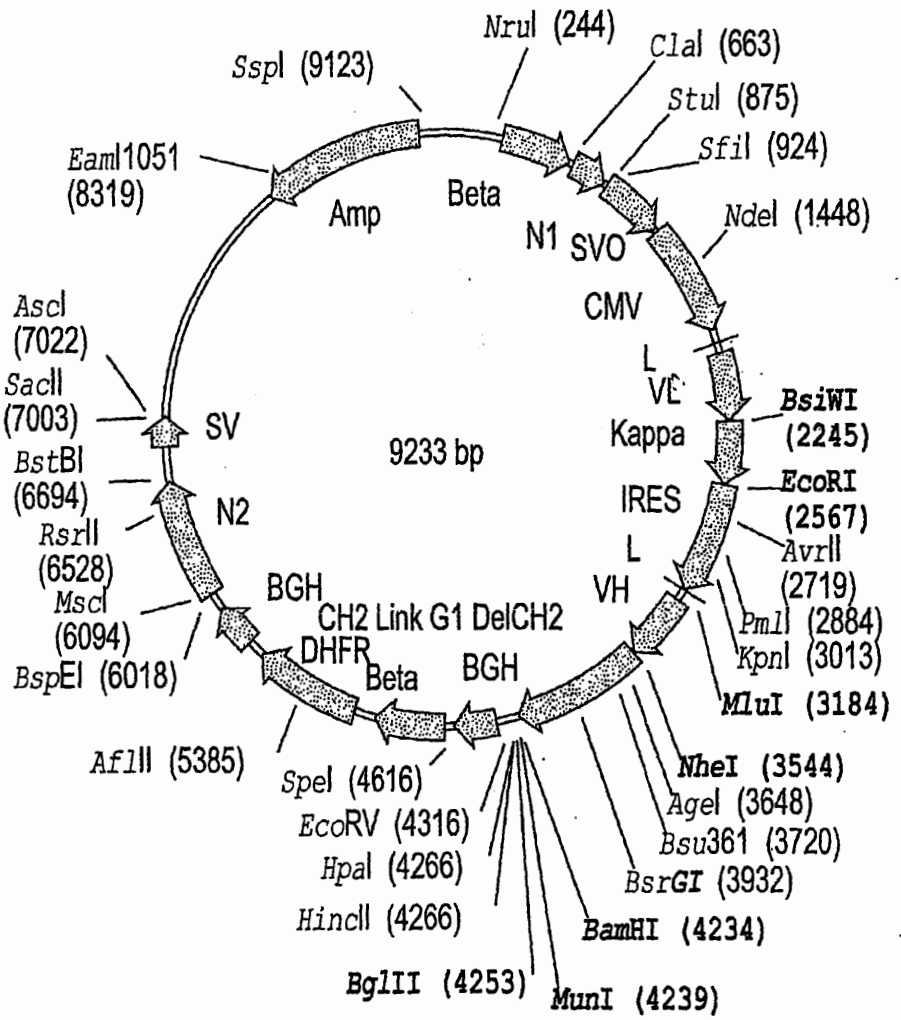

NruI (244)
ClaI (663)
StuI (875)
SfiI (924)
NdeI (1448)
BsiWI (2245)
EcoRI (2567)
AvrII (2719)
PmlI (2884)
KpnI (3013)
MluI (3184)
NheI (3544)
AgeI (3648)
Bsu361 (3720)
BsrGI (3932)
BamHI (4234)
MunI (4239)
BglII (4253)
HincII (4266)
HpaI (4266)
EcoRV (4316)
SpeI (4616)
AflII (5385)
BspEI (6018)
MscI (6094)
RsrII (6528)
BstBI (6694)
SacII (7003)
AscI (7022)
SspI (9123)
EamI1051 (8319)
Amp
Beta
N1
SVO
CMV
L
VL
Kappa
IRES
L
VH
BGH
CH2 Link G1 DelCH2
DHFR
Beta
BGH
SV
N2
9233 bp

FIG. 1

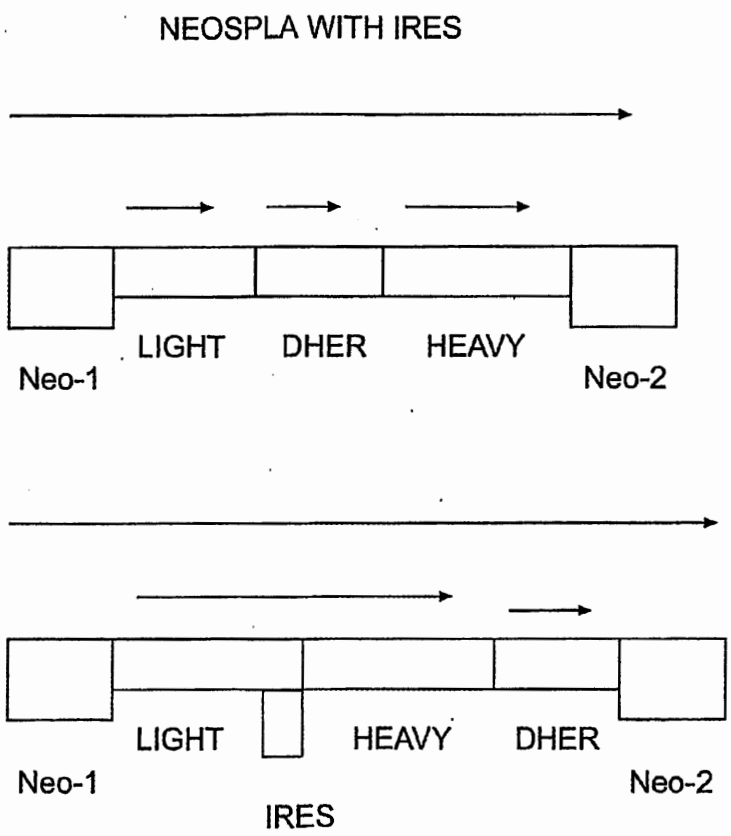

NEOSPLA WITH IRES
LIGHT
DHER
HEAVY
Neo-1
Neo-2
LIGHT
HEAVY
DHER
Neo-1
Neo-2
IRES

FIG. 2

Hucc49 CH2 Linker in N5KG1DelCH2

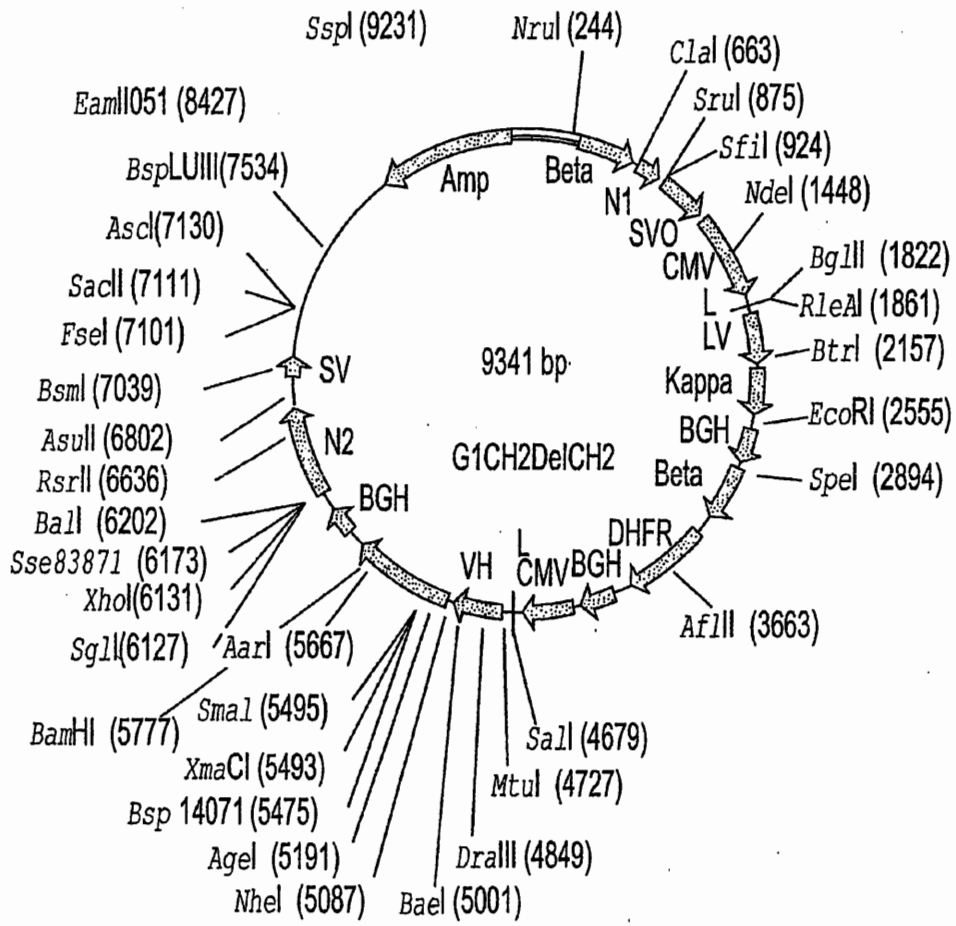


FIG. 3

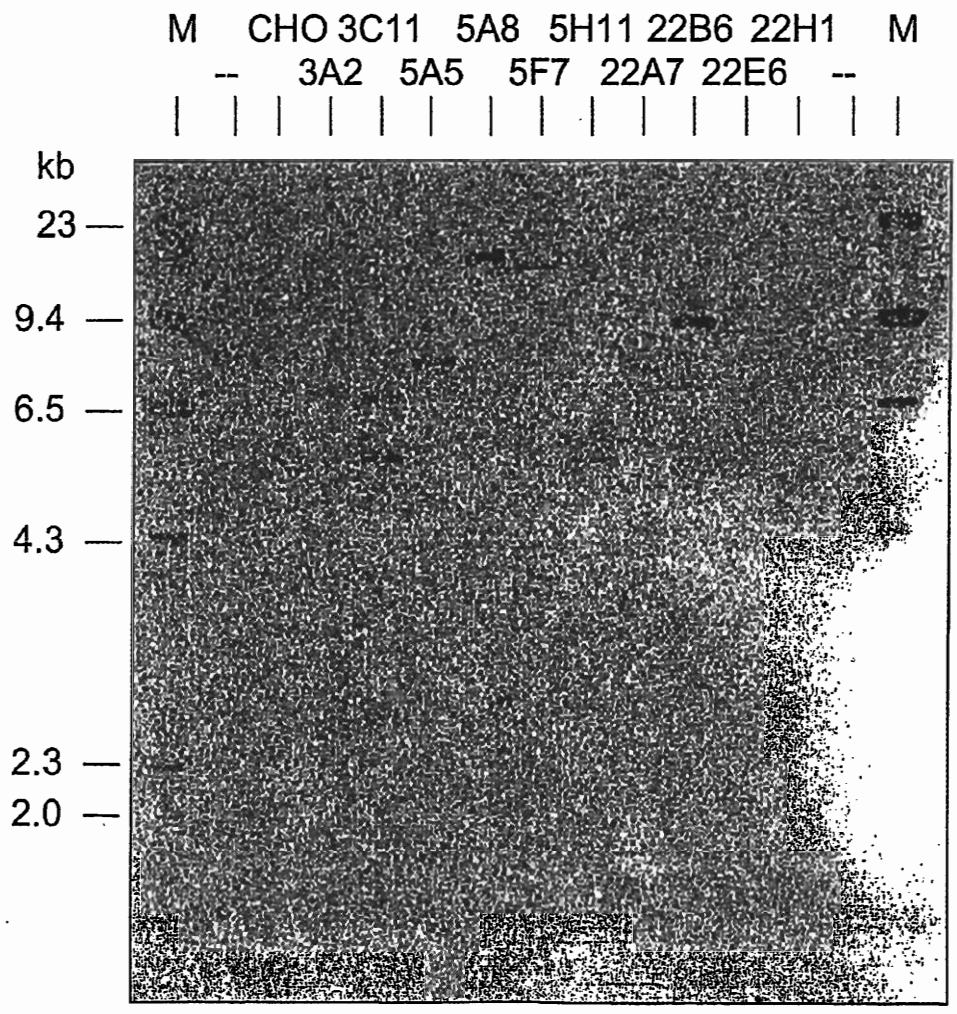

M
CHO
3C11
5A8
5H11
22B6
22H1
M
--
3A2
5A5
5F7
22A7
22E6
--
kb
23
9.4
6.5
4.3
2.3
2.0

FIG. 4

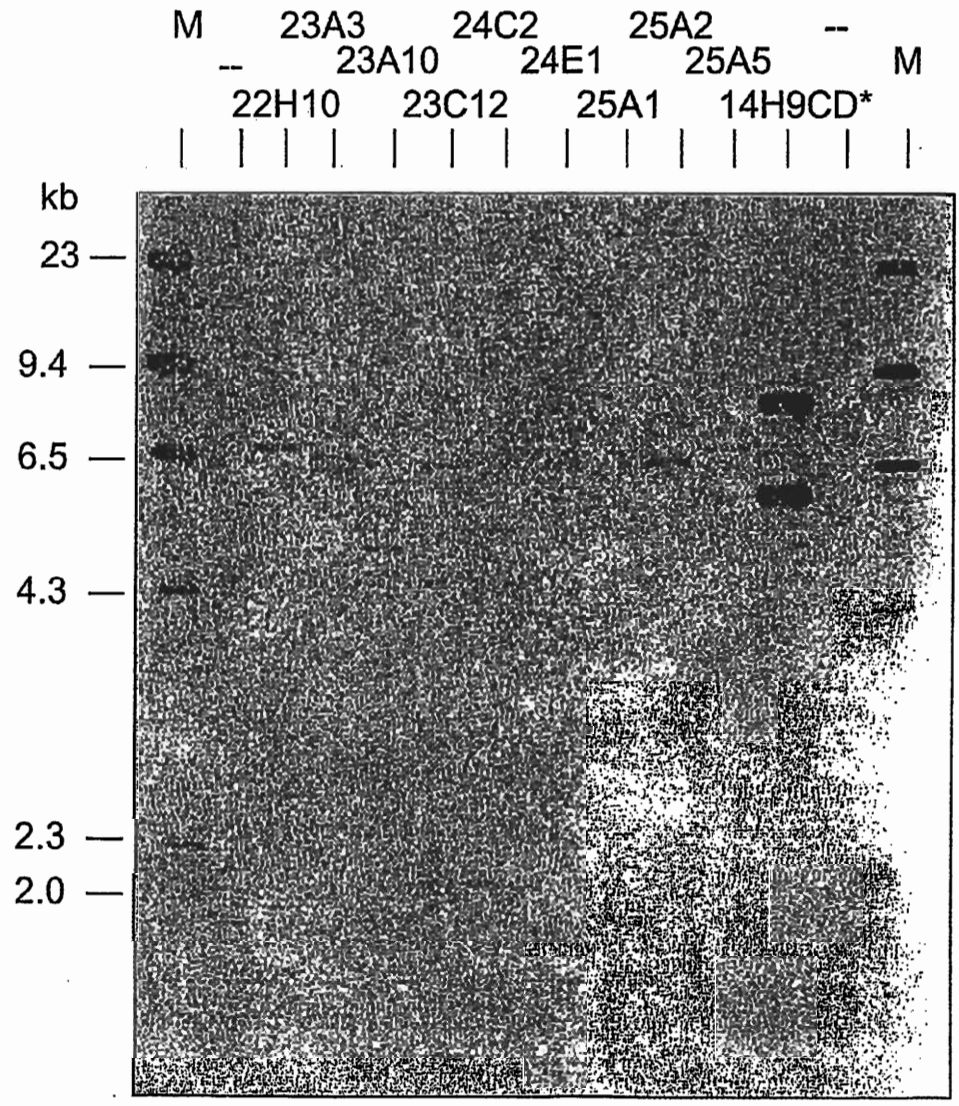

M
--
22H10
23A3
23A10
23C12
24C2
24E1
25A1
25A2
25A5
14H9CD*
--
M
kb
23
9.4
6.5
4.3
2.3
2.0

FIG. 5

```
1    CTGACGCGCC CTGTAGCGGC GCATTAAGCG CGGCGGGTGT GGTGGTTACG
     CGCAGCGTGA
 61  CCGCTACACT TGCCAGCGCC CTAGCGCCCG CTCCTTTCGC TTTCTTCCCT
     TCCTTTCTCG
121  CCACGTTCGC CGGCTTTCCC CGTCAAGCTC TAAATCGGGG GCTCCCTTTA
     GGGTTCCGAT
181  TTAGTGCTTT ACGGCACCTC GACCCCAAAA AACTTGATTA GGGTGATGGT
     TCACGTAGGG

     Beta

     -----------------
     NruI
     ------
241  TCGCGACGTA CCGGGCCCCC CCTCGATTAA TTAATCGAGC TACTAGCTTT
     GCTTCTCAAT
                                  Beta
     ----------------------------------------------------
     ---------
301  TTCTTATTTG CATAATGAGA AAAAAAGGAA AATTAATTTT AACACCAATT
     CAGTAGTTGA
                                  Beta
     ----------------------------------------------------
     ---------
361  TTGAGCAAAT GCGTTGCCAA AAAGGATGCT TTAGAGACAG TGTTCTCTGC
     ACAGATAAGG
                                  Beta
     ----------------------------------------------------
     ---------
421  ACAAACATTA TTCAGAGGGA GTACCCAGAG CTGAGACTCC TAAGCCAGTG
     AGTGGCACAG
                                  Beta
     ----------------------------------------------------
     ---------
481  CATCCAGGGA GAAATATGCT TGTCATCACC GAAGCCTGAT TCCGTAGAGC
     CACACCCTGG
                                  Beta
     ----------------------------------------------------
     ---------
541  TAAGGGCCAA TCTGCTCACA CAGGATAGAG AGGGCAGGAG CCAGGGCAGA
     GCATATAAGG
                             Beta
     ------------------------------------------------
601  TGAGGTAGGA TCAGTTGCTC CTCACATTTG CTTCTGACAT AGTTGTGCCA
     GCATGGAGGA
                                        N1
     ------------------------------------------------
     ClaI
```

FIG. 6A

```
      ------
661 ATCGATCCTC CATGCTTGAA CAAGATGGAT TGCACGCAGG TTCTCCGGCC
    GCTTGGGTGG
                                 N1
    ----------------------------------------------------
    ---------
721 AGAGGCTATT CGGCTATGAC TGGGCACAAC AGACAATCGG CTGCTCTGAT
    GCCGCCGTGT
                                 N1
    ----------------------------------------------------
    ----------
781 TCCGGCTGTC AGCGCAGGGG CGCCCGGTTC TTTTTGTCAA GACCGACCTG
    TCCGGTGCCC
          N1                                       SVO
    ----------------
    ---------------------------------
                                       StuI
                                      ------
841 TGAATGAACT GCAGGTAAGT GCGGCCGCTC TAGGCCTCCA AAAAAGCCTC
    CTCACTACTT
                                 SVO
    ----------------------------------------------------
    ---------
                     SfiI
                  --------------
901 CTGGAATAGC TCAGAGGCCG AGGCGGCCTC GGCCTCTGCA TAAATAAAAA
    AAATTAGTCA
                                 SVO
    ----------------------------------------------------
    ---------
961 GCCATGCATG GGGCGGAGAA TGGGCGGAAC TGGGCGGAGT TAGGGGCGGG
    ATGGGCGGAG
                                 SVO
    ----------------------------------------------------
    ---------
1021 TTAGGGGCGG GACTATGGTT GCTGACTAAT TGAGATGCAT GCTTTGCATA
    CTTCTGCCTG
                                 SVO
    ----------------------------------------------------
    ---------
```

FIG. 6B

```
1081 CTGGGGAGCC TGGGGACTTT CCACACCTGG TTGCTGACTA ATTGAGATGC
     ATGCTTTGCA
                                SVO
     ----------------------------------------------------
     ---------

1141 TACTTCTGCC TGCTGGGGAG CCTGGGGACT TTCCACACCC TAACTGACAC
     ACATTCCACA
     SVO                                  CMV
     -
     ------------------------------------------------
1201 GAATTAATTC CCCTAGTTAT TAATAGTAAT CAATTACGGG GTCATTAGTT
     CATAGCCCAT
                                CMV
     ----------------------------------------------------
     ---------
1261 ATATGGAGTT CCGCGTTACA TAACTTACGG TAAATGGCCC GCCTGGCTGA
     CCGCCCAACG
                                CMV
     ----------------------------------------------------
     ---------
1321 ACCCCCGCCC ATTGACGTCA ATAATGACGT ATGTTCCCAT AGTAACGCCA
     ATAGGGACTT
                                CMV
     ----------------------------------------------------
     ---------
1381 TCCATTGACG TCAATGGGTG GAGTATTTAC GGTAAACTGC CCACTTGGCA
     GTACATCAAG
                                CMV
     ----------------------------------------------------
     ---------
          Ndel
          -------
1441 TGTATCATAT GCCAAGTACG CCCCCTATTG ACGTCAATGA CGGTAAATGG
     CCCGCCTGGC
                                CMV
     ----------------------------------------------------
     ---------
1501 ATTATGCCCA GTACATGACC TTATGGGACT TTCCTACTTG GCAGTACATC
     TACGTATTAG
                                CMV
     ----------------------------------------------------
     ---------
```

FIG. 6C

```
1561 TCATCGCTAT TACCATGGTG ATGCGGTTTT GGCAGTACAT CAATGGGCGT
     GGATAGCGGT
                               CMV
     ----------------------------------------------------
     ---------
1621 TTGACTCACG GGGATTTCCA AGTCTCCACC CCATTGACGT CAATGGGAGT
     TTGTTTTGGC
                               CMV
     ----------------------------------------------------
     ---------
1681 ACCAAAATCA ACGGGACTTT CCAAAATGTC GTAACAACTC CGCCCCATTG
     ACGCAAATGG
                         CMV
     -------------------------------------------
1741 GCGGTAGGCG TGTACGGTGG GAGGTCTATA TAAGCAGAGC TGGGTACGTG
     AACCGTCAGA
                                                          L
     -----------------
1801 TCGCCTGGAG ACGCCATCAC AGATCAAAGC TTTGATCTCT CACCATGGAT
     AGCCAGGCCC

     VL
     -----------------
                       L
     ---------------------------------------------
                            RleAI
                            ------
1861 AGGTGCTCAT GCTCCTGCTG CTGTGGGTGA GCGGCACATG CGGCGACATC
     GTGATGAGCC
                                 VL
     ----------------------------------------------------------
     ---------
1921 AGTCTCCAGA CTCCCTGGCC GTGTCCCTGG GCGAGAGGGT GACTCTGAAT
     TGCAAGTCCA
                                 VL
     ----------------------------------------------------------
     ---------
1981 GCCAGTCCCT GCTCTATAGC GGAAATCAGA AGAACTATCT CGCCTGGTAT
     CAGCAGAAAC
                                 VL
     ----------------------------------------------------------
     ---------
```

FIG.6D

2041 CAGGGCAGAG CCCTAAACTG CTGATTTACT GGGCATCCGC TAGGGAATCC
GGCGTGCCTG

VL

2101 ATCGCTTCAG CGGCAGCGGA TCTGGGACAG ACTTCACTCT GACAATCAGC
AGCGTGCAGG

VL

2161 CAGAAGACGT GGCAGTCTAT TATTGTCAGC AGTATTATAG CTATCCCCTC
ACATTCGGCG

Kappa

VL

2221 CTGGCACCAA GCTGGAACTG AAACGTACGG TGGCTGCACC ATCTGTCTTC
ATCTTCCCGC

Kappa

2281 CATCTGATGA GCAGTTGAAA TCTGGAACTG CCTCTGTTGT GTGCCTGCTG
AATAACTTCT

Kappa

2341 ATCCCAGAGA GGCCAAAGTA CAGTGGAAGG TGGATAACGC CCTCCAATCG
GGTAACTCCC

Kappa

2401 AGGAGAGTGT CACAGAGCAG GACAGCAAGG ACAGCACCTA CAGCCTCAGC
AGCACCCTGA

Kappa

2461 CGCTGAGCAA AGCAGACTAC GAGAAACACA AAGTCTACGC CTGCGAAGTC
ACCCATCAGG

Kappa

FIG.6E

```
     IRES
     ----------------------------------------------------------
     ---------
                                                          EcoRI
                                                          -------
2521 GCCTGAGCTC GCCCGTCACA AAGAGCTTCA ACAGGGGAGA GTGTTGAATT
     CCTCCCTCCC
                                IRES
     ----------------------------------------------------------
     ---------
2581 CCCCCCCTAA CGTTACTGGC CGAAGCCGCT TGGAATAAGG CCGGTGTGCG
     TTTGTCTATA
                                IRES
     ----------------------------------------------------------
     ---------
2641 TGTTATTTTC CACCATATTG CCGTCTTTTG GCAATGTGAG GGCCCGGAAA
     CCTGGCCCTG
                                IRES
     ----------------------------------------------------------
     ---------
                    AvrII
                    -------
2701 TCTTCTTGAC GAGCATTCCT AGGGGTCTTT CCCCTCTCGC CAAAGGAATG
     CAAGGTCTGT
                                IRES
     ----------------------------------------------------------
     ---------
2761 TGAATGTCGT GAAGGAAGCA GTTCCTCTGG AAGCTTCTTG AAGACAAACA
     ACGTCTGTAG
                                IRES
     ----------------------------------------------------------
     ---------
2821 CGACCCTTTG CAGGCAGCGG AACCCCCCAC CTGGCGACAG GTGCCTCTGC
     GGCCAAAAGC
                                IRES
     ----------------------------------------------------------
     ---------
     PmaCI
     ------
```

