

FIGURE 1A

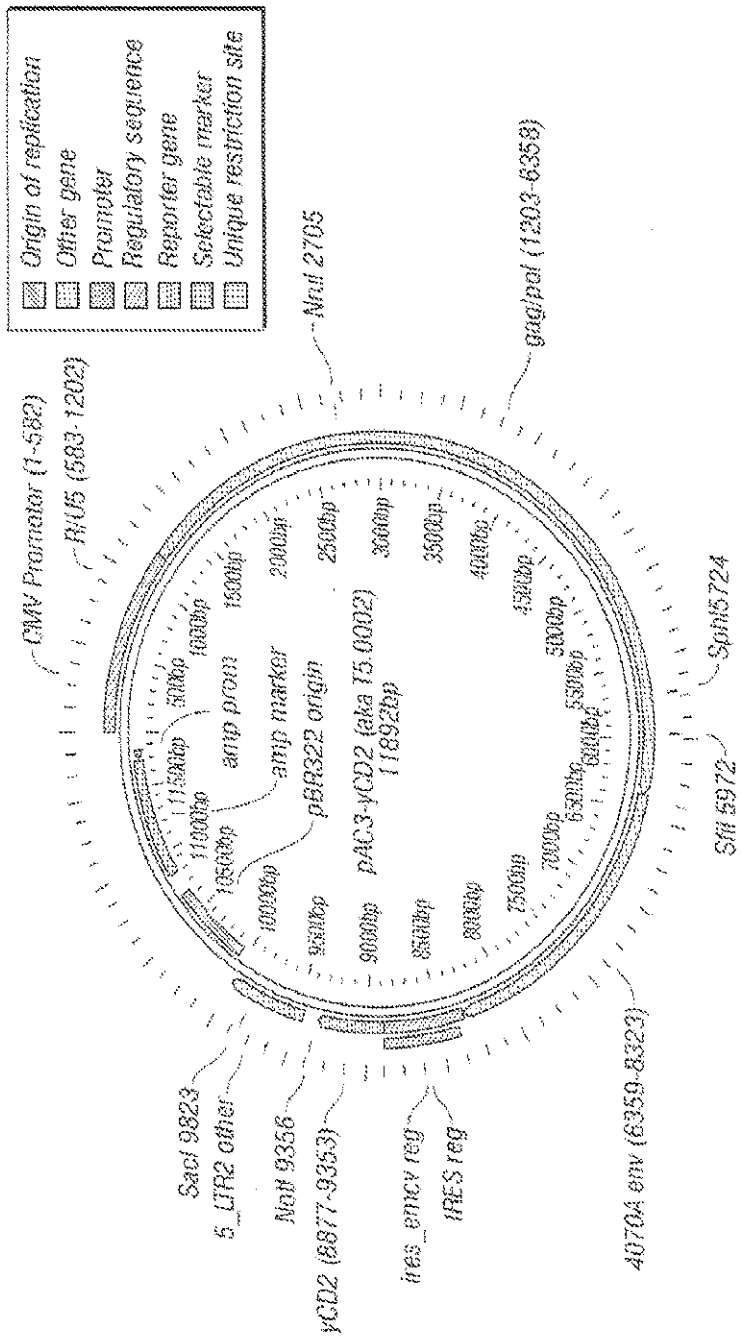


FIGURE 1B

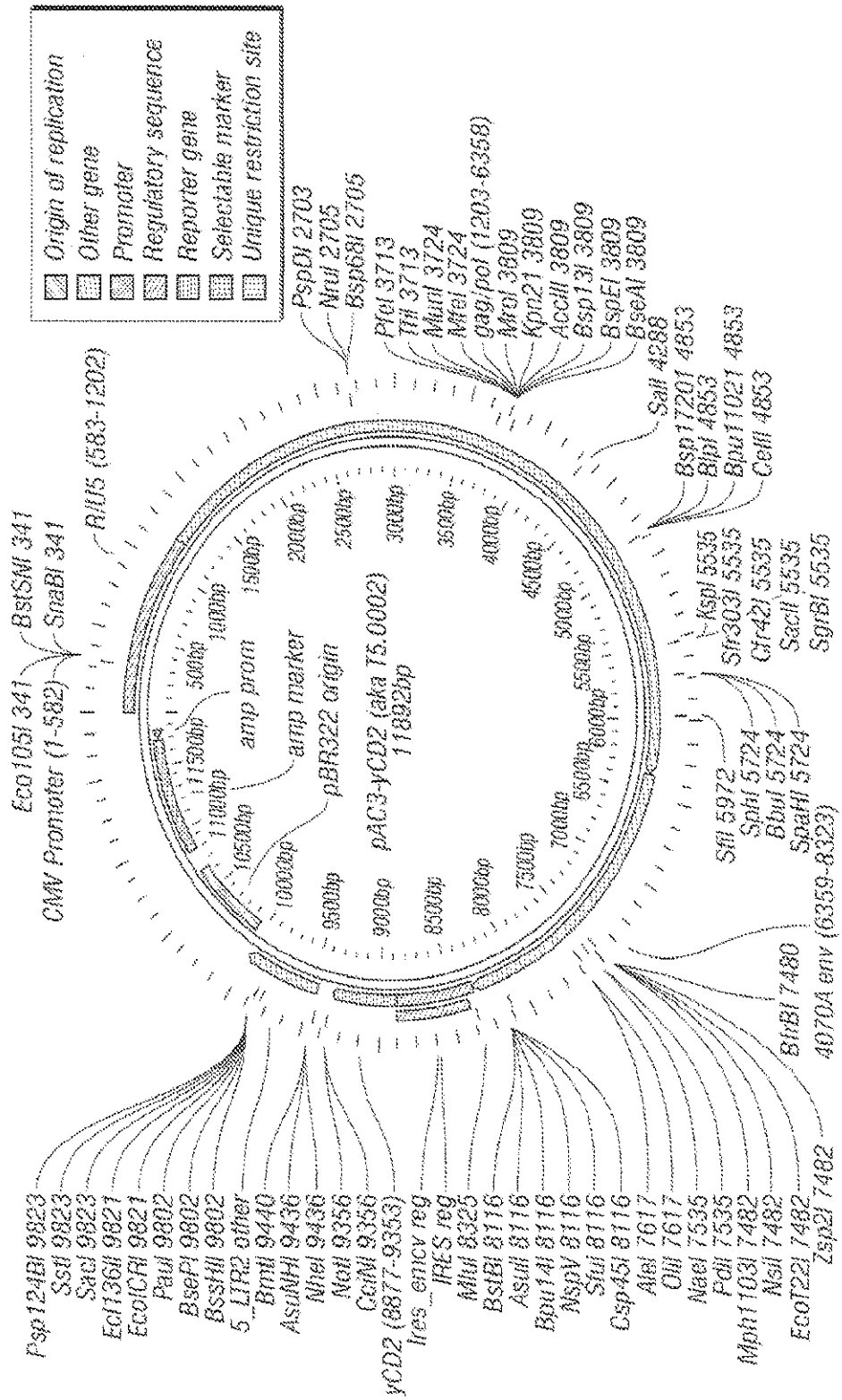

Origin of replication
Other gene
Promoter
Regulatory sequence
Reporter gene
Selectable marker
Unique restriction site
pAC3-yCD2 (aka T5.0002)
11892bp
amp marker
amp prom
pBR322 origin
CMV Promoter (1-582)
Eco105I 341
BstSWI 341
SnaBI 341
BlnI5 (583-1202)
PspOI 2703
NruI 2705
BspGSI 2705
PfoI 3713
TfiI 3713
MunI 3724
MfeI 3724
gag/pol (1203-6358)
MroI 3809
Kpn21 3809
AccIII 3809
Bsp13I 3809
BspEI 3809
BseAI 3809
SalI 4288
Bsp17201 4853
BipI 4853
Bpu11021 4853
CelII 4853
KspI 5535
Sfr303I 5535
Cfr42I 5535
SacII 5535
SgrBI 5535
SfiI 5972
SphI 5724
BbuI 5724
SnaHI 5724
BlnBI 7480
4070A env (6359-8323)
Zsp2I 7482
EcoT22I 7482
NsiI 7482
Mph1103I 7482
PdiI 7535
NaeI 7535
OliI 7617
AleI 7617
Csp45I 8116
SfuI 8116
MspV 8116
Bpu14I 8116
AsuII 8116
BstBI 8116
MluI 8325
IRES reg
Ires_emcv reg
yCD2 (8877-9353)
CelNI 9356
NotI 9356
MfeI 9436
AsuNHI 9436
BmtI 9440
5_LTR2 other
BssHII 9902
BseP1 9902
PauI 9902
EcoICRI 9921
Ecl136II 9921
SacI 9923
SstI 9923
Psp124BI 9923

FIGURE 1C



FIGURE 1D-1



FIGURE 1D-2



FIGURE 1D-3



FIGURE 1D-4



FIGURE 1D-4

```
                                                        U5 region (651-1202)>>>
                                                          |
601  ACTGAGTCGCCCGGGTACCCGTGTATCCAATAAACCCTCTTGCAGTTGCATCCGACTTGT 660
     TGACTCAGCGGGCCCATGGGCACATAGGTTATTTGGGAGAACGTCAACGTAGGCTGAACA

661  GGTCTCGCTGTTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGGGGTC 720
     CCAGAGCGACAAGGAACCCTCCCAGAGGAGACTCACTAACTGATGGGCAGTCGCCCCCAG

721  TTTCATTTGGGGGCTCGTCCGGGATCGGGAGACCCCTGCCCAGGGACCACCGACCCACCA 780
     AAAGTAAACCCCCGAGCAGGCCCTAGCCCTCTGGGGACGGGTCCCTGGTGGCTGGGTGGT

           5'SS (788)
             |
781  CCGGGAGGTAAGCTGGCCAGCAACTTATCTGTGTCTGTCCGATTGTCTAGTGTCTATGAC 840
     GGCCCTCCATTCGACCGGTCGTTGAATAGACACAGACAGGCTAACAGATCACAGATACTG

841  TGATTTTATGCGCCTGCGTCGGTACTAGTTAGCTAACTAGCTCTGTATCTGGCGGACCCG 900
```

FIGURE 1D-5

```
        ACTAAAATACGCGGACGCAGCCATGATCAATCGATTGATCGAGACATAGACCGCCTGGGC

901     TGGTGGAACTGACGAGTTCGGAACACCCGGCCGCAACCCTGGGAGACGTCCCAGGGACTT 960
        ACCACCTTGACTGCTCAAGCCTTGTGGGCCGGCGTTGGGACCCTCTGCAGGGTCCCTGAA

961     CGGGGGCCGTTTTTGTGGCCCGACCTGAGTCCAAAAATCCCGATCGTTTTGGACTCTTTG 1020
        GCCCCCGGCAAAAACACCGGGCTGGACTCAGGTTTTTAGGGCTAGCAAAACCTGAGAAAC

1021    GTGCACCCCCCTTAGAGGAGGGATATGTGGTTCTGGTAGGAGACGAGAACCTAAAACAGT 1080
        CACGTGGGGGGAATCTCCTCCCTATACACCAAGACCATCCTCTGCTCTTGGATTTTGTCA

1081    TCCCGCCTCCGTCTGAATTTTTGCTTTCGGTTTGGGACCGAAGCCGCGCCGCGCGTCTTG 1140
        AGGGCGGAGGCAGACTTAAAAACGAAAGCCAAACCCTGGCTTCGGCGCGGCGCGCAGAAC

1141    TCTGCTGCAGCATCGTTCTGTGTTGTCTCTGTCTGACTGTGTTTCTGTATTTGTCTGAGA 1200
        AGACGACGTCGTAGCAAGACACAACAGAGACAGACTGACACAAAGACATAAACAGACTCT

          q=g(1203,2819)>>>
          |
1201    ATATGGGCCAGACTGTTACCACTCCCTTAAGTTTGACCTTAGGTCACTGGAAAGATGTCG 1260
        TATACCCGGTCTGACAATGGTGAGGGAATTCAAACTGGAATCCAGTGACCTTTCTACAGC

1261    AGCGGATCGCTCACAACCAGTCGGTAGATGTCAAGAAGAGACGTTGGGTTACCTTCTGCT 1320
        TCGCCTAGCGAGTGTTGGTCAGCCATCTACAGTTCTTCTCTGCAACCCAATGGAAGACGA

1321    CTGCAGAATGGCCAACCTTTAACGTCGGATGGCCGCGAGACGGCACCTTTAACCGAGACC 1380
        GACGTCTTACCGGTTGGAAATTGCAGCCTACCGGCGCTCTGCCGTGGAAATTGGCTCTGG

1381    TCATCACCCAGGTTAAGATCAAGGTCTTTTCACCTGGCCCGCATGGACACCCAGACCAGG 1440
        AGTAGTGGGTCCAATTCTAGTTCCAGAAAAGTGGACCGGGGCGTACCTGTGGGTCTGGTCC

1441    TCCCCTACATCGTGACCTGGGAAGCCTTGGCTTTTGACCCCCCTCCCTGGGTCAAGCCCT 1500
        AGGGGATGTAGCACTGGACCCTTCGGAACCGAAAACTGGGGGGAGGGACCCAGTTCGGGA

1501    TTGTACACCCTAAGCCTCCGCCTCCTCTTCCTCCATCCGCCCCGTCTCTCCCCCTTGAAC 1560
        AACATGTGGGATTCGGAGGCGGAGGAGAAGGAGGTAGGCGGGGCAGACAGGGGGAACTTG

1561    CTCCTCGTTCGACCCCGCCTCGATCCTCCCTTTATCCAGCCCTCACTCCTTCTCTAGGCG 1620
        GAGGAGCAAGCTGGGGCGGAGCTAGGAGGGAAATAGGTCGGGAGTGAGGAAGAGATCCGC

1621    CCAAACCTAAACCTCAAGTTCTTTCTGACAGTGGGGGGCCGCTCATCGACCTACTTACAG 1680
        GGTTTGGATTTGGAGTTCAAGAAAGACTGTCACCCCCCGGCGAGTAGCTGGATGAATGTC

1681    AAGACCCCCCGCCTTATAGGGACCCAAGACCACCCCCTTCCGACAGGGACGGAAATGGTG 1740
        TTCTGGGGGGGCGGAATATCCCTGGGTTCTGGTGGGGGAAGGCTGTCCCTGCCTTTACCAC
```

