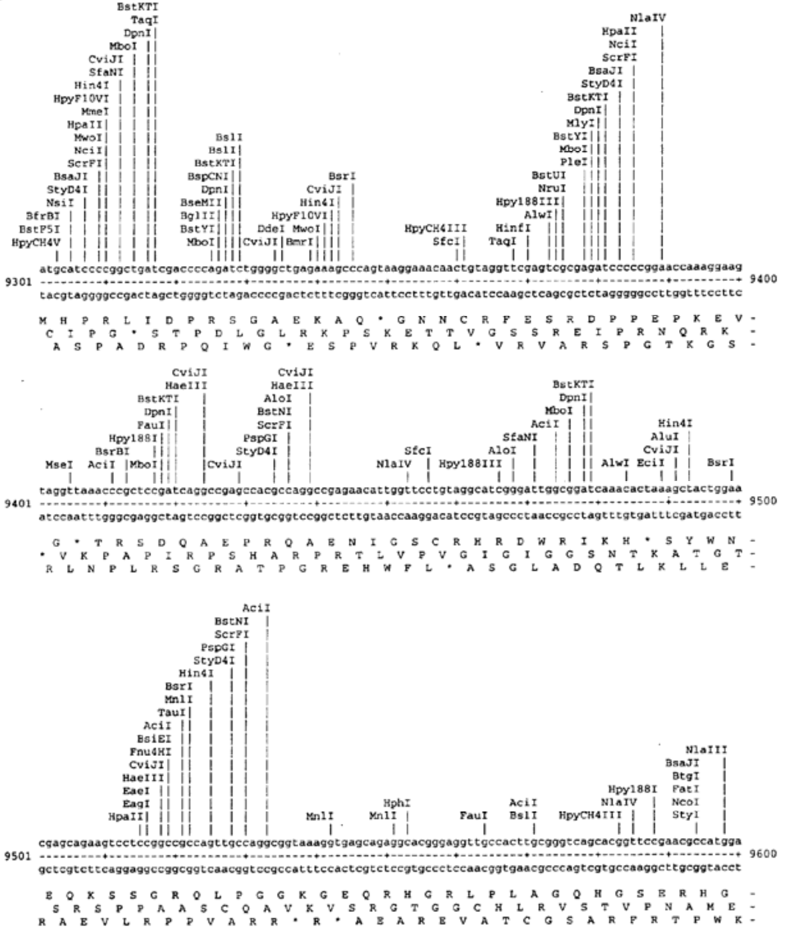
                                                                                                DdeI
                                                                                               AluI|
                                                                                              CviJI|
                                                                                        HpyF10VI ||
                                                                                      BspCNI   | ||
                                                                                      BbvCI|   | ||
                                                                                     Bpu10I|   | ||
                                                                                     BseMII|   | ||
                                                                                       DdeI|   | ||
                                                                                    MspA1I||   | ||
                                                          Hpy188III                   TauI||   | ||
                                                               SmlI                   AciI |||  | ||
                                                          BstKTI|                   Fnu4HI |||  | ||
               HpyCH4III                                   DpnI||                   CviJI| |||  | ||
                  MaeIII                                 MboI |||                   MnlI|| |||  | ||
                  Tsp45I                                 TaqI| |||                  BspCNI ||| |||  | ||
               MseI  |           AhdI                       || |||              BseMII| ||| |||MwoI| ||  HinP1I
              Hin4I| |           CviJI                      || |||    Hin4I      BpuEI   | ||| |||  ||  ||      |
                   || |              |                      || |||      |          |       || ||| |||  ||  ||      |
          cttattcatttctcgcttaaccgtgacaggctgtcgatcttgagaactatgccgacataataggaaatcgctggataaagccgctgaggaagctgagtgg
     9101 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 9200
          gaataagtaaagagcgaattggcactgtccgacagctagaactcttgatacggctgtattatcctttagcgacctatttcggcgactccttcgactcacc

a          Y  S  F  L  A  *  P  *  Q  A  V  D  L  E  N  Y  A  D  I  I  G  N  R  W  I  K  P  L  R  K  L  S  G  -
b         L  I  H  F  S  L  N  R  D  R  L  S  I  L  R  T  M  P  T  *  *  E  I  A  G  *  S  R  *  G  S  *  V  A -
c          L  F  I  S  R  L  T  V  T  G  C  R  S  *  E  L  C  R  H  N  R  K  S  L  D  K  A  A  E  E  A  E  W  -

                                                                                                    AloI
                                                                                                 CviJI |
                  HincII                                                   NlaIV                HaeIII |
                   Hpy8I                                                  NlaIV|              BslI   | |
                    TaiI|                                                AvaII||        HpyCH4III|   | |
                 AclI  ||                                             Eco0109I||             FokI||   | |
              HpyCH4IV ||                                        AloI    PpuMI||            SfaNI||   | |
     HaeII       Hin4I| ||                   BsrDI             RsaI |    SanDI||         BsmFI |||   | |
     KhaI|        Hpy8I|| || EcoRV           HphI| Hin4I      Csp6I| |  Sau96I||      Hpy188I  |||   | |
          ||          ||| ||    |               ||    |             || |        |||        |   |||   | |
          cgctatttctttagaagtgaacgttgacgatatcaactcccctatccattgctcaccgaatggtacaggtcggggacccgaagttccgactgtcggcctg
     9201 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 9300
          gcgataaagaaatcttcacttgcaactgctatagttgaggggataggtaacgagtggcttaccatgtccagcccctgggcttcaaggctgacagccggac

a           A  I  S  L  E  V  N  V  D  D  I  N  S  P  I  H  C  S  P  N  G  T  G  R  G  P  E  V  P  T  V  G  L  -
b            L  F  L  *  K  *  T  L  T  I  S  T  P  L  S  I  A  H  R  M  V  Q  V  G  D  P  K  F  R  L  S  A  *  -
c         R  Y  F  F  R  S  E  R  *  R  Y  Q  L  P  Y  F  L  L  T  E  W  Y  R  S  G  T  R  S  S  D  C  R  P  D -
```

Figure 19-EE



```
     atgcatccccggctgatcgaccccagatctggggctgagaaagcccagtaaggaaacaactgtaggttcgagtcgcgagatcccccggaaccaaaggaag
9301 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 9400
     tacgtaggggccgactagctggggtctagaccccgactctttcgggtcattcctttgttgacatccaagctcagcgctctagggggccttggtttccttc

a    M  H  P  R  L  I  D  P  R  S  G  A  E  K  A  Q  *  G  N  N  C  R  F  E  S  R  D  P  P  E  P  K  E  V -
b     C  I  P  G  *  S  T  P  D  L  G  L  R  K  P  S  K  E  T  T  V  G  S  S  R  E  I  P  R  N  Q  R  K  -
c      A  S  P  A  D  R  P  Q  I  W  G  *  E  S  P  V  R  K  Q  L  *  V  R  V  A  R  S  P  G  T  K  G  S  -

     taggttaaacccgctccgatcaggccgagccacgccaggccgagaacattggttcctgtaggcatcgggattggcggatcaaacactaaagctactggaa
9401 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 9500
     atccaatttgggcgaggctagtccggctcggtgcggtccggctcttgtaaccaaggacatccgtagccctaaccgcctagtttgtgatttcgatgacctt

a     G  *  T  R  S  D  Q  A  E  P  R  Q  A  E  N  I  G  S  C  R  H  R  D  W  R  I  K  H  *  S  Y  W  N  -
b    *  V  K  P  A  P  I  R  P  S  H  A  R  P  R  T  L  V  P  V  G  I  G  I  G  G  S  N  T  K  A  T  G  T -
c    R  L  N  P  L  R  S  G  R  A  T  P  G  R  E  H  W  F  L  *  A  S  G  L  A  D  Q  T  L  K  L  L  E  -

     cgagcagaagtcctccggccgccagttgccaggcggtaaaggtgagcagaggcacgggaggttgccacttgcgggtcagcacggttccgaacgccatgga
9501 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 9600
     gctcgtcttcaggaggccggcggtcaacggtccgccatttccactcgtctccgtgccctccaacggtgaacgcccagtcgtgccaaggcttgcggtacct

a     E  Q  K  S  S  G  R  Q  L  P  G  G  K  G  E  Q  R  H  G  R  L  P  L  A  G  Q  H  G  S  E  R  H  G  -
b      S  R  S  P  P  A  A  S  C  Q  A  V  K  V  S  R  G  T  G  G  C  H  L  R  V  S  T  V  P  N  A  M  E  -
c    R  A  E  V  L  R  P  P  V  A  R  R  *  R  *  A  E  A  R  E  V  A  T  C  G  S  A  R  F  R  T  P  W  K -
```

Figure 19-FF

```
                    Fnu4HI
                   MspA1I|
                     TseI|                  Fnu4HI
                   AciI ||                   HaeII
                  Cac8I ||                   HhaI|
               HpyF10VI ||                   TseI|
                  MwoI| ||                  AfeI||
                CviJI|| ||                  AlwI||
                 FauI|| ||               HinP1I|||
               HaeIII|| ||              BfaI  ||||
              Sau96I||| ||           BstKTI|  ||||
             BstNI |||| ||            DpnI||  ||||
             ScrFI |||| ||         BstYI |||  ||||
             BslI| |||| ||          MboI |||  ||||                             AciI                 BstNI
           PspGI|| |||| ||         HgaI| |||  ||||                            Cac8I                 ScrFI
          StyD4I|| |||| ||      BbvI  || |||  ||||                         HpyF10VI               BsaJI |
          AciI ||| |||| || Hpy99I  |  || |||  ||||                      HaeII     |               PspGI |
        BbvI | ||| |||| ||BsaHI |  |  || |||  ||||       HincII         HhaI|     |    AciI      StyD4I |
    AciI   | | ||| |||| ||FauI| |  |  || |||  ||||        Hpy8I     HinP1I || MwoI|   FauI|    CviJI  | |
       |   | | ||| |||| ||   || |  |  || |||  ||||            |          | ||    ||      ||        |  | |
     aaccgcccccgccaggcccgctgcgacgccgacaggatctagcgctgcgtttggtgtcaacaccaacagcgccacgcccgcagttccgcaaatagccccc
9601 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 9700
     ttggcgggggcggtccgggcgacgctgcggctgtcctagatcgcgacgcaaaccacagttgtggttgtcgcggtgcgggcgtcaaggcgtttatcggggg

a    N  R  P  R  Q  A  R  C  D  A  D  R  I  *  R  C  V  W  C  Q  H  Q  Q  R  H  A  R  S  S  A  N  S  P  Q  -
b     T  A  P  A  R  P  A  A  T  P  T  G  S  S  A  A  F  G  V  N  T  N  S  A  T  P  A  V  P  Q  I  A  P   -
c      P  P  P  P  G  P  L  R  R  R  Q  D  L  A  L  R  L  V  S  T  P  T  A  P  R  P  Q  F  R  K  *  P  P  -

                                                                                            BstUI
                                                                                             TauI
                                                                                           AciI |
                                                                                         Fnu4HI |
                                                                                        Hpy99I| |
                                                                                 HpyCH4III   || |
                                                                                HaeII    |   || |
                                                                                HhaI|    |   || |
                                                                            HinP1I ||    |   || |
                                                                      HpyCH4V    | ||    |   || |
                                                                     Fnu4HI |    | ||    |   || |
                                                                     AlwNI| |    | ||    |   || |
                                                                     CviJI| |    | ||    |   || |
                                                                      TauI| |    | ||    |   || |
                                                                      TseI| |    | ||    |   || |
                                                                     BccI|| |    | ||    |   || |     HpaII
                                         TauI                 Fnu4HI||| |    | ||    |   || |      NciI
      AciI                          Fnu4HI  |                  AciI|||| |    | ||    |   || |      ScrFI
  AvaII  |                            AciI| |        BbvI    MspA1I|||| |    | ||    |   || |  StyD4I |
 Sau96I  |      BccI   CviJI BfaI    BsrBI| |       BsgI|   TspDTI||||| |    | ||    |   || | AciI  | |
      |  |          |       |    |       || |          ||        |||||| |    | ||    |   || |     | | |
     aggaccgccatcaatcgtatcgggctacctagcagagcggcagagatgaacacgaccatcagcggctgcacagcgcctaccgtcgccgcgaccccgcccg
9701 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 9800
     tcctggcggtagttagcatagcccgatggatcgtctcgccgtctctacttgtgctggtagtcgccgacgtgtcgcggatggcagcggcgctggggcgggc

a      D  R  H  Q  S  Y  R  A  T  *  Q  S  G  R  D  E  H  D  H  Q  R  L  H  S  A  Y  R  R  R  D  P  A  R  -
b    R  T  A  I  N  R  I  G  L  P  S  R  A  A  E  M  N  T  T  I  S  G  C  T  A  P  T  V  A  A  T  P  P  G -
c     G  P  P  S  I  V  S  G  Y  L  A  E  R  Q  R  *  T  R  P  S  A  A  A  Q  R  L  P  S  P  R  P  R  P  -
```

Figure 19-GG

```
                                                                                       HinfI
                                                                                        TfiI
                                                                                      SfaNI|
                                                                                      MmeI||
                                                                                 TspDTI  |||
                                                                                 MboII|  |||
                                                                               FokI  ||  |||
                                                                            BstF5I|  ||  |||
          AciI                                                   FokI         HhaI|  ||  |||
         BslI|                                                SfaNI |       BsaBI||  ||  |||
       Cac8I||                                               BsaJI| |        FspI||  ||  |||
    HpyF10VI||      BpmI       Hpy188III                     HhaI|| |       FspAI||  ||  |||
       BglI|||   Eco57MI          AluI  |                HinPlI ||| |    HinPlI |||  ||  |||
       MwoI|||Hpy8I    |         CviJI  |           MseI      | ||| |      MmeI||||  ||  |||      HinfI
      FauI||||AccI|    |       TaqII |  |          SspI |MnlI | ||| | BstF5I   ||||  ||  |||XcmI   TfiI
         |||||   ||    |             |  |             | |   | | ||| |      |   ||||  ||  |||   |      |
         gcaggcggtagaccgaaataaacaacaagctccagaatagcgaaatattaagtgcgccgaggatgaagatgcgcatccaccagattcccgttggaatctg
    9801 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 9900
         cgtccgccatctggctttatttgttgttcgaggtcttatcgctttataattcacgcggctcctacttctacgcgtaggtggtctaagggcaaccttagac

a         Q  A  V  D  R  N  K  Q  Q  A  P  E  *  R  N  I  K  C  A  E  D  E  D  A  H  P  P  D  S  R  W  N  L   -
b          R  R  *  T  E  I  N  N  K  L  Q  N  S  E  I  L  S  A  P  R  M  K  M  R  I  H  Q  I  P  V  G  I  C  -
c        A  G  G  R  P  K  *  T  T  S  S  R  I  A  K  Y  *  V  R  R  G  *  R  C  A  S  T  R  F  P  L  E  S  V -
```

```
                                                    FauI
                                                 Fnu4HI|
                                                  TseI||
                                              Fnu4HI |||
                                               TseI| |||
                                            AciI  || |||
                                           Cac8I  || |||
                                        HpyF10VI  || |||
                                           MwoI|  || |||
                                    HpyF10VI   || || |||
                                       MwoI |  || || |||
                                      FauI ||  || || |||                               BanII
                 BssSI             Cac8I  |||  || || |||                           Bsp1286I
            Hpy188III               NaeI  |||  || || |||                              NlaIV|
            BstKTI   |            HpaII|  |||  || || |||      BbvI                  CviJI ||
             DpnI|   |          BsrFI ||  |||  || || |||   BbvI  |    CviJI     HpyF10VI |||
           MboI ||   |         NgoMIV ||  |||  || || ||| HpaII|  |   HaeIII        MnlI| |||       HpaII
    Hpy188I   | ||   |         AciI  |||  |||  || || |||BsrFI||  |BsaJI    | MnlI  MwoI| |||    SfaNI  |
           |  | ||   |             | |||  |||  || || |||    |||  |    |    |    |     || |||        |  |
         tcggacgatcatcacgagcaataaacccgccggcaacgcccgcagcagcataccggcgacccctcggcctcgctgttcgggctccacgaaaacgccggac
    9901 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
10000
         agcctgctagtagtgctcgttatttgggcggccgttgcgggcgtcgtcgtatggccgctggggagccggagcgacaagcccgaggtgcttttgcggcctg

a        S  D  D  H  H  E  Q  *  T  R  R  Q  R  P  Q  Q  H  T  G  D  P  S  A  S  L  F  G  L  H  E  N  A  G  Q -
b         R  T  I  I  T  S  N  K  P  A  G  N  A  R  S  S  I  P  A  T  P  R  P  R  C  S  G  S  T  K  T  P  D  -
c          G  R  S  S  R  A  I  N  P  P  A  T  P  A  A  A  Y  R  R  P  L  G  L  A  V  R  A  P  R  K  R  R  T  -
```

```
                                                                                               BsmI
                                                                                             BsaJI|
                                                                                              BtgI|
                                                                                       HpyF10VI  ||
                                                                                          MwoI|  ||
                                                                                       BbeI  ||  ||
                                                                                      HaeII  ||  ||
                                                                                      HhaI|  ||  ||
                                                                                    NlaIV||  ||  ||
                               CviJI                                                 SfoI||  ||  ||
                              HaeIII                                               BsaHI|||  ||  ||
               HpyF10VI       NlaIV|                      MboII  BstKTI           HinPlI|||  ||  ||
            HhaI      |     Sau96I||                    CviJI |   DpnI|             NarI|||  ||  ||
          HgaI |  MwoI| BsaJI    |||                   BceAI ||  TaqII|    Hpy99I  BanI||||  ||  ||
       HinPlI  |BceAI||  StyI    |||          MnlI    BbsI | || MboI ||    TaqI |  KasI||||  ||  ||
             | |    |||     |    |||              |      | | ||    | ||       | |     |||||  ||  ||
         agatgcgccttgtgagcgtccttggggccgtcctcctgtttgaagaccgacagcccaatgatctcgccgtcgatgtaggcgccgaatgccacggcatctc
   10001 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
10100
         tctacgcggaacactcgcaggaaccccggcaggaggacaaacttctggctgtcgggttactagagcggcagctacatccgcggcttacggtgccgtagag

a          M  R  L  V  S  V  L  G  A  V  L  L  F  E  D  R  Q  P  N  D  L  A  V  D  V  G  A  E  C  H  G  I  S  -
b        R  C  A  L  *  A  S  L  G  P  S  S  C  L  K  T  D  S  P  M  I  S  P  S  M  *  A  P  N  A  T  A  S  R -
c         D  A  P  C  E  R  P  W  G  R  P  P  V  *  R  P  T  A  Q  *  S  R  R  R  C  R  R  R  M  P  R  H  L  -
```

Figure 19-HH

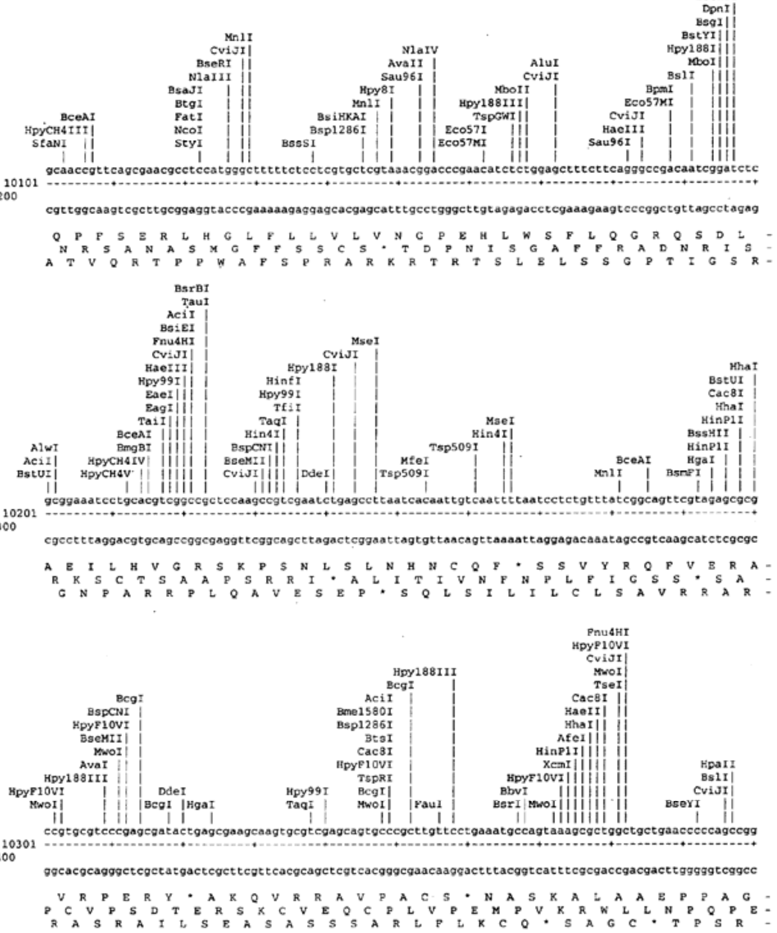

BstKTI
DpnI
BsgI
MnlI
BstYI
CviJI
NlaIV
Hpy188I
BseRI
AvaII
AluI
MboI
NlaIII
Sau96I
CviJI
BslI
BsaJI
Hpy8I
MboII
BpmI
BtgI
MnlI
Hpy188III
Eco57MI
BceAI
FatI
BsiHKAI
TspGWI
CviJI
HpyCH4III
NcoI
Bsp1286I
Eco57I
HaeIII
SfaNI
StyI
BssSI
Eco57MI
Sau96I
gcaaccgttcagcgaacgcctccatgggctttttctcctcgtgctcgtaaacggacccgaacatctctggagctttcttcagggccgacaatcggatctc
10101
10200
cgttggcaagtcgcttgcggaggtacccgaaaaagaggagcacgagcatttgcctgggcttgtagagacctcgaaagaagtcccggctgttagcctagag
a Q P F S E R L H G L F L L V L V N C P E H L W S F L Q G R Q S D L -
b N R S A N A S M G F F S S C S * T D P N I S G A F F R A D N R I S -
c A T V Q R T P P W A F S P R A R K R T R T S L E L S S G P T I G S R -
BsrBI
TauI
AciI
BsiEI
Fnu4HI
MseI
CviJI
CviJI
HaeIII
Hpy188I
MhaI
Hpy99I
HinfI
BstUI
EaeI
Hpy99I
Cac8I
EagI
TfiI
MhaI
TaiI
TaqI
MseI
HinP1I
BceAI
Hin4I
Hin4I
BssHII
AlwI
BmgBI
BspCNI
Tsp509I
HinP1I
AciI
HpyCH4IV
BseMII
MfeI
BceAI
HgaI
BstUI
HpyCH4V
CviJI
DdeI
Tsp509I
MnlI
BsmFI
gcggaaatcctgcacgtcggccgctccaagccgtcgaatctgagccttaatcacaattgtcaattttaatcctctgtttatcggcagttcgtagagcgcg
10201
10300
cgcctttaggacgtgcagccggcgaggttcggcagcttagactcggaattagtgttaacagttaaaattaggagacaaatagccgtcaagcatctcgcgc
a A E I L H V G R S K P S N L S L N H N C Q F * S S V Y R Q F V E R A -
b R K S C T S A A P S R R I * A L I T I V N F N P L F I G S S * S A -
c G N P A R R P L Q A V E S E P * S Q L S I L I L C L S A V R R A R -
Fnu4HI
HpyP10VI
CviJI
MwoI
Hpy188III
TseI
BcgI
BcgI
AciI
Cac8I
BspCNI
Bme1580I
HaeII
HpyF10VI
Bsp1286I
HhaI
BseMII
BtsI
AfeI
MwoI
Cac8I
HinP1I
AvaI
HpyF10VI
XcmI
HpaII
Hpy188III
TspRI
HpyF10VI
BslI
HpyF10VI
DdeI
Hpy99I
BcgI
BbvI
CviJI
MwoI
BcgI
HgaI
TaqI
MwoI
FauI
BsrI
MwoI
BseYI
ccgtgcgtcccgagcgatactgagcgaagcaagtgcgtcgagcagtgcccgcttgttcctgaaatgccagtaaagcgctggctgctgaacccccagccgg
10301
10400
ggcacgcagggctcgctatgactcgcttcgttcacgcagctcgtcacgggcgaacaaggactttacggtcatttcgcgaccgacgacttgggggtcggcc
a V R P E R Y * A K Q V R R A V P A C S * N A S K A L A A E P P A G -
b P C V P S D T E R S K C V E Q C P L V P E M P V K R W L L N P Q P E -
c R A S R A I L S E A S A S S S A R L P L K C Q * S A G C * T P S R -

Figure 19-II

```
                                                         MboII
                                                   Fnu4HI   |
                                                  MspA1I|   |
                                                     TauI|   |
                                                     TseI|   |
                                                   AciI ||   |
                 BstNI                           Fnu4HI ||   |
                 ScrFI                           CviJI| ||   |
                BsrDI |                         HaeIII| ||   |           HpyF10VI
        BfaI    PspGI |         BstNI          BstNI || ||   |               MwoI|
    CviJI |     SexAI |         ScrFI          ScrFI || ||   |             CviJI ||
   HaeIII |    StyD4I |        BsaJI |       PspGI | || ||   |           Cac8I | ||
 Eco0109I||   HpyCH4V | |      PspGI |      StyD4I | || ||   |          EarI | | ||
   Sau96I|| HpyCH4V | | |   StyD4I | BbvI  |    | || ||   |       MnlI | | | ||
         ||      |  | | |        |  |    |    |    | || ||   |          |  |  | | ||
       aactgaccccacaaggccctagcgtttgcaatgcaccaggtcatcattgacccaggcgtgttccaccaggccgctgcctcgcaactcttcgcaggcttcg
 10401 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
 10500
       ttgactggggtgttccgggatcgcaaacgttacgtggtccagtagtaactgggtccgcacaaggtggtccggcgacggagcgttgagaagcgtccgaagc

a       T  D  P  T  R  P  *  R  L  Q  C  T  R  S  S  L  T  Q  A  C  S  T  R  P  L  P  R  N  S  S  Q  A  S  -
b        L  T  P  Q  G  P  S  V  C  N  A  P  G  H  H  *  P  R  R  V  P  P  G  R  C  L  A  T  L  R  R  L  R -
c       N  *  P  H  K  A  L  A  F  A  M  H  Q  V  I  I  D  P  G  V  F  H  Q  A  A  A  S  Q  L  F  A  G  F  A-

                                                                                              FokI
                                                                                             AluI|
                                                                                            BceAI|
                                                                                            CviJI|
                                                                                          Cac8I ||
                                                                                     BpuEI    | ||
                                                                                  HpyF10VI    | ||
                                                                                     MwoI|    | ||
                                                    AciI                            HpaII ||    | ||
                                               HpyF10VI |                            NciI ||    | ||
                                                   MwoI| |                          ScrFI ||    | ||
                                                 NlaIII| |                       StyD4I | ||    | ||
                                               FatI   || |                       NlaIV| | ||    | ||
                                           MnlI |     || |                      CviJI|| | ||    | ||
                                          AciI| |     || |                  HpyF10VI ||| | ||    | ||
         MhaI                          BstKTI|| |     || |        EciI         MwoI| ||| | ||    | ||
       BspMI|                          DpnI||| |     || |        SmlI          RsaI|| ||| | ||    | ||
       BstUI||          AleI     Hpy188I |||| |     || |        AluI|         Csp6I||| ||| | ||    | ||
      HinP1I||          MslI   AlwI   | |||| |     || |       CviJI| AciI      |||| ||| | ||    | ||
       MboII||         AciI| HinfI    | |||| |     || |       FauI|| BsrBI    |||| ||| | ||    | ||
      Cac8I |||    FauI BstUI| TfiI MboI |||| |     || |       FauI||BsrBI     |||| ||| | ||    | ||
            |||     |     ||   |     | |||| |     || |         |||    |       |||| ||| | ||    | ||
       ccgacctgctcgcgccacttcttcacgcgggtggaatccgatccgcacatgaggcggaaggtttccagcttgagcgggtacggctcccggtgcgagctga
 10501 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
 10600
       ggctggacgagcgcggtgaagaagtgcgcccaccttaggctaggcgtgtactccgccttccaaaggtcgaactcgcccatgccgagggccacgctcgact

a       P  T  C  S  R  H  F  F  T  R  V  E  S  D  P  H  M  R  R  K  V  S  S  L  S  C  Y  G  S  R  C  E  L  K-
b        R  P  A  R  A  T  S  S  R  G  W  N  P  I  R  T  *  G  G  R  P  P  A  *  A  G  T  A  P  G  A  S  *  -
c         D  L  L  A  P  L  L  H  A  G  G  I  R  S  A  H  E  A  E  G  F  Q  L  E  R  V  R  L  P  V  R  A  E -

                                 RsaI
                                Csp6I|
          BstF5I     CviJI     AciI ||
        BceAI  |    HaeIII   Cac8I | ||          ApoI
         TaqI  |   Hpy99I |   AluI | | ||       Tsp509I
   TspGWI |    |   Sau96I |Hpy99I CviJI | | | ||    NdeI   |       TspDTI  Cac8I          Hpy99I
        | |    |        | |   |     | | | . ||      |   |          |       |              |
       aatagtcgaacatccgtcgggccgtcggcgacagcttgcggtacttctcccatatgaatttcgtgtagtggtcgccagcaaacagcacgacgatttcctc
 10601 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
 10700
       ttatcagcttgtaggcagcccggcagccgctgtcgaacgccatgaagagggtatacttaaagcacatcaccagcggtcgtttgtcgtgctgctaaaggag

a         *  S  N  I  R  R  A  V  G  D  S  L  R  Y  F  S  H  M  N  F  V  *  W  S  P  A  N  S  T  T  I  S  S  -
b       N  S  R  T  S  V  G  P  S  A  T  A  C  G  T  S  P  I  *  I  S  C  S  G  R  Q  Q  T  A  R  R  F  P  R -
c        I  V  E  H  P  S  G  R  R  R  Q  L  A  V  L  L  P  Y  E  F  R  V  V  V  A  S  K  Q  H  D  D  F  L  -
```

Figure 19-JJ

```
                    BstNI
                    ScrFI                                                                Bme1580I
                   AlwNI|                                                                Bsp1286I
                  PspGI||                                                                NlaIV  |
                 StyD4I||                                                                BanI|  |
                AvaII |||                         BstNI                               BsgI | |  |
             EcoO109I |||                         ScrFI                              BstNI | |  |
                PpuMI |||                        PfoI |                              ScrFI | |  |
               Sau96I |||                       PspGI |                              BslI| | |  |
          Hpy188III | |||                      StyD4I |                            PspGI|| | |  |         BmgBI
               MnlI | |||                     AvaII | |              Fnu4HI       StyD4I|| | |  |     HpyCH4IV|
            BstKTI| | |||                 HpyCH4III | |               TseI|       BbvI ||| | |  |       BceAI||
             DpnI|| | |||                    Sau96I | |            Fnu4HI||       MmeI ||| | |  |    Hpy188I|||
          Hpy99I||| | |||          TaiI   BsaJI   | | |  AciI   HpyCH4V| ||     HinfI| ||| | |  |    BsiEI ||||
           MboI|||| | |||  HpyCH4IV   |   BsmFI   | | | BstUI  AciI   || ||      TfiI| ||| | |  | AciI   | ||||
          TaqI||||| | ||| BslI     |  |    BtgI   | | | BslI| HgaI TseI| ||    BbvI || ||| | |  |BstUI   | ||||
             |||||| | |||    |     |  |       |   | | |    ||     |   || ||       | || ||| | |  |    |   | ||||
            gtcgatcaggacctggcaacgggacgttttcttgccacggtccaggacgcggaagcggtgcagcagcgacaccgattccaggtgcccaacgcggtcggac
      10701 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
10800
            cagctagtcctggaccgttgccctgcaaaagaacggtgccaggtcctgcgccttcgccacgtcgtcgctgtggctaaggtccacgggttgcgccagcctg

a            S  I  R  T  W  Q  R  D  V  F  L  P  R  S  R  T  R  K  R  C  S  S  D  T  D  S  R  C  P  T  R  S  D   -
b             R  S  G  P  G  N  G  T  F  S  C  H  G  P  G  R  G  S  G  A  A  A  T  P  I  P  G  A  Q  R  G  R  T  -
c           V  D  Q  D  L  A  T  G  R  F  L  A  T  V  Q  D  A  E  A  V  Q  Q  R  H  R  F  Q  V  P  N  A  V  G  R -
```

```
                                                                                              BstNI
                                                                                              ScrFI
                                                                                             AlwNI|
                                                                                              BslI|
                                                                                             PflMI|
                                                                                            PspGI||
                                                                                           StyD4I||
                                                                                          AvaII |||
                                                                                       EcoO109I |||
                                                                                          PpuMI |||
                                                                                         Sau96I |||
                                                                                        BstNI | |||
                                            BsmI                      CviJI             ScrFI | |||
                                      HpyF10VI |                     HaeIII  BstKTI   BsaJI | | |||
                             SfcI   BstUI    | |     CviJI           EaeI |    TaqI   PspGI | | |||
             CviJI       Hpy99I |    HhaI    | |    HaeIII         HpaII| |   DpnI|  StyD4I | | |||    AluI
          TaiI   |      BccI  | |HinPlI |MwoI| |BsaJI    | MnlI   BsrFI|| | MboI ||  CviJI| | | |||   CviJI
             |   |         |  | |     | |   || |    |    |    |       ||| |    | ||      || | | |||       |
            gtgaagcccatcgccgtcgcctgtaggcgcgacaggcattcctcggccttcgtgtaataccggccattgatcgaccagcccaggtcctggcaaagctcgt
      10801 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
10900
            cacttcgggtagcggcagcggacatccgcgctgtccgtaaggagccggaagcacattatggccggtaactagctggtcgggtccaggaccgtttcgagca

a           V  K  P  I  A  V  A  C  R  R  D  R  H  S  S  A  F  V  *  Y  R  P  L  I  D  Q  P  R  S  W  Q  S  S  * -
b            *  S  P  S  P  S  P  V  G  A  T  G  I  P  R  P  S  C  N  T  G  H  *  S  T  S  P  G  P  G  K  A  R   -
c             E  A  H  R  R  R  L  *  A  R  Q  A  F  L  G  L  R  V  I  P  A  I  D  R  P  A  Q  V  L  A  K  L  V  -
```

Figure 19-KK

```
                                                                                                        BbvI
                                                                                                      HpaII|
                                                                                                     BsrFI||
                                                                                                    Hpy99I||
                                                                                                     SgrAI||
                                                                                                   BsaHI |||
                                                                                                 FauI  | |||
                                                                                                 TaqI  | |||
                                                                                               AluI |  | |||
                                                                                              CviJI |  | |||
                                                                                           Fnu4HI | |  | |||
                           HphI                                                             TseI| | |  | |||
                        Cac8I |                                                           AciI || | |  | |||
                      CviJI | |                     BcgI                                 Cac8I || | |  | |||
                  BstKTI  | | |                  BbvI  |           AarI                CviJI | || | |  | |||
                   DpnI|  | | |                  RsaI  |          BspMI               HaeIII | || | |  | |||
           TaiI   BcgI||  | | |          HhaI  Csp6I|  |     Fnu4HI   |              Hpy99I| | || | |  | |||
    HpyCH4IV  |  MboI|||  | | |      HinPlI |BstUI ||  |      TseI|   |BsrI  MmeI    Sau96I| | || | |  | |||
           |  |     ||||  | | |           | |    | ||  |         ||   |   |     |         || | || | |  | |||
        agaacgtgaaggtgatcggctcgccgataggggtgcgcttcgcgtactccaacacctgctgccacaccagttcgtcatcgtcggcccgcagctcgacgcc
  10901 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
11000
        tcttgcacttccactagccgagcggctatccccacgcgaagcgcatgaggttgtggacgacggtgtggtcaagcagtagcagccgggcgtcgagctgcgg

a         N  V  K  V  I  G  S  P  I  G  V  R  F  A  Y  S  N  T  C  C  H  T  S  S  S  S  S  A  R  S  S  T  P -
b       R  T  *  R  *  S  A  R  R  *  G  C  A  S  R  T  P  T  P  A  A  T  P  V  R  H  R  R  P  A  A  R  R  R-
c        E  R  E  G  D  R  L  A  D  R  G  A  L  R  V  L  Q  H  L  L  P  H  Q  F  V  I  V  G  P  Q  L  D  A  -

                                                                   AciI
                                                                   BbvI
                                                                   BslI
                                                                  BstUI
                                                                   HhaI
                                                                BstUI |
                                                               HinPlI |
                                                             HpyF10VI |
                                                                MwoI| |
                        TaiI                                HaeII  || |
                       HphI|                                FauI|  || |
                     BmgBI||        TaiI                    HhaI|  || |
                 HpyCH4IV|||     BmgBI |                HinPlI ||  || |                                 AciI
              BstKTI    |||| HpyCH4IV| |              Fnu4HI | ||  || |             BstUI              BsrBI
        HgaI   DpnI|    |||| HincII || |            HpyCH4V| | ||  || |              HhaI   BceAI    HphI  |
       MboII MboI ||    ||||  Hpy8I || |               TseI| | ||  || |MnlI      HinPlI |  Hpy8I|FauI   |  |
           |    | ||    ||||      | || |                  || | ||  || |   |           | |      ||   |   |  |
        ggtgtaggtgatcttcacgtccttgttgacgtggaaaatgaccttgttttgcagcgcctcgcgcgggattttcttgttgcgcgtggtgaacagggcagag
  11001 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
11100
        ccacatccactagaagtgcaggaacaactgcaccttttactggaacaaaacgtcgcggagcgcgccctaaaagaacaacgcgcaccacttgtcccgtctc

a        V  *  V  I  F  T  S  L  L  T  W  K  M  T  L  F  C  S  A  S  R  G  I  F  L  L  R  V  V  N  R  A  E  -
b         C  R  *  S  S  R  P  C  *  R  G  K  *  P  C  F  A  A  P  R  A  G  F  S  C  C  A  W  *  T  G  Q  S -
c       G  V  G  D  L  H  V  L  V  D  V  E  N  D  L  V  L  Q  R  L  A  R  D  F  L  V  A  R  G  E  Q  G  R  A-

                                                  HhaI
                                              HinPlI |
                                          BsaJI    | |
       CviJI                               BtgI    | |                    BbvI
      HaeIII                             CviJI|    | |               HpyCH4V |        Fnu4HI
     Cac8I |                 SfaNI      HaeIII|    | |              Fnu4HI | |         TseI|
  HpyF10VI |               Cac8I |      EaeI ||    | |      BceAI    AluI| | |    BstKTI  ||
    Sau96I |            HpyF10VI |    HpaII| ||    | |  BbvI    |   CviJI| | |     DpnI|  ||
     MwoI| |               MwoI| |    SfaNI| ||    | |  TaqI    |    TseI| | |   MboI ||  ||
        || |                  || |        || ||    | |     |    |       || | |      | ||  ||
        cgggccgtgtcgtttggcatcgctcgcatcgtgtccggccacggcgcaatatcgaacaaggaaagctgcatttccttgatctgctgcttcgtgtgtttca
  11101 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
11200
        gcccggcacagcaaaccgtagcgagcgtagcacaggccggtgccgcgttatagcttgttcctttcgacgtaaaggaactagacgacgaagcacacaaagt

a       R  A  V  S  F  G  I  A  R  I  V  S  G  H  G  A  I  S  N  K  E  S  C  I  S  L  I  C  C  F  V  C  F  S-
b        G  P  C  R  L  A  S  L  A  S  C  P  A  T  A  Q  Y  R  T  R  K  A  A  F  P  *  S  A  A  S  C  V  S  -
c         G  R  V  V  W  H  R  S  H  R  V  R  P  R  R  N  I  E  Q  G  K  L  H  F  L  D  L  L  L  R  V  F  Q -
```

Figure 19-LL

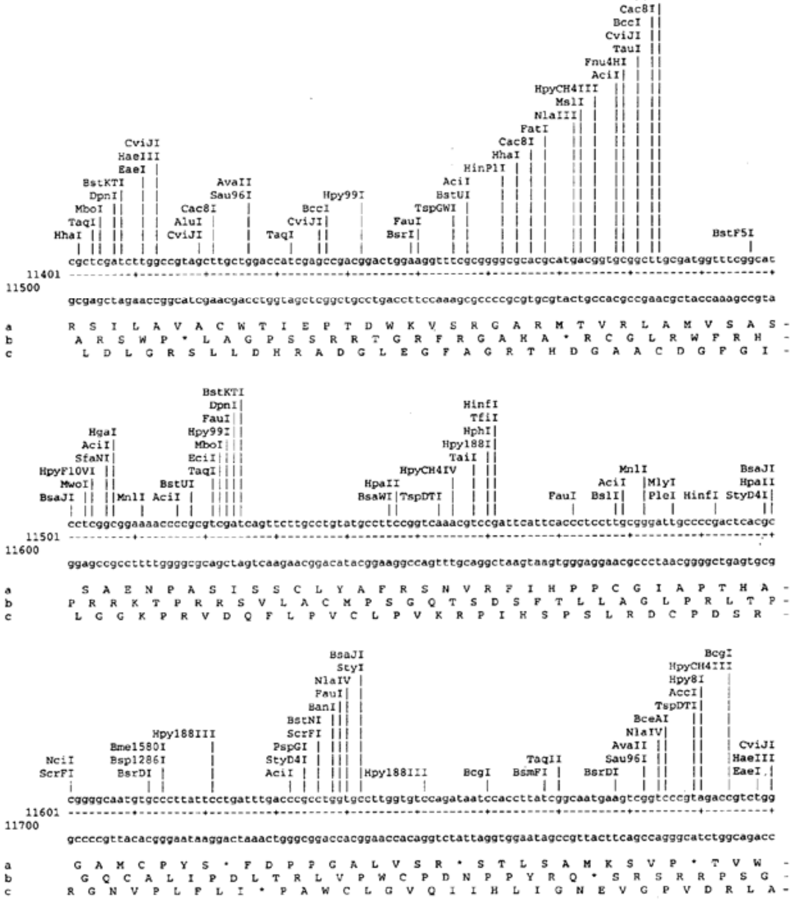
```
                       CviJI
                      HaeIII
                  HpyF10VI |                 AvaII         MnlI
                Cac8I    | |              EcoO109I       AciI |
              CviJI |    | |                 PpuMI    Cac8I | |
             HaeIII |    | |                Sau96I     NaeI | |
               TauI |    | |               BstNI |   HpaII| | |
           Fnu4HI | |BglI| |               ScrFI |  BsrFI|| | |
            AciI| | |MwoI| |             PspGI | | NgoMIV|| | |                             BccI MnlI     TaqI
           BstUI| | |SfiI| |       MnlI StyD4I | |  SgrAI|| | |                          BstUI|TaqI|BsaBI    |
               || | |   || |          |      | | |      ||| | |                               ||   ||    |   |
          gcaacgcggcctgcttggcctcgctgacctgttttgccaggtcctcgccggcggtttttcgcttcttggtcgtcatagttcctcgcgtgtcgatggtcat
     11201---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
11300
          cgttgcgccggacgaaccggagcgactggacaaaacggtccaggagcggccgccaaaaagcgaagaaccagcagtatcaaggagcgcacagctaccagta

a           N  A  A  C  L  A  S  L  T  C  F  A  R  S  S  P  A  V  F  R  F  L  V  V  I  V  P  R  V  S  M  V  I  -
b         A  T  R  P  A  W  P  R  *  P  V  L  P  G  P  R  R  R  F  F  A  S  W  S  S  *  F  L  A  C  R  W  S  S -
c          Q  R  G  L  L  G  L  A  D  L  F  C  Q  V  L  A  G  G  F  S  L  L  G  R  H  S  S  S  R  V  D  G  H   -
```

```
                                                                          HpyF10VI
                                                                        Cac8I    |
                                                                       BceAI|    |
                                                                       AciI||    |
                                                                      BstUI||    |
                                                                       HhaI||    |
                                                                   HinP1I |||    |
                                                                 HpyF10VI |||    |
                                                                FauI    | |||    |
                                    MnlI                      BsiEI|    | |||    |
                               Hpy188III|                    CviJI||    | |||    |
                              BsmAI    ||                   HaeIII||    | |||    |
                              BsmBI    ||                     TauI||    | |||    |               Cac8I
                           BspMI  |    ||                   EaeI |||    | |||    |          HpyCH4V  |
                          TauI |  |    ||                   EagI |||    | |||    |        BsrI     | |
                        AciI | |  |    ||                 Fnu4HI |||    | |||    |      CviJI|     | |
                      Fnu4HI | |  |    ||            BsaJI     | |||    | |||    |     NlaIV||     | |   BstUI
                 HpyF10VI  | | |  |    ||   BstUI     BtgI AciI| |||    | |||    | HpyF10VI|||     | |  HinP1I
                    MwoI|  | | |  |TaqI||  Hpy99I  HgaI  | BccI| |||MwoI| |||MwoI|    MwoI||||     | | BceAI |
                       ||  | | |  |   |||       |     |  |    || |||   || |||   ||       |||||     | |     | |
          cgacttcgccaaacctgccgcctcctgttcgagacgacgcgaacgctccacggcggccgatggcgcgggcagggcagggggagccagttgcacgctgtcg
     11301---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
11400
          gctgaagcggtttggacggcggaggacaagctctgctgcgcttgcgaggtgccgccggctaccgcgcccgtcccgtccccctcggtcaacgtgcgacagc

a          D  F  A  K  P  A  A  S  C  S  R  R  R  E  R  S  T  A  A  D  G  A  G  R  A  G  G  A  S  C  T  L  S  -
b            T  S  P  N  L  P  P  P  V  R  D  D  A  N  A  P  R  R  P  M  A  R  A  G  Q  G  E  P  V  A  R  C  R -
c         R  L  R  Q  T  C  R  L  L  F  E  T  T  R  T  L  H  G  G  R  W  R  G  Q  G  R  G  S  Q  L  H  A  V  A-
```

Figure 19-MM


FokI
Cac8I
BccI
CviJI
TauI
Fnu4HI
AciI
HpyCH4III
MslI
NlaIII
FatI
Cac8I
HhaI
HinP1I
AciI
BstUI
TspGWI
FauI
BsrI
CviJI
HaeIII
EaeI
BstKTI
DpnI
MboI
TaqI
HhaI
AvaII
Sau96I
Cac8I
AluI
CviJI
Hpy99I
BccI
CviJI
TaqI
BstF5I
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11401
11500
gcgagctagaaccggcatcgaacgacctggtagctcggctgcctgaccttccaaagcgccccgcgtgcgtactgccacgccgaacgctaccaaagccgta
a R S I L A V A C W T I E P T D W K V S R G A R M T V R L A M V S A S -
b A R S W P * L A G P S S R R T G R F R G A K A * R C G L R W F R H -
c L D L G R S L L D H R A D G L E G F A G R T H D G A A C D G F G I -
BstKTI
DpnI
FauI
Hpy99I
MboI
EciI
TaqI
HgaI
AciI
SfaNI
HpyF10VI
MwoI
BsaJI
MnlI
BstUI
AciI
HinfI
TfiI
HphI
Hpy188I
TaiI
HpyCH4IV
HpaII
BsaWI
TspDTI
FauI
MnlI
AciI
BslI
MlyI
PleI
HinfI
BsaJI
HpaII
StyD4I
cctcggcggaaaaccccgcgtcgatcagttcttgcctgtatgccttccggtcaaacgtccgattcattcaccctccttgcgggattgccccgactcacgc
11501
11600
ggagccgccttttggggcgcagctagtcaagaacggacatacggaaggccagtttgcaggctaagtaagtgggaggaacgccctaacggggctgagtgcg
a S A E N P A S I S S C L Y A F R S N V R F I H P P C G I A P T H A -
b P R R K T P R R S V L A C M P S G Q T S D S F T L L A G L P R L T P -
c L G G K P R V D Q F L P V C L P V K R P I H S P S L R D C P D S R -
BsaJI
StyI
NlaIV
FauI
BanI
BstNI
ScrFI
PspGI
StyD4I
AciI
Hpy188III
Bme1580I
Bsp1286I
BsrDI
NciI
ScrFI
Hpy188III
BcgI
TaqII
BsmFI
BcgI
HpyCH4III
Hpy8I
AccI
TspDTI
BceAI
NlaIV
AvaII
Sau96I
BsrDI
CviJI
HaeIII
EaeI
cggggcaatgtgcccttattcctgatttgacccgcctggtgccttggtgtccagataatccaccttatcggcaatgaagtcggtcccgtagaccgtctgg
11601
11700
gccccgttacacgggaataaggactaaactgggcggaccacggaaccacaggtctattaggtggaatagccgttacttcagccagggcatctggcagacc
a G A M C P Y S * F D P P G A L V S R * S T L S A M K S V P * T V W -
b G Q C A L I P D L T R L V P W C P D N P P Y R Q * S R S R R P S G -
c R G N V P L F L I * P A W C L G V Q I I H L I G N E V G P V D R L A -

Figure 19-NN

```
                                                                                                   SfaNI
                                                                                                 CviJI |
                                                                                               MnlI  | |
                                                                                            DdeI  |  | |
                                                                                         CviJI |  |  | |
                                                                                        HaeIII |  |  | |
                                                                                    BsaJI    | |  |  | |
                                                                                  BspCNI|    | |  |  | |
                                                                                   CviJI|    | |  |  | |
                                                                                  HaeIII|    | |  |  | |
                              HinfI                                              BseMII||    | |  |  | |
                               TfiI                                             Sau96I|||    | |  |  | |
                  RsaI     Hpy188I|                                          BsaJI   ||||    | |  |  | |
                Csp6I|    BsgI   ||     HpyCH4V              BceAI            BtgI   ||||    | |  |  | |
                    ||       |   ||           |                  |               |   ||||    | |  |  | |
         ccgtccttctcgtacttggtattccgaatcttgccctgcacgaataccagcgaccccttgcccaaatacttgccgtgggcctcggcctgagagccaaaac
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11800
         ggcaggaagagcatgaaccataaggcttagaacgggacgtgcttatggtcgctggggaacgggtttatgaacggcacccggagccggactctcggttttg

a        P  S  F  S  Y  L  V  F  R  I  L  P  C  T  N  T  S  D  P  L  P  K  Y  L  P  W  A  S  A  *  E  P  K  H -
b         R  P  S  R  T  W  Y  S  E  S  C  P  A  R  I  P  A  T  P  C  P  N  T  C  R  G  P  R  P  E  S  Q  N   -
c          V  L  L  V  L  G  I  P  N  L  A  L  H  E  Y  Q  R  P  L  A  Q  I  L  A  V  G  L  G  L  R  A  K  T  -

                                                                    TspDTI
                                            Cac8I                    RsaI|
                                             NaeI                  Csp6I||
                              HhaI         HpaII|        HhaI       FokI||
                          HinP1I |        BsrFI||      SfaNI|   BfaI   |||      BstF5I
             AciI          MboII |       NgoMIV||    HinP1I||   BslI   |||Tsp509I   |BsrI          SspI
                |              | |            |||         |||      |   |||      |   |   |             |
         acttgatgcggaagaagtcggtgcgctcctgcttgtcgccggcatcgttgcgccacatctaggtactaaaacaattcatccagtaaaatataatattta
   11801 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
11900
         tgaactacgccttcttcagccacgcgaggacgaacagcggccgtagcaacgcggtgtagatccatgattttgttaagtaggtcattttatattataaaat

a          L  M  R  K  K  S  V  R  S  C  L  S  P  A  S  L  R  H  I  *  V  L  K  Q  F  I  Q  *  N  I  I  F  Y  -
b        T  *  C  G  R  S  R  C  A  P  A  C  R  R  H  R  C  A  T  S  R  Y  *  N  N  S  S  S  K  I  *  Y  F  I -
c         L  D  A  E  E  V  G  A  L  L  L  V  A  G  I  V  A  P  H  L  G  T  K  T  I  H  P  V  K  Y  N  I  L   -

                                                                                       BsiEI
                              BsrI                                                     HpaII
                         BstKTI  |                                                    BsaWI|
                          DpnI|  |                    HpyCH4III                      MnlI ||
                        BmrI ||  |                   MboII    |                   BstKTI| ||
                        MboI ||  |                TaqI   |    |                     TaqI| ||
                    CviJI  | ||  |              AluI |   |    |                    DpnI|| ||
                   AlwI |  | ||  |             CviJI |   |    |       EcoRV      MboI ||| ||        HgaI
                      | |  | ||  |                 | |   |    |            |        | ||| ||           |
         ttttctcccaatcaggcttgatccccagtaagtcaaaaaatagctcgacatactgttcttccccgatatcctccctgatcgaccggacgcagaaggcaat
   11901 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
12000
         aaaagagggttagtccgaactaggggtcattcagttttttatcgagctgtatgacaagaaggggctataggagggactagctggcctgcgtcttccgtta

a         F  L  P  I  R  L  D  P  Q  *  V  K  K  *  L  D  I  L  F  F  P  D  I  L  P  D  R  P  D  A  E  G  N   -
b          F  S  Q  S  G  L  I  P  S  K  S  K  N  S  S  T  Y  C  S  S  P  I  S  S  L  I  D  R  T  Q  K  A  M  -
c        F  S  P  N  Q  A  *  S  P  V  S  Q  K  I  A  R  H  T  V  L  P  R  Y  P  P  *  S  T  G  R  R  R  Q  C -