FIG. 6F

```
2881 CACGTGTATA AGATACACCT GCAAAGGCGG CACAACCCCA GTGCCACGTT
     GTGAGTTGGA
                                IRES
     ----------------------------------------------------
     ---------
2941 TAGTTGTGGA AAGAGTCAAA TGGCTCTCCT CAAGCGTATT CAACAAGGGG
     CTGAAGGATG
                                IRES
     ----------------------------------------------------
     ---------
             KpnI
            -------
3001 CCCAGAAGGT ACCCCATTGT ATGGGATCTG ATCTGGGGCC TCGGTGCACA
     TGCTTTACAT
                                IRES
     ----------------------------------------------------
     ---------
3061 GTGTTTAGTC GAGGTTAAAA AACGTCTAGG CCCCCCGAAC CACGGGGACG
     TGGTTTTCCT
                                              L
     ------------------------------------------
             IRES
     ----------------------
3121 TTGAAAAACA CGATGATAAT ATGGGTTGGA GCCTCATCTT GCTCTTCCTT
     GTCGCTGTTG
             L
     -----------------
                                          VH
     ---------------------------------------------
        MluI
       ------
3181 CTACGCGTGT CCTGTCCCAG GTCCAGCTGG TGCAGTCCGG CGCTGAGGTG
     GTGAAACCTG
                               VH
     ----------------------------------------------------
     ---------
```

FIG. 6G

```
3241 GGGCTTCCGT GAAGATTTCC TGCAAGGCAA GCGGCTACAC CTTCACTGAT
     CACGCAATCC
                                VH
     ----------------------------------------------------------
     ---------
3301 ACTGGGTGAA ACAGAATCCT GGACAGCGCC TGGAGTGGAT TGGATATTTC
     TCTCCCGGAA
                                VH
     ----------------------------------------------------------
     ---------
3361 ACGATGATTT TAAGTACAAT GAGAGGTTCA AGGGCAAGGC CACACTGACT
     GCAGACACAT
                                VH
     ----------------------------------------------------------
     ---------
                                                          BaeI
     ------------
3421 CTGCCAGCAC TGCCTACGTG GAGCTCTCCA GCCTGAGATC CGAGGATACT
     GCAGTGTACT
                                VH
     ----------------------------------------------------------
     ---------
3481 TCTGCACAAG ATCCCTGAAT ATGGCCTACT GGGGACAGGG AACCCTGGTC
     ACCGTCTCCA
                          CH2 Link GlDelCH2
     ----------------------------------------------------------
     -------
     VH
     --
        NheI
       ------
3541 GCGCTAGCAC CAAGGGCCCA TCGGTCTTCC CCCTGGCACC CTCCTCCAAG
     AGCACCTCTG
                          CH2 Link GlDelCH2
     ----------------------------------------------------------
     ---------
                                                          AgeI
     -------
```

FIG. 6H

```
3601 GGGGCACAGC GGCCCTGGGC TGCCTGGTCA AGGACTACTT CCCCGAACCG
     GTGACGGTGT
                          CH2 Link GlDelCH2
     ----------------------------------------------------
     ---------
3661 CGTGGAACTC AGGCGCCCTG ACCAGCGGCG TGCACACCTT CCCGGCTGTC
     CTACAGTCCT
                          CH2 Link GlDelCH2
     ----------------------------------------------------
     ---------
3721 CAGGACTCTA CTCCCTCAGC AGCGTGGTGA CCGTGCCCTC CAGCAGCTTG
     GGCACCCAGA
                          CH2 Link GlDelCH2
     ----------------------------------------------------
     ---------
3781 CCTACATCTG CAACGTGAAT CACAAGCCCA GCAACACCAA GGTGGACAAG
     AAAGTTGAGC
                          CH2 Link GlDelCH2
     ----------------------------------------------------
     ---------
3841 CCAAATCTTG TGACAAAACT CACACATGCC CACCGTGCCC CATCGAGAAA
     ACCATCTCCA
                          CH2 Link GlDelCH2
     ----------------------------------------------------
     ---------
                                       Bsp1407I
                                       ------
3901 AAGCCAAAGG GCAGCCCCGA GAACCACAGG TGTACACCCT GCCCCCATCC
     CGGGATGAGC
                          CH2 Link GlDelCH2
     ----------------------------------------------------
     ---------
3961 TGACCAAGAA CCAGGTCAGC CTGACCTGCC TGGTCAAAGG CTTCTATCCC
     AGCGACATCG
                          CH2 Link GlDelCH2
     ----------------------------------------------------
     ---------
```

FIG. 6I

```
4021 CCGTGGAGTG GGAGAGCAAT GGGCAGCCGG AGAACAACTA CAAGACCACG
     CCTCCCGTGC
                          CH2 Link GlDelCH2
     ----------------------------------------------------
     ---------
4081 TGGACTCCGA CGGCTCCTTC TTCCTCTACA GCAAGCTCAC CGTGGACAAG
     AGCAGGTGGC
                          CH2 Link GlDelCH2
     ----------------------------------------------------
     ---------
4141 AGCAGGGGAA CGTCTTCTCA TGCTCCGTGA TGCATGAGGC TCTGCACAAC
     CACTACACGC
            CH2 Link GlDelCH2
     ----------------------------------
                                          MfeI
                                         -------
                                                  SrfI
                                                 ---------
                                      BamHI
     BglII                            ------
     ------
4201 AGAAGAGCCT CTCCCTGTCT CCGGGTAAAT GAGGATCCAA TTGGCCCGGG
     CAGATCTGAT
        HpaI
       ------
       HindII
     EcoRV
       ------
     ------
4261 CCGTTAACGG TTACCAACTA CCTAGACTGG ATTCGTGACA ACATGCGGCC
     GTGATATCTA
                                           BGH
     ----------------------------------------------------
4321 CGTATGATCA GCCTCGACTG TGCCTTCTAG TTGCCAGCCA TCTGTTGTTT
     GCCCCTCCCC
                                  BGH
     ----------------------------------------------------
     ---------
```

FIG. 6J

```
4381 CGTGCCTTCC TTGACCCTGG AAGGTGCCAC TCCCACTGTC CTTTCCTAAT
     AAAATGAGGA
                                BGH
     ----------------------------------------------------------
     ---------
4441 AATTGCATCG CATTGTCTGA GTAGGTGTCA TTCTATTCTG GGGGGTGGGG
     TGGGGCAGGA
                                BGH
     ----------------------------------------------------------
     ----------
4501 CAGCAAGGGG GAGGATTGGG AAGACAATAG CAGGCATGCT GGGGATGCGG
     TGGGCTCTAT
     BGH
     Beta
     --
     ---
                                                        SgfI
                                                      ---------
     SpeI
     ------
4561 GGCTTCTGAG GCGGAAAGAA CCAGCTGGGG CTCGACAGCG CTGCGATCGC
     CTCGACTAGT
                                Beta
     ----------------------------------------------------------
     ---------
4621 AGCTTTGCTT CTCAATTTCT TATTTGCATA ATGAGAAAAA AAGGAAAATT
     AATTTTAACA
                                Beta
     ----------------------------------------------------------
     ---------
4681 CCAATTCAGT AGTTGATTGA GCAAATGCGT TGCCAAAAAG GATGCTTTAG
     AGACAGTGTT
                                Beta
     ----------------------------------------------------------
     ---------
4741 CTCTGCACAG ATAAGGACAA ACATTATTCA GAGGGAGTAC CCAGAGCTGA
     GACTCCTAAG
                                Beta
     ----------------------------------------------------------
     ---------
```

FIG.6K

```
4801 CCAGTGAGTG GCACAGCATC CAGGGAGAAA TATGCTTGTC ATCACCGAAG
     CCTGATTCCG
                                Beta
     ----------------------------------------------------
     ---------
4861 TAGAGCCACA CCCTGGTAAG GGCCAATCTG CTCACACAGG ATAGAGAGGG
     CAGGAGCCAG
                                Beta
     ----------------------------------------------------
     ---------
4921 GGCAGAGCAT ATAAGGTGAG GTAGGATCAG TTGCTCCTCA CATTTGCTTC
     TGACATAGTT
     Beta
     -----

4981 GTGTTGGGAG CTTGGATAGC TTGGGGGGGG GACAGCTCAG GGCTGCGATT
     TCGCGCCAAA

     DHFR

     -------
5041 CTTGACGGCA ATCCTAGCGT GAAGGCTGGT AGGATTTTAT CCCCGCTGCC
     ATCATGGTTC
                                DHFR
     ----------------------------------------------------
     ---------
5101 GACCATTGAA CTGCATCGTC GCCGTGTCCC AAAATATGGG GATTGGCAAG
     AACGGAGACC
                                DHFR
     ----------------------------------------------------
     ---------
5161 TACCCTGGCC TCCGCTCAGG AACGAGTTCA AGTACTTCCA AAGAATGACC
     ACAACCTCTT
                                DHFR
     ----------------------------------------------------
     ---------
5221 CAGTGGAAGG TAAACAGAAT CTGGTGATTA TGGGTAGGAA AACCTGGTTC
     TCCATTCCTG
                                DHFR
     ----------------------------------------------------
     ----------
```

FIG. 6L

```
5281 AGAAGAATCG ACCTTTAAAG GACAGAATTA ATATAGTTCT CAGTAGAGAA
     CTCAAAGAAC
                                DHFR
     ----------------------------------------------------
     ---------
                                                    AflII
                                                    ------
5341 CACCACGAGG AGCTCATTTT CTTGCCAAAA GTTTGGATGA TGCCTTAAGA
     CTTATTGAAC
                                DHFR
     ----------------------------------------------------
     ---------
5401 AACCGGAATT GGCAAGTAAA GTAGACATGG TTTGGATAGT CGGAGGCAGT
     TCTGTTTACC
                                DHFR
     ----------------------------------------------------
     ---------
5461 AGGAAGCCAT GAATCAACCA GGCCACCTCA GACTCTTTGT GACAAGGATC
     ATGCAGGAAT
                                DHFR
     ----------------------------------------------------
     ---------
5521 TTGAAAGTGA CACGTTTTTC CCAGAAATTG ATTTGGGGAA ATATAAACTT
     CTCCCAGAAT
                                DHFR
     ----------------------------------------------------
     ---------
5581 ACCCAGGCGT CCTCTCTGAG GTCCAGGAGG AAAAAGGCAT CAAGTATAAG
     TTTGAAGTCT
           DHFR
     -------------------
5641 ACGAGAAGAA AGACTAACAG GAAGATGCTT TCAAGTTCTC TGCTCCCCTC
     CTAAAGCTAT

     BGH

     ------------
5701 GCATTTTTAT AAGACCATGG GACTTTTGCT GGCTTTAGAT CAGCCTCGAC
     TGTGCCTTCT
                                BGH
```

FIG. 6M

```
     ----------------------------------------------------------
     ---------
5761 AGTTGCCAGC CATCTGTTGT TTGCCCCTCC CCCGTGCCTT CCTTGACCCT
     GGAAGGTGCC
                                BGH
     ----------------------------------------------------------
     ---------
5821 ACTCCCACTG TCCTTTCCTA ATAAAATGAG GAAATTGCAT CGCATTGTCT
     GAGTAGGTGT
                                BGH
     ----------------------------------------------------------
     ---------
5881 CATTCTATTC TGGGGGGTGG GGTGGGGCAG GACAGCAAGG GGGAGGATTG
     GGAAGACAAT
                   BGH
     -----------------------------------
5941 AGCAGGCATG CTGGGGATGC GGTGGGCTCT ATGGCTTCTG AGGCGGAAAG
     AACCAGCTGG

     Sse8387I

     --
6001 GGCTCGAAGC GGCCGCTCCG GATCGAGGCC GCTACTAACT CTCTCCTCCC
     TCCTTTTTCC
                                   N2
     ----------------------------------------------------------
     ---------
     Sse8387I                        BalI
     ------                         ------
6061 TGCAGGACGA GGCAGCGCGG CTATCGTGGC TGGCCACGAC GGGCGTTCCT
     TGCGCAGCTG
                                N2
     ----------------------------------------------------------
     ---------
6121 TGCTCGACGT TGTCACTGAA GCGGGAAGGG ACTGGCTGCT ATTGGGCGAA
     GTGCCGGGGC
                                N2
     ----------------------------------------------------------
     ---------
```

FIG. 6N

```
6181 AGGATCTCCT GTCATCTCAC CTTGCTCCTG CCGAGAAAGT ATCCATCATG
     GCTGATGCAA
                                N2
     ----------------------------------------------------------
     ---------
6241 TGCGGCGGCT GCATACGCTT GATCCGGCTA CCTGCCCATT CGACCACCAA
     GCGAAACATC
                                N2
     ----------------------------------------------------------
     ---------
6301 GCATCGAGCG AGCACGTACT CGGATGGAAG CCGGTCTTGT CGATCAGGAT
     GATCTGGACG
                                N2
     ----------------------------------------------------------
     ---------
6361 AAGAGCCATCA GGGGCTCGCG CCAGCCGAAC TGTTCGCCAG GCTCAAGGCG
     CGCATGCCCG
                                N2
     ----------------------------------------------------------
     ---------
6421 ACGGCGAGGA TCTCGTCGTG ACCCATGGCG ATGCCTGCTT GCCGAATATC
     ATGGTGGAAA
                                N2
     ----------------------------------------------------------
     ---------
                                                          RsrII
     --------
6481 ATGGCCGCTT TTCTGGATTC ATCGACTGTG GCCGGCTGGG TGTGGCGGAC
     CGCTATCAGG
                                N2
     ----------------------------------------------------------
     ---------
6541 ACATAGCGTT GGCTACCCGT GATATTGCTG AAGAGCTTGG CGGCGAATGG
     GCTGACCGCT
                                N2
     ----------------------------------------------------------
     ---------
```

FIG. 6O

```
6601 TCCTCGTGCT TTACGGTATC GCCGCTCCCG ATTCGCAGCG CATCGCCTTC
     TATCGCCTTC
            N2
     ------------------
                                        AsuII
                                        ------
6661 TTGACGAGTT CTTCTGAGCG GGACTCTGGG GTTCGAAATG ACCGACCAAG
     CGACGCCCAA
6721 CCTGCCATCA CGAGATTTCG ATTCCACCGC CGCCTTCTAT GAAAGGTTGG
     GCTTCGGAAT
6781 CGTTTTCCGG GACGCCGGCT GGATGATCCT CCAGCGCGGG GATCTCATGC
     TGGAGTTCTT
                                       SV
     ----------------------------------------------------
6841 CGCCCACCCA ACTTGTTTAT TGCAGCTTAT AATGGTTACA AATAAAGCAA
     TAGCATCACA
                                   SV
     ----------------------------------------------------
     ---------
6901 AATTTCACAA ATAAAGCATT TTTTTCACTG CATTCTAGTT GTGGTTTGTC
     CAAACTCATC
               SV
     ------------------------
                                   FseI        SacII
     AscI
                                   -------     -------
     -
6961 AATGTATCTT ATCATGTCTG GATCGCGGCC GGCCGCCACC GCGGTGGAGC
     TTTAATTAAG
      AscI
     -------
7021 GCGCGCCAGC TCCAGCTTTT GTTCCCTTTA GTGAGGGTTA ATTTCGAGCT
     TGGCGTAATC
7081 ATGGTCATAG CTGTTTCCTG TGTGAAATTG TTATCCGCTC ACAATTCCAC
     ACAACATACG
7141 AGCCGGAAGC ATAAAGTGTA AAGCCTGGGG TGCCTAATGA GTGAGCTAAC
     TCACATTAAT
7201 TGCGTTGCGC TCACTGCCCG CTTTCCAGTC GGGAAACCTG TCGTGCCAGC
     TGCATTAATG
7261 AATCGGCCAA CGCGCGGGGA GAGGCGGTTT GCGTATTGGG CGCTCTTCCG
     CTTCCTCGCT
```

FIG. 6P

```
7321 CACTGACTCG CTGCGCTCGG TCGTTCGGCT GCGGCGAGCG GTATCAGCTC
     ACTCAAAGGC
7381 GGTAATACGG TTATCCACAG AATCAGGGGA TAACGCAGGA AAGAACATGT
     GAGCAAAAGG
7441 CCAGCAAAAG GCCAGGAACC GTAAAAAGGC CGCGTTGCTG GCGTTTTTCC
     ATAGGCTCCG
7501 CCCCCCTGAC GAGCATCACA AAAATCGACG CTCAAGTCAG AGGTGGCGAA
     ACCCGACAGG
7561 ACTATAAAGA TACCAGGCGT TTCCCCCTGG AAGCTCCCTC GTGCGCTCTC
     CTGTTCCGAC
7621 CCTGCCGCTT ACCGGATACC TGTCCGCCTT TCTCCCTTCG GGAAGCGTGG
     CGCTTTCTCA
7681 TAGCTCACGC TGTAGGTATC TCAGTTCGGT GTAGGTCGTT CGCTCCAAGC
     TGGGCTGTGT
7741 GCACGAACCC CCCGTTCAGC CCGACCGCTG CGCCTTATCC GGTAACTATC
     GTCTTGAGTC
7801 CAACCCGGTA AGACACGACT TATCGCCACT GGCAGCAGCC ACTGGTAACA
     GGATTAGCAG
7861 AGCGAGGTAT GTAGGCGGTG CTACAGAGTT CTTGAAGTGG TGGCCTAACT
     ACGGCTACAC
7921 TAGAAGGACA GTATTTGGTA TCTGCGCTCT GCTGAAGCCA GTTACCTTCG
     GAAAAAGAGT
7981 TGGTAGCTCT TGATCCGGCA AACAAACCAC CGCTGGTAGC GGTGGTTTTT
     TTGTTTGCAA
8041 GCAGCAGATT ACGCGCAGAA AAAAAGGATC TCAAGAAGAT CCTTTGATCT
     TTTCTACGGG
8101 GTCTGACGCT CAGTGGAACG AAAACTCACG TTAAGGGATT TTGGTCATGA
     GATTATCAAA
8161 AAGGATCTTC ACCTAGATCC TTTTAAATTA AAAATGAAGT TTTAAATCAA
     TCTAAAGTAT
8221 ATATGAGTAA ACTTGGTCTG ACAGTTACCA ATGCTTAATC AGTGAGGCAC
     CTATCTCAGC
     ------------------------------------
                                          Amp
                                     Eam1105I
                                     ----------
8281 GATCTGTCTA TTTCGTTCAT CCATAGTTGC CTGACTCCCC GTCGTGTAGA
     TAACTACGAT
     ------------------------------------------------------
     ---------
```

FIG. 6Q

```
                                        Amp
8341 ACGGGAGGGC TTACCATCTG GCCCCAGTGC TGCAATGATA CCGCGAGACC
     CACGCTCACC
     ---------------------------------------------------------
     ---------
                                        Amp
8401 GGCTCCAGAT TTATCAGCAA TAAACCAGCC AGCCGGAAGG GCCGAGCGCA
     GAAGTGGTCC
     ---------------------------------------------------------
     ---------
                                        Amp
8461 TGCAACTTTA TCCGCCTCCA TCCAGTCTAT TAATTGTTGC CGGGAAGCTA
     GAGTAAGTAG
     ---------------------------------------------------------
     ---------

                                        Amp
8521 TTCGCCAGTT AATAGTTTGC GCAACGTTGT TGCCATTGCT ACAGGCATCG
     TGGTGTCACG
     ---------------------------------------------------------
     ---------
                                        Amp
8581 CTCGTCGTTT GGTATGGCTT CATTCAGCTC CGGTTCCCAA CGATCAAGGC
     GAGTTACATG
     ---------------------------------------------------------
     ---------
                                        Amp
8641 ATCCCCCATG TTGTGCAAAA AAGCGGTTAG CTCCTTCGGT CCTCCGATCG
     TTGTCAGAAG
     ---------------------------------------------------------
     ---------
                                        Amp
8701 TAAGTTGGCC GCAGTGTTAT CACTCATGGT TATGGCAGCA CTGCATAATT
     CTCTTACTGT
     ---------------------------------------------------------
     ---------
                                        Amp
8761 CATGCCATCC GTAAGATGCT TTTCTGTGAC TGGTGAGTAC TCAACCAAGT
     CATTCTGAGA
     ---------------------------------------------------------
     ---------
                                        Amp
8821 ATAGTGTATG CGGCGACCGA GTTGCTCTTG CCCGGCGTCA ATACGGGATA
     ATACCGCGCC
     ---------------------------------------------------------
     ---------
```

FIG. 6R

```
                                        Amp
8881 ACATAGCAGA ACTTTAAAAG TGCTCATCAT TGGAAAACGT TCTTCGGGGC
     GAAAACTCTC
     ---------------------------------------------------------
     ---------
                                        Amp
8941 AAGGATCTTA CCGCTGTTGA GATCCAGTTC GATGTAACCC ACTCGTGCAC
     CCAACTGATC
     ---------------------------------------------------------
     ---------
                                        Amp
9001 TTCAGCATCT TTTACTTTCA CCAGCGTTTC TGGGTGAGCA AAAACAGGAA
     GGCAAAATGC
     ---------------------------------------------------------
     ---------
                                        Amp
     SspI
     -
9061 CGCAAAAAAG GGAATAAGGG CGACACGGAA ATGTTGAATA CTCATACTCT
     TCCTTTTTCA
     ---------------------------------------------------------
                                        Amp
     SspI
     ----
9121 ATATTATTGA AGCATTTATC AGGGTTATTG TCTCATGAGC GGATACATAT
     TTGAATGTAT
9181 TTAGAAAAAT AAACAAATAG GGGTTCCGCG CACATTTCCC CGAAAAGTGC
     CAC
```

FIG. 6S

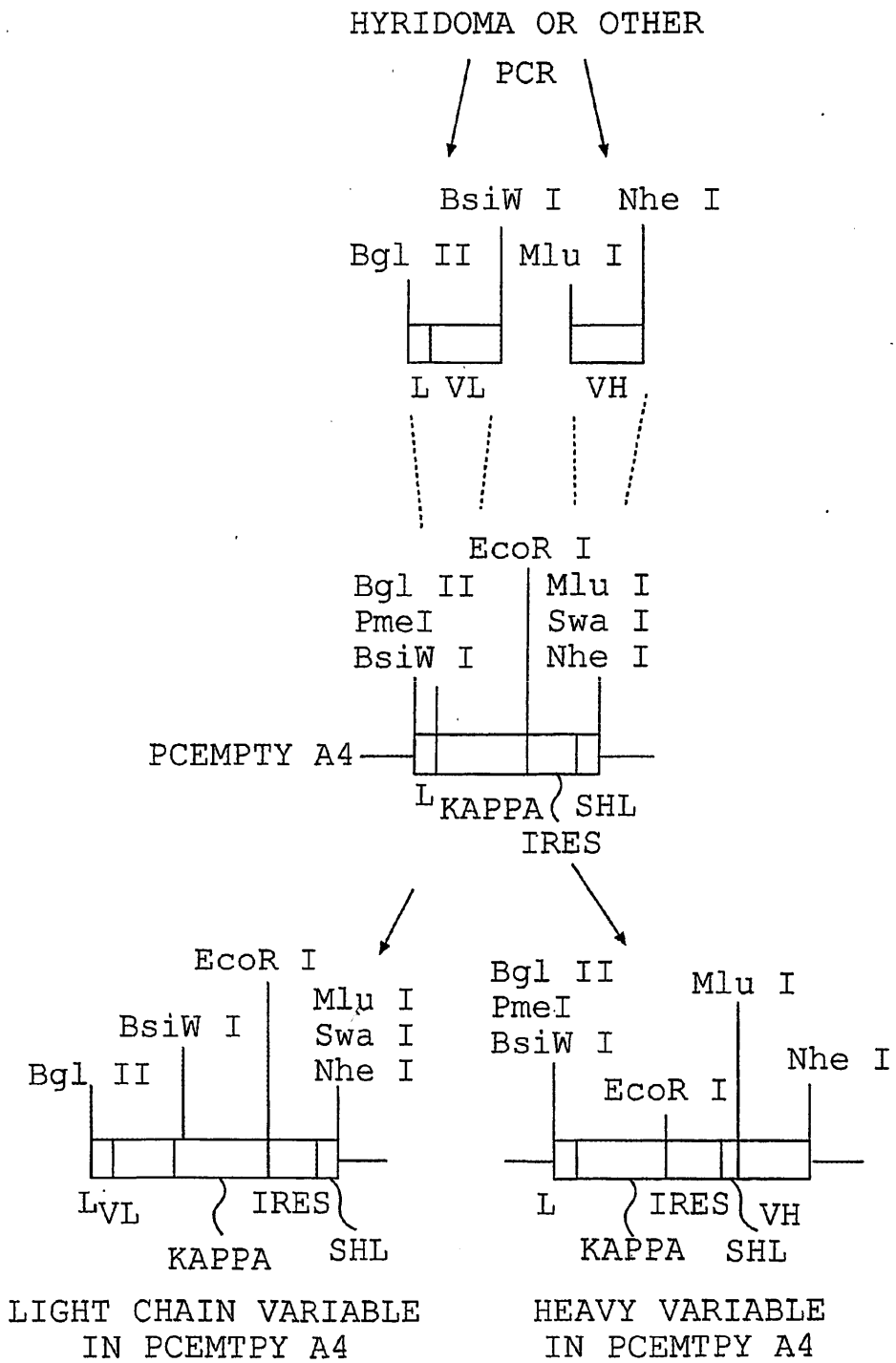

HYRIDOMA OR OTHER
PCR
BsiW I
Nhe I
Bgl II
Mlu I
L VL
VH
EcoR I
Bgl II
PmeI
BsiW I
Mlu I
Swa I
Nhe I
PCEMPTY A4
L
KAPPA
SHL
IRES
EcoR I
BsiW I
Mlu I
Swa I
Nhe I
Bgl II
L
VL
IRES
KAPPA
SHL
Bgl II
PmeI
BsiW I
Mlu I
Nhe I
EcoR I
L
IRES
VH
KAPPA
SHL
LIGHT CHAIN VARIABLE
IN PCEMTPY A4
HEAVY VARIABLE
IN PCEMTPY A4