FIGURE 1D-6


1741 GAGAAGCGACCCCTGCGGGAGAGGCACCGGACCCCTCCCCAATGGCATCTCGCCTACGTG 1800
CTCTTCGCTGGGGACGCCCTCTCCGTGGCCTGGGGAGGGGTTACCGTAGAGCGGATGCAC
1801 GGAGACGGGAGCCCCCTGTGGCCGACTCCACTACCTCGCAGGCATTCCCCCTCCGCGCAG 1860
CCTCTGCCCTCGGGGGACACCGGCTGAGGTGATGGAGCGTCCGTAAGGGGGAGGCGCGTC
1861 GAGGAAACGGACAGCTTCAATACTGGCCGTTCTCCTCTTCTGACCTTTACAACTGGAAAA 1920
CTCCTTTGCCTGTCGAAGTTATGACCGGCAAGAGGAGAAGACTGGAAATGTTGACCTTTT
1921 ATAATAACCCTTCTTTTTCTGAAGATCCAGGTAAACTGACAGCTCTGATCGAGTCTGTTC 1980
TATTATTGGGAAGAAAAAGACTTCTAGGTCCATTTGACTGTCGAGACTAGCTCAGACAAG
1981 TCATCACCCATCAGCCCACCTGGGACGACTGTCAGCAGCTGTTGGGGACTCTGCTGACCG 2040
AGTAGTGGGTAGTCGGGTGGACCCTGCTGACAGTCGTCGACAACCCCTGAGACGACTGGC
3121 ACTTTGAGGGATCAGGAGCCCAGGTTATGGGACCAATGGGGCAGCCCCTGCAAGTGTTGA 3180
TGAAACTCCCTAGTCCTCGGGTCCAATACCCTGGTTACCCCGTCGGGGACGTTCACAACT
3181 CCCTAAATATAGAAGATGAGCATCGGCTACATGAGACCTCAAAAGAGCCAGATGTTTCTC 3240
GGGATTTATATCTTCTACTCGTAGCCGATGTACTCTGGAGTTTTCTCGGTCTACAAAGAG
3241 TAGGGTCCACATGGCTGTCTGATTTTCCTCAGGCCTGGGCGGAAACCGGGGGCATGGGAC 3300
ATCCCAGGTGTACCGACAGACTAAAAGGAGTCCGGACCCGCCTTTGGCCCCCGTACCCTG
3'SS (3314)
3301 TGGCAGTTCGCCAAGCTCCTCTGATCATACCTCTGAAAGCAACCTCTACCCCCGTGTCCA 3360
ACCGTCAAGCGGTTCGAGGAGACTAGTATGGAGACTTTCGTTGGAGATGGGGGCACAGGT
3361 TAAAACAATACCCCATGTCACAAGAAGCCAGACTGGGGATCAAGCCCCACATACAGAGAC 3420
ATTTTGTTATGGGGTACAGTGTTCTTCGGTCTGACCCCTAGTTCGGGGTGTATGTCTCTG
3421 TGTTGGACCAGGGAATACTGGTACCCTGCCAGTCCCCCTGGAACACGCCCCTGCTACCCG 3480
ACAACCTGGTCCCTTATGACCATGGGACGGTCAGGGGGACCTTGTGCGGGGACGATGGGC
3481 TTAAGAAACCAGGGACTAATGATTATAGGCCTGTCCAGGATCTGAGAGAAGTCAACAAGC 3540
AATTCTTTGGTCCCTGATTACTAATATCCGGACAGGTCCTAGACTCTCTTCAGTTGTTCG
3541 GGGTGGAAGACATCCACCCCACCGTGCCCAACCCTTACAACCTCTTGAGCGGGCTCCCAC 3600
CCCACCTTCTGTAGGTGGGGTGGCACGGGTTGGGAATGTTGGAGAACTCGCCCGAGGGTG
3601 CGTCCCACCAGTGGTACACTGTGCTTGATTTAAAGGATGCCTTTTTCTGCCTGAGACTCC 3660
GCAGGGTGGTCACCATGTGACACGAACTAAATTTCCTACGGAAAAAGACGGACTCTGAGG
PfeI
TfiI
3661 ACCCCACCAGTCAGCCTCTCTTCGCCTTTGAGTGGAGAGATCCAGAGATGGGAATCTCAG 3720
TGGGGTGGTCAGTCGGAGAGAAGCGGAAACTCACCTCTCTAGGTCTCTACCCTTAGAGTC

FIGURE 1D-7

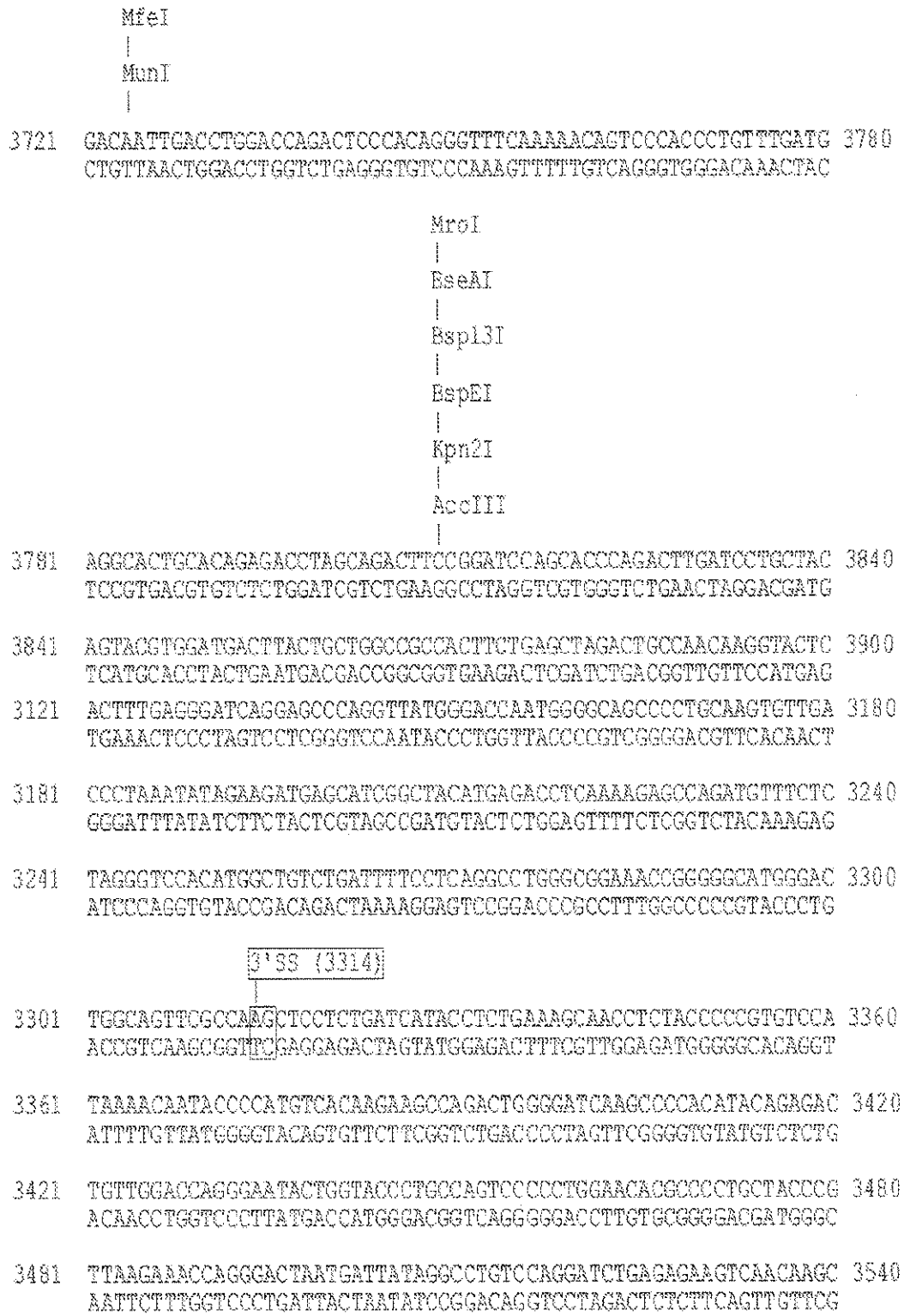

MfeI
MunI
3721 GACAATTGACCTGGACCAGACTCCCACAGGGTTTCAAAAACAGTCCCACCCTGTTTGATG 3780
CTGTTAACTGGACCTGGTCTGAGGGTGTCCCAAAGTTTTTGTCAGGGTGGGACAAACTAC
MroI
EseAI
Bsp13I
EspEI
Kpn2I
AccIII
3781 AGGCACTGCACAGAGACCTAGCAGACTTCCGGATCCAGCACCCAGACTTGATCCTGCTAC 3840
TCCGTGACGTGTCTCTGGATCGTCTGAAGGCCTAGGTCGTGGGTCTGAACTAGGACGATG
3841 AGTACGTGGATGACTTACTGCTGGCCGCCACTTCTGAGCTAGACTGCCAACAAGGTACTC 3900
TCATGCACCTACTGAATGACGACCGGCGGTGAAGACTCGATCTGACGGTTGTTCCATGAG
3121 ACTTTGAGGGATCAGGAGCCCAGGTTATGGGACCAATGGGGCAGCCCCTGCAAGTGTTGA 3180
TGAAACTCCCTAGTCCTCGGGTCCAATACCCTGGTTACCCCGTCGGGGACGTTCACAACT
3181 CCCTAAATATAGAAGATGAGCATCGGCTACATGAGACCTCAAAAGAGCCAGATGTTTCTC 3240
GGGATTTATATCTTCTACTCGTAGCCGATGTACTCTGGAGTTTTCTCGGTCTACAAAGAG
3241 TAGGGTCCACATGGCTGTCTGATTTTCCTCAGGCCTGGGCGGAAACCGGGGGCATGGGAC 3300
ATCCCAGGTGTACCGACAGACTAAAAGGAGTCCGGACCCGCCTTTGGCCCCCCGTACCCTG
3'SS (3314)
3301 TGGCAGTTCGCCAGGCTCCTCTGATCATACCTCTGAAAGCAACCTCTACCCCCGTGTCCA 3360
ACCGTCAAGCGGTCCGAGGAGACTAGTATGGAGACTTTCGTTGGAGATGGGGGCCACAGGT
3361 TAAAACAATACCCCATGTCACAAGAAGCCAGACTGGGGATCAAGCCCCACATACAGAGAC 3420
ATTTTGTTATGGGGTACAGTGTTCTTCGGTCTGACCCCTAGTTCGGGGTGTATGTCTCTG
3421 TGTTGGACCAGGGAATACTGGTACCCTGCCAGTCCCCCTGGAACACGCCCCTGCTACCCG 3480
ACAACCTGGTCCCTTATGACCATGGGACGGTCAGGGGGACCTTGTGCGGGGACGATGGGC
3481 TTAAGAAACCAGGGACTAATGATTATAGGCCTGTCCAGGATCTGAGAGAAGTCAACAAGC 3540
AATTCTTTGGTCCCTGATTACTAATATCCGGACAGGTCCTAGACTCTCTTCAGTTGTTCG