                                                                                            BstNI
                                                                                            ScrFI
                                                                                           BsmAI|
                              TauI       BstKTI                                           BsaJI||
         EciI               AciI |        DpnI|                             MslI          PspGI||  BsaJI
       BsrDI|       AciI  Fnu4HI |      MboI ||   CviJI                 BccI   |   BceAI StyD4I||   BtgI
           ||          |       | |         | ||       |                    |   |       |      |||      |
         gtcataccacttgtccgccctgccgcttctcccaagatcaataaagccacttactttgccatctttcacaaagatgttgctgtctcccaggtcgccgtgg
   12001 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
12100
         cagtatggtgaacaggcgggacggcgaagagggttctagttatttcggtgaatgaaacggtagaaagtgtttctacaacgacagagggtccagcggcacc

a        V  I  P  L  V  R  P  A  A  S  P  K  I  N  K  A  T  Y  F  A  I  F  H  K  D  V  A  V  S  Q  V  A  V  G -
b         S  Y  H  L  S  A  L  P  L  L  P  R  S  I  K  P  L  T  L  P  S  F  T  K  M  L  L  S  P  R  S  P  W   -
c          H  T  T  C  P  P  C  R  F  S  Q  D  Q  *  S  H  L  L  C  H  L  S  Q  R  C  C  C  L  P  G  R  R  G  -
```

Figure 19-OO

```
                                                                            MboII
                                                                          BbsI  |
                                                                         MboII  |
                                                                        AlwI |  |
                                                                       DraI| |  |
                                                                      MseI|| |  |
                                                                 BstKTI  ||| |  |
                                                                  DpnI|  ||| |  |
                                                               BstYI ||  ||| |  |
                                                                MboI ||  ||| |  |
                                                              AciI | ||  ||| |  |
                                                             BstUI | ||  ||| |  |
                                                              HhaI | ||  ||| |  |
                                                           BstUI | | ||  ||| |  |
                              MnlI                        HinP1I | | ||  ||| |  |
                            CviJI|        DraI           Cac8I | | | ||  ||| |  |
                           EarI ||       MseI|          AluI | | | | ||  ||| |  |
             MboII    TspGWI  | ||    FalI  ||         CviJI | | | | ||  ||| |  |   BmrI  BsrI
                 |         |  | ||       |  ||             | | | | | ||  ||| |  |      |     |
          gaaaagacaagttcctcttcgggcttttccgtctttaaaaaatcatacagctcgcgcggatctttaaatggagtgtcttcttcccagttttcgcaatcca
    12101 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
 12200
          cttttctgttcaaggagaagcccgaaaaggcagaaattttttagtatgtcgagcgcgcctagaaatttacctcacagaagaagggtcaaaagcgttaggt

 a          K  D  K  F  L  F  G  L  F  R  L  *  K  I  I  Q  L  A  R  I  F  K  W  S  V  F  F  P  V  F  A  I  H  -
 b        E  K  T  S  S  S  S  G  F  S  V  F  K  K  S  Y  S  S  R  G  S  L  N  G  V  S  S  S  Q  F  S  Q  S  T -
 c         K  R  Q  V  P  L  R  A  F  P  S  L  K  N  H  T  A  R  A  D  L  *  M  E  C  L  L  P  S  F  R  N  P   -

                                                              AluI
                                                             CviJI
                                                        HpyF10VI |
                BstKTI                              CviJI      | |
                 DpnI|                               TauI      | |
               MboI ||                           Fnu4HI |      | |                        TaqI
           CviJI  | ||                        BlpI    | |      | |                     BsmFI |
          HaeIII  | ||                        DdeI    | |  MwoI| |                    BccI | |
          EaeI |  | ||             Tsp509I  CviJI|AciI| | DdeI|| |              Hpy188I  | | |     SfaNI CviJI
             | |  | ||                   |      ||   || |    ||| |                    |  | | |         |     |
          catcggccagatcgttattcagtaagtaatccaattcggctaagcggctgtctaagctattcgtatagggacaatccgatatgtcgatggagtgaaagag
    12201 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
 12300
          gtagccggtctagcaataagtcattcattaggttaagccgattcgccgacagattcgataagcatatccctgttaggctatacagctacctcactttctc

 a         I  G  Q  I  V  I  Q  *  V  I  Q  F  G  *  A  A  V  *  A  I  R  I  G  T  I  R  Y  V  D  G  V  K  E   -
 b          S  A  R  S  L  F  S  K  *  S  N  S  A  K  R  L  S  K  L  F  V  *  G  Q  S  D  M  S  M  E  *  K  S  -
 c        H  R  P  D  R  Y  S  V  S  N  P  I  R  L  S  G  C  L  S  Y  S  Y  R  D  N  P  I  C  R  W  S  E  R  A -

                                                                                                    MnlI
                                                                                                  NlaIII
                                                                                            Hpy188III  |
                                                                                               BspHI|  |
                                                                                                FatI|  |
                                                                                               BpmI||  |
                                               MboII                                        Eco57MI||  |
                                              TspDTI                           BsaHI      BccI    |||  |
                             TaqI            CviJI |                        HpyF10VI    CviJI |   |||  |
          HpyCH4V          AluI |          BcgI  | |                  EarI     MwoI|   HaeIII |   |||  |
         BcgI   | AciI    CviJI |       TspDTI|  | |    MboII      Hpy188I BslI   ||    HgaI| |   |||  |
            |   |    |        | |            ||  | |        |            |    |   ||       || |   |||  |
          cctgatgcactccgcatacagctcgataatcttttcagggctttgttcatcttcatactcttccgagcaaaggacgccatcggcctcactcatgagcaga
    12301 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
 12400
          ggactacgtgaggcgtatgtcgagctattagaaaagtcccgaaacaagtagaagtatgagaaggctcgtttcctgcggtagccggagtgagtactcgtct

 a        P  D  A  L  R  I  Q  L  D  N  L  F  R  A  L  F  I  F  I  L  F  R  A  K  D  A  I  G  L  T  H  E  Q  I -
 b         L  M  H  S  A  Y  S  S  I  I  F  S  G  L  C  S  S  S  Y  S  S  E  Q  R  T  P  S  A  S  L  M  S  R   -
 c          *  C  T  P  H  T  A  R  *  S  P  Q  G  F  V  H  L  H  T  L  P  S  K  G  R  H  R  P  H  S  *  A  D  -
```

Figure 19-PP

```
                                   AvaII              AluI
                      BccI      EcoO109I             CviJI
                   NlaIII|         PpuMI            BsgI |                      SfaNI
                 FatI   ||        Sau96I          Fnu4HI |       CviJI       NlaIII |
     BceAI  CviJI   |   ||    HpyCH4V  |           TseI| |     BbvI  |     FatI   | |      BsmFI    XcmI
         |      |   |   ||          |  |              || |        |  |        |   | |          |       |
        ttgctccagccatcatgccgttcaaagtgcaggacctttggaacaggcagctttccttccagccatagcatcatgtccttttcccgttccacatcatagg
  12401 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
12500
        aacgaggtcggtagtacggcaagtttcacgtcctggaaaccttgtccgtcgaaaggaaggtcggtatcgtagtacaggaaaagggcaaggtgtagtatcc

a         A  P  A  I  M  P  F  K  V  Q  D  L  W  N  R  Q  L  S  F  Q  P  *  H  H  V  L  F  P  F  H  I  I  G  -
b       L  L  Q  P  S  C  R  S  K  C  R  T  F  G  T  G  S  F  P  S  S  H  S  I  M  S  F  S  R  S  T  S  *  V -
c        C  S  S  H  H  A  V  Q  S  A  G  P  L  E  Q  A  A  F  L  P  A  I  A  S  C  P  F  P  V  P  H  H  R   -

                    CviJI
       NlaIV     HpaII  |           TspDTI                                  BsmAI
     AvaII |    BsrFI|  |           DraI |                       AluI    Bpu10I |
    Sau96I | TspGWI ||  |          MseI| |                      CviJI      DdeI | TspGWI
         | |      | ||  |             || |                          |         | |      |
        tggtccctttataccggctgtccgtcatttttaaatataggttttcattttctcccaccagcttatataccttagcaggagacattccttccgtatcttt
  12501 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
12600
        accagggaaatatggccgacaggcagtaaaaatttatatccaaaagtaaaagagggtggtcgaatatatggaatcgtcctctgtaaggaaggcatagaaa

a        G  P  F  I  P  A  V  R  H  F  *  I  *  V  F  I  F  S  H  Q  L  I  Y  L  S  R  R  H  S  F  R  I  F   -
b         V  P  L  Y  R  L  S  V  I  F  K  Y  R  F  S  F  S  P  T  S  L  Y  T  L  A  G  D  I  P  S  V  S  F  -
c       W  S  L  Y  T  G  C  P  S  F  L  N  I  G  F  H  F  L  P  P  A  Y  I  P  *  Q  E  T  F  L  P  Y  L  L-

                       BstKTI
           AciI         DpnI|
         MspA1I       MboI ||          HpaII                                         HpyCH4III
       Fnu4HI |      TaqI| ||         BsaWI|                                            MnlI |  DraI
        TseI| |     BbvI|| ||   Tsp509I   ||          HphI CviJI                      SfcI | | MseI|
           || |        ||| ||         |   ||             |     |                         | | |    ||
        tacgcagcggtatttttcgatcagttttttcaattccggtgatattctcattttagccatttattatttccttcctcttttctacagtatttaaagatac
  12601 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
12700
        atgcgtcgccataaaaagctagtcaaaaaagttaaggccactataagagtaaaatcggtaaataataaaggaaggagaaaagatgtcataaatttctatg

a       Y  A  A  V  F  F  D  Q  F  F  Q  F  R  *  Y  S  H  F  S  H  L  L  F  P  S  S  F  L  Q  Y  L  K  I  P-
b        T  Q  R  Y  F  S  I  S  F  F  N  S  G  D  I  L  I  L  A  I  Y  Y  F  L  P  L  F  Y  S  I  *  R  Y   -
c         R  S  G  I  F  R  S  V  F  S  I  P  V  I  F  S  F  *  P  F  I  I  S  F  L  F  S  T  V  F  K  D  T  -

                                                    BsmI
                                                 HpyCH4V
            Tsp509I                            TspRI    |
             AluI |                    HpyCH4III  |    |                          AluI
            CviJI | PsiI         Tsp509I       |  |    |         MseI            CviJI
                |  |    |               |       |  |    |            |                |
        cccaagaagctaattataacaagacgaactccaattcactgttccttgcattctaaaaccttaaataccagaaaacagctttttcaaagttgttttcaaa
  12701 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
12800
        gggttcttcgattaatattgttctgcttgaggttaagtgacaaggaacgtaagattttggaatttatggtcttttgtcgaaaaagtttcaacaaaagttt

a         Q  E  A  N  Y  N  K  T  N  S  N  S  L  F  L  A  F  *  N  L  K  Y  Q  K  T  A  F  S  K  L  F  S  K  -
b       P  K  K  L  I  I  T  R  R  T  P  I  H  C  S  L  H  S  K  T  L  N  T  R  K  Q  L  F  Q  S  C  F  Q  S-
c        P  R  S  *  L  *  Q  D  E  L  Q  F  T  V  P  C  I  L  K  P  *  I  P  E  N  S  F  F  K  V  V  F  K   -

                                                   BstXI
                                                  MslI |
                                                 BbvI| |
                               CviJI            SfaNI| |
                              NlaIV|         Tsp509I|| |                                     MnlI
                           Hpy99I ||       TaqII   ||| |     Fnu4HI                        BpmI |
                        TaqI    | ||    TspGWI |   ||| |      TseI| HphI          BccI  Eco57MI |
                           |    | ||         | |   ||| |         ||    |             |        | |
        gttggcgtataacatagtatcgacggagccgattttgaaaccacaattatgggtgatgctgccaacttactgatttagtgtatgatggtgtttttgaggt
  12801 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
12900
        caaccgcatattgtatcatagctgcctcggctaaaactttggtgttaatacccactacgacggttgaatgactaaatcacatactaccacaaaaactcca

a        L  A  Y  N  I  V  S  T  E  P  I  L  K  P  Q  L  W  V  M  L  P  T  Y  *  F  S  V  *  W  C  F  *  G   -
b         W  R  I  T  *  Y  R  R  S  R  F  *  N  H  N  Y  G  *  C  C  Q  L  T  D  L  V  Y  D  G  V  F  E  V  -
c       V  G  V  *  H  S  I  D  G  A  D  F  E  T  T  I  M  G  D  A  A  N  L  L  I  *  C  M  M  V  F  L  R  C-
```

Figure 19-QQ

```
                   BsmFI
                TspRI |                                                                            HpyF10VI
               CviJI| |                                                                               MwoI|
           HpyF10VI || |                                                                           BceAI ||
              MwoI| || |          AluI              AlwNI                                         HaeII | ||
            BsrI || || |          CviJI         AluI  |                             BceAI          HhaI| | ||
        BsiHKAI| || || |          MspA1I        CviJI |                             HpaII|          AfeI|| | ||
       Bsp1286I| || || |          PvuII         MnlI| |          MaeIII          AciI ||        HinP1I||| | ||
               || || || |              |            || |              |              |  ||             |||| | ||
       gctccagtggcttctgtgtctatcagctgtccctcctgttcagctactgacggggtggtgcgtaacggcaaaagcaccgccggacatcagcgctatctct
 12901 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
13000
       cgaggtcaccgaagacacagatagtcgacagggaggacaagtcgatgactgccccaccacgcattgccgttttcgtggcggcctgtagtcgcgatagaga

a      A  P  V  A  S  V  S  I  S  C  P  S  C  S  A  T  D  G  V  V  R  N  G  K  S  T  A  G  H  Q  R  Y  L  C -
b       L  Q  W  L  L  C  L  S  A  V  P  P  V  Q  L  L  T  G  W  C  V  T  A  K  A  P  P  D  I  S  A  I  S  -
c        S  S  G  F  C  V  Y  Q  L  S  L  L  F  S  Y  *  R  G  G  A  *  R  Q  K  H  R  R  T  S  A  L  S  L -

                                                                                              SfaNI
                                                                RsaI                     NlaIII|
                                        Hpy8I                 Csp6I|                   FatI    ||
               TspRI                 PstI |                 HpaII ||                CviJI|     ||
       HpyF10VI  |               HpyCH4V | |                  NciI ||               HaeIII|     ||
          MwoI|  |       NlaIII       |  | |                 ScrFI ||           MslI  MscI|     ||
        BtsI ||  |     FatI   | SfcI  |  | |       AciI    StyD4I | ||          MmeI|EaeI ||     ||        MwoI
           | ||  |        |   |   |   |  | |          |       |  | ||             ||   |  ||     ||           |
       gctctcactgccgtaaaacatggcaactgcagttcacttacaccgcttctcaacccggtacgcaccagaaaatcattgatatggccatgaatggcgttgg
 13001 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
13100
       cgagagtgacggcattttgtaccgttgacgtcaagtgaatgtggcgaagagttgggccatgcgtggtcttttagtaactataccggtacttaccgcaacc

a       S  H  C  R  K  T  W  Q  L  Q  F  T  Y  T  A  S  Q  P  G  T  H  Q  K  I  I  D  M  A  M  N  G  V  G -
b      A  L  T  A  V  K  H  G  N  C  S  S  L  T  P  L  L  N  P  V  R  T  R  K  S  L  I  W  P  *  M  A  L  D -
c       L  S  L  P  *  N  M  A  T  A  V  H  L  H  R  F  S  T  R  Y  A  P  E  N  H  *  Y  G  H  E  W  R  W  -

                                                                                   BseMII
                                                                                   BstEII
                                                                                   MaeIII                 NciI
                                                                                  BspCNI|                ScrFI
        BstF5I                                                               TauI     ||                HpaII|
          NciI                                                              AciI |     ||               CviJI||
         ScrFI                                                  TaiI       Fnu4HI |     ||              StyD4I||
        HpaII|      AciI HpyF10VI                         MaeIII |         CviJI| |     ||           HpyF10VI |||
      StyD4I||      Cac8I    MwoI|    Hin4I                Tsp45I |         HaeIII| |     ||            HhaI  | |||
      TspDTI|||     CviJI |   FauI||   CviJI|            HpyCH4IV| |       Hin4I  || |     ||        BstUI |MnlI| |||
    HpyF10VI||||    FokI | |  BslI|||   HaeIII|            MnlI   || |MseI  DdeI | || |     ||       HinP1I |MwoI| |||
           ||||      |  | |     ||||       ||               |    || |  |      |  | || |     ||            | |   || |||
       atgccgggcaacagcccgcattatgggcgttggcctcaacacgatttacgtcacttaaaaactcaggccgcagtcggtaacctcgcgcatacagccgg
 13101 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
13200
       tacggcccgttgtcgggcgtaatacccgcaaccggagttgtgctaaaatgcagtgaatttttgagtccggcgtcagccattggagcgcgtatgtcggcc

a       C  R  A  T  A  R  I  M  G  V  G  L  N  T  I  L  R  H  L  K  N  S  G  R  S  R  *  P  R  A  Y  S  R  -
b        A  G  Q  Q  P  A  L  W  A  L  A  S  T  R  F  Y  V  T  *  K  T  Q  A  A  V  G  N  L  A  H  T  A  G -
c      M  P  G  N  S  P  H  Y  G  R  W  P  Q  H  D  F  T  S  L  K  K  L  R  P  Q  S  V  T  S  R  I  Q  P  G -

             DrdI                                                            CviJI
          AatII |                                                         Cac8I |
           TaiI |                                                        HaeII| |
          BtsI | |                                                        HhaI|| |
         TspRI | |                                                       AfeI||| |                        BsmAI
          ZraI | |                                                     HinP1I|||| |                        HpaII|
        BsaHI| | |                                                     Cac8I ||||| |                    Hpy188III|
     HpyCH4IV| | |        AciI                                     HhaI  | ||||| |         BstUI          BsaWI||
    MaeIII   || | |        BstUI              CviJI           BstUI |  | ||||| |     AflIII  |           BspEI||
    Tsp45I   || | | HinP1I  HhaI      HpyCH4III   TspRI|    CviJI  HinP1I |  | ||||| |       MluI |HpyCH4III   |||
         |   || | |      |  |              |    ||         |      |  |  | ||||| |          |  |         |   |||
       gcagtgacgtcatcgtctgcgcggaaatggacgaacagtggggctatgtcggggctaaatcgcgccagcgctggctgttttacgcgtatgacagtctccg
 13201 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
13300
       cgtcactgcagtagcagacgcgcctttacctgcttgtcaccccgatacagccccgatttagcgcggtcgcgaccgacaaaatgcgcatactgtcagaggc

a      A  V  T  S  S  S  A  R  K  W  T  N  S  G  A  M  S  G  L  N  R  A  S  A  G  C  F  T  R  M  T  V  S  G -
b       Q  *  R  H  R  L  R  G  N  G  R  T  V  G  L  C  R  G  *  I  A  P  A  L  A  V  L  R  V  *  Q  S  P  -
c        S  D  V  I  V  C  A  E  M  D  E  Q  W  G  Y  V  G  A  K  S  R  Q  R  W  L  F  Y  A  Y  D  S  L  R -
```

Figure 19-RR

```
                        TaiI
                     BsaAI |
                 HpyCH4IV| |                                          MaeIII
                   HhaI || |                    BseYI                 Tsp45I
           BbsI  FspI|  || |                  Hpy99I             Cac8I   |             TaiI          BstF5I
    HpyCH4III|HinP1I||  || |               HgaI    | BsaHI      CviJI |   |          BmgBI |           HphI |
       BslI  ||MboII||| || |     Hpy8I    HphI |     |  HgaI      HphI | |   |     HpyCH4IV| |        BccI | |
          |  ||    |||| || |        |        |  |     |     |          | |   |          || |          | | |
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 13301 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
13400
       cttctgccaacaacgcgtgcataagccacttgcgtgataccgctgcgaccccgcagaatactcggacgacagtgggaaactgcaccactatacctactgc

a        R  R  L  L  R  T  Y  S  V  N  A  L  W  R  R  W  G  V  L  *  A  C  C  H  P  L  T  W  *  Y  G  *  R  -
b      E  D  G  C  C  A  R  I  R  *  T  H  Y  G  D  A  G  A  S  Y  E  P  A  V  T  L  *  R  G  D  M  D  D  G -
c       K  T  V  V  A  H  V  F  G  E  R  T  M  A  T  L  G  R  L  M  S  L  L  S  P  F  D  V  V  I  W  M  T   -


                                                                                                    Fnu4HI
                                                                                           Hpy188I       |
                                                                                        HinfI    |       |
                                                                                         TfiI    |       |
                                                                                        MnlI|    |       |
             FokI                                                                  BspCNI ||    |       |
           TspGWI                                                                BseMII|  ||    |       |
          MspA1I|                                                              TauI   ||  ||    |       |
             TauI|                                                          Fnu4HI |   ||  ||    |       |
          AciI ||                                     Eco57I                  AciI| |   ||  ||    |       |
        Fnu4HI ||                                    Eco57MI                  BbvI| |   ||  ||    |       |
         CviJI| ||                                      TaiI |                BsrBI| |   ||  ||    |       |
        HaeIII| ||                                    BsaAI | |          HpyF10VI || |   ||  ||    |       |
        Cac8I || ||                               HpyCH4IV| | |       Tsp509I    | || |   ||  ||    |       |
         EaeI || ||                              HpyCH4V || | |    Fnu4HI     |    | || |   ||  ||    |       |
      BstF5I| || ||               TspDTI   Fnu4HI |  || | |       |      |    | || |   ||  ||    |       |
        FokI| || ||          BbvI       |   AluI| |  || | |     TseI|     |    | || |   ||  ||    |       |
       CviJI|| || || HinfI   BsgI| FauI|  CviJI| |  || | |  HpyF10VI ||     |    | || |   ||  ||    |       |
       CviJI|| || ||  TfiI  AciI||BslI||   TseI| |  || | | Cac8I   MwoI| ||     |MwoI| || |   ||  || DdeI|TseI|
            ||| || ||    |     |||    |||      || |  || | |     |       || ||     |  || || |   ||  ||    ||     ||
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13500
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a       M  A  G  R  C  M  N  P  A  *  R  E  S  C  T  *  S  A  S  D  I  R  S  E  L  S  G  I  T  *  I  *  G  -
b        W  L  A  A  V  *  I  P  P  E  G  K  A  A  R  N  Q  Q  A  I  Y  A  A  N  *  A  A  *  P  E  S  E  A  -
c      D  G  W  P  L  Y  E  S  R  L  K  G  K  L  H  V  I  S  K  R  Y  T  Q  R  I  E  R  H  N  L  N  L  R  Q -

                                                             Tth111I
                                                          NlaIII |
                                                         FatI |  |
          BstNI                                       HpyCH4V |  |
          ScrFI                              TspGWI    Fnu4HI |  |  |
         AlwNI|   BseYI                  BsmFI  |       AluI| |  |  |
         PspGI||  CviJI             BceAI     |  |      CviJI| |  |  |                          MmeI
        StyD4I||  BbvI |     PshAI     |     |  |  BbvI   TseI| |  |  |                 Hpy188I   |
              |||   |  |         |     |     |  |     |      || |  |  |                       |   |
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13600
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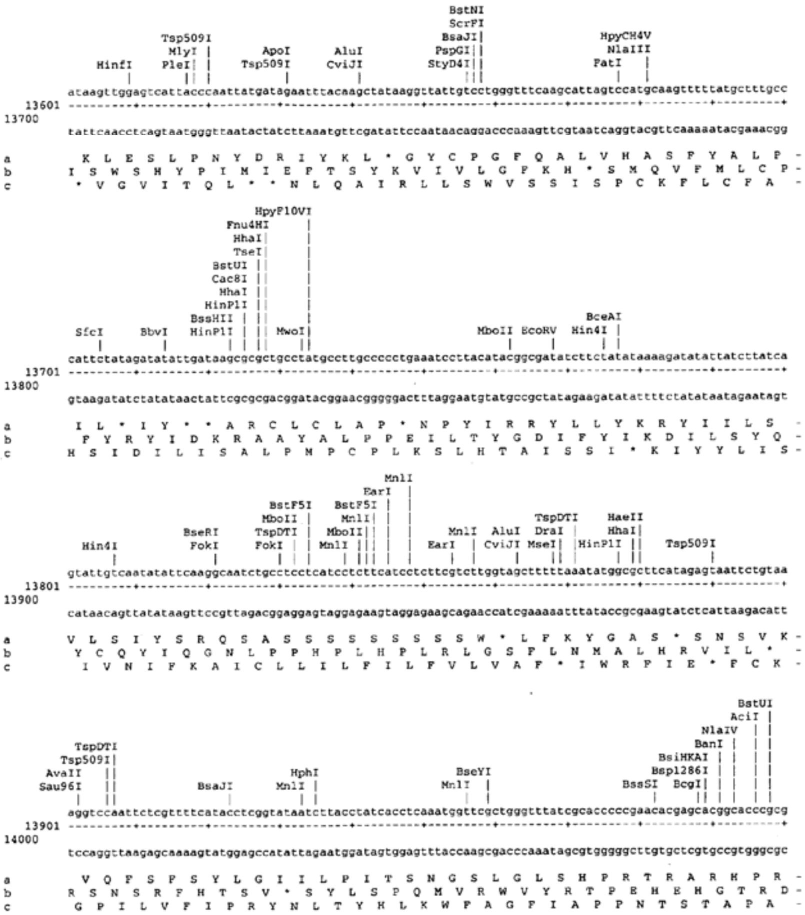
a      S  T  W  H  G  W  D  G  S  R  C  R  S  Q  N  R  W  S  C  M  T  K  S  S  G  I  I  *  T  *  N  T  I  N-
b       A  P  G  T  A  G  T  E  V  A  V  V  L  K  I  G  G  A  A  *  Q  S  H  R  A  L  S  E  H  K  T  L  S  -
c        H  L  A  R  L  G  R  K  S  L  S  P  S  K  S  V  E  L  H  D  K  V  I  G  H  Y  L  N  I  K  H  Y  Q  -
```

Figure 19-SS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MlyI ApoI AluI PspGI NlaIII
HinfI PleI Tsp509I CviJI StyD4I PatI
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a K L E S L P N Y D R I Y K L * G Y C P G F Q A L V H A S F Y A L P -
b I S W S H Y P I M I E F T S Y K V I V L G F K H * S M Q V F M L C P -
c * V G V I T Q L * * N L Q A I R L L S W V S S I S P C K F L C F A -
HpyF10VI
Fnu4HI
HhaI
TseI
BstUI
Cac8I
HhaI
HinP1I
BssHII BceAI
SfcI BbvI HinP1I MwoI MboII EcoRV Hin4I
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b F Y R Y I D K R A A Y A L P P E I L T Y G D I F Y I K D I L S Y Q -
c H S I D I L I S A L P M P C P L K S L H T A I S S I * K I Y Y L I S -
MnlI
EarI
BstF5I BstF5I
MboII MnlI TspDTI HaeII
BseRI TspDTI MboII MnlI AluI DraI HhaI
Hin4I FokI FokI MnlI EarI CviJI MseI HinP1I Tsp509I
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a V L S I Y S R Q S A S S S S S S S S S W * L F K Y G A S * S N S V K -
b Y C Q Y I Q G N L P P H P L H P L R L G S F L N M A L H R V I L * -
c I V N I F K A I C L L I L F I L F V L V A F * I W R P I E * F C K -
BstUI
AciI
NlaIV
BanI
BsiHKAI
TspDTI
Tsp509I
AvaII HphI BseYI Bsp1286I
Sau96I BsaJI MnlI MnlI BssSI BcgI
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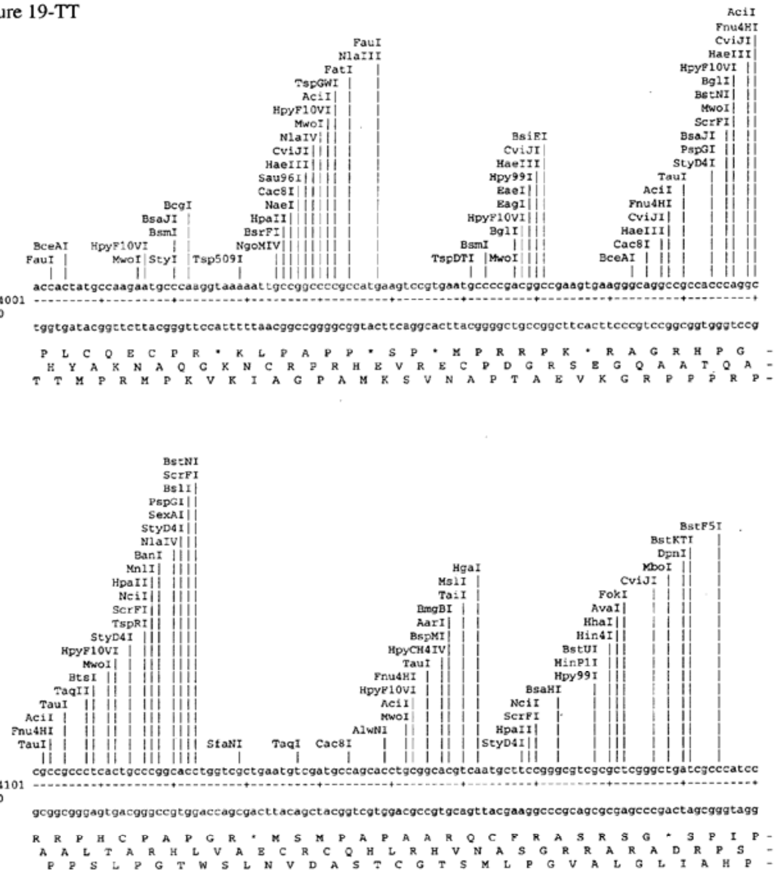
a V Q F S P S Y L G I I L P I T S N G S L G L S H P R T R A R H P R -
b R S N S R F H T S V * S Y L S P Q M V R W V Y R T P E H E H G T R D -
c G P I L V F I P R Y N L T Y H L K W P A G F I A P P N T S T A P A -

Figure 19-TT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Fnu4HI
CviJI
HaeIII
HpyF10VI
BglI
BstNI
MwoI
ScrFI
BsaJI
PspGI
StyD4I
TauI
AciI
Fnu4HI
CviJI
HaeIII
Cac8I
BceAI
FauI
NlaIII
FatI
TspGWI
AciI
HpyF10VI
MwoI
NlaIV
CviJI
HaeIII
Sau96I
Cac8I
NaeI
HpaII
BsrFI
NgoMIV
Tsp509I
BcgI
BsaJI
BsmI
BceAI
HpyF10VI
FauI
MwoI
StyI
BsiEI
CviJI
HaeIII
Hpy99I
EaeI
EagI
HpyF10VI
BglI
BsmI
TspDTI
MwoI
accactatgccaagaatgcccaaggtaaaaattgccggccccgccatgaagtccgtgaatgccccgacggccgaagtgaagggcaggccgccacccaggc
14001
14100
tggtgatacggttcttacgggttccatttttaacggccggggcggtacttcaggcacttacggggctgccggcttcacttcccgtccggcggtgggtccg
a P L C Q E C P R * K L P A P P * S P * M P R R P K * R A G R H P G -
b H Y A K N A Q G K N C R P R H E V R E C P D G R S E G Q A A T Q A -
c T T M P R M P K V K I A G P A M K S V N A P T A E V K G R P P P R P -
BstNI
ScrFI
BslI
PspGI
SexAI
StyD4I
NlaIV
BanI
MnlI
HpaII
NciI
ScrFI
TspRI
StyD4I
HpyF10VI
MwoI
BtsI
TaqII
TauI
AciI
Fnu4HI
TauI
SfaNI
TaqI
Cac8I
HgaI
MslI
TaiI
BmgBI
AarI
BspMI
HpyCH4IV
TauI
Fnu4HI
HpyF10VI
AciI
MwoI
AlwNI
BstF5I
BstKTI
DpnI
MboI
CviJI
FokI
AvaI
HhaI
Hin4I
BstUI
MinP1I
Hpy99I
BsaHI
NciI
ScrFI
HpaII
StyD4I
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14101
14200
gcggcgggagtgacgggccgtggaccagcgacttacagctacggtcgtggacgccgtgcagttacgaaggcccgcagcgcgagcccgactagcgggtagg
a R R P H C P A P G R * M S M P A P A A R Q C F R A S R S G * S P I P -
b A A L T A R H L V A E C R C Q H L R H V N A S G R R A R A D R P S -
c P P S L P G T W S L N V D A S T C G T S M L P G V A L G L I A H P -

Figure 19-UU

```
                                                                                                  BbvI
                                                  BceAI                                           MnlI
                                             Fnu4HI   |                                         BslI  |
                                              HaeII   |                                       BccI  | |
                                           HpyF10VI   |                     BsaJI           BstNI | | |
                                              HhaI|   |                     BsiEI           ScrFI | | |
                                              MwoI|   |                    CviJI|          AlwNI || | |
                     HpaII                    TseI|   |                   HaeIII|          BsaJI || | |
                      NciI                   AfeI||   |                     TauI|         BsaJI ||| | |
                     ScrFI                MinPlI|||   |                   EaeI ||         PspGI ||| | |
                     BslI|               Cac8I ||||   |                   EagI ||        StyD4I ||| | |
                  BstKTI||        HpyF10VI   | ||||   |                 Fnu4HI ||       CviJI | ||| | |
                  StyD4I||         BstAPI|   | ||||   |                  AciI| ||    Fnu4HI  || ||| | |
                   DpnI|||       BbvI   ||   | ||||   |                 BstUI| ||     HhaI|  || ||| | |
        BccI    Hin4I ||||     BsrDI|   ||   | ||||   | BslI     CviJI  HphI|| ||     TseI|  || ||| | |
    MaeIII |AlwI MboI |||| BslI    ||MwoI|   | ||||   | MnlI    HaeIII MnlI||| || HinPlI ||  || ||| | | BstF5I
         | |   |    ||||    |    ||   ||   | ||||   |    |         |     ||| ||      | ||  || ||| | |     |
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   14201 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
14300
         gcaatgacggggctagggccgttaccgttcctgacggtcgcgacggtaaaaccccactccggcaagcgccggctccccgcgtcggggaccccctaccc

a          L  L  P  R  S  R  Q  W  Q  G  L  P  A  L  P  F  L  G  *  G  R  S  R  P  R  G  A  A  P  G  G  M  G  -
b        R  Y  C  P  D  P  G  N  G  K  D  C  Q  R  C  H  F  W  G  E  A  V  R  G  R  G  A  Q  P  L  G  G  W  E -
c         V  T  A  P  I  P  A  M  A  R  T  A  S  A  A  I  F  G  V  R  P  F  A  A  E  G  R  S  P  W  G  D  G  -

                                                                                        BstNI
                                                                                        ScrFI
                                                                                      BsaJI  |
                                                                                      PspGI  |
                                                                                     StyD4I  |
                        NciI                                                          CviJI| |
                       ScrFI                                                      Fnu4HI  || |
                      HpaII|                                                        HhaI| || |
           BstUI     CviJI||                                                        TseI| || |
            FokI    HaeIII||                                    MaeIII         MinPlI  || || |
           FauI|    StyD4I||                                    Tsp45I       HpyF10VI  || || |
          AciI||   Cac8I |||                                    AciI  |          MwoI| || || |
         Cac8I||    MnlI |||                Bme1580I           BstUI  |    HpyF10VI|| || || |
       CviJI |||  Sau96I |||                Bsp1286I            HhaI  |            ||| || || |
      HaeIII |||  AciI | ||| Hpy188III       NlaIV|        HinPlI  | |BstUI  |    ||| || || | BbvI
     Sau96I| ||| FauI| | |||     TaqI|       BanI ||   BslI Cac8I | | |HinPlI |MwoI||| || || |MseI |
          || |||    || | |||        ||          | ||      |     | | | |     | |   |||| || || |   | |
         aggcccgcgttagcgggccgggagggttcgagaagggggggcaccccccttcggcgtgcgcggtcacgcgcacagggcgcagccctggttaaaaacaagg
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14400
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a         G  P  R  *  R  A  G  R  V  R  E  G  G  A  P  P  F  G  V  R  G  H  A  H  R  A  Q  P  W  L  K  T  R  -
b          A  R  V  S  G  P  G  G  F  E  K  G  G  H  P  P  S  A  C  A  V  T  R  T  G  R  S  P  G  *  K  Q  G  -
c        R  P  A  L  A  G  R  E  G  S  R  R  G  G  T  P  L  R  R  A  R  S  R  A  Q  G  A  A  L  V  K  N  K  V-

                      DraI                          CviJI
                     MseI|                         HaeIII
                 BspMI ||                          EaeI |                      EciI
         PsiI SspI   | ||      MseI           AciI   || BslI AciI     HpyCH4V  |        Hin4I   Hpy8I
            |    |   | ||         |              |    ||      |    |           |  |             |      |
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   14401 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
14500
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a        F  I  N  I  G  L  K  A  G  *  K  T  G  *  R  W  P  K  N  G  R  K  P  L  Q  M  L  D  F  L  P  V  D  S -
b         L  *  I  L  V  *  K  Q  V  K  R  Q  V  S  G  G  R  K  T  G  G  N  P  C  K  C  W  I  F  C  L  W  T  -
c          Y  K  Y  W  F  K  S  R  L  K  D  R  L  A  V  A  E  K  R  A  E  T  L  A  N  A  G  F  S  A  C  G  Q  -
```

Figure 19-VV

```
                                                                  AlwI
                                                                HhaI|
                                                              BstUI ||
                                                             HinP1I ||
                                                          BstKTI |  ||
                               HhaI                         DpnI||  ||                    HhaI
                         HinP1I |          MnlI           MboI |||  ||           MnlI  BstUI |
    CviJI         MnlI Hin4I  | |       BpuEI |       SmlI     MnlI | |||  ||          BpuEI| HinP1I |SmlI
        |             |     | | |           | |            |        | | ||| |||           ||       | |   |
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  14501 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
14600
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a        P  S  N  V  N  R  C  A  P  H  L  S  A  L  C  P  S  S  V  K  D  R  A  P  H  L  S  V  V  A  P  L  K  -
b       A  P  Q  M  S  I  G  A  P  L  I  C  Q  H  S  A  P  Q  V  S  R  I  A  P  L  I  C  Q  *  S  R  P  S  S -
c         P  L  K  C  Q  *  V  R  P  S  S  V  S  T  L  P  L  K  C  Q  G  S  R  P  S  S  V  S  S  R  A  P  Q  -
```

```
                                                                                                        AluI
                                                                                                       CviJI
                                                                                                     Cac8I |
                                                                                                    CviJI | |
                                                                                                   HaeIII | |
                                                                                                     MscI | |
                                      CviJI                                                        Cac8I | | |
                                  BstNI |                                                           EaeI | | |
                                  ScrFI |                                                       HpyF10VI | | |
                               BsaJI |  |                                                           MwoI|| | | |
                    Bme1580I   PspGI |  |                                                          CviJI||| | | |
    MnlI AciI   Bsp1286I    StyD4I | |  | Hpy8I   XcmI             BstUI                   MnlI      ||||| | | |
        |    |        |      |   | |  |     |      |               |                    |        ||| | | | |
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  14601 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
14700
        cacagttatggcgtcccgtgaataggggtccgaacaggtgtagtagacaccctttgagcgcattttagtccgcaaaagcggctaaacgctccgaccggtc

a        C  Q  Y  R  R  A  L  I  P  R  L  V  H  I  I  C  G  K  L  A  *  N  Q  A  F  S  P  I  C  E  A  G  Q  -
b         V  N  T  A  G  H  L  S  P  G  L  S  T  S  S  V  G  N  S  R  K  I  R  R  F  R  R  F  A  R  L  A  S -
c       V  S  I  P  Q  G  T  Y  P  Q  A  C  P  H  H  L  W  E  T  R  V  K  S  G  V  F  A  D  L  R  G  W  P  A -
```

```
                 BsiEI                                 BpuEI
                CviJI|                                  NciI
               HaeIII|                                 ScrFI
               Cac8I ||                               HpaII|
                EaeI ||                                HhaI||
                EagI ||                              StyD4I||
                NaeI ||                              BstUI |||
             HpaII|  ||                             HinP1I |||             SmlI
            BsrFI||  ||                               TauI |||             HphI|
           Hpy99I||  ||                                                    MlyI|
                                                     AciI | |||            PleI||                   AciI
           NgoMIV||  ||                                                  NlaIV|||                   TaiI|
                                                   Fnu4HI | |||         CviJI||||     HpyCH4IV        ||
            TaiI |||  ||          Cac8I            HincII | | |||       HaeIII|||||     HincII |       ||
         BmgBI |  |||  ||       CviJI |              Hpy8I | | |||      Sau96I||||||      Hpy8I |       ||         MnlI
     HpyCH4IV|  |  |||  ||   TaqI   |  |              MnlI  | | |||HinfI   ||||||EciI MnlI |       ||     MnlI |
            ||  |  |||  ||      |   |  |                |    | | |||    |   |||||||  |    |  |     ||        |  |
        ctccacgtcgccggccgaaatcgagcctgcccctcatctgtcaacgccgcgccgggtgagtcggcccctcaagtgtcaacgtccgcccctcatctgtcag
  14701 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
14800
        gaggtgcagcggccggctttagctcggacggggagtagacagttgcggcgcggcccactcagccggggagttcacagttgcaggcggggagtagacagtc

a       L  H  V  A  G  R  N  R  A  C  P  S  S  V  N  A  A  P  G  E  S  A  P  Q  V  S  T  S  A  P  H  L  S  V -
b        S  T  S  P  A  E  I  E  P  A  P  H  L  S  T  P  R  R  V  S  R  P  L  K  C  Q  R  P  P  L  I  C  Q  -
c         P  R  R  R  P  K  S  S  L  P  L  I  C  Q  R  R  A  G  *  V  G  P  S  S  V  N  V  R  P  S  S  V  S  -
```

Figure 19-WW

```
                                                  SacII
                                                  AciI|
                                                 BstUI|
                                                MspA1I|
                                                  TauI|
                                                AciI ||
                                               BsaJI ||
                                               BsiEI ||
                                                BtgI ||
                                              Fnu4HI ||
                                              CviJI| ||
                                             HaeIII| ||
                                               TauI| ||
                                             EaeI || ||
                                             EagI || ||                                          CviJI
                                           Fnu4HI || ||                                         HaeIII
                                             NotI || ||                                       Sau96I |
                                            AciI| || ||                                   HpyCH4V  | |
                                         Cac8I || || ||                                 BceAI   |  | |
                                          NaeI || || ||                               BstUI |   |  | |
                                        HpaII| || || ||                  Hpy99I        HhaI |   |  | |
           CviJI                       BciVI|| || || ||               HpyF10VI|    HinP1I | |   |  | |
          HaeIII       BstUI           BsrFI|| || || ||                  MwoI||HpyF10VI | | |   |  | |
        Sau96I |      AciI |          NgoMIV|| || || ||               TaqI  |||   MwoI| | | |   |  | |    EaeI
         TspRI |   MnlI  | |           SgrAI|| || || ||    BsmAI  CviJI  |  |||BceAI || | | |   |  | |    EagI
             | |      |  | |               ||| || || ||        |      |  |  |||    | || | | |   |  | |       |
          tgagggccaagtttccgcgaggtatccacaacgccggcggccgcggtgtctcgcacacggcttcgacggcgtttctggcgcgtttgcagggccatagac
    14801 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+
14900
          actcccggttcaaaggcgctccatagg tgttgcggccgccggcgccacagagcgtgtgccgaagctgccgcaaagaccgcgcaaacgtcccggtatctg

a           R  A  K  F  S  A  R  Y  P  Q  R  R  R  P  R  C  L  A  H  G  F  D  G  V  S  G  A  F  A  G  P  *  T  -
b         *  G  P  S  F  P  R  G  I  H  N  A  G  G  R  G  V  S  H  T  A  S  T  A  F  L  A  R  L  Q  G  H  R  R -
c          E  G  Q  V  F  R  E  V  S  T  T  P  A  A  A  V  S  R  T  R  L  R  R  R  F  W  R  V  C  R  A  I  D   -
```

```
                       HpyF10VI
                          MwoI|
                       TauI  ||
                    BceAI |  ||
                   Fnu4HI |  ||
                    AciI| |  ||
                  MspA1I| |  ||
              HpyF10VI || |  ||
                  MnlI || |  ||
                 MwoI| || |  ||
               BseYI|| || |  ||
              CviJI||| || |  ||
            Cac8I |||| || |  ||
           TauI | |||| || |  ||
         AciI | | |||| || |  ||      HpaII
        BsiEI | | |||| || |  ||       NciI
       Fnu4HI | | |||| || |  ||      ScrFI
       CviJI| | | |||| || |  ||    CviJI |
      HaeIII| | | |||| || |  ||   StyD4I |
           || | | |||| || |  ||        | |
          ggccgccagcccagcggcgagggcaaccagcccgg
    14901 ---------+---------+---------+----- 14935
          ccggcggtcgggtcgccgctcccgttggtcgggcc

a          A  A  S  P  A  A  R  A  T  S  P    -
b           P  P  A  Q  R  R  G  Q  P  A  R   -
c         G  R  Q  P  S  G  E  G  N  Q  P     -
```

Figure 19-XX

```
 Enzymes that do cut and were not excluded:

      AarI     AatII      AccI      AciI      AclI      AfeI     AflII    AflIII      AgeI      AhdI      AleI      AloI
AluI
      AlwI     AlwNI      ApaI     ApaLI      ApoI      AseI      AvaI     AvaII      BaeI     BamHI      BanI     BanII
BbeI
      BbsI      BbvI     BbvCI      BccI     BceAI      BcgI     BciVI      BclI      BfaI     BfrBI      BglI     BglII
BlpI
  Bme1580I     BmgBI      BmrI      BmtI      BplI      BpmI    Bpu10I     BpuEI      BsaI     BsaAI     BsaBI     BsaHI
BsaJI
     BsaWI     BsaXI    BseMII     BseRI     BseYI      BsgI     BsiEI   BsiHKAI      BslI      BsmI     BsmAI     BsmBI
BsmFI
  Bsp1286I    BspCNI     BspEI     BspHI     BspMI      BsrI     BsrBI     BsrDI     BsrFI    BssHII     BssSI    BstAPI
BstBI
    BstEII    BstF5I    BstKTI     BstNI     BstUI     BstXI     BstYI    Bsu36I      BtgI      BtsI     Cac8I      ClaI
Csp6I
     CviJI      DdeI      DpnI      DraI    DraIII      DrdI      EaeI      EagI      EarI      EciI    Eco57I   Eco57MI
EcoNI
  EcoO109I     EcoRI     EcoRV      FalI      FatI      FauI    Fnu4HI      FokI      FspI     FspAI     HaeII    HaeIII
HgaI
      HhaI     Hin4I    HinP1I    HincII   HindIII     HinfI      HpaI     HpaII      HphI     Hpy8I    Hpy99I   Hpy188I
Hpy188III
 HpyCH4III  HpyCH4IV   HpyCH4V  HpyF10VI      KasI    MaeIII      MboI     MboII      MfeI      MluI      MlyI      MmeI
MnlI
      MscI      MseI      MslI    MspA1I      MwoI      NaeI      NarI      NciI      NcoI      NdeI    NgoMIV      NheI
NlaIII
     NlaIV      NotI      NruI      NsiI      NspI      PciI     PflMI      PfoI      PleI      PmeI      PpiI     PpuMI
PshAI
      PsiI     PspGI    PspOMI      PsrI      PstI      PvuI     PvuII      RsaI     RsrII     SacII      SalI     SanDI
SapI
    Sau96I      SbfI      ScaI     ScrFI     SexAI     SfaNI      SfcI      SfiI      SfoI     SgrAI      SmlI      SpeI
SphI
      SspI      StyI    StyD4I      TaiI      TaqI     TaqII      TatI      TauI      TfiI      TseI    Tsp45I   Tsp509I
TspDTI
    TspGWI     TspRI   Tth111I      XbaI      XcmI      XhoI      XmnI      ZraI

 Enzymes that do not cut:

    Acc65I      AscI     AsiSI     AvrII     BsiWI     BsrGI   BstZ17I   EcoICRI      FseI      KpnI      PacI      PmlI
SacI
      SmaI     SnaBI      SrfI      StuI      SwaI      XmaI

 Enzymes excluded; MinCuts: 1  MaxCuts: 100000

   NONE
```

Figure 20-A

```
tgagcgtcgc aaaggcgctc ggtcttgcct tgctcgtcgg tgatgtactt caccagctcc 60
gcgaagtcgc tcttcttgat ggagcgcatg gggacgtgct tggcaatcac gcgcaccccc 120
cggccgtttt agcggctaaa aaagtcatgg ctctgccctc gggcggacca cgcccatcat 180
gaccttgcca agctcgtcct gcttctcttc gatcttcgcc agcagggcga ggatcgtggc 240
atcaccgaac cgcgccgtgc gcgggtcgtc ggtgagccag agtttcagca ggccgcccag 300
gcggcccagg tcgccattga tgcgggccag ctcgcggacg tgctcatagt ccacgacgcc 360
cgtgattttg tagccctggc cgacggccag caggtaggcc gacaggctca tgccggccgc 420
cgccgccttt tcctcaatcg ctcttcgttc gtctggaagg cagtacacct tgataggtgg 480
gctgcccttc ctggttggct tggtttcatc agccatccgc ttgccctcat ctgttacgcc 540
ggcggtagcc ggccagcctc gcagagcagg attcccgttg agcaccgcca ggtgcgaata 600
agggacagtg aagaaggaac acccgctcgc gggtgggcct acttcaccta tcctgcccgg 660
ctgacgccgt tggatacacc aaggaaagtc tacacgaacc ctttggcaaa atcctgtata 720
tcgtgcgaaa aaggatggat ataccgaaaa aatcgctata atgaccccga agcagggtta 780
tgcagcggaa aagcgccacg cttcccgaag ggagaaaggc ggacaggtat ccggtaagcg 840
gcagggtcgg aacaggagag cgcacgaggg agcttccagg gggaaacgcc tggtatcttt 900
atagtcctgt cgggtttcgc cacctctgac ttgagcgtcg atttttgtga tgctcgtcag 960
gggggcggag cctatggaaa aacgccagca acgcggcctt tttacggttc ctggcctttt 1020
gctggccttt tgctcacatg ttctttcctg cgttatcccc tgattctgtg gataaccgta 1080
ttaccgcctt tgagtgagct gataccgctc gccgcagccg aacgaccgag cgcagcgagt 1140
cagtgagcga ggaagcggaa gagcgccaga aggccgccag agaggccgag cgcggccgtg 1200
aggcttggac gctagggcag ggcatgaaaa agcccgtagc gggctgctac gggcgtctga 1260
cgcggtggaa agggggaggg gatgttgtct acatggctct gctgtagtga gtgggttgcg 1320
ctccggcagc ggtcctgatc aatcgtcacc ctttctcggt ccttcaacgt tcctgacaac 1380
gagcctcctt ttcgccaatc catcgacaat caccgcgagt ccctgctcga acgctgcgtc 1440
cggaccggct tcgtcgaagg cgtctatcgc ggcccgcaac agcggcgaga gcggagcctg 1500
ttcaacggtg ccgccgcgct cgccggcatc gctgtcgccg gcctgctcct caagcacggc 1560
cccaacagtg aagtagctga ttgtcatcag cgcattgacg gcgtccccgg ccgaaaaacc 1620
cgcctcgcag aggaagcgaa gctgcgcgtc ggccgtttcc atctgcggtg cgcccggtcg 1680
cgtgccggca tggatgcgcg cgccatcgcg gtaggcgagc agcgcctgcc tgaagctgcg 1740
ggcattcccg atcagaaatg agcgccagtc gtcgtcggct ctcggcaccg aatgcgtatg 1800
attctccgcc agcatggctt cggccagtgc gtcgagcagc gcccgcttgt tcctgaagtg 1860
ccagtaaagc gccggctgct gaacccccaa ccgttccgcc agtttgcgtg tcgtcagacc 1920
gtctacgccg acctcgttca acaggtccag ggcggcacgg atcactgtat tcggctgcaa 1980
ctttgtcatg cttgacactt tatcactgat aaacataata tgtccaccaa cttatcagtg 2040
ataaagaatc cgcgcgttca atcggaccag cggaggctgg tccggaggcc agacgtgaaa 2100
cccaacatac ccctgatcgt aattctgagc actgtcgcgc tcgacgctgt cggcatcggc 2160
ctgattatgc cggtgctgcc gggcctcctg cgcgatctgg ttcactcgaa cgacgtcacc 2220
gcccactatg gcattctgct ggcgctgtat gcgttggtgc aatttgcctg cgcacctgtg 2280
ctgggcgcgc tgtcggatcg tttcgggcgg cggccaatct tgctcgtctc gctggccggc 2340
gccagatctg gggaaccctg tggttggcat gcacatacaa atggacgaac ggataaacct 2400
tttcacgccc ttttaaatat ccgattattc taataaacgc tcttttctct taggtttacc 2460
cgccaatata tcctgtcaaa cactgatagt ttaaactgaa ggcgggaaac gacaatctga 2520
tcatgagcgg agaattaagg gagtcacgtt atgacccccg ccgatgacgc gggacaagcc 2580
gttttacgtt tggaactgac agaaccgcaa cgttgaagga gccactcagc cgcgggtttc 2640
tggagtttaa tgagctaagc acatacgtca gaaaccatta ttgcgcgttc aaaagtcgcc 2700
taaggtcact atcagctagc aaatatttct tgtcaaaaat gctccactga cgttccataa 2760
attcccctcg gtatccaatt agagtctcat attcactctc aatccaaata atctgcaccg 2820
gatctggatc gtttcgcatg attgaacaag atggattgca cgcaggttct ccggccgctt 2880
gggtggagag gctattcggc tatgactggg cacaacagac aatcggctgc tctgatgccg 2940
ccgtgttccg gctgtcagcg caggggcgcc cggttctttt tgtcaagacc gacctgtccg 3000
gtgccctgaa tgaactgcag gacgaggcag cgcggctatc gtggctggcc acgacgggcg 3060
```

Figure 20-B