FIG. 7A

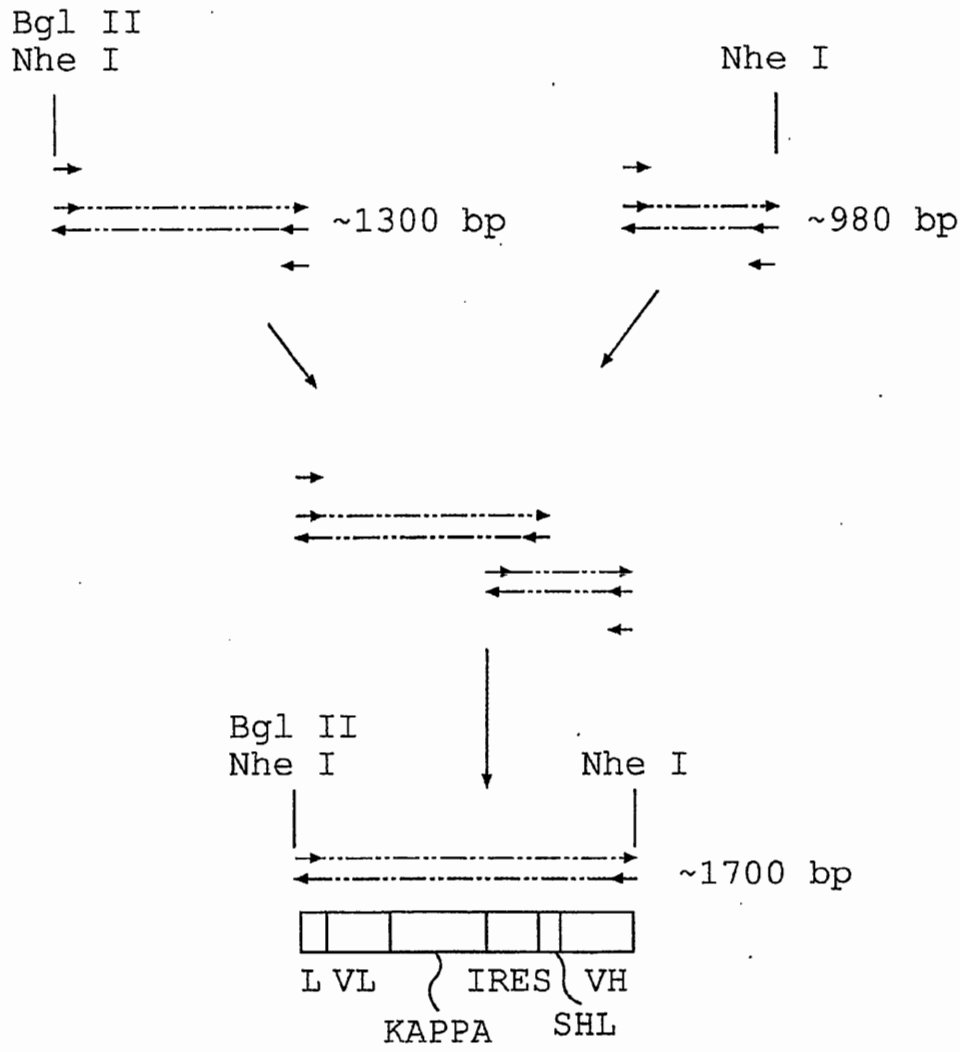
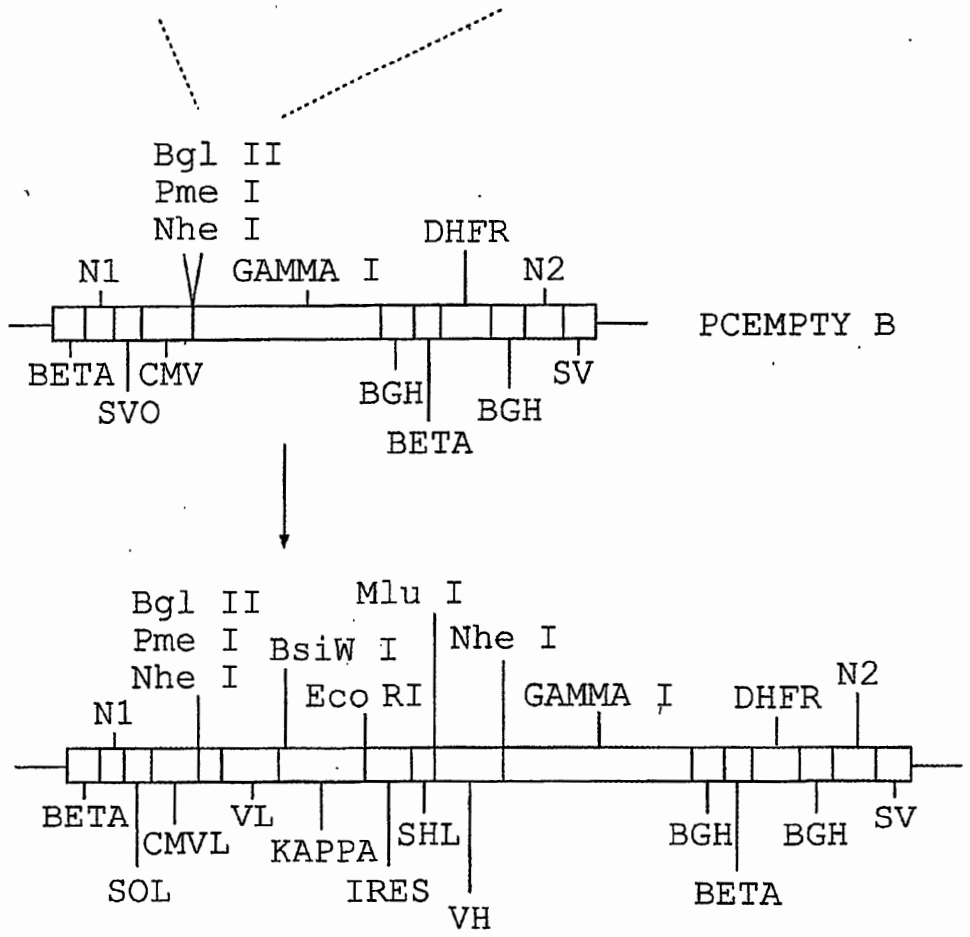

Bgl II
Nhe I
Nhe I
~1300 bp
~980 bp
Bgl II
Nhe I
Nhe I
~1700 bp
L VL
KAPPA
IRES
SHL
VH

FIG. 7B



FINAL EXPRESIION CONSTRUCT

FIG. 7C

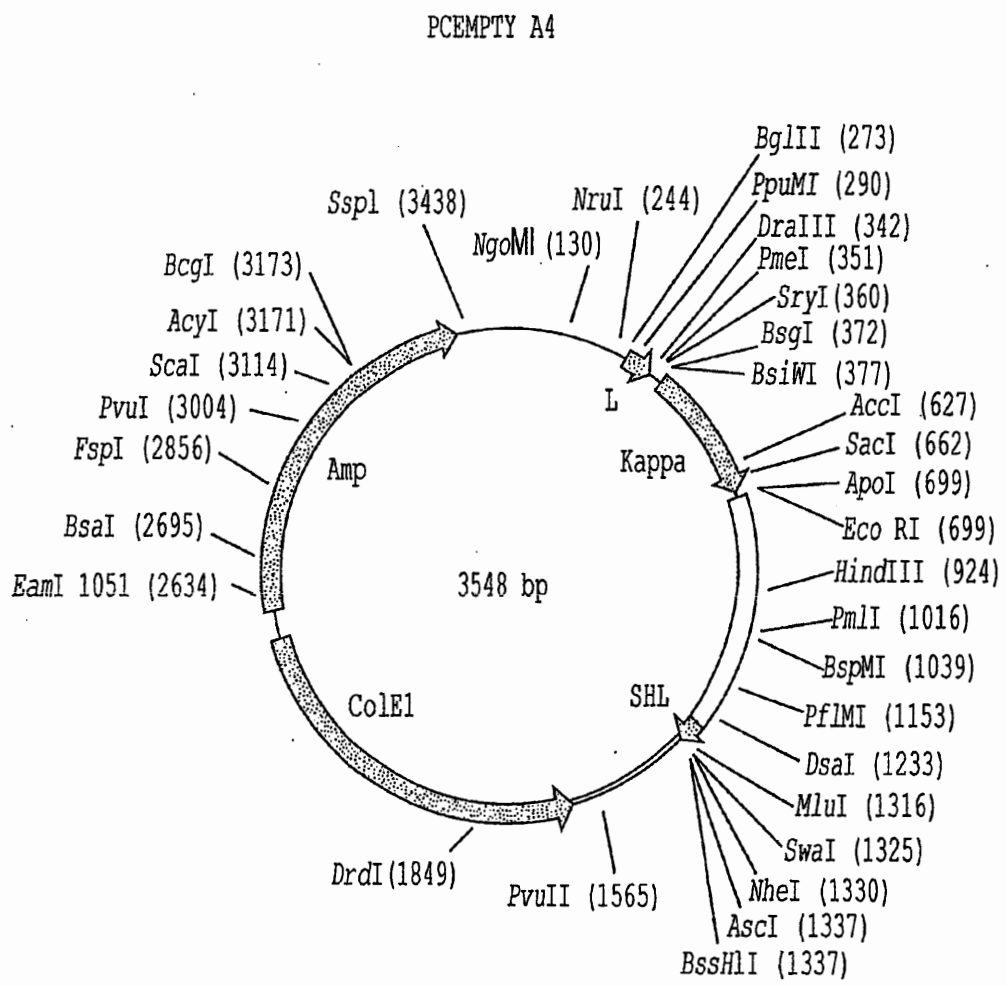

PCEMPTY A4
BglII (273)
PpuMI (290)
DraIII (342)
PmeI (351)
SryI (360)
BsgI (372)
BsiWI (377)
AccI (627)
SacI (662)
ApoI (699)
Eco RI (699)
HindIII (924)
PmlI (1016)
BspMI (1039)
PflMI (1153)
DsaI (1233)
MluI (1316)
SwaI (1325)
NheI (1330)
AscI (1337)
BssHlI (1337)
NruI (244)
NgoMI (130)
SspI (3438)
BcgI (3173)
AcyI (3171)
ScaI (3114)
PvuI (3004)
FspI (2856)
BsaI (2695)
EamI 1051 (2634)
L
Kappa
SHL
Amp
ColE1
3548 bp
DrdI (1849)
PvuII (1565)

FIG. 8

```
    1  CTGACGCGCC CTGTAGCGGC GCATTAAGCG CGGCGGGTGT
       GACTGCGCGG GACATCGCCG CGTAATTCGC GCCGCCCACA
   41  GGTGGTTACG CGCAGCGTGA CCGCTACACT TGCCAGCGCC
       CCACCAATGC GCGTCGCACT GGCGATGTGA ACGGTCGCGG
   81  CTAGCGCCCG CTCCTTTCGC TTTCTTCCCT TCCTTTCTCG
       GATCGCGGGC GAGGAAAGCG AAAGAAGGGA AGGAAAGAGC
              NgoMI
              -------
  121  CCACGTTCGC CGGCTTTCCC CGTCAAGCTC TAAATCGGGG
       GGTGCAAGCG GCCGAAAGGG GCAGTTCGAG ATTTAGCCCC
  161  GCTCCCTTTA GGGTTCCGAT TTAGTGCTTT ACGGCACCTC
       CGAGGGAAAT CCCAAGGCTA AATCACGAAA TGCCGTGGAG
  201  GACCCCAAAA AACTTGATTA GGGTGATGGT TCACGTAGGG
       CTGGGGTTTT TTGAACTAAT CCCACTACCA AGTGCATCCC
        NruI                               BglII
       ------                              ------
  241  TCGCGACGTA CCGGGCCCCC CCTCGATTAA TAGATCTCTC
       AGCGCTGCAT GGCCCGGGGG GGAGCTAATT ATCTAGAGAG
                             L
          ---------------------------------------
              PpuMI
             --------
  281  ACCATGAGGG TCCCCGCTCA GCTCCTGGGG CTCCTGCTGC
       TGGTACTCCC AGGGGCGAGT CGAGGACCCC GAGGACGACG
                 L
       ------------------------
                      DraIII       PmeI       StyI
                     ----------  ---------    --
  321  TCTGGCTCCC AGGTGCACGA TGTGATGTTT AAACGGTACC
       AGACCGAGGG TCCACGTGCT ACACTACAAA TTTGCCATGG
                                Kappa
                     ---------------------------
       StyI           BsiWI         BsgI
       ----           -------      -------
  361  AAGGTGGAAA TCAAACGTAC GGTGGCTGCA CCATCTGTCT
       TTCCACCTTT AGTTTGCATG CCACCGACGT GGTAGACAGA
                      Kappa
       ---------------------------------------
```

FIG. 9A

```
401  TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC
     AGTAGAAGGG CGGTAGACTA CTCGTCAACT TTAGACCTTG
                     Kappa
     ----------------------------------------
441  TGCCTCTGTT GTGTGCCTGC TGAATAACTT CTATCCCAGA
     ACGGAGACAA CACACGGACG ACTTATTGAA GATAGGGTCT
                     Kappa
     ----------------------------------------
481  GAGGCCAAAG TACAGTGGAA GGTGGATAAC GCCCTCCAAT
     CTCCGGTTTC ATGTCACCTT CCACCTATTG CGGGAGGTTA
                     Kappa
     ----------------------------------------
521  CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA
     GCCCATTGAG GGTCCTCTCA CAGTGTCTCG TCCTGTCGTT
                     Kappa
     ----------------------------------------
561  GGACAGCACC TACAGCCTCA GCAGCACCCT GACGCTGAGC
     CCTGTCGTGG ATGTCGGAGT CGTCGTGGGA CTGCGACTCG
                     Kappa
     ----------------------------------------
                              AccI
                             -------
601  AAAGCAGACT ACGAGAAACA CAAAGTCTAC GCCTGCGAAG
     TTTCGTCTGA TGCTCTTTGT GTTTCAGATG CGGACGCTTC
                    Kappa
     ----------------------------------------
                    SacI
                   -------
641  TCACCCATCA GGGCCTGAGC TCGCCCGTCA CAAAGAGCTT
     AGTGGGTAGT CCCGGACTCG AGCGGGCAGT GTTTCTCGAA
          Kappa                      IRES
     --------------------    ------------------
                     EcoRI
                    -------
                     ApoI
                    -------
681  CAACAGGGGA GAGTGTTGAA TTCCTCCCTC CCCCCCCCCT
     GTTGTCCCCT CTCACAACTT AAGGAGGGAG GGGGGGGGGA
                     IRES
```

FIG. 9B

```
721 AACGTTACTG GCCGAAGCCG CTTGGAATAA GGCCGGTGTG
     TTGCAATGAC CGGCTTCGGC GAACCTTATT CCGGCCACAC
                      IRES
761 CGTTTGTCTA TATGTTATTT TCCACCATAT TGCCGTCTTT
    GCAAACAGAT ATACAATAAA AGGTGGTATA ACGGCAGAAA
                      IRES
801 TGGCAATGTG AGGGCCCGGA AACCTGGCCC TGTCTTCTTG
    ACCGTTACAC TCCCGGGCCT TTGGACCGGG ACAGAAGAAC
                      IRES
841 ACGAGCATTC CTAGTGGTCT TTCCCCTCTC GCCAAAGGAA
    TGCTCGTAAG GATCACCAGA AAGGGGAGAG CGGTTTCCTT
                      IRES
881 TGCAAGGTCT GTTGAATGTC GTGAAGGAAG CAGTTCCTCT
    ACGTTCCAGA CAACTTACAG CACTTCCTTC GTCAAGGAGA
                      IRES
      HindIII
      ------
921 GGAAGCTTCT TGAAGACAAA CAACGTCTGT AGCGACCCTT
    CCTTCGAAGA ACTTCTGTTT GTTGCAGACA TCGCTGGGAA
                      IRES
961  TGCAGGCAGC GGAACCCCCC ACCTGGCGAC AGGTGCCTCT
    ACGTCCGTCG CCTTGGGGGG TGGACCGCTG TCCACGGAGA
                      IRES
                  PmlI            BspMI
                 ------           -------
1001 GCGGCCAAAA GCCACGTGTA TAAGATACAC CTGCAAAGGC
    CGCCGGTTTT CGGTGCACAT ATTCTATGTG GACGTTTCCG
                      IRES
1041 GGCACAACCC CAGTGCCAGG TTGTGAGTTG GATAGTTGTG
    CCGTGTTGGG GTCACGGTCC AACACTCAAC CTATCAACAC
                      IRES
1081 GAAAGAGTCA AATGGCTCTC CTCAAGCGTA TTCAACAAGG
    CTTTCTCAGT TTACCGAGAG GAGTTCGCAT AAGTTGTTCC
                      IRES
```

FIG. 9C

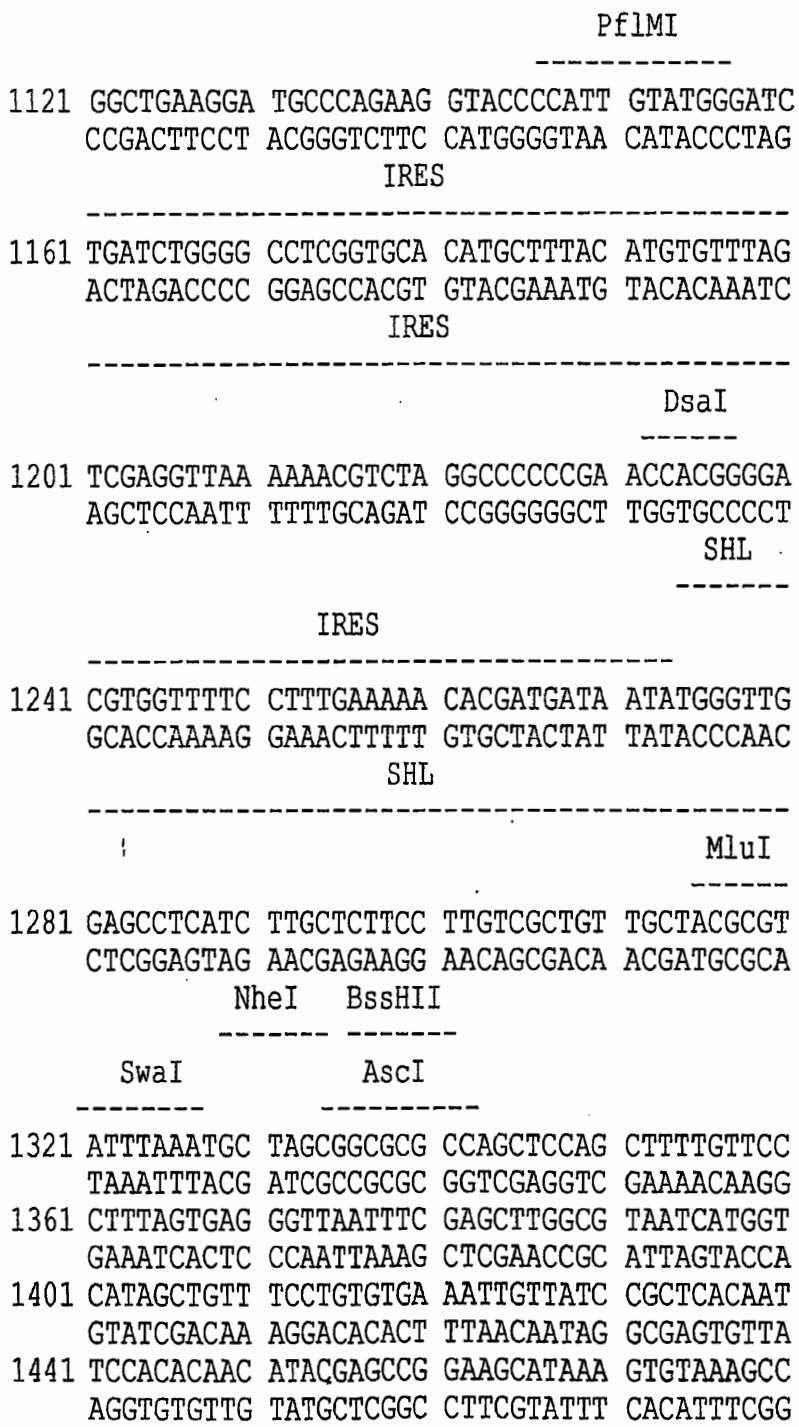

PflMI
1121 GGCTGAAGGA TGCCCAGAAG GTACCCCATT GTATGGGATC
CCGACTTCCT ACGGGTCTTC CATGGGGTAA CATACCCTAG
IRES
1161 TGATCTGGGG CCTCGGTGCA CATGCTTTAC ATGTGTTTAG
ACTAGACCCC GGAGCCACGT GTACGAAATG TACACAAATC
IRES
DsaI
1201 TCGAGGTTAA AAAACGTCTA GGCCCCCCGA ACCACGGGGA
AGCTCCAATT TTTTGCAGAT CCGGGGGGCT TGGTGCCCCT
SHL
IRES
1241 CGTGGTTTTC CTTTGAAAAA CACGATGATA ATATGGGTTG
GCACCAAAAG GAAACTTTTT GTGCTACTAT TATACCCAAC
SHL
MluI
1281 GAGCCTCATC TTGCTCTTCC TTGTCGCTGT TGCTACGCGT
CTCGGAGTAG AACGAGAAGG AACAGCGACA ACGATGCGCA
NheI BssHII
SwaI AscI
1321 ATTTAAATGC TAGCGGCGCG CCAGCTCCAG CTTTTGTTCC
TAAATTTACG ATCGCCGCGC GGTCGAGGTC GAAAACAAGG
1361 CTTTAGTGAG GGTTAATTTC GAGCTTGGCG TAATCATGGT
GAAATCACTC CCAATTAAAG CTCGAACCGC ATTAGTACCA
1401 CATAGCTGTT TCCTGTGTGA AATTGTTATC CGCTCACAAT
GTATCGACAA AGGACACACT TTAACAATAG GCGAGTGTTA
1441 TCCACACAAC ATACGAGCCG GAAGCATAAA GTGTAAAGCC
AGGTGTGTTG TATGCTCGGC CTTCGTATTT CACATTTCGG

FIG. 9D

```
1481 TGGGGTGCCT AATGAGTGAG CTAACTCACA TTAATTGCGT
     ACCCCACGGA TTACTCACTC GATTGAGTGT AATTAACGCA
1521 TGCGCTCACT GCCCGCTTTC CAGTCGGGAA ACCTGTCGTG
     ACGCGAGTGA CGGGCGAAAG GTCAGCCCTT TGGACAGCAC
      PvuII
      -----
1561 CCAGCTGCAT TAATGAATCG GCCAACGCGC GGGGAGAGGC
     GGTCGACGTA ATTACTTAGC CGGTTGCGCG CCCCTCTCCG
1601 GGTTTGCGTA TTGGGCGCTC TTCCGCTTCC TCGCTCACTG
     CCAAACGCAT AACCCGCGAG AAGGCGAAGG AGCGAGTGAC
                          ----------------------
                                    Col El
1641 ACTCGCTGCG CTCGGTCGTT CGGCTGCGGC GAGCGGTATC
     TGAGCGACGC GAGCCAGCAA GCCGACGCCG CTCGCCATAG
     ------------------------------------------
                     Col El
1681 AGCTCACTCA AAGGCGGTAA TACGGTTATC CACAGAATCA
     TCGAGTGAGT TTCCGCCATT ATGCCAATAG GTGTCTTAGT
     ------------------------------------------
                     Col El
1721 GGGGATAACG CAGGAAAGAA CATGTGAGCA AAAGGCCAGC
     CCCCTATTGC GTCCTTTCTT GTACACTCGT TTTCCGGTCG
     ------------------------------------------
                     Col El
1761 AAAAGGCCAG GAACCGTAAA AAGGCCGCGT TGCTGGCGTT
     TTTTCCGGTC CTTGGCATTT TTCCGGCGCA ACGACCGCAA
     ------------------------------------------
                     Col El
1801 TTTCCATAGG CTCCGCCCCC CTGACGAGCA TCACAAAAAT
     AAAGGTATCC GAGGCGGGGG GACTGCTCGT AGTGTTTTTA
     ------------------------------------------
                     Col El
          DrdI
      -------------
1841 CGACGCTCAA GTCAGAGGTG GCGAAACCCG ACAGGACTAT
     GCTGCGAGTT CAGTCTCCAC CGCTTTGGGC TGTCCTGATA
     ------------------------------------------
                     Col El
```

