```
             BssHII
             -------
          SacII
          ------
          MspAlI
          ------
        NotI   AscI                                                                                 AseI
        ----------------                                                                          -------
  1     GCGGCCGCGG CGCGCCACCT AAAGATGCCA TTCCTGTTAT TATATCCATA GGAAAGGATA GAGATGTTTG TGAACTATTA ATCTCATCTG ATAAAGCGTG
                             >>.......................................MVA164..........................................>

                                                               FokI
                                                               -----
                                                               BtsCI
                                                               -----
                                                   XcmI
                                                ---------------
                                           TsoI           NcoI
                                         -------         ------
101     TGCGTGTATA GAGTTAAATT CATATAAAGT AGCCATTCTT CCCATGGATG TTTCCTTTTT TACCAAAGGA AATGCATCAT TGATTATTCT CCTGTTTGAT
        >.................................................MVA164...................................................>

                                     SmlI                                            DrdI
                                    ------                                      -------------
                          BanI       AflII                                 XbaI        HgaI                    MunI
                         ------     ------                                -------     ------                  ------
201     TTCTCTATCG ATGCGGCACC TCTCTTAAGA AGTGTAACCG ATAATAATGT TATTATATCT AGACACCAGC GTCTACATGA CGAGCTTCCG AGTTCCAATT
        >.................................................MVA164...................................................>

                                                                                            SphI
                                                                                           ------
                                        MmeI                              BccI             NspI
                                      -------                            ------           ------
301     GGTTCAAGTT TTACATAAGT ATAAAGTCCG ACTATTGTTC TATATTATAT ATGGTTGTTG ATGGATCTGT GATGCATGCA ATAGCTGATA ATAGAACTTA
        >.................................................MVA164...................................................>
```