FIGURE 1D-8

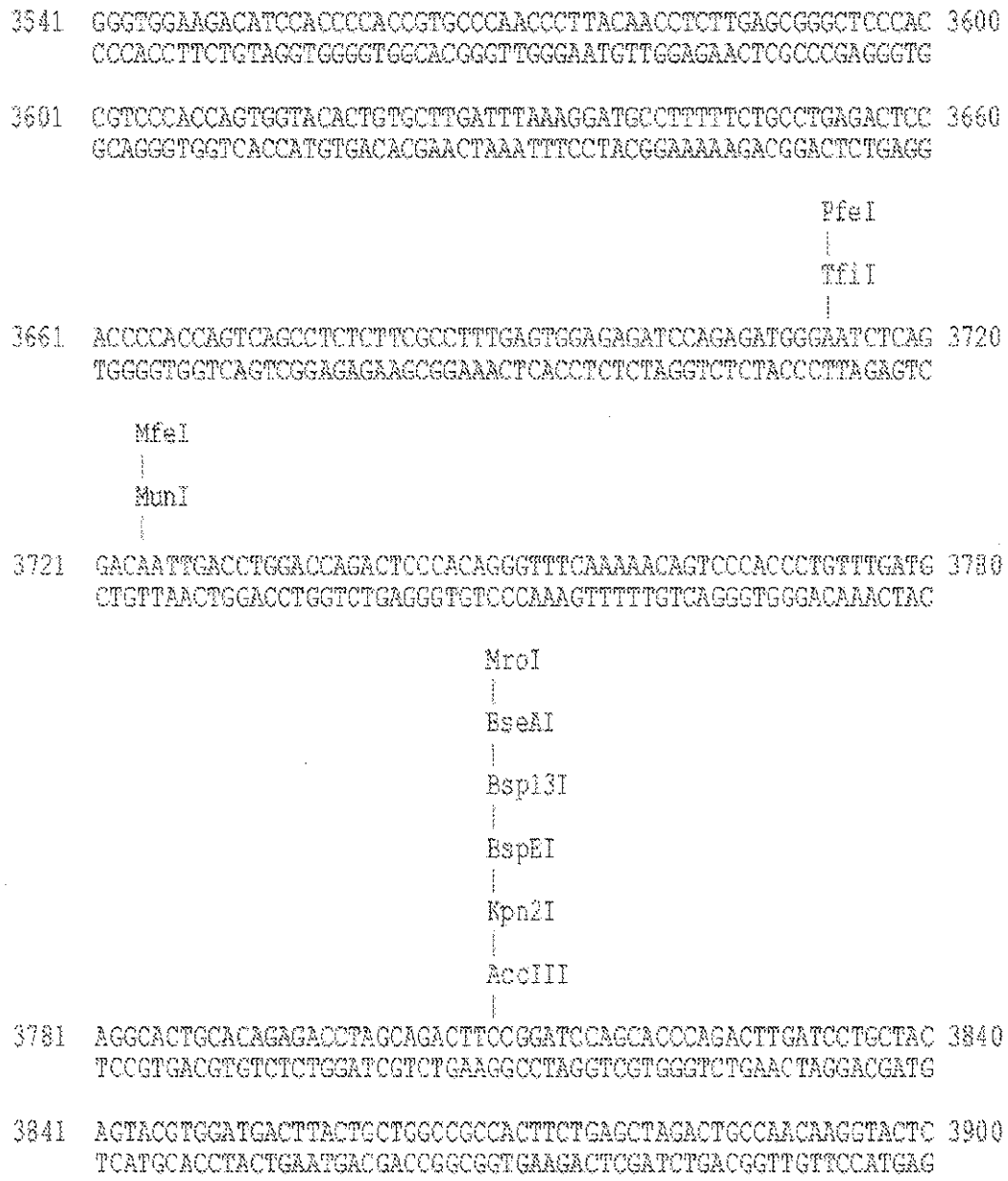

3541 GGGTGGAAGACATCCACCCCACCGTGCCCAACCCTTACAACCTCTTGAGCGGGCTCCCAC 3600
CCCACCTTCTGTAGGTGGGGTGGCACGGGTTGGGAATGTTGGAGAACTCGCCCGAGGGTG
3601 CGTCCCACCAGTGGTACACTGTGCTTGATTTAAAGGATGCCTTTTTCTGCCTGAGACTCC 3660
GCAGGGTGGTCACCATGTGACACGAACTAAATTTCCTACGGAAAAAGACGGACTCTGAGG
PfeI
TflI
3661 ACCCCACCAGTCAGCCTCTCTTCGCCTTTGAGTGGAGAGATCCAGAGATGGGAATCTCAG 3720
TGGGGTGGTCAGTCGGAGAGAAGCGGAAACTCACCTCTCTAGGTCTCTACCCTTAGAGTC
MfeI
MunI
3721 GACAATTGACCTGGACCAGACTCCCACAGGGTTTCAAAAACAGTCCCACCCTGTTTGATG 3780
CTGTTAACTGGACCTGGTCTGAGGGTGTCCCAAAGTTTTTGTCAGGGTGGGACAAACTAC
MroI
BseAI
Bsp13I
BspEI
Kpn2I
AccIII
3781 AGGCACTGCACAGAGACCTAGCAGACTTCCGGATCCAGCACCCAGACTTGATCCTGCTAC 3840
TCCGTGACGTGTCTCTGGATCGTCTGAAGGCCTAGGTCGTGGGTCTGAACTAGGACGATG
3841 AGTACGTGGATGACTTACTGCTGGCCGCCACTTCTGAGCTAGACTGCCAACAGGTACTC 3900
TCATGCACCTACTGAATGACGACCGGCGGTGAAGACTCGATCTGACGGTTGTTCCATGAG

FIGURE 1D-9

```
3901  GGGCCCTGTTACAAACCCTAGGGAACCTCGGGTATCGGGCCTCGGCCAAGAAAGCCCAAA 3960
      CCCGGGACAATGTTTGGGATCCCTTGGAGCCCATAGCCCGGAGCCGGTTCTTTCGGGTTT

3961  TTTGCCAGAAACAGGTCAAGTATCTGGGGTATCTTCTAAAAGAGGGTCAGAGATGGCTGA 4020
      AAACGGTCTTTGTCCAGTTCATAGACCCCATAGAAGATTTTCTCCCAGTCTCTACCGACT

4021  CTGAGGCCAGAAAAGAGACTGTGATGGGGCAGCCTACTCCGAAGACCCCTCGACAACTAA 4080
      GACTCCGGTCTTTTCTCTGACACTACCCCGTCGGATGAGGCTTCTGGGGAGCTGTTGATT

4081  GGGAGTTCCTAGGGACGGCAGGCTTCTGTCGCCTCTGGATCCCTGGGTTTGCAGAAATGG 4140
      CCCTCAAGGATCCCTGCCGTCCGAAGACAGCGGAGACCTAGGGACCCAAACGTCTTTACC

4141  CAGCCCCCTTGTACCCTCTCACCAAAACGGGGACTCTGTTTAATTGGGGCCCAGACCAAC 4200
      GTCGGGGGAACATGGGAGAGTGGTTTTGCCCCTGAGACAAATTAACCCCGGGTCTGGTTG

4201  AAAAGGCCTATCAAGAAATCAAGCAAGCTCTTCTAACTGCCCCAGCCCTGGGGTTGCCAG 4260
      TTTTCCGGATAGTTCTTTAGTTCGTTCGAGAAGATTGACGGGGTCGGGACCCCAACGGTC

                                  SalI
                                   |
4261  ATTTGACTAAGCCCTTTGAACTCTTTGTCGACGAGAAGCAGGGCTACGCCAAAGGTGTCC 4320
      TAAACTGATTCGGGAAACTTGAGAAACAGCTGCTCTTCGTCCCGATGCGGTTTCCACAGG

4321  TAACGCAAAAACTGGGACCTTGGCGTCGGCCGGTGGCCTACCTGTCCAAAAAGCTAGACC 4380
      ATTGCGTTTTTGACCCTGGAACCGCAGCCGGCCACCGGATGGACAGGTTTTTCGATCTGG

4381  CAGTAGCAGCTGGGTGGCCCCCTTGCCTACGGATGGTAGCAGCCATTGCCGTACTGACAA 4440
      GTCATCGTCGACCCACCGGGGGAACGGATGCCTACCATCGTCGGTAACGGCATGACTGTT

4441  AGGATGCAGGCAAGCTAACCATGGGACAGCCACTAGTCATTCTGGCCCCCCATGCAGTAG 4500
      TCCTACGTCCGTTCGATTGGTACCCTGTCGGTGATCAGTAAGACCGGGGGGTACGTCATC

4501  AGGCACTAGTCAAACAACCCCCCGACCGCTGGCTTTCCAACGCCCGGATGACTCACTATC 4560
      TCCGTGATCAGTTTGTTGGGGGGCTGGCGACCGAAAGGTTGCGGGCCTACTGAGTGATAG

4561  AGGCCTTGCTTTTGGACACGGACCGGGTCCAGTTCGGACCGGTGGTAGCCCTGAACCCGG 4620
      TCCGGAACGAAAACCTGTGCCTGGCCCAGGTCAAGCCTGGCCACCATCGGGACTTGGGCC

4621  CTACGCTGCTCCCACTGCCTGAGGAAGGGCTGCAACACAACTGCCTTGATATCCTGGCCG 4680
      GATGCGACGAGGGTGACGGACTCCTTCCCGACGTTGTGTTGACGGAACTATAGGACCGGC

4681  AAGCCCACGGAACCCGACCCGACCTAACGGACCAGCCGCTCCCAGACGCCGACCACACCT 4740
      TTCGGGTGCCTTGGGCTGGGCTGGATTGCCTGGTCGGCGAGGGTCTGCGGCTGGTGTGGA

4741  GGTACACGGATGGAAGCAGTCTCTTACAAGAGGGACAGCGTAAGGCGGGAGCTGCGGTGA 4800
      CCATGTGCCTACCTTCGTCAGAGAATGTTCTCCCTGTCGCATTCCGCCCTCGACGCCACT
```