FIG. 9E

1881 AAAGATACCA GGCGTTTCCC CCTGGAAGCT CCCTCGTGCG
TTTCTATGGT CCGCAAAGGG GGACCTTCGA GGGAGCACGC

Col El

1921 CTCTCCTGTT CCGACCCTGC CGCTTACCGG ATACCTGTCC
GAGAGGACAA GGCTGGGACG GCGAATGGCC TATGGACAGG

Col El

1961 GCCTTTCTCC CTTCGGGAAG CGTGGCGCTT TCTCATAGCT
CGGAAAGAGG GAAGCCCTTC GCACCGCGAA AGAGTATCGA

Col El

2001 CACGCTGTAG GTATCTCAGT TCGGTGTAGG TCGTTCGCTC
GTGCGACATC CATAGAGTCA AGCCACATCC AGCAAGCGAG

Col El

2041 CAAGCTGGGC TGTGTGCACG AACCCCCCGT TCAGCCCGAC
GTTCGACCCG ACACACGTGC TTGGGGGGCA AGTCGGGCTG

Col El

2081 CGCTGCGCCT TATCCGGTAA CTATCGTCTT GAGTCCAACC
GCGACGCGGA ATAGGCCATT GATAGCAGAA CTCAGGTTGG

Col El

2121 CGGTAAGACA CGACTTATCG CCACTGGCAG CAGCCACTGG
GCCATTCTGT GCTGAATAGC GGTGACCGTC GTCGGTGACC

Col El

2161 TAACAGGATT AGCAGAGCGA GGTATGTAGG CGGTGCTACA
ATTGTCCTAA TCGTCTCGCT CCATACATCC GCCACGATGT

Col El

2201 GAGTTCTTGA AGTGGTGGCC TAACTACGGC TACACTAGAA
CTCAAGAACT TCACCACCGG ATTGATGCCG ATGTGATCTT

Col El

2241 GAACAGTATT TGGTATCTGC GCTCTGCTGA AGCCAGTTAC
CTTGTCATAA ACCATAGACG CGAGACGACT TCGGTCAATG

Col El

FIG. 9F

```
2281 CTTCGGAAAA AGAGTTGGTA GCTCTTGATC CGGCAAACAA
     GAAGCCTTTT TCTCAACCAT CGAGAACTAG GCCGTTTGTT
     ----------------------------------------
                    Col El
2321 ACCACCGCTG GTAGCGGTGG TTTTTTTGTT TGCAAGCAGC
     TGGTGGCGAC CATCGCCACC AAAAAAACAA ACGTTCGTCG
     ----------------------------------------
                    Col El
2361 AGATTACGCG CAGAAAAAAA GGATCTCAAG AAGATCCTTT
     TCTAATGCGC GTCTTTTTTT CCTAGAGTTC TTCTAGGAAA
     ----------------------------------------
                    Col El
2401 GATCTTTTCT ACGGGGTCTG ACGCTCAGTG GAACGAAAAC
     CTAGAAAAGA TGCCCCAGAC TGCGAGTCAC CTTGCTTTTG
     ----------------------------------------
                    Col El
2441 TCACGTTAAG GGATTTTGGT CATGAGATTA TCAAAAAGGA
     AGTGCAATTC CCTAAAACCA GTACTCTAAT AGTTTTTCCT
     ----------------------------------------
                    Col El
2481 TCTTCACCTA GATCCTTTTA AATTAAAAAT GAAGTTTTAA
     AGAAGTGGAT CTAGGAAAAT TTAATTTTTA CTTCAAAATT
     ------------------
          Col El
                                              Amp
                                              -
2521 ATCAATCTAA AGTATATATG AGTAAACTTG GTCTGACAGT
     TAGTTAGATT TCATATATAC TCATTTGAAC CAGACTGTCA
                     Amp
     ----------------------------------------

2561 TACCAATGCT TAATCAGTGA GGCACCTATC TCAGCGATCT
     ATGGTTACGA ATTAGTCACT CCGTGGATAG AGTCGCTAGA
                     Amp
     ----------------------------------------
                                   Eam1105I
                                   ----------
2601 GTCTATTTCG TTCATCCATA GTTGCCTGAC TCCCCGTCGT
     CAGATAAAGC AAGTAGGTAT CAACGGACTG AGGGGCAGCA
```

FIG. 9G

```
                        Amp
     ----------------------------------------
2641 GTAGATAACT ACGATACGGG AGGGCTTACC ATCTGGCCCC
     CATCTATTGA TGCTATGCCC TCCCGAATGG TAGACCGGGG
                        Amp
     ----------------------------------------
                       EsaI
                      -------
2681 AGTGCTGCAA TGATACCGCG AGACCCACGC TCACCGGCTC
     TCACGACGTT ACTATGGCGC TCTGGGTGCG AGTGGCCGAG
                        Amp
     ----------------------------------------
2721 CAGATTTATC AGCAATAAAC CAGCCAGCCG GAAGGGCCGA
     GTCTAAATAG TCGTTATTTG GTCGGTCGGC CTTCCCGGCT
                        Amp
     ----------------------------------------
2761 GCGCAGAAGT GGTCCTGCAA CTTTATCCGC CTCCATCCAG
     CGCGTCTTCA CCAGGACGTT GAAATAGGCG GAGGTAGGTC
                        Amp
     ----------------------------------------
2801 TCTATTAATT GTTGCCGGGA AGCTAGAGTA AGTAGTTCGC
     AGATAATTAA CAACGGCCCT TCGATCTCAT TCATCAAGCG
                        Amp
     ----------------------------------------
                    FspI
                   ------
2841 CAGTTAATAG TTTGCGCAAC GTTGTTGCCA TTGCTACAGG
     GTCAATTATC AAACGCGTTG CAACAACGGT AACGATGTCC
                        Amp
     ----------------------------------------
2881 CATCGTGGTG TCACGCTCGT CGTTTGGTAT GGCTTCATTC
     GTAGCACCAC AGTGCGAGCA GCAAACCATA CCGAAGTAAG
                        Amp
     ----------------------------------------
2921 AGCTCCGGTT CCCAACGATC AAGGCGAGTT ACATGATCCC
     TCGAGGCCAA GGGTTGCTAG TTCCGCTCAA TGTACTAGGG
                        Amp
     ----------------------------------------
```

FIG. 9H

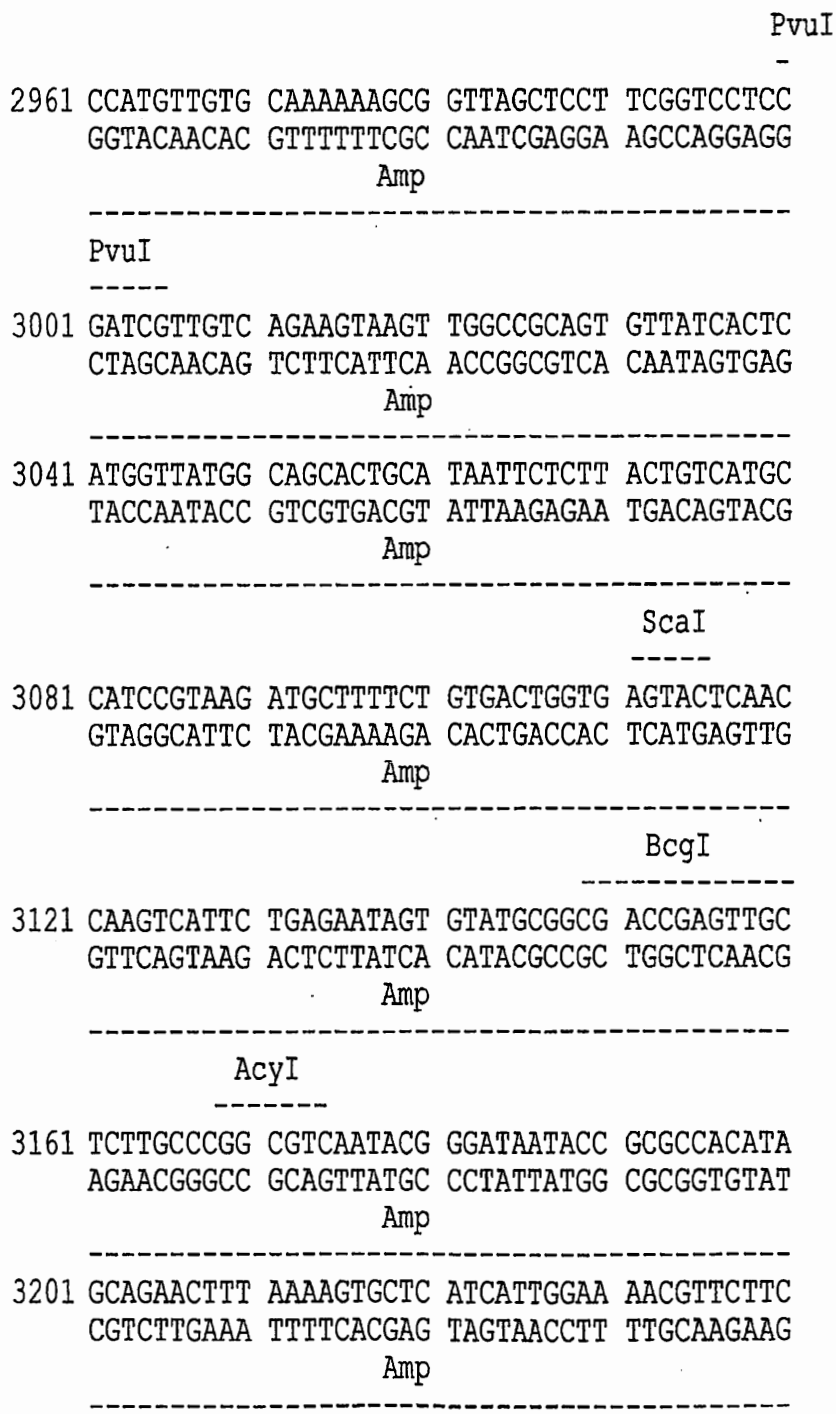

PvuI
2961 CCATGTTGTG CAAAAAAGCG GTTAGCTCCT TCGGTCCTCC
GGTACAACAC GTTTTTTCGC CAATCGAGGA AGCCAGGAGG
Amp
PvuI
3001 GATCGTTGTC AGAAGTAAGT TGGCCGCAGT GTTATCACTC
CTAGCAACAG TCTTCATTCA ACCGGCGTCA CAATAGTGAG
Amp
3041 ATGGTTATGG CAGCACTGCA TAATTCTCTT ACTGTCATGC
TACCAATACC GTCGTGACGT ATTAAGAGAA TGACAGTACG
Amp
ScaI
3081 CATCCGTAAG ATGCTTTTCT GTGACTGGTG AGTACTCAAC
GTAGGCATTC TACGAAAAGA CACTGACCAC TCATGAGTTG
Amp
BcgI
3121 CAAGTCATTC TGAGAATAGT GTATGCGGCG ACCGAGTTGC
GTTCAGTAAG ACTCTTATCA CATACGCCGC TGGCTCAACG
Amp
AcyI
3161 TCTTGCCCGG CGTCAATACG GGATAATACC GCGCCACATA
AGAACGGGCC GCAGTTATGC CCTATTATGG CGCGGTGTAT
Amp
3201 GCAGAACTTT AAAAGTGCTC ATCATTGGAA AACGTTCTTC
CGTCTTGAAA TTTTCACGAG TAGTAACCTT TTGCAAGAAG
Amp

FIG. 9I

```
3241 GGGGCGAAAA CTCTCAAGGA TCTTACCGCT GTTGAGATCC
     CCCCGCTTTT GAGAGTTCCT AGAATGGCGA CAACTCTAGG
                      Amp
     ----------------------------------------
3281 AGTTCGATGT AACCCACTCG TGCACCCAAC TGATCTTCAG
     TCAAGCTACA TTGGGTGAGC ACGTGGGTTG ACTAGAAGTC
                      Amp
     ----------------------------------------
3321 CATCTTTTAC TTTCACCAGC GTTTCTGGGT GAGCAAAAAC
     GTAGAAAATG AAAGTGGTCG CAAAGACCCA CTCGTTTTTG
                      Amp
     ----------------------------------------
3361 AGGAAGGCAA AATGCCGCAA AAAAGGGAAT AAGGGCGACA
     TCCTTCCGTT TTACGGCGTT TTTTCCCTTA TTCCCGCTGT
            Amp
     ---------------------
                                          SspI
                                          ------
3401 CGGAAATGTT GAATACTCAT ACTCTTCCTT TTTCAATATT
     GCCTTTACAA CTTATGAGTA TGAGAAGGAA AAAGTTATAA
3441 ATTGAAGCAT TTATCAGGGT TATTGTCTCA TGAGCGGATA
     TAACTTCGTA AATAGTCCCA ATAACAGAGT ACTCGCCTAT
3481 CATATTTGAA TGTATTTAGA AAAATAAACA AATAGGGGTT
     GTATAAACTT ACATAAATCT TTTTATTTGT TTATCCCCAA
3521 CCGCGCACAT TTCCCCGAAA AGTGCCAC
     GGCGCGTGTA AAGGGGCTTT TCACGGTG
```

FIG. 9J

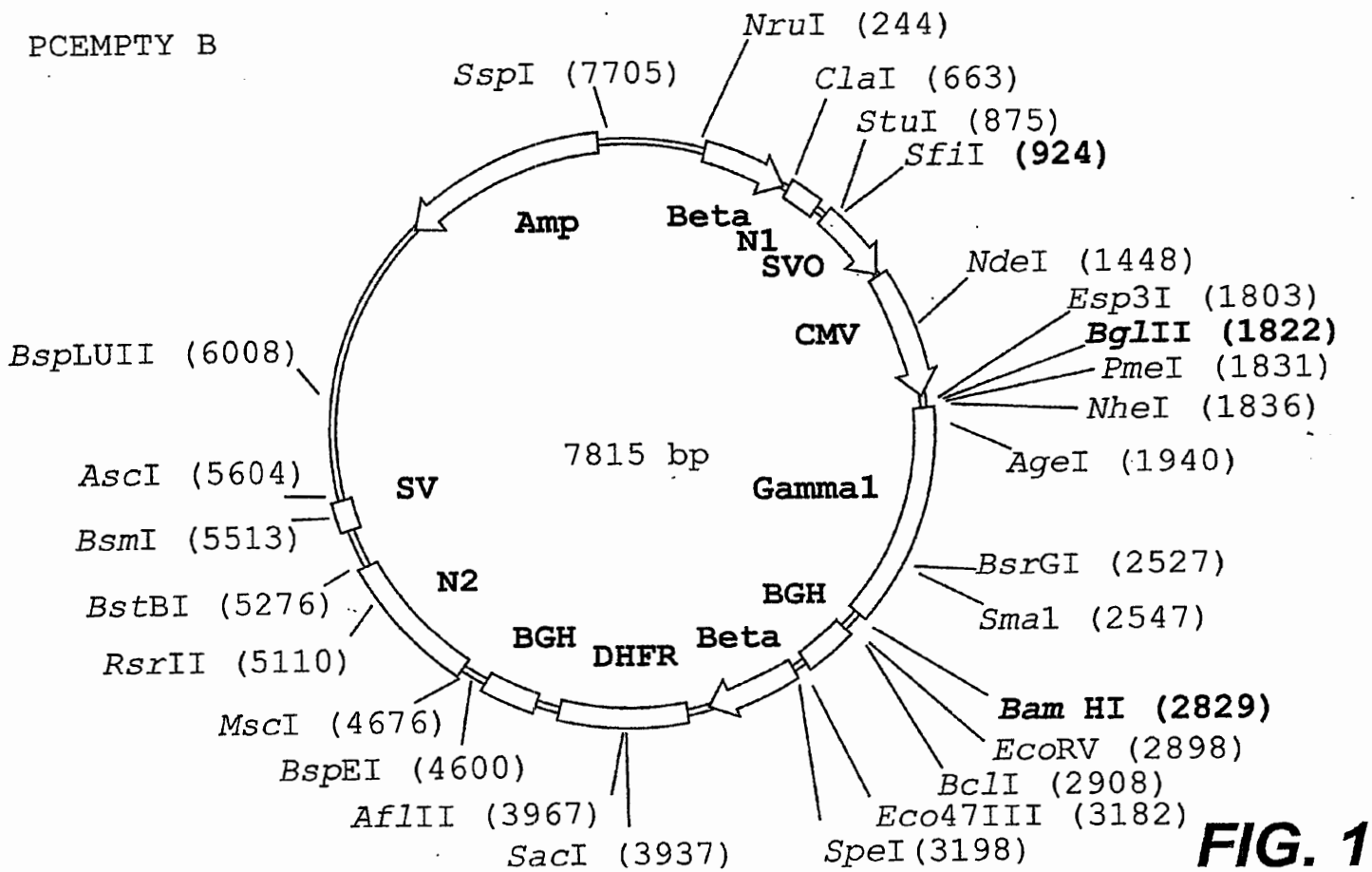

PCEMPTY B
NruI (244)
SspI (7705)
ClaI (663)
StuI (875)
SfiI (924)
Amp
Beta
N1
SVO
NdeI (1448)
Esp3I (1803)
BglII (1822)
CMV
PmeI (1831)
BspLUII (6008)
NheI (1836)
7815 bp
AgeI (1940)
AscI (5604)
SV
Gamma1
BsmI (5513)
BsrGI (2527)
N2
BstBI (5276)
BGH
Sma1 (2547)
BGH
DHFR
Beta
RsrII (5110)
Bam HI (2829)
MscI (4676)
EcoRV (2898)
BspEI (4600)
BclI (2908)
AflII (3967)
Eco47III (3182)
SacI (3937)
SpeI(3198)

FIG. 10

```
1    CTGACGCGCC CTGTAGCGGC GCATTAAGCG CGGCGGGTGT
     GACTGCGCGG GACATCGCCG CGTAATTCGC GCCGCCCACA
 41  GGTGGTTACG CGCAGCGTGA CCGCTACACT TGCCAGCGCC
     CCACCAATGC GCGTCGCACT GGCGATGTGA ACGGTCGCGG
 81  CTAGCGCCCG CTCCTTTCGC TTTCTTCCCT TCCTTTCTCG
     GATCGCGGGC GAGGAAAGCG AAAGAAGGGA AGGAAAGAGC
121  CCACGTTCGC CGGCTTTCCC CGTCAAGCTC TAAATCGGGG
     GGTGCAAGCG GCCGAAAGGG GCAGTTCGAG ATTTAGCCCC
161  GCTCCCTTTA GGGTTCCGAT TTAGTGCTTT ACGGCACCTC
     CGAGGGAAAT CCCAAGGCTA AATCACGAAA TGCCGTGGAG
201  GACCCCAAAA AACTTGATTA GGGTGATGGT TCACGTAGGG
     CTGGGGTTTT TTGAACTAAT CCCACTACCA AGTGCATCCC
      NruI
     -------
241  tCGCGACGTA CCGGGCCCCC CCTCGATTAA TTAATCGAGC
     AGCGCTGCAT GGCCCGGGGG GGAGCTAATT AATTAGCTCG
                        Beta
     ------------------------------------

281  TACTAGCTTT GCTTCTCAAT TTCTTATTTG CATAATGAGA
     ATGATCGAAA CGAAGAGTTA AAGAATAAAC GTATTACTCT
                        Beta
     ------------------------------------------

321  AAAAAAGGAA AATTAATTTT AACACCAATT CAGTAGTTGA
     TTTTTTCCTT TTAATTAAAA TTGTGGTTAA GTCATCAACT
                        Beta
     ------------------------------------------

361  TTGAGCAAAT GCGTTGCCAA AAAGGATGCT TTAGAGACAG
     AACTCGTTTA CGCAACGGTT TTTCCTACGA AATCTCTGTC
                        Beta
     ------------------------------------------

401  TGTTCTCTGC ACAGATAAGG ACAAACATTA TTCAGAGGGA
     ACAAGAGACG TGTCTATTCC TGTTTGTAAT AAGTCTCCCT
                        Beta
     ------------------------------------------

441  GTACCCAGAG CTGAGACTCC TAAGCCAGTG AGTGGCACAG
     CATGGGTCTC GACTCTGAGG ATTCGGTCAC TCACCGTGTC
                        Beta
     ------------------------------------------
```

FIG. 11A

```
481  CATCCAGGGA GAAATATGCT TGTCATCACC GAAGCCTGAT
     GTAGGTCCCT CTTTATACGA ACAGTAGTGG CTTCGGACTA
                       Beta
     ----------------------------------------
521  TCCGTAGAGC CACACCCTGG TAAGGGCCAA TCTGCTCACA
     AGGCATCTCG GTGTGGGACC ATTCCCGGTT AGACGAGTGT
                       Beta
     ----------------------------------------
561  CAGGATAGAG AGGGCAGGAG CCAGGGCAGA GCATATAAGG
     GTCCTATCTC TCCCGTCCTC GGTCCCGTCT CGTATATTCC
                       Beta
     ----------------------------------------
601  TGAGGTAGGA TCAGTTGCTC CTCACATTTG CTTCTGACAT
     ACTCCATCCT AGTCAACGAG GAGTGTAAAC GAAGACTGTA
      Beta                                 Nl
     -------                              ---------

                            ClaI
                           ------
641  AGTTGTGCCA GCATGGAGGA ATCGATCCTC CATGCTTGAA
     TCAACACGGT CGTACCTCCT TAGCTAGGAG GTACGAACTT
                       Nl
     ----------------------------------------
681  CAAGATGGAT TGCACGCAGG TTCTCCGGCC GCTTGGGTGG
     GTTCTACCTA ACGTGCGTCC AAGAGGCCGG CGAACCCACC
                       Nl
     ----------------------------------------
721  AGAGGCTATT CGGCTATGAC TGGGCACAAC AGACAATCGG
     TCTCCGATAA GCCGATACTG ACCCGTGTTG TCTGTTAGCC
                       Nl
     ----------------------------------------
761  CTGCTCTGAT GCCGCCGTGT TCCGGCTGTC AGCGCAGGGG
     GACGAGACTA CGGCGGCACA AGGCCGACAG TCGCGTCCCC
                       Nl
     ----------------------------------------
801  CGCCCGGTTC TTTTTGTCAA GACCGACCTG TCCGGTGCCC
     GCGGGCCAAG AAAAACAGTT CTGGCTGGAC AGGCCACGGG
           Nl                           SVO
     ---------------                 ------------

                                        StuI
                                       ------
```

FIG. 11B

```
 841 TGAATGAACT GCAGGTAAGT GCGGCCGCTC TAGGCCTCCA
     ACTTACTTGA CGTCCATTCA CGCCGGCGAG ATCCGGAGGT
                       SVO
     ----------------------------------------
                                          SfiI
                                          -----
 881 AAAAAGCCTC CTCACTACTT CTGGAATAGC TCAGAGGCCG
     TTTTTCGGAG GAGTGATGAA GACCTTATCG AGTCTCCGGC
                       SVO
     ----------------------------------------
       SfiI
     --------
 921 AGGCGGCCTC GGCCTCTGCA TAAATAAAAA AAATTAGTCA
     TCCGCCGGAG CCGGAGACGT ATTTATTTTT TTTAATCAGT
                       SVO
     ----------------------------------------
 961 GCCATGCATG GGGCGGAGAA TGGGCGGAAC TGGGCGGAGT
     CGGTACGTAC CCCGCCTCTT ACCCGCCTTG ACCCGCCTCA
                       SVO
     ----------------------------------------
1001 TAGGGGCGGG ATGGGCGGAG TTAGGGGCGG GACTATGGTT
     ATCCCCGCCC TACCCGCCTC AATCCCCGCC CTGATACCAA
                       SVO
     ----------------------------------------
1041 GCTGACTAAT TGAGATGCAT GCTTTGCATA CTTCTGCCTG
     CGACTGATTA ACTCTACGTA CGAAACGTAT GAAGACGGAC
                       SVO
     ----------------------------------------
1081 CTGGGGAGCC TGGGGACTTT CCACACCTGG TTGCTGACTA
     GACCCCTCGG ACCCCTGAAA GGTGTGGACC AACGACTGAT
                       SVO
     ----------------------------------------
1121 ATTGAGATGC ATGCTTTGCA TACTTCTGCC TGCTGGGGAG
     TAACTCTACG TACGAAACGT ATGAAGACGG ACGACCCCTC
                       SVO
     ----------------------------------------
1161 CCTGGGGACT TTCCACACCC TAACTGACAC ACATTCCACA
     GGACCCCTGA AAGGTGTGGG ATTGACTGTG TGTAAGGTGT
```