```
ttccttgcgc agctgtgctc gacgttgtca ctgaagcggg aagggactgg ctgctattgg 3120
gcgaagtgcc ggggcaggat ctcctgtcat ctcaccttgc tcctgccgag aaagtatcca 3180
tcatggctga tgcaatgcgg cggctgcata cgcttgatcc ggctacctgc ccattcgacc 3240
accaagcgaa acatcgcatc gagcgagcac gtactcggat ggaagccggt cttgtcgatc 3300
aggatgatct ggacgaagag catcaggggc tcgcgccagc cgaactgttc gccaggctca 3360
aggcgcgcat gcccgacggc gatgatctcg tcgtgaccca tggcgatgcc tgcttgccga 3420
atatcatggt ggaaaatggc cgcttttctg gattcatcga ctgtggccgg ctgggtgtgg 3480
cggaccgcta tcaggacata gcgttggcta cccgtgatat tgctgaagag cttggcggcg 3540
aatgggctga ccgcttcctc gtgctttacg gtatcgccgc tcccgattcg cagcgcatcg 3600
ccttctatcg ccttcttgac gagttcttct gagcgggact ctggggttcg aaatgaccga 3660
ccaagcgacg cccaacctgc catcacgaga tttcgattcc accgccgcct tctatgaaag 3720
gttgggcttc ggaatcgttt tccgggacgc cggctggatg atcctccagc gcggggatct 3780
catgctggag ttcttcgccc acgggatctc tgcggaacag gcggtcgaag gtgccgatat 3840
cattacgaca gcaacggccg acaagcacaa cgccacgatc ctgagcgaca atatgatcgg 3900
gcccggcgtc cacatcaacg gcgtcggcgg cgactgccca ggcaagaccg agatgcaccg 3960
cgatatcttg ctgcgttcgg atattttcgt ggagttcccg ccacagaccc ggatgatccc 4020
cgatcgttca aacatttggc aataaagttt cttaagattg aatcctgttg ccggtcttgc 4080
gatgattatc atataatttc tgttgaatta cgttaagcat gtaataatta acatgtaatg 4140
catgacgtta tttatgagat gggtttttat gattagagtc ccgcaattat acatttaata 4200
cgcgatagaa aacaaaatat agcgcgcaaa ctaggataaa ttatcgcgcg cggtgtcatc 4260
tatgttacta gatcgggcct cctgtcaatg ctggcggcgg ctctggtggt ggttctggtg 4320
gcggctctga gggtggtggc tctgagggtg gcggttctga gggtggcggc tctgagggag 4380
gcggttccgg tggtggctct ggttccggtg attttgatta tgaaaagatg gcaaacgcta 4440
ataagggggc tatgaccgaa aatgccgatg aaaacgcgct acagtctgac gctaaaggca 4500
aacttgattc tgtcgctact gattacggtg ctgctatcga tggtttcatt ggtgacgttt 4560
ccggccttgc taatggtaat ggtgctactg gtgattttgc tggctctaat tcccaaatgg 4620
ctcaagtcgg tgacggtgat aattcacctt taatgaataa tttccgtcaa tatttacctt 4680
ccctccctca atcggttgaa tgtcgccctt ttgtctttgg cccaatacgc aaaccgcctc 4740
tccccgcgcg ttggccgatt cattaatgca gctggcacga caggtttccc gactggaaag 4800
cgggcagtga gcgcaacgca attaatgtga gttagctcac tcattaggca ccccaggctt 4860
tacactttat gcttccggct cgtatgttgt gtggaattgt gagcggataa caatttcaca 4920
caggaaacag ctatgaccat gattacgcca agcttgcatg cctgcaggtc cccagattag 4980
ccttttcaat ttcagaaaga atgctaaccc acagatggtt agagaggctt acgcagcagg 5040
tctcatcaag acgatctacc cgagcaataa tctccaggaa atcaaatacc ttcccaagaa 5100
ggttaaagat gcagtcaaaa gattcaggac taactgcatc aagaacacag agaaagatat 5160
atttctcaag atcagaagta ctattccagt atggacgatt caaggcttgc ttcacaaacc 5220
aaggcaagta atagagattg gagtctctaa aaaggtagtt cccactgaat caaaggccat 5280
ggagtcaaag attcaaatag aggacctaac agaactcgcc gtaaagactg gcgaacagtt 5340
catacagagt ctcttacgac tcaatgacaa gaagaaaatc ttcgtcaaca tggtggagca 5400
cgacacactt gtctactcca aaaatatcaa agatacagtc tcagaagacc aaagggcaat 5460
tgagactttt caacaaaggg taatatccgg aaacctcctc ggattccatt gcccagctat 5520
ctgtcacttt attgtgaaga tagtggaaaa ggaaggtggc tcctacaaat gccatcattg 5580
cgataaagga aaggccatcg ttgaagatgc ctctgccgac agtggtccca aagatggacc 5640
cccacccacg aggagcatcg tggaaaaaga agacgttcca accacgtctt caaagcaagt 5700
ggattgatgt gatatctcca ctgacgtaag ggatgacgca caatcccact atccttcgca 5760
agacccttcc tctatataag gaagttcatt tcatttggag agaacacggg ggactctaga 5820
ggatccatgt ttatttcttt attatttctt actctcacta gtggtagtga ccttgaccgg 5880
tgcaccactt ttgatgatgt tcaagctcct aattacactc aacatacttc atctatgagg 5940
ggggtttact atcctgatga aatttttaga tcagacactc tttatttaac tcaggattta 6000
tttcttccat tttattctaa tgttacaggg tttcatacta ttaatcatac gtttggcaac 6060
cctgtcatac cttttaagga tggtatttat tttgctgcca cagagaaatc aaatgttgtc 6120
cgtggttggg tttttggttc taccatgaac aacaagtcac agtcggtgat tattattaac 6180
aattctacta atgttgttat acgagcatgt aactttgaat tgtgtgacaa ccctttcttt 6240
```

Figure 20-C

```
gctgtttcta aacccatggg tacacagaca catactatga tattcgataa tgcatttaat 6300
tgcactttcg agtacatatc tgatgccttt tcgcttgatg tttcagaaaa gtcaggtaat 6360
tttaaacact tacgagagtt tgtgtttaaa aataaagatg ggtttctcta tgtttataag 6420
ggctatcaac ctatagatgt agttcgtgat ctaccttctg gttttaacac tttgaaacct 6480
atttttaagt tgcctcttgg tattaacatt acaaatttta gagccattct tacagccttt 6540
tcacctgctc aagacatttg ggcacgtca gctgcagcct attttgttgg ctatttaaag 6600
ccaactacat ttatgctcaa gtatgatgaa aatggtacaa tcacagatgc tgttgattgt 6660
tctcaaaatc cacttgctga actcaaatgc tctgttaaga gctttgagat tgacaaagga 6720
atttaccaga cctctaattt cagggttgtt ccctcaggag atgttgtgag attccctaat 6780
attacaaact tgtgtccttt tggagaggtt tttaatgcta ctaaattccc ttctgtctat 6840
gcatgggaga gaaaaaaaat ttctaattgt gttgctgatt actctgtgct ctacaactca 6900
acatttttt caacctttaa gtgctatggc gtttctgcca ctaagttgaa tgatctttgc 6960
ttctccaatg tctatgcaga ttcttttgta gtcaagggag atgatgtaag acaaatagcg 7020
ccaggacaaa ctggtgttat tgctgattat aattataaat tgccagatga tttcatgggt 7080
tgtgtccttg cttggaatac taggaacatt gatgctactt caactggtaa ttataattat 7140
aaatataggt atcttagaca tggcaagctt aggccctttg agagagacat atctaatgtg 7200
cctttctccc ctgatggcaa accttgcacc ccacctgctc ttaattgtta ttggccatta 7260
aatgattatg gtttttacac cactactggc attggctacc aaccttacag agttgtagta 7320
ctttcttttg aacttttaaa tgcaccggcc acggtttgtg gaccaaaatt atccactgac 7380
cttattaaga accagtgtgt caattttaat tttaatggac tcactggtac tggtgtgtta 7440
actccttctt caaagagatt tcaaccattt caacaatttg gccgtgatgt ttctgatttc 7500
actgattccg ttcgagatcc taaaacatct gaaatattag acatttcacc ttgctctttt 7560
gggggtgtaa gtgtaattac acctggaaca aatgcttcat ctgaagttgc tgttctatat 7620
caagatgtta actgcactga tgtttctaca gcaattcatg cagatcaact cacaccagct 7680
tggcgcatat attctactgg aaacaatgta ttccagactc aagcaggctg tcttatagga 7740
gctgagcatg tcgacacttc ttatgagtgc gacattccta ttggagctgg catttgtgct 7800
attaccatac agttagacta gaaaagggcg aattctgcag atatccatca cactggcggc 7860
cgctcgacct cgaggggggg cccggtacag ctcgaatttc cccgatcgtt caaacatttg 7920
gcaataaagt ttcttaagat tgaatcctgt tgccggtctt gcgatgatta tcatataatt 7980
tctgttgaat tacgttaagc atgtaataat taacatgtaa tgcatgacgt tatttatgag 8040
atgggttttt atgattagag tcccgcaatt atacatttaa tacgcgatag aaaacaaaat 8100
atagcgcgca aactaggata aattatcgcg cgcggtgtca tctatgttac tagatcggga 8160
attcactggc cgtcgtttta caacgtcgtg actgggaaaa ccctggcgtt acccaactta 8220
atcgccttgc agcacatccc cctttcgcca gctggcgtaa tagcgaagag gcccgcaccg 8280
atcgcccttc ccaacagttg cgcagcctga atggcgcccg ctcctttcgc tttcttccct 8340
tcctttctcg ccacgttcgc cggctttccc cgtcaagctc taaatcgggg gctcccttta 8400
gggttccgat ttagtgcttt acggcacctc gaccccaaaa aacttgattt gggtgatggt 8460
tcacgtagtg ggccatcgcc ctgatagacg gtttttcgcc ctttgacgtt ggagtccacg 8520
ttctttaata gtggactctt gttccaaact ggaacaacac tcaaccctat ctcgggctat 8580
tcttttgatt tataagggat tttgccgatt tcggaaccac catcaaacag gattttcgcc 8640
tgctggggca aaccagcgtg gaccgcttgc tgcaactctc tcagggccag gcggtgaagg 8700
gcaatcagct gttgcccgtc tcactggtga aaagaaaaac caccccagta cattaaaaac 8760
gtccgcaatg tgttattaag ttgtctaagc gtcaatttgt ttacaccaca atatatcctg 8820
ccaccagcca gccaacagct ccccgaccgg cagctcggca caaaatcacc actcgataca 8880
ggcagcccat cagtccggga cggcgtcagc gggagagccg ttgtaaggcg gcagactttg 8940
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cctatccatt gctcaccgaa tggtacaggt cggggacccg aagttccgac tgtcggcctg 9300
atgcatcccc ggctgatcga ccccagatct ggggctgaga aagcccagta aggaaacaac 9360
```

Figure 20-D

```
tgtaggttcg agtcgcgaga tcccccggaa ccaaaggaag taggttaaac ccgctccgat 9420
caggccgagc cacgccaggc cgagaacatt ggttcctgta ggcatcggga ttggcggatc 9480
aaacactaaa gctactggaa cgagcagaag tcctccggcc gccagttgcc aggcggtaaa 9540
ggtgagcaga ggcacgggag gttgccactt gcgggtcagc acggttccga acgccatgga 9600
aaccgccccc gccaggcccg ctgcgacgcc gacaggatct agcgctgcgt ttggtgtcaa 9660
caccaacagc gccacgcccg cagttccgca aatagccccc aggaccgcca tcaatcgtat 9720
cgggctacct agcagagcgg cagagatgaa cacgaccatc agcggctgca cagcgcctac 9780
cgtcgccgcg accccgcccg gcaggcggta gaccgaaata aacaacaagc tccagaatag 9840
cgaaatatta agtgcgccga ggatgaagat gcgcatccac cagattcccg ttggaatctg 9900
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cttggggccg tcctcctgtt tgaagaccga cagcccaatg atctcgccgt cgatgtaggc 10080
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cctgatgcac tccgcataca gctcgataat cttttcaggg ctttgttcat cttcatactc 12360
ttccgagcaa aggacgccat cggcctcact catgagcaga ttgctccagc catcatgccg 12420
```

Figure 20-E

```
ttcaaagtgc aggacctttg gaacaggcag ctttccttcc agccatagca tcatgtcctt 12480
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gttttcattt tctcccacca gcttatatac cttagcagga gacattcctt ccgtatcttt 12600
tacgcagcgg tatttttcga tcagtttttt caattccggt gatattctca ttttagccat 12660
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aagacgaact ccaattcact gttccttgca ttctaaaacc ttaaatacca gaaaacagct 12780
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cgtaacggca aaagcaccgc cggacatcag cgctatctct gctctcactg ccgtaaaaca 13020
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atggccatga atggcgttgg atgccgggca acagcccgca ttatgggcgt tggcctcaac 13140
acgattttac gtcacttaaa aaactcaggc cgcagtcggt aacctcgcgc atacagccgg 13200
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cggaaaccct tgcaaatgct ggattttctg cctgtggaca gcccctcaaa tgtcaatagg 14520
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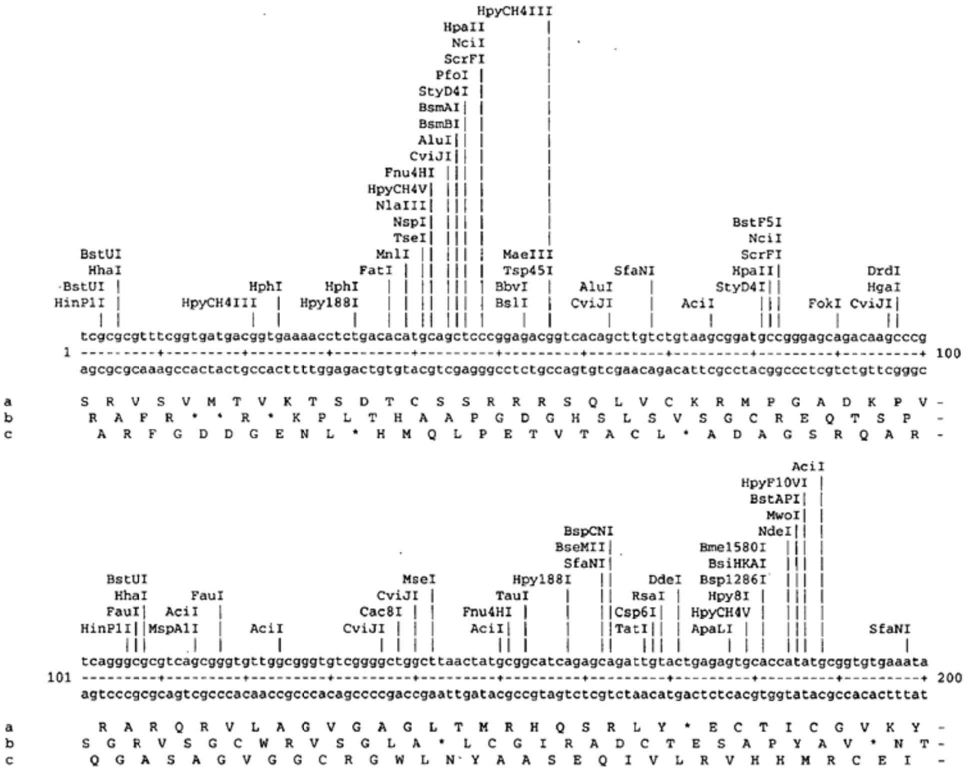
tcggcccctc aagtgtcaac gtccgcccct catctgtcag tgagggccaa gttttccgcg 14820
aggtatccac aacgccggcg gccgcggtgt ctcgcacacg gcttcgacgg cgtttctggc 14880
gcgtttgcag ggccatagac ggccgccagc ccagcggcga gggcaaccag cccgg      14935
```

Figure 21-A



```
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  1 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 100
    agcgcgcaaagccactactgccacttttggagactgtgtacgtcgagggcctctgccagtgtcgaacagacattcgcctacggccctcgtctgttcgggc

a   S  R  V  S  V  M  T  V  K  T  S  D  T  C  S  S  R  R  R  S  Q  L  V  C  K  R  M  P  G  A  D  K  P  V  -
b    R  A  F  R  *  *  R  *  K  P  L  T  H  A  A  P  G  D  G  H  S  L  S  V  S  G  C  R  E  Q  T  S  P   -
c     A  R  F  G  D  D  G  E  N  L  *  H  M  Q  L  P  E  T  V  T  A  C  L  *  A  D  A  G  S  R  Q  A  R  -

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101 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 200
    agtcccgcgcagtcgcccacaaccgcccacagccccgaccgaattgatacgccgtagtctcgtctaacatgactctcacgtggtatacgccacactttat

a     R  A  R  Q  R  V  L  A  G  V  G  A  G  L  T  M  R  H  Q  S  R  L  Y  *  E  C  T  I  C  G  V  K  Y  -
b   S  G  R  V  S  G  C  W  R  V  S  G  L  A  *  L  C  G  I  R  A  D  C  T  E  S  A  P  Y  A  V  *  N  T -
c    Q  G  A  S  A  G  V  G  G  C  R  G  W  L  N  Y  A  A  S  E  Q  I  V  L  R  V  H  H  M  R  C  E  I  -
```

Figure 21-B

```
                                    HpyF10VI
                                       MwoI|
                                      BbvI||                                   CviJI
                                     BbeI|||                                  HaeIII
                                    HaeII|||                                 Cac8I |
                                    HhaI||||                                Sau96I |
                                   SfaNI||||          HpyCH4III              AciI| |
                                  NlaIV|||||           HhaI   |            MboII|| |
                                   SfoI|||||          FspI|   |        HpyF10VI||| |
                                 BsaHI||||||       HinP1I||   |           MwoI|||| |
                                HinP1I||||||     Fnu4HI |||   |        BsiEI ||||| |
                              HpyF10VI||||||     CviJI| |||   |       BstKTI ||||| |
                                  NarI||||||      TseI| |||   |         PvuI ||||| |
                                 BanI|||||||HpyF10VI || |||   |        DpnI| ||||| |
                                 KasI|||||||   BglI| || |||   |       FauI|| ||||| |      MnlI
 AciI                     AciI   MwoI|||||||   MwoI| || |||   |      MboI||| ||||| |   EarI  |
    |                        |      ||||||||      || || |||   |         |||| ||||| |      |  |
    ccgcacagatgcgtaaggagaaaataccgcatcaggcgccattcgccattcaggctgcgcaactgttgggaagggcgatcggtgcgggcctcttcgctat
201 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 300
    ggcgtgtctacgcattcctcttttatggcgtagtccgcggtaagcggtaagtccgacgcgttgacaacccttcccgctagccacgcccggagaagcgata

a    R  T  D  A  *  G  E  N  T  A  S  G  A  I  R  H  S  G  C  A  T  V  G  K  G  D  R  C  G  P  L  R  Y   -
b     A  Q  M  R  K  E  K  I  P  H  Q  A  P  F  A  I  Q  A  A  Q  L  L  G  R  A  I  G  A  G  L  F  A  I  -
c   P  H  R  C  V  R  R  K  Y  R  I  R  R  H  S  P  F  R  L  R  N  C  W  E  G  R  S  V  R  A  S  S  L  L -

                                                                              TaiI
          Cac8I                                        BstNI               Hpy99I|
         AluI |                                        ScrFI           HpyCH4IV ||          BsrI
        CviJI |             HpyCH4V                   BsaJI|      Hpy188III   | ||        CviJI|
       MspA1I |            Fnu4HI |                  PspGI||      MaeIII  |   | ||       HaeIII|
        PvuII |           BstF5I| |                 StyD4I||      Tsp45I  |   | ||      Hpy99I|| HindIII
      Cac8I | |BbvI         TseI| |FokI MseI  MaeIII     |||BmrI  BsrI |  |   | ||       EaeI|||  TspRI|
          | | |   |            || |   |    |       |     |||   |     | |  |   | ||          ||||      ||
    tacgccagctggcgaaagggggatgtgctgcaaggcgattaagttgggtaacgccagggttttcccagtcacgacgttgtaaaacgacggccagtgccaa
301 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 400
    atgcggtcgaccgctttccccctacacgacgttccgctaattcaacccattgcggtcccaaaagggtcagtgctgcaacattttgctgccggtcacggtt

a   Y  A  S  W  R  K  G  D  V  L  Q  G  D  *  V  G  *  R  Q  G  F  P  S  H  D  V  V  K  R  R  P  V  P  S -
b    T  P  A  G  E  R  G  M  C  C  K  A  I  K  L  G  N  A  R  V  F  P  V  T  T  L  *  N  D  G  Q  C  Q   -
c     R  Q  L  A  K  G  G  C  A  A  R  R  L  S  W  V  T  P  G  F  S  Q  S  R  R  C  K  T  T  A  S  A  K  -

                                                 BstF5I           BslI
  BceAI                                           RsaI|     Tsp509I  |
 AluI |           BsmFI                          Csp6I||   FokI    |  |               HpyCH4III
CviJI |     Tsp509I   |                   BslI  TatI|||MseI  |    |  |          BceAI        | CviJI
    | |           |   |                      |     ||||   |  |    |  |              |        |     |
    gcttgaaagagataaattgaacaagtatggtcgtcccctgttgggatgtactattaaacctaaattggggttatctgctaaaaactacggtagagccgtt
401 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 500
    cgaactttctctatttaacttgttcataccagcaggggacaaccctacatgataatttggatttaaccccaatagacgattttgatgccatctcggcaa

a     L  K  E  I  N  *  T  S  M  V  V  P  C  W  D  V  L  L  N  L  N  W  G  Y  L  L  K  T  T  V  E  P  F  -
b   A  *  K  R  *  I  E  Q  V  W  S  S  P  V  G  M  Y  Y  *  T  *  I  G  V  I  C  *  K  L  R  *  S  R  L -
c    L  E  R  D  K  L  N  K  Y  G  R  P  L  L  G  C  T  I  K  P  K  L  G  L  S  A  K  N  Y  G  R  A  V   -
```

Figure 21-C

```
                      Hpy8I                             MmeI
                   TspDTI |                           Hpy8I|               PpiI    BstKTI
     BbsI         AciI  | |                           TaiI||              XcmI|     DpnI|
    MboII   XmnI BstUI  | |              PpiI  HpyCH4IV  |||          BsaXI  ||   MboI ||           BsaXI
        |      |     |  | |                 |         |  |||               | ||      | ||               |
        tatgaatgtcttcgcggtggacttgatttactaaagatgatgagaacgtgaactcacaaccatttatgcgttggagagatcgtttcttattttgtgccg
    501 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 600
        atacttacagaagcgccacctgaactaaaatgatttctactactcttgcacttgagtgttggtaaatacgcaacctctctagcaaagaataaaacacggc

a        M  N  V  F  A  V  D  L  I  L  L  K  M  M  R  T  *  T  H  N  H  L  C  V  G  E  I  V  S  Y  F  V  P   -
b         *  M  S  S  R  W  T  *  F  Y  *  R  *  *  E  R  E  L  T  T  I  Y  A  L  E  R  S  F  L  I  L  C  R  -
c       Y  E  C  L  R  G  G  L  D  F  T  K  D  D  E  N  V  N  S  Q  P  P  F  M  R  W  R  D  R  F  L  F  C  A  E -

                                                                           NlaIII
                                                                         FatI   |
                                                                        RsaI|   |
                                                                      Csp6I||   |         MboII
                                                                    PstI  |||   |      BstKTI |
                                                              HpyCH4V   | |||   |       DpnI| |     HpyF10VI
                                                                 SfcI | | |||   |     BclI || |  AluI      |
              PsiI        CviJI               HphI       BspMI BsmI | | | |||NspI     MboI || | CviJI  MwoI|
                 |          |                    |           |    | | | | |||   |        | || |     |     ||
        aagcactttataaagcacaggctgaaacaggtgaaatcaaagggcattacttgaatgctactgcaggtacatgcgaagaaatgatcaaaagagctgtatt
    601 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 700
        ttcgtgaaatatttcgtgtccgactttgtccactttagtttcccgtaatgaacttacgatgacgtccatgtacgcttctttactagttttctcgacataa

a       K  H  F  I  K  H  R  L  K  Q  V  K  S  K  G  I  T  *  M  L  L  Q  V  H  A  K  K  *  S  K  E  L  Y  L -
b        S  T  L  *  S  T  G  *  N  R  *  N  Q  R  A  L  L  E  C  Y  C  R  Y  M  R  R  N  D  Q  K  S  C  I   -
c         A  L  Y  K  A  Q  A  E  T  G  E  I  K  G  H  Y  L  N  A  T  A  G  T  C  E  E  M  I  K  R  A  V  F  -

                           BsiEI
                          BstKTI     NlaIII
                            PvuI     NsiI |                                                          Hpy8I
              BcgI         DpnI|  BfrBI | |       HphI                   AluI                        AccI|
         Tsp509I |   Hpy188I  ||   FatI | |    BcgI  |HinfI             CviJI                      FokI ||
       BfaI    | |       MboI ||HpyCH4V | |  MseI  | | TfiI  AciI     BfaI  |CviJI                MboII ||
          |    | |          | ||      | | |     |  | |    |     |        |  |    |                    | ||
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a         L  E  N  W  A  F  R  S  *  C  M  T  T  *  R  G  D  S  P  Q  I  L  A  W  L  I  I  A  E  I  M  V  Y  -
b       C  *  R  I  G  R  S  D  R  N  A  *  L  L  N  G  G  I  H  R  K  Y  *  L  G  S  L  L  P  R  *  W  S  T -
c        A  R  E  L  G  V  P  I  V  M  H  D  Y  L  T  G  G  F  T  A  N  T  S  L  A  H  Y  C  R  D  N  G  L   -
```

Figure 21-D

```
                                 AciI
                               NlaIII
                                 NspI
                                 SphI
                              BsrDI |
                              Cac8I |
                           HpyF10VI |
                               NsiI |
                            BstAPI| |
                              MwoI| |
                            BfrBI|| |                                  BciVI
                             FatI|| |                        MboII      NciI                   TaiI
                          HpyCH4V|| |                      NlaIII|     ScrFI                BsaAI |
                     HpyCH4V    ||| |                   FatI    ||     BslI|                SnaBI |
                HpyCH4III  |    ||| |               HinfI  |    ||    HpaII|            HpyCH4IV| |
           BstF5I       |  |    ||| |                TfiI  |    ||  StyD4I||          MaeIII   || |
                |       |  |    ||| |                   |  |    ||       |||               |   || |
         cttcttcacatccaccgtgcaatgcatgcggttattgatagacagaagaatcatggtatccacttccgggtattagcaaaagcgttacgtatgtctggtg
     801 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 900
         gaagaagtgtaggtggcacgttacgtacgccaataactatctgtcttcttagtaccataggtgaaggcccataatcgttttcgcaatgcatacagaccac

a         F  F  T  S  T  V  Q  C  M  R  L  L  I  D  R  R  I  M  V  S  T  S  G  Y  *  Q  K  R  Y  V  C  L  V   -
b          S  S  H  P  P  C  N  A  C  G  Y  *  *  T  E  E  S  W  Y  P  L  P  G  I  S  K  S  V  T  Y  V  W  W  -
c        L  L  H  I  H  R  A  M  H  A  V  I  D  R  Q  K  N  H  G  I  H  F  R  V  L  A  K  A  L  R  M  S  G  G -

                       HpyCH4III
                           KpnI|
                        NlaIV ||
        BstKTI           RsaI ||
         DpnI|         Csp6I| ||
       BaeI ||       Acc65I|| ||        BaeI    BaeI
       MboI || BaeI    BanI|| ||     Hpy8I |   BsmAI       HphI     CviJI
          | ||    |       ||| ||         | |       |          |         |
         gagatcatattcactctggtaccgtagtaggtaaacttgaaggtgaaagagacataactttgggctttgttgatttactgcgtgatgattttgttgaaca
     901 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 1000
         ctctagtataagtgagaccatggcatcatccatttgaacttccactttctctgtattgaaacccgaaacaactaaatgacgcactactaaaacaacttgt

a        E  I  I  F  T  L  V  P  *  *  V  N  L  K  V  K  E  T  *  L  W  A  L  L  I  Y  C  V  M  I  L  L  N  K -
b         R  S  Y  S  L  W  Y  R  S  R  *  T  *  R  *  K  R  H  N  F  G  L  C  *  F  T  A  *  *  F  C  *  T   -
c          D  H  I  H  S  G  T  V  V  G  K  L  E  G  E  R  D  I  T  L  G  F  V  D  L  L  R  D  D  F  V  E  Q  -
```

Figure 21-E

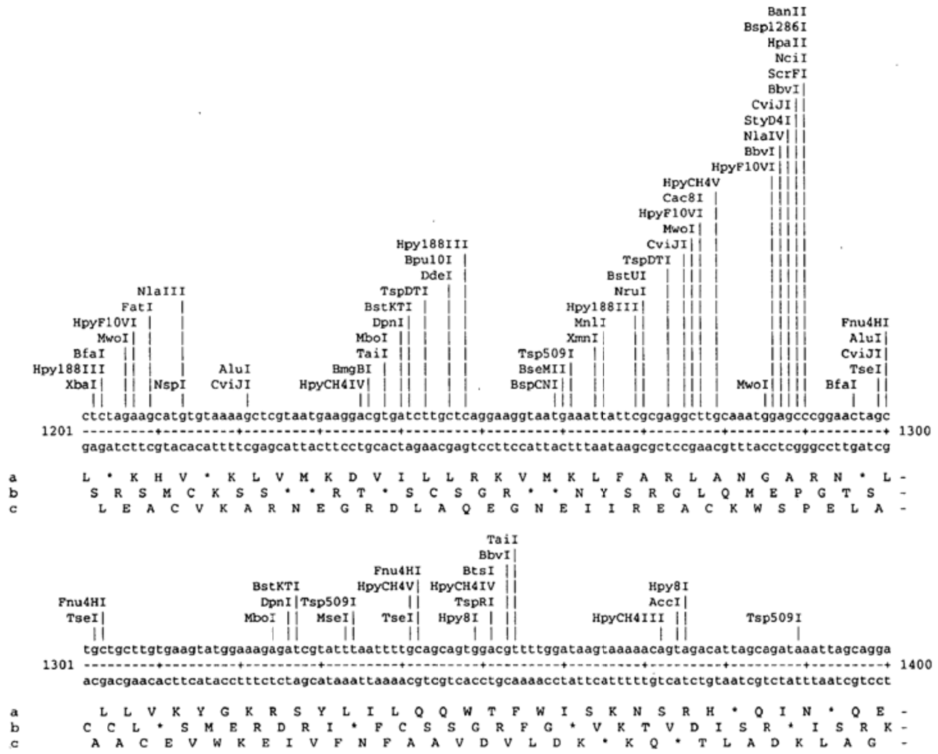
```
                                                            Hin4I
                                                       Eco57I   |
                                                      Eco57MI   |
                                                     BstNI  |   |
                                                     ScrFI  |   |
                                                   PspGI |  |   |
        BstKTI                                     SexAI |  |   |     Hpy188III
          TaqI    AciI        Hpy188III           StyD4I |  |   |     CviJI   |
         DpnI|   BpuEI           SmlI |          BsaI  | |  |   |BsaJI    |   |           TaiI
       MboI ||   BstUI      Hin4I   | |         BsmAI  | |  |   | BtgI MnlI   |    HpyCH4IV  |  NdeI Cac8I
          | ||       |          |   | |             |  | |  |   |    |    |   |           |  |     |     |
          agatcgaagtcgcggtatttatttcactcaagattgggtctctttaccaggtgttctacccgtggcttcaggaggtattcacgtttggcatatgcctgct
     1001 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 1100
          tctagcttcagcgccataaataaagtgagttctaacccagagaaatggtccacaagatgggcaccgaagtcctccataagtgcaaaccgtatacggacga

 a          I  E  V  A  V  F  I  S  L  K  I  G  S  L  Y  Q  V  F  Y  P  W  L  Q  E  V  F  T  F  G  I  C  L  L -
 b        R  S  K  S  R  Y  L  F  H  S  R  L  G  L  F  T  R  C  S  T  R  G  F  R  R  Y  S  R  L  A  Y  A  C  S -
 c         D  R  S  R  G  I  Y  F  T  Q  D  W  V  S  L  P  G  V  L  P  V  A  S  G  G  I  H  V  W  H  M  P  A   -

                                           MnlI
                                    HpyCH4III |
                                     FokI   | |
                                     SfcI   | |
                                   RsaI |   | |
                                 Csp6I| |   | |                                       NlaIV
                            BstF5I   || |   | |                                   HpyF10VI|
                           HinfI |   || |   | |                                      BanI||
                            TfiI |   || |   | |                                      MwoI||
                        TaqII  | |   || |   | |                                   BstNI |||
                   TspGWI   |  | |   || |   | |                                   ScrFI |||
               BstKTI   |   |  | |   || |   | |                                  HhaI | |||
                DpnI|   |   |  | |   || |   | |                                 PspGI | |||
             BglII ||   |   |  | |   || |   | |                   BsaJI        StyD4I | |||
             BstYI ||   |   |  | |   || |   | |                    StyI      HinP1I | | |||   AluI        AluI
     Hpy188I  MboI ||   |   |  | |   || |   | |   FokI       BstF5I   | BceAI     | | | |||  CviJI TaqI  CviJI
           |     | ||   |   |  | |   || |   | |      |            |   |     |     | | | |||      |    |      |
          ctgaccgagatctttggggatgattccgtactacagttcggtggaggaactttaggacatccttggggtaatgcgccaggtgccgtagctaatcgagtag
     1101 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 1200
          gactggctctagaaacccctactaaggcatgatgtcaagccacctccttgaaatcctgtaggaaccccattacgcggtccacggcatcgattagctcatc

 a         *  P  R  S  L  G  M  I  P  Y  Y  S  S  V  E  E  L  *  D  I  L  G  V  M  R  Q  V  P  *  L  I  E  *   -
 b          D  R  D  L  W  G  *  F  R  T  T  V  R  W  R  N  F  R  T  S  L  G  *  C  A  R  C  R  S  *  S  S  S  -
 c        L  T  E  I  F  G  D  D  S  V  L  Q  F  G  G  G  T  L  G  H  P  W  G  N  A  P  G  A  V  A  N  R  V  A-
```

Figure 21-F



```
     ctctagaagcatgtgtaaaagctcgtaatgaaggacgtgatcttgctcaggaaggtaatgaaattattcgcgaggcttgcaaatggagcccggaactagc
1201 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 1300
     gagatcttcgtacacattttcgagcattacttcctgcactagaacgagtccttccattactttaataagcgctccgaacgtttacctcgggccttgatcg

a     L  *  K  H  V  *  K  L  V  M  K  D  V  I  L  L  R  K  V  M  K  L  F  A  R  L  A  N  G  A  R  N  *  L -
b      S  R  S  M  C  K  S  S  *  *  R  T  *  S  C  S  G  R  *  *  N  Y  S  R  G  L  Q  M  E  P  G  T  S  -
c       L  E  A  C  V  K  A  R  N  E  G  R  D  L  A  Q  E  G  N  E  I  I  R  E  A  C  K  W  S  P  E  L  A -

     tgctgcttgtgaagtatggaaagagatcgtatttaattttgcagcagtggacgttttggataagtaaaaacagtagacattagcagataaattagcagga
1301 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 1400
     acgacgaacacttcatacctttctctagcataaattaaaacgtcgtcacctgcaaaacctattcatttttgtcatctgtaatcgtctatttaatcgtcct

a      L  L  V  K  Y  G  K  R  S  Y  L  I  L  Q  Q  W  T  F  W  I  S  K  N  S  R  H  *  Q  I  N  *  Q  E  -
b     C  C  L  *  S  M  E  R  D  R  I  *  F  C  S  S  G  R  F  G  *  V  K  T  V  D  I  S  R  *  I  S  R  K -
c      A  A  C  E  V  W  K  E  I  V  F  N  F  A  A  V  D  V  L  D  K  *  K  Q  *  T  L  A  D  K  L  A  G  -
```

Figure 21-G

```
                                                                 MseI
                                                           Tsp509I   |
                                                         HpyCH4V|    |
                                                     Tsp509I    ||   |    CviJI
                              Tsp509I            Tsp509I    |   ||   |   HaeIII
            BpuEI          SmlI     |              MseI|    |   ||   |  Sau96I|                     CviJI
               |              |     |                 ||    |   ||   |       ||                         |
     aataaagaaggataaggagaaagaactcaagtaattatccttcgttctcttaattgaattgcaattaaactcggcccaatcttttactaaaaggattgag
1401 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 1500
     ttatttcttcctattcctctttcttgagttcattaataggaagcaagagaattaacttaacgttaatttgagccgggttagaaaatgattttcctaactc

a     I  K  K  D  K  E  K  E  L  K  *  L  S  F  V  L  L  I  E  L  Q  L  N  S  A  Q  S  F  T  K  R  I  E   -
b       *  R  R  I  R  R  K  N  S  S  N  Y  P  S  F  S  *  L  N  C  N  *  T  R  P  N  L  L  L  K  G  L  S   -
c    N  K  E  G  *  G  E  R  T  Q  V  I  I  L  R  S  L  N  *  I  A  I  K  L  G  P  I  F  Y  *  K  D  *  A -

                                                                                   BfaI
               HinfI                                                          Hpy188III              MlyI
                TfiI  HpyCH4V         DdeI            BfaI                        XbaI|              PleI
                   |        |            |               |                           ||                 |
     ccgaatacaacaaagattctattgcatatatttgactaagtatatacttacctagatatacaagatttgaaatacaaaatctagaaaactaaatcaaaa
1501 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 1600
     ggcttatgttgtttctaagataacgtatataaaactgattcatatatgaatggatctatatgttctaaactttatgttttagatcttttgatttagtttt

a    P  N  T  T  K  I  L  L  H  I  F  *  L  S  I  Y  L  P  R  Y  T  R  F  E  I  Q  N  L  E  N  *  I  K  I -
b     R  I  Q  Q  R  F  Y  C  I  Y  F  D  *  V  Y  T  Y  L  D  I  Q  D  L  K  Y  K  I  *  K  T  K  S  K    -
c      E  Y  N  K  D  S  I  A  Y  I  L  T  K  Y  I  L  T  *  I  Y  K  I  *  N  T  K  S  R  K  L  N  Q  N   -
```

Figure 21-H

```
                                                        HincII
                                                         Hpy8I
                                                          AccI |
                                                         TaqI ||
                                                        SalI |||
                                                       PstI ||||
                                                   HpyCH4V |||||
                                                   Cac8I | |||||
                                                    SfcI | |||||
                                                NlaIII | | |||||
                                                  NspI | | |||||
                                                  SphI | | |||||
                                               Cac8I | | | |||||
                                              FatI | | | | |||||
                                           HpyCH4V | | | | |||||
                                           Cac8I | | | | | |||||
                                          AluI | | | | | | |||||
                                         CviJI | | | | | | |||||
                                        AlwI | | | | | | | |||||
                                      TaqI | | | | | | | | |||||
                                BstKTI |   | | | | | | | | |||||                              RsaI
      HinfI                      DpnI ||   | | | | | | | | |||||                            Csp6I ||
 DdeI     |                    MboI | ||   | | | | | | | | ||||| HpyCH4III    Hpy188I       TatI |||
      |   |                         | ||   | | | | | | | | |||||         |          |            |||
     tctaagactcaaatctttctattgttgtcttggatcatcgagcttgcatgcctgcagtcgactttcacagtttccattctgaaatgttctctgtactata
1601 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 1700
     agattctgagtttagaaagataacaacagaacctagtagctcgaacgtacggacgtcagctgaaagtgtcaaaggtaagactttacaagagacatgatat

a      *  D  S  N  L  S  I  V  V  L  D  H  R  A  C  M  P  A  V  D  F  H  S  F  H  S  E  M  F  S  V  L  *  -
b    S  K  T  Q  I  F  L  L  L  S  W  I  I  E  L  A  C  L  Q  S  T  F  T  V  S  I  L  K  C  S  L  Y  Y  N -
c     L  R  L  K  S  F  Y  C  C  L  G  S  S  S  L  H  A  C  S  R  L  S  Q  F  P  F  *  N  V  L  C  T  I   -

                                         Hpy8I            MnlI
               HinfI                     MboII           EarI |
                TfiI           Tsp509I   AccI |     Hpy188I   |    CviJI                        HpyCH4V
                   |                  |      ||            |  |        |                            |
     ataaatagtaagtgaatcaacttactactaaaaaattagtagacttcctcttcggaatagaaatagcctatttctacatagggaaagtcgtgtgcaatg
1701 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 1800
     tatttatcattcacttagttgaatgatgatttttttaatcatctgaaggagaagccttatctttatcggataaagatgtatccctttcagcacacgttac

a     *  I  V  S  E  S  T  Y  Y  *  K  N  *  *  T  S  S  S  E  *  K  *  P  I  S  T  *  G  K  S  C  A  M   -
b      K  *  *  V  N  Q  L  T  T  K  K  I  S  R  L  P  L  R  N  R  N  S  L  F  L  H  R  E  S  R  V  Q  *  -
c    I  N  S  K  *  I  N  L  L  L  K  K  L  V  D  F  L  F  G  I  E  I  A  Y  F  Y  I  G  K  V  V  C  N  E -
```

Figure 21-I

```
                                                                                                      MlyI
                                                                                                     PleI|
                                                                                                   MmeI ||
                                                                                                   NciI ||
                                                                                                  ScrFI ||
                                                                                                   SmaI ||
                                                                                      NciI       HpaII| ||
                                                                                     ScrFI        NciI| ||
                                                                                    HpaII|       ScrFI| ||
                                                                                  StyD4I||       AvaI|| ||
                                                                               BsmFI   |||      BsaJI|| ||
                                                                               BccI|   |||     StyD4I|| ||
                 TspDTI                                                        BfaI|   |||       XmaI|| ||
              Cac8I   |                                                       SpeI||   |||    StyD4I||| ||
          HpyCH4V |   |                                 Tsp509I          Hpy188I |||   |||  HinfI  |||| ||
       BsrDI    | |   | MnlI                 MaeIII       FokI|      BstF5I    | |||   ||| TaqI |  |||| ||
           |    | |   |    |                      |          ||           |    | |||   |||    | |  |||| ||
          aaaaatgcaagcacgatttggggagaggtttttctctattgtaacaaggaataattatctactccatccgactagttccgggttcgagtcccgggcaac
     1801 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 1900
          ttttacgttcgtgctaaacccctctccaaaaaagagataacattgttccttattaatagatgaggtaggctgatcaaggcccaagctcagggcccgttg

a         K  N  A  S  T  I  W  G  E  V  F  S  L  L  *  Q  G  I  I  I  Y  S  I  R  L  V  P  G  S  S  P  G  Q  P-
b          K  M  Q  A  R  F  G  E  R  F  F  L  Y  C  N  K  E  *  L  S  T  P  S  D  *  F  R  V  R  V  P  G  N  -
c           K  C  K  H  D  L  G  R  G  F  F  S  I  V  T  R  N  N  Y  L  L  H  P  T  S  S  G  F  E  S  R  A  T -

                       BspCNI
                      BseMII|  Hpy188I                            ApoI             ApoI
         NdeI     BfaI     ||    DdeI|      TspDTI             Tsp509I          Tsp509I
            |        |     ||       ||           |                   |                |
          ccatatggaaactagaaaggagcaatctgagttttgattttcactcacttcatttacaaaatttttggtttggtaaattttgttgtatggatatacaa
     1901 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 2000
          ggtatacctttgatctttcctcgttagactcaaaactaaaaagtgagtgaagtaaatgttttaaaaaccaaaccatttaaaacaacatacctatatgtt

a           I  W  K  L  E  R  S  N  L  S  F  D  F  S  L  T  S  F  T  K  F  F  G  L  V  N  F  V  V  W  I  Y  N -
b         P  Y  G  N  *  K  G  A  I  *  V  L  I  F  H  S  L  H  L  Q  N  F  L  V  W  *  I  L  L  Y  G  Y  T  T-
c          H  M  E  T  R  K  E  Q  S  E  F  *  F  F  T  H  F  I  Y  K  I  F  W  F  G  K  F  C  C  M  D  I  Q  -

                                                                                               TaiI
                                                                                            BsaAI |
                                                                                          AflIII| |
                  CviJI                                                                 HpyCH4IV| |
                Cac8I | HincII                          MseI                           MseI    || |
   HpyCH4III  CviJI | |  Hpy8I                   HpyCH4III |      CviJI            BfaI   |    || |    HinfI
           |      | | |      |                           | |          |               |   |    || |        |
          ctgtcggggctggcttggttgacattggtatatagtctatattatactgttaaataacaagccttctattatctttctagttaatacgtgtgcttgggag
     2001 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 2100
          gacagccccgaccgaaccaactgtaaccatatatcagatataatatgacaatttattgttcggaagataatagaaagatcaattatgcacacgaaccctc

a          C  R  G  W  L  G  *  H  W  Y  I  V  Y  I  I  L  L  N  N  K  P  S  I  I  F  L  V  N  T  C  A  W  E  -
b           V  G  A  G  L  V  D  I  G  I  *  S  I  L  Y  C  *  I  T  S  L  L  L  S  F  *  L  I  R  V  L  G  S -
c         L  S  G  L  A  W  L  T  L  V  Y  S  L  Y  Y  T  V  K  *  Q  A  F  Y  Y  L  S  S  *  Y  V  C  L  G  V-
```

Figure 21-J

```
                                                                                   MaeIII
                                                                                   Tsp45I
                                                                                FauI     |
                                                                               BslI |    |
                                                                             BfaI | |    |
                                                                           AciI | | |    |
                                                                           ApaI | | |    |
                                                                          BanII | | |    |
                                                                       Bme1580I | | |    |
                                                                       Bsp1286I | | |    |
                                                                          Cac8I | | |    |
                                                                        CviJI | | | |    |
                                                                       HaeIII | | | |    |
                                                                        NlaIV | | | |    |
                                                                       NlaIV| | | | |    |
                                                                      Sau96I| | | | |    |
                                                                    EcoO109I|| | | | |    |
                                                                      PspOMI|| | | | |    |
                                      AciI                            Sau96I|| | | | |    |
                                     BstUI                            SacII |||| | | |    |
                                      HhaI                            AciI| |||| | | |    |
                                   BstUI |                           BstUI| |||| | | |    |
                                  HinP1I |                          MspA1I| |||| | | |    |
                                    TauI |                           AciI|| |||| | | |    |
                                  AciI | |                          BsaJI|| |||| | | |    |
                                 Fnu4HI| |                           BtgI|| |||| | | |    |
                                 CviJI|| |                      AvaII |  || |||| | | |    |
                                HaeIII|| |                     NlaIII |  || |||| | | |    |
                               NlaIII||| |                     Sau96I |  || |||| | | |    |
                                 EaeI||| |                     FauI | |  || |||| | | |    |
                                 FauI||| |                   FatI | | |  || |||| | | |    |
                          BsaJI |||||| |                    MslI| | | |  || |||| | | |    |
                  BstKTI    | |||||| |                       || | | |  || |||| | | |    |
       MlyI        DpnI| BtgI |||||| |                       || | | |  || |||| | | |    |
    Tsp509I      BglII || FatI |||||| |                       || | | |  || |||| | | |    |          AgeI
   HpyCH4V|      BstYI || NcoI |||||| |                       || | | |  || |||| | | |    |          BsaWI
      PleI|       MboI || StyI |||||| |                       || | | |  || |||| | | |    |          BsrFI
          ||        | || |    |||||| |                       || | | |  || |||| | | |    |           |
     tccttgcaatttgaataaaccaagatcttaccatggccgcgcggggttctcatcatcatcatcatggtccgcgggggcccgctagtggtagtgaccttga
2101 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 2200
     aggaacgttaaacttatttggttctagaatggtaccggcgcgccccaagagtagtagtagtagtaccaggcgcccccgggcgatcaccatcactggaact

a    S  L  Q  F  E  *  T  K  I  L  P  W  P  R  G  V  L  I  I  I  I  M  V  R  G  G  P  L  V  V  V  T  L  T  -
b     P  C  N  L  N  K  P  R  S  Y  H  G  R  A  G  F  S  S  S  S  S  W  S  A  G  A  R  *  W  *  *  P  *   -
c      L  A  I  *  I  N  Q  D  L  T  M  A  A  R  G  S  H  H  H  H  H  G  P  R  G  P  A  S  G  S  D  L  D  -

     Bme1580I
      BsiHKAI
     Bsp1286I
       Hpy8I |
     HpyCH4V |                                                                                  Hpy188I
       ApaLI | |                     Tsp509I                                                    TspDTI|
     HpaII | | |                        AluI  |                          Hpy188III   ApoI      BstKTI||
         | | | |                       CviJI  |   TspDTI       MnlI      Hpy8I      |Tsp509I    DpnI|||
         | | | |                           |   |      |           |            |     |      |   MboI ||||
     ccggtgcaccacttttgatgatgttcaagctcctaattacactcaacatacttcatctatgaggggggtttactatcctgatgaaatttttagatcagac
2201 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 2300
     ggccacgtggtgaaaactactacaagttcgaggattaatgtgagttgtatgaagtagatactccccccaaatgataggactactttaaaaatctagtctg

a      G  A  P  L  L  M  M  F  K  L  L  I  T  L  N  I  L  H  L  *  G  G  F  T  I  L  M  K  F  L  D  Q  T  -
b     P  V  H  H  F  *  *  C  S  S  S  *  L  H  S  T  Y  F  I  Y  E  G  G  L  L  S  *  *  N  F  *  I  R  H -
c      R  C  T  T  F  D  D  V  Q  A  P  N  Y  T  Q  H  T  S  S  M  R  G  V  Y  Y  P  D  E  I  F  R  S  D  -
```

Figure 21-K

```
                     MboII                                                    TaiI
            Hpy188III  |                                             HpyCH4IV   |
              DdeI  |  |   BseMII           TspDTI              AseI         |  |               MseI
         MseI     | |  | BspCNI |          MaeIII |             MseI         |  |                BccI |
              |   | |  |       ||                ||                  |       |  |                    ||
     actctttatttaactcaggatttatttcttccattttattctaatgttacagggtttcatactattaatcatacgtttggcaaccctgtcatacctttta
2301 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 2400
     tgagaaataaattgagtcctaaataaagaaggtaaaataagattacaatgtcccaaagtatgataattagtatgcaaaccgttgggacagtatggaaaat

a     L  F  I  *  L  R  I  Y  F  F  H  F  I  L  M  L  Q  G  F  I  L  L  I  I  R  L  A  T  L  S  Y  L  L   -
b      S  L  F  N  S  G  F  I  S  S  I  L  F  *  C  Y  R  V  S  Y  Y  *  S  Y  V  W  Q  P  C  H  T  F  *  -
c    T  L  Y  L  T  Q  D  L  F  L  P  F  Y  S  N  V  T  G  F  H  T  I  N  H  T  F  G  N  P  V  I  P  F  K -

                                                                                HpyCH4III
                 Fnu4HI                                                            TspDTI |
       BstF5I      TseI |                    BsaJI                    NlaIII  MaeIII     ||
     BbvI    | FokI    ||       TspGWI       BtgI  BslI           FatI      | Tsp45I     ||          MseI
          |  |      |  ||             |          |     |                |   |       |    ||             |
     aggatggtatttatttgctgccacagagaaatcaaatgttgtccgtggttgggtttttggttctaccatgaacaacaagtcacagtcggtgattattat
2401 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 2500
     tcctaccataaataaaacgacggtgtctctttagtttacaacaggcaccaacccaaaaaccaagatggtacttgttgttcagtgtcagccactaataata

a    R  M  V  F  I  L  L  P  Q  R  N  Q  M  L  S  V  V  G  F  L  V  L  P  *  T  T  S  H  S  R  *  L  L  L -
b     G  W  Y  L  F  C  C  H  R  E  I  K  C  C  P  W  L  G  F  W  F  Y  H  E  Q  Q  V  T  V  G  D  Y  Y  -
c      D  G  I  Y  F  A  A  T  E  K  S  N  V  V  R  G  W  V  F  G  S  T  M  N  N  K  S  Q  S  V  I  I  I -