FIGURE 1D-10

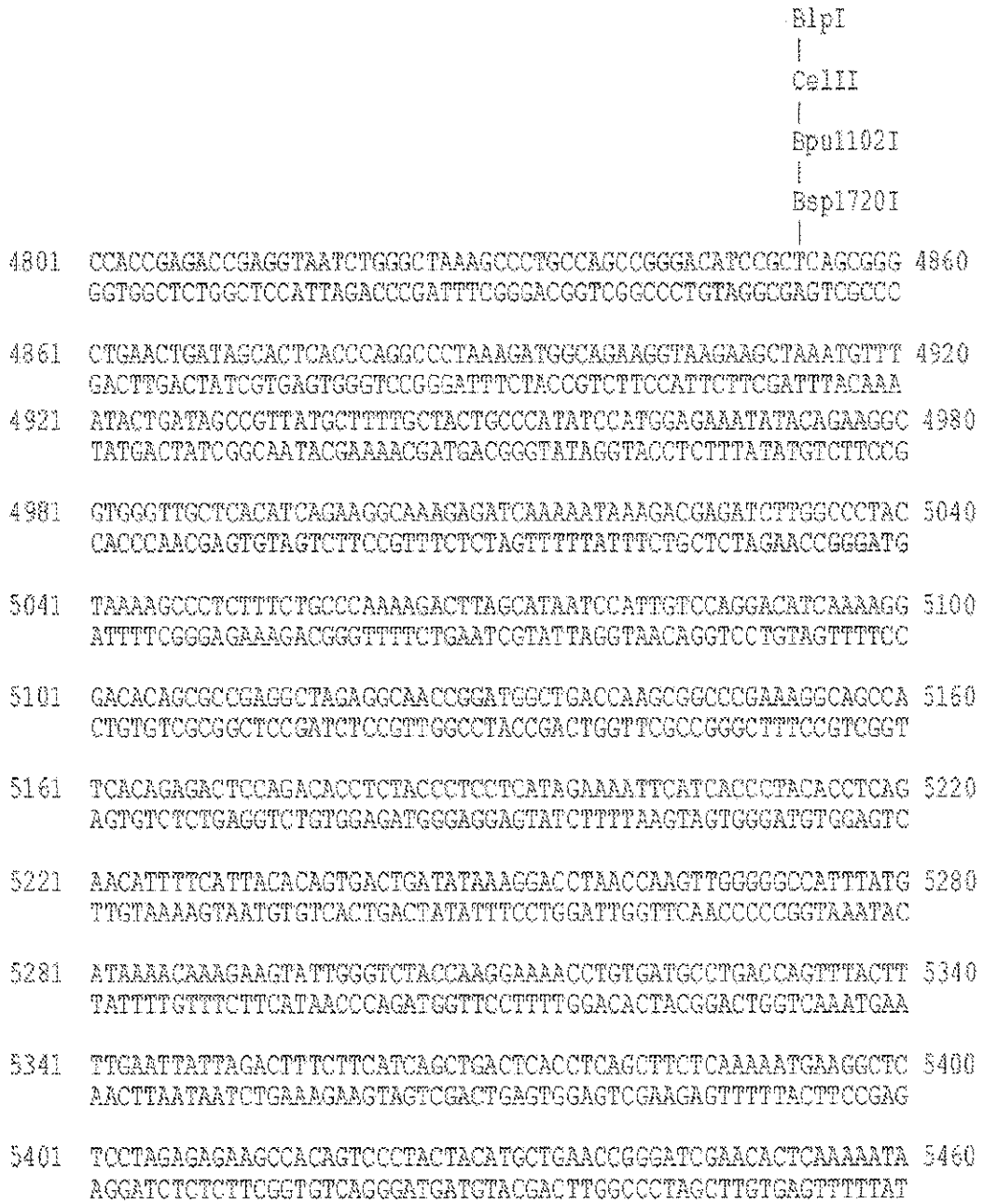

BlpI
CelII
Bpu1102I
Bsp1720I
4801 CCACCGAGACCGAGGTAATCTGGGCTAAAGCCCTGCCAGCCGGGACATCGCTCAGCGGG 4860
GGTGGCTCTGGCTCCATTAGACCCGATTTCGGGACGGTCGGCCCTGTAGCGAGTCGCCC
4861 CTGAACTGATAGCACTCACCCAGGCCCTAAAGATGGCAGAAGGTAAGAAGCTAAATGTTT 4920
GACTTGACTATCGTGAGTGGGTCCGGGATTTCTACCGTCTTCCATTCTTCGATTTACAAA
4921 ATACTGATAGCCGTTATGCTTTTGCTACTGCCCATATCCATGGAGAAATATACAGAAGGC 4980
TATGACTATCGGCAATACGAAAACGATGACGGGTATAGGTACCTCTTTATATGTCTTCCG
4981 GTGGGTTGCTCACATCAGAAGGCAAAGAGATCAAAAATAAAGACGAGATCTTGGCCCTAC 5040
CACCCAACGAGTGTAGTCTTCCGTTTCTCTAGTTTTTATTTCTGCTCTAGAACCGGGATG
5041 TAAAAGCCCTCTTTCTGCCCAAAAGACTTAGCATAATCCATTGTCCAGGACATCAAAAGG 5100
ATTTTCGGGAGAAAGACGGGTTTTCTGAATCGTATTAGGTAACAGGTCCTGTAGTTTTCC
5101 GACACAGCGCCGAGGCTAGAGGCAACCGGATGGCTGACCAAGCGGCCCGAAAGGCAGCCA 5160
CTGTGTCGCGGCTCCGATCTCCGTTGGCCTACCGACTGGTTCGCCGGGCTTTCCGTCGGT
5161 TCACAGAGACTCCAGACACCTCTACCCTCCTCATAGAAAATTCATCACCCTACACCTCAG 5220
AGTGTCTCTGAGGTCTGTGGAGATGGGAGGCAGTATCTTTTAAGTAGTGGGATGTGGAGTC
5221 AACATTTTCATTACACAGTGACTGATATAAAGGACCTAACCAAGTTGGGGGCCATTTATG 5280
TTGTAAAAGTAATGTGTCACTGACTATATTTCCTGGATTGGTTCAACCCCCGGTAAATAC
5281 ATAAAACAAAGAAGTATTGGGTCTACCAAGGAAAACCTGTGATGCCTGACCAGTTTACTT 5340
TATTTTGTTTCTTCATAACCCAGATGGTTCCTTTTGGACACTACGGACTGGTCAAATGAA
5341 TTGAATTATTAGACTTTCTTCATCAGCTGACTCACCTCAGCTTCTCAAAAATGAAGGCTC 5400
AACTTAATAATCTGAAAGAAGTAGTCGACTGAGTGGAGTCGAAGAGTTTTTACTTCCGAG
5401 TCCTAGAGAGAAGCCACAGTCCCTACTACATGCTGAACCGGGATCGAACACTCAAAAATA 5460
AGGATCTCTCTTCGGTGTCAGGGATGATGTACGACTTGGCCCTAGCTTGTGAGTTTTTAT

FIGURE 1D-11

```
5461  TCACTGAGACCTGCAAAGCTTGTGCACAAGTCAACGCCAGCAAGTCTGCCGTTAAACAGG 5520
      AGTGACTCTGGACGTTTCGAACACGTGTTCAGTTGCGGTCGTTCAGACGGCAATTTGTCC

                        SacII
                        |
                        SgrBI
                        |
                        Cfr42I
                        |
                        Sfr303I
                        |
                        KspI
                        |
5521  GAACTAGGGTCCGCGGGCATCGGCCCGGCACTCATTGGGAGATCGATTTCACCGAGATAA 5580
      CTTGATCCCAGGCGCCCGTAGCCGGGCCGTGAGTAACCCTCTAGCTAAAGTGGCTCTATT

5581  AGCCCGGATTGTATGGCTATAAATATCTTCTAGTTTTTATAGATACCTTTTCTGGCTGGA 5640
      TCGGGCCTAACATACCGATATTTATAGAAGATCAAAAATATCTATGGAAAAGACCGACCT

5641  TAGAAGCCTTCCCAACCAAGAAAGAAACCGCCAAGGTCGTAACCAAGAAGCTACTAGAGG 5700
      ATCTTCGGAAGGGTTGGTTCTTTCTTTGGCGGTTCCAGCATTGGTTCTTCGATGATCTCC

                              PaeI
                              |
                              BbuI
                              |
                              SpaHI
                              |
                              SphI
                              |
5701  AGATCTTCCCCAGGTTCGGCATGCCTCAGGTATTGGGAACTGACAATGGGCCTGCCTTCG 5760
      TCTAGAAGGGGTCCAAGCCGTACGGAGTCCATAACCCTTGACTGTTACCCGGACGGAAGC

6901  CTTCCAAGGGGCTACTCGAGGGGGCAGATGCAACCCTCTAGTCCTAGAATTCACTGATGC 6960
      GAAGGTTCCCCGATGAGCTCCCCCGTCTACGTTGGGAGATCAGGATCTTAAGTGACTACG

6961  AGGAAAAAAGGCTAACTGGGACGGGCCCAAATCGTGGGGACTGAGACTGTACCGGACAGG 7020
      TCCTTTTTTCCGATTGACCCTGCCCGGGTTTAGCACCCCTGACTCTGACATGGCCTGTCC

7021  AACAGATCCTATTACCATGTTCTCCCTGACCCGGCAGGTCCTTAATGTGGGACCCCGAGT 7080
      TTGTCTAGGATAATGGTACAAGAGGGACTGGGCCGTCCAGGAATTACACCCTGGGGCTCA

7081  CCCCATAGGGCCCAACCCAGTATTACCCGACCAAAGACTCCCTTCCTCACCAATAGAGAT 7140
      GGGGTATCCCGGGTTGGGTCATAATGGGCTGGTTTCTGAGGGAAGGAGTGGTTATCTCTA

7141  TGTACCGGCTCCACAGCCACCTAGCCCCCTCAATACCAGTTACCCCCCTTCCACTACCAG 7200
      ACATGGCCGAGGTGTCGGTGGATCGGGGGAGTTATGGTCAATGGGGGGAAGGTGATGGTC

7201  TACACCCTCAACCTCCCCTACAAGTCCAAGTGTCCCACAGCCACCCCCAGGAACTGGAGA 7260
      ATGTGGGAGTTGGAGGGGATGTTCAGGTTCACAGGGTGTCGGTGGGGGTCCTTGACCTCT

7261  TAGACTACTAGCTCTAGTCAAAGGAGCCTATCAGGCGCTTAACCTCACCAATCCCGACAA 7320
      ATCTGATGATCGAGATCAGTTTCCTCGGATAGTCCGCGAATTGGAGTGGTTAGGGCTGTT
```

FIGURE 1D-12


7321 GACCCAAGAATGTTGGCTGTGCTTAGTGTCGGGACCTCCTTATTACGAAGGAGTAGCGGT 7380
CTGGGTTCTTACAACCGACACGAATCACAGCCCTGGAGGAATAATGCTTCCTCATCGCCA
7381 CGTGGGCACTTATACCAATCATTCCACCGCTCCGGCCAACTGTACGGCCACTTCCCAACA 7440
GCACCCGTGAATATGGTTAGTAAGGTGGCGAGGCCGGTTGACATGCCGGTGAAGGGTTGT
EcoT22I
NsiI
Mph1103I
Zsp2I
BfrBI
7441 TAAGCTTACCCTATCTGAAGTGACAGGACAGGGCCTATGCATGGGGGCAGTACCTAAAAC 7500
ATTCGAATGGGATAGACTTCACTGTCCTGTCCCGGATACGTACCCCCGTCATGGATTTTG
NaeI
PdiI
MroNI
NgoMIV
7501 TCACCAGGCCTTATGTAACACCACCCAAAGCGCCGGCTCAGGATCCTACTACCTTGCAGC 7560
AGTGGTCCGGAATACATTGTGGTGGGTTTCGCGGCCGAGTCCTAGGATGATGGAACGTCG
AleI
OliI
7561 ACCCGCCGGAACAATGTGGGCTTGCAGCACTGGATTGACTCCCTGCTTGTCCACCACGGT 7620
TGGGCGGCCTTGTTACACCCGAACGTCGTGACCTAACTGAGGGACGAACAGGTGGTGCCA
7621 GCTCAATCTAACCACAGATTATTGTGTATTAGTTGAACTCTGGCCCAGAGTAATTTACCA 7680
CGAGTTAGATTGGTGTCTAATAACACATAATCAACTTGAGACCGGGTCTCATTAAATGGT