FIG. 11C

```
     SVO                          CMV
     -                ----------------------------
1201 GAATTAATTC CCCTAGTTAT TAATAGTAAT CAATTACGGG
     CTTAATTAAG GGGATCAATA ATTATCATTA GTTAATGCCC
                       CMV
     ----------------------------------------------
1241 GTCATTAGTT CATAGCCCAT ATATGGAGTT CCGCGTTACA
     CAGTAATCAA GTATCGGGTA TATACCTCAA GGCGCAATGT
                       CMV
     ----------------------------------------------
1281 TAACTTACGG TAAATGGCCC GCCTGGCTGA CCGCCCAACG
     ATTGAATGCC ATTTACCGGG CGGACCGACT GGCGGGTTGC
                       CMV
     ----------------------------------------------
1321 ACCCCCGCCC ATTGACGTCA ATAATGACGT ATGTTCCCAT
     TGGGGGCGGG TAACTGCAGT TATTACTGCA TACAAGGGTA
                       CMV
     ----------------------------------------------
1361 AGTAACGCCA ATAGGGACTT TCCATTGACG TCAATGGGTG
     TCATTGCGGT TATCCCTGAA AGGTAACTGC AGTTACCCAC
                       CMV
     ----------------------------------------------
1401 GAGTATTTAC GGTAAACTGC CCACTTGGCA GTACATCAAG
     CTCATAAATG CCATTTGACG GGTGAACCGT CATGTAGTTC
                       CMV
     ----------------------------------------------
          NdeI
         --------
1441 TGTATCATAT GCCAAGTACG CCCCCTATTG ACGTCAATGA
     ACATAGTATA CGGTTCATGC GGGGGATAAC TGCAGTTACT
                       CMV
1481 CGGTAAATGG CCCGCCTGGC ATTATGCCCA GTACATGACC
     GCCATTTACC GGGCGGACCG TAATACGGGT CATGTACTGG
                       CMV
     ----------------------------------------------
1521 TTATGGGACT TTCCTACTTG GCAGTACATC TACGTATTAG
     AATACCCTGA AAGGATGAAC CGTCATGTAG ATGCATAATC
                       CMV
     ----------------------------------------------
```

FIG. 11D

```
1561 TCATCGCTAT TACCATGGTG ATGCGGTTTT GGCAGTACAT
     AGTAGCGATA ATGGTACCAC TACGCCAAAA CCGTCATGTA
                       CMV
     ----------------------------------------
1601 CAATGGGCGT GGATAGCGGT TTGACTCACG GGGATTTCCA
     GTTACCCGCA CCTATCGCCA AACTGAGTGC CCCTAAAGGT
                       CMV
     ----------------------------------------
1641 AGTCTCCACC CCATTGACGT CAATGGGAGT TTGTTTTGGC
     TCAGAGGTGG GGTAACTGCA GTTACCCTCA AACAAAACCG
                       CMV
     ----------------------------------------
1681 ACCAAAATCA ACGGGACTTT CCAAAATGTC GTAACAACTC
     TGGTTTTAGT TGCCCTGAAA GGTTTTACAG CATTGTTGAG
                       CMV
     ----------------------------------------
1721 CGCCCCATTG ACGCAAATGG GCGGTAGGCG TGTACGGTGG
     GCGGGGTAAC TGCGTTTACC CGCCATCCGC ACATGCCACC
            CMV
     ----------------------
1761 GAGGTCTATA TAAGCAGAGC TGGGTACGTG AACCGTCAGA
     CTCCAGATAT ATTCGTCTCG ACCCATGCAC TTGGCAGTCT
                                          GammaI
                                          ------
                                  PmeI
                                 ---------
           Esp3I          BglII            NheI
           -------        ------           -----
1801 TCGCCTGGAG ACGCCATCAC AGATCTGTTT AAACGCTAGC
     AGCGGACCTC TGCGGTAGTG TCTAGACAAA TTTGCGATCG
                      Gamma1
     ----------------------------------------
1841 ACCAAGGGCC CATCGGTCTT CCCCCTGGCA CCCTCCTCCA
     TGGTTCCCGG GTAGCCAGAA GGGGGACCGT GGGAGGAGGT
                      Gamma1
     ----------------------------------------
1881 AGAGCACCTC TGGGGGCACA GCGGCCCTGG GCTGCCTGGT
     TCTCGTGGAG ACCCCCGTGT CGCCGGGACC CGACGGACCA
                      Gamma1
```

FIG. 11E

```
                                        AgeI
                                       -------
1921 CAAGGACTAC TTCCCCGAAC CGGTGACGGT GTCGTGGAAC
     GTTCCTGATG AAGGGGCTTG GCCACTGCCA CAGCACCTTG
                        Gamma1
2001 TCAGGCGCCC TGACCAGCGG CGTGCACACC TTCCCGGCTG
     AGTCCGCGGG ACTGGTCGCC GCACGTGTGG AAGGGCCGAC
                        Gamma1
2041 TCCTACAGTC CTCAGGACTC TACTCCCTCA GCAGCGTGGT
     AGGATGTCAG GAGTCCTGAG ATGAGGGAGT CGTCGCACCA
                        Gamma1
2081 GACCGTGCCC TCCAGCAGCT TGGGCACCCA GACCTACATC
     CTGGCACGGG AGGTCGTCGA ACCCGTGGGT CTGGATGTAG
                        Gamma1
2121 TGCAACGTGA ATCACAAGCC CAGCAACACC AAGGTGGACA
     ACGTTGCACT TAGTGTTCGG GTCGTTGTGG TTCCACCTGT
                        Gamma1
2161 AGAAAGTTGA GCCCAAATCT TGTGACAAAA CTCACACATG
     TCTTTCAACT CGGGTTTAGA ACACTGTTTT GAGTGTGTAC
                        Gamma1
2201 CCCACCGTGC CCAGCACCTG AACTCCTGGG GGGACCGTCA
     GGGTGGCACG GGTCGTGGAC TTGAGGACCC CCCTGGCAGT
                        Gamma1
2241 GTCTTCCTCT TCCCCCCAAA ACCCAAGGAC ACCCTCATGA
     CAGAAGGAGA AGGGGGGTTT TGGGTTCCTG TGGGAGTACT
                        Gamma1
2281 TCTCCCGGAC CCCTGAGGTC ACATGCGTGG TGGTGGACGT
     AGAGGGCCTG GGGACTCCAG TGTACGCACC ACCACCTGCA
                        Gamma1
```

FIG. 11F

```
2281 GAGCCACGAA GACCCTGAGG TCAAGTTCAA CTGGTACGTG
     CTCGGTGCTT CTGGGACTCC AGTTCAAGTT GACCATGCAC
                    Gamma1
     ----------------------------------------
2321 GACGGCGTGG AGGTGCATAA TGCCAAGACA AAGCCGCGGG
     CTGCCGCACC TCCACGTATT ACGGTTCTGT TTCGGCGCCC
                    Gamma1
     ----------------------------------------
2361 AGGAGCAGTA CAACAGCACG TACCGTGTGG TCAGCGTCCT
     TCCTCGTCAT GTTGTCGTGC ATGGCACACC AGTCGCAGGA
                    Gamma1
     ----------------------------------------
2401 CACCGTCCTG CACCAGGACT GGCTGAATGG CAAGGAGTAC
     GTGGCAGGAC GTGGTCCTGA CCGACTTACC GTTCCTCATG
                    Gamma1
     ----------------------------------------
2441 AAGTGCAAGG TCTCCAACAA AGCCCTCCCA GCCCCCATCG
     TTCACGTTCC AGAGGTTGTT TCGGGAGGGT CGGGGGTAGC
                    Gamma1
     ----------------------------------------
2481 AGAAAACCAT CTCCAAAGCC AAAGGGCAGC CCCGAGAACC
     TCTTTTGGTA GAGGTTTCGG TTTCCCGTCG GGGCTCTTGG
                    Gamma1
     ----------------------------------------
          BsrGI                SmaI
          -------              ------
2521 ACAGGTGTAC ACCCTGCCCC CATCCCGGGA TGAGCTGACC
     TGTCCACATG TGGGACGGGG GTAGGGCCCT ACTCGACTGG
                    Gamma1
     ----------------------------------------
2561 AAGAACCAGG TCAGCCTGAC CTGCCTGGTC AAAGGCTTCT
     TTCTTGGTCC AGTCGGACTG GACGGACCAG TTTCCGAAGA
                    Gamma1
     ----------------------------------------
2601 ATCCCAGCGA CATCGCCGTG GAGTGGGAGA GCAATGGGCA
     TAGGGTCGCT GTAGCGGCAC CTCACCCTCT CGTTACCCGT
                    Gamma1
     ----------------------------------------
```

FIG. 11G

```
2641 GCCGGAGAAC AACTACAAGA CCACGCCTCC CGTGCTGGAC
     CGGCCTCTTG TTGATGTTCT GGTGCGGAGG GCACGACCTG
                    Gammal
     ----------------------------------------
2681 TCCGACGGCT CCTTCTTCCT CTACAGCAAG CTCACCGTGG
     AGGCTGCCGA GGAAGAAGGA GATGTCGTTC GAGTGGCACC
                    Gammal
     ----------------------------------------
2721 ACAAGAGCAG GTGGCAGCAG GGGAACGTCT TCTCATGCTC
     TGTTCTCGTC CACCGTCGTC CCCTTGCAGA AGAGTACGAG
                    Gammal
     ----------------------------------------
2761 CGTGATGCAT GAGGCTCTGC ACAACCACTA CACGCAGAAG
     GCACTACGTA CTCCGAGACG TGTTGGTGAT GTGCGTCTTC
              Gammal
     ---------------------------
                                  BamHI
                                  -------
2801 AGCCTCTCCC TGTCTCCGGG TAAATGAGGA TCCAATTCGA
     TCGGAGAGGG ACAGAGGCCC ATTTACTCCT AGGTTAAGCT
2841 CTGATGCAAC GGTTACCAAC TACCTAGACT GGATTCGTGA
     GACTACGTTG CCAATGGTTG ATGGATCTGA CCTAAGCACT
                                                BGH
                                                -
                  EcoRV          BclI
                  -------        -------
2881 CAACATGCGG CCGTGATATC TACGTATGAT CAGCCTCGAC
     GTTGTACGCC GGCACTATAG ATGCATACTA GTCGGAGCTG
                      BGH
     ----------------------------------------
2921 TGTGCCTTCT AGTTGCCAGC CATCTGTTGT TTGCCCCTCC
     ACACGGAAGA TCAACGGTCG GTAGACAACA AACGGGGAGG
                      BGH
     ----------------------------------------
2961 CCCGTGCCTT CCTTGACCCT GGAAGGTGCC ACTCCCACTG
     GGGCACGGAA GGAACTGGGA CCTTCCACGG TGAGGGTGAC
                      BGH
     ----------------------------------------
```

FIG. 11H

```
3001 TCCTTTCCTA ATAAAATGAG GAAATTGCAT CGCATTGTCT
     AGGAAAGGAT TATTTTACTC CTTTAACGTA GCGTAACAGA
                      BGH
     ----------------------------------------
3041 GAGTAGGTGT CATTCTATTC TGGGGGGTGG GGTGGGGCAG
     CTCATCCACA GTAAGATAAG ACCCCCCACC CCACCCCGTC
                      BGH
     ----------------------------------------
3081 GACAGCAAGG GGGAGGATTG GGAAGACAAT AGCAGGCATG
     CTGTCGTTCC CCCTCCTAAC CCTTCTGTTA TCGTCCGTAC
               BGH
     -------------------------
3121 CTGGGGATGC GGTGGGCTCT ATGGCTTCTG AGGCGGAAAG
     GACCCCTACG CCACCCGAGA TACCGAAGAC TCCGCCTTTC
                                              Beta
                                              -
                        Eco47III           SpeI
                        -------            ----
3161 AACCAGCTGG GGCTCGACAG CGCTGCGATC GCCTCGACTA
     TTGGTCGACC CCGAGCTGTC GCGACGCTAG CGGAGCTGAT
                      Beta
     ----------------------------------------
     SpeI
     --
3201 GTAGCTTTGC TTCTCAATTT CTTATTTGCA TAATGAGAAA
     CATCGAAACG AAGAGTTAAA GAATAAACGT ATTACTCTTT
                      Beta
     ----------------------------------------
3241 AAAAGGAAAA TTAATTTTAA CACCAATTCA GTAGTTGATT
     TTTTCCTTTT AATTAAAATT GTGGTTAAGT CATCAACTAA
                      Beta
     ----------------------------------------
3281 GAGCAAATGC GTTGCCAAAA AGGATGCTTT AGAGACAGTG
     CTCGTTTACG CAACGGTTTT TCCTACGAAA TCTCTGTCAC
                      Beta
     ----------------------------------------
3321 TTCTCTGCAC AGATAAGGAC AAACATTATT CAGAGGGAGT
     AAGAGACGTG TCTATTCCTG TTTGTAATAA GTCTCCCTCA
                      Beta
     ----------------------------------------
```

FIG. 11I

```
3361 ACCCAGAGCT GAGACTCCTA AGCCAGTGAG TGGCACAGCA
     TGGGTCTCGA CTCTGAGGAT TCGGTCACTC ACCGTGTCGT
     ------------------------------------------
                       Beta
3401 TCCAGGGAGA AATATGCTTG TCATCACCGA AGCCTGATTC
     AGGTCCCTCT TTATACGAAC AGTAGTGGCT TCGGACTAAG
                       Beta
     ------------------------------------------
3441 CGTAGAGCCA CACCCTGGTA AGGGCCAATC TGCTCACACA
     GCATCTCGGT GTGGGACCAT TCCCGGTTAG ACGAGTGTGT
                       Beta
     ------------------------------------------
3481 GGATAGAGAG GGCAGGAGCC AGGGCAGAGC ATATAAGGTG
     CCTATCTCTC CCGTCCTCGG TCCCGTCTCG TATATTCCAC
                       Beta
     ------------------------------------------
3521 AGGTAGGATC AGTTGCTCCT CACATTTGCT TCTGACATAG
     TCCATCCTAG TCAACGAGGA GTGTAAACGA AGACTGTATC
      Beta
     -------
3561 TTGTGTTGGG AGCTTGGATA GCTTGGGGGG GGGACAGCTC
     AACACAACCC TCGAACCTAT CGAACCCCCC CCCTGTCGAG
3601 AGGGCTGCGA TTTCGCGCCA AACTTGACGG CAATCCTAGC
     TCCCGACGCT AAAGCGCGGT TTGAACTGCC GTTAGGATCG
                                          DHFR
                                          -----
3641 GTGAAGGCTG GTAGGATTTT ATCCCCGCTG CCATCATGGT
     CACTTCCGAC CATCCTAAAA TAGGGGCGAC GGTAGTACCA
                       DHFR
     ------------------------------------------
3681 TCGACCATTG AACTGCATCG TCGCCGTGTC CCAAAATATG
     AGCTGGTAAC TTGACGTAGC AGCGGCACAG GGTTTTATAC
                       DHFR
     ------------------------------------------
3721 GGGATTGGCA AGAACGGAGA CCTACCCTGG CCTCCGCTCA
     CCCTAACCGT TCTTGCCTCT GGATGGGACC GGAGGCGAGT
                       DHFR
     ------------------------------------------
```

FIG. 11J

```
3761 GGAACGAGTT CAAGTACTTC CAAAGAATGA CCACAACCTC
     CCTTGCTCAA GTTCATGAAG GTTTCTTACT GGTGTTGGAG
                       DHFR
     ----------------------------------------
3801 TTCAGTGGAA GGTAAACAGA ATCTGGTGAT TATGGGTAGG
     AAGTCACCTT CCATTTGTCT TAGACCACTA ATACCCATCC
                       DHFR
     ----------------------------------------
3841 AAAACCTGGT TCTCCATTCC TGAGAAGAAT CGACCTTTAA
     TTTTGGACCA AGAGGTAAGG ACTCTTCTTA GCTGGAAATT
                       DHFR
     ----------------------------------------
3881 AGGACAGAAT TAATATAGTT CTCAGTAGAG AACTCAAAGA
     TCCTGTCTTA ATTATATCAA GAGTCATCTC TTGAGTTTCT
                       DHFR
     ----------------------------------------
                  SacI
                 ------
3921 ACCACCACGA GGAGCTCATT TTCTTGCCAA AAGTTTGGAT
     TGGTGGTGCT CCTCGAGTAA AAGAACGGTT TTCAAACCTA
                       DHFR
     ----------------------------------------
          AflII
         -------
3961 GATGCCTTAA GACTTATTGA ACAACCGGAA TTGGCAAGTA
     CTACGGAATT CTGAATAACT TGTTGGCCTT AACCGTTCAT
                       DHFR
     ----------------------------------------
4001 AAGTAGACAT GGTTTGGATA GTCGGAGGCA GTTCTGTTTA
     TTCATCTGTA CCAAACCTAT CAGCCTCCGT CAAGACAAAT
                       DHFR
     ----------------------------------------
4041 CCAGGAAGCC ATGAATCAAC CAGGCCACCT CAGACTCTTT
     GGTCCTTCGG TACTTAGTTG GTCCGGTGGA GTCTGAGAAA
                       DHFR
     ----------------------------------------
4081 GTGACAAGGA TCATGCAGGA ATTTGAAAGT GACACGTTTT
     CACTGTTCCT AGTACGTCCT TAAACTTTCA CTGTGCAAAA
                       DHFR
     ----------------------------------------
```

FIG. 11K

```
4121 TCCCAGAAAT TGATTTGGGG AAATATAAAC TTCTCCCAGA
     AGGGTCTTTA ACTAAACCCC TTTATATTTG AAGAGGGTCT
                       DHFR
     ----------------------------------------
4161 ATACCCAGGC GTCCTCTCTG AGGTCCAGGA GGAAAAAGGC
     TATGGGTCCG CAGGAGAGAC TCCAGGTCCT CCTTTTTCCG
                       DHFR
     ----------------------------------------
4201 ATCAAGTATA AGTTTGAAGT CTACGAGAAG AAAGACTAAC
     TAGTTCATAT TCAAACTTCA GATGCTCTTC TTTCTGATTG
4241 AGGAAGATGC TTTCAAGTTC TCTGCTCCCC TCCTAAAGCT
     TCCTTCTACG AAAGTTCAAG AGACGAGGGG AGGATTTCGA
4281 ATGCATTTTT ATAAGACCAT GGGACTTTTG CTGGCTTTAG
     TACGTAAAAA TATTCTGGTA CCCTGAAAAC GACCGAAATC
                              BGH
                 ------------------------------
4321 ATCAGCCTCG ACTGTGCCTT CTAGTTGCCA GCCATCTGTT
     TAGTCGGAGC TGACACGGAA GATCAACGGT CGGTAGACAA
                       BGH
     ----------------------------------------
4361 GTTTGCCCCT CCCCCGTGCC TTCCTTGACC CTGGAAGGTG
     CAAACGGGGA GGGGGCACGG AAGGAACTGG GACCTTCCAC
                       BGH
     ----------------------------------------
4401 CCACTCCCAC TGTCCTTTCC TAATAAAATG AGGAAATTGC
     GGTGAGGGTG ACAGGAAAGG ATTATTTTAC TCCTTTAACG
                       BGH
     ----------------------------------------
4441 ATCGCATTGT CTGAGTAGGT GTCATTCTAT TCTGGGGGGT
     TAGCGTAACA GACTCATCCA CAGTAAGATA AGACCCCCCA
                       BGH
     ----------------------------------------
4481 GGGGTGGGGC AGGACAGCAA GGGGGAGGAT TGGGAAGACA
     CCCCACCCCG TCCTGTCGTT CCCCCTCCTA ACCCTTCTGT
                       BGH
     ----------------------------------------
4521 ATAGCAGGCA TGCTGGGGAT GCGGTGGGCT CTATGGCTTC
     TATCGTCCGT ACGACCCCTA CGCCACCCGA GATACCGAAG
                                              BspEI
                                              --
```

FIG. 11L

```
4561 TGAGGCGGAA AGAACCAGCT GGGGCTCGAA GCGGCCGCTC
     ACTCCGCCTT TCTTGGTCGA CCCCGAGCTT CGCCGGCGAG
     EspEI
     ----
4601 CGGATCGAGG CCGCTACTAA CTCTCTCCTC CCTCCTTTTT
     GCCTAGCTCC GGCGATGATT GAGAGAGGAG GGAGGAAAAA
                          N2
          ----------------------------------
                                        MscI
                                        ------
4641 CCTGCAGGAC GAGGCAGCGC GGCTATCGTG GCTGGCCACG
     GGACGTCCTG CTCCGTCGCG CCGATAGCAC CGACCGGTGC
                       N2
     ----------------------------------------
4681 ACGGGCGTTC CTTGCGCAGC TGTGCTCGAC GTTGTCACTG
     TGCCCGCAAG GAACGCGTCG ACACGAGCTG CAACAGTGAC
                       N2
     ----------------------------------------
4721 AAGCGGGAAG GGACTGGCTG CTATTGGGCG AAGTGCCGGG
     TTCGCCCTTC CCTGACCGAC GATAACCCGC TTCACGGCCC
                       N2
     ----------------------------------------
4761 GCAGGATCTC CTGTCATCTC ACCTTGCTCC TGCCGAGAAA
     CGTCCTAGAG GACAGTAGAG TGGAACGAGG ACGGCTCTTT
                       N2
     ----------------------------------------
4801 GTATCCATCA TGGCTGATGC AATGCGGCGG CTGCATACGC
     CATAGGTAGT ACCGACTACG TTACGCCGCC GACGTATGCG
                       N2
     ----------------------------------------
4841 TTGATCCGGC TACCTGCCCA TTCGACCACC AAGCGAAACA
     AACTAGGCCG ATGGACGGGT AAGCTGGTGG TTCGCTTTGT
                       N2
     ----------------------------------------
4881 TCGCATCGAG CGAGCACGTA CTCGGATGGA AGCCGGTCTT
     AGCGTAGCTC GCTCGTGCAT GAGCCTACCT TCGGCCAGAA
                       N2
     ----------------------------------------
```

FIG. 11M

```
4921 GTCGATCAGG ATGATCTGGA CGAAGAGCAT CAGGGGCTCG
     CAGCTAGTCC TACTAGACCT GCTTCTCGTA GTCCCCGAGC
                       N2
     ----------------------------------------
4961 CGCCAGCCGA ACTGTTCGCC AGGCTCAAGG CGCGCATGCC
     GCGGTCGGCT TGACAAGCGG TCCGAGTTCC GCGCGTACGG
                       N2
     ----------------------------------------
5001 CGACGGCGAG GATCTCGTCG TGACCCATGG CGATGCCTGC
     GCTGCCGCTC CTAGAGCAGC ACTGGGTACC GCTACGGACG
                       N2
     ----------------------------------------
5041 TTGCCGAATA TCATGGTGGA AAATGGCCGC TTTTCTGGAT
     AACGGCTTAT AGTACCACCT TTTACCGGCG AAAAGACCTA
                       N2
     ----------------------------------------
                                  RsrII
                                 --------
5081 TCATCGACTG TGGCCGGCTG GGTGTGGCGG ACCGCTATCA
     AGTAGCTGAC ACCGGCCGAC CCACACCGCC TGGCGATAGT
                       N2
     ----------------------------------------
5121 GGACATAGCG TTGGCTACCC GTGATATTGC TGAAGAGCTT
     CCTGTATCGC AACCGATGGG CACTATAACG ACTTCTCGAA
                       N2
     ----------------------------------------
5161 GGCGGCGAAT GGGCTGACCG CTTCCTCGTG CTTTACGGTA
     CCGCCGCTTA CCCGACTGGC GAAGGAGCAC GAAATGCCAT
                       N2
     ----------------------------------------
5201 TCGCCGCTCC CGATTCGCAG CGCATCGCCT TCTATCGCCT
     AGCGGCGAGG GCTAAGCGTC GCGTAGCGGA AGATAGCGGA
            N2
     --------------------
                                        BstBI
                                        ------
5241 TCTTGACGAG TTCTTCTGAG CGGGACTCTG GGGTTCGAAA
     AGAACTGCTC AAGAAGACTC GCCCTGAGAC CCCAAGCTTT
```

FIG. 11N

```
5281 TGACCGACCA AGCGACGCCC AACCTGCCAT CACGAGATTT
     ACTGGCTGGT TCGCTGCGGG TTGGACGGTA GTGCTCTAAA
5321 CGATTCCACC GCCGCCTTCT ATGAAAGGTT GGGCTTCGGA
     GCTAAGGTGG CGGCGGAAGA TACTTTCCAA CCCGAAGCCT
5361 ATCGTTTTCC GGGACGCCGG CTGGATGATC CTCCAGCGCG
     TAGCAAAAGG CCCTGCGGCC GACCTACTAG GAGGTCGCGC
                                        SV
                                       ---------
5401 GGGATCTCAT GCTGGAGTTC TTCGCCCACC CAACTTGTTT
     CCCTAGAGTA CGACCTCCAG AAGCGGGTGG GTTGAACAAA
                         SV
     ----------------------------------------
5441 ATTGCAGCTT ATAATGGTTA CAAATAAAGC AATAGCATCA
     TAACGTCGAA TATTACCAAT GTTTATTTCG TTATCGTAGT
                         SV
     ----------------------------------------
                                       BsmI
                                      ------
5481 CAAATTTCAC AAATAAAGCA TTTTTTTCAC TGCATTCTAG
     GTTTAAAGTG TTTATTTCGT AAAAAAAGTG ACGTAAGATC
                         SV
     ----------------------------------------
5521 TTGTGGTTTG TCCAAACTCA TCAATGTATC TTATCATGTC
     AACACCAAAC AGGTTTGAGT AGTTACATAG AATAGTACAG
      SV
     ----
5561 TGGATCGCGG CCGGCCGCCA CCGCGGTGGA GCTTTAATTA
     ACCTAGCGCC GGCCGGCGGT GGCGCCACCT CGAAATTAAT
        AscI
      --------
5601 AGGCGCGCCA GCTCCAGCTT TTGTTCCCTT TAGTGAGGGT
     TCCGCGCGGT CGAGGTCGAA AACAAGGGAA ATCACTCCCA
5641 TAATTTCGAG CTTGGCGTAA TCATGGTCAT AGCTGTTTCC
     ATTAAAGCTC GAACCGCATT AGTACCAGTA TCGACAAAGG
5681 TGTGTGAAAT TGTTATCCGC TCACAATTCC ACACAACATA
     ACACACTTTA ACAATAGGCG AGTGTTAAGG TGTGTTGTAT
5721 CGAGCCGGAA GCATAAAGTG TAAAGCCTGG GGTGCCTAAT
     GCTCGGCCTT CGTATTTCAC ATTTCGGACC CCACGGATTA
5761 GAGTGAGCTA ACTCACATTA ATTGCGTTGC GCTCACTGCC
     CTCACTCGAT TGAGTGTAAT TAACGCAACG CGAGTGACGG
```