                                                                                      Hpy8I
                                                                                      RsaI |
                                                                                     Csp6I||
                                                                                 NlaIII  |||
                                                                              BsaJI    | |||
                                NlaIII                                         BtgI    | |||
                                  NspI        MaeIII                           FatI    | |||
  Tsp509I                      MaeIII |       Tsp45I                           NcoI    | |||
  HphI   |                     FatI  || Tsp509I     |                          StyI    | |||
      |  |                        |  ||       |     |                              |   | |||
     taacaattctactaatgttgttatacgagcatgtaactttgaattgtgtgacaaccctttctttgctgtttctaaacccatgggtacacagacacatact
2501 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 2600
     attgttaagatgattacaacaatatgctcgtacattgaaacttaacacactgttgggaaagaaacgacaaagatttgggtacccatgtgtctgtgtatga

a      T  I  L  L  M  L  L  Y  E  H  V  T  L  N  C  V  T  T  L  S  L  L  F  L  N  P  W  V  H  R  H  I  L  -
b    *  Q  F  Y  *  C  C  Y  T  S  M  *  L  *  I  V  *  Q  P  F  L  C  C  F  *  T  H  G  Y  T  D  T  Y  Y -
c     N  N  S  T  N  V  V  I  R  A  C  N  F  E  L  C  D  N  P  F  F  A  V  S  K  P  M  G  T  Q  T  H  T   -
```

Figure 21-L

```
                                              HpyCH4V
                             Hin4I|
                        Tsp509I   ||       RsaI
                          MseI|   ||     Csp6I|
                        NsiI ||   ||     SfaNI|
                     BfrBI | ||   ||     TatI||                                              DraI
              TaqI HpyCH4V | ||   ||  TaqI  ||| Hpy188I       Hin4I     Hpy188I     Tsp509I MseI|
                 |       | | ||   ||     |  |||       |           |           |           |    ||
          atgatattcgataatgcatttaattgcactttcgagtacatatctgatgccttttcgcttgatgtttcagaaaagtcaggtaattttaaacacttacgag
     2601 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 2700
          tactataagctattacgtaaattaacgtgaaagctcatgtatagactacggaaaagcgaactacaaagtcttttcagtccattaaaatttgtgaatgctc

a          *  Y  S  I  M  H  L  I  A  L  S  S  T  Y  L  M  P  F  R  L  M  F  Q  K  S  Q  V  I  L  N  T  Y  E   -
b           D  I  R  *  C  I  *  L  H  F  R  V  H  I  *  C  L  F  A  *  C  F  R  K  V  R  *  F  *  T  L  T  R -
c         M  I  F  D  N  A  F  N  C  T  F  E  Y  I  S  D  A  F  S  L  D  V  S  E  K  S  G  N  F  K  H  L  R  E -

                                                                              BstKTI
                                                                               DpnI|
                 DraI                                                        MboI ||
               MseI|BccI                      PsiI CviJI     SfcI     Hpy188III | ||          MseI
                   ||   |                        |     |        |             | | ||             |
          agtttgtgtttaaaaataaagatgggtttctctatgtttataagggctatcaacctatagatgtagttcgtgatctaccttctggttttaacactttgaa
     2701 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 2800
          tcaaacacaaatttttatttctacccaaagagatacaaatattcccgatagttggatatctacatcaagcactagatggaagaccaaaattgtgaaactt

a         S  L  C  L  K  I  K  M  G  F  S  M  F  I  R  A  I  N  L  *  M  *  F  V  I  Y  L  L  V  L  T  L  *  N -
b          V  C  V  *  K  *  R  W  V  S  L  C  L  *  G  L  S  T  Y  R  C  S  S  *  S  T  F  W  F  *  H  F  E  -
c           F  V  F  K  N  K  D  G  F  L  Y  V  Y  K  G  Y  Q  P  I  D  V  V  R  D  L  P  S  G  F  N  T  L  K -

                                                                                                      PstI
                                                                                                   Fnu4HI|
                                                                                                 HpyCH4V||
                                                                                                    TseI||
                                                                                                Fnu4HI |||
                                                                                                  SfcI |||
                                                                                                 AluI| |||
                                                                                                CviJI| |||
                                                                                               MspA1I| |||
                                                                                                PvuII| |||
                                                                                                 TseI| |||
                                                                                               TaiI || |||
                                                                                           BmgBI |  || |||
                                                                                  AarI     Bme1580I| |  || |||
                                                                 CviJI           BspMI     Bsp1286I| |  || |||
                                 MnlI      ApoI               BpuEI |      Hpy188III |     HpyCH4IV| |  || |||
               MseI              MseI   Tsp509I     CviJI      HphI |         SmlI | |  BbvI      || |  || |||
                  |                 |         |         |         | |            | | |     |      || |  || |||
          acctattttaagttgcctcttggtattaacattacaaatttagagccattcttacagccttttcacctgctcaagacatttggggcacgtcagctgca
     2801 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 2900
          tggataaaattcaacggagaaccataattgtaatgtttaaatctcggtaagaatgtcggaaaagtggacgagttctgtaaaccccgtgcagtcgacgt

a          L  F  L  S  C  L  L  V  L  T  L  Q  I  L  E  P  F  L  Q  P  F  H  L  L  K  T  F  G  A  R  Q  L  Q   -
b         T  Y  F  *  V  A  S  W  Y  *  H  Y  K  F  *  S  H  S  Y  S  L  F  T  C  S  R  H  L  G  H  V  S  C  S -
c           P  I  F  K  L  P  L  G  I  N  I  T  N  F  R  A  I  L  T  A  F  S  P  A  Q  D  I  W  G  T  S  A  A  -
```

Figure 21-M

```
                         BpuEI                                  TspDTI
                        CviJI|                               RsaI    |
              CviJI  DraI   ||                              SfaNI    |
 CviJI     BbvI   | MseI|   ||           SmlI              Csp6I|    |   AlwNI
     |        |   |    ||   ||              |                  ||    |       |
     gcctattttgttggctatttaaagccaactacatttatgctcaagtatgatgaaaatggtacaatcacagatgctgttgattgttctcaaaatccacttg
2901 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 3000
     cggataaaacaaccgataaatttcggttgatgtaaatacgagttcatactacttttaccatgttagtgtctacgacaactaacaagagttttaggtgaac

a     P  I  L  L  A  I  *  S  Q  L  H  L  C  S  S  M  M  K  M  V  Q  S  Q  M  L  L  I  V  L  K  I  H  L  -
b      L  F  C  W  L  F  K  A  N  Y  I  Y  A  Q  V  *  *  K  W  Y  N  H  R  C  C  *  L  F  S  K  S  T  C  -
c    A  Y  F  V  G  Y  L  K  P  T  T  F  M  L  K  Y  D  E  N  G  T  I  T  D  A  V  D  C  S  Q  N  P  L  A -

                                                                                              HinfI
                                                                           Hpy188III           TfiI
                                                                            Bsu36I |      BseMII  |
                          AluI              ApoI                              DdeI |     BspCNI|  |
                    MseI CviJI           Tsp509I         Tsp509I  MnlI   BsaXI   | |   MnlI   ||  |
                       |     |                 |               |     |       |   | |      |   ||  |
     ctgaactcaaatgctctgttaagagctttgagattgacaaaggaatttaccagacctctaatttcagggttgttccctcaggagatgttgtgagattccc
3001 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 3100
     gacttgagtttacgagacaattctcgaaactctaactgtttccttaaatggtctggagattaaagtcccaacaagggagtcctctacaacactctaaggg

a    L  N  S  N  A  L  L  R  A  L  R  L  T  K  E  F  T  R  P  L  I  S  G  L  F  P  Q  E  M  L  *  D  S  L -
b     *  T  Q  M  L  C  *  E  L  *  D  *  Q  R  N  L  P  D  L  *  F  Q  G  C  S  L  R  R  C  C  E  I  P  -
c      E  L  K  C  S  V  K  S  F  E  I  D  K  G  I  Y  Q  T  S  N  F  R  V  V  P  S  G  D  V  V  R  F  P  -

                                                                    NlaIII
                                                                      NsiI
                                                                   BfrBI |            Tsp509I
     SspI                                       ApoI                FatI |        ApoI      |
   BsaXI|              MnlI          MseI    Tsp509I           HpyCH4V | |     Tsp509I      |
       ||                 |             |          |                 | | |           |      |
     taatattacaaacttgtgtccttttggagaggtttttaatgctactaaattcccttctgtctatgcatgggagagaaaaaaaatttctaattgtgttgct
3101 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 3200
     attataatgtttgaacacaggaaaacctctccaaaaattacgatgatttaagggaagacagatacgtaccctctcttttttttaaagattaacacaacga

a      I  L  Q  T  C  V  L  L  E  R  F  L  M  L  L  N  S  L  L  S  M  H  G  R  E  K  K  F  L  I  V  L  L  -
b    *  Y  Y  K  L  V  S  F  W  R  G  F  *  C  Y  *  I  P  F  C  L  C  M  G  E  K  K  N  F  *  L  C  C  * -
c     N  I  T  N  L  C  P  F  G  E  V  F  N  A  T  K  F  P  S  V  Y  A  W  E  R  K  K  I  S  N  C  V  A  -

                                                                             BstKTI
            BsiHKAI                                                      DpnI|
           Bsp1286I                       MseI                    DdeI      MboI ||               HpyCH4V
                  |                          |                       |         | ||                     |
     gattactctgtgctctacaactcaacatttttttcaacctttaagtgctatggcgtttctgccactaagttgaatgatctttgcttctccaatgtctatg
3201 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 3300
     ctaatgagacacgagatgttgagttgtaaaaaaagttggaaattcacgataccgcaaagacggtgattcaacttactagaaacgaagaggttacagatac

a     I  T  L  C  S  T  T  Q  H  F  F  Q  P  L  S  A  M  A  F  L  P  L  S  *  M  I  F  A  S  P  M  S  M  -
b      L  L  C  A  L  Q  L  N  I  F  F  N  L  *  V  L  W  R  F  C  H  *  V  E  *  S  L  L  L  Q  C  L  C  -
c    D  Y  S  V  L  Y  N  S  T  F  F  S  T  F  K  C  Y  G  V  S  A  T  K  L  N  D  L  C  F  S  N  V  Y  A -
```

Figure 21-N

```
                                                   BstNI
                                                   ScrFI
                                                  HaeII|
                                                  HhaI||
                                                 PspGI||                                  TspDTI
                                                StyD4I||                            Tsp509I    |
        HinfI                                   BsaXI|||                     Tsp509I      |    |
         TfiI     BsaXI                       HinP1I||||         BsrI          PsiI| PsiI |    |          FatI
            |         |                            |||||            |              ||    | |    |          |
          cagattcttttgtagtcaagggagatgatgtaagacaaatagcgccaggacaaactggtgttattgctgattataattataaattgccagatgatttcat
     3301 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 3400
          gtctaagaaaacatcagttccctctactacattctgtttatcgcggtcctgtttgaccacaataacgactaatattaatatttaacggtctactaaagta

a         Q  I  L  L  *  S  R  E  M  M  *  D  K  *  R  Q  D  K  L  V  L  L  L  I  I  I  I  N  C  Q  M  I  S  W -
b          R  F  F  C  S  Q  G  R  *  C  K  T  N  S  A  R  T  N  W  C  Y  C  *  L  *  L  *  I  A  R  *  F  H  -
c           D  S  F  V  V  K  G  D  D  V  R  Q  I  A  P  G  Q  T  G  V  I  A  D  Y  N  Y  K  L  P  D  D  F  M -

                                                                                                    CviJI
                                                                                                   HaeIII
                                                                                                Eco0109I|
                                                                                                  Sau96I|
                                                                                              Bpu10I   ||
                                                                                                DdeI   ||
                                                                                               AluI|   ||
                                                                                              CviJI|   ||
                                                                                            Cac8I ||   ||
                                                           Tsp509I                        HindIII ||   ||
                              SfaNI       BsrI      |                           NlaIII  | ||   ||
     NlaIII                   BfaI|    Tsp509I PsiI| PsiI          DdeI FatI   |  | ||   ||
          |                      ||           |    ||    |             |    |   |  | ||   ||
          gggttgtgtccttgcttggaatactaggaacattgatgctacttcaactggtaattataattataaatataggtatcttagacatggcaagcttaggccc
     3401 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 3500
          cccaacacaggaacgaaccttatgatccttgtaactacgatgaagttgaccattaatattaatatttatatccatagaatctgtaccgttcgaatccggg

a           V  V  S  L  L  G  I  L  G  T  L  M  L  L  Q  L  V  I  I  I  I  N  I  G  I  L  D  M  A  S  L  G  P  -
b         G  L  C  P  C  L  E  Y  *  E  H  *  C  Y  F  N  W  *  L  *  L  *  I  *  V  S  *  T  W  Q  A  *  A  L -
c          G  C  V  L  A  W  N  T  R  N  I  D  A  T  S  T  G  N  Y  N  Y  K  Y  R  Y  L  R  H  G  K  L  R  P  -

                                                     HpyCH4V           AarI       CviJI
                                                  HpyF10VI |          BspMI      HaeIII
                                                   BstAPI| |        Tsp509I        MscI
       BsmAI                          BccI           MwoI| |          MseI|      EaeI |MseI
           |                             |              || |             ||         |  |   |
          tttgagagagacatatctaatgtgcctttctcccctgatggcaaaccttgcaccccacctgctcttaattgttattggccattaaatgattatggttttt
     3501 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 3600
          aaactctctctgtatagattacacggaaagaggggactaccgtttggaacgtggggtggacgagaattaacaataaccggtaatttactaataccaaaaa

a          L  R  E  T  Y  L  M  C  L  S  P  L  M  A  N  L  A  P  H  L  L  L  I  V  I  G  H  *  M  I  M  V  F  -
b           *  E  R  H  I  *  C  A  F  L  P  *  W  Q  T  L  H  P  T  C  S  *  L  L  L  A  I  K  *  L  W  F  L -
c         F  E  R  D  I  S  N  V  P  F  S  P  D  G  K  P  C  T  P  P  A  L  N  C  Y  W  P  L  N  D  Y  G  F  Y -
```

Figure 21-O

```
                                                                                       HpyCH4III
                                                                                        BsaJI   |
                                                                                          BtgI  |
                                                                                        CviJI|  |
                                                                                       HaeIII|  |
                                                                                        EaeI ||  |
                                                                                      HpaII| ||  |
                                                       RsaI                           BsrFI|| ||  |     Tsp509I
                                                       ScaI                     HpyCH4V ||| ||  |  AvaII     |
                    CviJI                             Csp6I|                       DraI  | ||| ||  |  Hpy8I     |
                 BsrI     |                           TatI||                      MseI|  | ||| ||  | Sau96I     |
                    |     |                              |||                        ||  | ||| ||  |    |       |
       acaccactactggcattggctaccaaccttacagagttgtagtactttcttttgaacttttaaatgcaccggccacggtttgtggaccaaaattatccac
  3601 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 3700
       tgtggtgatgaccgtaaccgatggttggaatgtctcaacatcatgaaagaaaacttgaaaatttacgtggccggtgccaaacacctggttttaataggtg

a      T  P  L  L  A  L  A  T  N  L  T  E  L  *  Y  F  L  L  N  F  *  M  H  R  P  R  F  V  D  Q  N  Y  P  L -
b       H  H  Y  W  H  W  L  P  T  L  Q  S  C  S  T  F  F  *  T  F  K  C  T  G  H  G  L  W  T  K  I  I  H  -
c        T  T  T  G  I  G  Y  Q  P  Y  R  V  V  V  L  S  F  E  L  L  N  A  P  A  T  V  C  G  P  K  L  S  T  -

                                                                           HincII
                                                                             HpaI
                                                             BsrI            Hpy8I
                           Tsp509I MlyI                      RsaI           MboII
                     Tsp509I     | MseI  BaeI               TspRI            MseI|
       TspRI MseI   BsrI  TspRI  | MseI| PleI HinfI         Csp6I|  BsrI     ||          BaeI          BceAI Tsp509I
         |    |       |      | |     ||   |     |              ||     |      ||            |               |      |
       tgaccttattaagaaccagtgtgtcaattttaattttaatggactcactggtactggtgtgttaactccttcttcaaagagatttcaaccatttcaacaa
  3701 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 3800
       actggaataattcttggtcacacagttaaaattaaaattacctgagtgaccatgaccacacaattgaggaagaagtttctctaaagttggtaaagttgtt

a       T  L  L  R  T  S  V  S  I  L  I  L  M  D  S  L  V  L  V  C  *  L  L  L  Q  R  D  F  N  H  F  N  N  -
b      *  P  Y  *  E  P  V  C  Q  F  *  F  *  W  T  H  W  Y  W  C  V  N  S  F  F  K  E  I  S  T  I  S  T  I -
c       D  L  I  K  N  Q  C  V  N  F  N  F  N  G  L  T  G  T  G  V  L  T  P  S  S  K  R  F  Q  P  F  Q  Q  -

                                          BstKTI
                                            DpnI|
                                          BstYI ||
                                           MboI ||
                                 Hpy188III | ||
       CviJI                     TspRI    | | ||
       HaeIII          TspGWI  HinfI |  TaqI| | ||
       EaeI |     Hpy188I   |   TfiI |AlwI || | ||          Hpy188I SspI  HphI                             Tsp509I
         | |           |    |      | |   | || | ||              |     |   |                                   |
       tttggccgtgatgtttctgatttcactgattccgttcgagatcctaaaacatctgaaatattagacatttcaccttgctcttttggggtgtaagtgtaa
  3801 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 3900
       aaaccggcactacaaagactaaagtgactaaggcaagctctaggattttgtagactttataatctgtaaagtggaacgagaaaaccccccacattcacatt

a       L  A  V  M  F  L  I  S  L  I  P  F  E  I  L  K  H  L  K  Y  *  T  F  H  L  A  L  L  G  V  *  V  *  -
b        W  P  *  C  F  *  F  H  *  F  R  S  R  S  *  N  I  *  N  I  R  H  F  T  L  L  F  W  G  C  K  C  N -
c      F  G  R  D  V  S  D  F  T  D  S  V  R  D  P  K  T  S  E  I  L  D  I  S  P  C  S  F  G  G  V  S  V  I -
```

Figure 21-P

```
                                                                                        BstKTI
                                                                                         DpnI|
                                                                                      MboI  ||
                                                                                 HpyCH4V  | ||
                                                                                  NlaIII  | ||
                                                                              HpyF10VI  | | ||
         TspDTI                                         HpyCH4V                 BstAPI| | | ||
       BstNI  |                              Eco57I HincII    |           Tsp509I    || | | ||
       ScrFI  |                             Eco57MI   HpaI    |        SfcI     |    || | | ||
     PspGI |  |                          Hpy188III|  Hpy8I    |     TspDTI|     | MwoI| | | ||
    StyD4I |  |        Hpy188I           BsgI    ||  MseI|    |  TspRI   ||     |FatI|| | | ||
         | |  |               |              |   ||     ||    |      |   ||     |   ||| | | ||
     ttacacctggaacaaatgcttcatctgaagttgctgttctatatcaagatgttaactgcactgatgtttctacagcaattcatgcagatcaactcacacc
3901 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 4000
     aatgtggaccttgtttacgaagtagacttcaacgacaagatatagttctacaattgacgtgactacaaagatgtcgttaagtacgtctagttgagtgtgg

a    L  H  L  E  Q  M  L  H  L  K  L  L  F  Y  I  K  M  L  T  A  L  M  F  L  Q  Q  F  M  Q  I  N  S  H  Q-
b     Y  T  W  N  K  C  F  I  *  S  C  C  S  I  S  R  C  *  L  H  *  C  F  Y  S  N  S  C  R  S  T  H  T  -
c      T  P  G  T  N  A  S  S  E  V  A  V  L  Y  Q  D  V  N  C  T  D  V  S  T  A  I  H  A  D  Q  L  T  P -

                                                                           HincII
                                                                            Hpy8I
                                                                            AccI|
                                          SmlI                              TaqI|
         HhaI                          HinfI  |                  BlpI    NlaIII||
      HinP1I |                   Hpy188III  | |                  DdeI      NspI||
   AluI    | |             BpuEI   MlyI  |  | |    CviJI BspCNI   AluI|    SalI2|
  CviJI    | |            BsrI |   PleI  |  | |  Cac8I |BseMII|  CviJI|FatI   |||
      |    | |               | |      |  |  | |      | |     ||      ||   |   |||
     agcttggcgcatatattctactggaaacaatgtattccagactcaagcaggctgtcttataggagctgagcatgtcgacacttcttatgagtgcgacatt
4001 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 4100
     tcgaaccgcgtatataagatgacctttgttacataaggtctgagttcgtccgacagaatatcctcgactcgtacagctgtgaagaatactcacgctgtaa

a      L  G  A  Y  I  L  L  E  T  M  Y  S  R  L  K  Q  A  V  L  *  E  L  S  M  S  T  L  L  M  S  A  T  F -
b    S  L  A  H  I  F  Y  W  K  Q  C  I  P  D  S  S  R  L  S  Y  R  S  *  A  C  R  H  F  L  *  V  R  H  S-
c     A  W  R  I  Y  S  T  G  N  N  V  F  Q  T  Q  A  G  C  L  I  G  A  E  H  V  D  T  S  Y  E  C  D  I  -
```

Figure 21-Q

```
                                                                                          ClaI
                                                                                          TaqI
                                                                                      TauI   |
                                                                                     AciI |  |
                                                                                    BsiEI |  |
                                                                                   Fnu4HI |  |
                                                                                   CviJI| |  |
                                                                                  HaeIII| |  |
                                                                                    TauI| |  |
                                                                    BsaBI               | |  |
                                                                  EcoRV |          BsrI|| |  |   Tsp509I
                                                                 PstI | |          EaeI|| |  |   BanII  |
                                                           HpyCH4V |  | |          EagI|| |  |  BsiHKAI  |
                                                        HpyF10VI | |  | |        Fnu4HI|| |  | Bsp1286I  |
                                                            SfcI | |  | |          NotI|| |  |    SacI  |
                                                           MwoI| | |  | |         TspRI|| |  |   AluI | |
            Cac8I                                      ApoI   || | |  | |        AciI| || |  |  CviJI | |
           AluI |                                     EcoRI   || | |  | |     BccI  || || |  |EcoICRI | |
          CviJI |             HpyCH4III   BfaI     Tsp509I    || | |  | |   BstXI|  || || |  |SfaNI|  | |
              | |                      |      |           |   || | |  | |       ||  || || |  |    ||  | |
     cctattggagctggcatttgtgctattaccatacagTTAGACTAGAAaagggcgaattctgcagatatccatcacactggcggccgcatcgatgagctct
4101 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 4200
     ggataacctcgaccgtaaacacgataatggtatgtcAATCTGATCTTtcccgcttaagacgtctataggtagtgtgaccgccggcgtagctactcgaga

a     L  L  E  L  A  F  V  L  L  P  Y  S  *  T  R  K  G  R  I  L  Q  I  S  I  T  L  A  A  A  S  M  S  S   -
b      Y  W  S  W  H  L  C  Y  Y  H  T  V  R  L  E  K  G  E  F  C  R  Y  P  S  H  W  R  P  H  R  *  A  L  -
c    P  I  G  A  G  I  C  A  I  T  I  Q  L  D  *  K  R  A  N  S  A  D  I  H  H  T  G  G  R  I  D  E  L  * -

        MseI
        PacI                                          BfaI
  Tsp509I  |                                         AluI|
    AseI|  |                                        CviJI|                                    Eco57I
    MseI|  |CviJI            Tsp509I                MboII|                                   Eco57MI
       ||  |    |                   |                   ||                                          |
     aattaattaaggcttttctgctaacatatagcaattttgaagaaaggaaagctagaaatacccaatatcttgctgaagcaagatattgggtatttcttt
4201 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 4300
     ttaattaattccgaaaagacgattgtatatcgttaaaacttctttcctttcgatctttatgggttatagaacgacttcgttctataacccataaagaaa

a    N  *  L  R  L  F  C  *  H  I  A  I  F  E  E  R  K  A  R  N  T  Q  Y  L  A  E  A  R  Y  W  V  F  L  F -
b     I  N  *  G  F  S  A  N  I  *  Q  F  L  K  K  G  K  L  E  I  P  N  I  L  L  K  Q  D  I  G  Y  F  F   -
c      L  I  K  A  P  L  L  T  Y  S  N  F  *  R  K  E  S  *  K  Y  P  I  S  C  *  S  K  I  L  G  I  S  F  -

                                      Hin4I                                                          ApoI
                              ApoI   HincII                                                         EcoRI
                             EcoRI     HpaI                    HpyCH4V                            Tsp509I
              HinfI        Tsp509I    Hpy8I                     BciVI|     Hpy188III              RsaI  |
               TfiI       Hpy188I|    MseI| Hpy99I        TspDTI    ||Hin4I BssSI  |            Csp6I|  |
                  |             ||       ||      |              |   ||    |      | |                ||  |
     tttttttatttgaatctttctattctgaattcagttaacgacgagatttagtatcctttcttgcactttcataactcgtgaaatgccgagttggtacga
4301 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 4400
     aaaaaaataaaacttagaaagataagacttaagtcaattgctgctctaaatcataggaaagaacgtgaaagtattgagcactttacggctcaaccatgct

a      F  L  F  *  I  F  L  F  *  I  Q  L  T  T  R  F  S  I  L  S  C  T  F  I  T  R  E  M  P  S  W  Y  E  -
b    F  F  Y  F  E  S  F  Y  S  E  F  S  *  R  R  D  L  V  S  F  L  A  L  S  *  L  V  K  C  R  V  G  T  N -
c     F  F  I  L  N  L  S  I  L  N  S  V  N  D  E  I  *  Y  P  F  L  H  F  H  N  S  *  N  A  E  L  V  R   -
```

Figure 21-R

```
                                                                                        BsrDI
                                                                                       FauI |
                                                                        BstUI      CviJI  | |
                                                                         NruI     HaeIII  | |
                                                                   Hpy188III|       MscI  | |
                         BslI                                     HinfI    ||    EaeI  |  | |     SfaNI
     Tsp509I         EcoNI  |                                       TfiI   || TspDTI|  |  | | AciI    |
            |             ! |                                          |   ||       || |  | |    |    |
     attcccccaatttgcgacctaccataggatttgttatgtaaataggtatatgttcctttccattatgaatcgcgattgtatggccaaccattgcgggtag
4401 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 4500
     taagggggttaaacgctggatggtatcctaaacaatacatttatccatatacaaggaaaggtaatacttagcgctaacataccggttggtaacgcccatc

a     F  P  Q  F  A  T  Y  H  R  I  C  Y  V  N  R  Y  M  F  L  S  I  M  N  R  D  C  M  A  N  H  C  G  *   -
b      S  P  N  L  R  P  T  I  G  F  V  M  *  I  G  I  C  S  F  P  L  *  I  A  I  V  W  P  T  I  A  G  R  -
c    I  P  P  I  C  D  L  P  *  D  L  L  C  K  *  V  Y  V  P  F  H  Y  E  S  R  L  Y  G  Q  P  L  R  V  E -

                         TaiI
                   MaeIII   |
                  HpyCH4IV| |
                NlaIV    || |
                AvaII|   || |
               Sau96I|   || |
               NciI ||   || |
              ScrFI ||   || |
               SmaI ||   || |
             HpaII| ||   || |
              NciI| ||   || |
             ScrFI| ||   || |
             AvaI|| ||   || |
            BsaJI|| ||   || |                                                            KpnI
           StyD4I|| ||   || |                                                         NlaIV |
             XmaI|| ||   || |                                                          RsaI |
          StyD4I||| ||   || |                            AluI                        Csp6I| |
       BsmI    |||| ||   || |  BseRI                    CviJI               BccI   Acc65I|| |      MnlI
      BfaI|    |||| ||   || |BsmFI |TspDTI           MnlI    |          Hin4I  |    BanI||| |   AciI  |
         ||    |||| ||   || |    | |     |              |    |              |  |        ||| |      |  |
     aatgctagatgcccgggaccacgttactattgtttctttctcctccttcatattgagcttttctatttttgccaataaatgatggtacctcccccgcca
4501 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 4600
     ttacgatctacgggccctggtgcaatgataacaaagaaagaggaggaagtataactcgaaaagataaaaacggttatttactaccatggagggggcggt

a    N  A  R  C  P  G  P  R  Y  Y  C  F  F  L  L  L  H  I  E  L  F  Y  F  C  Q  *  M  M  V  P  P  P  A  T -
b     M  L  D  A  R  D  H  V  T  I  V  S  F  S  S  F  I  L  S  F  S  I  F  A  N  K  *  W  Y  L  P  P  P   -
c      C  *  M  P  G  T  T  L  L  L  F  L  S  P  P  S  Y  *  A  F  L  F  L  P  I  N  D  G  T  S  P  R  H  -
```

Figure 21-S

```
        BsiEI
       BstKTI
        Hin4I
         PvuI                                                                          CviJI            HaeII
         TaqI                                                                       BstNI  |            HhaI|
        DpnI|                                TaiI                 BpmI              ScrFI  |           AfeI||
       FauI||                             BmgBI |              Eco57MI            PspGI |  |        HinP1I|||
     MboI|||       MnlI     CviJI     HpyCH4IV| |            CviJI    |          StyD4I |  |  Hpy188I    ||||
        ||||          |         |            || |               |     |               | |  |         |   ||||
        cgatcgaacgggaatggataagaggcttgtgggattgacgtgatagggtagggttggctatactgctggtggcgaactccaggctaataatctgaagcgc
   4601 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 4700
        gctagcttgcccttacctattctccgaacaccctaactgcactatcccatcccaaccgatatgacgaccaccgcttgaggtccgattattagacttcgcg

a         I  E  R  E  W  I  R  G  L  W  D  *  R  D  R  V  G  L  A  I  L  L  V  A  N  S  R  L  I  I  *  S  A -
b       R  S  N  G  N  G  *  E  A  C  G  I  D  V  I  G  *  G  W  L  Y  C  W  W  R  T  P  G  *  *  S  E  A  L-
c        D  R  T  G  M  D  K  R  L  V  G  L  T  *  *  G  R  V  G  Y  T  A  G  G  E  L  Q  A  N  N  L  K  R  -

                             AlwI
                           NlaIII
                       BsaJI    |
                        BtgI    |
                        FatI    |
                        NcoI    |
                        StyI    |
                      BstKTI|   |
                       DpnI||   |
                     NlaIV|||   |
                    BamHI1|||   |                                      BstNI
                    BstYI |||   |                                      ScrFI
               Eco57I   | |||   |                                     PfoI |
              Eco57MI   | |||   |       RsaI                 MseI    PspGI |
               AlwI|    | |||   |     Csp6I|HpyCH4III      AluI |   StyD4I |           BfaI
            MnlI   ||MboI |||   | HpyCH4III||  MnlI  |    CviJI |   BseRI| |        NlaIV |
               |   ||   | |||   |         |||     |  |        | |        |||           |  |
        ttggaagttgtagggaGGATCCATGgcagacaacggtactattaccgttgaggagcttaaacaactcctggaacaatggaacctagtaataggtttccta
   4701 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 4800
        aaccttcaacatccctCCTAGGTACcgtctgttgccatgataatggcaactcctcgaatttgttgaggaccttgttaccttggatcattatccaaaggat

a        W  K  L  *  G  G  S  M  A  D  N  G  T  I  T  V  E  E  L  K  Q  L  L  E  Q  W  N  L  V  I  G  F  L  -
b         G  S  C  R  E  D  P  W  Q  T  T  V  L  L  P  L  R  S  L  N  N  S  W  N  N  G  T  *  *  *  V  S  Y -
c       L  E  V  V  G  R  I  H  G  R  Q  R  Y  Y  Y  R  *  G  A  *  T  T  P  G  T  M  E  P  S  N  R  F  P  I-
```

Figure 21-T

```
                                                                                               MaeIII
                                                                                               BsrI |
                                                                                             CviJI| |
                                                                                            HaeIII| |
         BstNI                                                                                MscI| |
         ScrFI                                                                              EaeI || |
       CviJI |                                             RsaI                         HpyF10VI || |
       PspGI |                                           Csp6I|       AluI                 MwoI| || |
      StyD4I |                                          BsrGI||      CviJI               MnlI || || |
     BfaI  | |  MaeIII Tsp509I            Hpy188I        TatI||  HindIII |          CviJI   | || || |
        |  | |       |       |                  |           |||        | |              |   | || || |
     ttcctagcctggattatgttactacaatttgcctattctaatcggaacaggttttgtacataataaagcttgttttcctctggctcttgtggccagtaa
4801 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 4900
     aaggatcggacctaatacaatgatgttaaacggataagattagccttgtccaaaaacatgtattatttcgaacaaaaggagaccgagaacaccggtcatt

a    F  L  A  W  I  M  L  L  Q  F  A  Y  S  N  R  N  R  F  L  Y  I  I  K  L  V  F  L  W  L  L  W  P  V  T -
b     S  *  P  G  L  C  Y  Y  N  L  P  I  L  I  G  T  G  F  C  T  *  *  S  L  F  S  S  G  S  C  G  Q  *   -
c      P  S  L  D  Y  V  T  T  I  C  L  F  *  S  E  Q  V  F  V  H  N  K  A  C  F  P  L  A  L  V  A  S  N  -

                                    Tsp509I
                                      AseI|
                                      MseI|
                                Tsp509I  ||                                                          AluI
                                TaqII |  ||                                                         CviJI
                             Hpy8I  | |  ||   FauI       HphI                                    BlpI   |
                              SfcI  | |  ||MaeIII|    BsrI  |            BsrDI                   DdeI   |
                   Cac8I     AccI|  | |  ||Tsp45I|   AciI|  |   HpyCH4V CviJI|       CviJI     CviJI|   |
                       |        ||  | |  ||     ||      ||  |         |     ||           |         ||   |
     cacttgcttgttttgtgcttgctgttgtctacagaattaattgggtgactggcgggattgcgattgcaatggcttgtattgtaggcttgatgtggcttag
4901 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 5000
     gtgaacgaacaaaacacgaacgacaacagatgtcttaattaacccactgaccgccctaacgctaacgttaccgaacataacatccgaactacaccgaatc

a      L  A  C  F  V  L  A  V  V  Y  R  I  N  W  V  T  G  G  I  A  I  A  M  A  C  I  V  G  L  M  W  L  S  -
b    H  L  L  V  L  C  L  L  L  S  T  E  L  I  G  *  L  A  G  L  R  L  Q  W  L  V  L  *  A  *  C  G  L  A -
c     T  C  L  F  C  A  C  C  C  L  Q  N  *  L  G  D  W  R  D  C  D  C  N  G  L  Y  C  R  L  D  V  A  *   -

                                                                                             BslI
                                                                                             NciI
                                       BsrBI                                                ScrFI
                                      AciI |                                               BsaJI|   MfeI
 Eco57I                            RsaI  | |                                               HpaII|Tsp509I
Eco57MI               CviJI      Csp6I|  | | FauI                MboII                   StyD4I||MnlI  |
     |                    |          ||  | |    |                    |                        |||   |  |
     ctacttcgttgcttccttcaggctgtttgctcgtacccgctcaatgtggtcattcaacccagaaacaaacattcttctcaatgtgcctctccggggaca
5001 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 5100
     gatgaagcaacgaaggaagtccgacaaacgagcatgggcgagttacaccagtaagttgggtctttgtttgtaagaagagttacacggagaggcccctgt

a     Y  F  V  A  S  F  R  L  F  A  R  T  R  S  M  W  S  F  N  P  E  T  N  I  L  L  N  V  P  L  R  G  T   -
b      T  S  L  L  P  S  G  C  L  L  V  P  A  Q  C  G  H  S  T  Q  K  Q  T  F  F  S  M  C  L  S  G  G  Q  -
c    L  L  R  C  F  L  Q  A  V  C  S  Y  P  L  N  V  V  I  Q  P  R  N  K  H  S  S  Q  C  A  S  P  G  D  N -
```

Figure 21-U

```
                                                                                             MaeIII
                                                                                             Tsp45I
                                                                                             HaeII|
                    NlaIII                                                                   HhaI||
                  FatI   |                                                               HinP1I |||
               BsrBI |   |                       BstKTI                   HpaII       BfaI    | |||
                XcmI |   |                        DpnI|                  CviJI|     AvrII|    | |||
  MaeIII      AciI | |   |                      BclI ||  MaeIII         HaeIII|     BsaJI|    | |||
  Tsp45I BsmFI   | | |   |  Hpy8I               MboI ||  Tsp45I         EaeI ||      StyI|    | |||
       |     |   | | |   |      |                  | ||       |            | ||         ||    | |||
     attgtgaccagaccgctcatggaaagtgaacttgtcattggtgctgtgatcattcgtggtcacttgcgaatggccggacactccctagggcgctgtgaca
5101 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 5200
     taacactggtctggcgagtacctttcacttgaacagtaaccacgacactagtaagcaccagtgaacgcttaccggcctgtgagggatcccgcgacactgt

a    I  V  T  R  P  L  M  E  S  E  L  V  I  G  A  V  I  I  R  G  H  L  R  M  A  G  H  S  L  G  R  C  D  I -
b     L  *  P  D  R  S  W  K  V  N  L  S  L  V  L  *  S  F  V  V  T  C  E  W  P  D  T  P  *  G  A  V  T   -
c      C  D  Q  T  A  H  G  K  *  T  C  H  W  C  C  D  H  S  W  S  L  A  N  G  R  T  L  P  R  A  L  *  H  -

                                 Hpy188III
                              CviJI      |
                             TspRI|      |
     AvaII            HpyCH4III  ||      |                                               TspRI
  Eco0109I           BstKTI   |  ||      |                                             HinfI |
     PpuMI            DpnI|   |  ||      |                             Fnu4HI           TfiI |
    Sau96I          MboI ||   |  ||      |             Tsp509I        Hpy99I|          BbvI| |    Fnu4HI
  MseI   |      BspMI  | ||   |  ||      |   XmnI       HgaI |          TseI|       BbvI  || |      TseI|
     |   |          |  | ||   |  ||      |      |          | |             ||          |  || |         ||
     ttaaggacctgccaaaagagatcactgtggctacatcacgaacgctttcttattacaaattaggagcgtcgcagcgtgtaggcactgattcaggttttgc
5201 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 5300
     aattcctggacggttttctctagtgacaccgatgtagtgcttgcgaaagaataatgtttaatcctcgcagcgtcgcacatccgtgactaagtccaaaacg

a      K  D  L  P  K  E  I  T  V  A  T  S  R  T  L  S  Y  Y  K  L  G  A  S  Q  R  V  G  T  D  S  G  F  A  -
b   L  R  T  C  Q  K  R  S  L  W  L  H  H  E  R  F  L  I  T  N  *  E  R  R  S  V  *  A  L  I  Q  V  L  L -
c    *  G  P  A  K  R  D  H  C  G  Y  I  T  N  A  F  L  L  Q  I  R  S  V  A  A  C  R  H  *  F  R  F  C   -

                                                                                          ApoI
                                                                                         EcoRI
                                                                                       Tsp509I
                                                                                     BcgI    |
                                                                                HpyCH4III    |
                                                                                  RsaI  |    |       ApoI
                                                   HpaII                        Csp6I|  |    |      EcoRI
             HpyCH4III              MseI           BcgI|                        TatI||  |    |    Tsp509I
HpyCH4V    AciI      |        Tsp509I  |          BsrFI|            SspI      BfaI |||  |    |   CviJI  |
      |       |      |              |  |              ||               |         | |||  |    |       |  |
     tgcatacaaccgctaccgtattggaaactataaattaaatacagaccacgccggtagcaacgacaatattgctttgctagtacagtaaGAATTCaagccg
5301 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 5400
     acgtatgttggcgatggcataacctttgatatttaatttatgtctggtgcggccatcgttgctgttataacgaaacgatcatgtcattCTTAAGttcggc

a     A  Y  N  R  Y  R  I  G  N  Y  K  L  N  T  D  H  A  G  S  N  D  N  I  A  L  L  V  Q  *  E  F  K  P   -
b      H  T  T  A  T  V  L  E  T  I  N  *  I  Q  T  T  P  V  A  T  T  I  L  L  C  *  Y  S  K  N  S  S  R  -
c    C  I  Q  P  L  P  Y  W  K  L  *  I  K  Y  R  P  R  R  *  Q  R  Q  Y  C  F  A  S  T  V  R  I  Q  A  E -
```

Figure 21-V

```
                                                   MseI
                                                   PacI
                                            Tsp509I |
                                               AseI||
                                               MseI||
                          AlwI         Tsp509I |  ||
                          BfaI           BanII |  ||
                          SpeI|         BsiHKAI |  ||
                      Hin4I ||        Bsp1286I |  ||
                    MaeIII | ||           SacI |  ||
                    BsiEI| | ||           AluI |  ||
                   CviJI|| | ||           AlwI |  ||
                  HaeIII|| | ||          CviJI |  ||
                    TauI|| | ||        EcoICRI |  ||
                   BsrI ||| | ||     Hpy188I | |  ||
                   EaeI ||| | ||     BstKTI | | |  ||
                   EagI ||| | ||      DpnI|| | |  ||
                 Fnu4HI ||| | ||     NlaIV|| | |  ||
                  TspRI ||| | ||    BamHI2|| | |  ||
                   AciI|||| | ||    BstYI || | |  ||  |CviJI                                   BfaI
     BceAI   BstXI    |||| | ||     MboI || | |  ||  |Hin4I             Tsp509I           AluI|
                                                                                          CviJI|
                                                                                          MboII|
       |       |    || |||| | ||       |  ||| | |  ||  |    |                   |                 ||
     aattccagcacactggcggccgttactagtggatccgagctctaattaattaaggcttttctgctaacatatagcaattttgaagaaaggaaagctaga
5401 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 5500
     ttaaggtcgtgtgaccgccggcaatgatcacctaggctcgagattaattaattccgaaaagacgattgtatatcgttaaaacttctttcctttcgatct

a    N  S  S  T  L  A  A  V  T  S  G  S  E  L  *  L  I  K  A  F  L  L  T  Y  S  N  F  *  R  K  E  S  *  K -
b     I  P  A  H  W  R  P  L  L  V  D  P  S  S  N  *  L  R  L  F  C  *  H  I  A  I  F  E  E  R  K  A  R  -
c      F  Q  H  T  G  G  R  Y  *  W  I  R  A  L  I  N  *  G  F  S  A  N  I  *  Q  F  L  K  K  G  K  L  E  -

                                                                            Hin4I
                                                                     ApoI   HincII
                                                                    EcoRI    HpaI
                                   Eco57I           HinfI         Tsp509I   Hpy8I
                                  Eco57MI            TfiI         Hpy188I|   MseI| Hpy99I
                                        |                |              ||       ||      |
     aatacccaatatcttgctgaagcaagatattgggtatttcttttttttttttatttgaatctttctattctgaattcagttaacgacgagatttagtatcc
5501 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 5600
     ttatgggttatagaacgacttcgttctataacccataaagaaaaaaaaaaataaacttagaaagataagacttaagtcaattgctgctctaaatcatagg

a      Y  P  I  S  C  *  S  K  I  L  G  I  S  F  F  F  I  L  N  L  S  I  L  N  S  V  N  D  E  I  *  Y  P  -
b    N  T  Q  Y  L  A  E  A  R  Y  W  V  F  L  F  F  L  F  *  I  F  L  F  *  I  Q  L  T  T  R  F  S  I  L -
c     I  P  N  I  L  L  K  Q  D  I  G  Y  F  F  F  F  Y  F  E  S  F  Y  S  E  F  S  *  R  R  D  L  V  S  -
```

Figure 21-W

```
                                            ApoI
                                           EcoRI
           HpyCH4V                       Tsp509I
            BciVI|      Hpy188III           RsaI |                           BslI
        TspDTI  ||Hin4I   BssSI |          Csp6I| |  Tsp509I           EcoNI |
             |   ||    |      | |              || |        |              | |
     tttcttgcactttcataactcgtgaaatgccgagttggtacgaattcccccaatttgcgacctaccataggatttgttatgtaaataggtatatgttcct
5601 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 5700
     aaagaacgtgaaagtattgagcactttacggctcaaccatgcttaagggggttaaacgctggatggtatcctaaacaatacatttatccatatacaagga

a     F  L  H  F  H  N  S  *  N  A  E  L  V  R  I  P  P  I  C  D  L  P  *  D  L  L  C  K  *  V  Y  V  P  -
b      S  C  T  F  I  T  R  E  M  P  S  W  Y  E  F  P  Q  F  A  T  Y  H  R  I  C  Y  V  N  R  Y  M  F  L -
c    F  L  A  L  S  *  L  V  K  C  R  V  G  T  N  S  P  N  L  R  P  T  I  G  F  V  M  *  I  G  I  C  S  F -

                                                                TaiI
                                                          MaeIII |
                                                       HpyCH4IV| |
                                                      NlaIV   || |
                                                    AvaII|    || |
                                                   Sau96I|    || |
                                                     NciI ||  || |
                                                    ScrFI ||  || |
                                                     SmaI ||  || |
                                                   HpaII| ||  || |
                                                    NciI| ||  || |
                                                   ScrFI| ||  || |
                             BsrDI                  AvaI|| ||  || |
                            FauI |                 BsaJI|| ||  || |
             BstUI      CviJI  | |                StyD4I|| ||  || |
              NruI     HaeIII  | |                  XmaI|| ||  || |
        Hpy188III|       MscI  | |               StyD4I||| ||  || |                      AluI
            HinfI ||      EaeI |  | |    SfaNI   BsmI   |||| ||  || | BseRI               CviJI
             TfiI ||  TspDTI| |  | | AciI    |  BfaI|   |||| ||  || |BsmFI |TspDTI      MnlI  |
                |    ||      || |  | |    |    |   ||   |||| ||  || |    | |    |          |  |
     ttccattatgaatcgcgattgtatggccaaccattgcgggtagaatgctagatgcccgggaccacgttactattgtttctttctcctccttcatattgag
5701 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 5800
     aaggtaatacttagcgctaacataccggttggtaacgcccatcttacgatctacgggccctggtgcaatgataacaaagaaagaggaggaagtataactc

a    F  H  Y  E  S  R  L  Y  G  Q  P  L  R  V  E  C  *  M  P  G  T  T  L  L  L  F  L  S  P  P  S  Y  *  A -
b     S  I  M  N  R  D  C  M  A  N  H  C  G  *  N  A  R  C  P  G  P  R  Y  Y  C  F  F  L  L  L  H  I  E  -
c      P  L  *  I  A  I  V  W  P  T  I  A  G  R  M  L  D  A  R  D  H  V  T  I  V  S  F  S  S  F  I  L  S  -
```

Figure 21-X

```
                                                   BsiEI
                                                  BstKTI
                                                   Hin4I
                                                    PvuI
                                    KpnI            TaqI
                                 NlaIV |           DpnI|
                                  RsaI |          FauI||
                                Csp6I| |         MboI|||                                 TaiI
                       BccI   Acc65I|| |      MnlI  ||||                              BmgBI |
                   Hin4I  |     BanI|| |   AciI  |  ||||       MnlI     CviJI     HpyCH4IV| |           CviJI
                       |  |        ||| |      |  |  ||||          |         |            || |               |
         cttttctatttttgccaataaatgatggtacctccccccgccacgatcgaacgggaatggataagaggcttgtgggattgacgtgatagggtagggttgg
    5801 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 5900
         gaaaagataaaaacggttatttactaccatggaggggggcggtgctagcttgcccttacctattctccgaacaccctaactgcactatcccatcccaacc

a          F  L  F  L  P  I  N  D  G  T  S  P  R  H  D  R  T  G  M  D  K  R  L  V  G  L  T  *  *  G  R  V  G  -
b        L  F  Y  F  C  Q  *  M  M  V  P  P  P  A  T  I  E  R  E  W  I  R  G  L  W  D  *  R  D  R  V  G  L  A -
c         F  S  I  F  A  N  K  *  W  Y  L  P  P  P  R  S  N  G  N  G  *  E  A  C  G  I  D  V  I  G  *  G  W   -

                                                                  BstKTI
                                                                   DpnI|               HpyF10VI
                                                                  NlaIV|            AciI      |
                                                                BamHI3||      HpyF10VI |      |
                              CviJI            HaeII            BstYI ||         MwoI| |      |
                            BstNI |            HhaI|       Eco57I   | || Hpy188III  || |      |        HinfI
                            ScrFI |           AfeI||      Eco57MI   | ||   BssSI |  || |      |       TaqI |
          BpmI              PspGI |        HinP1I|||        AlwI|   | ||  CviJI| |  || |      |   MlyI   | |
       Eco57MI            StyD4I| |   Hpy188I   ||||    MnlI   ||MboI || AlwI || |  || |  MwoI|   PleI   | |
             |                 || |        |   ||||       |   ||   | ||    | || |  || |     ||      |   | |
         ctatactgctggtggcgaactccaggctaataatctgaagcgcttggaagttgtagggaggatcctatggctcgtgaagcggttatcgccgaagtatcga
    5901 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 6000
         gatatgacgaccaccgcttgaggtccgattattagacttcgcgaaccttcaacatccctcctaggataccgagcacttcgccaatagcggcttcatagct

a         Y  T  A  G  G  E  L  Q  A  N  N  L  K  R  L  E  V  V  G  R  I  L  W  L  V  K  R  L  S  P  K  Y  R   -
b          I  L  L  V  A  N  S  R  L  I  I  *  S  A  W  K  L  *  G  G  S  Y  G  S  *  S  G  Y  R  R  S  I  D  -
c        L  Y  C  W  W  R  T  P  G  *  *  S  E  A  L  G  S  C  R  E  D  P  M  A  R  E  A  V  I  A  E  V  S  T-
```

Figure 21-Y

```
                                                               RsaI
                                                             Csp6I|
                                                          CviJI  ||
                                                         HaeIII  ||
                                                        Cac8I |  ||
                                                     TaiI   | |  ||
                                                  Hpy99I|   | |  ||
                                              HpyCH4IV ||   | |  ||                         CviJI
                                             BccI    | ||   | |  ||                        HaeIII
                                           BceAI|    | ||   | |  ||                          TauI
                                          TaqI ||    | ||   | |  ||             BccI       BstF5I
                                    Hpy188III| ||    | ||   | |  ||           AciI |       Fnu4HI
                                    HaeII   || ||    | ||   | |  ||        NlaIV | |       AciI |
            HgaI                    HhaI|   || ||    | ||   | |  ||       CviJI| | |     BceAI| |
         Hpy188I                HinP1I ||   || ||    | ||   | |  ||    RsaI   || | |    BtsI || | CviJI
      MnlI     |      BsaHI   TaqI   | ||   || ||    | ||EaeI |  ||  Csp6I|   || | |  TspRI| || |FokI |
         |     |          |      |   | ||   || ||    | ||   | |  ||      ||   || | |      || || |   | |
     ctcaactatcagaggtagttggcgtcatcgagcgccatctcgaaccgacgttgctggccgtacatttgtacggctccgcagtggatggcggcctgaagcc
6001 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 6100
     gagttgatagtctccatcaaccgcagtagctcgcggtagagcttggctgcaacgaccggcatgtaaacatgccgaggcgtcacctaccgccggacttcgg

a     L  N  Y  Q  R  *  L  A  S  S  S  A  I  S  N  R  R  C  W  P  Y  I  C  T  A  P  Q  W  M  A  A  *  S  H -
b      S  T  I  R  G  S  W  R  H  R  A  P  S  R  T  D  V  A  G  R  T  F  V  R  L  R  S  G  W  R  P  E  A   -
c       Q  L  S  E  V  V  G  V  I  E  R  H  L  E  P  T  L  L  A  V  H  L  Y  G  S  A  V  D  G  G  L  K  P  -

                                                                AluI
                                                               CviJI
                                                             Cac8I |
                               HpyCH4III                    TspDTI |                               BstNI
             Eco57I         BstEII     |                    TauI | |                               ScrFI
            Eco57MI      HpyCH4III     |                Fnu4HI | | | BstKTI                      BsaJI |
          TspRI   |         MaeIII     |                  AciI | | |  DpnI|                      PspGI |
    DraIII    |   |         Tsp45I     | CviJI          BstUI| | | |BclI ||                     StyD4I |
 HpyCH4III    |   |  MaeIII      |     |  HphI      Hin4I   || | | |MboI ||         Hin4I   CviJI    | |
         |    |   |       |      |     |     |          |   || | | |   | ||             |       |    | |
     acacagtgatattgatttgctggttacggtgaccgtaaggcttgatgaaacaacgcggcgagctttgatcaacgaccttttggaaacttcggcttcccct
6101 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 6200
     tgtgtcactataactaaacgaccaatgccactggcattccgaactactttgttgcgccgctcgaaactagttgctggaaaacctttgaagccgaagggga

a       T  V  I  L  I  C  W  L  R  *  P  *  G  L  M  K  Q  R  G  E  L  *  S  T  T  F  W  K  L  R  L  P  L  -
b     T  Q  *  Y  *  F  A  G  Y  G  D  R  K  A  *  *  N  N  A  A  S  F  D  Q  R  P  F  G  N  F  G  F  P  W -
c      H  S  D  I  D  L  L  V  T  V  T  V  R  L  D  E  T  T  R  R  A  L  I  N  D  L  L  E  T  S  A  S  P   -
```

Figure 21-Z