FIGURE ONE

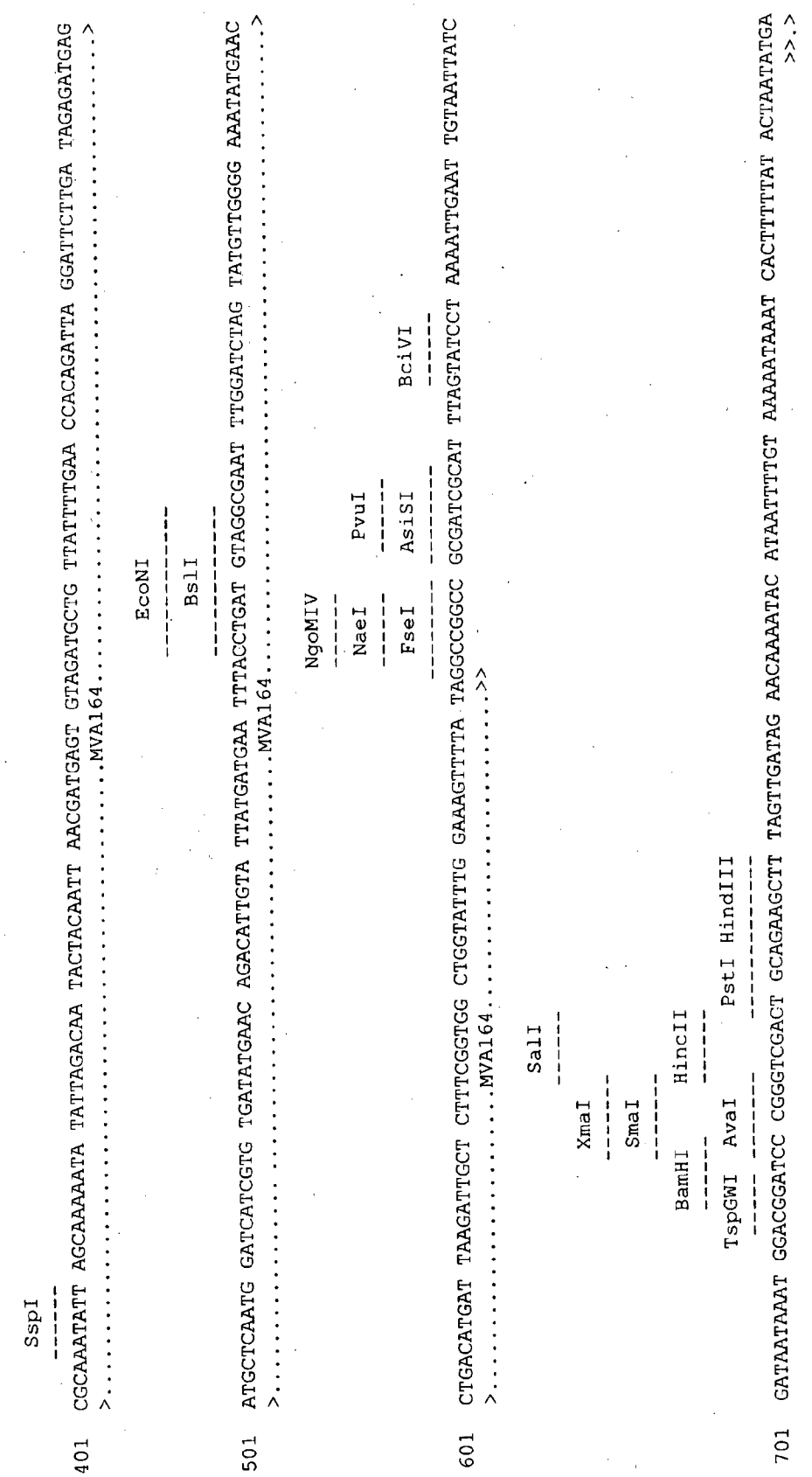


FIGURE ONE (cont)

```
                                     Bst1107I
                                     -------
801  CACGATTACC AATACTTTTG TTACTAATAT CATTAGTATA CGCTACACCT TTTCCTCAGA CATCTAAAAA AATAGGTGAT GATGCAACTT TATCATGTAA
     >.............................................MVA165.........................................................>

                                                                                                ZraI
                                                                                                ------
                                                 Bsp1286I                      TseI             BsaHI
                                                 -------                       -----            ------
                                                  BanII                        BbvI             AatII
                                                 -------                       -----            ------
901  TCGAAATAAT ACAAATGACT ACGTTGTTAT GAGTGCTTGG TATAAGGAGC CCAATTCCAT TATTCTTTTA GCTGCTAAAA GCGACGTCTT GTATTTTGAT
     >.............................................MVA165.........................................................>

                            PleI                                                                          RsaI
                            ------                                                                        ----
                            MlyI                                                                          CviQI
                            ------                                                                        ----
1001 AATTATACCA AGGATAAAAT ATCTTACGAC TCTCCATACG ATGATCTAGT TACAACTATC ACAATTAAAT CATTGACTGC TAGAGATGCC GGTACTTATG
     >.............................................MVA165.........................................................>

        BsmI         BtgZI            TspRI
       -------      -------          -----
1101 TATGTGCATT CTTTATGACA TCGCCTACAA ATGACACTGA TAAAGTAGAT TATGAAGAAT ACTCCACAGA GTTGATTGTA AATACAGATA GTGAATCGAC
     >.............................................MVA165.........................................................>

                                    BsaWI    SpeI                                                          BstBI
                                   ------   ------                                                        ------
1201 TATAGACATA ATACTATCTG GATCTACACA TTCACCGGAA ACTAGTTCTG AGAAACCTGA TTATATAGAT AATTCTAATT GCTCGTCGGT ATTCGAAATC
     >.............................................MVA165........................................................>>

       NotI
     --------
1301 GCGGCCGC
```

FIGURE ONE (cont)