FIG. 11O

```
5801 CGCTTTCCAG TCGGGAAACC TGTCGTGCCA GCTGCATTAA
     GCGAAAGGTC AGCCCTTTGG ACAGCACGGT CGACGTAATT
5841 TGAATCGGCC AACGCGCGGG GAGAGGCGGT TTGCGTATTC
     ACTTAGCCGG TTGCGCGCCC CTCTCCGCCA AACGCATAAC
5881 GGCGCTCTTC CGCTTCCTCG CTCACTGACT CGCTGCGCTC
     CCGCGAGAAG GCGAAGGAGC GAGTGACTGA GCGACGCGAG
5921 GGTCGTTCGG CTGCGGCGAG CGGTATCAGC TCACTCAAAG
     CCAGCAAGCC GACGCCGCTC GCCATAGTCG AGTGAGTTTC
5961 GCGGTAATAC GGTTATCCAC AGAATCAGGG GATAACGCAG
     CGCCATTATG CCAATAGGTG TCTTAGTCCC CTATTGCGTC
           BspLUII
           -------
6001 GAAAGAACAT GTGAGCAAAA GGCCAGCAAA AGGCCAGGAA
     CTTTCTTGTA CACTCGTTTT CCGGTCGTTT TCCGGTCCTT
6041 CCGTAAAAAG GCCGCGTTGC TGGCGTTTTT CCATAGGCTC
     GGCATTTTTC CGGCGCAACG ACCGCAAAAA GGTATCCGAG
6081 CGCCCCCCTG ACGAGCATCA CAAAAATCGA CGCTCAAGTC
     GCGGGGGGAC TGCTCGTAGT GTTTTTAGCT GCGAGTTCAG
6121 AGAGGTGGCG AAACCCGACA GGACTATAAA GATACCAGGC
     TCTCCACCGC TTTGGGCTGT CCTGATATTT CTATGGTCCG
6161 GTTTCCCCCT GGAAGCTCCC TCGTGCGCTC TCCTGTTCCG
     CAAAGGGGGA CCTTCGAGGG AGCACGCGAG AGGACAAGGC
6201 ACCCTGCCGC TTACCGGATA CCTGTCCGCC TTTCTCCCTT
     TGGGACGGCG AATGGCCTAT GGACAGGCGG AAAGAGGGAA
6241 CGGGAAGCGT GGCGCTTTCT CATAGCTCAC GCTGTAGGTA
     GCCCTTCGCA CCGCGAAAGA GTATCGAGTG CGACATCCAT
6281 TCTCAGTTCG GTGTAGGTCG TTCGCTCCAA GCTGGGCTGT
     AGAGTCAAGC CACATCCAGC AAGCGAGGTT CGACCCGACA
6321 GTGCACGAAC CCCCCGTTCA GCCCGACCGC TGCGCCTTAT
     CACGTGCTTG GGGGGCAAGT CGGGCTGGCG ACGCGGAATA
6361 CCGGTAACTA TCGTCTTGAG TCCAACCCGG TAAGACACGA
     GGCCATTGAT AGCAGAACTC AGGTTGGGGC ATTCTGTGCT
6401 CTTATCGCCA CTGGCAGCAG CCACTGGTAA CAGGATTAGC
     GAATAGCGGT GACCGTCGTC GGTGACCATT GTCCTAATCG
6441 AGAGCGAGGT ATGTAGGCGG TGCTACAGAG TTCTTGAAGT
     TCTCGCTCCA TACATCCGCC ACGATGTCTC AAGAACTTCA
6481 GGTGGCCTAA CTACGGCTAC ACTAGAAGAA CAGTATTTGG
     CCACCGGATT GATGCCGATG TGATCTTCTT GTCATAAACC
```

FIG. 11P

```
6521 TATCTGCGCT CTGCTGAAGC CAGTTACCTT CGGAAAAAGA
     ATAGACGACA GACGACTTCG GTCAATGGAA GCCTTTTTCT
6561 GTTGGTAGCT CTTGATCCGG CAAACAAACC ACCGCTGGTA
     CAACCATCGA GAACTAGGCC GTTTGTTTGG TGGCGACCAT
6601 GCGGTGGTTT TTTTGTTTGC AAGCAGCAGA TTACGCGCAG
     CGCCACCAAA AAAACAAACG TTCGTCGTCT AATGCGCGTC
6641 AAAAAAAGGA TCTCAAGAAG ATCCTTTGAT CTTTTCTACG
     TTTTTTTCCT AGAGTTCTTC TAGGAAACTA GAAAAGATGC
6681 GGGTCTGACG CTCAGTGGAA CGAAAACTCA CGTTAAGGGA
     CCCAGACTGC GAGTCACCTT GCTTTTGAGT GCAATTCCCT
6721 TTTTGGTCAT GAGATTATCA AAAAGGATCT TCACCTAGAT
     AAAACCAGTA CTCTAATAGT TTTTCCTAGA AGTGGATCTA
6761 CCTTTTAAAT TAAAAATGAA GTTTTAAATC AATCTAAAGT
     GGAAAATTTA ATTTTTACTT CAAAATTTAG TTAGATTTCA
6801 ATATATGAGT AAACTTGGTC TGACAGTTAC CAATGCTTAA
     TATATACTCA TTTGAACCAG ACTGTCAATG ATTACGAATT
                                      ----------
                                        Amp
6841 TCAGTGAGGC ACCTATCTCA GCGATCTGTC TATTTCGTTC
     AGTCACTCCG TGGATAGAGT CGCTAGACAG ATAAAGCAAG
     ----------------------------------------
                    Amp
6881 ATCCATAGTT GCCTGACTCC CCGTCGTGTA GATAACTACG
     TAGGTATCAA CGGACTGAGG GGCAGCACAT CTATTGATGC
     ----------------------------------------
                    Amp
6921 ATACGGGAGG GCTTACCATC TGGCCCCAGT GCTGCAATGA
     TATGCATGGC CGAATGGTAG ACCGGGGGCA CGACGTTACT
     ----------------------------------------
                    Amp
6961 TACCGCGAGA CCCACGCTCA CCGGCTCCAG ATTTATCAGC
     ATGGCGCTCT GGGTGCGAGT GGCCGAGGTC TAAATAGTCG
     ----------------------------------------
7001 AATAAACCAG CCAGCCGGAA GGGCCGAGCG CAGAAGTGGT
     TTATTTGGTC GGTCGGCCTT CCCGGCTCGC GTCTTCACCA
     ----------------------------------------
                    Amp
7041 CCTGCAACTT TATCCGCCTC CATCCAGTCT ATTAATTGTT
     GGACGTTGAA ATAGGCGGAG GTAGGTCAGA TAATTAACAA
```

FIG. 11Q

```
     ----------------------------------------

                       Amp
7081 GCCGGGAAGC TAGAGTAAGT AGTTCGCCAG TTAATAGTTT
     CGGCCCTTCG ATCTCATTCA TCAAGCGGTC AATTATCAAA
     ----------------------------------------

                       Amp
7121 GCGCAACGTT GTTGCCATTG CTACAGGCAT CGTGGTGTCA
     CGCGTTGCAA CAACGGTAAC GATGTCCGTA GCACCACAGT
     ----------------------------------------

                       Amp
7161 CGCTCGTCGT TTGGTATGGC TTCATTCAGC TCCGGTTCCC
     GCGAGCAGCA AACCATACCG AAGTAAGTCG AGGCCAAGGG
     ----------------------------------------

                       Amp
7201 AACGATCAAG GCGAGTTACA TGATCCCCCA TGTTGTGCAA
     TTGCTAGTTC CGCTCAATGT ACTAGGGGGT ACAACACGTT
     ----------------------------------------

                       Amp
7241 AAAAGCGGTT AGCTCCTTCG GTCCTCCGAT CGTTGTCAGA
     TTTTCGCCAA TCGAGGAAGC CAGGAGGCTA GCAACAGTCT
     ----------------------------------------

                       Amp
7281 AGTAAGTTGG CCGCAGTGTT ATCACTCATG GTTATGGCAG
     TCATTCAACC GGCGTCACAA TAGTGAGTAC CAATACCGTC
     ----------------------------------------

                       Amp
7321 CACTGCATAA TTCTCTTACT GTCATGCCAT CCGTAAGATG
     GTGACGTATT AAGAGAATGA CAGTACGGTA GGCATTCTAC
     ----------------------------------------

                       Amp
7361 CTTTTCTGTG ACTGGTGAGT ACTCAACCAA GTCATTCTGA
     GAAAAGACAC TGACCACTCA TGAGTTGGTT CAGTAAGACT
     ----------------------------------------

                       Amp
7401 GAATAGTGTA TGCGGCGACC GAGTTGCTCT TGCCCGGCGT
     CTTATCACAT ACGCCGCTGG CTCAACGAGA ACGGGCCGCA
     ----------------------------------------

                       Amp
```

FIG. 11R

```
7441 CAATACGGGA TAATACCGCG CCACATAGCA GAACTTTAAA
     GTTATGCCCT ATTATGGCGC GGTGTATCGT CTTGAAATTT
     ------------------------------------------
                     Amp
7481 AGTGCTCATC ATTGGAAAAC GTTCTTCGGG GCGAAAACTC
     TCACGAGTAG TAACCTTTTG CAAGAAGCCC CGCTTTTGAG
     ------------------------------------------
                     Amp
7521 TCAAGGATCT TACCGCTGTT GAGATCCAGT TCGATGTAAC
     AGTTCCTAGA ATGGCGACAA CTCTAGGTCA AGCTACATTG
     ------------------------------------------
                     Amp
7561 CCACTCGTGC ACCCAACTGA TCTTCAGCAT CTTTTACTTT
     GGTGAGCACG TGGGTTGACT AGAAGTCGTA GAAAATGAAA
     ------------------------------------------
                     Amp
7601 CACCAGCGTT TCTGGGTGAG CAAAAACAGG AAGGCAAAAT
     GTGGTCGCAA AGACCCACTC GTTTTTGTCC TTCCGTTTTA
     ------------------------------------------
                     Amp
7641 GCCGCAAAAA AGGGAATAAG GGCGACACGG AAATGTTGAA
     CGGCGTTTTT TCCCTTATTC CCGCTGTGCC TTTACAACTT
     ------------------------------------------
                     Amp
                           SspI
                           ------
7681 TACTCATACT CTTCCTTTTT CAATATTATT GAAGCATTTA
     ATGAGTATGA GAAGGAAAAA GTTATAATAA CTTCGTAAAT
     -------
        Amp
7721 TCAGGGTTAT TGTCTCATGA GCGGATACAT ATTTGAATGT
     AGTCCCAATA ACAGAGTACT CGCCTATGTA TAAACTTACA
7761 ATTTAGAAAA ATAAACAAAT AGGGGTTCCG CGCACATTTC
     TAAATCTTTT TATTTGTTTA TCCCCAAGGC GCGTGTAAAG
7801 CCCGAAAAGT GCCAC
     GGGCTTTTCA CGGTG
```

FIG. 11S

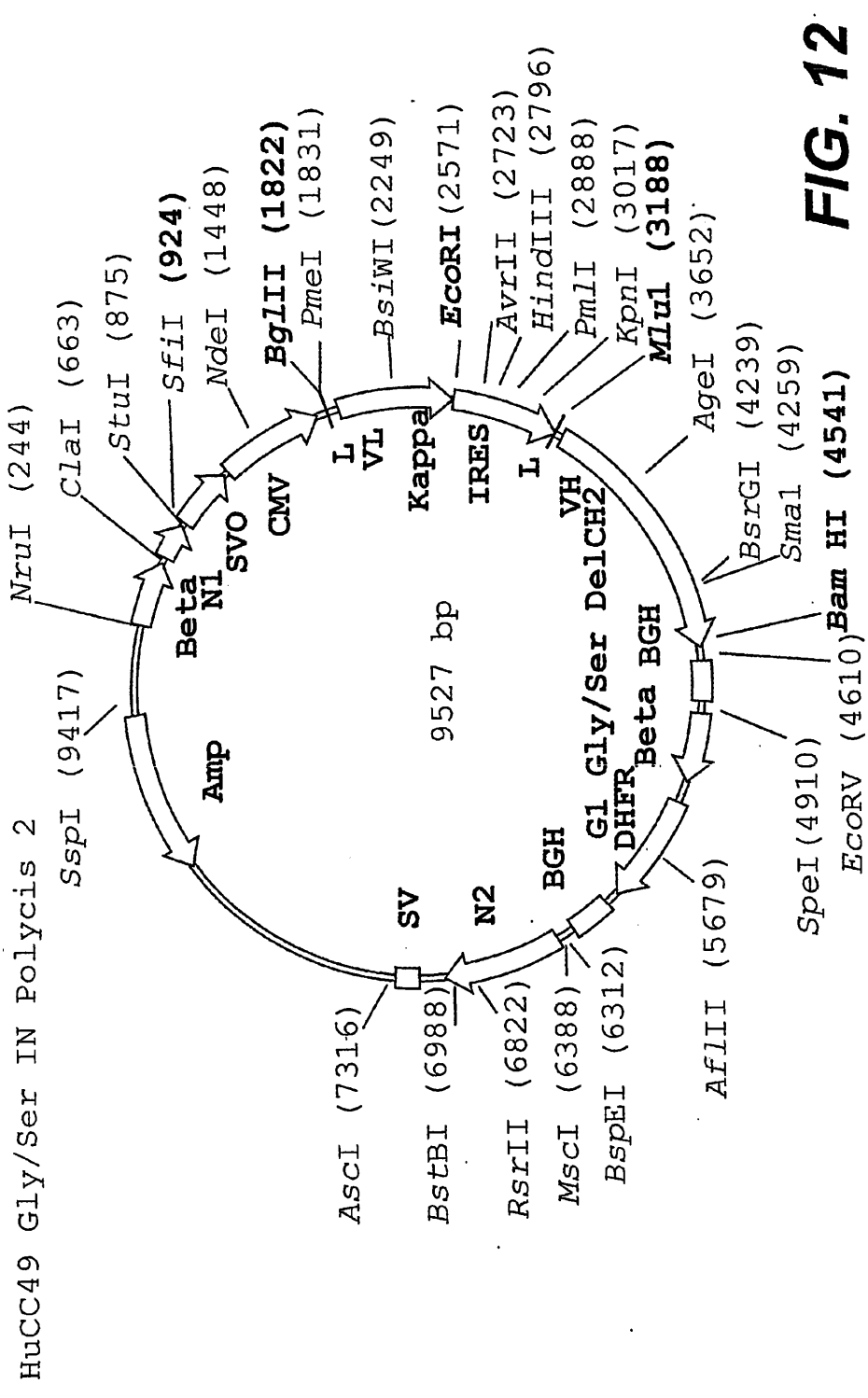

HuCC49 Gly/Ser IN Polycis 2
9527 bp
NruI (244)
ClaI (663)
StuI (875)
SfiI (924)
NdeI (1448)
BglII (1822)
PmeI (1831)
BsiWI(2249)
EcoRI(2571)
AvrII (2723)
HindIII (2796)
PmlI (2888)
KpnI (3017)
MluI (3188)
AgeI (3652)
BsrGI (4239)
SmaI (4259)
BamHI (4541)
EcoRV (4610)
SpeI(4910)
AflII (5679)
BspEI (6312)
MscI (6388)
RsrII (6822)
BstBI (6988)
AscI (7316)
SspI (9417)
Beta N1
SVO
CMV
L
VL
Kappa
IRES
L
VH
G1 Gly/Ser DelCH2
Beta BGH
DHFR
BGH
N2
SV
Amp

FIG. 12

```
1       CTGACGCGCC CTGTAGCGGC GCATTAAGCG CGGCGGGTGT
        GACTGCGCGG GACATCGCCG CGTAATTCGC GCCGCCCACA
  41    GGTGGTTACG CGCAGCGTGA CCGCTACACT TGCCAGCGCC
        CCACCAATGC GCGTCGCACT GGCGATGTGA ACGGTCGCGG
  81    CTAGCGCCCG CTCCTTTCGC TTTCTTCCCT TCCTTTCTCG
        GATCGCGGGC GAGGAAAGCG AAAGAAGGGA AGGAAAGAGC
 121    CCACGTTCGC CGGCTTTCCC CGTCAAGCTC TAAATCGGGG
        GGTGCAAGCG GCCGAAAGGG GCAGTTCGAG ATTTAGCCCC
 161    GCTCCCTTTA GGGTTCCGAT TTAGTGCTTT ACGGCACCTC
        CGAGGGAAAT CCCAAGGCTA AATCACGAAA TGCCGTGGAG
 201    GACCCCAAAA AACTTGATTA GGGTGATGGT TCACGTAGGG
        CTGGGGTTTT TTGAACTAAT CCCACTACCA AGTGCATCCC
         NruI
        ------
 241    TCGCGACGTA CCGGGCCCCC CCTCGATTAA TTAATCGAGC
        AGCGCTGCAT GGCCCGGGGG GGAGCTAATT AATTAGCTCG
                          Beta
            ---------------------------------------
 281    TACTAGCTTT GCTTCTCAAT TTCTTATTTG CATAATGAGA
        ATGATCGAAA CGAAGAGTTA AAGAATAAAC GTATTACTCT
                        Beta
        ---------------------------------------
 321    AAAAAAGGAA AATTAATTTT AACACCAATT CAGTAGTTGA
        TTTTTTCCTT TTAATTAAAA TTGTGGTTAA GTCATCAACT
                        Beta
        ---------------------------------------
 361    TTGAGCAAAT GCGTTGCCAA AAAGGATGCT TTAGAGACAG
        AACTCGTTTA CGCAACGGTT TTTCCTACGA AATCTCTGTC
                        Beta
        ---------------------------------------
 401    TGTTCTCTGC ACAGATAAGG ACAAACATTA TTCAGAGGGA
        ACAAGAGACG TGTCTATTCC TGTTTGTAAT AAGTCTCCCT
                        Beta
        ---------------------------------------
 441    GTACCCAGAG CTGAGACTCC TAAGCCAGTG AGTGGCACAG
        CATGGGTCTC GACTCTGAGG ATTCGGTCAC TCACCGTGTC
              Beta
        ---------------------------------------
```

FIG. 13A

```
481  CATCCAGGGA GAAATATGCT TGTCATCACC GAAGCCTGAT
     GTAGGTCCCT CTTTATACGA ACAGTAGTGG CTTCGGACTA
                  Beta
     ----------------------------------------
521  TCCGTAGAGC CACACCCTGG TAAGGGCCAA TCTGCTCACA
     AGGCATCTCG GTGTGGGACC ATTCCCGGTT AGACGAGTGT
                   Beta
     ----------------------------------------
561  CAGGATAGAG AGGGCAGGAG CCAGGGCAGA GCATATAAGG
     GTCCTATCTC TCCCGTCCTC GGTCCCGTCT CGTATATTCC
                    Beta
     ----------------------------------------
601  TGAGGTAGGA TCAGTTGCTC CTCACATTTG CTTCTGACAT
     ACTCCATCCT AGTCAACGAG GAGTGTAAAC GAAGACTGTA
      Beta                                 N1
     -------                              ---------
                           ClaI
                          ------
641  AGTTGTGCCA GCATGGAGGA ATCGATCCTC CATGCTTGAA
     TCAACACGGT CGTACCTCCT TAGCTAGGAG GTACGAACTT
                       N1
     ----------------------------------------
681  CAAGATGGAT TGCACGCAGG TTCTCCGGCC GCTTGGGTGG
     GTTCTACCTA ACGTGCGTCC AAGAGGCCGG CGAACCCACC
                       N1
     ----------------------------------------
721  AGAGGCTATT CGGCTATGAC TGGGCACAAC AGACAATCGG
     TCTCCGATAA GCCGATACTG ACCCGTGTTG TCTGTTAGCC
                       N1
     ----------------------------------------
761  CTGCTCTGAT GCCGCCGTGT TCCGGCTGTC AGCGCAGGGG
     GACGAGACTA CGGCGGCACA AGGCCGACAG TCGCGTCCCC
                       N1
     ----------------------------------------
801  CGCCCGGTTC TTTTTGTCAA GACCGACCTG TCCGGTGCCC
     GCGGGCCAAG AAAAACAGTT CTGGCTGGAC AGGCCACGGG
          N1                            SVO
     ---------                        ----------
```

FIG. 13B

```
                                                 StuI
                                                 ------
 841  TGAATGAACT GCAGGTAAGT GCGGCCGCTC TAGGCCTCCA
      ACTTACTTGA CGTCCATTCA CGCCGGCGAG ATCCGGAGGT
                         SVO
      ----------------------------------------
                                               SfiI
                                               ----
 881  AAAAAGCCTC CTCACTACTT CTGGAATAGC TCAGAGGCCG
      TTTTTCGGAG GAGTGATGAA GACCTTATCG AGTCTCCGGC
                         SVO
      ----------------------------------------
        SfiI
      --------
 921  AGGCGGCCTC GGCCTCTGCA TAAATAAAAA AAATTAGTCA
      TCCGCCGGAG CCGGAGACGT ATTTATTTTT TTTAATCAGT
                         SVO
      ----------------------------------------
 961  GCCATGCATG GGGCGGAGAA TGGGCGGAAC TGGGCGGAGT
      CGGTACGTAC CCCGCCTCTT ACCCGCCTTG ACCCGCCTCA
                         SVO
      ----------------------------------------
1001  TAGGGGCGGG ATGGGCGGAG TTAGGGGCGG GACTATGGTT
      ATCCCCGCCC TACCCGCCTC AATCCCCGCC CTGATACCAA
                         SVO
      ----------------------------------------
1041  GCTGACTAAT TGAGATGCAT GCTTTGCATA CTTCTGCCTG
      CGACTGATTA ACTCTACGTA CGAAACGTAT GAAGACGGAC
                         SVO
      ----------------------------------------
1081  CTGGGGAGCC TGGGGACTTT CCACACCTGG TTGCTGACTA
      GACCCCTCGG ACCCCTGAAA GGTGTGGACC AACGACTGAT
                         SVO
      ----------------------------------------
1121  ATTGAGATGC ATGCTTTGCA TACTTCTGCC TGCTGGGGAG
      TAACTCTACG TACGAAACGT ATGAAGACGG ACGACCCCTC
                         SVO
      ----------------------------------------
1161  CCTGGGGACT TTCCACACCC TAACTGACAC ACATTCCACA
      GGACCCCTGA AAGGTGTGGG ATTGACTGTG TGTAAGGTGT
      SVO                      CMV
      -                ------------------------
```

FIG. 13C

```
1201  GAATTAATTC CCCTAGTTAT TAATAGTAAT CAATTACGGG
      CTTAATTAAG GGGATCAATA ATTATCATTA GTTAATGCCC
                        CMV
      ----------------------------------------
1241  GTCATTAGTT CATAGCCCAT ATATGGAGTT CCGCGTTACA
      CAGTAATCAA GTATCGGGTA TATACCTCAA GGCGCAATGT
                        CMV
      ----------------------------------------
1281  TAACTTACGG TAAATGGCCC GCCTGGCTGA CCGCCCAACG
      ATTGAATGCC ATTTACCGGG CGGACCGACT GGCGGGTTGC
                        CMV
      ----------------------------------------
1321  ACCCCCGCCC ATTGACGTCA ATAATGACGT  ATGTTCCCAT
      TGGGGGCGGG TAACTGCAGT TATTACTGCA TACAAGGGTA
                        CMV
      ----------------------------------------
1361  AGTAACGCCA ATAGGGACTT TCCATTGACG TCAATGGGTG
      TCATTGCGGT TATCCCTGAA AGGTAACTGC AGTTACCCAC
                        CMV
      ----------------------------------------
1401  GAGTATTTAC GGTAAACTGC CCACTTGGCA GTACATCAAG
      CTCATAAATG CCATTTGACG GGTGAACCGT CATGTAGTTC
                        CMV
      ----------------------------------------
           NdeI
          -------
1441  TGTATCATAT GCCAAGTACG CCCCCTATTG ACGTCAATGA
      ACATAGTATA CGGTTCATGC GGGGGATAAC TGCAGTTACT
                        CMV
      ----------------------------------------
1481  CGGTAAATGG CCCGCCTGGC ATTATGCCCA GTACATGACC
      GCCATTTACC GGGCGGACCG TAATACGGGT CATGTACTGG
                        CMV
      ----------------------------------------
1521  TTATGGGACT TTCCTACTTG GCAGTACATC TACGTATTAG
      AATACCCTGA AAGGATGAAC CGTCATGTAG ATGCATAATC
                        CMV
      ----------------------------------------
```