FIGURE 1D-13

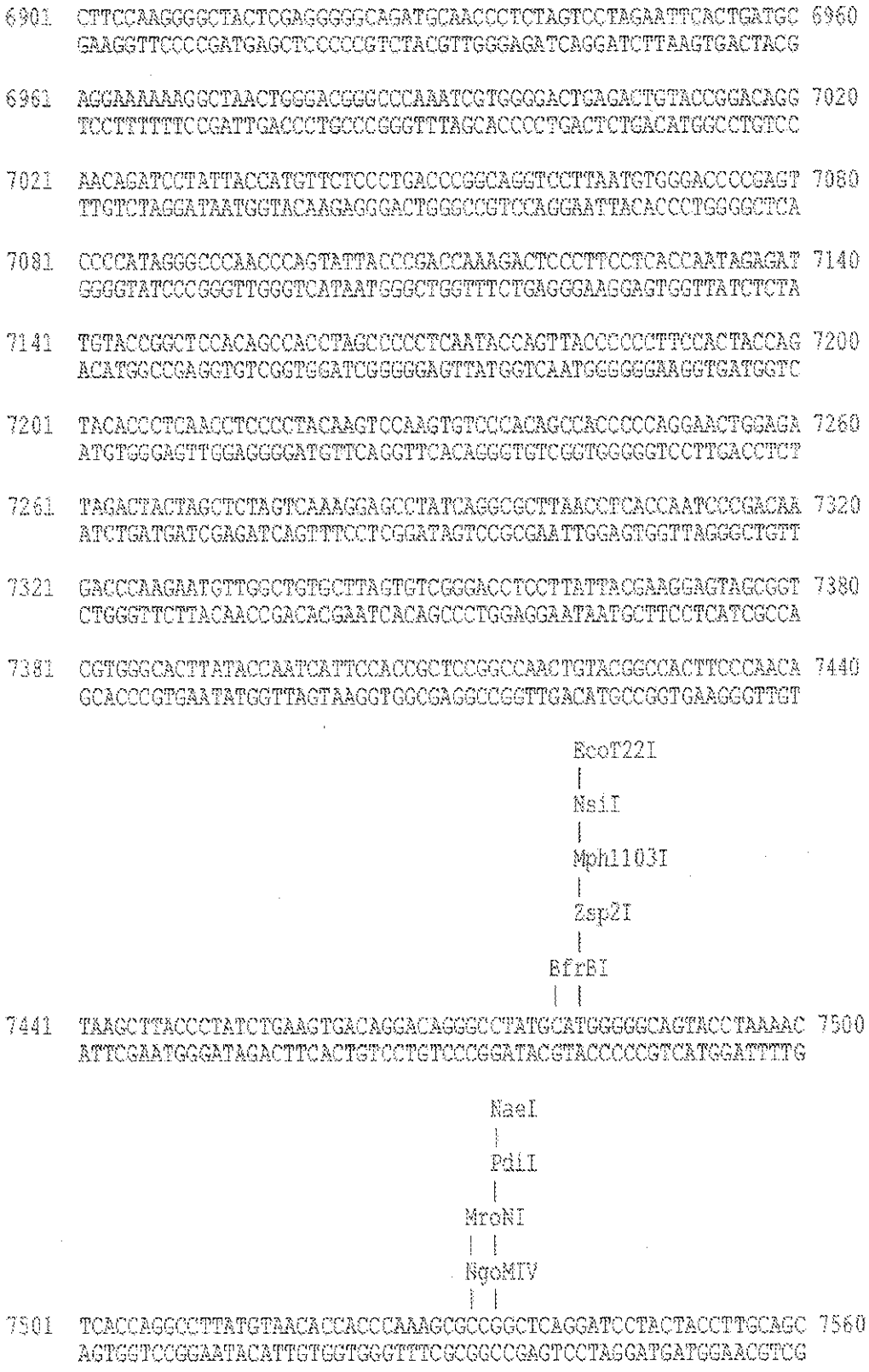

6901 CTTCCAAGGGGCTACTCGAGGGGGCAGATGCAACCCTCTAGTCCTAGAATTCACTGATGC 6960
GAAGGTTCCCCGATGAGCTCCCCCCGTCTACGTTGGGAGATCAGGATCTTAAGTGACTACG
6961 AGGAAAAAAGGCTAACTGGGACGGGCCCCAAATCGTGGGGACTGAGACTGTACCGGACAGG 7020
TCCTTTTTTCCGATTGACCCTGCCCGGGTTTAGCACCCCTGACTCTGACATGGCCTGTCC
7021 AACAGATCCTATTACCATGTTCTCCCTGACCCGGCAGGTCCTTAATGTGGGACCCCGAGT 7080
TTGTCTAGGATAATGGTACAAGAGGGACTGGGCCGTCCAGGAATTACACCCTGGGGCTCA
7081 CCCCATAGGGCCCAACCCAGTATTACCCGACCAAAGACTCCCTTCCTCACCAATAGAGAT 7140
GGGGTATCCCGGGTTGGGTCATAATGGGCTGGTTTCTGAGGGAAGGAGTGGTTATCTCTA
7141 TGTACCGGCTCCACAGCCACCTAGCCCCCTCAATACCAGTTACCCCCCTTCCACTACCAG 7200
ACATGGCCGAGGTGTCGGTGGATCGGGGGAGTTATGGTCAATGGGGGGAAGGTGATGGTC
7201 TACACCCTCAACCTCCCCTACAAGTCCAAGTGTCCCACAGCCACCCCCAGGAACTGGAGA 7260
ATGTGGGAGTTGGAGGGGATGTTCAGGTTCACAGGGTGTCGGTGGGGGTCCTTGACCTCT
7261 TAGACTACTAGCTCTAGTCAAAGGAGCCTATCAGGCGCTTAACCTCACCAATCCCGACAA 7320
ATCTGATGATCGAGATCAGTTTCCTCGGATAGTCCGCGAATTGGAGTGGTTAGGGCTGTT
7321 GACCCAAGAATGTTGGCTGTGCTTAGTGTCGGGACCTCCTTATTACGAAGGAGTAGCGGT 7380
CTGGGTTCTTACAACCGACACGAATCACAGCCCTGGAGGAATAATGCTTCCTCATCGCCA
7381 CGTGGGCACTTATACCAATCATTCCACCGCTCCGGCCAACTGTACGGCCACTTCCCAACA 7440
GCACCCGTGAATATGGTTAGTAAGGTGGCGAGGCCGGTTGACATGCCGGTGAAGGGTTGT
EcoT22I
NsiI
Mph1103I
Zsp2I
BfrBI
7441 TAAGCTTACCCTATCTGAAGTGACAGCACAGGGCCTATGCATGGGGGCAGTACCTAAAAC 7500
ATTCGAATGGGATAGACTTCACTGTCCTGTCCCGGATACGTACCCCCGTCATGGATTTTG
NaeI
PdiI
MroNI
NgoMIV
7501 TCACCAGGCCTTATGTAACACCACCCAAAGCGCCGGCTCAGGATCCTACTACCTTGCAGC 7560
AGTGGTCCGGAATACATTGTGGTGGGTTTCGCGGCCGAGTCCTAGGATGATGGAACGTCG

FIGURE 1D-14

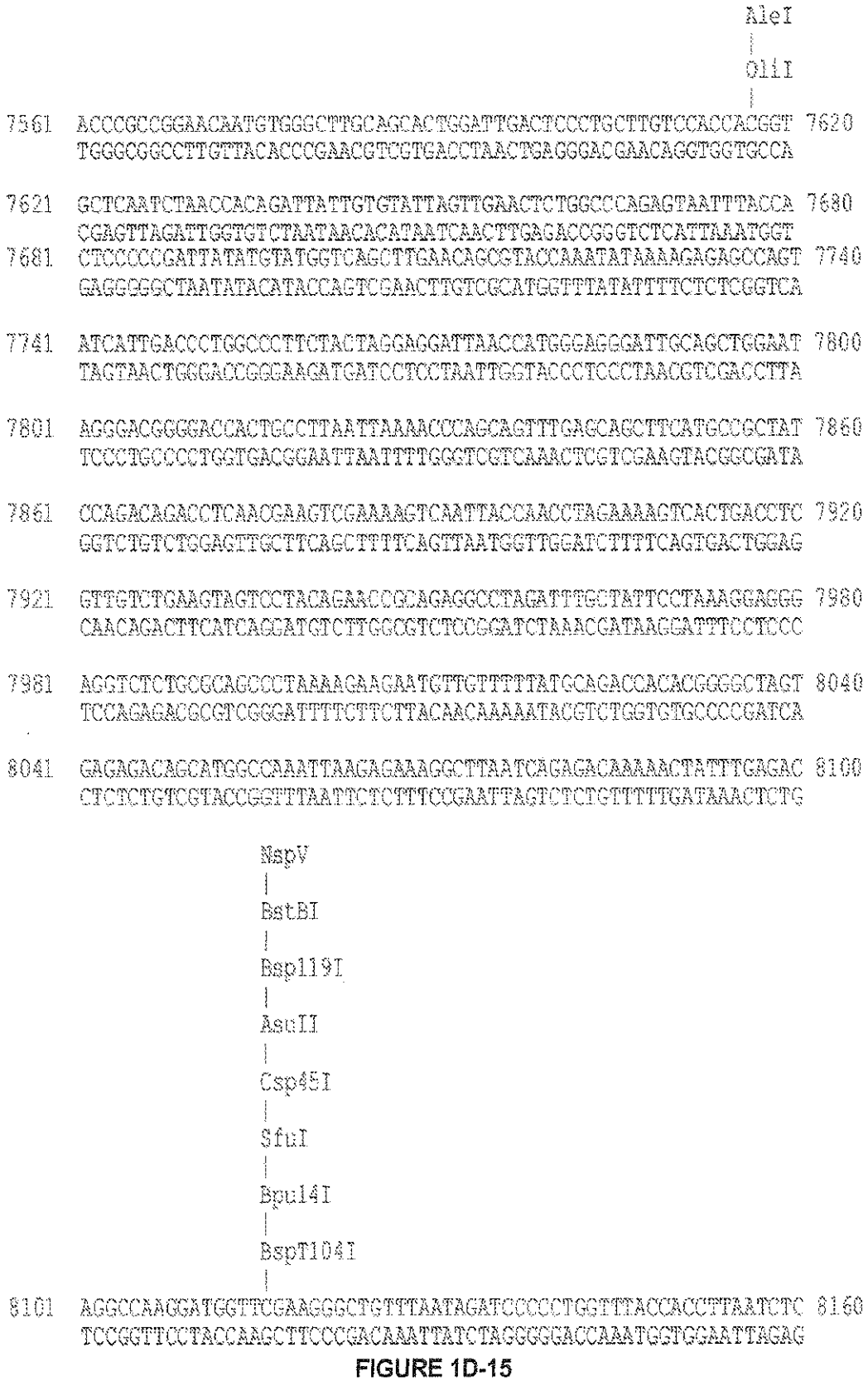

AleI
OliI
7561 ACCCGCCGGAACAATGTGGGCTTGCAGCACTGGATTGACTCCCTGCTTGTCCACCACGGT 7620
TGGGCGGCCTTGTTACACCCGAACGTCGTGACCTAACTGAGGGACGAACAGGTGGTGCCA
7621 GCTCAATCTAACCACAGATTATTGTGTATTAGTTGAACTCTGGCCCAGAGTAATTTACCA 7680
CGAGTTAGATTGGTGTCTAATAACACATAATCAACTTGAGACCGGGTCTCATTAAATGGT
7681 CTCCCCCGATTATATGTATGGTCAGCTTGAACAGCGTACCAAATATAAAAGAGAGCCAGT 7740
GAGGGGGCTAATATACATACCAGTCGAACTTGTCGCATGGTTTATATTTTCTCTCGGTCA
7741 ATCATTGACCCTGGCCCTTCTACTAGGAGGATTAACCATGGGAGGGATTGCAGCTGGAAT 7800
TAGTAACTGGGACCGGGAAGATGATCCTCCTAATTGGTACCCTCCCTAACGTCGACCTTA
7801 AGGGACGGGGACCACTGCCTTAATTAAAACCCAGCAGTTTGAGCAGCTTCATGCCGCTAT 7860
TCCCTGCCCCTGGTGACGGAATTAATTTTGGGTCGTCAAACTCGTCGAAGTACGGCGATA
7861 CCAGACAGACCTCAACGAAGTCGAAAAGTCAATTACCAACCTAGAAAAGTCACTGACCTC 7920
GGTCTGTCTGGAGTTGCTTCAGCTTTTCAGTTAATGGTTGGATCTTTTCAGTGACTGGAG
7921 GTTGTCTGAAGTAGTCCTACAGAACCGCAGAGGCCTAGATTTGCTATTCCTAAAGGAGGG 7980
CAACAGACTTCATCAGCATGTCTTGGCGTCTCCGGATCTAAACGATAAGGATTTCCTCCC
7981 AGGTCTCTGCGGCAGCCCTAAAAGAAGAATGTTGTTTTTATGCAGACCACACGGGGCTAGT 8040
TCCAGAGACGCGTCGGGATTTTCTTCTTACAACAAAAATACGTCTGGTGTGCCCCGATCA
8041 GAGAGACAGCATGGCCAAATTAAGAGAAAGGCTTAATCAGAGACAAAAACTATTTGAGAC 8100
CTCTCTGTCGTACCGGTTTAATTCTCTTTCCGAATTAGTCTCTGTTTTTGATAAACTCTG
MspV
BstBI
Bsp119I
AscII
Csp45I
SfuI
Bpu14I
BspT104I
8101 AGGCCAAGGATGGTTCGAAGGGCTGTTTAATAGATCCCCCTGGTTTACCACCTTAATCTC 8160
TCCGGTTCCTACCAAGCTTCCCGACAAATTATCTAGGGGGACCAAATGGTGGAATTAGAG