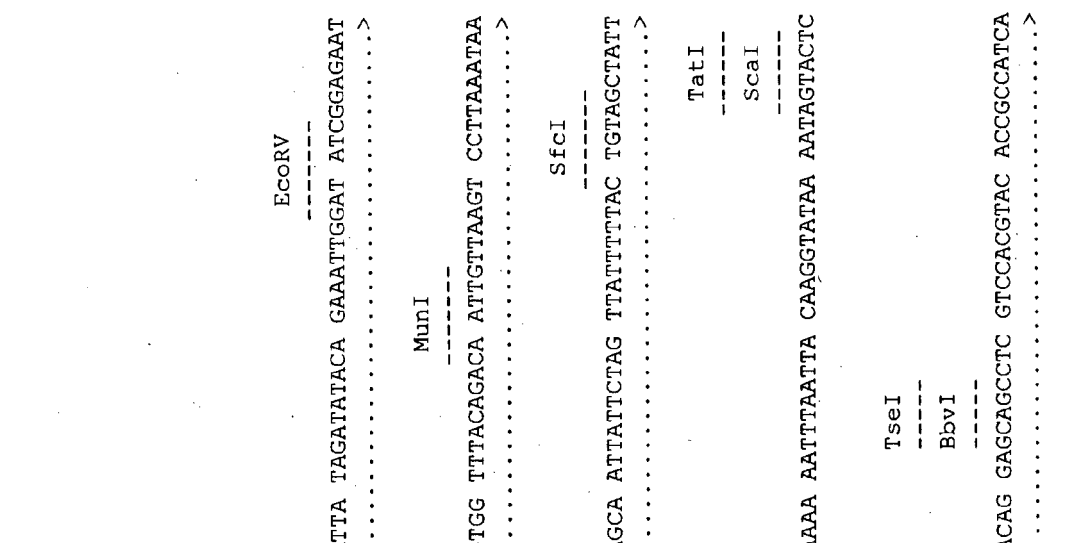

BssHII
NotI AscI BciVI
EcoRV
1 GCGGCCGCGG CGCGCCCGGT ATCCAAGCTA GAAAAGAACT GTAATGCGTA TGCGGAGGTT AATAATATTA TAGATATACA GAAATTGGAT ATCGGAGAAT
>>.....F9L.....>
MunI
EciI HincII
101 GTTCGGCTCC GCCCGGTCAA CATATGCTTT TACAGATAGT TAATACAGGA TCCGCGGAAG CAAATTGTGG TTTACAGACA ATTGTTAAGT CCTTAAATAA
>.....F9L.....>
SfcI
BceAI TaqII
201 AATATACGTT CCACCTATTA TCGAAAACCG ATTGCCGTAT TACGATCCGT GGTTTCTAGT GGGTGTAGCA ATTATTCTAG TTATTTTTAC TGTAGCTATT
>.....F9L.....>
TatI
ScaI
AclI PacI
301 TGTTCTATTA GACGAAATCT GGCTCTTAAA TACAGATACG GAACGTTTTT ATACGTTTAA TTAATAAAAA AATTTAATTA CAAGGTATAA AATAGTACTC
>.....F9L.....>>
TseI
BbvI
DrdI
NruI
401 CATCTACGCA ATCGCGATAA TGGAGGGATC TAAACGCAGA CACGACAGTC GGCGACTACA ACAAGAACAG GAGCAGCCTC GTCCACGTAC ACCGCCATCA
>>.....F8L.....>
SmlI
AflII

FIGURE TWO

```
                                                    -------
501  TATGAAGAAA TTGCAAAATA TGGACACTCA TTTAACGTGA AAAGATTTAC GAATGAAGAA ATGTGTCTTA AGAATGATTA TCCACGAATT ATATCATATA
     >.....F8L.....>

                    NgoMIV
                    -------
                     NaeI     PvuI                                  Bst1107I
                    -------  ------                                 --------
                     FseI     AsiSI HindIII                 BspHI   AccI
                    ------------------------               -------  ------
601  ATCCTCCACC AAAATAGTTT TTTTTGGCCG GCCGCGATCG CAAGCTTAGT ATATATATAT CATCATTTCA TGATGTATAC TACTGACATA GTTTCAATGT
     >.....F8L.....>>

                                                                                                      PshAI
                                                                                                      --------
701  GAACTTTTCA CTTTCTTGCC GGTTATGAAG AATATTTTTA TTTTAATGGT CATTACTAAT CGTATATTAT AATTGAAAAT GGATTAGTTT AATATGACGC
                                                                                                        >>F7L.>

                          Tsp45I
                          -----
801  TCGTCATGGG ATCCTGCTGT GGTAGATTCT GTGACGCTAA GAATAAGAAT AAGAAGGAAG ATGTAGAAGA GGGAAGAGAA GGATGTTACA ATTATAAGAA
     >.....F7L.....>

                                      Sau96I
                                      -----
                          AflIII      BmgT120I
                          ------      --------
                          PmlI        AvaII
                          ------      -----
901  CCTTAATGAT CTGGATGAAT CCGAAGCACG TGTAGAATTT GGACCATTAT ATATGATAAA TGAAGAAAAA TCAGACATAA ATACATTGGA TATAAAAAGA
     >.....F7L.....>

1001 AGATATAGAC ACACGATAGA GTCTGTATAT TTCTAAAAGT TTTTATAAAA AATGAGTAAA ATACTCACGT TTGTTAAAAA TAAGATAATT GACTTGATTA
```