FIG. 13D

```
1561  TCATCGCTAT TACCATGGTG ATGCGGTTTT GGCAGTACAT
      AGTAGCGATA ATGGTACCAC TACGCCAAAA CCGTCATGTA
                        CMV
      ----------------------------------------
1601  CAATGGGCGT GGATAGCGGT TTGACTCACG GGGATTTCCA
      GTTACCCGCA CCTATCGCCA AACTGAGTGC CCCTAAAGGT
                        CMV
      ----------------------------------------
1641  AGTCTCCACC CCATTGACGT CAATGGGAGT TTGTTTTGGC
      TCAGAGGTGG GGTAACTGCA GTTACCCTCA AACAAAACCG
                        CMV
      ----------------------------------------
1681  ACCAAAATCA ACGGGACTTT CCAAAATGTC GTAACAACTC
      TGGTTTTAGT TGCCCTGAAA GGTTTTACAG CATTGTTGAG
                        CMV
      ----------------------------------------
1721  CGCCCCATTG ACGCAAATGG GCGGTAGGCG TGTACGGTGG
      GCGGGGTAAC TGCGTTTACC CGCCATCCGC ACATGCCACC
                        CMV
      ----------------------------------------
1761  GAGGTCTATA TAAGCAGAGC TGGGTACGTG AACCGTCAGA
      CTCCAGATAT ATTCGTCTCG ACCCATGCAC TTGGCAGTCT
                                  PmeI
                                 ---------
                           Bg1II
                           ------
1801  TCGCCTGGAG ACGCCATCAC AGATCTGTTT AAACGCTAGC
      AGCGGACCTC TGCGGTAGTG TCTAGACAAA TTTGCGATCG
                            L
            ---------------------------------
1841  CTCTCACCAT GGATAGCCAG GCCCAGGTGC TCATGCTCCT
      GAGAGTGGTA CCTATCGGTC CGGGTCCACG AGTACGAGGA
                                        VL
                                    ------------
                  L
      ----------------------------
```

FIG. 13E

```
1881  GCTGCTGTGG GTGAGCGGCA CATGCGGCGA CATCGTGATG
      CGACGACACC CACTCGCCGT GTACGCCGCT GTAGCACTAC
                         VL
      ----------------------------------------
1921  AGCCAGTCTC CAGACTCCCT GGCCGTGTCC CTGGGCGAGA
      TCGGTCAGAG GTCTGAGGGA CCGGCACAGG GACCCGCTCT
                         VL
      ----------------------------------------
1961  GGGTGACTCT GAATTGCAAG TCCAGCCAGT CCCTGCTCTA
      CCCACTGAGA CTTAACGTTC AGGTCGGTCA GGGACGAGAT
                         VL
      ----------------------------------------
2001  TAGCGGAAAT CAGAAGAACT ATCTCGCCTG GTATCAGCAG
      ATCGCCTTTA GTCTTCTTGA TAGAGCGGAC CATAGTCGTC
                         VL
      ----------------------------------------
2041  AAACCAGGGC AGAGCCCTAA ACTGCTGATT TACTGGGCAT
      TTTGGTCCCG TCTCGGGATT TGACGACTAA ATGACCCGTA
                         VL
      ----------------------------------------
2081  CCGCTAGGGA ATCCGGCGTG CCTGATCGCT TCAGCGGCAG
      GGCGATCCCT TAGGCCGCAC GGACTAGCGA AGTCGCCGTC
                         VL
      ----------------------------------------
2121  CGGATCTGGG ACAGACTTCA CTCTGACAAT CAGCAGCGTG
      GCCTAGACCC TGTCTGAAGT GAGACTGTTA GTCGTCGCAC
                         VL
      ----------------------------------------
2161  CAGGCAGAAG ACGTGGCAGT CTATTATTGT CAGCAGTATT
      GTCCGTCTTC TGCACCGTCA GATAATAACA GTCGTCATAA
                         VL
      ----------------------------------------
2201  ATAGCTATCC CCTCACATTC GGCGCTGGCA CCAAGCTGGA
      TATCGATAGG GGAGTGTAAG CCGCGACCGT GGTTCGACCT
                          Kappa
            ---------------------------------
        VL
      -------
```

FIG. 13F

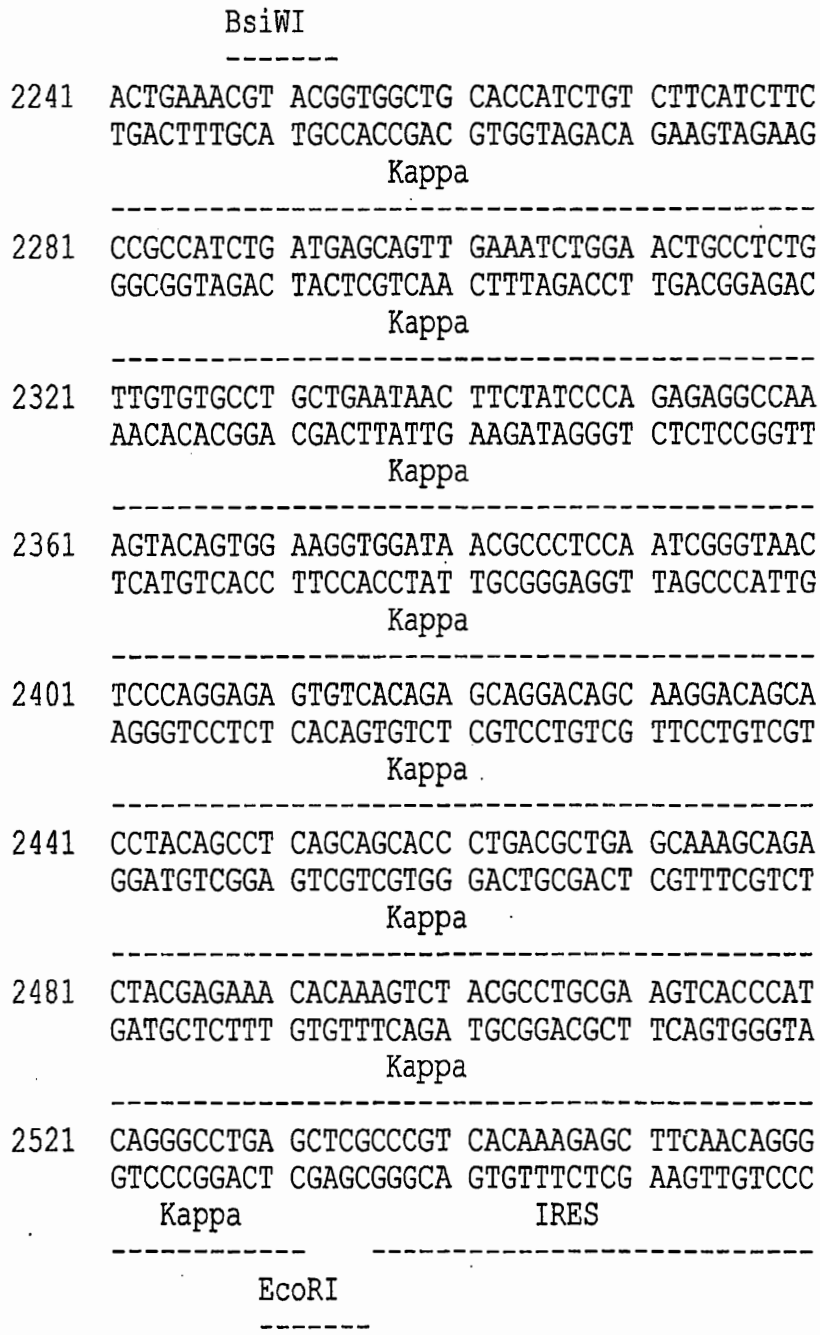

BsiWI
2241 ACTGAAACGT ACGGTGGCTG CACCATCTGT CTTCATCTTC
TGACTTTGCA TGCCACCGAC GTGGTAGACA GAAGTAGAAG
Kappa
2281 CCGCCATCTG ATGAGCAGTT GAAATCTGGA ACTGCCTCTG
GGCGGTAGAC TACTCGTCAA CTTTAGACCT TGACGGAGAC
Kappa
2321 TTGTGTGCCT GCTGAATAAC TTCTATCCCA GAGAGGCCAA
AACACACGGA CGACTTATTG AAGATAGGGT CTCTCCGGTT
Kappa
2361 AGTACAGTGG AAGGTGGATA ACGCCCTCCA ATCGGGTAAC
TCATGTCACC TTCCACCTAT TGCGGGAGGT TAGCCCATTG
Kappa
2401 TCCCAGGAGA GTGTCACAGA GCAGGACAGC AAGGACAGCA
AGGGTCCTCT CACAGTGTCT CGTCCTGTCG TTCCTGTCGT
Kappa
2441 CCTACAGCCT CAGCAGCACC CTGACGCTGA GCAAAGCAGA
GGATGTCGGA GTCGTCGTGG GACTGCGACT CGTTTCGTCT
Kappa
2481 CTACGAGAAA CACAAAGTCT ACGCCTGCGA AGTCACCCAT
GATGCTCTTT GTGTTTCAGA TGCGGACGCT TCAGTGGGTA
Kappa
2521 CAGGGCCTGA GCTCGCCCGT CACAAAGAGC TTCAACAGGG
GTCCCGGACT CGAGCGGGCA GTGTTTCTCG AAGTTGTCCC
Kappa
IRES
EcoRI

FIG. 13G

```
2561  GAGAGTGTTG AATTCCTCCC TCCCCCCCCC CTAACGTTAC
      CTCTCACAAC TTAAGGAGGG AGGGGGGGGG GATTGCAATG
                      IRES
      ----------------------------------------
2601  TGGCCGAAGC CGCTTGGAAT AAGGCCGGTG TGCGTTTGTC
      ACCGGCTTCG GCGAACCTTA TTCCGGCCAC ACGCAAACAG
                      IRES
      ----------------------------------------
2641  TATATGTTAT TTTCCACCAT ATTGCCGTCT TTTGGCAATG
      ATATACAATA AAAGGTGGTA TAACGGCAGA AAACCGTTAC
                      IRES
      ----------------------------------------
2681  TGAGGGCCCG GAAACCTGGC CCTGTCTTCT TGACGAGCAT
      ACTCCCGGGC CTTTGGACCG GGACAGAAGA ACTGCTCGTA
                      IRES
      ----------------------------------------
      AvrII
      ------
2721  TCCTAGGGGT CTTTCCCCTC TCGCCAAAGG AATGCAAGGT
      AGGATCCCCA GAAAGGGGAG AGCGGTTTCC TTACGTTCCA
                      IRES
      ----------------------------------------
                                          HindIII
                                          ------
2761  CTGTTGAATG TCGTGAAGGA AGCAGTTCCT CTGGAAGCTT
      GACAACTTAC AGCACTTCCT TCGTCAAGGA GACCTTCGAA
                      IRES
      ----------------------------------------
2801  CTTGAAGACA AACAACGTCT GTAGCGACCC TTTGCAGGCA
      GAACTTCTGT TTGTTGCAGA CATCGCTGGG AAACGTCCGT
                      IRES
      ----------------------------------------
2841  GCGGAACCCC CCACCTGGCG ACAGGTGCCT CTGCGGCCAA
      CGCCTTGGGG GGTGGACCGC TGTCCACGGA GACGCCGGTT
                      IRES
      ----------------------------------------
           PmlI
          -------
```

FIG. 13H

```
2881  AAGCCACGTG TATAAGATAC ACCTGCAAAG GCGGCACAAC
      TTCGGTGCAC ATATTCTATG TGGACGTTTC CGCCGTGTTG
                        IRES
      ----------------------------------------
2921  CCCAGTGCCA CGTTGTGAGT TGGATAGTTG TGGAAAGAGT
      GGGTCACGGT GCAACACTCA ACCTATCAAC ACCTTTCTCA
                        IRES
      ----------------------------------------
2961  CAAATGGCTC TCCTCAAGCG TATTCAACAA GGGGCTGAAG
      GTTTACCGAG AGGAGTTCGC ATAAGTTGTT CCCCGACTTC
                        IRES
      ----------------------------------------
                   KpnI
                  ------
3001  GATGCCCAGA AGGTACCCCA TTGTATGGGA TCTGATCTGG
      CTACGGGTCT TCCATGGGGT AACATACCCT AGACTAGACC
                        IRES
      ----------------------------------------
3041  GGCCTCGGTG CACATGCTTT ACATGTGTTT AGTCGAGGTT
      CCGGAGCCAC GTGTACGAAA TGTACACAAA TCAGCTCCAA
                        IRES
      ----------------------------------------
3081  AAAAAACGTC TAGGCCCCCC GAACCACGGG GACGTGGTTT
      TTTTTTGCAG ATCCGGGGGG CTTGGTGCCC CTGCACCAAA
                                      L
                                 -----------------
               IRES
      --------------------------
3121  TCCTTTGAAA AACACGATGA TAATATGGGT TGGAGCCTCA
      AGGAAACTTT TTGTGCTACT ATTATACCCA ACCTCGGAGT
                        L
      ----------------------------------------
                                   MluI
                                  -------
3161  TCTTGCTCTT CCTTGTCGCT GTTGCTACGC GTGTCCTGTC
      AGAACGAGAA GGAACAGCGA CAACGATGCG CACAGGACAG
      L
      -
```

FIG. 13I

```
                        VH
      ----------------------------------------
3201  CCAGGTCCAG CTGGTGCAGT CCGGCGCTGA GGTGGTGAAA
      GGTCCAGGTC GACCACGTCA GGCCGCGACT CCACCACTTT
                        VH
      ----------------------------------------
3241  CCTGGGGCTT CCGTGAAGAT TTCCTGCAAG GCAAGCGGCT
      GGACCCCGAA GGCACTTCTA AAGGACGTTC CGTTCGCCGA
                        VH
      ----------------------------------------
3281  ACACCTTCAC TGATCACGCA ATCCACTGGG TGAAACAGAA
      TGTGGAAGTG ACTAGTGCGT TAGGTGACCC ACTTTGTCTT
                        VH
      ----------------------------------------
3321  TCCTGGACAG CGCCTGGAGT GGATTGGATA TTTCTCTCCC
      AGGACCTGTC GCGGACCTCA CCTAACCTAT AAAGAGAGGG
                        VH
      ----------------------------------------
3361  GGAAACGATG ATTTTAAGTA CAATGAGAGG TTCAAGGGCA
      CCTTTGCTAC TAAAATTCAT GTTACTCTCC AAGTTCCCGT
                        VH
      ----------------------------------------
3401  AGGCCACACT GACTGCAGAC ACATCTGCCA GCACTGCCTA
      TCCGGTGTGA CTGACGTCTG TGTAGACGGT CGTGACGGAT
                        VH
      ----------------------------------------
3441  CGTGGAGCTC TCCAGCCTGA GATCCGAGGA TACTGCAGTG
      GCACCTCGAG AGGTCGGACT CTAGGCTCCT ATGACGTCAC
                        VH
      ----------------------------------------
3481  TACTTCTGCA CAAGATCCCT GAATATGGCC TACTGGGGAC
      ATGAAGACGT GTTCTAGGGA CTTATACCGG ATGACCCCTG
                                 G1 G1y/Ser DelCH2
                                 --------------
            VH
      --------------------------
```

FIG. 13J

```
3521  AGGGAACCCT GGTCACCGTC TCCAGCGCTA GCACCAAGGG
      TCCCTTGGGA CCAGTGGCAG AGGTCGCGAT CGTGGTTCCC
                Gl Gly/Ser DelCH2
      ----------------------------------------
3561  CCCATCGGTC TTCCCCCTGG CACCCTCCTC CAAGAGCACC
      GGGTAGCCAG AAGGGGGACC GTGGGAGGAG GTTCTCGTGG
                Gl Gly/Ser DelCH2
      ----------------------------------------
3601  TCTGGGGGCA CAGCGGCCCT GGGCTGCCTG GTCAAGGACT
      AGACCCCCGT GTCGCCGGGA CCCGACGGAC CAGTTCCTGA
                Gl Gly/Ser DelCH2
      ----------------------------------------
                 AgeI
                ------
3641  ACTTCCCCGA ACCGGTGACG GTGTCGTGGA ACTCAGGCGC
      TGAAGGGGCT TGGCCACTGC CACAGCACCT TGAGTCCGCG
                Gl Gly/Ser DelCH2
      ----------------------------------------
3681  CCTGACCAGC GGCGTGCACA CCTTCCCGGC TGTCCTACAG
      GGACTGGTCG CCGCACGTGT GGAAGGGCCG ACAGGATGTC
                G1 Gly/Ser DelCH2
      ----------------------------------------
3721  TCCTCAGGAC TCTACTCCCT CAGCAGCGTG GTGACCGTGC
      AGGAGTCCTG AGATGAGGGA GTCGTCGCAC CACTGGCACG
                G1 Gly/Ser DelCH2
      ----------------------------------------
3761  CCTCCAGCAG CTTGGGCACC CAGACCTACA TCTGCAACGT
      GGAGGTCGTC GAACCCGTGG GTCTGGATGT AGACGTTGCA
                G1 Gly/Ser DelCH2
      ----------------------------------------
3801  GAATCACAAG CCCAGCAACA CCAAGGTGGA CAAGAAAGTT
      CTTAGTGTTC GGGTCGTTGT GGTTCCACCT GTTCTTTCAA
                G1 Gly/Ser DelCH2
      ----------------------------------------
3841  GAGCCCAAAT CTTGTGACAA AACTCACACA TGCCCACCGT
      CTCGGGTTTA GAACACTGTT TTGAGTGTGT ACGGGTGGCA
                G1 Gly/Ser DelCH2
      ----------------------------------------
```

FIG. 13K

```
3881  GCCCAGCACC TGAACTCCTG GGGGGACCGT CAGTCTTCCT
      CGGGTCGTGG ACTTGAGGAC CCCCCTGGCA GTCAGAAGGA
                 G1 Gly/Ser DelCH2
      ----------------------------------------
3921  CTTCCCCCCA AAACCCAAGG ACACCCTCAT GATCTCCCGG
      GAAGGGGGGT TTTGGGTTCC TGTGGGAGTA CTAGAGGGCC
                 G1 Gly/Ser DelCH2
      ----------------------------------------
3961  ACCCCTGAGG TCACATGCGT GGTGGTGGAC GTGAGCCACG
      TGGGGACTCC AGTGTACGCA CCACCACCTG CACTCGGTGC
                 G1 Gly/Ser DelCH2
      ----------------------------------------
4001  AAGACCCTGA GGTCAAGTTC AACTGGTACG TGGACGGCGT
      TTCTGGGACT CCAGTTCAAG TTGACCATGC ACCTGCCGCA
                 G1 Gly/Ser DelCH2
      ----------------------------------------
4041  GGAGGTGCAT AATGCCAAGA CAAAGCCGCG GGAGGAGCAG
      CCTCCACGTA TTACGGTTCT GTTTCGGCGC CCTCCTCGTC
                 G1 Gly/Ser DelCH2
      ----------------------------------------
4081  TACAACAGCA CGTACCGTGT GGTCAGCGTC CTCACCGTCC
      ATGTTGTCGT GCATGGCACA CCAGTCGCAG GAGTGGCAGG
                 G1 Gly/Ser DelCH2
      ----------------------------------------
4121  TGCACCAGGA CTGGCTGAAT GGCAAGGAGT ACAAGTGCAA
      ACGTGGTCCT GACCGACTTA CCGTTCCTCA TGTTCACGTT
                 G1 Gly/Ser DelCH2
      ----------------------------------------
4161  GGTCTCCAAC AAAGCCCTCC CAGCCCCCAT CGAGAAAACC
      CCAGAGGTTG TTTCGGGAGG GTCGGGGGTA GCTCTTTTGG
                 G1 Gly/Ser DelCH2
      ----------------------------------------
                                              BsrGI
                                              ---
4201  ATCTCCAAAG CCAAAGGGCA GCCCCGAGAA CCACAGGTGT
      TAGAGGTTTC GGTTTCCCGT CGGGGCTCTT GGTGTCCACA
```

FIG. 13L

```
                G1 Gly/Ser DelCH2
      ----------------------------------------
      BsrGI            SmaI
      ---              -------
4241  ACACCCTGCC CCCATCCCGG GATGAGCTGA CCAAGAACCA
      TGTGGGACGG GGGTAGGGCC CTACTCGACT GGTTCTTGGT
                G1 Gly/Ser DelCH2
      ----------------------------------------
4281  GGTCAGCCTG ACCTGCCTGG TCAAAGGCTT CTATCCCAGC
      CCAGTCGGAC TGGACGGACC AGTTTCCGAA GATAGGGTCG
                G1 Gly/Ser DelCH2
      ----------------------------------------
4321  GACATCGCCG TGGAGTGGGA GAGCAATGGG CAGCCGGAGA
      CTGTAGCGGC ACCTCACCCT CTCGTTACCC GTCGGCCTCT
                G1 Gly/Ser DelCH2
      ----------------------------------------
4361  ACAACTACAA GACCACGCCT CCCGTGCTGG ACTCCGACGG
      TGTTGATGTT CTGGTGCGGA GGGCACGACC TGAGGCTGCC
                G1 Gly/Ser DelCH2
      ----------------------------------------
4401  CTCCTTCTTC CTCTACAGCA AGCTCACCGT GGACAAGAGC
      GAGGAAGAAG GAGATGTCGT TCGAGTGGCA CCTGTTCTCG
                G1 Gly/Ser DelCH2
      ----------------------------------------
4441  AGGTGGCAGC AGGGGAACGT CTTCTCATGC TCCGTGATGC
      TCCACCGTCG TCCCCTTGCA GAAGAGTACG AGGCACTACG
                G1 Gly/Ser DelCH2
      ----------------------------------------
4481  ATGAGGCTCT GCACAACCAC TACACGCAGA AGAGCCTCTC
      TACTCCGAGA CGTGTTGGTG ATGTGCGTCT TCTCGGAGAG
       G1 Gly/Ser DelCH2
      ------------------
                        BamHI
                        -------
4521  CCTGTCTCCG GGTAAATGAG CATCCAATTC GACTGATGCA
      GGACAGAGGC CCATTTACTC CTAGGTTAAG CTGACTACGT
```

FIG. 13M

```
4561  ACGGTTACCA ACTACCTAGA CTGGATTCGT GACAACATGC
      TGCCAATGGT TGATGGATCT GACCTAAGCA CTGTTGTACG
                                          BGH
                                         ---------

            EcoRV
            -------
4601  GGCCGTGATA TCTACGTATG ATCAGCCTCG ACTGTGCCTT
      CCGGCACTAT AGATGCATAC TAGTCGGAGC TGACACGGAA
                        BGH
      ----------------------------------------
4641  CTAGTTGCCA GCCATCTGTT GTTTGCCCCT CCCCCGTGCC
      GATCAACGGT CGGTAGACAA CAAACGGGGA GGGGGCACGG
                        BGH
      ----------------------------------------
4681  TTCCTTGACC CTGGAAGGTG CCACTCCCAC TGTCCTTTCC
      AAGGAACTGG GACCTTCCAC GGTGAGGGTG ACAGGAAAGG
                        BGH
      ----------------------------------------
4721  TAATAAAATG AGGAAATTGC ATCGCATTGT CTGAGTAGGT
      ATTATTTTAC TCCTTTAACG TAGCGTAACA GACTCATCCA
                        BGH
      ----------------------------------------
4761  GTCATTCTAT TCTGGGGGGT GGGGTGGGGC AGGACAGCAA
      CAGTAAGATA AGACCCCCCA CCCCACCCCG TCCTGTCGTT
                        BGH
      ----------------------------------------
4801  GGGGGAGGAT TGGGAAGACA ATAGCAGGCA TGCTGGGGAT
      CCCCCTCCTA ACCCTTCTGT TATCGTCCGT ACGACCCCTA
            BGH
      ----------------
4841  GCGGTGGGCT CTATGGCTTC TGAGGCGGAA AGAACCAGCT
      CGCCACCCGA GATACCGAAG ACTCCGCCTT TCTTGGTCGA
                                            Beta
                                           ---------
                                     SpeI
                                    -------
```