FIGURE 1D-15

```
8161  CACCATCATGGGACCTCTAATAGTACTCTTACTGATCTTACTCTTTGGACCTTGCATTCT 8220
      GTGGTAGTACCCTGGAGATTATCATGAGAATGACTAGAATGAGAAACCTGGAACGTAAGA

8221  CAATCGATTGGTCCAATTTGTTAAAGACAGGATCTCAGTGGTCCAGGCTCTGGTTTTGAC 8280
      GTTAGCTAACCAGGTTAAACAATTTCTGTCCTAGAGTCACCAGGTCCGAGACCAAAACTG
                                                    IRES reg(8327,8876)>>>
                                                      |
                                                    MluI(8325)
                                                    |  |
8281  TCAGCAATATCACCAGCTAAAACCCATAGAGTACGAGCCATGAACGCGTTACTGGCCGAA 8340
      AGTCGTTATAGTGGTCGATTTTGGGTATCTCATGCTCGGTACTTGCGCAATGACCGGCTT

                                                ires_emcv reg(8378,8876)>>>
                                                |
8341  GCCGCTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTATTTTCCACCATATTGCCGT 8400
      CGGCGAACCTTATTCCGGCCACACGCAAACAGATATACAATAAAAGGTGGTATAACGGCA

8401  CTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCTGTCTTCTTGACGAGCATTCCTAGGG 8460
      GAAAACCGTTACACTCCCGGGCCTTTGGACCGGGACAGAAGAACTGCTCGTAAGGATCCC
8461  GTCTTTCCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTC 8520
      CAGAAAGGGGAGAGCGGTTTCCTTACGTTCCAGACAACTTACAGCACTTCCTTCGTCAAG

8521  CTCTGGAAGCTTCTTGAAGACAAACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACC 8580
      GAGACCTTCGAAGAACTTCTGTTTGTTGCAGACATCGCTGGGAAACGTCCGTCGCCTTGG

8581  CCCCACCTGGCGACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAA 8640
      GGGGTGGACCGCTGTCCACGGAGACGCCGGTTTTCGGTGCACATATTCTATGTGGACGTT

8641  AGGCGGCACAACCCCAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGC 8700
      TCCGCCGTGTTGGGGTCACGGTGCAACACTCAACCTATCAACACCTTTCTCAGTTTACCG

8701  TCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCCAGAAGGTACCCCATTGTATGG 8760
      AGAGGAGTTCGCATAAGTTGTTCCCCGACTTCCTACGGGTCTTCCATGGGGTAACATACC

8761  GATCTGATCTGGGGCCTCGGTGCACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAAAC 8820
      CTAGACTAGACCCCGGAGCCACGTGTACGAAATGTACACAAATCAGCTCCAATTTTTTTG
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FIGURE 1D-16

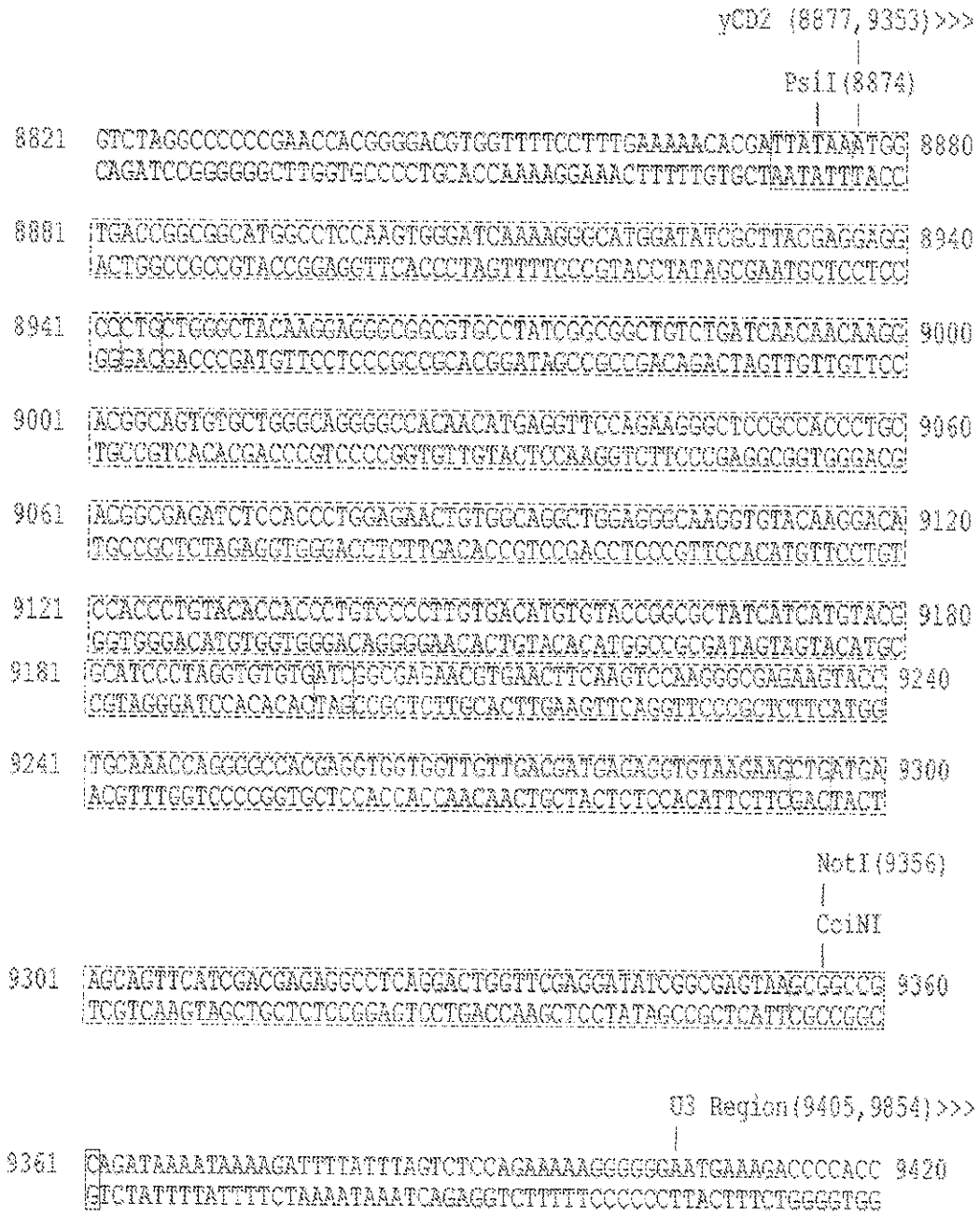

yCD2 (8877,9353)>>>
PsiI(8874)
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CAGATCCGGGGGGCTTGGTGCCCCTGCACCAAAAGGAAACTTTTTGTGCTAATATTTACC
8881 TGACCGGCGGCATGGCCTCCAAGTGGGATCAAAAGGGCATGGATATCGCTTACGAGGAGG 8940
ACTGGCCGCCGTACCGGAGGTTCACCCTAGTTTTCCCGTACCTATAGCGAATGCTCCTCC
8941 CCCTGCTGGGCTACAAGGAGGGCGGCGTGCCTATCGGCGGCTGTCTGAACAACAAGG 9000
GGGACGACCCGATGTTCCTCCCGCCGCACGGATAGCCGCCGACAGACTAGTTGTTGTTCC
9001 ACGGCAGTGTGCTGGGCAGGGGCCACAACATGAGGTTCCAGAAGGGCTCCGCCACCCTGC 9060
TGCCGTCACACGACCCGTCCCCGGTGTTGTACTCCAAGGTCTTCCCGAGGCGGTGGGACG
9061 ACGGCGAGATCTCCACCCTGGAGAACTGTGGCAGGCTGGAGGGCAAGGTGTACAAGGCAC 9120
TGCCGCTCTAGAGGTGGGACCTCTTGACACCGTCCGACCTCCCGTTCCACATGTTCCTGT
9121 CCACCCTGTACACCACCCTGTCCCCTTGTGACATGTGTACCGGCGCTATCATCATGTACG 9180
GGTGGGACATGTGGTGGGACAGGGGAACACTGTACACATGGCCGCGATAGTAGTACATGC
9181 GCATCCCTAGGTGTGTGATCGCCGAGAACCTGAACTTCAAGTCCAAGGGCGAGAAGTACC 9240
CGTAGGGATCCACACACTAGCGGCTCTTGCACTTGAAGTTCAGGTTCCCGCTCTTCATGG
9241 TGCAAACCAGGGCCCACGAGGTGGTGGTTCTTCAGCATGAGAGGTGTAAGAAGCTCATGA 9300
ACGTTTGGTCCCCGGTGCTCCACCACCAACAACTGCTACTCTCCACATTCTTCGACTACT
NotI(9356)
CciNI
9301 AGCAGTTCATCGACGAGAGGCCTCAGGACTGGTTCGAGGATATCGGCGAGTAAGCGGCCG 9360
TCGTCAAGTAGCTGCTCTCCGGAGTCCTGACCAAGCTCCTATAGCCGCTCATTCGCCGGC
U3 Region(9405,9854)>>>
9361 CAGATAAAATAAAAGATTTTATTTAGTCTCCAGAAAAAGGGGGGAATGAAAGACCCCACC 9420
GTCTATTTTATTTTCTAAAATAAATCAGAGGTCTTTTTCCCCCCTTACTTTCTGGGGTGG

FIGURE 1D-17

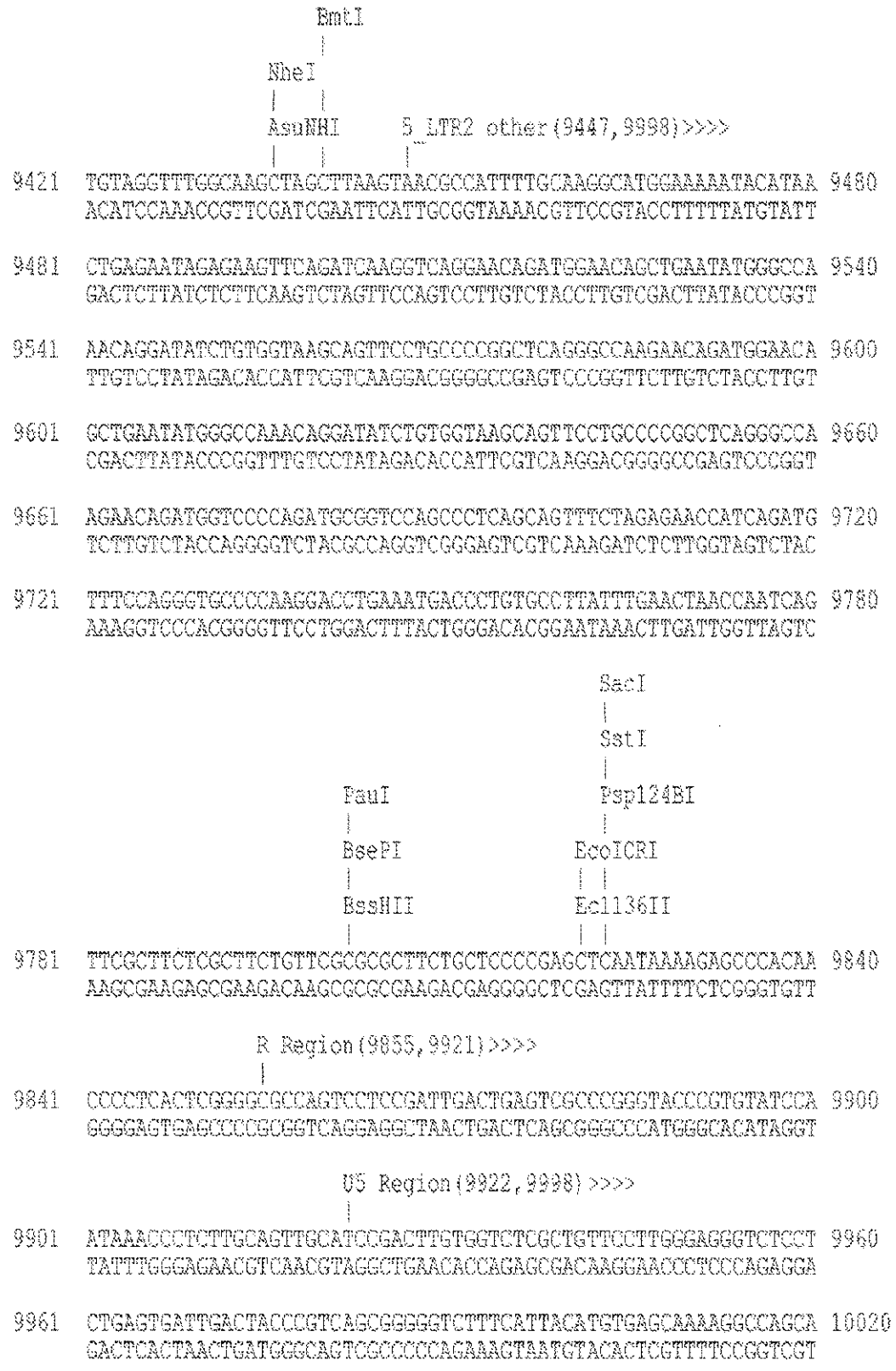

EmlI
NheI
AsuNHI
5_LTR2 other(9447,9998)>>>>
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ACATCCAAACCGTTCGATCGAATTCATTGCGGTAAAACGTTCCGTACCTTTTTATGTATT
9481 CTGAGAATAGAGAAGTTCAGATCAAGGTCAGGAACAGATGGAACAGCTGAATATGGGCCA 9540
GACTCTTATCTCTTCAAGTCTAGTTCCAGTCCTTGTCTACCTTGTCGACTTATACCCGGT
9541 AACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGAACA 9600