```
                                                                                              Tsp509I
                                                        Hpy99I                               HpyCH4V|
                              HphI                    TspGWI |                            HpyF10VI ||
                             SfcI|               Bme1580I  | |                          BstUI    | ||
                            HhaI||                BsiHKAI  | |                           HhaI    | ||
                         BpmI  |||               Bsp1286I  | |                       HinP1I |    | ||
                        BstUI  |||                Hpy8I |  | |                     BlpI   | |    | ||
                      Eco57MI  |||              HpyCH4V |  | |                     DdeI   | |    | ||
                 HinfI HinP1I  |||MaeIII        ApaLI | |  | |    BsaJI           AluI|   | |    | ||
                  TfiI  AciI | |||Tsp45I      MslI  | | |  | |     BtgI          CviJI|   | |MwoI| ||
                     |     | | |||     |         |  | | |  | |        |              ||   | |   || ||
          ggagagagcgagattctccgcgctgtagaagtcaccattgttgtgcacgacgacatcattccgtggcgttatccagctaagcgcgaactgcaatttggag
     6201 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 6300
          cctctctcgctctaagaggcgcgacatcttcagtggtaacaacacgtgctgctgtagtaaggcaccgcaataggtcgattcgcgcttgacgttaaacctc

a          E  R  A  R  F  S  A  L  *  K  S  P  L  L  C  T  T  T  S  F  R  G  V  I  Q  L  S  A  N  C  N  L  E   -
b           R  E  R  D  S  P  R  C  R  S  H  H  C  C  A  R  R  H  H  S  V  A  L  S  S  *  A  R  T  A  I  W  R  -
c         G  E  S  E  I  L  R  A  V  E  V  T  I  V  V  H  D  D  I  I  P  W  R  Y  P  A  K  R  E  L  Q  F  G  E -

                                                      BsiEI
                                                     BstKTI
                HhaI       HpyCH4V             CviJI   PvuI         CviJI
            HinP1I |   BbvI      |           Cac8I |   TaqI    BstKTI   |
          Fnu4HI | |  BsrDI      |         CviJI | |  DpnI|     DpnI|   |                                BsaJI
           TseI| | |BspMI | MboII|      TaqI   | | |MboI ||   MboI ||   |                                 StyI
              || | |    | |     ||         |   | | |   | ||      | ||   |                                    |
          aatggcagcgcaatgacattcttgcaggtatcttcgagccagccacgatcgacattgatctggctatcttgctgacaaaagcaagagaacatagcgttgc
     6301 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 6400
          ttaccgtcgcgttactgtaagaacgtccatagaagctcggtcggtgctagctgtaactagaccgatagaacgactgttttcgttctcttgtatcgcaacg

a         N  G  S  A  M  T  F  L  Q  V  S  S  S  Q  P  R  S  T  L  I  W  L  S  C  *  Q  K  Q  E  N  I  A  L  P -
b          M  A  A  Q  *  H  S  C  R  Y  L  R  A  S  H  D  R  H  *  S  G  Y  L  A  D  K  S  K  R  T  *  R  C   -
c           W  Q  R  N  D  I  L  A  G  I  F  E  P  A  T  I  D  I  D  L  A  I  L  L  T  K  A  R  E  H  S  V  A  -

                                          Hpy188III
                       AciI                 NlaIV |
                       TauI             HpaII   | |
                   Fnu4HI |            BsaWI|   | |     BstKTI
                    AciI| |           BstKTI|   | |       MnlI        HaeII
                  MspA1I| |            DpnI||   | |      DpnI|        HhaI|                            TauI
             AvaII     || |           EciI|||   | |   BstYI ||    HinP1I ||                          AciI |
            Sau96I MnlI|| |     AlwI MboI||||   | |    MboI || AlwI    | ||        MseI TspDTI     Fnu4HI |
                 |    ||| |        |    |||||   | |       | ||    |    | ||           |      |          | |
          cttggtaggtccagcggcggaggaactctttgatccggttcctgaacaggatctatttgaggcgctaaatgaaaccttaacgctatggaactcgccgccc
     6401 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 6500
          gaaccatccaggtcgccgcctccttgagaaactaggccaaggacttgtcctagataaactccgcgatttactttggaattgcgataccttgagcggcggg

a           W  *  V  Q  R  R  R  N  S  L  I  R  F  L  N  R  I  Y  L  R  R  *  M  K  P  *  R  Y  G  T  R  R  P  -
b         L  G  R  S  S  G  G  G  T  L  *  S  G  S  *  T  G  S  I  *  G  A  K  *  N  L  N  A  M  E  L  A  A  R -
c          L  V  G  P  A  A  E  E  L  F  D  P  V  P  E  Q  D  L  F  E  A  L  N  E  T  L  T  L  W  N  S  P  P   -
```

Figure 21-AA

```
                                                                   HpaII
                                                                  BsrFI |
                                                             MaeIII    ||
                                                              HhaI |   ||
                                                          HinP1I | |   ||
                BmrI                                   RsaI    | | |   ||        BbvI
           Cac8I   |                                  Csp6I|   | | |   ||        HhaI         Fnu4HI   BglI
           BsrI |  |                    TaiI        FauI  ||   | | |   ||     BstUI  |         TseI|   MwoI
         CviJI  |  |       BsmFI  HpyCH4IV  | AciI BslI | ||   | | |   ||     HinP1I |      BstF5I|| FokI  |
              | |  |           |         |  |    |    | | ||   | | |   ||          | |           |||    |  |
        gactgggctggcgatgagcgaaatgtagtgcttacgttgtcccgcatttggtacagcgcagtaaccggcaaaatcgcgccgaaggatgtcgctgccgact
   6501 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 6600
        ctgacccgaccgctactcgctttacatcacgaatgcaacagggcgtaaaccatgtcgcgtcattggccgttttagcgcggcttcctacagcgacggctga

a        T  G  L  A  M  S  E  M  *  C  L  R  C  P  A  F  G  T  A  Q  *  P  A  K  S  R  R  R  M  S  L  P  T   -
b         L  G  W  R  *  A  K  C  S  A  Y  V  V  P  H  L  V  Q  R  S  N  R  Q  N  R  A  E  G  C  R  C  R  L  -
c       D  W  A  G  D  E  R  N  V  V  L  T  L  S  R  I  W  Y  S  A  V  T  G  K  I  A  P  K  D  V  A  A  D  W -

                                                                                                        DpnI
                                                                                                      MboI |
                                                                                                      MnlI |
                                                                                                    HhaI | |
                                                                                                 BstUI | | |
                           BsrI                                                                  Cac8I | | |
                        CviJI |                                                                   HhaI | | |
                       HaeIII |                                                                HinP1I | | |
                      Sau96I| |                                                              HpyF10VI | | |
                      Cac8I|| |                                                                  MwoI| | | |
                       NaeI|| |                                                               BssHII|| | | |
                     HpaII||| |                                                                BstUI|| | | |
                     BmrI|||| |                                                               HinP1I|| | | |
                    BsrFI|||| |                                                           CviJI    ||| | | |
                   NgoMIV|||| |                                                          HaeIII    ||| | | |
                  Cac8I ||||| |                                                           MboII    ||| | | |
                 HaeII| ||||| |                             CviJI                        MmeI |    ||| | | |
                 HhaI|| ||||| |                        HpyF10VI |                      MboII| |    ||| | | |
             HinP1I ||| ||||| |                      BfaI     | |                 BstKTI   || |    ||| | | |
       BsrI  BsrDI| ||| ||||| |                     AluI|     | |                  DpnI|   || |    ||| | | |
 HpyF10VI | BmrI || ||| ||||| |    CviJI           CviJI| MwoI| |                MboI ||   || |    ||| | | |
        | |    | || ||| ||||| |        |               ||    || |                   | ||   || |    ||| | | |
        gggcaatggagcgcctgccggcccagtatcagcccgtcatacttgaagctagacaggcttatcttggacaagaagaagatcgcttggcctcgcgcgcaga
   6601 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 6700
        cccgttacctcgcggacggccgggtcatagtcgggcagtatgaacttcgatctgtccgaatagaacctgttcttcttctagcgaaccggagcgcgcgtct

a       G  Q  W  S  A  C  R  P  S  I  S  P  S  Y  L  K  L  D  R  L  I  L  D  K  K  K  I  A  W  P  R  A  Q  I -
b        G  N  G  A  P  A  G  P  V  S  A  R  H  T  *  S  *  T  G  L  S  W  T  R  R  R  S  L  G  L  A  R  R   -
c         A  M  E  R  L  P  A  Q  Y  Q  P  V  I  L  E  A  R  Q  A  Y  L  G  Q  E  E  D  R  L  A  S  R  A  D  -
```

Figure 21-BB

```
                                TaiI                            Hpy188III
                             BsaAI |            BcgI                 TaqI|
                            DraIII |           DdeI|                AvaI||
                         HpyCH4IV| |      BstKTI  ||                SmlI||
                ApoI    MboII   || |       DpnI|  ||                XhoI||        Tsp509I
    BstKTI   Tsp509I   Hpy8I|   || |     MboI ||  ||           BsmAI   ||| DdeI   BcgI  |
         |         |       ||   || |        | ||  ||               |   |||   |       |  |
         tcagttggaagaatttgtccactacgtgaaaggcgagatcactaaggtagttggcaaataactcgagactaagtggataaaattagatagaaaaaaggtc
    6701 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 6800
         agtcaaccttcttaaacaggtgatgcactttccgctctagtgattccatcaaccgtttattgagctctgattcacctattttaatctatcttttttccag

a          S  W  K  N  L  S  T  T  *  K  A  R  S  L  R  *  L  A  N  N  S  R  L  S  G  *  N  *  I  E  K  R  S  -
b        S  V  G  R  I  C  P  L  R  E  R  R  D  H  *  G  S  W  Q  I  T  R  D  *  V  D  K  I  R  *  K  K  G  L -
c         Q  L  E  E  F  V  H  Y  V  K  G  E  I  T  K  V  V  G  K  *  L  E  T  K  W  I  K  L  D  R  K  K  V   -

                                BstKTI                Tsp509I
                                 DpnI|                Hin4I   |                            MseI
                               MboI ||              HpyCH4V   |                      Tsp509I  |        BsmAI
            EarI      Hin4I MboII | ||   MaeIII        MboII   | MboII      Tsp509I  HpyCH4V|  |        BsmBI
               |          |     | | ||        |           |   |     |            |        ||  |            |
         taaataaaaaagaagagaaatagaaagatcaaaaatcagttacgaaaatgcagtaattcttcttttttcttctaattgattgcaattaaactcgtctcaa
    6801 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 6900
         atttattttttcttctctttatctttctagtttttagtcaatgcttttacgtcattaagaagaaaaaagaagattaactaacgttaatttgagcagagtt

a         K  *  K  R  R  E  I  E  R  S  K  I  S  Y  E  N  A  V  I  L  L  F  S  S  N  *  L  Q  L  N  S  S  Q   -
b          N  K  K  E  E  K  *  K  D  Q  K  S  V  T  K  M  Q  *  F  F  F  F  L  L  I  D  C  N  *  T  R  L  N  -
c        *  I  K  K  K  R  N  R  K  I  K  N  Q  L  R  K  C  S  N  S  S  F  F  F  *  L  I  A  I  K  L  V  S  I -

                                                   NlaIII
                                             Hpy188III  |
                                                BspHI|  |
                                               BstKTI|  |
                                                 FatI|  |
                                                DpnI||  |            HinfI
                              DraI              BsmAI|||  |             TfiI
     Hpy188I         CviJI  MseI||            MboI||||  |     Hpy188III   |          MnlI               MboII
           |             |      ||               |||||  |              |  |             |                   |
         tctgaaaaaagattgagccgagtttaaatagattttgatacgatcatgagacttgacaaatcgggattcctctattctatatatttagaagatataaagg
    6901 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 7000
         agacttttttctaactcggctcaaatttatctaaaactatgctagtactctgaactgtttagccctaaggagataagatatataaatcttctatatttcc

a        S  E  K  R  L  S  R  V  *  I  D  F  D  T  I  M  R  L  D  K  S  G  F  L  Y  S  I  Y  L  E  D  I  K  V-
b         L  K  K  D  *  A  E  F  K  *  I  L  I  R  S  *  D  L  T  N  R  D  S  S  I  L  Y  I  *  K  I  *  R   -
c          *  K  K  I  E  P  S  L  N  R  F  *  Y  D  H  E  T  *  Q  I  G  I  P  L  F  Y  I  F  R  R  Y  K  G  -
```

Figure 21-CC

```
                                         Bsu36I
                                   TaqI    DdeI
                            BfaI  AlwI| BstKTI|
                       Hpy188III AluI|| DpnI| |                                           HinfI
                           XbaI|CviJI||MboI|| |                           SfcI             TfiI CviJI
                              ||    |||  | || |                              |                |     |
        tataatacaataaataaatacaatctagaagctcgatgatccttaggattggtatattcttttctatcctgtagtttgtagtttccctgaatcaagccaa
   7001 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 7100
        atattatgttatttatttatgttagatcttcgagctactaggaatcctaaccatataagaaaagataggacatcaaacatcaaagggacttagttcggtt

a         *  Y  N  K  *  I  Q  S  R  S  S  M  I  L  R  I  G  I  F  F  S  I  L  *  F  V  V  S  L  N  Q  A  K   -
b       Y  N  T  I  N  K  Y  N  L  E  A  R  *  S  L  G  L  V  Y  S  F  L  S  C  S  L  *  F  P  *  I  K  P  S  -
c        I  I  Q  *  I  N  T  I  *  K  L  D  D  P  *  D  W  Y  I  L  F  Y  P  V  V  C  S  F  P  E  S  S  Q    -

                      BstF5I                                                               ApoI
                      BsmFI|                                          Tsp509I             Tsp509I
             FokI      MnlI|  BccI TspGWI                             MseI|              MseI |
                |         ||      |     |                                ||                  ||
        gtatcacacctctttctacccatcctgtatattgtcccctttgttccgtgttgaaatagaaccttaatttattacttatttttttattaaattttagatt
   7101 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 7200
        catagtgtggagaaagatgggtaggacatataacaggggaaacaaggcacaactttatcttggaattaaataatgaataaaaaaataatttaaaatctaa

a        Y  H  T  S  F  Y  P  S  C  I  L  S  P  L  F  R  V  E  I  E  P  *  F  I  T  Y  F  F  I  K  F  *  I    -
b         I  T  P  L  S  T  H  P  V  Y  C  P  L  C  S  V  L  K  *  N  L  N  L  L  L  I  F  L  L  N  F  R  F   -
c       V  S  H  L  F  L  P  I  L  Y  I  V  P  F  V  P  C  *  N  R  T  L  I  Y  Y  L  F  F  Y  *  I  L  D  L  -

                                                                                                ApoI
                                                                                             Tsp509I
                                                                     MnlI                    Hin4I |
                                         Tsp509I                  Hin4I |          SfaNI  TaqI    ||
                                               |                       ||              |      |   ||
        tgttagtgattagatattagtattagacgagattttacgaaacaattatttttttatttctttataggagaggacaaatctcttttttcgatgcgaattt
   7201 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 7300
        acaatcactaatctataatcataatctgctctaaaatgctttgttaataaaaaaataaagaaatatcctctcctgtttagagaaaaaagctacgcttaaa

a       C  *  *  L  D  I  S  I  R  R  D  F  T  K  Q  L  F  F  Y  F  F  I  G  E  D  K  S  L  F  S  M  R  I  *  -
b        V  S  D  *  I  L  V  L  D  E  I  L  R  N  N  Y  F  F  I  S  L  *  E  R  T  N  L  F  F  R  C  E  F    -
c         L  V  I  R  Y  *  Y  *  T  R  F  Y  E  T  I  I  F  L  F  L  Y  R  R  G  Q  I  S  F  F  D  A  N  L   -

                         TauI
                       AciI |
                     Fnu4HI |   Tsp509I        DraI                             AseI
                     CviJI| |   MseI  |  FalI MseI|                    NlaIV    MseI         MmeI
                         || |      |  |    |     ||                       |        |            |
        gacacgacataggagaagccgccctttattaaaaattatattattttaaataatataaagggggttccaacatattaatatatagtgaagtgttcccccca
   7301 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 7400
        ctgtgctgtatcctcttcggcgggaaataatttttaatataataaaatttattatatttcccccaaggttgtataattatatatcacttcacaagggggt

a         H  D  I  G  E  A  A  L  Y  *  K  L  Y  Y  F  K  *  Y  K  G  G  S  N  I  L  I  Y  S  E  V  F  P  Q   -
b       D  T  T  *  E  K  P  P  F  I  K  N  Y  I  I  L  N  N  I  K  G  V  P  T  Y  *  Y  I  V  K  C  S  P  R  -
c        T  R  H  R  R  S  R  P  L  L  K  I  I  L  F  *  I  I  *  R  G  F  Q  H  I  N  I  *  *  S  V  P  P    -
```

Figure 21-DD

```
       Hpy188I
    HinfI    |                                                               Hpy188I
     TfiI    |                              MseI     BfaI                DdeI      |
        |    |                                 |        |                   |      |
        gattcagaacttttttttcaatactcacaatccttattagttaataatcctagtgattggatttctatgcttagtctgataggaaataagatattcaaata
   7401 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 7500
        ctaagtcttgaaaaaaagttatgagtgttaggaataatcaattattaggatcactaacctaaagatacgaatcagactatcctttattctataagtttat

a        I  Q  N  F  F  S  I  L  T  I  L  I  S  *  *  S  *  *  L  D  F  Y  A  *  S  D  R  K  *  D  I  Q  I   -
b         F  R  T  F  F  Q  Y  S  Q  S  L  L  V  N  N  P  S  D  W  I  S  M  L  S  L  I  G  N  K  I  F  K  *  -
c       D  S  E  L  F  F  N  T  H  N  P  Y  *  L  I  I  L  V  I  G  F  L  C  L  V  *  *  E  I  R  Y  S  N  K -

                                             HpyCH4V
                                              NlaIII
                TspDTI                       Hin4I |                                    Tsp509I
    Tsp509I  Hin4I   |          TspDTI      FatI | |                      BccI          MseI|TaqI      MseI
          |      |   |              |          | | |                        |              ||   |         |
        aataattttatagcgaatgactattcatctattgtattttcatgcaaatagggggcaagaaaactctatggaaagatggtggtttaattcgatgttgttt
   7501 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 7600
        ttattaaaatatcgcttactgataagtagataacataaaagtacgtttatcccccgttcttttgagatacctttctaccaccaaattaagctacaacaaa

a       N  N  F  I  A  N  D  Y  S  S  I  V  F  S  C  K  *  G  A  R  K  L  Y  G  K  M  V  V  *  F  D  V  V  * -
b        I  I  L  *  R  M  T  I  H  L  L  Y  F  H  A  N  R  G  Q  E  N  S  M  E  R  W  W  F  N  S  M  L  F   -
c         *  F  Y  S  E  *  L  F  I  Y  C  I  F  M  Q  I  G  G  K  K  T  L  W  K  D  G  G  L  I  R  C  C  L  -

              BstBI                                                              BsaBI     TspDTI
               TaqI                                                         BstKTI |    MmeI  |
            AarI  |                                                          DpnI| |TspDTI |  |
           BspMI  |                                    AvaII                BstYI || |MboII| |  |
           XmnI|  |           CviJI                   Sau96I              AlwI MboI || |TaqI|| |  |
              ||  |               |                        |                 |   |  || |   ||| |  |
        aagaaggagttcgaacgcaggtgtgggctaaataaatcaatgggcagtcttggtcctattgaaaataccaatgaagatccaaatcgaaaagtgaaaaaca
   7601 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 7700
        ttcttcctcaagcttgcgtccacacccgatttatttagttacccgtcagaaccaggataacttttatggttacttctaggtttagcttttcactttttgt

a         E  G  V  R  T  Q  V  W  A  K  *  I  N  G  Q  S  W  S  Y  *  K  Y  Q  *  R  S  K  S  K  S  E  K  H  -
b       K  K  E  F  E  R  R  C  G  L  N  K  S  M  G  S  L  G  P  I  E  N  T  N  E  D  P  N  R  K  V  K  N  I -
c        R  R  S  S  N  A  G  V  G  *  I  N  Q  W  A  V  L  V  L  L  K  I  P  M  K  I  Q  I  E  K  *  K  T   -

                        Tsp509I
                 Hpy188III    |
                    MaeIII    |                                               ApoI
                    Tsp45I    |    HpyCH4V                                 Tsp509I
        MnlI     HinfI   |    |    BsaXI |                                Hpy188I|
     BsaXI |      TfiI   |    | BfaI   | |                       MseI TspDTI    ||       Hpy188I
         | |         |   |    |    |   | |                          |       |   ||           |
        ttcatagttggaggaatcgtgacaattctagttgcagtaatgttgattatttattcggcgttaaagacattcggaatttcatctctgatgacactttttt
   7701 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 7800
        aagtatcaacctccttagcactgttaagatcaacgtcattacaactaataaataagccgcaatttctgtaagccttaaagtagagactactgtgaaaaaa

a        S  *  L  E  E  S  *  Q  F  *  L  Q  *  C  *  L  F  I  R  R  *  R  H  S  E  F  H  L  *  *  H  F  F   -
b         H  S  W  R  N  R  D  N  S  S  C  S  N  V  D  Y  L  F  G  V  K  D  I  R  N  F  I  S  D  D  T  F  L  -
c       F  I  V  G  G  I  V  T  I  L  V  A  V  M  L  I  I  Y  S  A  L  K  T  F  G  I  S  S  L  M  T  L  F  * -
```

Figure 21-EE

```
                                                                             BspCNI
                                                                            BseMII|
                                                                           BstKTI||
                                                                            DpnI|||  Hpy188I  BfaI
            BsmAI  HpyCH4III     BccI                                   MboI ||||    DdeI|Hpy8I  |
                |          |              |                                   | ||||       ||    |  |
     agttagtgataggaatggagacagttattccatctattttgatattgaaaatcatatttttgagattgacaacgatcattcttttctgagtgaactagaa
7801 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 7900
     tcaatcactatccttacctctgtcaataaggtagataaaactataacttttagtataaaaactctaactgttgctagtaagaaaagactcacttgatctt

a    S  *  *  *  E  W  R  Q  L  F  H  L  F  *  Y  *  K  S  Y  F  *  D  *  Q  R  S  F  F  S  E  *  T  R  K -
b     V  S  D  R  N  G  D  S  Y  S  I  Y  F  D  I  E  N  H  I  F  E  I  D  N  D  H  S  F  L  S  E  L  E  -
c      L  V  I  G  M  E  T  V  I  P  S  I  L  I  L  K  I  I  F  L  R  L  T  T  I  I  L  F  *  V  N  *  K -

                                                                                 NlaIII
                                                                                   NspI
                                                       BstKTI                   MmeI |
                                                         DpnI|              AflIII | |
               Tsp509I                                 BstYI ||  Tsp509I      FatI | |
            TaqI  TaqI | Hpy188I                  AlwI MboI  ||  MboII |      PciI | |
                |     || |         |                 |     | ||       ||         | | |
     agttctttttatagttatcgaaactcgaattatcggaataatggatttaggggcgaagatccctactataattcttacatgtatgatactcaatatagtt
7901 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 8000
     tcaagaaaaatatcaatagctttgagcttaatagccttattacctaaatccccgcttctagggatgatattaagaatgtacatactatgagttatatcaa

a       F  F  L  *  L  S  K  L  E  L  S  E  *  W  I  *  G  R  R  S  L  L  *  F  L  H  V  *  Y  S  I  *  L -
b    S  S  F  Y  S  Y  R  N  S  N  Y  R  N  N  G  F  R  G  E  D  P  Y  Y  N  S  Y  M  Y  D  T  Q  Y  S  W -
c     V  L  F  I  V  I  E  T  R  I  I  G  I  M  D  L  G  A  K  I  P  T  I  I  L  T  C  M  I  L  N  I  V  -

                                                                                                 BceAI
                                                                                             HpyCH4III
                                                                                                MaeIII
                                                                                         HpyCH4III   |
              HpyCH4V                                                                     MaeIII   |
           AseI Eco57I|    BsaBI                                                                    |
           MseI Eco57MI|MboII  |            BsmAI                  PsiI       Tsp509I Tsp45I   |
               |        ||   |   |             |                       |          |     |     |
     ggaataatcacattaatagttgcattgatagttatcttcagtctcaaatctgtatagatacttccattataagtggtagtgagaattacggtgacagtta
8001 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 8100
     ccttattagtgtaattatcaacgtaactatcaatagaagtcagagtttagacatatctatgaaggtaatattcaccatcactcttaatgccactgtcaat

a     E  *  S  H  *  *  L  H  *  *  L  S  S  V  S  N  L  Y  R  Y  F  H  Y  K  W  *  *  E  L  R  *  Q  L  -
b      N  N  H  I  N  S  C  I  D  S  Y  L  Q  S  Q  I  C  I  D  T  S  I  I  S  C  S  E  N  Y  G  D  S  Y -
c    G  I  I  T  L  I  V  A  L  I  V  I  F  S  L  K  S  V  *  I  L  P  L  *  V  V  V  R  I  T  V  T  V  T-

              CviJI                                                         Hpy8I                   MseI
             HaeIII                        HphI                          BsrI   |        HpyF10VI   BtsI|
         HphI Sau96I |                TaqI     |      MnlI           NlaIV |AccI|           MwoI|   TspRI|
            |      | |                    |    |       |            |  |   ||                ||        ||
     catttatagggccgtttgtggtggtgaaagtcgaaatagtagtgaaaacgagggttccagtagacgaactcgcacgaagggcagtgatttaactataaga
8101 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 8200
     gtaaatatcccggcaaacaccaccactttcagctttatcatcacttttgctcccaaggtcatctgcttgagcgtgcttcccgtcactaaattgatattct

a    H  L  *  G  R  L  W  W  *  K  S  K  *  *  *  K  R  G  F  Q  *  T  N  S  H  E  G  Q  *  F  N  Y  K  R -
b     I  Y  R  A  V  C  G  G  E  S  R  N  S  S  E  N  E  G  S  S  R  R  T  R  T  K  G  S  D  L  T  I  R  -
c      F  I  G  P  F  V  V  V  K  V  E  I  V  V  K  T  R  V  P  V  D  E  L  A  R  R  A  V  I  *  L  *  E -
```

Figure 21-FF

```
                    MaeIII
                  TaqI   |
                 AvaI|   |
            Hpy188III|   |
                 SmlI|   |
                 XhoI|   |
              BstKTI||   |
               DpnI|||   |                                                            ApoI
             MboI ||||   |                                               Tsp509I   Tsp509I
             MnlI ||||   |                                 Tsp509I        MseI | PsiI    |
                | ||||   |                                       |           | |    |    |
     gaaagttctaatgatctcgaggtaactcaaaaatacaggcatttgtgggttcaatgcgaaaattgttatggattaaattataagaaatttttgaaatcaa
8201 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 8300
     ctttcaagattactagagctccattgagtttttatgtccgtaaacacccaagttacgcttttaacaatacctaatttaatattctttaaaaactttagtt

a      K  F  *  *  S  R  G  N  S  K  I  Q  A  F  V  G  S  M  R  K  L  L  W  I  K  L  *  E  I  F  E  I  K  -
b    E  S  S  N  D  L  E  V  T  Q  K  Y  R  H  L  W  V  Q  C  E  N  C  Y  G  L  N  Y  K  K  F  L  K  S  K -
c     K  V  L  M  I  S  R  *  L  K  N  T  G  I  C  G  F  N  A  K  I  V  M  D  *  I  I  R  N  F  *  N  Q   -

                                                         ApoI
                                                        EcoRI
                 TspDTI                               Tsp509I       NlaIII   AluI
         SspI  Hpy8I  |    EcoRV                Hpy188I     |      FatI  |  CviJI        Tsp509I
            |      |  |        |                      |     |         |  |      |              |
     aaatgaatatttgtgaacaatgtggatatcatttgaaaatgagtagttcagatagaattcgtaatcatggtcatagctgtttcctgtgtgaaattgttat
8301 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 8400
     tttacttataaacacttgttacacctatagtaaactttttactcatcaagtctatcttaagcattagtaccagtatcgacaaaggacacactttaacaata

a     N  E  Y  L  *  T  M  W  I  S  F  E  N  E  *  F  R  *  N  S  *  S  W  S  *  L  F  P  V  *  N  C  Y   -
b      M  N  I  C  E  Q  C  G  Y  H  L  K  M  S  S  S  D  R  I  R  N  H  G  H  S  C  F  L  C  E  I  V  I  -
c    K  *  I  F  V  N  N  V  D  I  I  *  K  *  V  V  Q  I  E  F  V  I  M  V  I  A  V  S  C  V  K  L  L  S -

                                                          NlaIV
                                                      HpyF10VI|
                                                    BstNI    ||
                                                    ScrFI    ||                                   HpyF10VI
                                                   BsaJI|    ||                                      MwoI|
       Tsp509I                                    CviJI||    ||                   Tsp509I          BtsI ||
    BsrBI    |                HpaII               PspGI||BanI||          AluI       AseI|        HhaI | ||
   AciI |    |               CviJI|              StyD4I||MwoI||         CviJI       MseI|    HinP1I | | ||
      | |    |                   ||                   |||   |||             |          ||         | | | ||
     ccgctcacaattccacacaacatacgagccggaagcataaagtgtaaagcctggggtgcctaatgagtgagctaactcacattaattgcgttgcgctcac
8401 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 8500
     ggcgagtgttaaggtgtgttgtatgctcggccttcgtatttcacatttcggaccccacggattactcactcgattgagtgtaattaacgcaacgcgagtg

a    P  L  T  I  P  H  N  I  R  A  G  S  I  K  C  K  A  W  G  A  *  *  V  S  *  L  T  L  I  A  L  R  S  L -
b     R  S  Q  F  H  T  T  Y  E  P  E  A  *  S  V  K  P  G  V  P  N  E  *  A  N  S  H  *  L  R  C  A  H   -
c      A  H  N  S  T  Q  H  T  S  R  K  H  K  V  *  S  L  G  C  L  M  S  E  L  T  H  I  N  C  V  A  L  T  -
```

Figure 21-GG

```
                                                               AciI
                                                              BstUI
                                                               HhaI
                                                               MnlI
                                                              BslI|
                                             AseI           TspDTI|
                                             MseI           BstUI||
                                       HpyCH4V  |          HinPlI||
                                      Fnu4HI | |         BsaXI |||                        HaeII
                                       AluI| | |       FauI  | |||                        HhaI|
                                      CviJI| | |     CviJI|  | |||                     BsaXI ||
                                     MspA1I| | |    HaeIII|  | |||                    HinPlI ||
        AciI   Hpy188III              PvuII| | |    EaeI ||  | |||                HpyF10VI | || EarI
       Cac8I   BsrI    |               TseI| | |HinfI  | ||  | |||                   MwoI| | || SapI
       TspRI   FauI    |  BbvI      Cac8I || |  | TfiI  | ||  | |||      AciI       MboII|| | ||AciI|
           |      |    |     |          | || |  |    |  | ||  | |||         |           ||| | ||   ||
        tgcccgctttccagtcgggaaacctgtcgtgccagctgcattaatgaatcggccaacgcgcggggagaggcggtttgcgtattgggcgctcttccgcttc
   8501 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 8600
        acgggcgaaaggtcagccctttggacagcacggtcgacgtaattacttagccggttgcgcgcccctctccgccaaacgcataacccgcgagaaggcgaag

a         P  A  F  Q  S  G  N  L  S  C  Q  L  H  *  *  I  G  Q  R  A  G  R  G  G  L  R  I  G  R  S  S  A  S  -
b       C  P  L  S  S  R  E  T  C  R  A  S  C  I  N  E  S  A  N  A  R  G  E  A  V  C  V  L  G  A  L  P  L  P-
c        A  R  F  P  V  G  K  P  V  V  P  A  A  L  M  N  R  P  T  R  G  E  R  R  F  A  Y  W  A  L  F  R  F   -

                                                         AluI
                                                        CviJI
                                                  HpyF10VI  |
                         BbvI                   AciI     |  |
                         HhaI                  BsrBI     |  |
                     HinPlI |                Cac8I |     |  |
                   Fnu4HI | |               TauI | |     |  |
                    TseI| | |           Fnu4HI | | |     |  |
                TaqII  || | |            AciI| | | |     |  |
         MlyI   TspRI  || | |        Fnu4HI || | | |     |  |
         PleI HinfI |  || | |        CviJI| || | | |     |  |                           HinfI
       BbvI | MnlI| |  || | | BsiEI   TseI| || | | | MwoI|  |       AciI HpyCH4III       TfiI
          | |    || |  || | |     |      || || | | |    ||  |          |         |          |
        ctcgctcactgactcgctgcgctcggtcgttcggctgcggcgagcggtatcagctcactcaaaggcggtaatacggttatccacagaatcaggggataac
   8601 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 8700
        gagcgagtgactgagcgacgcgagccagcaagccgacgccgctcgccatagtcgagtgagtttccgccattatgccaataggtgtcttagtcccctattg

a        S  L  T  D  S  L  R  S  V  V  R  L  R  R  A  V  S  A  H  S  K  A  V  I  R  L  S  T  E  S  G  D  N   -
b         R  S  L  T  R  C  A  R  S  F  G  C  G  E  R  Y  Q  L  T  Q  R  R  *  Y  G  Y  P  Q  N  Q  G  I  T  -
c       L  A  H  *  L  A  A  L  G  R  S  A  A  A  S  G  I  S  S  L  K  G  G  N  T  V  I  H  R  I  R  G  *  R-
```

Figure 21-HH

```
                                               HpyCH4III              Cac8I
                                                NlaIV  |           HpyF10VI
                                            BstNI   |  |       BstUI      |
                                            ScrFI   |  |        TauI      |
                   NlaIII                 CviJI |   |  |      AciI |      |
                     NspI                HaeIII |   |  |    Fnu4HI |      |
               AflIII   |        Cac8I    PspGI |   |  |    CviJI| |      |               AciI
                 FatI   |      CviJI |   StyD4I |   |  |   HaeIII| |      |            NlaIV  |
                 PciI   |     HaeIII | BslI   | |   |  | BslI   || |  MwoI|    EciI    CviJI| |
                    |   |          | |    |   | |   |  |     |  || |     ||        |       || |
          gcaggaaagaacatgtgagcaaaaggccagcaaaaggccaggaaccgtaaaaaggccgcgttgctggcgtttttccataggctccgcccccctgacgagc
     8701 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 8800
          cgtcctttcttgtacactcgttttccggtcgttttccggtccttggcatttttccggcgcaacgaccgcaaaaaggtatccgaggcggggggactgctcg

a         A  G  K  N  M  *  A  K  G  Q  Q  K  A  R  N  R  K  K  A  A  L  L  A  F  F  H  R  L  R  P  P  D  E  H -
b          Q  E  R  T  C  E  Q  K  A  S  K  R  P  G  T  V  K  R  P  R  C  W  R  F  S  I  G  S  A  P  L  T  S    -
c           R  K  E  H  V  S  K  R  P  A  K  G  Q  E  P  *  K  G  R  V  A  G  V  F  P  *  A  P  P  P  *  R  A   -

                            Hpy188I
                            HgaI  |
                         DrdI  |  |                                                                MnlI
                         MnlI  |  |                                           BstNI              HhaI  |
                       SmlI  | |  |                              BstNI        ScrFI         HinPlI  | |
                    Hpy99I | | |  |                              ScrFI      BsaJI |      BssSI     | | |
                 TaqI     || | |  |                            PspGI |      PspGI |  AluI     |    | | |
       BpuEI SfaNI   |    || | |  |                           StyD4I |     StyD4I | CviJI     |    | | |
           |     |   |    || | |  |                                 ||          | |      |    |    | | |
          atcacaaaaatcgacgctcaagtcagaggtggcgaaacccgacaggactataaagataccaggcgtttccccctggaagctccctcgtgcgctctcctgt
     8801 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 8900
          tagtgttttagctgcgagttcagtctccaccgctttgggctgtcctgatatttctatggtccgcaaagggggaccttcgagggagcacgcgagaggaca

a           H  K  N  R  R  S  S  Q  R  W  R  N  P  T  G  L  *  R  Y  Q  A  F  P  P  G  S  S  L  V  R  S  P  V   -
b         I  T  K  I  D  A  Q  V  R  G  G  E  T  R  Q  D  Y  K  D  T  R  R  F  P  L  E  A  P  S  C  A  L  L  F -
c          S  Q  K  S  T  L  K  S  E  V  A  K  P  D  R  T  I  K  I  P  G  V  S  P  W  K  L  P  R  A  L  S  C    -

                         EciI
                        HpaII|
                       BsaWI||
                        BslI||
                   BciVI   |||
                    TauI|  |||                                  HaeII
                  AciI ||  |||      AciI                         HhaI|     AluI                        BseMII
      Hpy188I  Fnu4HI  ||  |||  MmeI    |     Hpy188III      HinPlI ||    CviJI   SfcI      DdeI       BspCNI|
             |       | ||  |||      |   |              |          | ||         |      |         |           ||
          tccgaccctgccgcttaccggatacctgtccgcctttctcccttcgggaagcgtggcgctttctcatagctcacgctgtaggtatctcagttcggtgtag
     8901 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 9000
          aggctgggacggcgaatggcctatggacaggcggaaagagggaagcccttcgcaccgcgaaagagtatcgagtgcgacatccatagagtcaagccacatc

a          P  T  L  P  L  T  G  Y  L  S  A  F  L  P  S  G  S  V  A  L  S  H  S  S  R  C  R  Y  L  S  S  V  *    -
b           R  P  C  R  L  P  D  T  C  P  P  F  S  L  R  E  A  W  R  F  L  I  A  H  A  V  G  I  S  V  R  C  R   -
c         S  D  P  A  A  Y  R  I  P  V  R  L  S  P  F  G  K  R  G  A  F  S  *  L  T  L  *  V  S  Q  F  G  V  G -
```

Figure 21-II

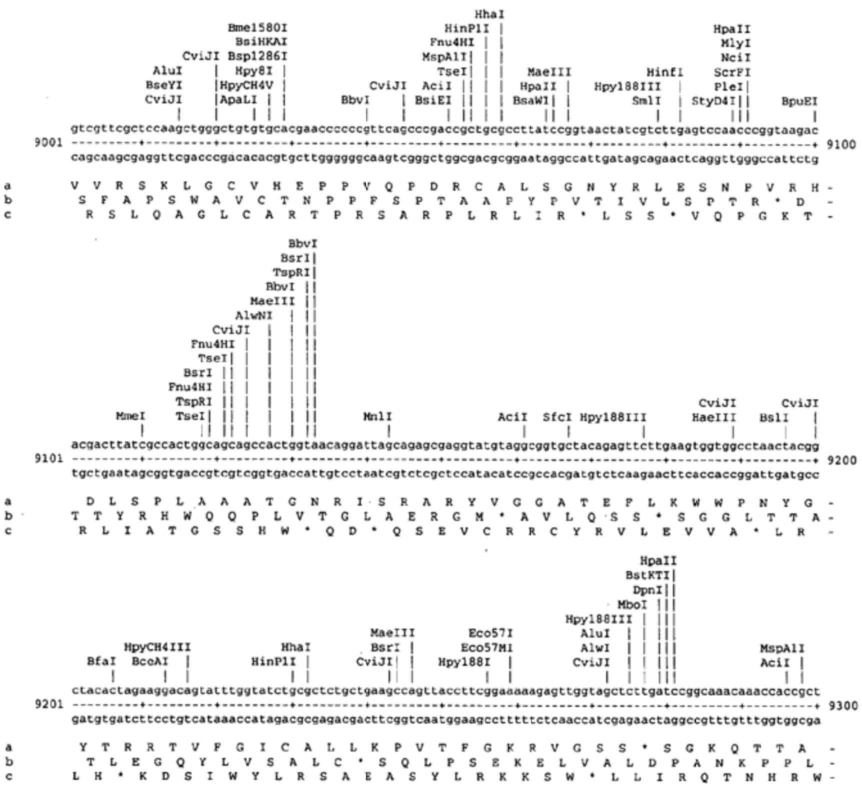

HhaI
Bme1580I
BsiHKAI
CviJI Bsp1286I
AluI Hpy8I
BseYI HpyCH4V
CviJI ApaLI
BbvI
CviJI
HinP1I
Fnu4HI
MspA1I
TseI
AciI
BsiEI
MaeIII
HpaII
BsaWI
Hpy188III
HinfI
SmlI
HpaII
MlyI
NciI
ScrFI
PleI
StyD4I
BpuEI
gtcgttcgctccaagctgggctgtgtgcacgaacccccgttcagcccgaccgctgcgccttatccggtaactatcgtcttgagtccaacccggtaagac
9001
9100
cagcaagcgaggttcgacccgacacacgtgcttgggggcaagtcgggctggcgacgcggaataggccattgatagcagaactcaggttgggccattctg
a V V R S K L G C V H E P P V Q P D R C A L S G N Y R L E S N P V R H -
b S F A P S W A V C T N P P F S P T A A P Y P V T I V L S P T R * D -
c R S L Q A G L C A R T P R S A R P L R L I R * L S S * V Q P G K T -
BbvI
BsrI
TspRI
BbvI
MaeIII
AlwNI
CviJI
Fnu4HI
TseI
BsrI
Fnu4HI
TspRI
MmeI TseI
MnlI
AciI SfcI Hpy188III
CviJI
HaeIII
BslI
CviJI
acgacttatcgccactggcagcagccactggtaacaggattagcagagcgaggtatgtaggcggtgctacagagttcttgaagtggtggcctaactacgg
9101
9200
tgctgaatagcggtgaccgtcgtcggtgaccattgtcctaatcgtctcgctccatacatccgccacgatgtctcaagaacttcaccaccggattgatgcc
a D L S P L A A A T G N R I S R A R Y V G G A T E F L K W W P N Y G -
b T T Y R H W Q Q P L V T G L A E R G M * A V L Q S S * S G G L T T A -
c R L I A T G S S H W * Q D * Q S E V C R R C Y R V L E V V A * L R -
HpaII
BstKTI
DpnI
MboI
Hpy188III
AluI
AlwI
CviJI
HpyCH4III
BfaI BccAI
HhaI
HinP1I
MaeIII
BsrI
CviJI
Eco57I
Eco57MI
Hpy188I
MspA1I
AciI
ctacactagaaggacagtatttggtatctgcgctctgctgaagccagttaccttcggaaaaagagttggtagctcttgatccggcaaacaaaccaccgct
9201
9300
gatgtgatcttcctgtcataaaccatagacgcgagacgacttcggtcaatggaagcctttttctcaaccatcgagaactaggccgtttgtttggtggcga
a Y T R R T V F G I C A L L K P V T F G K R V G S S * S G K Q T T A -
b T L E G Q Y L V S A L C * S Q L P S E K E L V A L D P A N K P P L -
c L H * K D S I W Y L R S A E A S Y L R K K S W * L L I R Q T N H R W -

Figure 21-JJ

```
                                                                 BstKTI
                                                                  DpnI|
                                                               BstYI ||
                                                                MboI ||
                                                             AlwI  | ||
                                         BpuEI             AlwI |  | ||
                                          HhaI        Hpy188III |  | ||
                                        BbvI |           SmlI | |  | ||
                           Fnu4HI      BstUI |        BstKTI| | |  | ||  BstKTI
                            TseI|     HinP1I |         DpnI|| | |  | ||   DpnI|                 DdeI
                         Cac8I || HpyF10VI | |      BstYI ||| | |  | ||  MboII|                PpiI|
      AciI           HpyCH4V | ||    MwoI| | |       MboI ||| | |  | || MboI ||         Hpy188I   || HgaI
         |                 | | ||       || | |          | ||| | |  | ||    | ||               |   ||    |
     ggtagcggtggtttttttgtttgcaagcagcagattacgcgcagaaaaaaaggatctcaagaagatcctttgatcttttctacggggtctgacgctcagt
9301 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 9400
     ccatcgccaccaaaaaaacaaacgttcgtcgtctaatgcgcgtcttttttttcctagagttcttctaggaaactagaaaagatgccccagactgcgagtca

a    G  S  G  G  F  F  V  C  K  Q  Q  I  T  R  R  K  K  G  S  Q  E  D  P  L  I  F  S  T  G  S  D  A  Q  W -
b     V  A  V  V  F  L  F  A  S  S  R  L  R  A  E  K  K  D  L  K  K  I  L  *  S  F  L  R  G  L  T  L  S   -
c      *  R  W  F  F  C  L  Q  A  A  D  Y  A  Q  K  K  R  I  S  R  R  S  P  D  L  F  Y  G  V  *  R  S  V  -

                                                               BstKTI
                  MseI                             BstKTI       DpnI|
                  TaiI                              DpnI|    BstYI ||
           HpyCH4IV  |            NlaIII         BstYI ||     MboI ||      MseI
        BseMII    |  |      Hpy188III  |          MboI ||   BfaI | ||Tsp509I  |
       BspCNI|    |  |         BspHI|  |        HphI | || AlwI | | ||  DraI|  |           DraI
   TspRI    ||    |  |     PpiI FatI|  |    MboII  | | ||AlwI| | | || MseI||  |          MseI|TspDTI
       |    ||    |  |        |    ||  |        |  | | ||   || | | ||    |||  |             ||     |
     ggaacgaaaactcacgttaagggattttggtcatgagattatcaaaaaggatcttcacctagatccttttaaattaaaaatgaagttttaaatcaatcta
9401 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 9500
     ccttgcttttgagtgcaattccctaaaaccagtactctaatagtttttcctagaagtggatctaggaaaatttaatttttacttcaaaatttagttagat

a      N  E  N  S  R  *  G  I  L  V  M  R  L  S  K  R  I  F  T  *  I  L  L  N  *  K  *  S  F  K  S  I  *  -
b    G  T  K  T  H  V  K  G  F  W  S  *  D  Y  Q  K  G  S  S  P  R  S  F  *  I  K  N  E  V  L  N  Q  S  K -
c     E  R  K  L  T  L  R  D  F  G  H  E  I  I  K  K  D  L  H  L  D  P  F  K  L  K  M  K  F  *  I  N  L   -

                                                                          BseMII
                                                                         BspCNI|
                                                                       TspDTI ||
                                                                         FokI | ||
                         HpyCH4III                    NlaIV         BstKTI| | ||              MlyI
                            MaeIII          MnlI     BanI |          DpnI|| | ||              PleI
               Hpy8I   Hpy188I   |        MseI |    TspRI |   DdeI MboI ||| | ||  BstF5I  Hin4I  | HinfI
                   |         |   |           | |        | |      |    | ||| | ||       |      |  |     |
     aagtatatatgagtaaacttggtctgacagttaccaatgcttaatcagtgaggcacctatctcagcgatctgtctatttcgttcatccatagttgcctga
9501 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 9600
     ttcatatatactcatttgaaccagactgtcaatggttacgaattagtcactccgtggatagagtcgctagacagataaagcaagtaggtatcaacggact

a     S  I  Y  E  *  T  W  S  D  S  Y  Q  C  L  I  S  E  A  P  I  S  A  I  C  L  F  R  S  S  I  V  A  *   -
b      V  Y  M  S  K  L  G  L  T  V  T  N  A  *  S  V  R  H  L  S  Q  R  S  V  Y  F  V  H  P  *  L  P  D  -
c    K  Y  I  *  V  N  L  V  *  Q  L  P  M  L  N  Q  *  G  T  Y  L  S  D  L  S  I  S  F  I  H  S  C  L  T -
```

Figure 21-KK

```
                                                       BsrI                    BpmI
                                                     BccI |                 Eco57MI
                                                    NlaIV |              BstUI    |
                                                   CviJI| |             AciI |    |        Hpy188III
                                                  HaeIII| | HpyCH4V   BsaI | |    |          NlaIV |
                                                 Sau96I|| |  TspRI|  BsmAI | |    |         CviJI| |
             Hpy99I          MnlI                BmrI ||| |Fnu4HI||  BsrDI | |    |    HpaII    || |
         AhdI      |      Hin4I |      CviJI   BbvI | ||| | TseI||| Hin4I| | | HphI    BsrFI|   || |Hin4I
            |      |          | |          |      | | ||| |    ||||      ||| |    |         ||  || |    |
         ctccccgtcgtgtagataactacgatacgggagggcttaccatctggccccagtgctgcaatgataccgcgagacccacgctcaccggctccagatttat
    9601 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 9700
         gaggggcagcacatctattgatgctatgccctcccgaatggtagaccggggtcacgacgttactatggcgctctgggtgcgagtggccgaggtctaaata

a        L  P  V  V  *  I  T  T  I  R  E  G  L  P  S  G  P  S  A  A  M  I  P  R  D  P  R  S  P  A  P  D  L  S -
b         S  P  S  C  R  *  L  R  Y  G  R  A  Y  H  L  A  P  V  L  Q  *  Y  R  E  T  H  A  H  R  L  Q  I  Y  -
c          P  R  R  V  D  N  Y  D  T  G  G  L  T  I  W  P  Q  C  C  N  D  T  A  R  P  T  L  T  G  S  R  F  I -

                                       HhaI
                                   HinP1I |
                               CviJI    | |
                              HaeIII    | |
                          HpyF10VI |    | |
                       HpaII     | |    | |             FokI                   Tsp509I     NciI
                      CviJI|Sau96I |    | |       HpyCH4V  |                   BccI  |    ScrFI   BfaI
                    Cac8I || BglI| |    | |   AvaII     |  |       BstF5I   MnlI|AseI|    HpaII|  AluI|
                  CviJI | || MwoI| |    | |  Sau96I EciI|  |   AciI     |BsrI  ||MseI|  StyD4I|| CviJI|
                      | | ||    || |    | |       |    ||  |      |     |   |  ||   ||       |||     ||
         cagcaataaaccagccagccggaagggccgagcgcagaagtggtcctgcaactttatccgcctccatccagtctattaattgttgccgggaagctagagt
    9701 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 9800
         gtcgttatttggtcggtcggccttcccggctcgcgtcttcaccaggacgttgaaataggcggaggtaggtcagataattaacaacggcccttcgatctca

a          A  I  N  Q  P  A  G  R  A  E  R  R  S  G  P  A  T  L  S  A  S  I  Q  S  I  N  C  C  R  E  A  R  V -
b        Q  Q  *  T  S  Q  P  E  G  P  S  A  E  V  V  L  Q  L  Y  P  P  P  S  S  L  L  I  V  A  G  K  L  E  * -
c         S  N  K  P  A  S  R  K  G  R  A  Q  K  W  S  C  N  F  I  R  L  H  P  V  Y  *  L  L  P  G  S  *  S  -

                                      TaiI
                                   AclI  |                                                              NlaIV
                               HpyCH4IV  |                     MaeIII                              HpaII   |
                                HhaI  |  |                      SfaNI                             BsaWI|   |
                    MseI       FspI|  |  |                     Tsp45I         TspDTI              AluI ||   |
                BsrI   |    HinP1I||  |  | BsrDI  SfcI       MslI   |       Hpy99I |   CviJI     CviJI ||   |
                   |   |         |||  |  |     |     |          |   |            | |       |         | ||   |
         aagtagttcgccagttaatagtttgcgcaacgttgttgccattgctacaggcatcgtggtgtcacgctcgtcgtttggtatggcttcattcagctccggt
    9801 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 9900
         ttcatcaagcggtcaattatcaaacgcgttgcaacaacggtaacgatgtccgtagcaccacagtgcgagcagcaaaccataccgaagtaagtcgaggcca

a         S  S  S  P  V  N  S  L  R  N  V  V  A  I  A  T  G  I  V  V  S  R  S  S  F  G  M  A  S  F  S  S  G  -
b          V  V  R  Q  L  I  V  C  A  T  L  L  P  L  L  Q  A  S  W  C  H  A  R  R  L  V  W  L  H  S  A  P  V -
c        K  *  F  A  S  *  *  F  A  Q  R  C  C  H  C  Y  R  H  R  G  V  T  L  V  V  W  Y  G  F  I  Q  L  R  F -
```

Figure 21-LL