FIGURE TWO (cont)

```
>.....F7L.....>>                    >>.....F6L.....>
                                          SphI
                                          ------
                                BsaWI     NspI  TsoI
                                ------    ------------
                          XbaI  AgeI      ------------
                          ------
1101 ATAATGACCA AATTAAATAT TCTAGAGTTA TAATGATAGA AGAGTCCGAT AGTCTTTTAC CGGTTGATGA GGTGCATGCT AACCACGGAT TTGACTGTGT
     >.....F6L.....>
                                    NotI
                                    ---------
                    BsrDI           ---------
                    ------
1201 GGAGATGATA GATGAAAATA TAAGCAATGA GAATATCGAA CAGTATAAGC GGCCGC
     >.....F6L.....>>
```

FIGURE TWO (cont)

```
          EagI
         -------
      EcoRI
      ------
       ApoI   FseI          BciVI                      ClaI
      ---------------     -------                    ------
  1   GAATTCGGCC GGCCATTTAG TATCCTAAAA TTGAATTGTA ATTATCGATA ATAAATGGGC
                                                              >>...>

 61   GTGAGGAACT CCGTGCTGTC CGGCAAGAAG GCCGACGAGC TGGAGAAGAT CAGGCTGAGG
      >.............................gag.............................>

121   CCCAACGGCA AGAAGAAGTA CATGCTGAAG CACGTGGTGT GGGCCGCCAA CGAGCTGGAC
      >.............................gag.............................>

181   AGGTTCGGCC TGGCCGAGTC CCTGCTGGAG AACAAGGAGG GCTGCCAGAA GATCCTGTCC
      >.............................gag.............................>

241   GTGCTGGCCC CCCTGGTGCC CACCGGCTCC GAGAACCTGA AGTCCCTGTA CAACACCGTG
      >.............................gag.............................>

301   TGCGTGATCT GGTGCATCCA CGCCGAGGAG AAGGTGAAGC ACACCGAGGA GGCCAAGCAG
      >.............................gag.............................>

   BstAPI
  -----------
361   ATCGTGCAGA GGCACCTGGT GGTGGAGACC GGCACCACCG AGACCATGCC CAAGACCTCC
      >.............................gag.............................>

421   AGGCCCACCG CCCCCTCCTC CGGCAGGGGC GGCAACTACC CCGTGCAGCA GATCGGCGGC
      >.............................gag.............................>

481   AACTACGTGC ACCTGCCCCT GTCCCCCAGG ACCCTGAACG CCTGGGTGAA GCTGATCGAG
      >.............................gag.............................>

          XmnI
         -----------
541   GAGAAGAAGT TCGGCGCCGA GGTGGTGCCC GGCTTCCAGG CCCTGTCCGA GGGCTGCACC
      >.............................gag.............................>

601   CCCTACGACA TCAACCAGAT GCTGAACTGC GTGGGCGACC ACCAGGCCGC CATGCAGATC
      >.............................gag.............................>

661   ATCAGGGACA TCATCAACGA GGAGGCCGCC GACTGGGACC TCCAGCACCC CCAGCCCGCC
      >.............................gag.............................>

721   CCCCAGCAGG GCCAGCTGAG GGAGCCCTCC GGCTCCGACA TCGCCGGCAC CACCTCCTCC
      >.............................gag.............................>

781   GTGGACGAGC AGATCCAGTG GATGTACAGG CAGCAGAACC CCATCCCCGT GGGCAACATC
      >.............................gag.............................>

841   TACAGGAGGT GGATTCAGCT GGGCCTGCAA AAGTGCGTGA GGATGTACAA CCCCACCAAC
      >.............................gag.............................>

901   ATCCTGGACG TGAAGCAGGG CCCCAAGGAG CCCTTCCAGT CCTACGTGGA CAGGTTCTAC
      >.............................gag.............................>
```