TTGTCCTATAGACACCATTCGTCAAGGACGGGGCCGAGTCCCGGTTCTTGTCTACCTTGT
9601 GCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCA 9660
CGACTTATACCCGGTTTGTCCTATAGACACCATTCGTCAAGGACGGGGCCGAGTCCCGGT
9661 AGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGAGAACCATCAGATG 9720
TCTTGTCTACCAGGGGTCTACGCCAGGTCGGGAGTCGTCAAAGATCTCTTGGTAGTCTAC
9721 TTTCCAGGGTGCCCCAAGGACCTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAG 9780
AAAGGTCCCACGGGGTTCCTGGACTTTACTGGGACACGGAATAAACTTGATTGGTTAGTC
SacI
SstI
PauI
Psp124BI
BsePI
EcoICRI
BssHII
Ecl136II
9781 TTCGCTTCTCGCTTCTGTTCGCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCCACAA 9840
AAGCGAAGAGCGAAGACAAGCGCGCGAAGACGAGGGGCTCGAGTTATTTTCTCGGGTGTT
R Region(9855,9921)>>>>
9841 CCCCTCACTCGGGGCGCCAGTCCTCCGATTGACTGAGTCGCCCGGGTACCCGTGTATCCA 9900
GGGGAGTGAGCCCCGCGGTCAGGAGGCTAACTGACTCAGCGGGCCCATGGGCACATAGGT
U5 Region(9922,9998)>>>>
9901 ATAAACCCTCTTGCAGTTGCATCCGACTTGTGGTCTCGCTGTTCCTTGGGAGGGTCTCCT 9960
TATTTGGGACAACGTCAACGTAGGCTGAACACCAGAGCGACAAGGAACCCTCCCAGAGGA
9961 CTGAGTGATTGACTACCCGTCAGCGGGGGTCTTTCATTACATGTGAGCAAAAGGCCAGCA 10020
GACTCACTAACTGATGGGCAGTCGCCCCCAGAAAGTAATGTACACTCGTTTTCCGGTCGT

FIGURE 1D-18

pBR322 origin(10045,10664)<<<

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10021 AAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCC 10080
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10081 TGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATA 10140
      ACTGCTCGTAGTGTTTTTAGCTGCGAGTTCAGTCTCCACCGCTTTGGGCTGTCCTGATAT

10141 AAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCC 10200
      TTCTATGGTCCGCAAAGGGGGACCTTCGAGGGAGCACGCGAGAGGACAAGGCTGGGACGG
10201 GCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAATGCTC 10260
      CGAATGGCCTATGGACAGGCGGAAAGAGGGAAGCCCTTCGCACCGCGAAAGAGTTACGAG

10261 ACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGA 10320
      TGCGACATCCATAGAGTCAAGCCACATCCAGCAAGCGAGGTTCGACCCGACACACGTGCT

10321 ACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCC 10380
      TGGGGGGCAAGTCGGGCTGGCGACGCGGAATAGGCCATTGATAGCAGAACTCAGGTTGGG

10381 GGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAG 10440
      CCATTCTGTGCTGAATAGCGGTGACCGTCGTCGGTGACCATTGTCCTAATCGTCTCGCTC

10441 GTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAG 10500
      CATACATCCGCCACGATGTCTCAAGAACTTCACCACCGGATTGATGCCGATGTGATCTTC

10501 GACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAG 10560
      CTGTCATAAACCATAGACGCGACGACTTCGGTCAATGGAAGCCTTTTTCTCAACCATC

10561 CTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCA 10620
      GAGAACTAGGCCGTTTGTTTGGTGGCGACCATCGCCACCAAAAAAACAAACGTTCGTCGT

10621 GATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGA 10680
      CTAATGCGCGTCTTTTTTTCCTAGAGTTCTTCTAGGAAACTAGAAAAGATGCCCCAGACT

10681 CGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGAT 10740
      GCGAGTCACCTTGCTTTTGAGTGCAATTCCCTAAAACCAGTACTCTAATAGTTTTTCCTA

10741 CTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGA 10800
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FIGURE 1D-19

amp marker(10813,11679)<<<

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      CATTTGAACCAGACTGTCAATGGTTACGAATTAGTCACTCCGTGGATAGAGTCGCTAGAC

10861 TCTATTTCGTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGA 10920
      AGATAAAGCAAGTAGGTATCAACGGACTGAGGGGCAGCACATCTATTGATGCTATGCCCT

10921 GGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACCGGCTCC 10980
      CCCGAATGGTAGACCGGGGTCACGACGTTACTATGGCGCTCTGGGTGCGAGTGGCCGAGG

10981 AGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAAC 11040
      TCTAAATAGTCGTTATTTGGTCGGTCGGCCTTCCCGGCTCGCGTCTTCACCAGGACGTTG

11041 TTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGCC 11100
      AAATAGGCGGAGGTAGGTCAGATAATTAACAACGGCCCTTCGATCTCATTCATCAAGCGG

11101 AGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTGCAGGCATCGTGGTGTCACGCTCGTC 11160
      TCAATTATCAAACGCGTTGCAACAACGGTAACGACGTCCGTAGCACCACAGTGCGAGCAG

11161 GTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCC 11220