```
                                                                                    Hpy188I
                                                                                  MnlI    |
                              BstKTI                                          BsiEI  |    |
                               DpnI|                                         BstKTI  |    |           TauI
                            NlaIII||                                           PvuI  |    |         AciI |
                             MboI|||                         AluI             DpnI|  |    |       Fnu4HI |
            BstKTI        FatI  ||||      HpyCH4V           CviJI        Hpy188I ||  |    |       CviJI| |
             DpnI|      AlwI |  ||||  NlaIII    |       TaqII   |   AvaII      | ||  |    |      HaeIII| |
           MboI ||  MaeIII | |  ||||FatI   |    |     AciI  |   |  Sau96I   MboI ||  |    |      EaeI || |
              | ||       | | |  ||||   |   |    |        |  |   |       |      | ||  |    |         | || |
        tcccaacgatcaaggcgagttacatgatcccccatgttgtgcaaaaaagcggttagctccttcggtcctccgatcgttgtcagaagtaagttggccgcag
   9901 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 10000
        agggttgctagttccgctcaatgtactagggggtacaacacgttttttcgccaatcgaggaagccaggaggctagcaacagtcttcattcaaccggcgtc

a       S  Q  R  S  R  R  V  T  *  S  P  M  L  C  K  K  A  V  S  S  F  G  P  P  I  V  V  R  S  K  L  A  A  V -
b        P  N  D  Q  G  E  L  H  D  P  P  C  C  A  K  K  R  L  A  P  S  V  L  R  S  L  S  E  V  S  W  P  Q   -
c         P  T  I  K  A  S  Y  M  I  P  H  V  V  Q  K  S  G  *  L  L  R  S  S  D  R  C  Q  K  *  V  G  R  S  -

                                     BbvI             BstF5I
                                 Tsp509I|              SfaNI
                                  TspRI||          NlaIII|                            RsaI
                              HpyCH4V |||       FatI   ||                             ScaI
                   MslI     BtsI    | |||   HpyCH4III |   ||                          Csp6I|   BspCNI
        BtsI    NlaIII| Fnu4HI |    | |||      TspGWI |   ||             MaeIII       TatI||  BseMII|
       TspRI  FatI   ||  TseI| |    | ||| FokI      | |   ||   BccI      Tsp45I     BsrI |||  HphI ||
           |     |   ||     || |    | |||    |      | |   ||      |           |        | |||     | ||
        tgttatcactcatggttatggcagcactgcataattctcttactgtcatgccatccgtaagatgcttttctgtgactggtgagtactcaaccaagtcatt
  10001 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 10100
        acaatagtgagtaccaataccgtcgtgacgtattaagagaatgacagtacggtaggcattctacgaaaagacactgaccactcatgagttggttcagtaa

a         L  S  L  M  V  M  A  A  L  H  N  S  L  T  V  M  P  S  V  R  C  F  S  V  T  G  E  Y  S  T  K  S  F  -
b       C  Y  H  S  W  L  W  Q  H  C  I  I  L  L  L  S  C  H  P  *  D  A  F  L  *  L  V  S  T  Q  P  S  H  S -
c        V  I  T  H  G  Y  G  S  T  A  *  F  S  Y  C  H  A  I  R  K  M  L  F  C  D  W  *  V  L  N  Q  V  I   -

                                               BcgI
                                            BsaHI |
                                         HpaII  | |
                                          NciI  | |
                          BsiEI          ScrFI  | |                 HhaI
                       TauI   |         TaqII|  | |              BstUI |
   Hpy188I         Fnu4HI |   |       StyD4I||  | |             HinP1I |             DraI  BsiHKAI
     DdeI|   BcgI   AciI| |   |   HgaI     |||  | |             AciI | |            MseI| Bsp1286I    MboII
        ||      |      || |   |      |     |||  | |                |  | |               ||        |        |
        ctgagaatagtgtatgcggcgaccgagttgctcttgcccggcgtcaatacgggataataccgcgccacatagcagaactttaaaagtgctcatcattgga
  10101 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 10200
        gactcttatcacatacgccgctggctcaacgagaacgggccgcagttatgccctattatggcgcggtgtatcgtcttgaaattttcacgagtagtaacct

a        *  E  *  C  M  R  R  P  S  C  S  C  P  A  S  I  R  D  N  T  A  P  H  S  R  T  L  K  V  L  I  I  G   -
b         E  N  S  V  C  G  D  R  V  A  L  A  R  R  Q  Y  G  I  I  P  R  H  I  A  E  L  *  K  C  S  S  L  E  -
c       L  R  I  V  Y  A  A  T  E  L  L  L  P  G  V  N  T  G  *  Y  R  A  T  *  Q  N  F  K  S  A  H  H  W  K -
```

Figure 21-MM

```
                                                                                   MboII
                                                                              Bme1580I |
                                                                               BsiHKAI |
                                                                              Bsp1286I |
                                                                               Hpy8I | |
                                                                             HpyCH4V | |
               BpuEI                            AlwI     BsrI                ApaLI | | |
             TaiI  |                 BstKTI MspA1I |  BstKTI|               Eco57I | | |
          AclI  |  |                  DpnI| AciI | |   DpnI||              Eco57MI | | |  BstKTI
      HpyCH4IV  |  |               BstYI || AlwI | |BstYI |||   MaeIII    BssSI  | | | |   DpnI|          SfaNI
          XmnI  |  |           SmlI MboI ||PpiI| | | MboI |||TaqI    |      PpiI  | | | | MboI ||TaqII  HphI   |
             |  |  |              |    | ||   || | |    | |||    |   |        |  | | | |    | ||    |     |   |
           aaacgttcttcggggcgaaaactctcaaggatcttaccgctgttgagatccagttcgatgtaacccactcgtgcacccaactgatcttcagcatctttta
     10201 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 10300
           tttgcaagaagccccgcttttgagagttcctagaatggcgacaactctaggtcaagctacattgggtgagcacgtgggttgactagaagtcgtagaaaat

a          K  R  S  S  G  R  K  L  S  R  I  L  P  L  L  R  S  S  S  M  *  P  T  R  A  P  N  *  S  S  A  S  F  T -
b           N  V  L  R  G  E  N  S  Q  G  S  Y  R  C  *  D  P  V  R  C  N  P  L  V  H  P  T  D  L  Q  H  L  L   -
c            T  F  F  G  A  K  T  L  K  D  L  T  A  V  E  I  Q  F  D  V  T  H  S  C  T  Q  L  I  F  S  I  F  Y  -

                                                       TauI
                                                     AciI |                                 MboII
             TaqII                    HphI         Fnu4HI |                      MslI      TspGWI         EarI
                 |                       |              | |                         |           |            |
           ctttcaccagcgtttctgggtgagcaaaaacaggaaggcaaaatgccgcaaaaaagggaataagggcgacacggaaatgttgaatactcatactcttcct
     10301 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 10400
           gaaagtggtcgcaaagacccactcgtttttgtccttccgttttacggcgttttttcccttattcccgctgtgcctttacaacttatgagtatgagaagga

a            F  T  S  V  S  G  *  A  K  T  G  R  Q  N  A  A  K  K  G  I  R  A  T  R  K  C  *  I  L  I  L  F  L  -
b          L  S  P  A  F  L  G  E  Q  K  Q  E  G  K  M  P  Q  K  R  E  *  G  R  H  G  N  V  E  Y  S  Y  S  S  F -
c           F  H  Q  R  F  W  V  S  K  N  R  K  A  K  C  R  K  K  G  N  K  G  D  T  E  M  L  N  T  H  T  L  P   -

                                                    AciI
                                                   BsrBI
                                                NlaIII |
                                               BciVI | |                                               HhaI
                                               BsmAI | |                                            BstUI |
                                          Hpy188III| | |                                          HinP1I  |
                                             BspHI|| | |                                           AciI  ||
               SspI                           FatI|| | |                                       NlaIV    |||
                  |                              ||| | |                                             |  |||
           ttttcaatattattgaagcatttatcagggttattgtctcatgagcggatacatatttgaatgtatttagaaaaataaacaaataggggttccgcgcaca
     10401 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 10500
           aaaagttataataacttcgtaaatagtcccaataacagagtactcgcctatgtataaacttacataaatctttttatttgtttatccccaaggcgcgtgt

a           F  Q  Y  Y  *  S  I  Y  Q  G  Y  C  L  M  S  G  Y  I  F  E  C  I  *  K  N  K  Q  I  G  V  P  R  T   -
b            F  N  I  I  E  A  F  I  R  V  I  V  S  *  A  D  T  Y  L  N  V  F  R  K  I  N  K  *  G  F  R  A  H  -
c          F  S  I  L  L  K  H  L  S  G  L  L  S  H  E  R  I  H  I  *  M  Y  L  E  K  *  T  N  R  G  S  A  H  I -
```

Figure 21-NN

```
                                                                                     CviJI
                                DdeI                                                HaeIII
                              AatII|                                              EcoO109I|
                               TaiI|               NlaIII                           Sau96I|
                             ZraI ||         Hpy188III  |                      BssSI    ||
                        BsaHI| ||              BspHI|  |                Hpy188III    ||
                     HpyCH4IV| ||               FatI|  |MseI               MnlI   |    ||
                               || ||                || |   |                  |   |    ||
         tttccccgaaaagtgccacctgacgtctaagaaaccattattatcatgacattaacctataaaaataggcgtatcacgaggccctttcgtc
   10501 ---------+---------+---------+---------+---------+---------+---------+---------+---------+- 10591
         aaaggggcttttcacggtggactgcagattctttggtaataatagtactgtaattggatatttttatccgcatagtgctccgggaaagcag

a        F  P  R  K  V  P  P  D  V  *  E  T  I  I  I  M  T  L  T  Y  K  N  R  R  I  T  R  P  F  R    -
b         F  P  E  K  C  H  L  T  S  K  K  P  L  L  S  *  H  *  P  I  K  I  G  V  S  R  G  P  F  V   -
c          S  P  K  S  A  T  *  R  L  R  N  H  Y  Y  H  D  I  N  L  *  K  *  A  Y  H  E  A  L  S     -

Enzymes that do cut and were not excluded:

      AarI     AatII      AccI    Acc65I      AciI      AclI      AfeI    AflIII      AgeI      AhdI      AluI      AlwI     AlwNI
      ApaI     ApaLI      ApoI      AseI      AvaI     AvaII     AvrII      BaeI     BamHI      BanI     BanII      BbeI      BbsI
      BbvI      BccI     BceAI      BcgI     BciVI      BclI      BfaI     BfrBI      BglI     BglII      BlpI  Bme1580I     BmgBI
      BmrI      BpmI    Bpu10I     BpuEI      BsaI     BsaAI     BsaBI     BsaHI     BsaJI     BsaWI     BsaXI    BseMII     BseRI
     BseYI      BsgI     BsiEI   BsiHKAI      BslI      BsmI     BsmAI     BsmBI     BsmFI  Bsp1286I    BspCNI     BspHI     BspMI
      BsrI     BsrBI     BsrDI     BsrFI     BsrGI    BssHII     BssSI    BstAPI     BstBI    BstEII    BstF5I    BstKTI     BstNI
     BstUI     BstXI     BstYI    Bsu36I      BtgI      BtsI     Cac8I      ClaI     Csp6I     CviJI      DdeI      DpnI      DraI
    DraIII      DrdI      EaeI      EagI      EarI      EciI    Eco57I   EcoICRI   Eco57MI     EcoNI  EcoO109I     EcoRI     EcoRV
      FalI      FatI      FauI    Fnu4HI      FokI      FspI     HaeII    HaeIII      HgaI      HhaI     Hin4I    HinP1I    HincII
   HindIII     HinfI      HpaI     HpaII      HphI     Hpy8I    Hpy99I   Hpy188I Hpy188III HpyCH4III  HpyCH4IV   HpyCH4V  HpyF10VI
      KasI      KpnI    MaeIII      MboI     MboII      MfeI      MlyI      MmeI      MnlI      MscI      MseI      MslI    MspA1I
      MwoI      NaeI      NarI      NciI      NcoI      NdeI    NgoMIV    NlaIII     NlaIV      NotI      NruI      NsiI      NspI
      PacI      PciI      PfoI      PleI      PpiI     PpuMI      PsiI     PspGI    PspOMI      PstI      PvuI     PvuII      RsaI
      SacI     SacII      SalI      SapI    Sau96I      ScaI     ScrFI     SexAI     SfaNI      SfcI      SfoI      SmaI      SmlI
     SnaBI      SpeI      SphI      SspI      StyI    StyD4I      TaiI      TaqI     TaqII      TatI      TauI      TfiI      TseI
    Tsp45I   Tsp509I    TspDTI    TspGWI     TspRI      XbaI      XcmI      XhoI      XmaI      XmnI      ZraI

Enzymes that do not cut:

     AflII      AleI      AloI      AscI     AsiSI     BbvCI      BmtI      BplI     BsiWI     BspEI   BstZ17I      FseI     FspAI
      MluI      NheI     PflMI      PmeI      PmlI     PshAI      PsrI     RsrII     SanDI      SbfI      SfiI     SgrAI      SrfI
      StuI      SwaI   Tth111I

Enzymes excluded; MinCuts: 1  MaxCuts: 100000
```

Figure 22-A

pCV6 sequence

```
tcgcgcgttt cggtgatgac ggtgaaaacc tctgacacat gcagctcccg gagacggtca 60
cagcttgtct gtaagcggat gccgggagca gacaagcccg tcagggcgcg tcagcgggtg 120
ttggcgggtg tcggggctgg cttaactatg cggcatcaga gcagattgta ctgagagtgc 180
accatatgcg gtgtgaaata ccgcacagat gcgtaaggag aaaataccgc atcaggcgcc 240
attcgccatt caggctgcgc aactgttggg aagggcgatc ggtgcgggcc tcttcgctat 300
tacgccagct ggcgaaaggg ggatgtgctg caaggcgatt aagttgggta acgccagggt 360
tttcccagtc acgacgttgt aaaacgacgg ccagtgccaa gcttgaaaga gataaattga 420
acaagtatgg tcgtcccctg ttgggatgta ctattaaacc taaattgggg ttatctgcta 480
aaaactacgg tagagccgtt tatgaatgtc ttcgcggtgg acttgatttt actaaagatg 540
atgagaacgt gaactcacaa ccatttatgc gttggagaga tcgtttctta ttttgtgccg 600
aagcacttta taaagcacag gctgaaacag gtgaaatcaa agggcattac ttgaatgcta 660
ctgcaggtac atgcgaagaa atgatcaaaa gagctgtatt tgctagagaa ttgggcgttc 720
cgatcgtaat gcatgactac ttaacggggg gattcaccgc aaatactagc ttggctcatt 780
attgccgaga taatggtcta cttcttcaca tccaccgtgc aatgcatgcg gttattgata 840
gacagaagaa tcatggtatc cacttccggg tattagcaaa agcgttacgt atgtctggtg 900
gagatcatat tcactctggt accgtagtag gtaaacttga aggtgaaaga gacataactt 960
tgggctttgt tgatttactg cgtgatgatt ttgttgaaca agatcgaagt cgcggtattt 1020
atttcactca agattgggtc tctttaccag gtgttctacc cgtggcttca ggaggtattc 1080
acgtttggca tatgcctgct ctgaccgaga tctttgggga tgattccgta ctacagttcg 1140
gtggaggaac tttaggacat ccttggggta atgcgccagg tgccgtagct aatcgagtag 1200
ctctagaagc atgtgtaaaa gctcgtaatg aaggacgtga tcttgctcag gaaggtaatg 1260
aaattattcg cgaggcttgc aaatggagcc cggaactagc tgctgcttgt gaagtatgga 1320
aagagatcgt atttaatttt gcagcagtgg acgttttgga taagtaaaaa cagtagacat 1380
tagcagataa attagcagga aataaagaag gataaggaga aagaactcaa gtaattatcc 1440
ttcgttctct taattgaatt gcaattaaac tcggcccaat cttttactaa aaggattgag 1500
ccgaatacaa caaagattct attgcatata ttttgactaa gtatatactt acctagatat 1560
acaagatttg aaatacaaaa tctagaaaac taaatcaaaa tctaagactc aaatctttct 1620
attgttgtct tggatcatcg agcttgcatg cctgcagtcg actttcacag tttccattct 1680
gaaatgttct ctgtactata ataaatagta agtgaatcaa cttactacta aaaaaattag 1740
tagacttcct cttcggaata gaaatagcct atttctacat agggaaagtc gtgtgcaatg 1800
aaaaatgcaa gcacgatttg gggagaggtt ttttctctat tgtaacaagg aataattatc 1860
tactccatcc gactagttcc gggttcgagt cccgggcaac ccatatggaa actagaaagg 1920
agcaatctga gttttgattt ttcactcact tcatttacaa aatttttttgg tttggtaaat 1980
tttgttgtat ggatatacaa ctgtcggggc tggcttggtt gacattggta tatagtctat 2040
attatactgt taaataacaa gccttctatt atctttctag ttaatacgtg tgcttgggag 2100
tccttgcaat ttgaataaac caagatctta ccatggccgc gcggggttct catcatcatc 2160
atcatggtcc gcgggggccc gctagtggta gtgaccttga ccggtgcacc acttttgatg 2220
atgttcaagc tcctaattac actcaacata cttcatctat gaggggggtt tactatcctg 2280
atgaaatttt tagatcagac actctttatt taactcagga tttatttctt ccatttttatt 2340
ctaatgttac agggtttcat actattaatc atacgtttgg caaccctgtc ataccttttta 2400
aggatggtat ttattttgct gccacagaga aatcaaatgt tgtccgtggt tgggtttttg 2460
gttctaccat gaacaacaag tcacagtcgg tgattattat taacaattct actaatgttg 2520
ttatacgagc atgtaacttt gaattgtgtg acaacccttt ctttgctgtt tctaaaccca 2580
tgggtacaca gacacatact atgatattcg ataatgcatt taattgcact ttcgagtaca 2640
tatctgatgc cttttcgctt gatgtttcag aaaagtcagg taattttaaa cacttacgag 2700
agtttgtgtt taaaaataaa gatgggtttc tctatgttta taagggctat caacctatag 2760
atgtagttcg tgatctacct tctggtttta acactttgaa acctattttt aagttgcctc 2820
ttggtattaa cattacaaat tttagagcca ttcttacagc cttttcacct gctcaagaca 2880
```

Figure 22-B

```
tttggggcac gtcagctgca gcctattttg ttggctattt aaagccaact acatttatgc 2940
tcaagtatga tgaaaatggt acaatcacag atgctgttga ttgttctcaa aatccacttg 3000
ctgaactcaa atgctctgtt aagagctttg agattgacaa aggaatttac cagacctcta 3060
atttcagggt tgttccctca ggagatgttg tgagattccc taatattaca aacttgtgtc 3120
cttttggaga ggtttttaat gctactaaat tcccttctgt ctatgcatgg gagagaaaaa 3180
aaatttctaa ttgtgttgct gattactctg tgctctacaa ctcaacattt ttttcaacct 3240
ttaagtgcta tggcgtttct gccactaagt tgaatgatct ttgcttctcc aatgtctatg 3300
cagattcttt tgtagtcaag ggagatgatg taagacaaat agcgccagga caaactggtg 3360
ttattgctga ttataattat aaattgccag atgatttcat gggttgtgtc cttgcttgga 3420
atactaggaa cattgatgct acttcaactg gtaattataa ttataaatat aggtatctta 3480
gacatggcaa gcttaggccc tttgagagag acatatctaa tgtgcctttc tcccctgatg 3540
gcaaaccttg caccccacct gctcttaatt gttattggcc attaaatgat tatggttttt 3600
acaccactac tggcattggc taccaacctt acagagttgt agtactttct tttgaacttt 3660
taaatgcacc ggccacggtt tgtggaccaa aattatccac tgaccttatt aagaaccagt 3720
gtgtcaattt taattttaat ggactcactg gtactggtgt gttaactcct tcttcaaaga 3780
gatttcaacc atttcaacaa tttggccgtg atgtttctga tttcactgat tccgttcgag 3840
atcctaaaac atctgaaata ttagacattt caccttgctc ttttgggggt gtaagtgtaa 3900
ttacacctgg aacaaatgct tcatctgaag ttgctgttct atatcaagat gttaactgca 3960
ctgatgtttc tacagcaatt catgcagatc aactcacacc agcttggcgc atatattcta 4020
ctggaaacaa tgtattccag actcaagcag gctgtcttat aggagctgag catgtcgaca 4080
cttcttatga gtgcgacatt cctattggag ctggcatttg tgctattacc atacagttag 4140
actagaaaag ggcgaattct gcagatatcc atcacactgg cggccgcatc gatgagctct 4200
aattaattaa ggcttttctg ctaacatata gcaattttttg aagaaaggaa agctagaaat 4260
acccaatatc ttgctgaagc aagatattgg gtatttcttt ttttttatt ttgaatcttt 4320
ctattctgaa ttcagttaac gacgagattt agtatccttt cttgcacttt cataactcgt 4380
gaaatgccga gttggtacga attcccccaa tttgcgacct accataggat ttgttatgta 4440
aataggtata tgttcctttc cattatgaat cgcgattgta tggccaacca ttgcgggtag 4500
aatgctagat gcccgggacc acgttactat tgtttctttc tcctccttca tattgagctt 4560
ttctattttt gccaataaat gatggtacct ccccccgcca cgatcgaacg ggaatggata 4620
agaggcttgt gggattgacg tgatagggta gggttggcta tactgctggt ggcgaactcc 4680
aggctaataa tctgaagcgc ttggaagttg tagggaggat ccatggcaga caacggtact 4740
attaccgttg aggagcttaa acaactcctg gaacaatgga acctagtaat aggtttccta 4800
ttcctagcct ggattatgtt actacaattt gcctattcta atcggaacag gtttttgtac 4860
ataataaagc ttgttttcct ctggctcttg tggccagtaa cacttgcttg ttttgtgctt 4920
gctgttgtct acagaattaa ttgggtgact ggcgggattg cgattgcaat ggcttgtatt 4980
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attgtgacca gaccgctcat ggaaagtgaa cttgtcattg gtgctgtgat cattcgtggt 5160
cacttgcgaa tggccggaca ctccctaggg cgctgtgaca ttaaggacct gccaaaagag 5220
atcactgtgg ctacatcacg aacgctttct tattacaaat taggagcgtc gcagcgtgta 5280
ggcactgatt caggttttgc tgcatacaac cgctaccgta ttggaaacta taaattaaat 5340
acagaccacg ccggtagcaa cgacaatatt gctttgctag tacagtaaga attcaagccg 5400
aattccagca cactggcggc cgttactagt ggatccgagc tctaattaat taaggctttt 5460
ctgctaacat atagcaattt ttgaagaaag gaaagctaga aatacccaat atcttgctga 5520
agcaagatat tgggtatttc tttttttttt attttgaatc tttctattct gaattcagtt 5580
aacgacgaga tttagtatcc tttcttgcac tttcataact cgtgaaatgc cgagttggta 5640
cgaattcccc caatttgcga cctaccatag gatttgttat gtaaataggt atatgttcct 5700
ttccattatg aatcgcgatt gtatggccaa ccattgcggg tagaatgcta gatgcccggg 5760
accacgttac tattgtttct ttctcctcct tcatattgag cttttctatt tttgccaata 5820
aatgatggta cctccccccg ccacgatcga acgggaatgg ataagaggct tgtgggattg 5880
acgtgatagg gtagggttgg ctatactgct ggtggcgaac tccaggctaa taatctgaag 5940
cgcttggaag ttgtagggag gatcctatgg ctcgtgaagc ggttatcgcc gaagtatcga 6000
ctcaactatc agaggtagtt ggcgtcatcg agcgccatct cgaaccgacg ttgctggccg 6060
```

Figure 22-C

```
tacatttgta cggctccgca gtggatggcg gcctgaagcc acacagtgat attgatttgc 6120
tggttacggt gaccgtaagg cttgatgaaa caacgcggcg agctttgatc aacgaccttt 6180
tggaaacttc ggcttcccct ggagagagcg agattctccg cgctgtagaa gtcaccattg 6240
ttgtgcacga cgacatcatt ccgtggcgtt atccagctaa gcgcgaactg caatttggag 6300
aatggcagcg caatgacatt cttgcaggta tcttcgagcc agccacgatc gacattgatc 6360
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gggcaatgga gcgcctgccg gcccagtatc agcccgtcat acttgaagct agacaggctt 6660
atcttggaca agaagaagat cgcttggcct cgcgcgcaga tcagttggaa gaatttgtcc 6720
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tctgaaaaaa gattgagccg agtttaaata gattttgata cgatcatgag acttgacaaa 6960
tcgggattcc tctattctat atatttagaa gatataaagg tataatacaa taaataaata 7020
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gtttccctga atcaagccaa gtatcacacc tctttctacc catcctgtat attgtcccct 7140
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gccctttatt aaaaattata ttattttaaa taatataaag gggttccaa catattaata 7380
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taataatcct agtgattgga tttctatgct tagtctgata ggaaataaga tattcaaata 7500
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tgagattgac aacgatcatt cttttctgag tgaactagaa agttcttttt atagttatcg 7920
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gtatgatact caatatagtt ggaataatca cattaatagt tgcattgata gttatcttca 8040
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taatgagtga gctaactcac attaattgcg ttgcgctcac tgcccgcttt ccagtcggga 8520
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attgggcgct cttccgcttc ctcgctcact gactcgctgc gctcggtcgt tcggctgcgg 8640
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ttgctggcgt ttttccatag gctccgcccc cctgacgagc atcacaaaaa tcgacgctca 8820
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aagtggtggc ctaactacgg ctacactaga aggacagtat ttggtatctg cgctctgctg 9240
```

Figure 22-D

```
aagccagtta ccttcggaaa aagagttggt agctcttgat ccggcaaaca aaccaccgct 9300
ggtagcggtg gtttttttgt ttgcaagcag cagattacgc gcagaaaaaa aggatctcaa 9360
gaagatcctt tgatcttttc tacggggtct gacgctcagt ggaacgaaaa ctcacgttaa 9420
gggattttgg tcatgagatt atcaaaaagg atcttcacct agatcctttt aaattaaaaa 9480
tgaagtttta aatcaatcta aagtatatat gagtaaactt ggtctgacag ttaccaatgc 9540
ttaatcagtg aggcacctat ctcagcgatc tgtctatttc gttcatccat agttgcctga 9600
ctccccgtcg tgtagataac tacgatacgg gagggcttac catctggccc cagtgctgca 9660
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ggaagggccg agcgcagaag tggtcctgca actttatccg cctccatcca gtctattaat 9780
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ttcggtcctc cgatcgttgt cagaagtaag ttggccgcag tgttatcact catggttatg 10020
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```

Figure 23

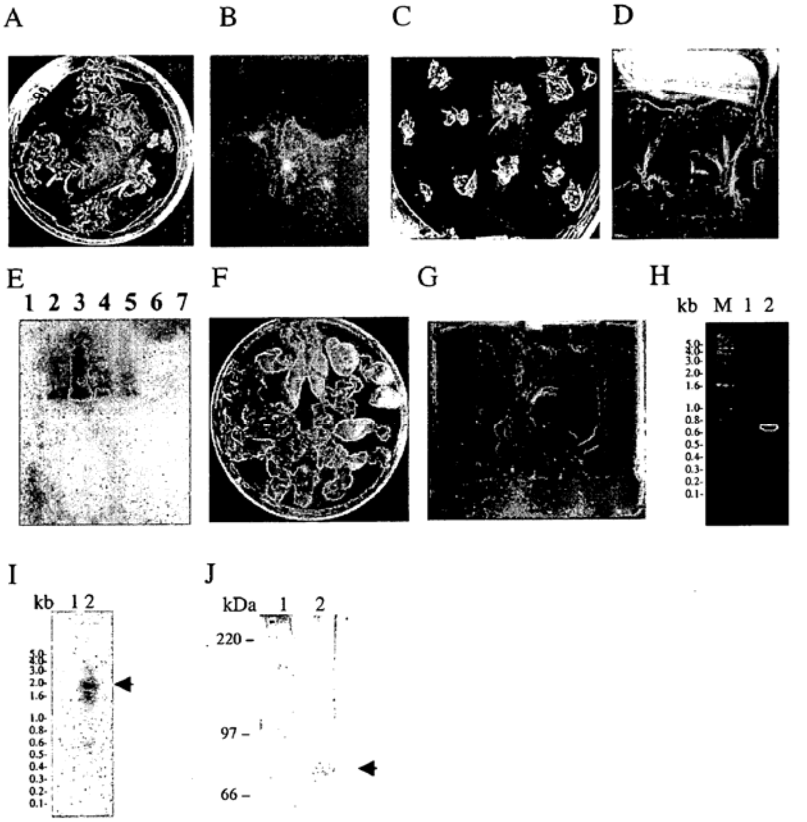
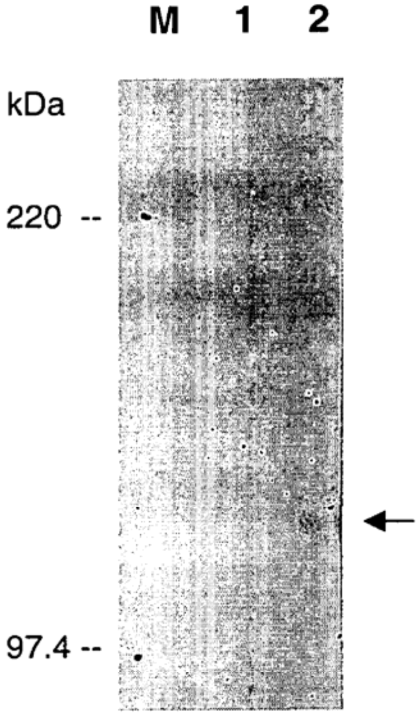

A
B
C
D
E
1 2 3 4 5 6 7
F
G
H
kb M 1 2
5.0
4.0
3.0
2.0
1.6
1.0
0.8
0.6
0.5
0.4
0.3
0.2
0.1
I
kb 1 2
5.0
4.0
3.0
2.0
1.6
1.0
0.8
0.6
0.5
0.4
0.3
0.2
0.1
J
kDa 1 2
220
97
66

Figure 24



# GENETICALLY MODIFIED PLANTS COMPRISING SARS-COV VIRAL NUCLEOTIDE SEQUENCES AND METHODS OF USE THEREOF FOR IMMUNIZATION AGAINST SARS

**[0001]** This application claims priority of U.S. Ser. No. 60/527,637, filed Dec. 5, 2003, the contents of which are hereby incorporated by reference into this application.

**[0002]** Throughout this application, certain publications are referenced. Full citations for these publications, as well as additional related references, may be found immediately preceding the claims. The disclosures of these publications are hereby incorporated by reference into this application in order to more fully describe the state of the art as of the date of the invention described and claimed herein.

## BACKGROUND OF THE INVENTION

**[0003]** Recently, there has been an outbreak of atypical pneumonia in Guangdong province in mainland China. Between November 2002 and March 2003, there were 792 reported cases with 31 fatalities (WHO, Severe Acute Respiratory Syndrome (SARS), *Weekly Epidemiol. Rec.* (2003) Vol. 78, page 86). In response to this crisis, the Hospital Authority in Hong Kong has increased the surveillance on patients with severe atypical pneumonia. In the course of this investigation, a number of clusters of health care workers with the disease were identified. In addition, there were clusters of pneumonia incidents among persons in close contact with those infected. The disease was unusual in its severity and its progression in spite of the antibiotic treatment typical for the bacterial pathogens that are known to be commonly associated with atypical pneumonia. Some of the present inventors were one of the groups involved in the investigation of these patients. The disease was given the acronym Severe Acute Respiratory Syndrome ("SARS"), which is caused by a novel coronavirus (Peiris et al., 2003, *Lancet* Vol. 61, pages 1319-25; Fouchier et al., 2003, *Nature* Vol. 423, page 240) known as the SARS-CoV virus. The SARS-associated coronavirus is distinct from previously characterized members of the family Coronaviridae that cause respiratory and enteric diseases in animals including humans.

**[0004]** Plants play a critical role as nutrients for animals, including humans, and for the production of substances useful as pharmaceuticals, cosmetics and the like. The generation of transgenic plants by plant nuclear transformation has successfully produced mucosal vaccines against cholera, Norwalk virus, Hepatitis B, foot-and-mouth disease (Walmsley and Arntzen, 2003, *Curr. Opin. Biotech. Vol.* 14, pages 145-150). Viral antigens expressed in transgenic plants are effective in inducing mucosal and serum immune responses in animals, irrespective of parenteral or oral delivery (Daniell et al., 2001, *Trends Plant Sci*. Vol. 6, pages 219-226).

**[0005]** Plastid transformation offers great benefits for recombinant DNA technology. In the plant cell, the mere presence of up to 10,000 more copies of the plastid genome as compared to a nuclear genome, ensures enhanced yield of the plastid-expressed foreign protein, or antigen in the case of vaccine production. Further, maternal inheritance of plastids would result in foreign gene containment due to the lack of pollen transmission (Daniell et al., 2002, *Trends Plant Sci*. Vol. 7, pages 84-91). Human somatotropin accumulates to 7% total soluble protein, which is 300-fold greater than from nuclear-transformed tobacco (Staub et al., 2000, *Plant Journal* Vol. 6, pages 547-553), while human serum albumin accumulates to 11.1% total soluble protein, which is 500-fold more than nuclear-transformed leaves (Fernandez-San Millan et al., 2003, *Plant Biotech* Vol. 1, pages 71-79). The cholera toxin B subunit, the first plant-derived vaccine arising from plastid transformation, accumulates to 4.1% total soluble protein in tobacco leaves (Daniell et al., 2001, *J. Mol. Biol*. Vol. 311, pages 1001-1009). In comparison, the yield of foreign protein from nuclear-transformed plants rarely exceeds 1% total soluble protein (Daniell et al., 2001, *Trends Plant Sci*. Vol. 6, pages 219-226).

## SUMMARY OF THE INVENTION

**[0006]** The present invention is based on the observation of the present inventors that genetically modified plants and progeny thereof expressing SARS-CoV viral antigens can be used as vaccines against SARS. When the genetically modified plants or progeny thereof are ingested by animals, or extracts from genetically modified plants or progeny thereof are injected into or ingested by animals, preferably human, antibodies are generated against the SARS-CoV viral antigens. An edible vaccine against the SARS-CoV virus, deliverable as fruits (e.g., tomato), leaves (e.g., lettuce), tubers (e.g., potato), seeds (e.g., rice or corn), flowers, stems or roots, would obliterate costly purification procedures required of recombinant vaccines from microorganisms. It has further advantages in easy storage, transport and administration by direct ingestion. Also, edible vaccines in the form of fruits, leaves, tubers, seeds, flowers, stems or roots can be grown and easily distributed in developing countries, cutting the costs of immunization programs, and omitting the need for refrigeration and delivery by injection which requires trained health personnel.

**[0007]** In accordance with the present invention, plant transformation vectors are engineered to provide SARS-CoV viral antigens for eliciting an immune response of an animal for the prevention and treatment of SARS. The antigen includes proteinaceous agent or molecules of the SARS-CoV virus, natural or artificial variants, or mutants thereof. The plant vectors comprising the SARS-CoV viral sequences may be engineered to provide one, two, three or more nucleotide sequences of the SARS-CoV virus. In accordance with the present invention, the antigenic sequences may be derived from the SARS-CoV virus, natural or artificial variants, or mutants thereof.

**[0008]** The present invention provides plant transformation vectors comprising SARS-CoV nucleotide sequences which encode fragments, derivatives, analogs, or variants of polypeptides of SARS-CoV virus. In a specific embodiment, the invention provides for transgenic and/or transplastomic tobacco plants. The present invention provides modified plants that comprise SARS-CoV antigens, including SARS-CoV viral polypeptides or fragments, derivatives, analogs, or variants thereof, or molecules having similar activities as the polypeptides of the SARS-CoV virus. These activities include functional activities as well as immunogenic abilities. The present invention also provides a method of producing the modified plants which comprises transforming a plant with plastid and/or nuclear transformation vector comprising SARS-CoV viral sequences, fragments, derivatives, analogs, or variants thereof. In preferred embodiments, the present invention provides for modified plants that express less than the entire genome of the SARS-CoV virus. In preferred embodiments, the modified plants provide less than 95%, less than 90%, less than 85%, less than 80%, less than 75%, less than 70%, less than 65%, less than 60%, less than 55%, less than 50%, less than 45%, less than 40%, less than 35%, less than 30%, less than 25%, less than 20%, less than 15%, less than 10%, less than 5%, or less than 1% of the entire genome of SARS-CoV virus. In preferred embodiments, the modified plants provide at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 polypeptides, fragments, derivatives, analogs and variants of the SARS-CoV virus.

**[0009]** In another specific embodiment, the invention provides a vaccine against SARS. The vaccine comprises the modified plant, its proteins, or extracts. The present invention also provides a method of immunization against SARS. The method comprises administering the modified plants to an animal so as to elicit the production of antibodies in the animal against the SARS-CoV viral antigens, which include SARS-CoV viral polypeptides, or fragments, derivatives, analogs, or variants thereof, or molecules having the similar activities as the polypeptide of the SARS-CoV virus.

**[0010]** In another specific embodiment, plant transformation vectors are engineered to provide SARS-CoV viral antigens for use as reagents in serological tests. One aspect of the invention relates to methods of detecting an antibody to a SARS-CoV viral antigen in a sample by incubating plant-derived SARS-CoV viral antigens with the sample and detecting the presence of antibodies bound to the plant-derived SARS-CoV viral antigens. The sample may be a biological fluid, such as blood, serum, plasma, saliva, urine, stool, sputum, nasopharyngeal aspirates, cells and tissues. Such plant-derived antigens would be cheaper alternative to those generated by infected cell lines for antibody detection.

**[0011]** In one embodiment, the invention relates to compositions comprising a SARS-CoV viral antigen produced by a transformed plant cell or plant. Methods of using the compositions to detect an antibody to a SARS-CoV viral antigen are also encompassed. In a specific embodiment, a method comprises contacting a sample with a composition comprising a SARS-CoV viral antigen produced by a transformed plant cell or plant, and detecting the presence of an antibody bound to the SARS-CoV viral antigen.

**[0012]** In one specific embodiment, the invention provides for a plastid transformation vector comprising the nucleotide sequences of the SARS-CoV virus encoding fragments, derivatives, analogs, or variants of polypeptides of SARS-CoV virus. In another embodiment, the invention provides for a plastid transformation vector which expresses SARS-CoV viral polypeptides, fragments, derivatives, analogs, or variants thereof, or molecules having the similar activities as the polypeptide of the SARS-CoV virus. In a specific embodiment, the vector devoid of viral DNA is pMLVHisA. In a specific embodiment, the present invention provides a method of producing SARS-CoV viral antigens via the plastid transformation vector pCV1, pCV6 or pCV8, and its derivatives containing an S1 with nucleotide (but not amino acid) changes to optimize codon usage for expression in plants.

**[0013]** In another specific embodiment, the invention provides for a nuclear transformation vector comprising the nucleotide sequences of the SARS-CoV virus, fragments, derivatives, analogs, or variants thereof. In another embodiment, the invention provides for a nuclear transformation vector which expresses SARS-CoV viral polypeptides, fragments, derivatives, analogs, or variants thereof, or molecules having the similar activities as the polypeptide of the SARS-CoV virus. In a specific embodiment, the vector devoid of viral DNA is pSa7. In a specific embodiment, the present invention provides a method of producing SARS-CoV viral antigens via the nuclear transformation vector pCV2, pCV4 or pCV12, and its derivatives containing an S1 with nucleotide (but not amino acid) changes to optimize codon usage for expression in plants.

**[0014]** In a specific embodiment, the present invention further provides transplastomic tobacco plants having therein a vector comprising a promoter derived from the rice plastid gene psbA, and a terminator. Plant cells containing a vector comprising a nucleotide sequence of the SARS-CoV virus is also an aspect of this invention. Plant parts of the modified plants, such as for example, fruits, leaves, tubers, seeds, flowers, stems or roots, which comprise cells expressing the SARS-CoV polypeptides, derivatives, analogs, or variants thereof are provided in the invention. The plant parts include parts that are separated from the whole plant or attached onto the whole plant. In a specific embodiment, the present invention further utilizes a selectable marker gene aadA, which specifies spectinomycin-resistance. In another embodiment, the present invention utilizes a start codon for recombinant $(His)_5$-tagged protein and an rbcL terminator. In a preferred embodiment, the modified plant further comprises heterologous nucleotide sequences that express protease inhibitor protein.

**[0015]** In another specific embodiment, the invention provides for the construction of a nuclear transformation vector for expression of SARS-CoV antigens including polypeptides of the SARS-CoV virus, or fragments, derivatives, analogs, or variants thereof, or molecules having similar activities as the polypeptides of the SARS-CoV virus. In a specific embodiment, the present invention provides plant nuclear transformation vectors pCV2, pCV4 and pCV12.

**[0016]** In another specific embodiment, the invention provides for the construction of a plastid transformation vector for expression of SARS-CoV antigens including polypeptides of the SARS-CoV virus, or fragments, derivatives, analogs, or variants thereof, or molecules having similar activities as the polypeptides of the SARS-CoV virus. In a specific embodiment, the present invention provides plant plastid transformation vectors pCV1, pCV6 and pCV8.

**[0017]** In a specific embodiment, a nuclear transformation vector is used to express one or more SARS-CoV antigens, including polypeptides of the SARS-CoV virus, or fragments, derivatives, analogs, or variants thereof, or molecules having similar activities as the polypeptides of the SARS-CoV virus.

**[0018]** In a specific embodiment, a plastid transformation vector is used to express one or more SARS-CoV antigens, including polypeptides of the SARS-CoV virus, or fragments, derivatives, analogs, or variants thereof, or molecules having similar activities as the polypeptides of the SARS-CoV virus.

**[0019]** In a specific embodiment, a plastid transformation vector and a nuclear transformation vector are used to express one or more SARS-CoV antigens, including polypeptides of the SARS-CoV virus, or fragments, derivatives, analogs, or variants thereof, or molecules having similar activities as the polypeptides of the SARS-CoV virus.

**[0020]** The present invention provides a method of producing SARS-CoV viral antigens in plants, the antigens include polypeptides of the SARS-CoV virus, or fragments, derivatives, analogs, or variants thereof, or molecules having similar activities as the polypeptides of the SARS-CoV virus. The method comprises transforming a plant with a vector which comprises a promoter, operably associated with a coding sequence for one or more SARS-CoV viral polypeptides, and a terminator. Plant cells containing a vector which comprises one or more nucleic acid sequences encoding for the SARS-CoV viral antigens, including polypeptides of the SARS-CoV virus, or fragments, derivatives, analogs, or variants thereof, or molecules having the similar activities as the polypeptides of the SARS-CoV virus, are also an aspect of this invention. Alternatively, the plant cells may contain one or more vectors of the present invention. The present invention provides plant parts, such as for example, fruits, leaves, tubers, seeds, flowers, stems, roots, and all other anatomical parts of the modified plant.

**[0021]** The present invention provides for a vaccine that elicits an immune response against SARS-CoV antigens, including SARS-CoV viral polypeptides, or fragments, derivatives, analogs, or variants thereof, or molecules having similar activities as the polypeptides of the SARS-CoV virus. In one specific embodiment, the invention provides a method of immunization against SARS. The method comprises ingesting an edible transformed plant parts comprising nucleic acid molecules of the SARS-CoV viral sequences encoding the SARS-CoV viral polypeptides. In another embodiment, the method comprises the consumption of the modified plant or intravenous injection or ingestion of an extract of the modified plant, which plant expresses SARS-CoV viral antigens, including SARS-CoV viral polypeptides, or fragments, derivatives, analogs, or variants thereof, or molecules having similar activities as the polypeptides of the SARS-CoV virus. In another specific embodiment, the present invention provides a method of immunization against SARS by feeding the modified plant of the present invention or injecting to or ingestion of an extract of the modified plant of the present invention by a rabbit, goat, cow, pig, sheep, horse, primate, civet, rodent, raccoon, raccoon dog, dog, ferret, ferret Badger, cat, avian, or any other species of animal, including human. The present invention further provides extracting antibodies from an immunized animal. The antibodies are immunospecific to SARS-CoV antigens, including viral polypeptides of the SARS-CoV virus, or fragments, derivatives, analogs, or variants thereof, or molecules having similar activities as the polypeptides of the SARS-CoV virus.

## BRIEF DESCRIPTION OF THE FIGURES

**[0022]** **FIGS. 1A-1W** show restriction sites of pCV1.

**[0023]** **FIGS. 2A-2C** show the nucleic acid sequence of pCV1 (SEQ ID NO:1).

**[0024]** **FIGS. 3A-3B** show restriction maps of pCV1 with specific restriction enzymes.

**[0025]** **FIG. 4** shows the pMLVHisA plastid transformation vector from which pCV1, pCV6 and pCV8 were derived. The flanking regions rbcL and accD are derived from the tobacco plastid genome for homologous recombination during plastid transformation. $P_{psbA}$ represents the promoter for the expression of the inserted gene. $T_{psbA}$ represents the terminator. $P_{rrn}$ represents the promoter driving expression of the spectinomycin-resistance marker aadA. $T_{rbcL}$ represents the rbcL terminator. Met represents the start codon for recombinant $(His)_5$-tagged protein. (A) shows the sequence (SEQ ID NO:2) and restriction sites of pCV8. (B) shows a restriction map of pCV8 with specific restriction enzymes. (C) shows a restriction map of pCV8 with specific restriction enzymes. (D) shows a restriction map of pCV8 with specific restriction enzymes.

**[0026]** **FIG. 5** shows the pSa7 nuclear transformation vector from which pCV2 and pCV4 were derived. RB and LB represent the right and left borders of T(transferred)-DNA for random insertion into the plant nuclear genome. NOS-Pro represents the nopaline synthase (NOS) promoter. NOS-ter represents the NOS-terminator. NPTII ($Kan^R$) represents neomycin phosphotransferase specifying kanamycin-resistance. CaMV35S-Pro represents the Cauliflower Mosaic Virus 35S promoter. SaPIN2a cDNA represents the cDNA encoding *Solanum americanum* proteinase inhibitor IIA.

**[0027]** **FIGS. 6A-6I** show the entire nucleic acid sequence of the SARS virus (SEQ ID NO:7).

**[0028]** FIGS. **7A-7**LL show restriction sites of pCV8.

**[0029]** **FIGS. 8A-8D** show the nucleic acid sequence of pCV8 (SEQ ID NO:2).

**[0030]** **FIG. 9** shows a restriction map of pCV8 with specific restriction enzymes.

**[0031]** **FIG. 10** shows a restriction map of pCV8 with specific restriction enzymes.

**[0032]** **FIG. 11** shows a restriction map of pCV8 with specific restriction enzymes.

**[0033]** **FIG. 12** shows the pCV12 nuclear transformation vector for expression of a protein fusion consisting of the SARS-CoV S1 protein fused with green fluorescent protein (GFP). RB and LB represent the right and left borders of T(transferred)-DNA for random insertion into the plant nuclear genome. NOS-ter represents the NOS-terminator. CaMV35S-Pro represents the Cauliflower Mosaic Virus 35S promoter. S1 represents the SARS-CoV S1 protein and GFP, the green fluorescent protein.

**[0034]** **FIG. 13A-13B** show the genomic DNA sequence of the M-gene (SEQ ID NO: 3), and the amino acid sequence of the M protein (SEQ ID NO:4), respectively.

**[0035]** **FIGS. 14A-14B** show the genomic DNA sequence of the S-gene (SEQ ID NO:5).

**[0036]** **FIG. 15** show the amino acid sequence of the S protein (SEQ ID NO:6).

**[0037]** FIGS. **16A-16**NN show the deduced amino acid sequences obtained from SEQ ID NO:7 in three frames. An aster (*) indicates a stop codon which marks the end of a peptide.

**[0038]** FIGS. **17**A-**17**NN show the deduced amino acid sequences obtained from the complement of SEQ ID NO:7 in three frames. An aster (*) indicates a stop codon which marks the end of a peptide.

**[0039]** FIGS. **18**A-D show transient expression of S1:GFP in agroinfiltrated tobacco leaves. Representative tobacco leaf epidermal cells are shown by confocal microscopy 2 days following agroinfiltration (Yang Y. et al., In vivo analysis of plant promoters and transcription factors by agroinfiltration of tobacco leaves. *Plant J.* 2000; 22: 543-551) of *Agrobacterium tumefaciens* LBA4404 harboring plasmid pCV12 expressing S1:GFP fusion protein (A, C) or LBA4404 harboring pGDG expressing GFP alone (B, D). Bar represents 20 μm.

**[0040]** FIGS. **19**A-**19**XX show restriction sites of pCV2.

**[0041]** **FIGS. 20A-20E** show the nucleic acid sequence of pCV2 (SEQ ID NO:8).

**[0042]** FIGS. **21**A-**21**NN show restriction sites of pCV6.

**[0043]** **FIGS. 22A-22D** show the nucleic acid sequence of pCV6 (SEQ ID NO:9).

**[0044]** **FIGS. 23A-23I** show plants obtained following transformation and their analysis. **FIGS. 23A-23E** show the regenerated plantlets obtained following *Agrobacterium*-mediated transformation of tobacco and lettuce using nuclear transformation vector pCV2 and analysis of these plantlets by PCR using primers 35S and NOS-ter followed by Southern blot analysis with a $^{32}$P-radiolabeled S1 probe. **FIGS. 23F-23I** show the regenerated plantlets obtained following plastid transformation of tobacco using plastid transformation vector pCV1, PCR analysis of these plantlets using S1 primers and Northern blot analysis with a $^{32}$P-radiolabeled S1 probe. **FIG. 23A** shows the plants regenerated from tobacco leaves after *Agrobacterium*-mediated transformation. **FIG. 23B** shows the regenerated tobacco shoot used in the PCR analysis. **FIG. 23C** shows the plants regenerated from lettuce cotyledons after *Agrobacterium*-mediated transformation. **FIG. 23D** shows the regenerated lettuce shoot used in the PCR analysis. **FIG. 23E** shows the presence of a 2.1-kb S1 hybridizing band (arrowed) in two independent tobacco lines (lanes 2 and 3), and two independent lettuce lines (lanes 4 and 5), and the absence of this band in wild-type tobacco (lane 6) and wild-type lettuce (lane 7). One other tobacco line tested negative (lane 1). **FIGS. 23F and 23G** show the plantlets regenerated from tobacco after particle bombardment. **FIG. 23H** shows the specific 0.7-kb PCR band in regenerated tobacco (lane 2) which is absent in wild-type (lane 1). **FIG. 231** shows the presence of a 2.1-kb hybridizing S1 mRNA band (arrowed) in a tobacco line (lane 2) which is absent in wild-type (lane 1).). **FIG. 23J** shows western blot analysis of transplastomic tobacco expressing S1 using Ni-NTA conjugate in detection of His-tagged S1 protein. The arrow indicates the expected 73-kDa (His)$_5$—S1 band.

**[0045]** **FIG. 24** shows a Western blot analysis using antibodies against GFP show transient expression of S1:GFP in tobacco leaves following agroinfiltration. Total protein (200 μg) extracted from tobacco leaves, infiltrated with plasmid pGDG expressing GFP alone (lane 1) or plasmid pCV12 expressing S1:GFP fusion (lane 2), were separated on a 8% SDS-PAGE gel, blotted onto Hybond-C filters according to Sambrook et al. (1989. Molecular Cloning: A Laboratory Manual. Cold Spring Harbor Laboratory Press, Cold Spring Harbor), and cross-reacted with antibodies against GFP (Clontech). Arrow indicates cross-reacting S1:GFP band (calculated size 99.1 kDa). M, molecular mass marker.

## DETAILED DESCRIPTION OF THE INVENTION

Definitions of Terms:

**[0046]** As used herein, the term "modified plant or plant parts" refers to a plant or plant part, whether it is attached or detached from the whole plant. It also includes progeny of the modified plant or plant parts that are produced through sexual or asexual reproduction.

**[0047]** As used herein, the term "variant" refers either to a naturally occurring genetic mutant of SARS-CoV or a recombinantly prepared variation of the SARS-CoV virus, each of which contain one or more mutations in its genome compared to the SARS-CoV virus of a deposited virus, CCTCC-V200303, which sequence is shown in **FIG. 6A-6I** (SEQ ID NO:7). The term "variant" may also refer to either a naturally occurring variation of a given peptide or a recombinantly prepared variation of a given peptide or protein in which one or more amino acid residues have been modified by amino acid substitution, addition, or deletion. A natural variant of SARS-CoV has a sequence that is different from the genomic sequence of the SARS-CoV virus due to one or more naturally occurred mutations, including, but not limited to, point mutations, rearrangements, insertions, deletions, etc., to the genomic sequence that may or may not result in a phenotypic change. Preferably, the variants include less than 25, less than 20, less than 15, less than 10, less than 5, less than 4, less than 3, or less than 2 amino acid substitutions, rearrangements, insertions, and/or deletions relative to the SARS-CoV virus.

**[0048]** In preferred embodiments, the variants have conservative amino acid substitutions that are made at one or more predicted non-essential amino acid residues (i.e., amino acid residues which are not critical for the expression of the biological activities of the virus, e.g., infectivity, replication ability, protein synthesis ability, assembling ability, and cytotoxic effect). A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a side chain with a similar charge. Families of amino acid residues having side chains with similar charges have been defined in the art. These families include amino acids with basic side chains (e.g., lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (e.g., threonine, valine, isoleucine), and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine). In another embodiment, the variants have non-conservative amino acid substitution, i.e., amino acid residues are replaced by an amino acid that does not have a side chain with a similar charge.