FIGURE 3

```
 961  AAGTCCCTGA GGGCCGAGCA GACCGACGCC GCCGTGAAGA ACTGGATGAC CCAGACCCTG
      >.............................gag.............................>

1021  CTGATCCAGA ACGCCAACCC CGACTGCAAG CTGGTGCTGA AGGGCCTGGG CGTGAACCCC
      >.............................gag.............................>

1081  ACCCTGGAGG AGATGCTGAC CGCCTGCCAG GGCGTGGGCG GCCCCGGCCA GAAGGCCAGG
      >.............................gag.............................>

1141  CTGATGGCCG AGGCCCTGAA GGAGGCCCTG GCCCCCGTGC CCATCCCCTT CGCCGCCGCC
      >.............................gag.............................>

                                                                 EciI
                                                                 ------
1201  CAGCAGAGGG GCCCCAGGAA GCCCATCAAG TGCTGGAACT GCGGCAAGGA GGGCCACTCC
      >.............................gag.............................>

           BsrDI              BbsI
          -------            ------
1261  GCCAGGCAAT GCAGAGCCCC AAGAAGACAG GGATGCTGGA AATGTGGAAA AATGGACCAT
      >.............................gag.............................>
             >>.........................pol.........................>

1321  GTTATGGCCA AATGCCCAGA CAGACAGGCG GGTTTTTTAG GCCTTGGTCC ATGGGGAAAG
      >.............................gag.............................>
      >.............................pol.............................>

                              SmlI
                             ------
                             BpuEI
                             ------
1381  AAGCCCCGCA ATTTCCCCAT GGCTCAAGTG CATCAGGGGC TGATGCCAAC TGCTCCCCCA
      >.............................gag.............................>
      >.............................pol.............................>

1441  GAGGACCCAG CTGTGGATCT GCTAAAGAAC TACATGCAGT TGGGCAAGCA GCAGAGAGAA
      >.............................gag.............................>
      >.............................pol.............................>

1501  AAGCAGAGAG AAAGCAGAGA GAAGCCTTAC AAGGAGGTGA CAGAGGATTT GCTGCACCTC
      >.............................gag.............................>
      >.............................pol.............................>

1561  AATTCTCTCT TTGGAGGAGA CCAGTAGTGA CCGCCCACAT CGAGGGCCAG CCCGTGGAGG
      >...........gag............>>
      >.............................pol.............................>

1621  TGCTGCTGGA CACCGGCGCC GACGACTCCA TCGTGACCGG CATCGAGCTG GGCCCCCACT
      >.............................pol.............................>

1681  ACACCCCCAA GATCGTGGGC GGCATCGGCG GCTTCATCAA CACCAAGGAG TACAAGAACG
      >.............................pol.............................>

                                                    BspHI
                                                   -------
1741  TGGAGATCGA GGTGCTGGGC AAGAGGATCA AGGGCACCAT CATGACCGGC GACACCCCCA
      >.............................pol.............................>
```