      CAAACCATACCGAAGTAAGTCGAGGCCAAGGGTTGCTAGTTCCGCTCAATGTACTAGGGG

11221 CATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTT 11280
      GTACAACACGTTTTTTCGCCAATCGAGGAAGCCAGGAGGCTAGCAACAGTCTTCATTCAA

11281 GGCCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGCC 11340
      CCGGGCGTCACAATAGTGAGTACCAATACCGTCGTGACGTATTAAGAGAATGACAGTACGG

11341 ATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTG 11400
      TAGGCATTCTACGAAAAGACACTGACCACTCATGAGTTGGTTCAGTAAGACTCTTATCAC

11401 TATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAACACGGGATAATACCGCGCCACATAG 11460
      ATACGCCGCTGGCTCAACGAGAACGGGCCGCAGTTGTGCCCTATTATGGCGCGGTGTATC

11461 CAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAACTCTCAAGGAT 11520
      GTCTTGAAATTTTCACGAGTAGTAACCTTTTGCAAGAAGCCCCGCTTTTGAGAGTTCCTA

11521 CTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAGC 11580
      GAATGGCGACAACTCTAGGTCAAGCTACATTGGGTGAGCACGTGGGTTGACTAGAAGTCG

11581 ATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAA 11640
      TAGAAAATGAAAGTGGTCGCAAAGACCCACTCGTTTTTGTCCTTCCGTTTTACGGCGTTT

11641 AAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTTTCAATATTA 11700
      TTTCCCTTATTCCCGCTGTGCCTTTACAACTTATGAGTATGAGAAGGAAAAAGTTATAAT
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FIGURE 1D-20

amp prom(11721,11749)<<<

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11701 TTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAA 11760
      AACTTCGTAAATAGTCCCAATAACAGAGTACTCGCCTATGTATAAACTTACATAAATCTT

11761 AAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGA 11820
      TTTATTTGTTTATCCCCAAGGCGCGTGTAAAGGGGCTTTTCACGGTGGACTGCAGATTCT

11821 AACCATTATTATCATGACATTAACCTATAAAAATAGGCGTATCACGAGGCCCTTTCGTCT 11880
      TTGGTAATAATAGTACTGTAATTGGATATTTTTATCCGCATAGTGCTCCGGGAAAGCAGA

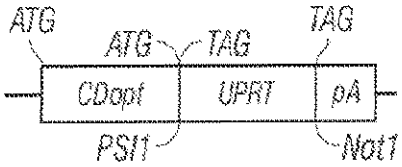
11881 TCAAGAATTCAT 11892
      AGTTCTTAAGTA
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FIGURE 1D-21

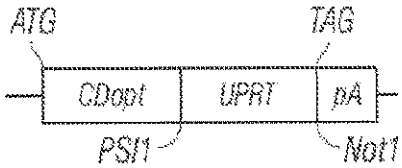
1. Separate synthesis of CDopt and UPRT genes with PSI1/Not1 sites



2. Digest with PSI1 and perform blunt end ligation



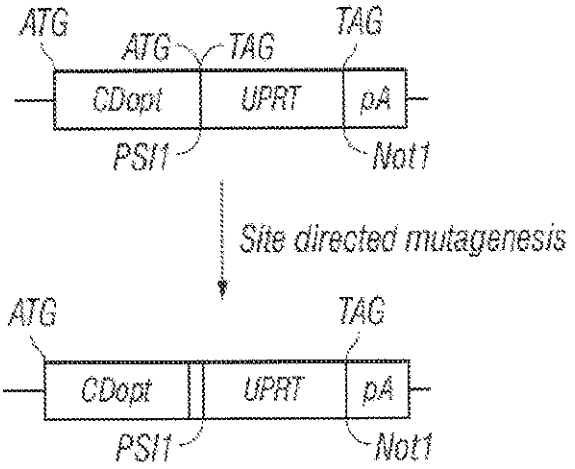
3. Deletion of CDopt gene STOP and UPRT START codon by site directed mutagenesis



4. CDopt-UPRT gene size: 1.3 kb

FIGURE 2A

1. Synthesis of CDopt-LINKER-UPRT: Site directed mutagenesis insertion of linker



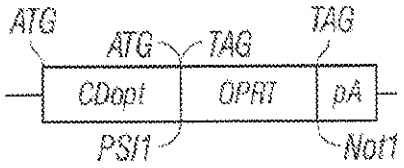
2. CDopt-Linker-UPRT gene size: 1.36 kb

FIGURE 2B

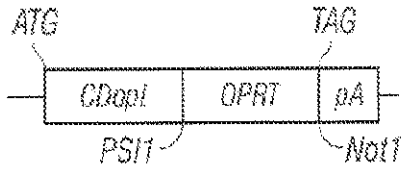
1. Separate synthesis of CDopt gene and OPRT domain with PSI1/Not1 sites



2. Digest with PSI1 and perform blunt end ligation



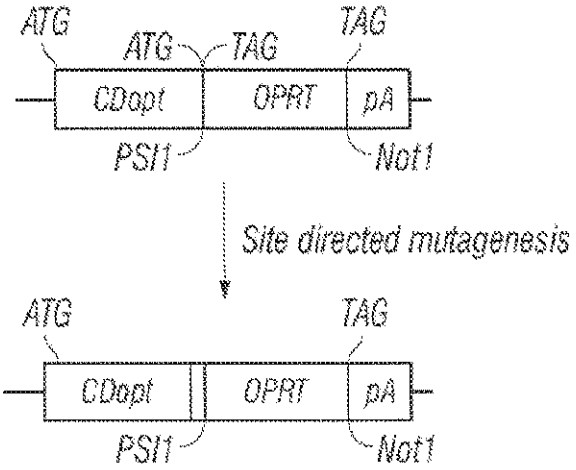
3. Deletion of CDopt gene STOP and OPRT START codon by site directed mutagenesis



4. CDopt-OPRT gene size: 1.3 kb

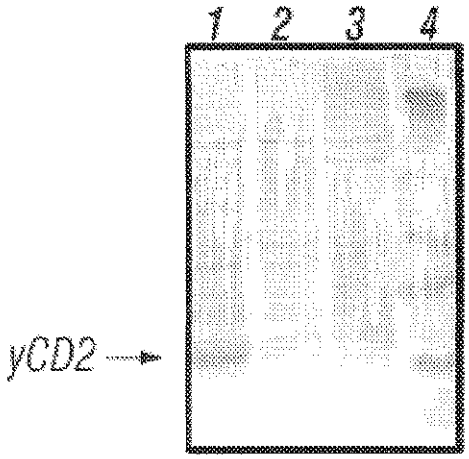
FIGURE 2C

1. Synthesis of CDopt-LINKER-OPRT: Site directed mutagenesis insertion of linker



2. CD-OPRT gene size: 1.33 kb

FIGURE 2D



1 - U87 + AC3-yCD2 (V)
2 - U87 + ACE-yCD (V)
3 - U87 (uninfected)
4 - Molecular Weight Standards

FIGURE 3

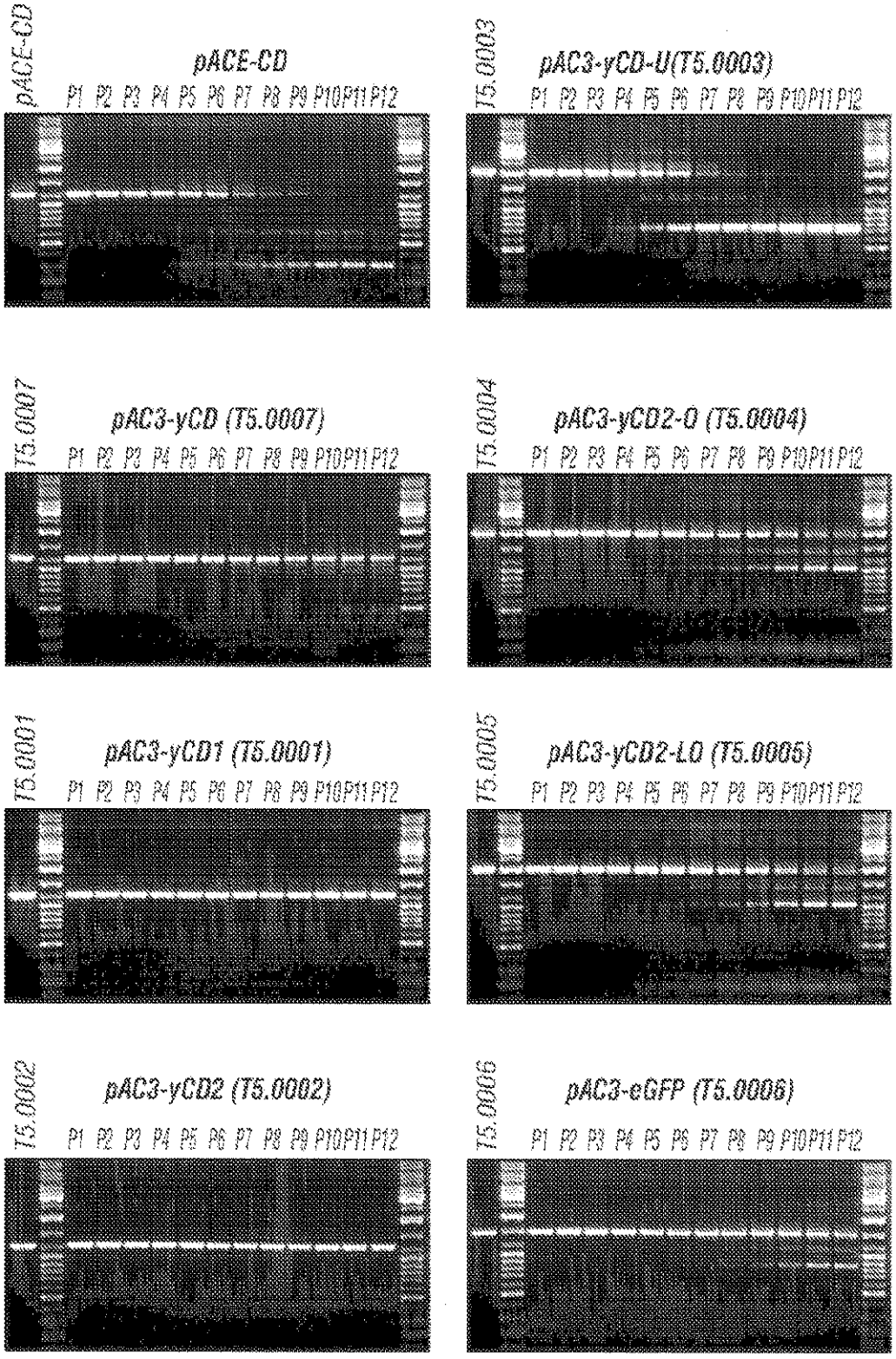

pACE-CD
P1 P2 P3 P4 P5 P6 P7 P8 P9 P10 P11 P12
T5.0003
pAC3-yCD-U(T5.0003)
P1 P2 P3 P4 P5 P6 P7 P8 P9 P10 P11 P12
T5.0007
pAC3-yCD (T5.0007)
P1 P2 P3 P4 P5 P6 P7 P8 P9 P10 P11 P12
T5.0004
pAC3-yCD2-O (T5.0004)
P1 P2 P3 P4 P5 P6 P7 P8 P9 P10 P11 P12
T5.0001
pAC3-yCD1 (T5.0001)
P1 P2 P3 P4 P5 P6 P7 P8 P9 P10 P11 P12
T5.0005
pAC3-yCD2-LO (T5.0005)
P1 P2 P3 P4 P5 P6 P7 P8 P9 P10 P11 P12
T5.0002
pAC3-yCD2 (T5.0002)
P1 P2 P3 P4 P5 P6 P7 P8 P9 P10 P11 P12
T5.0006
pAC3-eGFP (T5.0006)
P1 P2 P3 P4 P5 P6 P7 P8 P9 P10 P11 P12

FIGURE 4

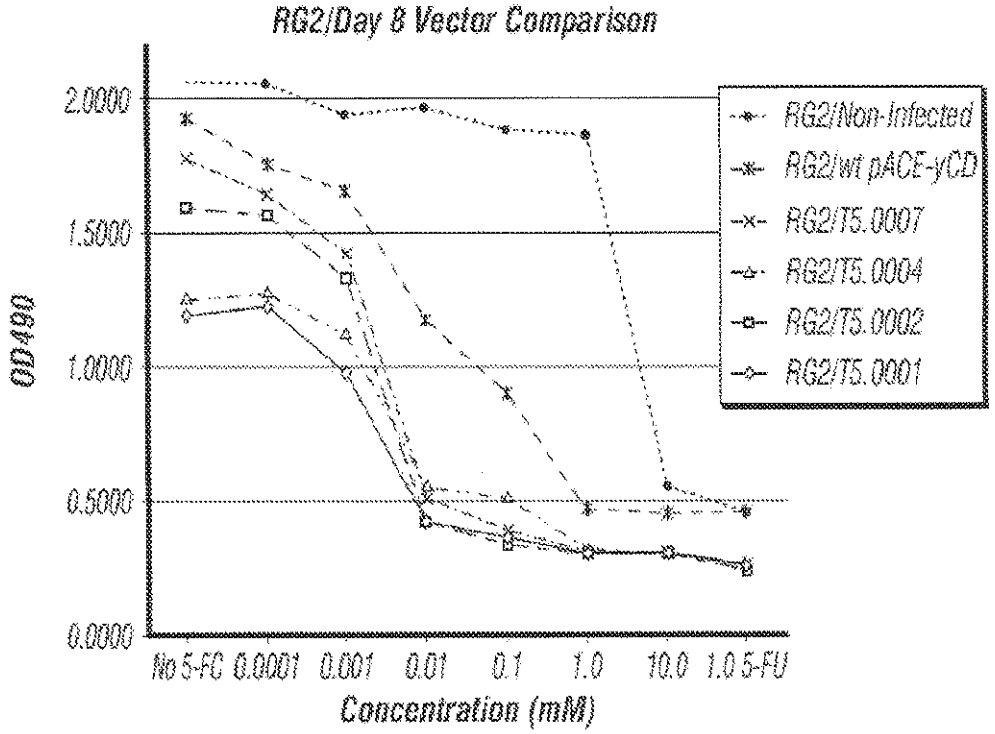


FIGURE 5A

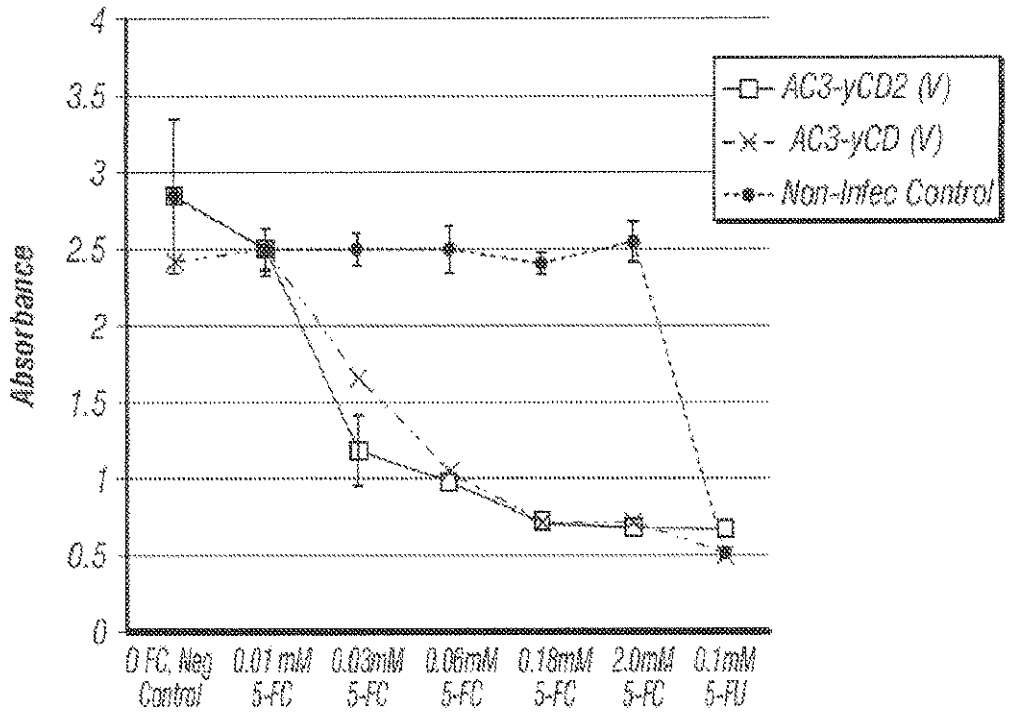


FIGURE 5B

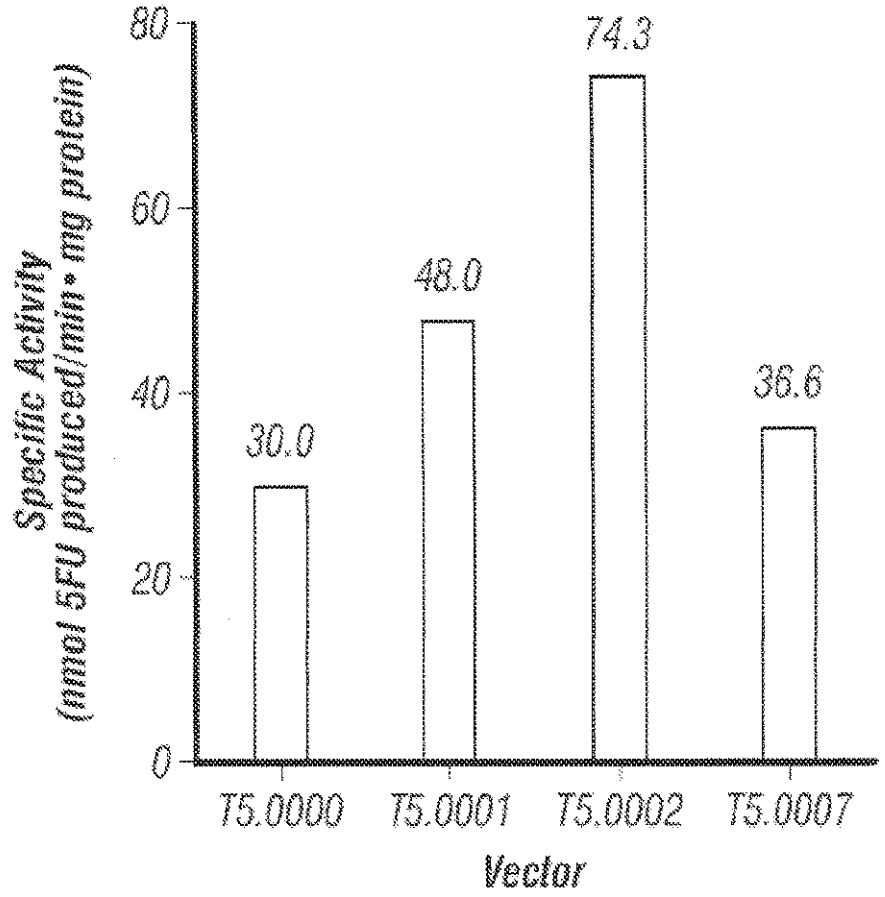

Specific Activity
(nmol 5FU produced/min • mg protein)
80
60
40
20
0
30.0
48.0
74.3
36.6
T5.0000
T5.0001
T5.0002
T5.0007
Vector

FIGURE 6