**[0049]** In a specific embodiment, the SARS-CoV sequences that may be used in the present invention include those deposited with GenBank® having accession nos. NC_004718, AY304495, AY304494, AY304493,

AY304492, AY304491, AY304490, AY304489, AY304488, AY304487, AY304486, AY360146, AY278491, AY310120, AY278489, AY362699, AY362698, AY283798, AY283797, AY283796, AY283795, AY283794, AY268070, AY278741, AY340092, AY351680, AP006561, AP006560, AP006559, AP006558, AP006557, AY278554, AY348314, AY338175, AY338174, AY323977, AY322199, AY322198, AY322197, AH013000, AY322208, AY322207, AY322206, AY322205, AH012999, AY321118, AY323976, AY323975, AY323974, AY286320, AY290752, AY291315, AY307165, AY279354, AY278490, AY278487, AY297028, AY286402, AY274119, AY291451, AY271716, AY282752, AY278488, AY268049, AY269391, all of which are incorporated herein by reference in their entireties.

**[0050]** The SARS-CoV viral nucleotide sequences used in the present invention may be derived from a mutant SARS-CoV virus. Mutations can be introduced randomly along all or part of the coding sequence of the SARS-CoV virus or variants thereof, such as by saturation mutagenesis, and the resultant mutants can be screened for biological activity to identify mutants that retain activity. In preferred embodiments, the mutant polypeptides do not retain activity of the wild-type polypeptide. In specific embodiments, the mutant polypeptides do not retain the virulent activity of the SARS-CoV virus. Techniques for mutagenesis known in the art can also be used, including but not limited to, point-directed mutagenesis, chemical mutagenesis, in vitro site-directed mutagenesis, using, for example, the QuikChange® Site-Directed Mutagenesis Kit (Stratagene), etc. Non-limiting examples of such modifications include substitutions of amino acids to cysteines toward the formation of disulfide bonds; substitution of amino acids to tyrosine and subsequent chemical treatment of the polypeptide toward the formation of dityrosine bonds, as disclosed in detail herein; one or more amino acid substitutions and/or biological or chemical modification toward generating a binding pocket for a small molecule (substrate or inhibitor), and/or the introduction of side-chain specific tags (e.g., to characterize molecular interactions or to capture protein-protein interaction partners). Biological modifications that are useful in the present invention comprises alkylation, phosphorylation, sulfation, oxidation or reduction, ADP-ribosylation, hydroxylation, glycosylation, glucosylphosphatidylinositol addition, ubiquitination, etc. Chemical modifications that are useful in the present invention comprise, e.g., altering the charge of the recombinant virus. A positive or negative charge is chemically added to an amino acid residue where a charged amino acid residue is modified to an uncharged residue.

**[0051]** As used herein, the terms "antibody" and "antibodies" refer to monoclonal antibodies, bispecific antibodies, multispecific antibodies, human antibodies, humanized antibodies, chimeric antibodies, camelised antibodies, single domain antibodies, single-chain Fvs (scFv), single chain antibodies, Fab fragments, F(ab') fragments, disulfide-linked Fvs (sdFv), and anti-idiotypic (anti-Id) antibodies (including, e.g., anti-Id antibodies to antibodies of the invention), and epitope-binding fragments of any of the above. In particular, antibodies include immunoglobulin molecules and immunologically active fragments of immunoglobulin molecules, i.e., molecules that contain an antigen binding site. Immunoglobulin molecules can be of any type (e.g., IgG, IgE, IgM, IgD, IgA and IgY), class (e.g., IgG1, IgG2, IgG3, IgG4, IgA1 and IgA2) or subclass.

**[0052]** As used herein, the term "an antibody that immunospecifically binds a polypeptide of the SARS-CoV virus" refers to an antibody that immunospecifically binds to the polypeptide encoded by SARS-CoV virus and does not non-specifically bind to other polypeptides. An antibody that immunospecifically binds to the polypeptide of the SARS-CoV virus does not cross-react with other antigens. Preferably, an antibody that immunospecifically binds to a polypeptide of the SARS-CoV virus does not cross-react with other antigens. An antibody that immunospecifically binds to the polypeptide of the SARS-CoV virus can be identified by, for example, immunoassays or other techniques known to those skilled in the art.

**[0053]** As used herein, the term "epitope" refers to a fragment of a SARS-CoV virus, polypeptide or protein having antigenic or immunogenic activity in an animal, preferably a mammal, and most preferably in a human. An epitope having immunogenic activity is a fragment of a polypeptide that elicits an antibody response in an animal. An epitope having antigenic activity is a fragment of a polypeptide or protein to which an antibody immunospecifically binds as determined by any method well known in the art, for example, by the immunoassays described herein. Antigenic epitopes need not necessarily be immunogenic.

**[0054]** As used herein, the term "antigenicity" refers to the ability of a substance (e.g., foreign objects, microorganisms, drugs, antigens, proteins, peptides, polypeptides, nucleic acids, DNA, RNA, etc.) to trigger an immune response in a particular organism, tissue, and/or cell. Sometimes, the term "antigenic" is synonymous with the term "immunogenic".

**[0055]** As used herein, the term "immunogenicity" refers to the property of a substance (e.g., foreign objects, microorganisms, drugs, antigens, proteins, peptides, polypeptides, nucleic acids, DNA, RNA, etc.) being able to evoke an immune response within an organism. Immunogenicity depends partly upon the size of the substance in question and partly upon how unlike the host molecules is the substance. Highly conserved proteins tend to have rather low immunogenicity.

**[0056]** As used herein, the term "hybridizes under stringent conditions" describes conditions for hybridization and washing under which nucleotide sequences having at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, or at least 95% identity to each other typically remain hybridized to each other. Such hybridization conditions are described in, for example but not limited to, Current Protocols in Molecular Biology, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6; Basic Methods in Molecular Biology, Elsevier Science Publishing Co., Inc., N.Y. (1986), pp. 75-78, and 84-87; and Molecular Cloning, Cold Spring Harbor Laboratory, N.Y. (1982), pp. 387-389, and are well known to those skilled in the art. The conditions under which hybridization and/or washing can be carried out can range from 42-68° C. and the washing buffer can comprise from 0.1× sodium chloride/sodium citrate (SSC), 0.5% SDS to 6×SSC, 0.5% SDS. Typically, hybridization can be carried out overnight at 65° C. (high stringency conditions), 60° C. (medium stringency conditions), or 55° C. (low stringency conditions). The filters can be washed for 2×15 minutes with 0.1×SSC, 0.5% SDS at 65° C. (high stringency washing). The filters were washed for

2×15 minutes with 0.1×SSC, 0.5% SDS at 63° C. (medium stringency washing). For low stringency washing, the filters were washed at 60° C. for 2×15 minutes at 2×SSC, 0.5% SDS. A preferred, non-limiting example of stringent hybridization conditions is hybridization in 6×SSC, 0.5% SDS at about 68° C. followed by one or more washes in 2×SSC, 0.5% SDS at room temperature. Another preferred, non-limiting example of stringent hybridization conditions is hybridization in 6×SSC at about 45° C. followed by one or more washes in 0.2×SSC, 0.1% SDS at about 50-65° C.

**[0057]** An "isolated" or "purified" antibody is substantially free of cellular material or other contaminating proteins from the biological fluid from which the antibody is derived. The language "substantially free of cellular material" includes preparations of an antibody in which the antibody is separated from cellular components of the cells from which it is isolated. Thus, an antibody that is substantially free of cellular material includes preparations of the antibody having less than about 30%, 20%, 10%, 5%, 2.5%, or 1%, (by dry weight) of contaminating protein. In a preferred embodiment of the present invention, the antibody is isolated or purified.

**[0058]** As used herein, the term "having a biological activity of the polypeptides of the SARS-CoV virus" refers to the characteristics of the polypeptides or proteins having a common biological activity similar or identical structural domain and/or having sufficient amino acid identity to SARS polypeptides or the polypeptides having the amino acid sequences as shown in **FIGS. 13B, 15, 16**A-**16**NN, and **17**A-**17**NN, or a fragment thereof. Such common biological activities of the polypeptides of the invention include antigenicity and immunogenicity.

**[0059]** As used herein, the term "molecules having the similar activities as the polypeptide of the SARS-CoV virus" refers to polypeptides or proteins having similar biological activities and similar or identical structural domain and/or having sufficient amino acid identity to the polypeptides of the SARS-CoV virus. Such biological activities can include, but are not limited to, antigenicity, immunogenicity, cytotoxicity, hormonal activities, binding properties and affinities, pharmacological activities, stimulation or inhibition of growth proliferation and differentiation, induction of changes in cells, antiviral, antibacterial, antifungal and antiparasitic activities, etc. In preferred embodiments, polypeptides that are useful for the present invention may retain at least one, two, three, four, five, or more biological activities of the wild-type SARS-CoV virus (e.g., infectivity, replication ability, protein synthesis ability, assembling ability, and cytotoxic effect).

**[0060]** As used herein, the term "portion" or "fragment" refers to a fragment of a nucleic acid molecule containing at least about 25, 30, 35, 40, 45, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1,000, 1,050, 1,100, 1,150, 1,200, 1,500, 2,000, 2,500, 3,000, 3,500, 4,000, 5,000, 6,000, 7,000, 8,000, 9,000, 10,000, 15,000, 20,000, 25,000, or more contiguous nucleic acids in length of the relevant nucleic acid molecule and having at least one functional feature of the nucleic acid molecule (or the encoded protein has one functional feature of the protein encoded by the nucleic acid molecule); or a fragment of a protein or a polypeptide containing at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 90, 100, 120, 140, 160, 180, 200, 220, 240, 260, 280, 300, 320, 340, 360, 380, 400, 450, 500, 600, 700, 800, 900, 1,000, 2,000, 3,000, 4,000, 5,000, 6,000, 7,000, 8,000, or more contiguous amino acid residues in length of the relevant protein or polypeptide and having at least one functional feature of the protein or polypeptide.

**[0061]** As used herein, the term "analog" in the context of proteinaceous agent (e.g., proteins, polypeptides, peptides, and antibodies) refers to a proteinaceous agent that possesses a similar or identical function as a second proteinaceous agent but does not necessarily comprise a similar or identical amino acid sequence of the second proteinaceous agent, or possess a similar or identical structure of the second proteinaceous agent. In a specific embodiment, antibody analogs immunospecifically bind to the same epitope as the original antibodies from which the analogs were derived. In an alternative embodiment, antibody analogs immunospecifically bind to different epitopes than the original antibodies from which the analogs were derived. A proteinaceous agent that has a similar amino acid sequence refers to a second proteinaceous agent that satisfies at least one of the following: (a) a proteinaceous agent having an amino acid sequence that is at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% identical to the amino acid sequence of a second proteinaceous agent; (b) a proteinaceous agent encoded by a nucleotide sequence that hybridizes under stringent conditions to a nucleotide sequence encoding a second proteinaceous agent of at least 5 contiguous amino acid residues, at least 10 contiguous amino acid residues, at least 15 contiguous amino acid residues, at least 20 contiguous amino acid residues, at least 25 contiguous amino acid residues, at least 40 contiguous amino acid residues, at least 50 contiguous amino acid residues, at least 60 contiguous amino residues, at least 70 contiguous amino acid residues, at least 80 contiguous amino acid residues, at least 90 contiguous amino acid residues, at least 100 contiguous amino acid residues, at least 125 contiguous amino acid residues, or at least 150 contiguous amino acid residues; and (c) a proteinaceous agent encoded by a nucleotide sequence that is at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% identical to the nucleotide sequence encoding a second proteinaceous agent. A proteinaceous agent with similar structure to a second proteinaceous agent refers to a proteinaceous agent that has a similar secondary, tertiary or quaternary structure to the second proteinaceous agent. The structure of a proteinaceous agent can be determined by methods known to those skilled in the art, including but not limited to, peptide sequencing, X ray crystallography, nuclear magnetic resonance, circular dichroism, and crystallographic electron microscopy.

**[0062]** To determine the percent identity of two amino acid sequences or of two nucleic acid sequences, the sequences are aligned for optimal comparison purposes (e.g., gaps can be introduced in the sequence of a first amino acid or nucleic acid sequence for optimal alignment with a second amino acid or nucleic acid sequence). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are identical at that position. The percent identity between the two sequences is a function of the number of identical positions shared by the sequences (i.e., % identity=number of identical overlapping positions/total number of positions×100%). In one embodiment, the two sequences are the same length.

**[0063]** The determination of percent identity between two sequences can also be accomplished using a mathematical algorithm. A preferred, non limiting example of a mathematical algorithm utilized for the comparison of two sequences is the algorithm of Karlin and Altschul, 1990, *Proc. Natl. Acad. Sci. U.S.A*. Vol. 87, pages 2264-2268, modified as in Karlin and Altschul, 1993, *Proc. Natl. Acad. Sci. U.S.A*. Vol. 90, pages 5873-5877. Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul et al., 1990, *J. Mol. Biol*. Vol. 215, page 403. BLAST nucleotide searches can be performed with the NBLAST nucleotide program parameters set, e.g., for score=100, wordlength=12 to obtain nucleotide sequences homologous to a nucleic acid molecules of the present invention. BLAST protein searches can be performed with the XBLAST program parameters set, e.g., to score 50, wordlength=3 to obtain amino acid sequences homologous to a protein molecule of the present invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al., 1997, *Nucleic Acids Res*. Vol. 25, pages 3389-3402. Alternatively, PSI BLAST can be used to perform an iterated search which detects distant relationships between molecules (Id.). When utilizing BLAST, Gapped BLAST, and PSI Blast programs, the default parameters of the respective programs (e.g., of XBLAST and NBLAST) can be used (see, e.g., the NCBI website). Another preferred, non limiting example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller, 1988, *CABIOS* Vol. 4, pages 11-17. Such an algorithm is incorporated in the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. The percent identity between two sequences can be determined using techniques similar to those described above, with or without allowing gaps. In calculating percent identity, typically only exact matches are counted.

**[0064]** As used herein, the term "analog" in the context of a non-proteinaceous analog refers to a second organic or inorganic molecule which possesses a similar or identical function as a first organic or inorganic molecule and is structurally similar to the first organic or inorganic molecule.

**[0065]** As used herein, the term "derivative" in the context of proteinaceous agent (e.g., proteins, polypeptides, peptides, and antibodies) refers to a proteinaceous agent that comprises an amino acid sequence which has been altered by the introduction of amino acid residue substitutions, deletions, and/or additions. The term "derivative" as used herein also refers to a proteinaceous agent which has been modified, i.e., by the covalent attachment of any type of molecule to the proteinaceous agent. For example, but not by way of limitation, an antibody may be modified, e.g., by glycosylation, acetylation, pegylation, phosphorylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, linkage to a cellular ligand or other protein, etc. A derivative of a proteinaceous agent may be produced by chemical modifications using techniques known to those of skill in the art, including, but not limited to specific chemical cleavage, acetylation, formylation, metabolic synthesis of tunicamycin, etc. Further, a derivative of a proteinaceous agent may contain one or more non-classical amino acids. A derivative of a proteinaceous agent possesses a similar or identical function as the proteinaceous agent from which it was derived.

**[0066]** As used herein, the term "derivative" in the context of a non-proteinaceous derivative refers to a second organic or inorganic molecule that is formed based upon the structure of a first organic or inorganic molecule. A derivative of an organic molecule includes, but is not limited to, a molecule modified, e.g., by the addition or deletion of a hydroxyl, methyl, ethyl, carboxyl or amine group. An organic molecule may also be esterified, alkylated and/or phosphorylated.

**[0067]** As used herein, the terms "subject" and "patient" are used interchangeably. As used herein, the terms "subject" and "subjects" refer to an animal, preferably a mammal including a non-primate (e.g., rabbits, goats, cows, pigs, sheep, horses, civets, rodents, raccoons, raccoon dogs, dogs, ferrets, ferret Badger, cats, and avian species) and a primate (e.g., monkeys such as a cynomolgous monkey and humans), and more preferably a human.

**[0068]** As used herein, the terms "SARS" or "SARS related symptoms" include various clinical indications and classifications. As described herein, SARS include (1) asymptomatic or mild respiratory illness; (2) moderate respiratory illness; or (3) severe respiratory illness.

**[0069]** As used herein, the term "carrier" is a substance used to support or convey another substance such as a pigment, catalyst, or radioactive material.

**[0070]** As used herein, the term "vehicle" is a substance that facilitates the use of a drug, pigment, or other material mixed with it.

**[0071]** As used herein, the term "excipients" refers to inert substances which are commonly used as a diluent, vehicle, preservatives, binders, or stabilizing agent for drugs and includes, but not limited to, proteins (e.g., serum albumin, etc.), amino acids (e.g., aspartic acid, glutamic acid, lysine, arginine, glycine, histidine, etc.), fatty acids and phospholipids (e.g., alkyl sulfonates, caprylate, etc.), surfactants (e.g., SDS, polysorbate, nonionic surfactant, etc.), saccharides (e.g., sucrose, maltose, trehalose, etc.) and polyols (e.g., mannitol, sorbitol, etc.). Also see *Remington's Pharmaceutical Sciences* (by Joseph P. Remington, 18th ed., Mack Publishing Co., Easton, Pa.), which is hereby incorporated in its entirety.

**[0072]** As used herein, the term "operably associated" or "operably linked" refers to an association in which the regulatory regions (e.g., promoter, enhancer) and the nucleic acid sequence to be expressed are covalently joined and positioned in such a way as to permit transcription, and under the appropriate condition, translation.

## PREFERRED EMBODIMENTS AND EXPERIMENTAL DETAILS

**[0073]** The present invention provides transgenic and transplastomic plants and their progeny that are generated by plastid and/or nuclear transformation vectors thereby producing a mucosal vaccine against SARS-CoV viral antigens. Viral antigens expressed in transgenic plants are effective in inducing mucosal and serum immune responses in animals, irrespective of parenteral or oral delivery. Viral antigens expressed in transgenic plants are also useful as reagents for antibody detection in serological tests. The present invention seeks to transform various types of plants with plant vectors comprising nucleotide sequences from the SARS-CoV virus including but not limited to nucleotide sequences of the SARS-CoV virus which encodes fragments, derivatives, analogs, or variants of polypeptides of SARS-CoV virus, or that it encodes an epitope or a proteinaceous molecule having similar activities as the polypeptides, fragments, derivatives, analogs, or variants thereof, of the SARS-CoV virus.

**[0074]** Analysis of the genome sequence of the SARS-associated coronavirus revealed that four of its eleven predicted open reading frames encode structural proteins including a spike glycoprotein (S) of 1255 deduced amino acids and a membrane glycoprotein (M) of 221 deduced amino acids; S and M presumably associate to form the viral envelope. The S glycoprotein, a type I membrane protein, functions in attachment to host receptors and has an N-terminal signal sequence (S1; amino acids 1-658) and a C-terminal transmembrane region followed by a cytoplasmic tail (Marra et al., 2003; Rota et al, 2003). The N-terminal region of M also includes an uncleavable signal sequence and is exposed to the surface of the virus while its C-terminus resides within the viral membrane. While both S and M are believed to be targeted to the plasma membrane, M was also believed to be localized at the endoplasmic reticulum in plant cells. In preferred embodiments, the modified plant or plant parts or progeny of the modified plant comprise SARS-CoV viral sequences that encode the spike protein (S or S1) of the SARS-CoV virus, or fragments, derivatives, analogs, or variants thereof. In a preferred embodiment, the modified plant or plant parts or progeny of the modified plant comprises nucleotide sequences that encode the N-terminal region (S1) of the spike protein (S) and/or the membrane protein (M) of the SARS-CoV virus, or fragments, derivatives, analogs, or variants thereof, or molecule having the similar activities as the polypeptide of the SARS-CoV virus. In preferred embodiments, the plant or plant parts comprises the nucleotide sequence of SEQ ID NO:3, 5, or 7, or a fragment thereof, or that immunospecifically binds to the polypeptide having the nucleotide sequence of SEQ ID NO:3, 5, or 7, or an analog, derivative, or fragment thereof, and/or polypeptides encoded by the nucleotide sequence of SEQ ID NO:3, 5, or 7, or a fragment thereof. The present invention also relates to a method of producing modified plants comprising one or more plastid and/or nuclear transformation vectors comprising one or more SARS-CoV nucleotide sequences which encode fragments, derivatives, analogs or variants of polypeptides of SARS-CoV virus. All varieties of plants may be used for the present invention. In a preferred embodiment, the plant is tobacco, lettuce, potato, tomato, banana, corn, rice, cereals, wheat, maize, barley, apple, pear, strawberry, carrot, sugar beets, yam, kiwifruit, or spinach.

Construction of Transformation Vectors

**[0075]** The present invention relates to plant vectors comprising one or more nucleotide sequences of the SARS-CoV virus, or fragments, derivatives, analogs or variants thereof. In a preferred embodiment, the plant vectors are plastid and nuclear transformation vectors. In preferred embodiments, the nucleotide sequence is the M-gene and/or S-gene of the SARS-CoV virus. The present invention also relates to the construction of plastid and nuclear transformation vectors comprising one or more SARS-CoV viral nucleotide sequences, or fragments, derivatives, analogs or artificial or natural variants thereof. In specific embodiments, the invention provides plant transformation vectors that comprise one or more nucleotide sequences that are at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 100, 150, 200, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1,000, 1,050, 1,100, 1,150, 1,200, 2,000, 3,000, 4,000, 5,000, 6,000, 7,000, 8,000, 9,000, 10,000, 11,000, 12,000, 13,000, 14,000, 15,000, 16,000, 17,000, 18,000, 19,000, 20,000, 21,000, 22,000, 23,000, 24,000, 25,000, 26,000, 27,000, 28,000, 29,000, or more contiguous nucleotides of SEQ ID NO:7, or a complement thereof, or a nucleotide comprising a nucleotide sequence that hybridizes to the nucleotide sequences of the SARS-CoV virus under stringent conditions. In specific embodiments, the invention provides plant transformation vectors that comprise one or more nucleotide sequences that are at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 100, 150, 200, 300, 350, 400, 450, 500, 550, 600, 650, or more contiguous nucleotides of SEQ ID NO:3, or a nucleotide comprising a nucleotide sequence that hybridizes to the nucleotide sequences of the SARS-CoV virus under stringent conditions. In specific embodiments, the invention provides plant transformation vectors that comprise one or more nucleotide sequences that are at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 100, 150, 200, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1,000, 1,050, 1,100, 1,150, 1,200, 2,000, 3,000, 3,500, or more contiguous nucleotides of SEQ ID NO:5, or a nucleotide comprising a nucleotide sequence that hybridizes to the nucleotide sequences of the SARS-CoV virus under stringent conditions. In specific embodiments, the invention provides plant transformation vectors that comprise one or more nucleotide sequences that encode polypeptides that are at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 100, 150, 200, or more contiguous amino acids of SEQ ID NO:4. In specific embodiments, the invention provides plant transformation vectors that comprise one or more nucleotide sequences that encode polypeptides that are at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 100, 150, 200, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1,000, 1,050, 1,100, 1,150, 1,200, or more contiguous amino acids of SEQ ID NO:6. In one embodiment, the plant vector comprises nucleotide sequences that encode amino acids 14-1195 of S. In preferred embodiments, the plant vector comprises nucleotide sequences that encode at least 20, 30, 40, 50, 60, 80, 100, 200, 300, 400, 500, or more contiguous amino acids in length of amino acids 14-1195 of S. In specific embodiments, the polypeptides are those shown in FIGS. **16A-16**NN and **17A-17**NN, or fragments, derivatives or analogs thereof. In specific embodiments, the invention provides plant transformation vectors that comprise one or more nucleotide sequences that encode any of the genes, or portions thereof, or variants, fragments, analogs, or derivatives, from the SARS-CoV virus. These genes include, but are not limited to, envelop protein (E protein), integral membrane protein (M protein), spike protein (S protein), nucleocapsid protein (N protein), hemagglutinin esterase (HE protein), and RNA-dependent RNA polymerase. Particularly useful are also those proteinaceous substances that are encoded by recombinant nucleic acid fragments of the SARS-CoV genome. Preferred are those that are within the open reading frames (ORFs), in particular, for eliciting SARS-CoV specific antibody or T cell responses, whether in vivo (e.g., for protective or therapeutic purposes or for providing diagnostic antibodies) or in vitro (e.g., by phage display technology or another technique useful for generating synthetic antibodies).

**[0076]** The viral vectors can be engineered to provide antigenic molecules, including nucleotide sequences, or polypeptides of the SARS-CoV virus, including recombinant and chimeric forms of the virus, or subunits of the virus, or fragments, derivatives, analogs, or variants thereof, or molecules having similar activities as the polypeptides of the SARS-CoV virus. The present invention further provides methods of preparing recombinant or chimeric forms of SARS-CoV antigen.

**[0077]** In another specific embodiment, the present invention provides methods for treating, ameliorating, managing, or preventing SARS by administering a vaccine preparations or antibodies of SARS-CoV virus alone or in combination with antivirals (e.g., amantadine, rimantadine, zanamivir, abacavir, combivir, emtricitabine, tenofovir, trizivir, enfuvirtide, gancyclovir, acyclovir, ribavirin, penciclovir, oseltamivir, foscarnet zidovudine (AZT), didanosine (ddI), lamivudine (3TC), zalcitabine (ddC), stavudine (d4T), nevirapine, delavirdine, efavirenz, fosamprenavir, amprenavir, atazanavir, kaletra, indinavir, ritonavir, vidarabine, nelfinavir, saquinavir, relenza, tamiflu, pleconaril, interferons, etc.), steroids and corticosteroids such as prednisone, cortisone, fluticasone and glucocorticoid, antibiotics, analgesics, bronchodialaters, or other treatments for respiratory and/or viral infections. In another specific embodiment, the methods of the present invention provides the use of herbs, herbal extracts, Chinese medicine and other remedies in combination with the modified plants of the present invention for the prevention and treatment of SARS.

**[0078]** Furthermore, the present invention provides pharmaceutical compositions comprising anti-viral agents of the present invention and a pharmaceutically acceptable carrier, vehicle or excipient. In addition, the present invention provides pharmaceutical compositions comprising liposomally encapsulated plant extracts, preferably purified, or anti-viral agents of the present invention. The present invention also provides kits comprising the pharmaceutical compositions of the present invention.

**[0079]** The present invention encompasses the use of a nucleotide sequence that encodes a chimeric polypeptide of the SARS-CoV virus. In a specific embodiment, the chimeric polypeptide comprises amino acid sequences from two or more different strains of the SARS-CoV virus. In accordance with the present invention, the modified plants of the present invention further comprise a nucleotide sequence that is non-native to the viral genome. The nucleotide sequence that may be useful for the present invention includes a portion of the SARS-CoV viral sequence which further comprises a heterologous nucleotide sequence. A heterologous nucleotide sequence may be from a virus, bacteria, animal, or plant. In a preferred embodiment, the heterologous nucleotide sequence encodes a proteinase inhibitor. The heterologous nucleotide sequence renders the expressed SARS-CoV polypeptide more stable and reduces programmed cell death and increases shelf life of the modified plant of the present invention. In a specific embodiment, the heterologous nucleotide sequence (e.g., SaPIN2a or SaPIN2b) renders the expressed SARS-CoV polypeptides more stable so that the modified plants that express the SARS-CoV polypeptide may be processed before ingestion, injection, or other methods of administration. SaPIN2a and SaPIN2b, which are proteinase inhibitor II genes isolated from *Solanum americanum*, a weed belonging to the Solanaceae family, encode serine proteinase inhibitor II proteins which confer insect resistance in transgenic plants (See U.S. Provisional Application No. 60/429,992 filed Nov. 29, 2002; and U.S. application Ser. No. 10/725,829, Attorney Docket No. 9661-043-999, filed Dec. 1, 2003, each of which is incorporated by reference herein in its entirety). SaPIN2a and SaPIN2b are highly expressed in the phloem and have possible involvement in regulating proteolysis in the sieve elements (See, Xu et al., 2001, *Plant Mol. Biol*. Vol. 47, pages 727-738; and Xu et al., 2003, *Planta* Vol. 218, pages 623-629, each of which is incorporated by reference herein in its entirety).

**[0080]** In certain embodiments, the present invention relates to vectors and nucleic acid molecules comprising the nucleotide sequence that encodes a chimeric polypeptide of the SARS-CoV virus. In a specific embodiment, a vector comprises a heterologous nucleotide sequence of SARS-CoV. In another embodiment, such heterologous nucleotide sequences have been added, inserted or substituted for native or non-native sequences. In accordance with the present invention, the nucleotide sequence of the SARS-CoV virus may be derived from different strains or variants of SARS-CoV virus.

**[0081]** A plant vector comprising chimeric SARS-CoV viral sequences may be of particular use for the generation of recombinant vaccines protecting against two or more viruses (Tao et al., *J. Virol.* 72: 2955-2961; Durbin et al., 2000, *J. Virol.* 74: 6821-6831; Skiadopoulos et al., 1998, *J. Virol.* 72: 1762-1768 (1998); Teng et al., 2000, *J. Virol.* 74: 9317-9321). For example, it can be envisaged that a plant vector comprising the SARS-CoV viral nucleotide sequences may express one or more peptides from variants of the SARS-CoV virus, and will protect a subject against infections by both the native SARS-CoV and the variant.

**[0082]** In accordance with the present invention, the plant vectors can be engineered to provide antigenic sequences which confer protection against infection by the SARS-CoV and natural variants thereof when ingested by a subject. The plant vectors may be engineered to provide one or more antigenic sequences of SARS-CoV virus. In accordance with the present invention, the antigenic sequences may be derived from the same virus, from different strains or variants of the same type of virus, or from different viruses.

**[0083]** The invention provides a host cell comprising a vector according to the invention. Plant plastid or nuclear transformation vector containing the nucleotide sequences of the SARS-CoV virus such as containing the full-length, portions or fragments of the SARS-CoV genome for the expression of SARS-CoV viral nucleic acids. These plant vectors may contain other sequences for the generation of chimeric SARS-CoV viral polypeptides which may contain mutations, deletions or insertions of the SARS-CoV polypeptides. Nucleotide sequences which encode SARS-CoV virus, fragments, derivatives, analogs, or variants of polypeptides of SARS-CoV virus include, but are not limited to, those deposited with GenBank® having accession nos. NC_004718, AY304495, AY304494, AY304493, AY304492, AY304491, AY304490, AY304489, AY304488, AY304487, AY304486, AY360146, AY278491, AY310120, AY278489, AY362699, AY362698, AY283798, AY283797, AY283796, AY283795, AY283794, AY268070, AY278741, AY340092, AY351680, AP006561, AP006560, AP006559, AP006558, AP006557, AY278554, AY348314, AY338175, AY338174, AY323977, AY322199, AY322198, AY322197, AH013000, AY322208, AY322207, AY322206, AY322205, AH012999, AY321118, AY323976, AY323975, AY323974, AY286320, AY290752, AY291315, AY307165, AY279354, AY278490, AY278487, AY297028, AY286402, AY274119, AY291451, AY271716, AY282752, AY278488, AY268049, AY269391, all of which are incorporated herein by reference in their entireties.

**[0084]** In one specific embodiment, plant cells may be transiently or stably expressing one or more nucleotide sequences of the SARS-CoV virus. Plants cells are modified by transfection (proteins or nucleic acid vectors), infection (viral vectors) or transduction (viral vectors). The modified plant may be used to modulate a subject's immune system by stimulating a humoral immune response, a cellular immune response or by stimulating tolerance to an antigen. As used herein, a subject means: humans, primates, rabbits, goats, cows, pigs, sheep, horses, civets, rodents, raccoons, raccoon dogs, dogs, ferrets, ferret Badger, cat, cats, avian species, or other non-human animals.

**[0085]** The nucleotide molecules encoding the SARS-CoV viral antigen proteins may be cloned by amplification. The term "amplified" refers to the process of making multiple copies of the nucleic acid from a single polynucleotide molecule. The amplification of polynucleotides can be carried out in vitro by biochemical processes known to those of skill in the art. The amplification agent may be any compound or system that will function to accomplish the synthesis of primer extension products, including enzymes. Suitable enzymes for this purpose include, for example, *E. coli* DNA polymerase I, Taq polymerase, Klenow fragment of *E. coli* DNA polymerase I, T4 DNA polymerase, other available DNA polymerases, polymerase mutants, reverse transcriptase, ligase, and other enzymes, including heat-stable enzymes (i.e., those enzymes that perform primer extension after being subjected to temperatures sufficiently elevated to cause denaturation). Suitable enzymes will facilitate combination of the nucleotides in the proper manner to form the primer extension products that are complementary to each mutant nucleotide strand. Generally, the synthesis will be initiated at the 3'-end of each primer and proceed in the 5'-direction along the template strand, until synthesis terminates, producing molecules of different lengths. There may be amplification agents, however, that initiate synthesis at the 5'-end and proceed in the other direction, using the same process as described above. In any event, the method of the invention is not to be limited to the embodiments of amplification described herein.

**[0086]** One method of in vitro amplification, which can be used according to this invention, is the polymerase chain reaction (PCR) described in U.S. Pat. Nos. 4,683,202 and 4,683,195. The term "polymerase chain reaction" refers to a method for amplifying a DNA base sequence using a heat-stable DNA polymerase and two oligonucleotide primers, one complementary to the (+)-strand at one end of the sequence to be amplified and the other complementary to the (−)-strand at the other end. Because the newly synthesized DNA strands can subsequently serve as additional templates for the same primer sequences, successive rounds of primer annealing, strand elongation, and dissociation produce rapid and highly specific amplification of the desired sequence. The polymerase chain reaction is used to detect the presence of polynucleotides encoding cytokines in the sample. Many polymerase chain methods are known to those of skill in the art and may be used in the method of the invention. For example, DNA can be subjected to 30 to 35 cycles of amplification in a thermocycler as follows: 95° C. for 30 sec, 52-60° C. for 1 min, and 72° C. for 1 min, with a final extension step of 72° C. for 5 min. For another example, DNA can be subjected to 35 polymerase chain reaction cycles in a thermocycler at a denaturing temperature of 95° C. for 30 sec, followed by varying annealing temperatures ranging from 54-58° C. for 1 min, an extension step at 70° C. for 1 min and a final extension step at 70° C.

**[0087]** The primers for use in amplifying the nucleotide sequences that encodes the proteinaceous molecules of the SARS-CoV virus, or fragments, derivatives, analogs, or variants thereof, or molecules having the similar activities as the polypeptides of the SARS-CoV virus may be prepared using any suitable method, such as conventional phosphotriester and phosphodiester methods or automated embodiments thereof so long as the primers are capable of hybridizing to the polynucleotides of interest. One method for synthesizing oligonucleotides on a modified solid support is described in U.S. Pat. No. 4,458,066. The exact length of primer will depend on many factors, including temperature, buffer, and nucleotide composition. The primer must prime the synthesis of extension products in the presence of the inducing agent for amplification.

**[0088]** Primers used according to the method of the invention are complementary to each strand of nucleotide sequence to be amplified. The term "complementary" means that the primers must hybridize with their respective strands under conditions, which allow the agent for polymerization to function. In other words, the primers that are complementary to the flanking sequences hybridize with the flanking sequences and permit amplification of the nucleotide sequence. Preferably, the 3' terminus of the primer that is extended has perfectly base paired complementarity with the complementary flanking strand. Primers and probes for the nucleotide sequence encoding the antigens, polypeptides of the SARS-CoV or fragments, derivatives, analogs, or variants thereof, or molecules having the similar activities as the polypeptides of the SARS-CoV virus can be developed using known methods combined with the present disclosure.

**[0089]** Those of ordinary skill in the art will know of various amplification methodologies that can also be utilized to increase the copy number of target nucleic acid. The polynucleotides that may be used for the present invention can be further evaluated, detected, cloned, sequenced, and the like, either in solution or after binding to a solid support, by any method usually applied to the detection of a specific nucleic acid sequence such as another polymerase chain reaction, oligomer restriction (Saiki et al., 1985*, Bio/Technology Vol.* 3, pages 1008-1012), allele-specific oligonucleotide (ASO) probe analysis (Conner et al., 1983, *Proc. Natl. Acad. Sci. USA* Vol. 80, page 278), oligonucleotide ligation assays (OLAs) (Landegren et al., 1988, *Science* Vol. 241, page 1077), RNase Protection Assay (RPA) and the like. Molecular techniques for DNA analysis have been reviewed (Landegren et al, 1988, *Science* Vol. 242, pages 229-237). Following DNA amplification, the reaction product may be detected by Southern blot analysis, without using radioactive probes. In such a process, for example, a small sample of DNA containing the polynucleotides obtained from the tissue or subject are amplified, and analyzed via a Southern blotting technique. The use of non-radioactive probes or labels is facilitated by the high level of the amplified signal.

**[0090]** The size of the primers used to amplify nucleotide sequences that encode antigens, polypeptides of the SARS-CoV or fragments, derivatives, analogs, or variants thereof, or molecules having the similar activities as the polypeptides of the SARS-CoV virus is at least 10, 15, 20, 25, 30 nucleotide in length. In particular, primers that amplify the M-gene or S-gene is most preferred. Preferably, the G:C ratio should be above 30%, 35%, 40%, 45%, 50%, 55%, 60% so as to prevent hair-pin structure on the primer. Furthermore, the amplicon should be sufficiently long enough to be detected by standard molecular biology methodologies. Preferably, the amplicon is at least 40, 60, 100, 200, 300, 400, 500, 600, 800, 1000, or more base pair in length.

**[0091]** The polynucleotides that may be used in the present invention include polynucleotides having the DNA sequences presented herein, and additionally include any nucleotide sequences encoding an epitope comprising contiguous and functional antigens, polypeptides of the SARS-CoV or fragments, derivatives, analogs, or variants thereof, or molecules having the similar activities as the polypeptides of the SARS-CoV virus encoding open reading frame (ORF) that hybridizes to a complement of the DNA sequences presented herein under highly stringent conditions. By way of example and not limitation, high stringency hybridization conditions can be defined as follows: The filter-bound DNA were hybridized in a solution containing 50% deionized formamide, 6×SSC, 5× Denhardt's, 1% SDS, 100 μg/ml denatured salmon sperm DNA at 42° C. overnight (about 4-16 hours), and washing in 0.1× SSC, 0.1% SDS at 65° C. (Ausubel F. M. et al., eds., 1989, *Current Protocols in Molecular Biology*, Vol. 1, Green Publishing Associates, Inc., and John Wiley & sons, Inc., New York) and encodes a functionally equivalent gene product. For oligonucleotide probes, by way of example and not limitation, highly stringent conditions may refer, e.g., to washing in 6×SSC/0.05% sodium pyrophosphate at 37° C. (for 14-base oligos), 48° C. (for 17-base oligos), 55° C. (for 20-base oligos), and 60° C. (for 23-base oligos).

**[0092]** Additionally contemplated polynucleotides that may be used in the present invention include any nucleotide sequences that hybridize under moderately stringent conditions to the complement of the DNA sequences that encode antigens, polypeptides of the SARS-CoV or fragments, derivatives, analogs, or variants thereof, or molecules having the similar activities as the polypeptides of the SARS-CoV virus. By way of example but not limitation, such moderately stringent conditions may include, e.g., washing in 0.2×SSC/0.1% SDS at 42° C. (Ausubel et al., 1989, supra).

**[0093]** Additionally contemplated polynucleotides that may be used in the present invention include any nucleotide sequences that hybridize under low stringency conditions to the complement of the DNA sequences that encode antigens, polypeptides of the SARS-CoV or fragments, derivatives, analogs, or variants thereof, or molecules having the similar activities as the polypeptides of the SARS-CoV virus. By way of example and not limitation, procedures using such conditions of low stringency are described in Shilo and Weinberg, 1981, *Proc. Natl. Acad. Sci. USA* Vol. 78, pages 6789-6792. A variant may comprise one or more changes in the amino acid sequence of the protein, e.g., by way of addition, substitution, or deletion of one or more amino acids, compared with the wild type protein. Any change should not abolish the ability of the protein to perform its function, though it may increase or decrease this ability depending on the nature of the changes. Preferably, the amino acid changes are conservative.

**[0094]** In various embodiments, antigen, polypeptide of the SARS-CoV virus or fragment, variant, analog, or derivative may be expressed as a fusion, or chimeric protein product (comprising the enzyme, fragment, analog, or derivative joined via a peptide bond to a heterologous protein sequence (of a different protein)). Such a chimeric gene product can be made by ligating the appropriate nucleic acid sequences encoding the desired amino acid sequences to each other by methods known in the art, in the proper coding frame, and expressing the chimeric product by methods commonly known in the art. Alternatively, such a chimeric product may be made by protein synthetic techniques, e.g., by use of a peptide synthesizer. Preferably, the fragment, analog, and derivative of the enzyme in the fusion protein retains the ability to perform the enzyme's function.

**[0095]** For the construction of plant nuclear transformation vectors, the expression of the SARS-CoV nucleotide sequences, genes, fragments, derivatives, analogs or variants thereof may be driven by any of a number of regulatory elements. For example, viral promoters such as the 35S RNA and 19S RNA promoters of CaMV (Brisson et al., 1984, *Nature* Vol. 310, pages 511-514), or the coat protein promoter of TMV (Takamatsu et al., 1987, *EMBO J*. Vol. 6, pages 307-311) may be used; alternatively, plant promoters such as the small subunit of RUBISCO (Coruzzi et al., 1984, *EMBO J*. Vol. 3, pages 1671-1680; Broglie et al., 1984, *Science* Vol. 224, pages 838-843); or heat shock promoters, e.g., soybean hsp17.5-E or hsp17.3-B (Gurley et al., 1986, *Mol. Cell. Biol*. Vol. 6, pages 559-565) may be used. These constructs can be introduced into plant cells using Ti plasmids, R1 plasmids, plant virus vectors, direct DNA transformation, biolistics/particle bombardment, microinjection, electroporation, etc. For reviews of such techniques see, for example, Weissbach & Weissbach, 1988, *Methods for Plant Molecular Biology*, Academic Press, New York, Section VIII, pp. 421-463; and Grierson & Corey, 1988, *Plant Molecular Biology,* 2d Ed., Blackie, London, Ch. 7-9. As used herein, regulatory elements include but are not limited to inducible and non-inducible promoters, enhancers, operators and other elements known to those skilled in the art that drive and regulate expression. Preferably the promoter is capable of directing expression in a particular tissue of the plant and/or at particular stages of development of the plant. The promoter may be heterologous or homologous to the plant. Preferably the promoter directs expression to the fruit, e.g., tomato, the leaves, e.g., lettuce, the endosperm of the plant seed or to the roots or tuber of the plant. A preferred promoter is the high molecular weight glutenin (HMWG) gene of wheat. Other suitable promoters will be known to the skilled man, such as the promoters of gliadin, branching enzyme, ADPG pyrophosphorylase, starch synthase and actin, for example.

**[0096]** A transformed plant with the ability to express SARS-CoV antigens including polypeptides of the SARS-CoV virus, or fragments, derivatives, analogs, or variants thereof, or molecules having the similar activities as the polypeptides of the SARS-CoV virus may be engineered by transforming a plant cell with a vector comprising a sequence encoding antigens, including polypeptides of the SARS-CoV or fragments, derivatives, analogs, or variants thereof, or molecules having the similar activities as the polypeptides of the SARS-CoV virus. In one embodiment, a plant promoter is operably associated with a sequence encoding the desired antigens. As used herein, the term "Operably associated" or "operably linked" refers to an association in which the regulatory regions (e.g., promoter, enhancer) and the nucleic acid sequence to be expressed are covalently joined and positioned in such a way as to permit transcription, and under the appropriate condition, translation. In a preferred embodiment of the present invention, the associated promoter for nuclear transformation is a strong and non tissue- or developmental-specific plant promoter (e.g., a promoter that strongly expresses in many or all plant tissue types). Examples of such strong, "constitutive" promoters include, but are not limited to, the CaMV 35S promoter (Odell et al., 1985, *Nature* 313:810-812), the T-DNA mannopine synthetase promoter, and their various derivatives. In another preferred embodiment, an inducible or repressible promoter is used to express the SARS-CoV virus of interest in a plant, for example, a tet operator promoter as described in Weinmann et al., 1994, *The Plant Journal* 5: 559-569; or a glucocorticoid-inducible promoter as described in McNellis et al., 1998, *The Plant Journal* 14: 247-257; or an ethanol inducible promoter as described in Caddick et al., 1998, *Nature Biotechnology* 16: 177-180. See, also, Gatz, 1995, *Methods In Cell Biology* 50: 411-424, which describes inducible and repressible gene expression systems for plants.

**[0097]** The promoters used for plastid transformation include strong and constitutive promoters in plastid expression including the psbA promoter (the psbA gene encodes the photosystem II 32 kD protein) and the 16S rRNA operon (rrn) promoter, or modifications thereof of these promoters which have enhanced expression (Suzuki et al., 2003, *Plant Cell* 15: 195-205; see also PCT publication no. WO 00/03012).

**[0098]** In one embodiment of the invention, SARS-CoV antigens will be localized in the apoplastic space from nuclear expression. The SARS-CoV antigens may be directed to the apoplastic space, when expressed in a plant, by expressing the antigens as fusion proteins together with a peptide that acts as a signal or transporter so that the antigen is localized in the apoplastic space of the transgenic plant. A variety of signal or transporter peptides can be used, for example, the PR1b signal sequence as described in Lund et al., 1992, *Plant Molecular Biology* 18: 47-53; or the PR-1a, b and c signal sequences as described in Pfitzner et al., 1987, *Nucleic Acids Research* 15: 4449-4465. A fusion protein comprising a signal or transporter peptide and an SARS-CoV antigen may be constructed by linking polynucleotides specific for each component to each other (e.g., the polynucleotides are linked in frame) so that the desired fusion protein is made when the fusion polynucleotide is expressed in a transgenic plant. A skilled artisan would know how to construct a polynucleotide useful for expressing SARS-CoV antigens, including polypeptides of the SARS-CoV or fragments, derivatives, analogs, or variants thereof, or molecules having the similar activities as the polypeptides of the SARS-CoV virus in the apoplastic space of a transgenic plant.

**[0099]** In another embodiment of the present invention, it may be advantageous to engineer a plant with a vector comprising a sequence SARS-CoV antigens, polypeptides of the SARS-CoV or fragments, derivatives, analogs, or variants thereof, or molecules having the similar activities as the polypeptides of the SARS-CoV virus operably associated with a tissue- or developmental-specific promoter, such as, but not limited to, the tomato E8 fruit-specific promoter, the chalcone synthase (CHS) promoter, the patatin promoter.

**[0100]** In yet another embodiment of the present invention, it may be advantageous to transform a plant with a vector comprising a sequence encoding SARS-CoV antigens, polypeptides of the SARS-CoV or fragments, derivatives, analogs, or variants thereof, or molecules having the similar activities as the polypeptides of the SARS-CoV virus operably linked to a modified or artificial promoter. Typically, such promoters, constructed by recombining structural elements of different promoters, have unique expression patterns and/or levels not found in natural promoters. See, e.g., Salina et al., 1992, *Plant Cell* 4: 1485-1493, for examples of artificial promoters constructed from combining cis-regulatory elements with a promoter core.

**[0101]** In yet an additional embodiment of the present invention, the expression of SARS-CoV antigens, polypeptides of the SARS-CoV or fragments, derivatives, analogs, or variants thereof, or molecules having the similar activities as the polypeptides of the SARS-CoV virus may be engineered by increasing the copy number of the gene encoding the desired protein or polypeptide using techniques known in the art.

**[0102]** The present invention provides a vector capable of directing the expression of SARS-CoV viral nucleotide sequences, fragments, derivatives, analogs or variants thereof, in a genetically modified plant or progeny thereof including, for example, transgenic and transplastomic plants. The plant vector is constructed using general recombinant DNA and cloning techniques known in the art of biotechnology, see, e.g., Sambrook et al., supra; Ausubel et al., supra. Such a polynucleotide construct typically comprises a polynucleotide sequence that encodes an engineered gene product and one or more regulatory polynucleotide sequence. Regulatory sequences useful for the polynucleotide construct of the invention include, but are not limited to, a promoter, an enhancer, an intron, a splice donor, a splice acceptor, a polyadenylation sequence, a RNA stability regulating sequence, or an element of any one of the above (e.g., promoter elements including, but not limited to, a TATA box). The regulatory elements useful for the present invention are capable of directing expression in a plant species in which expression of the nucleotide sequences that encode the SARS-CoV viral antigens is desired. In another preferred aspect, the regulatory elements are capable of directing expression in a cell type in which expression of the engineered gene product is desired in the plant species of interest.

**[0103]** Regulatory elements useful for the present invention are known to those of skill in the art, for example, promoter and enhancer elements of genes known to be expressed in the cell type and plant species of interest. A promoter useful for expression of the SARS-CoV viral antigens in a plant species of interest may also be isolated using routine experimentation, for example, by isolating a promoter region of a gene known to be expressed in the desired fashion. For example, one may screen a genomic library with a cDNA probe specific for the 5' end of a messenger RNA known to be expressed in the cell type of interest of the plant species of interest. Such a 5' end cDNA probe should preferably be only about 100 base pairs to about 300 base pairs so that the clones identified in the genomic library are likely to include the 5' end of the gene possibly including the promoter region of the gene for which the probe is specific. The promoter region typically includes about 1,000 to about 2,000 base pairs upstream of the transcription initiation site. Thus, a promoter useful for the expression of the engineered SARS-CoV nucleotide sequences, genes, fragments, derivatives, analogs or variants thereof of the present invention is a polynucleotide from about 2,000 base pairs upstream to about 50 base pairs downstream of the transcription initiation site of a gene known to be expressed in the cell type of interest in the plant species of interest, or is a portion of the polynucleotide.

**[0104]** In order to facilitate the proper processing of the SARS-CoV viral antigens, it may be necessary to include a nucleotide sequence that encodes a peptide sequence necessary for such processing. For example, a peptide sequence which is recognized by and functional in the transgenic host plant, for example, to facilitate the entry of the antigen into the endoplasmic reticulum may be necessary, i.e., signal Sequence.

Transformation of Plants and Plant Cells

**[0105]** Plants and plant cells nuclei and plastids may be transformed using any method known in the art. In an embodiment of the present invention, *Agrobacterium* is employed to introduce the vector of the present invention in nuclear transformation. Such transformation preferably uses binary *Agrobacterium* T-DNA vectors (Bevan, 1984, *Nuc. Acid Res.* Vol. 12, pages 8711-8721) and the co-cultivation procedure (Horsch et al., 1985, *Science* Vol. 227, pages 1229-1231). Generally, the *Agrobacterium* transformation system is used to engineer dicotyledonous plants (Bevan et al., 1982, *Ann. Rev. Genet* Vol. 16, pages 357-384; Rogers et al., 1986, *Methods Enzymol*. Vol. 118, pages 627-641). The *Agrobacterium* transformation system may also be used to transform, as well as transfer, DNA to monocotyledonous plants and plant cells (see Hernasteen et al., 1984, *EMBO J.* Vol. 3: pages 3039-3041; Hooykaas-Van Slogteren et al., 1984, *Nature* Vol. 311, pages 763-764; Grimsley et al., 1987, *Nature* Vol. 325, pages 1677-179; Boulton et al., 1989, *Plant Mol. Biol*. Vol. 12, pages 31-40; and Gould et al., 1991, *Plant Physiol*. Vol. 95, pages 426-434).

**[0106]** In other embodiments, various alternative methods for introducing recombinant nucleic acid constructs into plants and plant cells may also be utilized. These other methods are particularly useful where the target is a monocotyledonous plant or plant cell. Alternative gene transfer and transformation methods include, but are not limited to, particle gun bombardment (biolistics), protoplast transformation through calcium-, polyethylene glycol (PEG)- or electroporation-mediated uptake of naked DNA (see Paszkowski et al., 1984, *EMBO J*. Vol. 3, pages 2717-2722; Potrykus et al. 1985, *Molec. Gen. Genet*. Vol. 199, pages 169-177; Fromm et al., 1985, *Proc. Nat. Acad. Sci. USA* Vol. 82, pages 5824-5828; and Shimamoto, 1989, *Nature* Vol. 338, pages 274-276) and electroporation of plant tissues (D'Halluin et al., 1992, *Plant Cell* Vol. 4, pages 1495-1505). Additional methods for plant cell transformation include microinjection, silicon carbide mediated DNA uptake (Kaeppler et al., 1990, *Plant Cell Reporter* Vol. 9, pages 415-418), and microprojectile bombardment (see Klein et al., 1988, *Proc. Nat. Acad. Sci. USA* Vol. 85, pages 4305-4309; and Gordon-Kamm et al., 1990, *Plant Cell* Vol. 2, pages 603-618). In any methods, selectable markers may be used, at least initially, in order to determine whether transformation has actually occurred. Useful selectable markers include enzymes which confer resistance to an antibiotic, such as gentamycin, hygromycin, kanamycin and the like. Alternatively, markers which provide a compound identifiable by a color change, such as GUS, or luminescence, such as luciferase, may be used.

**[0107]** The chimeric gene may also comprise a gene switch mechanism which determines under what conditions or when the coding sequence is to be expressed. The gene switch may be a chemically induced promoter or a temperature controlled promoter, for example.