FIG. 13N

```
4881  GGGGCTCGAC AGCGCTGCGA TCGCCTCGAC TAGTAGCTTT
      CCCCGAGCTG TCGCGACGCT AGCGGAGCTG ATCATCGAAA
                        Beta
      ----------------------------------------
4921  GCTTCTCAAT TTCTTATTTG CATAATGAGA AAAAAAGGAA
      CGAAGAGTTA AAGAATAAAC GTATTACTCT TTTTTTCCTT
                        Beta
      ----------------------------------------
4961  AATTAATTTT AACACCAATT CAGTAGTTGA TTGAGCAAAT
      TTAATTAAAA TTGTGGTTAA GTCATCAACT AACTCGTTTA
                        Beta
      ----------------------------------------
5001  GCGTTGCCAA AAAGGATGCT TTAGAGACAG TGTTCTCTGC
      CGCAACGGTT TTTCCTACGA AATCTCTGTC ACAAGAGACG
                        Beta
      ----------------------------------------
5041  ACAGATAAGG ACAAACATTA TTCAGAGGGA GTACCCAGAG
      TGTCTATTCC TGTTTGTAAT AAGTCTCCCT CATGGGTCTC
                        Beta
      ----------------------------------------
5081  CTGAGACTCC TAAGCCAGTG AGTGGCACAG CATCCAGGGA
      GACTCTGAGG ATTCGGTCAC TCACCGTGTC GTAGGTCCCT
                        Beta
      ----------------------------------------
5121  GAAATATGCT TGTCATCACC GAAGCCTGAT TCCGTAGAGC
      CTTTATACGA ACAGTAGTGG CTTCGGACTA AGGCATCTCG
                        Beta
      ----------------------------------------
5161  CACACCCTGG TAAGGGCCAA TCTGCTCACA CAGGATAGAG
      GTGTGGGACC ATTCCCGGTT AGACGAGTGT GTCCTATCTC
                        Beta
      ----------------------------------------
5201  AGGGCAGGAG CCAGGGCAGA GCATATAAGG TGAGGTAGGA
      TCCCGTCCTC GGTCCCGTCT CGTATATTCC ACTCCATCCT
                        Beta
      ----------------------------------------
```

FIG. 13O

```
5241  TCAGTTGCTC CTCACATTTG CTTCTGACAT AGTTGTGTTG
      AGTCAACGAG GAGTGTAAAC GAAGACTGTA TCAACACAAC
5281  GGAGCTTGGA TAGCTTGGGG GGGGGACAGC TCAGGGCTGC
      CCTCGAACCT ATCGAACCCC CCCCCTGTCG AGTCCCGACG
5321  GATTTCGCGC CAAACTTGAC GGCAATCCTA GCGTGAAGGC
      CTAAAGCGCG GTTTGAACTG CCGTTAGGAT CGCACTTCCG
                                        DHFR
                                    ----------
5361  TGGTAGGATT TTATCCCCGC TGCCATCATG GTTCGACCAT
      ACCATCCTAA AATAGGGGCG ACGGTAGTAC CAAGCTGGTA
                        DHFR
      ----------------------------------------
5401  TGAACTGCAT CGTCGCCGTG TCCCAAAATA TGGGGATTGG
      ACTTGACGTA GCAGCGGCAC AGGGTTTTAT ACCCCTAACC
                        DHFR
      ----------------------------------------
5441  CAAGAACGGA GACCTACCCT GGCCTCCGCT CAGGAACGAG
      GTTCTTGCCT CTGGATGGGA CCGGAGGCGA GTCCTTGCTC
                        DHFR
      ----------------------------------------
5481  TTCAAGTACT TCCAAAGAAT GACCACAACC TCTTCAGTGG
      AAGTTCATGA AGGTTTCTTA CTGGTGTTGG AGAAGTCACC
                        DHFR
      ----------------------------------------
5521  AAGGTAAACA GAATCTGGTG ATTATGGGTA GGAAAACCTG
      TTCCATTTGT CTTAGACCAC TAATACCCAT CCTTTTGGAC
                        DHFR
      ----------------------------------------
5561  GTTCTCCATT CCTGAGAAGA ATCGACCTTT AAAGGACAGA
      CAAGAGGTAA GGACTCTTCT TAGCTGGAAA TTTCCTGTCT
                        DHFR
      ----------------------------------------
5601  ATTAATATAG TTCTCAGTAG AGAACTCAAA GAACCACCAC
      TAATTATATC AAGAGTCATC TCTTGAGTTT CTTGGTGGTG
                        DHFR
      ----------------------------------------
                                            AflII
                                            ---
```

FIG. 13P

AMENDED SHEET

```
5641  GAGGAGCTCA TTTTCTTGCC AAAAGTTTGG ATGATGCCTT
      CTCCTCGAGT AAAAGAACGG TTTTCAAACC TACTACGGAA
                        DHFR
      ----------------------------------------
      AflII
      ---
5681  AAGACTTATT GAACAACCGG AATTGGCAAG TAAAGTAGAC
      TTCTGAATAA CTTGTTGGCC TTAACCGTTC ATTTCATCTG
                        DHFR
      ----------------------------------------
5721  ATGGTTTGGA TAGTCGGAGG CAGTTCTGTT TACCAGGAAG
      TACCAAACCT ATCAGCCTCC GTCAAGACAA ATGGTCCTTC
                        DHFR
      ----------------------------------------
5761  CCATGAATCA ACCAGGCCAC CTCAGACTCT TTGTGACAAG
      GGTACTTAGT TGGTCCGGTG GAGTCTGAGA AACACTGTTC
                        DHFR
      ----------------------------------------
5801  GATCATGCAG GAATTTGAAA GTGACACGTT TTTCCCAGAA
      CTAGTACGTC CTTAAACTTT CACTGTGCAA AAAGGGTCTT
                        DHFR
      ----------------------------------------
5841  ATTGATTTGG GGAAATATAA ACTTCTCCCA GAATACCCAG
      TAACTAAACC CCTTTATATT TGAAGAGGGT CTTATGGGTC
                        DHFR
      ----------------------------------------
5881  GCGTCCTCTC TGAGGTCCAG GAGGAAAAAG GCATCAAGTA
      CGCAGGAGAG ACTCCAGGTC CTCCTTTTTC CGTAGTTCAT
                   DHFR
      ---------------------------------
5921  TAAGTTTGAA GTCTACGAGA AGAAAGACTA ACAGGAAGAT
      ATTCAAACTT CAGATGCTCT TCTTTCTGAT TGTCCTTCTA
5961  GCTTTCAAGT TCTCTGCTCC CCTCCTAAAG CTATGCATTT
      CGAAAGTTCA AGAGACGAGG GGAGGATTTC GATACGTAAA
6001  TTATAAGACC ATGGGACTTT TGCTGGCTTT AGATCAGCCT
      AATATTCTGG TACCCTGAAA ACGACCGAAA TCTAGTCGGA
                           BGH
         -------------------------------------
```

FIG. 13Q

```
6041  CGACTGTGCC TTCTAGTTGC CAGCCATCTG TTGTTTGCCC
      GCTGACACGG AAGATCAACG GTCGGTAGAC AACAAACGGG
                        BGH
      ----------------------------------------
6081  CTCCCCCGTG CCTTCCTTGA CCCTGGAAGG TGCCACTCCC
      GAGGGGGCAC GGAAGGAACT GGGACCTTCC ACGGTGAGGG
                        BGH
      ----------------------------------------
6121  ACTGTCCTTT CCTAATAAAA TGAGGAAATT GCATCGCATT
      TGACAGGAAA GGATTATTTT ACTCCTTTAA CGTAGCGTAA
                        BGH
      ----------------------------------------
6161  GTCTGAGTAG GTGTCATTCT ATTCTGGGGG GTGGGGTGGG
      CAGACTCATC CACAGTAAGA TAAGACCCCC CACCCCACCC
                        BGH
      ----------------------------------------
6201  GCAGGACAGC AAGGGGGAGG ATTGGGAAGA CAATAGCAGG
      CGTCCTGTCG TTCCCCCTCC TAACCCTTCT GTTATCGTCC
                 BGH
      ------------------------------
6241  CATGCTGGGG ATGCGGTGGG CTCTATGGCT TCTGAGGCGG
      GTACGACCCC TACGCCACCC GAGATACCGA AGACTCCGCC
                                        BspEI
                                        ------
6281  AAAGAACCAG CTGGGGCTCG AAGCGGCCGC TCCGGATCGA
      TTTCTTGGTC GACCCCGAGC TTCGCCGGCG AGGCCTAGCT
                                                N2
                                                -
6321  GGCCGCTACT AACTCTCTCC TCCCTCCTTT TTCCTGCAGG
      CCGGCGATGA TTGAGAGAGG AGGGAGGAAA AAGGACGTCC
                        N2
      ----------------------------------------
                               MscI
                               -------
6361  ACGAGGCAGC GCGGCTATCG TGGCTGGCCA CGACGGGCGT
      TGCTCCGTCG CGCCGATAGC ACCGACCGGT GCTGCCCGCA
                        N2
      ----------------------------------------
```

FIG. 13R

```
6401  TCCTTGCGCA GCTGTGCTCG ACGTTGTCAC TGAAGCGGGA
      AGGAACGCGT CGACACGAGC TGCAACAGTG ACTTCGCCCT
                        N2
      ----------------------------------------
6441  AGGGACTGGC TGCTATTGGG CGAAGTGCCG GGGCAGGATC
      TCCCTGACCG ACGATAACCC GCTTCACGGC CCCGTCCTAG
                        N2
      ----------------------------------------
6481  TCCTGTCATC TCACCTTGCT CCTGCCGAGA AAGTATCCAT
      AGGACAGTAG AGTGGAACGA GGACGGCTCT TTCATAGGTA
                        N2
      ----------------------------------------
6521  CATGGCTGAT GCAATGCGGC GGCTGCATAC GCTTGATCCG
      GTACCGACTA CGTTACGCCG CCGACGTATG CGAACTAGGC
                        N2
      ----------------------------------------
6561  GCTACCTGCC CATTCGACCA CCAAGCGAAA CATCGCATCG
      CGATGGACGG GTAAGCTGGT GGTTCGCTTT GTAGCGTAGC
                        N2
      ----------------------------------------
6601  AGCGAGCACG TACTCGGATG GAAGCCGGTC TTGTCGATCA
      TCGCTCGTGC ATGAGCCTAC CTTCGGCCAG AACAGCTAGT
                        N2
      ----------------------------------------
6641  GGATGATCTG GACGAAGAGC ATCAGGGGCT CGCGCCAGCC
      CCTACTAGAC CTGCTTCTCG TAGTCCCCGA GCGCGGTCGG
                        N2
      ----------------------------------------
6681  GAACTGTTCG CCAGGCTCAA GGCGCGCATG CCCGACGGCG
      CTTGACAAGC GGTCCGAGTT CCGCGCGTAC GGGCTGCCGC
                        N2
      ----------------------------------------
6721  AGGATCTCGT CGTGACCCAT GGCGATGCCT GCTTGCCGAA
      TCCTAGAGCA GCACTGGGTA CCGCTACGGA CGAACGGCTT
                        N2
      ----------------------------------------
```

FIG. 13S

```
6761  TATCATGGTG GAAAATGGCC GCTTTTCTGG ATTCATCGAC
      ATAGTACCAC CTTTTACCGG CGAAAAGACC TAAGTAGCTG
                        N2
      ----------------------------------------

                         RsrII
                        --------
6801  TGTGGCCGGC TGGGTGTGGC GGACCGCTAT CAGGACATAG
      ACACCGGCCG ACCCACACCG CCTGGCGATA GTCCTGTATC
                        N2
      ----------------------------------------
6841  CGTTGGCTAC CCGTGATATT GCTGAAGAGC TTGGCGGCGA
      GCAACCGATG GGCACTATAA CGACTTCTCG AACCGCCGCT
                        N2
      ----------------------------------------
6881  ATGGGCTGAC CGCTTCCTCG TGCTTTACGG TATCGCCGCT
      TACCCGACTG GCGAAGGAGC ACGAAATGCC ATAGCGGCGA
                        N2
      ----------------------------------------
6921  CCCGATTCGC AGCGCATCGC CTTCTATCGC CTTCTTGACG
      GGGCTAAGCG TCGCGTAGCG GAAGATAGCG GAAGAACTGC
          N2
      ------------

                                 BstBI
                                -------
6961  AGTTCTTCTG AGCGGGACTC TGGGGTTCGA AATGACCGAC
      TCAAGAAGAC TCGCCCTGAG ACCCCAAGCT TTACTGGCTG
7001  CAAGCGACGC CCAACCTGCC ATCACGAGAT TTCGATTCCA
      GTTCGCTGCG GGTTGGACGG TAGTGCTCTA AAGCTAAGGT
7041  CCGCCGCCTT CTATGAAAGG TTGGGCTTCG GAATCGTTTT
      GGCGGCGGAA GATACTTTCC AACCCGAACD CTTAGCAAAA
7081  CCGGGACGCC GGCTGGATGA TCCTCCAGGC CGGGGATCTC
      GGCCCTGCGG CCGACCTACT AGGAGGTCGC GCCCCTAGAG
                                        SV
                                 ----------------
7121  ATGCTGGAGT TCTTCGCCCA CCCAACTTGT TTATTGCAGC
      TACGACCTCA AGAAGCGGGT GGGTTGAACA AATAACGTCG
                        SV
      ----------------------------------------
```

FIG. 13T

```
7161  TTATAATGGT TACAAATAAA GCAATAGCAT CACAAATTTC
      AATATTACCA ATGTTTATTT CGTTATCGTA GTGTTTAAAG
                         SV
      ----------------------------------------
7202  ACAAATAAAG CATTTTTTTC ACTGCATTCT AGTTGTGGTT
      TGTTTATTTC GTAAAAAAAG TGACGTAAGA TCAACACCAA
                       SV
      -------------------------------------
7241  TGTCCAAACT CATCAATGTA TCTTATCATG TCTGGATCGC
      ACAGGTTTGA GTAGTTACAT AGAATAGTAC AGACCTAGCG
                                            AscI
                                           -------
7281  GGCCGGCCGC CACCGCGGTG GAGCTTTAAT TAAGGCGCGC
      CCGGCCGGCG GTGGCGCCAC CTCGAAATTA ATTCCGCGCG
      AscI
      -
7321  CAGCTCCAGC TTTTGTTCCC TTTAGTGAGG GTTAATTTCG
      GTCGAGGTCG AAAACAAGGG AAATCACTCC CAATTAAAGC
7361  AGCTTGGCGT AATCATGGTC ATAGCTGTTT CCTGTGTGAA
      TCGAACCGCA TTAGTACCAG TATCGACAAA GGACACACTT
7401  ATTGTTATCC GCTCACAATT CCACACAACA TACGAGCCGG
      TAACAATAGG CGAGTGTTAA GGTGTGTTGT ATGCTCGGCC
7441  AAGCATAAAG TGTAAAGCCT GGGGTGCCTA ATGAGTGAGC
      TTCGTATTTC ACATTTCGGA CCCCACGGAT TACTCACTCG
7481  TAACTCACAT TAATTGCGTT GCGCTCACTG CCCGCTTTCC
      ATTGAGTGTA ATTAACGCAA CGCGAGTGAC GGGCGAAAGG
7521  AGTCGGGAAA CCTGTCGTGC CAGCTGCATT AATGAATCGG
      TCAGCCCTTT GGACAGCACG GTCGACGTAA TTACTTAGCC
7561  CCAACGCGCG GGGAGAGGCG GTTTGCGTAT TGGGCGCTCT
      GGTTGCGCGC CCCTCTCCGC CAAACGCATA ACCCGCGAGA
7601  TCCGCTTCCT CGCTCACTGA CTCGCTGCGC TCGGTCGTTC
      AGGCGAAGGA GCGAGTGACT GAGCGACGCG AGCCAGCAAG
7641  GGCTGCGGCG AGCGGTATCA GCTCACTCAA AGGCGGTAAT
      CCGACGCCGC TCGCCATAGT CGAGTGAGTT TCCGCCATTA
7681  ACGGTTATCC ACAGAATCAG GGGATAACGC AGGAAAGAAC
      TGCCAATAGG TGTCTTAGTC CCCTATTGCG TCCTTTCTTG
7721  ATGTGAGCAA AAGGCCAGCA AAAGGCCAGG AACCGTAAAA
      TACACTCGTT TTCCGGTCGT TTTCCGGTCC TTGGCATTTT
7761  AGGCCGCGTT GCTGGCGTTT TTCCATAGGC TCCGCCCCCC
      TCCGGCGCAA CGACCGCAAA AAGGTATCCG AGGCGGGGGG
```

FIG. 13U

```
7801  TGACGAGCAT CACAAAAATC GACGCTCAAG TCAGAGGTGG
      ACTGCTCGTA GTGTTTTTAG CTGCGAGTTC AGTCTCCACC
7841  CGAAACCCGA CAGGACTATA AAGATACCAG GCGTTTCCCC
      GCTTTGGGCT GTCCTGATAT TTCTATGGTC CGCAAAGGGG
7881  CTGGAAGCTC CCTCGTGCGC TCTCCTGTTC CGACCCTGCC
      GACCTTCGAG GGAGCACGCG AGAGGACAAG GCTGGGACGG
7921  GCTTACCGGA TACCTGTCCG CCTTTCTCCC TTCGGGAAGC
      CGAATGGCCT ATGGACAGGC GGAAAGAGGG AAGCCCTTCG
7961  GTGGCGCTTT CTCATAGCTC ACGCTGTAGG TATCTCAGTT
      CACCGCGAAA GAGTATCGAG TGCGACATCC ATAGAGTCAA
8001  CGGTGTAGGT CGTTCGCTCC AAGCTGGGCT GTGTGCACGA
      GCCACATCCA GCAAGCGAGG TTCGACCCGA CACACGTGCT
8041  ACCCCCCGTT CAGCCCGACC GCTGCGCCTT ATCCGGTAAC
      TGGGGGGCAA GTCGGGCTGG CGACGCGGAA TAGGCCATTG
8081  TATCGTCTTG AGTCCAACCC GGTAAGACAC GACTTATCGC
      ATAGCAGAAC TCAGGTTGGG CCATTCTGTG CTGAATAGCG
8121  CACTGGCAGC AGCCACTGGT AACAGGATTA GCAGAGCGAG
      GTGACCGTCG TCGGTGACCA TTGTCCTAAT CGTCTCGCTC
8161  GTATGTAGGC GGTGCTACAG AGTTCTTGAA GTGGTGGCCT
      CATACATCCG CCACGATGTC TCAAGAACTT CACCACCGGA
8201  AACTACGGCT ACACTAGAAG AACAGTATTT GGTATCTGCG
      TTGATGCCGA TGTGATCTTC TTGTCATAAA CCATAGACGC
8241  CTCTGCTGAA GCCAGTTACC TTCGGAAAAA GAGTTGGTAG
      GAGACGACTT CGGTCAATGG AAGCCTTTTT CTCAACCATC
8281  CTCTTGATCC GGCAAACAAA CCACCGCTGG TAGCGGTGGT
      GAGAACTAGG CCGTTTGTTT GGTGGCGACC ATCGCCACCA
8321  TTTTTTGTTT GCAAGCAGCA GATTACGCGC AGAAAAAAAG
      AAAAAACAAA CGTTCGTCGT CTAATGCGCG TCTTTTTTTC
8361  GATCTCAAGA AGATCCTTTG ATCTTTTCTA CGGGGTCTGA
      CTAGAGTTCT TCTAGGAAAC TAGAAAAGAT GCCCCAGACT
8401  CGCTCAGTGG AACGAAAACT CACGTTAAGG GATTTTGGTC
      GCGAGTCACC TTGCTTTTGA GTGCAATTCC CTAAAACCAG
8441  ATGAGATTAT CAAAAAGGAT CTTCACCTAG ATCCTTTTAA
      TACTCTAATA GTTTTTCCTA GAAGTGGATC TAGGAAAATT
8481  ATTAAAAATG AAGTTTTAAA TCAATCTAAA GTATATATGA
      TAATTTTTAC TTCAAAATTT AGTTAGATTT CATATATACT
8521  GTAAACTTGG TCTGACAGTT ACCAATGCTT AATCAGTGAG
      CATTTGAACC AGACTGTCAA TGGTTACGAA TTAGTCACTC
                        ----------------------
                                Amp
```

FIG. 13V

```
8561  GCACCTATCT CAGCGATCTG TCTATTTCGT TCATCCATAG
      CGTGGATAGA GTCGCTAGAC AGATAAAGCA AGTAGGTATC
      ------------------------------------------
                          Amp
8601  TTGCCTGACT CCCCGTCGTG TAGATAACTA CGATACGGGA
      AACGGACTGA GGGGCAGCAC ATCTATTGAT GCTATGCCCT
      ------------------------------------------
                          Amp
8641  GGGCTTACCA TCTGGCCCCA GTGCTGCAAT GATACCGCGA
      CCCGAATGGT AGACCGGGGT CACGACGTTA CTATGGCGCT
      ------------------------------------------
                          Amp
8681  GACCCACGCT CACCGGCTCC AGATTTATCA GCAATAAACC
      CTGGGTGCGA GTGGCCGAGG TCTAAATAGT CGTTATTTGG
      ------------------------------------------
                          Amp
8721  AGCCAGCCGG AAGGGCCGAG CGCAGAAGTG GTCCTGCAAC
      TCGGTCGGCC TTCCCGGCTC GCGTCTTCAC CAGGACGTTG
      ------------------------------------------
                          Amp
8761  TTTATCCGCC TCCATCCAGT CTATTAATTG TTGCCGGGAA
      AAATAGGCGG AGGTAGGTCA GATAATTAAC AACGGCCCTT
      ------------------------------------------
                          Amp
8801  GCTAGAGTAA GTAGTTCGCC AGTTAATAGT TTGCGCAACG
      CGATCTCATT CATCAAGCGG TCAATTATCA AACGCGTTGC
      ------------------------------------------
                          Amp
8841  TTGTTGCCAT TGCTACAGGC ATCGTGGTGT CACGCTCGTC
      AACAACGGTA ACGATGTCCG TAGCACCACA GTGCGAGCAG
      ------------------------------------------
                          Amp
8881  GTTTGGTATG GCTTCATTCA GCTCCGGTTC CCAACGATCA
      CAAACCATAC CGAAGTAAGT CGAGGCCAAG GGTTGCTAGT
      ------------------------------------------
                          Amp
8921  AGGCGAGTTA CATGATCCCC CATGTTGTGC AAAAAAGCGG
      TCCGCTCAAT GTACTAGGGG GTACAACACG TTTTTTCGCC
      ------------------------------------------
                          Amp
```

FIG. 13W

```
8961  TTAGCTCCTT CGGTCCTCCG ATCGTTGTCA GAAGTAAGTT
      AATCGAGGAA GCCAGGAGGC TAGCAACAGT CTTCATTCAA
      ------------------------------------------
                        Amp
9001  GGCCGCAGTG TTATCACTCA TGGTTATGGC AGCACTGCAT
      CCGGCGTCAC AATAGTGAGT ACCAATACCG TCGTGACGTA
      ------------------------------------------
                        Amp
9041  AATTCTCTTA CTGTCATGCC ATCCGTAAGA TGCTTTTCTG
      TTAAGAGAAT GACAGTACGG TAGGCATTCT ACGAAAAGAC
      ------------------------------------------
                        Amp
9081  TGACTGGTGA GTACTCAACC AAGTCATTCT GAGAATAGTG
      ACTGACCACT CATGAGTTGG TTCAGTAAGA CTCTTATCAC
      ------------------------------------------
                        Amp
9121  TATGCGGCGA CCGAGTTGCT CTTGCCCGGC GTCAATACGG
      ATACGCCGCT GGCTCAACGA GAACGGGCCG CAGTTATGCC
      ------------------------------------------
                        Amp
9161  GATAATACCG CGCCACATAG CAGAACTTTA AAAGTGCTCA
      CTATTATGGC GCGGTGTATC GTCTTGAAAT TTTCACGAGT
      ------------------------------------------
                        Amp
9201  TCATTGGAAA ACGTTCTTCG GGGCGAAAAC TCTCAAGGAT
      AGTAACCTTT TGCAAGAAGC CCCGCTTTTG AGAGTTCCTA
      ------------------------------------------
                        Amp
9241  CTTACCGCTG TTGAGATCCA GTTCGATGTA ACCCACTCGT
      GAATGGCGAC AACTCTAGGT CAAGCTACAT TGGGTGAGCA
      ------------------------------------------
                        Amp
9281  GCACCCAACT GATCTTCAGC ATCTTTTACT TTCACCAGCG
      CGTGGGTTGA CTAGAAGTCG TAGAAAATGA AAGTGGTCGC
      ------------------------------------------
                        Amp
9321  TTTCTGGGTG AGCAAAAACA GGAAGGCAAA ATGCCGCAAA
      AAAGACCCAC TCGTTTTTGT CCTTCCGTTT TACGGCGTTT
      ------------------------------------------
                        Amp
```

FIG. 13X

```
9361  AAAGGGAATA AGGGCGACAC GGAAATGTTG AATACTCATA
      TTTCCCTTAT TCCCGCTGTG CCTTTACAAC TTATGAGTAT
      ----------------------------------------
                        Amp
                     SsPI
                    ------
9401  CTCTTCCTTT TTCAATATTA TTGAAGCATT TATCAGGGTT
      GAGAAGGAAA AAGTTATAAT AACTTCGTAA ATAGTCCCAA
9441  ATTGTCTCAT GAGCGGATAC ATATTTGAAT GTATTTAGAA
      TAACAGAGTA CTCGCCTATG TATAAACTTA CATAAATCTT
9481  AAATAAACAA ATAGGGGTTC CGCGCACATT TCCCCGAAAA
      TTTATTTGTT TATCCCCAAG GCGCGTGTAA AGGGGCTTTT
9521  GTGCCAC
      CACGGTG
```

FIG. 13Y