**[0108]** In a specific embodiment, each plastid transformation construct (pCV1, pCV6 or pCV8, and its derivatives containing an S1 with nucleotide (but not amino acid) changes to optimize codon usage for expression in plants) was introduced by particle gun bombardment into tobacco (Staub and Maliga, 1994, *Plant Journal* Vol. 6, pages 547-553) and tomato (Ruf et al., 2001, *Nature Biotech* Vol. 19, pages 870-875). In a specific embodiment, production of transgenic tobacco and transgenic lettuce expressing S1 or M antigen by nuclear transformation was carried out using *Agrobacterium*-mediated transformation (Horsch et al., 1985, *Science* Vol. 227, pages 1227-1231) with plasmids pCV2 [and its derivative containing an S1 with nucleotide (but not amino acid) changes to optimize codon usage for expression in plants] and pCV4, respectively. In another specific embodiment, production of transgenic tomato expressing S1 or M antigen by nuclear transformation is carried out.

**[0109]** According to the present invention, a wide variety of plants and plant cell systems may be engineered for the desired physiological and agronomic characteristics described herein using the nucleic acid constructs of the present invention and the various transformation methods mentioned above. In preferred embodiments, target plants and plant cells for engineering include, but are not limited to, those monocotyledonous and dicotyledonous plants, such as crops including grain crops (e.g., wheat, maize, rice, millet, barley), tobacco, fruit crops (e.g., tomato, apple, pear, strawberry, orange), forage crops (e.g., alfalfa), root vegetable crops (e.g., carrot, potato, sugar beets, yam), leafy vegetable crops (e.g., lettuce, spinach); flowering plants (e.g., petunia, rose, chrysanthemum), conifers and pine trees (e.g., pine fir, spruce); plants used in phytoremediation (e.g., heavy metal accumulating plants); oil crops (e.g., sunflower, rape seed); and plants used for experimental purposes (e.g., *Arabidopsis*).

Screening of Transformed Plants and Plant Cells

**[0110]** According to the present invention, desired plants may be obtained by engineering one or more of the vectors expressing SARS-CoV antigens as described herein into a variety of plant cell types, including but not limited to, protoplasts, tissue culture cells, tissue and organ explants, pollens, embryos, as well as whole plants. In an embodiment of the present invention, the engineered plant material is selected or screened for transformants (those that have incorporated or integrated the introduced gene construct(s)) following the approaches and methods described below. An isolated transformant may then be regenerated into a plant and progeny thereof via sexual or asexual reproduction or growth. Alternatively, the engineered plant material may be regenerated into a plant before subjecting the derived plant to selection or screening for the marker gene traits. Procedures for regenerating plants from plant cells, tissues or organs, either before or after selecting or screening for marker gene(s), are well known to those skilled in the art.

**[0111]** A transformed plant cell, callus, tissue or plant may be identified and isolated by selecting or screening the engineered plant material for traits encoded by the marker genes present on the transforming DNA. For instance, selection may be performed by growing the engineered plant material on media containing inhibitory amount of the antibiotic or herbicide to which the transforming gene construct confers resistance. Further, transformed plants and plant cells may also be identified by screening for the activities of any visible marker genes (e.g., the β-glucuronidase, luciferase, B or Cl genes) that may be present on the vector of the present invention. Such selection and screening methodologies are well known to those skilled in the art.

**[0112]** Physical and biochemical methods may also be used to identify plant or plant cell transformants containing the gene constructs of the present invention. These methods include but are not limited to: 1) Southern analysis or PCR amplification for detecting and determining the structure of the recombinant DNA insert; 2) Northern blot, S1 RNase protection, primer-extension or reverse transcriptase-PCR amplification for detecting and examining RNA transcripts of the gene constructs; 3) enzymatic assays for detecting enzyme activity, where such gene products are encoded by the gene construct; 4) protein gel electrophoresis (PAGE), Western blot techniques, immunoprecipitation, or enzyme-linked immunoassays, where the gene construct products are proteins. Additional techniques, such as in situ hybridization, enzyme staining, and immunostaining, also may be used to detect the presence or expression of the recombinant construct in specific plant organs and tissues. The methods for doing all these assays are well known to those skilled in the art.

**[0113]** In a specific embodiment, the selectable marker gene aadA, which specifies spectinomycin-resistance, is driven from the rice plastid 16S rRNA operon (rrn) promoter in plastid transformation. In a specific embodiment, the selectable marker gene nptII, which specifies kanamycin-resistance, is driven by the NOS (nopaline synthase) promoter in nuclear transformation.

**[0114]** The present invention relates to transgenic and transplastomic plants that express one or more epitopes of the SARS-CoV virus. A transgenic or transplastomic plant expressing a SARS-CoV antigen elicits the production of antibodies against SARS-CoV by the subject after ingestion of the modified plant or plant parts by a subject; or administration of plant extract to a subject using methods known in the art.

**[0115]** Examples of plants are monocots, dicots, crop plants (i.e., any plant species grown for purposes of agriculture, food production for animals including humans, plants that are typically grown in groups of more than about 10 plants in order to harvest the entire plant or a part of the plant, e.g., a fruit, a flower or a crop, e.g., tobacco, grain, that the plants bear, etc.), trees (i.e., fruit trees, trees grown for wood production, trees grown for decoration, etc.), flowers of any kind (i.e., plants grown for purposes of decoration, for example, following their harvest), cactuses

**[0116]** Further examples of plants in which the SARS-CoV viral antigens may be expressed include Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Euphyllophytes, Spermatophyta, Magnoliophyta, Liliopsida, Commelinidae, Poales, Poaceae, *Oryza, Oryza sativa, Zea, Zea mays, Hordeum, Hordeum vulgare, Triticum, Triticum aestivum*, Eudicotyledons, Core eudicots, Asteridae, Euasterids, Rosidae, Eurosids II, Brassicales, Brassicaceae, *Arabidopsis*, Magnoliopsida, Solananae, Solanales, Solanaceae, *Solanum*, and *Nicotiana*.

**[0117]** Also included are, for example, crops of particular interest including Solanaceae, including processing and fresh market tomatoes, pepper and eggplant; leafy plants, including lettuce and spinach; *Brassicas*, including broccoli, brussels sprouts, calabrese, cale, cauliflower, red cabbage and white cabbage; cucurbits, including cucumber, melon, watermelon, zucchini and squash; large seeded plants, including peas, beans and sweetcorn; rooted plants, including carrots and onions; vegetatively propagated plants, including berries, grapes, banana, pineapple, kiwifruit, and rosaceous fruit and nut crops; and tropical crops, including mango and papaya.

**[0118]** Thus, the invention has use over a broad range of plants including, but not limited to, species from the genera *Anacardium, Arachis*, Asparagus, *Atropa, Avena, Brassica, Citrus, Citrullus, Capsicum, Carthamus, Cocos, Coffea, Cucumis, Cucurbita, Daucus, Elaeis, Fragaria, Glycine, Gossypium, Helianthus, Heterocallis, Hordeum, Hyoscyamus, Lactuca, Linum, Lolium, Lupinus, Lycopersicon, Malus, Manihot, Majorana, Medicago, Nicotiana, Olea, Oryza, Panieum, Panneserum, Persea, Phaseolus, Pistachia, Pisum, Pyrus, Prunus, Raphanus, Ricinus, Secale, Senecio, Sinapis, Solanum, Sorghum, Theobromus, Trigonella, Titicum, Vicia, Vitis, Vigna*, and *Zea*.

Vaccine Formulations and Administration

**[0119]** The invention also provides vaccine formulations containing extracts of the modified plants of the present invention, which are suitable for administration to elicit a protective immune (humoral and/or cell mediated) response against certain antigens, e.g., for the treatment and prevention of SARS.

**[0120]** Suitable preparations of such vaccines include injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid prior to injection, may also be prepared. The preparation may also be emulsified, or the proteinaceous molecules encapsulated in liposomes. The active immunogenic ingredients are often mixed with carriers, vehicles or excipients which are pharmaceutically acceptable and compatible with the active ingredient. Suitable excipients are, for example, water, saline, buffered saline, dextrose, glycerol, ethanol, sterile isotonic aqueous buffer or the like and combinations thereof. In addition, if desired, the vaccine preparation may also include minor amounts of auxiliary substances such as wetting or emulsifying agents, pH buffering agents, and/or adjuvants which enhance the effectiveness of the vaccine.

**[0121]** Examples of adjuvants which may be effective, include, but are not limited to: aluminum hydroxide, N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-MDP), N-acetyl-nor-muramyl-L-alanyl-D-isoglutamine, N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-sn-glycero-3-hydroxyphosphoryloxy)-ethylamine.

**[0122]** The effectiveness of an adjuvant may be determined by measuring the induction of anti-idiotype antibodies directed against the injected modified plant extract formulated with the particular adjuvant.

**[0123]** The composition can be a liquid solution, suspension, emulsion, tablet, pill, capsule, sustained release formulation, or powder. Oral formulation can include standard carriers such as pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium carbonate.

**[0124]** In another embodiment, the composition can be delivered in a vesicle, in particular a liposome (see Langer, 1990, *Science* 249:1527-1533; Treat et al., in Liposomes in the Therapy of Infectious Disease and Cancer, Lopez-Berestein and Fidler (eds.), Liss, New York, pp. 353-365 (1989); *Lopez*-Berestein, ibid., pp. 317-327; see generally ibid.).

**[0125]** Generally, the ingredients are supplied either separately or mixed together in unit dosage form, for example, as a dry lyophilized powder or water-free concentrate in a hermetically sealed container such as an ampoule or sachette indicating the quantity of active agent. Where the composition is administered by injection, an ampoule of sterile diluent can be provided so that the ingredients may be mixed prior to administration.

**[0126]** In a specific embodiment, the lyophilized modified immunoglobulin of the invention is provided in a first container; a second container comprises diluent consisting of an aqueous solution of 50% glycerin, 0.25% phenol, and an antiseptic (e.g., 0.005% brilliant green).

**[0127]** The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the vaccine formulations of the invention. Associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration.

**[0128]** The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may for example comprise metal or plastic foil, such as a blister pack or transdermal patch. The pack or dispenser device may be accompanied by instructions for administration. Composition comprising an extract of the invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

**[0129]** The subject to which the vaccine is administered is preferably a mammal, most preferably a human, but can also be a non-human animal including but not limited to rabbits, goats, cows, pigs, sheep, horses, civets, rodents, raccoons, raccoon dogs, dogs, ferrets, ferret Badger, cats, and avian species.

**[0130]** Many methods may be used to introduce the vaccine formulations of the invention; these include but are not limited to oral, intracerebral, intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, intranasal routes, and via scarification (scratching through the top layers of skin, e.g., using a bifurcated needle) or any other standard routes of immunization. In a specific embodiment, scarification is employed.

**[0131]** The precise dose of the extract of the modified plant to be employed in the formulation will also depend on the route of administration, and the nature of the patient, and should be decided according to the judgment of the practitioner and each patient's circumstances according to standard clinical techniques. An effective immunizing amount is that amount sufficient to produce an immune response to the SARS-CoV viral epitope in the host (i.e., an anti-idiotype reaction) to which the vaccine preparation is administered. Effective doses may also be extrapolated from dose-response curves derived from animal model test systems.

**[0132]** The present invention provides methods of vaccination against SARS. The methods comprise administering whole modified plants or plant parts, extracts, to a subject for the production of antibodies against SARS-CoV viral antigens. In preferred embodiments, the vaccine is administered by ingestion of the modified plants or injection of the modified plant extracts. In certain embodiments, a first vaccine comprising a modified plant extract transformed by a vector for expression of a S antigen may be administered prior to, simultaneously with, or after administration of a second vaccine comprising a modified plant extract transformed by a vector for expression of a M antigen. The term "concurrently" is not limited to the administration of prophylactic or therapeutic composition at exactly the same time, but rather it is meant that the composition of the present invention and the other agent are administered to a mammal in a sequence and within a time interval such that the composition comprising the polynucleotides can act together with the other composition to provide an increased benefit than if they were administered otherwise. In various embodiments, the prophylactic or therapeutic compositions are administered less than 1 hour apart, at about 1 hour apart, at about 1 hour to about 2 hours apart, at about 2 hours to about 3 hours apart, at about 3 hours to about 4 hours apart, at about 4 hours to about 5 hours apart, at about 5 hours to about 6 hours apart, at about 6 hours to about 7 hours apart, at about 7 hours to about 8 hours apart, at about 8 hours to about 9 hours apart, at about 9 hours to about 10 hours apart, at about 10 hours to about 11 hours apart, at about 11 hours to about 12 hours apart, no more than 24 hours apart or no more than 48 hours apart. In preferred embodiments, two or more components are administered within the same patient visit.

**[0133]** In other embodiments, the prophylactic or therapeutic compositions are administered at about 30 minutes, at about 1 hour apart, at about 1 hour to about 2 hours apart, at about 2 hours to about 3 hours apart, at about 3 hours to about 4 hours apart, at about 4 hours to about 5 hours apart, at about 5 hours to about 6 hours apart, at about 6 hours to about 7 hours apart, at about 7 hours to about 8 hours apart, at about 8 hours to about 9 hours apart, at about 9 hours to about 10 hours apart, at about 10 hours to about 11 hours apart, at about 11 hours to about 12 hours apart, at about 1 to 2 days apart, at about 2 to 4 days apart, at about 4 to 6 days apart, at about 1 week part, at about 1 to 2 weeks apart, or more than 2 weeks apart. One skilled in the art would be able to determine such a time frame by determining the half life of the administered compositions.

**[0134]** In certain embodiments, the prophylactic or therapeutic compositions of the invention are cyclically administered to a subject. Cycling therapy involves the administration of a first composition for a period of time, followed by the administration of a second composition and/or third composition for a period of time and repeating this sequential administration. Cycling therapy can reduce the development of resistance to one or more of the therapies, avoid or reduce the side effects of one of the therapies, and/or improves the efficacy of the treatment.

**[0135]** In certain embodiments, prophylactic or therapeutic compositions are administered in a cycle of less than about 3 weeks, about once every two weeks, about once every 10 days or about once every week. One cycle can comprise the administration of a therapeutic or prophylactic composition by infusion over about 90 minutes every cycle, about 1 hour every cycle, about 45 minutes every cycle. Each cycle can comprise at least 1 week of rest, at least 2 weeks of rest, at least 3 weeks of rest. The number of cycles administered is from about 1 to about 12 cycles, more typically from about 2 to about 10 cycles, and more typically from about 2 to about 8 cycles.

**[0136]** In yet other embodiments, the therapeutic and prophylactic compositions of the invention are administered in metronomic dosing regiments, either by continuous infusion or frequent administration without extended rest periods. Such metronomic administration can involve dosing at constant intervals without rest periods. The dosing regimens encompass the chronic daily administration of relatively low doses for extended periods of time. In preferred embodiments, the use of lower doses can minimize toxic side effects and eliminate rest periods. In certain embodiments, the therapeutic and prophylactic compositions are delivered by chronic low-dose or continuous infusion ranging from about 24 hours to about 2 days, to about 1 week, to about 2 weeks, to about 3 weeks to about 1 month to about 2 months, to about 3 months, to about 4 months, to about 5 months, to about 6 months. The scheduling of such dose regimens can be optimalized by the skilled physician.

**[0137]** The dosage amounts and frequencies of administration provided herein are encompassed by the terms therapeutically effective and prophylactically effective. The dosage and frequency further will typically vary according to factors specific for each patient depending on the specific therapeutic or prophylactic composition administered, the severity and type of disease or disorder, the route of administration, as well as age, body weight, response, and the past medical history of the patient. Suitable regimens can be selected by one skilled in the art by considering such factors and by following, for example, dosages reported in the literature and recommended in the *Physician's Desk Reference* (56th ed., 2002).

**[0138]** Various delivery systems are known and can be used to administer the therapeutic or prophylactic composition of the present invention, e.g., encapsulation in liposomes, microparticles, microcapsules, recombinant cells capable of expressing the antibody or antibody fragment, receptor-mediated endocytosis (see, e.g., Wu and Wu, *J. Biol. Chem.* 262:4429-4432 (1987)), construction of a nucleic acid as part of a retroviral or other vector, etc. Methods of administering a prophylactic or therapeutic composition of the invention include, but are not limited to, parenteral administration (e.g., intradermal, intramuscular, intraperitoneal, intravenous and subcutaneous), epidural, and mucosal (e.g., intranasal and oral routes). In a specific embodiment, prophylactic or therapeutic composition of the invention is administered intramuscularly, intravenously, or subcutaneously. The prophylactic or therapeutic composition may be administered by any convenient route, for example by infusion or bolus injection, by absorption through epithelial or mucocutaneous linings (e.g., oral mucosa, rectal and intestinal mucosa, etc.) and may be administered together with other biologically active agents. Administration can be systemic or local.

**[0139]** In a specific embodiment, it may be desirable to administer the prophylactic or therapeutic composition of the invention locally to the area in need of treatment; this may be achieved by, for example, and not by way of limitation, local infusion, by injection, or by means of an implant, said implant being of a porous, non-porous, or gelatinous material, including membranes, such as sialastic membranes, or fibers.

**[0140]** In yet another embodiment, the prophylactic or therapeutic composition can be delivered in a controlled release or sustained release system. In one embodiment, a pump may be used to achieve controlled or sustained release (see Langer, supra; Sefton, 1987*, CRC Crit. Ref. Biomed. Eng.* 14:20; Buchwald et al., 1980, *Surgery* 88:507; Saudek et al., 1989, *N. Engl. J. Med.* 321:574). In another embodiment, polymeric materials can be used to achieve controlled or sustained release of the therapeutic or prophylactic composition of the invention (see e.g., Medical Applications of Controlled Release, Langer and Wise (eds.), CRC Pres., Boca Raton, Fla. (1974); Controlled Drug Bioavailability, Drug Product Design and Performance, Smolen and Ball (eds.), Wiley, New York (1984); Ranger and Peppas, 1983, *J., Macromol. Sci. Rev. Macromol. Chem.* 23:61; see also Levy et al., 1985, *Science* 228:190; During et al., 1989, *Ann. Neurol.* 25:351; Howard et al., 1989, *J. Neurosurg.* 7 1:105); U.S. Pat. No. 5,679,377; U.S. Pat. No. 5,916,597; U.S. Pat. No. 5,912,015; U.S. Pat. No. 5,989,463; U.S. Pat. No. 5,128,326; PCT Publication No. WO 99/15154; and PCT Publication No. WO 99/20253. Examples of polymers used in sustained release formulations include, but are not limited to, poly(2-hydroxy ethyl methacrylate), poly(methyl methacrylate), poly(acrylic acid), poly(ethylene-co-vinyl acetate), poly(methacrylic acid), polyglycolides (PLG), polyanhydrides, poly(N-vinyl pyrrolidone), poly(vinyl alcohol), polyacrylamide, poly(ethylene glycol), polylactides (PLA), poly(lactide-co-glycolides) (PLGA), and polyorthoesters. In a preferred embodiment, the polymer used in a sustained release formulation is inert, free of leachable impurities, stable on storage, sterile, and biodegradable. In yet another embodiment, a controlled or sustained release system can be placed in proximity of the prophylactic or therapeutic target, thus requiring only a fraction of the systemic dose (see, e.g., Goodson, in Medical Applications of Controlled Release, supra, vol. 2, pp. 115-138 (1984)).

**[0141]** Controlled release systems are discussed in the review by Langer (1990, Science 249:1527-1533). Any technique known to one skilled in the art can be used to produce sustained release formulations comprising one or more therapeutic composition of the invention. See, e.g., U.S. Pat. No. 4,526,938, PCT publication WO 91/05548, PCT publication WO 96/20698, Ning et al., 1996, "Intratumoral Radioimmunotheraphy of a Human Colon Cancer Xenograft Using a Sustained-Release Gel," Radiotherapy & Oncology 39:179-189, Song et al., 1995, "Antibody Mediated Lung Targeting of Long-Circulating Emulsions," PDA Journal of Pharmaceutical Science & Technology 50:372-397, Cleek et al., 1997, "Biodegradable Polymeric Carriers for a bFGF Antibody for Cardiovascular Application," Pro. Int'l. Symp. Control. Rel. Bioact. Mater. 24:853-854, and Lam et al., 1997, "Microencapsulation of Recombinant Humanized Monoclonal Antibody for Local Delivery," Proc. Int'l. Symp. Control Rel. Bioact. Mater. 24:759-760, each of which is incorporated herein by reference in their entireties.

**[0142]** Antibodies may be isolated from a subject after administration of the vaccine of the present invention. Methods of production of antibodies against SARS comprise administering an effective amount of modified plant to a subject and isolating antibodies from a sample of the subject after a period of time. The sample may be a biological fluid, such as blood, serum, plasma, saliva, urine, stool, sputum, nasopharyngeal aspirates, cells and tissues.

Demonstration of Prophylactic and Therapeutic Utility

**[0143]** The present invention provides methods for preventing, treating, ameliorating, and/or managing SARS by administration of the modified plants of the present invention to a subject in need thereof. Modified plants that are useful for the methods of the invention can be screened or assayed in a variety of ways for efficacy in treating or preventing SARS.

**[0144]** First, the immunopotency of a vaccine formulation containing the modified plant or extracts of the plant of the invention can be determined by monitoring the immune response of test animals following immunization with the vaccine. Generation of a humoral response may be taken as an indication of a generalized immune response, other components of which, particularly cell-mediated immunity, may be important for protection against a disease. Test animals may include mice, rabbits, chimpanzees and eventually human subjects. A vaccine made in this invention can be made to infect chimpanzees experimentally. However, since chimpanzees are a protected species, the antibody response to a vaccine of the invention can first be studied in a number of smaller, less expensive animals, with the goal of finding one or two best candidate modified plants that produce the best combinations of SARS-CoV viral epitopes to use be used in chimpanzee efficacy studies.

**[0145]** The safety of the vaccine can also be determined by observing or monitoring symptoms of subjects after administration of vaccine to a test subject. In a specific embodiment, the entire genome of SARS-CoV is used in the vaccine. In preferred embodiment, the plant express less than 10%, less than 20%, less than 25%, less than 30%, less than 35%, less than 40%, less than 45%, less than 50%, less than 55%, less than 60%, less than 65%, less than 70%, less than 80%, less than 90% of the SARS-CoV polypeptides.

**[0146]** The immune response of the test subjects can be analyzed by various approaches such as the reactivity of the resultant immune serum to antigens, as assayed by known techniques, e.g., enzyme linked immunosorbent assay (ELISA), immunoblots, radioimmunoprecipitations, etc.; or protection from infection and/or attenuation of disease symptoms in immunized hosts.

**[0147]** As one example of suitable animal testing, the vaccine composition of the invention may be tested in rabbits for the ability to induce an immune response to the SARS viral antigens. For example, male specific-pathogen-free (SPF) young adult New Zealand White rabbits may be used. The test group of rabbits each receives an effective amount of the vaccine, via any route of administration, e.g., ingestion of modified plant or injection of modified plant extract. A control group of rabbits receives an injection in 1 mM Tris-HCl pH 9.0 of the vaccine containing the same kind of plant extract from an unmodified plant of the same type. Blood samples may be drawn from the rabbits every one or two weeks, and serum analyzed for antibodies specific for the viral antigen was directed using, e.g., a radioimmunoassay (Abbott Laboratories). The presence of antibodies may be assayed using an ELISA. Because rabbits may give a variable response due to their outbred nature, it may also be useful to test the vaccines in mice.

**[0148]** In one embodiment, the invention relates to biological material collected from subjects to which the modified plants and/or plant extracts were administered, either by injection or ingestion. The biological material can be tested for the presence of SARS-CoV polypeptides or fragments thereof. Biological materials include, but are not limited to, blood, serum, plasma, saliva, urine, stool, sputum, nasopharyngeal aspirates, cells and tissues. The biological material can be collected 1 hour, 2 hours, 6 hours, 12 hours, 24 hours, 2 days, 3 days, or 1 week after administration of the modified plant and/or plant extracts of the present invention.

**[0149]** In addition, a modified plant of the invention may be tested by first administering the modified plant to a test subject, either animal or human, and then isolating the anti-anti-idiotypic antibodies (i.e., the Ab3 antibodies) generated as part of the anti-idiotype response to the viral antigens. The isolated Ab3 may then be tested for the ability to bind the particular viral antigen (e.g., by any immunoassays known in the art, for example, but not limited to, radioimmunoassays, ELISA, "sandwich" immunoassay, gel diffusion precipitin reactions, immunodiffusion assays, western blots, precipitation reactions, agglutination assays, complement fixation assays, immunofluorescence assays, protein A assays, immunoelectrophoresis assays, etc.)

**[0150]** In one aspect where the vaccine is directed against SARS-CoV viral antigen, the efficacy of the isolated Ab3 for treating SARS is screened by culturing SARS-CoV virus infected cells from a culture or a patient, contacting the cells with the Ab3 antibody to be tested, and comparing the proliferation or survival of the contacted cells with the proliferation or survival of cells not so contacted with the Ab3 antibody, wherein a lower level of proliferation or survival of the contacted cells indicates that the Ab3 antibody (which was elicited by immunization with the SARS-CoV viral antigen) is effective to treat the SARS in the patient. Many assays standard in the art can be used to assess such survival and/or growth; for example, cell proliferation can be assayed by measuring $^3$H-thymidine incorporation, by direct cell count, by detecting changes in transcriptional activity of known genes such as proto-oncogenes (e.g., fos, myc) or cell cycle markers; cell viability can be assessed by trypan blue staining, differentiation can be assessed visually based on changes in morphology.

**[0151]** The present invention also provides antibodies against the SARS-CoV virus subsequent to the administration of the modified plant of the invention to a subject in need thereof. An antibody that immunospecifically binds an antigen of the SARS-CoV virus may also be tested directly in vivo. To monitor the effect of an antibody of the invention, the level of the antigen is measured at suitable time intervals before, during, or after administration of the vaccine. Any change or absence of change in the amount of the antigen can be identified and correlated with the effect of the treatment on the subject.

**[0152]** In particular, in the case of SARS, the serum levels of a SARS-CoV antigen bears a direct relationship with severity of SARS. Generally, a decrease in the level of antigen is associated with efficacious treatment. The serum levels of SARS-CoV antigens in a treated subject can be measured every 1 hour, 2 hours, 3 hours, 6 hours, 12 hours, 24 hours, 2 days, 3 days, or 1 week after administration of the modified plant and/or plant extracts of the present invention to said subject.

**[0153]** In a preferred aspect, the approach that can be taken is to determine the levels of antigen at different time points and to compare these values with a baseline level. The baseline level can be either the level of the marker present in normal, disease free individuals; and/or the levels present prior to treatment, or during periods of stability. These levels can then be correlated with the disease course or treatment outcome.

**[0154]** The levels of antigen can be determined by any method well known in the art. For example, SARS-CoV viral antigen can be quantitated by known immunodiagnostic methods such as western blotting immunoprecipitation using any antibody against SARS-CoV antigen.

**[0155]** The strength of the immune response in vivo to the viral antigen may be determined by any method known in the art, for example, but not limited to, delayed hypersensitivity skin tests and assays of the activity of cytolytic T-lymphocytes in vitro.

**[0156]** Delayed hypersensitivity skin tests are of great value in the testing of the overall immunocompetence and cellular immunity to an antigen. Proper technique of skin testing requires that the antigens be stored sterile at 4° C., protected from light and reconstituted shortly before use. A 25- or 27-gauge need ensures intradermal, rather than subcutaneous, administration of antigen. Twenty-four and 48 hours after intradermal administration of the antigen, the largest dimensions of both erythema and induration are measured with a ruler. Hypoactivity to any given antigen or group of antigens is confirmed by testing with higher concentrations of antigen or, in ambiguous circumstances, by a repeat test with an intermediate test.

**[0157]** To test the activity of cytolytic T-lymphocytes, T-lymphocytes isolated from the immunized subject, e.g., by the Ficoll-Hypaque centrifugation gradient technique, are re-stimulated with cells bearing the antigen against SARS was directed in 3 ml RPMI medium containing 10% fetal calf serum. In some experiments, 33% secondary mixed lymphocyte culture supernatant or IL-2 is included in the culture medium as a source of T cell growth factors. In order to measure the primary response of cytolytic T-lymphocytes after immunization, the isolated T cells are cultured with or without the cells bearing the antigen. After six days, the cultures are tested for cytotoxity in a 4 hour $^{51}$Cr-release assay. The spontaneous $^{51}$Cr-release of the targets should reach a level less than 20% if immunization was effective (Heike et al., *J. Immunotherapy* Vol. 15, pages 15-174).

**[0158]** The efficacy of the antibody can be assayed by administering the antibody to a subject (either a human subject or an animal model for the disease) and then monitoring either the levels of the SARS-CoV viral antigens or symptoms of the particular infectious disease. The levels of the SARS-CoV viral antigens may be determined by any method known in the art for assaying the levels of SARS-CoV viral antigens, e.g., the viral titer, in the case of a virus, or bacterial levels (for example, by culturing of a sample from the patient), etc. A decrease in the levels of the viral antigens or an elimination, amelioration or reduction in the number of symptoms of SARS indicates that the antibody is effective. Symptoms of SARS include, but are not limited to, temperature of greater than 100.4° F. (>38° C.) (according to the CDC), chills, headache, malaise, body aches, cough, shortness of breath, difficulty breathing, and hypoxia. Radiographic evidence of pneumonia, respiratory distress syndrome, and autopsy findings are also useful to determine whether a subject is inflicted with, recovering from, or free of SARS.

Efficacy of the Prophylactic and Therapeutic Utilities

**[0159]** Toxicity and efficacy of the prophylactic and/or therapeutic protocols of the instant invention can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the $LD_{50}$ (the dose lethal to 50% of the population) and the $ED_{50}$ (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio $LD_{50}/ED_{50}$. Prophylactic and/or therapeutic agents that exhibit large therapeutic indices are preferred. While prophylactic and/or therapeutic agents that exhibit toxic side effects may be used, care should be taken to design a delivery system that targets such agents to the site of affected tissue in order to minimize potential damage to uninfected cells and, thereby, reduce side effects.

**[0160]** The data obtained from the cell culture assays and animal studies can be used in formulating a range of dosage of the prophylactic and/or therapeutic agents for use in humans. The dosage of such agents lies preferably within a range of circulating concentrations that include the $ED_{50}$ with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. For any agent used in the method of the invention, the therapeutically effective dose can be estimated initially from cell culture assays. A dose may be formulated in animal models to achieve a circulating plasma concentration range that includes the $IC_{50}$ (i.e., the concentration of the test compound that achieves a half-maximal inhibition of symptoms) as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Levels in plasma may be measured, for example, by high performance liquid chromatography.

## EXAMPLES

**[0161]** The following examples illustrate the generation of transgenic or transplastomic tobacco plants that comprise the M and/or S1 proteins of the SARS-CoV virus.

### Plasmid Construction

**[0162]** The backbone for construction of these plastid transformation vectors is derived from plasmid pVSR326 (Reddy et al., 2002, *Mol Breeding* 9: 259-269; PCT international application no. PCT/EP00/12446, international publication no. WO 01/42441). Plasmid pVSR326 utilizes the tobacco plastid genome sequences spanning rbcL-accD to target the reporter gene encoding β-glucuronidase (GUS) into the chloroplast genome by homologous recombination (Reddy et al., 2002). The promoter and terminator for GUS are derived from the rice plastid gene psbA; the psbA gene encoding the photosystem II 32 kD protein. The selectable marker gene aadA, which specifies spectinomycin-resistance, is driven from the rice plastid 16S rRNA operon (rrn) promoter and aadA is located adjacent to *GUS* (Reddy et al., 2002). In the pMLVHis vectors, other than unique restriction sites at this region, a start codon plus a $(His)_5$-tag is incorporated to facilitate the cloning and expression of $(His)_5$-tagged recombinant proteins.

### Construction of pCV1, a Plastid Transformation Vector for Expression of the S1 Antigen

**[0163]** The 2-kb SpeI-NotI fragment encoding S1 minus its start codon and signal peptide from pCRII-S1 was cloned into the NheI and NotI sites of pMLVHisA (**FIG. 4**). The plasmid pCRII-S1 was derived from pCRII (Invitrogen) and contains a PCR-amplified fragment of S1. In the resultant derivative, designated pCV1 (**FIG. 1**), amino acids 12-658 of S1 are fused in-frame to seventeen pMLVHisA-derived residues, including the 'ATG' start codon and a $(His)_5$-tag. Plasmid pMLVHisA is designed with a $(His)_5$-tag enabling recognition of the recombinant protein using antisera against the $(His)_5$-tag in western blot analysis. Also, the $(His)_5$-tag enables easy purification of the recombinant protein, if and when required, using Ni-NTA Agarose (Qiagen) affinity columns. The rice plastid psbA promoter drives expression of the recombinant protein and the terminator is also psbA-derived. The presence of flanking rbcL and accD sequences from the tobacco plastid genome enables homologous recombination to occur, resulting in the incorporation of S1 (and aadA) into the plastid genome of the target plant.

**[0164]** Since plant chloroplast genome sequences are highly-conserved, the same construct was used for plastid transformation of tobacco and tomato, both belonging to the same family Solanaceae.

### Construction of pCV2, a Nuclear Transformation Vector for Expression of the S1 Antigen

**[0165]** The 2-kb BamHI-XhoI fragment of S1 encoding amino acids 1-658 from pCRII-S1 was cloned into the BamHI and SalI sites of pSa7 (**FIG. 5**), a plant nuclear transformation vector. In this case, the signal peptide of S1 (amino acids 1-13) is retained because previous reports suggest that the presence of endoplasmic reticulum-targeting signals on plant nuclear-expressed foreign proteins results in improved protein stability (Richter et al., 2000, *Nature Biotech* 18: 1167-1171; Sojikul et al., 2003, *Proc. Natl. Acad. Sci.* 100: 2209-2214). In the resultant plasmid, pCV2 (**FIG. 19**), S1 is placed between the strong and constitutive Cauliflower Mosaic Virus 35S promoter and the nopaline synthase (NOS) terminator. This plasmid was introduced from *Escherichia coli* to *Agrobacterium tumefaciens* strain LBA4404 in the presence of *E. coli* helper strain HB101/pRK2013 by triparental mating (Horsch et al., 1985, *Science* 227: 1227-1231).

### Construction of pCV8, a Plastid Transformation Vector for Expression of the M Antigen

**[0166]** The 0.7-kb NcoI-SacI fragment encoding M from plasmid pCRII-M was cloned into the NcoI and SacI sites of pMLVHisA (**FIG. 4**) to generate pCV7. The plasmid pCRII-M was derived from pCRII (Invitrogen) and contains a PCR-amplified fragment of M. Subsequently, plasmid pCV7 was digested with NcoI and a $(His)_6$-tag was introduced into this site using annealed oligomers ML527 (5'-CATGGCCGCGCGGGGTTCTCATCATCATCATCATCATGG-3'; SEQ ID NO:10) and ML528 (5'-CATGCCATGATGATGATGATGATGAGAACCCCGCGCGGC-3'; SEQ ID NO:11) to create pCV8 (**FIG. 7**). The resultant M expressed from pCV8 is a $(His)_6$-tagged protein.

### Construction of pCV4, a Nuclear Transformation Vector for Expression of the M Antigen

**[0167]** The 0.7-kb BamHI fragment encoding M from plasmid pCRII-M was cloned into the BamHI site of plant nuclear transformation vector pSal3. Plasmid pSal3 was derived from plasmid pSa7 (**FIG. 5**) by removal of a 0.58-kb SalI fragment of SaPIN2a cDNA followed by religation.

### Construction of pCV6, a Plastid Transformation Vector for Co-Expression of the S1 and M Antigens

**[0168]** A 1.2-kb partial BamHI fragment consisting of the M-gene fused to the psbA terminator and the rrn promoter, in this order, from plasmid pCV3 was cloned into the BamHI unique site of plasmid pCV1 to generate plastid transformation vector pCV6 (**FIG. 21**) that co-expresses the S1 and M antigens. Plasmid pCV3 was obtained by cloning a 0.7-kb EcoRV-SacI fragment encoding M from pCRII-M in the StuI-SacI sites of pMLVHisA.

### Codon Usage Optimization of SARS-CoV S1 Gene by Site Directed Mutagenesis

**[0169]** Plasmid pCRII-S1 was used as a mutagenesis template for generating derivatives of codon usage optimization. Mutagenesis was carried out by PCR with PfuTurbo DNA polymerase using the 'QuikChange Multi site-directed mutagenesis kit' (Stratagene), according to the manufacturer's specifications. Table 1 shows the oligonucleotides used for site-directed mutagenesis. The amplification procedure included denaturation at 95° C. for 1 min, followed by 30 cycles of denaturation (95° C. for 1 min), annealing (55° C. for 1 min) and extension (65° C. for 12 min). The amplified product was treated with DpnI to remove template DNA and the mutated DNA was used in transformation of *E. coli* XL10-Gold cells. DNA sequencing analysis was performed to confirm each mutation. A total of 13 nucleotide changes (as summarized in Table 1) incorporated in an "optimized" S1 was then used for cloning in plastid and nuclear transformation vectors.

TABLE 1

Oligonucleotides used for site-directed mutagenesis of S1 for codon optimization

| Affected Residue | Sequence of primer | |
|---|---|---|
| | Forward primers: | |
| R18 | 5'-GGTAGTGACCTTGAC*A*G*A*TGCACCACTT TTGAT-3'; | SEQ ID NO:12 |
| T75 | 5'-GGGTTTCATACTATTAATCATAC*T*TTTG GCAACCCTGTCATAC-3'; | SEQ ID NO:13 |
| S113 | 5'-CCATGAACAACAAGTCACAGTC*T*GTGAT TATTATTAACAATTCTACT-3'; | SEQ ID NO:14 |
| S169 | 5'-AGTACATATCTGATGCCTTTTC*T*CTTGA TGTTTCAGAAAAGTC-3'; | SEQ ID NO:15 |
| L209 | 5'-CCTATAGATGTAGTTCGTGATCT*T*CCTT CTGGTTTTAACACTTTG-3'; | SEQ ID NO:16 |
| T247 | 5'-CAAGACATTTGGGGCAC*T*TCAGCTGCAG CCTAT-3'; | SEQ ID NO:17 |
| A398 | 5'-GATGATGTAAGACAAATAGC*T*CCAGGAC AAACTGG-3'; | SEQ ID NO:18 |
| P507 | 5'-TCTTTTGAACTTTTAAATGCACC*T*GCCA CGGTTTGTGGACC-3'; | SEQ ID NO:19 |
| T509 | 5'-CTTTTAAATGCACCTGCCAC*T*GTTTGTG GACCAAAATTATC-3'; | SEQ ID NO:20 |
| L597 | 5'-CTTCATCTGAAGTTGCTGTTCT*T*ATCAA GATGTTAACTGCAC-3'; | SEQ ID NO:21 |
| R620 | 5'-CAACTCACACCAGCTTGG*A*G*A*ATATATT CTACTGGAAACAATG-3'; | SEQ ID NO:22 |
| | Reverse primers: | |
| R18 | 5'-ATCAAAAGTGGTGCA*T*C*T*GTCAAGGTCA CTACC-3'; | SEQ ID NO:23 |
| R620 | 5'-CATTGTTTCCAGTAGAATATAT*T*C*T*CCA AGCTGGTGTGAGTTG-3'; | SEQ ID NO:24 |

*nucleotides in italics are mutated. The affected codons are underlined.

Plant Transformation

Plastid Transformation of Tobacco and Tomato for Expression of the S1 and/or M Antigens

**[0170]** Each plastid transformation construct (pCV1, pCV6 or pCV8, and its derivatives containing an S1 with nucleotide (but not amino acid) changes to optimize codon usage for expression in plants) was introduced by particle gun bombardment into tobacco (Staub and Maliga, 1994, *Plant Journal* 6: 547-553) and tomato (Ruf et al., 2001, *Nature Biotech* 19: 870-875).

Plastid Transformation of *Lycopersicon esculentum* cv. UC82B

**[0171]** Plastid transformation was carried out following Ruf et al., 2001, by bombardment of young leaves with tungsten particles coated with the desired DNA (pCV1, pCV6 or pCV8, and its derivatives containing an S1 with nucleotide (but not amino acid) changes to optimize codon usage for expression in plants).

**[0172]** Aseptical seeds were germinated on Murashige and Skoog (MS) medium (Murashige and Skoog, 1962, *Physiol. Plant.* 15: 473-497), supplemented with agar (5 g/liter) and sucrose (30 g/liter). For bombardment, young leaves from outgrowing axillary meristem were placed abaxial side facing up on RMOP medium containing MS salts, 6-benzylaminopurine (1 mg/liter), α-naphthalene acetic acid (0.1 mg/liter), thiamine (1 mg/liter), myo-inositol (100 mgaiter), agar (5 g/liter) at pH 5.7 and sucrose (30 g/liter). Bombardment was carried out using the particle delivery system, PDS1000-He (Bio-Rad) and its accessories. Tungsten particles (M 17) were coated with desired DNA and leaves bombarded. After bombardment, leaves were cut into small pieces and placed on RMOP selection medium containing spectinomycin dihydrochloride (250 mg/liter). Greenish yellow calli were passaged for few more cycles in the selection medium to obtain homoplastomic plastid-containing calli. From this calli plant regeneration will be achieved.

Plastid Transformation of *N. tabacum* cv. *xanthi*

**[0173]** Plastid transformation was carried out following Svab and Maliga (Svab et al., 1993, *Proc. Natl. Acad. Acad. Sci. USA* 90: 913-917) by bombardment of leaves with tungsten particles coated with the desired DNA (pCV1, pCV6 or pCV8, and its derivatives containing an S1 with nucleotide (but not amino acid) changes to optimize codon usage for expression in plants).

**[0174]** Aseptical seeds were germinated on Murashige and Skoog (MS) medium (Murashige and Skoog, 1962, *Physiol. Plant.* 15: 473-497), supplemented with agar (5 g/liter) and sucrose (30 g/liter). For bombardment, leaves were placed abaxial side facing up on RMOP medium containing MS salts, 6-benzylaminopurine (1 mg/liter), α-naphthalene acetic acid (0.1 mg/liter), thiamine (1 mg/liter), myo-inositol (100 mg/liter), agar (5 g/liter) at pH 5.7 and sucrose (30 g/liter). Bombardment was carried out using the particle delivery system, PDS 1000-He (Bio-Rad) and its accessories. Tungsten particles (M 17) were coated with desired DNA and leaves bombarded. After bombardment, leaves were cut into small pieces and placed on RMOP selection medium containing spectinomycin dihydrochloride (500 mg/liter). The regenerated plantlets obtained following plastid transformation of tobacco using vector pCV1 (**FIG. 23F-23G**) were passaged for five more cycles in selection medium to obtain homoplastomic plastid-containing plants. Results of PCR analysis (**FIG. 23H**) using S1 primers ML560 (5'-CAGAGAGAGTTTCCCGGATTC-3'; SEQ ID NO:25) and ML567 (5'-CAACCTATAGATGTAGTTCG-3'; SEQ ID NO:26) and of northern blot analysis (**FIG. 23I**) using an $^{32}$P-radiolabeled S1 probe are shown. **FIG. 23J** shows western blot analysis of transplastomic tobacco expressing a modified S1 (with nucleotide changes as stipulated in Table 1) using Ni-NTA conjugate in detection of a His-tagged S1 protein. The arrow indicates the expected 73-kDa $(His)_5$-S1 band.

Nuclear Transformation of Tobacco and Lettuce for Expression of S1 or M Antigen

**[0175]** Production of transgenic tobacco and transgenic lettuce expressing S1 or M antigen by nuclear transformation was carried out using *Agrobacterium*-mediated transformation (Horsch et al., 1985, *Science* 227: 1227-1231) with plasmids pCV2 [and its derivative containing an S1 with nucleotide (but not amino acid) changes to optimize codon usage for expression in plants] and pCV4, respectively.

**[0176]** Following *Agrobacterium*-mediated transformation, shoots of tobacco **(FIG. 23A)** and lettuce **(FIG. 23C)** were rooted and the regenerated shoots **(FIG. 23**, B, D) were used in PCR analysis using primers 35S and NOS-ter that are located within the CaMV 35S promoter and the NOS-terminator, respectively. Southern blot analysis using a $^{32}$P-labeled S1 probe of these PCR-amplified DNA is shown in **FIG. 23E**. A 2.1-kb hybridizing band confirms the presence of S1-containing transgenic lines **(FIG. 23E**; lanes 2-5).

Nuclear Transformation of Tobacco for Expression of S1:GFP Antigen

**[0177]** Production of transgenic tobacco expressing a protein fusion consisting of the SARS-CoV S1 protein fused with green fluorescent protein (GFP) was carried out using *Agrobacterium*-mediated transformation (Horsch et al. supra.) with plasmid pCV12.

**[0178]** Two days after agroinfiltration, representative tobacco leaf epidermal cells were selected and observed by confocal microscopy (Yang Y. et al., In vivo analysis of plant promoters and transcription factors by agroinfiltration of tobacco leaves. *Plant J*. 2000; 22: 543-551) of *Agrobacterium tumefaciens* LBA4404 harboring plasmid pCV12 expressing S1:GFP fusion protein **(FIG. 18**, A, C) or LBA4404 harboring pGDG expressing GFP alone **(FIG. 18**, B, D). Bar represents 20 μm.

**[0179]** Western blot analysis was performed using antibodies against GFP and showed transient expression of S1:GFP in the tobacco leaves following agroinfiltration. Total protein (200 μg) extracted from tobacco leaves, infiltrated with plasmid pGDG expressing GFP alone **(FIG. 23**, lane 1) or plasmid pCV12 expressing S1:GFP fusion **(FIG. 23**, lane 2), were separated on a 8% SDS-PAGE gel, blotted onto Hybond-C filters according to Sambrook et al. (1989. Molecular Cloning: A Laboratory Manual. Cold Spring Harbor Laboratory Press, Cold Spring Harbor), and cross-reacted with antibodies against GFP (Clontech). The results are shown in **FIG. 24**, wherein arrow indicates cross-reacting S1:GFP band (calculated size 99.1 kDa) and M is the molecular mass marker.

**[0180]** Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

**[0181]** All publications, patents and patent applications mentioned in this specification are herein incorporated by reference into the specification to the same extent as if each individual publication, patent or patent application was specifically and individually indicated to be incorporated herein by reference.

**[0182]** Citation or discussion of a reference herein shall not be construed as an admission that such is prior art to the present invention.

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## SEQUENCE LISTING

The patent application contains a lengthy “Sequence Listing” section. A copy of the “Sequence Listing” is available in electronic form from the USPTO web site (http://seqdata.uspto.gov/?pageRequest=docDetail&DocID=US20060053516A1). An electronic copy of the “Sequence Listing” will also be available from the USPTO upon request and payment of the fee set forth in 37 CFR 1.19(b)(3).

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**1**. A vector comprising an isolated nucleic acid which nucleic acid sequence is set forth in SEQ ID NO:708 or 709, or a fragment, derivative or analog thereof.

**2**. The vector in accordance with claim 1, wherein the vector is a plastid transformation vector.

**3**. The vector in accordance with claim 2, wherein the vector is pCV1, pCV6, pCV8, or a derivative thereof containing an S1 with at least one nucleotide change.

**4**. The vector in accordance with claim 1, wherein the vector is a nuclear transformation vector.

**5**. The vector in accordance with claim 4, wherein the vector is pCV2, pCV4, pCV12, or a derivative thereof containing an S1 with at least one nucleotide change.

**6**. The vector in accordance with claim 1, wherein the isolated nucleic acid encodes the S protein of the SARS-CoV virus, the M protein of the SARS-CoV virus, or both.

**7**. The vector in accordance with claim 1, wherein the isolated nucleic acid comprises the nucleic acid sequence as set forth in SEQ ID NO:4023, 4025, or a fragment, derivative or analog thereof.

**8**. The vector in accordance with claim 1, wherein the isolated nucleic acid encodes the amino acid sequence as set forth in SEQ ID NO:4024 or 4026, or a fragment, derivative or analog thereof.

**9**. The vector in accordance with claim 1, wherein the isolated nucleic acid hybridizes under high stringency conditions to the nucleic acid sequence of SEQ ID NO:4023, 4025, 708, or 709, or a complement thereof.

**10**. A plant cell comprising an isolated nucleic acid which nucleic acid sequence is set forth in SEQ ID NO:708, 709, or a fragment, derivative or analog thereof.

**11**. The plant cell in accordance with claim 10, wherein the isolated nucleic acid encodes the S protein of the SARS-CoV virus, the M protein of the SARS-CoV virus, or both.

**12**. The plant cell in accordance with claim 10, wherein the isolated nucleic acid comprises the nucleic acid sequence as set forth in SEQ ID NO:4023, 4025, or a fragment, derivative or analog thereof.

**13**. The plant cell in accordance with claim 10, wherein the isolated nucleic acid encodes the amino acid sequence as set forth in SEQ ID NO:4024 or 4026, or a fragment, derivative or analog thereof.

**14**. The plant cell in accordance with claim 10, wherein the isolated nucleic acid hybridizes under high stringency conditions to the nucleic acid sequence of SEQ ID NO:4023, 4025, 708, or 709, or a complement thereof.

**15**. The plant cell in accordance with claim 10, wherein the plant cell is isolated from a plant selected from the group consisting of tobacco, lettuce, tomato, potato, banana, corn, rice, cereals, wheat, maize, barley, apple, pear, strawberry, carrot, sugar beets, yam, kiwifruit, or spinach.

**16**. A plant cell comprising the vector in accordance with claim 1.

**17**. A method of immunization against SARS comprising administering to a subject a plant, wherein the plant comprises an isolated nucleic acid which nucleic acid sequence is set forth in SEQ ID NO:708, 709, or a fragment, derivative, analog, or vector thereof.

**18**. The method in accordance to claim 17, wherein the isolated nucleic acid encodes the S protein of the SARS-CoV virus, the M protein of the SARS-CoV virus, or both.

**19**. The method in accordance to claim 17, wherein the isolated nucleic acid comprises the nucleic acid sequence as set forth in SEQ ID NO:4023, 4025, or a fragment, derivative or analog thereof.

**20**. The method in accordance to claim 17, wherein the isolated nucleic acid encodes the amino acid sequence as set forth in SEQ ID NO:4024 or 4026, or a fragment, derivative or analog thereof.

**21**. The method in accordance to claim 17, wherein the isolated nucleic acid hybridizes under high stringency conditions to the nucleic acid sequence of SEQ ID NO:4023, 4025, 708, or 709, or a complement thereof.

**22**. The method in accordance to claim 17, where the administering to the subject is oral administration.

**23**. The method in accordance to claim 17, wherein subject is human.

**24**. A method of immunization against SARS comprising administering to a subject a vector in accordance with claim 1 and an acceptable pharmaceutical carrier.

**25**. The method in accordance to claim 24, wherein the subject is human.

**26**. A plant comprising the isolated nucleic acid which nucleic acid sequence is set forth in SEQ ID NO:708, 709, or a fragment, derivative or analog thereof.

**27**. The plant in accordance with claim 26, which is selected from the group consisting of tobacco, lettuce, tomato, potato, banana, corn, rice, cereals, wheat, maize, barley, apple, pear, strawberry, carrot, sugar beets, yam, kiwifruit, or spinach.

**28**. A composition comprising a SARS-CoV viral antigen produced by the plant cell of claim 10.

**29**. A composition comprising a SARS-CoV viral antigen produced by the plant cell of claim 16.

**30**. A composition comprising a SARS-CoV viral antigen produced by the plant of claim 26.

**31**. A method of detecting an antibody to a SARS-CoV viral antigen in a sample comprising:

(a) contacting the sample with the composition of claim 28; and

(b) detecting the presence of an antibody bound to the composition of claim 28, thereby detecting an antibody to a SARS-CoV viral antigen.

**32**. The method in accordance with claim 31, wherein the sample is a biological fluid.

**33**. The method in accordance with claim 32, wherein the biological fluid is blood, serum, plasma, saliva, urine, stool, sputum, nasopharyngeal aspirates, cells or tissues.

**34**. A method of detecting an antibody to a SARS-CoV viral antigen in a sample comprising:

(a) contacting the sample with the composition of claim 29; and

(b) detecting the presence of an antibody bound to the composition of claim 29, thereby detecting an antibody to a SARS-CoV viral antigen.

**35**. The method in accordance with claim 34, wherein the sample is a biological fluid.

**36**. The method in accordance with claim 35, wherein the biological fluid is blood, serum, plasma, saliva, urine, stool, sputum, nasopharyngeal aspirates, cells or tissues.

**37**. A method of detecting an antibody to a SARS-CoV viral antigen in a sample comprising:

(a) contacting the sample with the composition of claim 30; and

(b) detecting the presence of an antibody bound to the composition of claim 30, thereby detecting an antibody to a SARS-CoV viral antigen.

**38**. The method in accordance with claim 37, wherein the sample is a biological fluid.

**39**. The method in accordance with claim 38, wherein the biological fluid is blood, serum, plasma, saliva, urine, stool, sputum, nasopharyngeal aspirates, cells or tissues.

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