FIGURE 3 (cont)

```
1801  TCAACATCTT CGGCAGGAAC CTGCTGACCG CCCTGGGCAT GTCCCTGAAC TTCCCCATCG
      >.............................pol.............................>

1861  CCAAGGTGGA GCCCGTGAAG GTGGCCCTGA AGCCCGGCAA GGACGGCCCC AAGCTGAAGC
      >.............................pol.............................>

1921  AGTGGCCCCT GTCCAAGGAG AAGATCGTGG CCCTGAGGGA GATCTGCGAG AAGATGGAGA
      >.............................pol.............................>

1981  AGGACGGCCA GCTGGAGGAG GCCCCCCCCA CCAACCCCTA CAACACCCCC ACCTTCGCCA
      >.............................pol.............................>

2041  TCAAGAAGAA GGACAAGAAC AAGTGGAGGA TGCTGATCGA CTTCAGGGAG CTGAACAGGG
      >.............................pol.............................>

                    AleI
                   -----------
2101  TGACCCAGGA CTTCACCGAG GTGCAGCTGG GCATCCCCCA CCCCGCCGGC CTGGCCAAGA
      >.............................pol.............................>

        EarI
       ------
2161  GGAAGAGGAT CACCGTGCTG GACATCGGCG ACGCCTACTT CTCCATCCCC CTGGACGAGG
      >.............................pol.............................>

2221  AGTTCAGGCA GTACACCGCC TTCACCCTGC CCTCCGTGAA CAACGCCGAG CCCGGCAAGA
      >.............................pol.............................>

2281  GGTACATCTA CAAGGTGCTG CCCCAGGGCT GGAAGGGCTC CCCCGCCATC TTCCAGTACA
      >.............................pol.............................>

2341  CCATGAGGCA CGTGCTGGAG CCCTTCAGGA AGGCCAACCC CGACGTGACC CTGGTGCAGT
      >.............................pol.............................>

2401  ACATGGACGA CATCCTGATC GCCTCCGACA GGACCGACCT GGAGCACGAC AGGGTGGTGC
      >.............................pol.............................>

2461  TCCAGTCCAA GGAGCTGCTG AACTCCATCG GCTTCTCCAC CCCCGAGGAG AAGTTCCAGA
      >.............................pol.............................>

2521  AGGACCCCCC CTTCCAGTGG ATGGGCTACG AGCTGTGGCC CACCAAGTGG AAGCTGCAAA
      >.............................pol.............................>

2581  AGATCGAGCT GCCCCAGAGG GAGACCTGGA CCGTGAACGA CATCCAGAAG CTGGTGGGCG
      >.............................pol.............................>

2641  TGCTGAACTG GGCCGCCCAG ATCTACCCCG GCATCAAGAC CAAGCACCTG TGCAGGCTGA
      >.............................pol.............................>

2701  TCAGGGGCAA GATGACCCTG ACCGAGGAGG TGCAGTGGAC CGAGATGGCC GAGGCCGAGT
      >.............................pol.............................>

2761  ACGAGGAGAA CAAGATCATC CTGTCCCAGG AGCAGGAGGG CTGCTACTAC CAGGAGGGCA
      >.............................pol.............................>

2821  AGCCCCTGGA GGCCACCGTG ATCAAGTCCC AGGACAACCA GTGGTCCTAC AAGATCCACC
      >.............................pol.............................>
```

FIGURE 3 (cont)

```
2881  AGGAGGACAA GATCCTGAAG GTGGGCAAGT TCGCCAAGAT CAAGAACACC CACACCAACG
      >.............................pol.............................>

2941  GCGTGAGGCT GCTGGCCCAC GTGATCCAGA AGATCGGCAA GGAGGCCATC GTGATCTGGG
      >.............................pol.............................>

                                              AflIII
                                              -------
3001  GCCAGGTGCC CAAGTTCCAC CTGCCCGTGG AGAAGGACGT GTGGGAGCAG TGGTGGACCG
      >.............................pol.............................>

3061  ACTACTGGCA GGTGACCTGG ATTCCCGAGT GGGACTTCAT CTCCACCCCC CCCCTGGTGA
      >.............................pol.............................>

3121  GGCTGGTGTT CAACCTGGTG AAGGACCCCA TCGAGGGCGA GGAGACCTAC TACACCGACG
      >.............................pol.............................>

3181  GCTCCTGCAA CAAGCAGTCC AAGGAGGGCA AGGCCGGCTA CATCACCGAC AGGGGCAAGG
      >.............................pol.............................>

3241  ACAAGGTGAA GGTGCTGGAG CAGACCACCA ACCAGCAGGC CGAGCTGGAG GCCTTCCTGA
      >.............................pol.............................>

3301  TGGCCCTGAC CGACTCCGGC CCCAAGGCCA ACATCATCGT GGACTCCCAG TACGTGATGG
      >.............................pol.............................>

3361  GCATCATCAC CGGCTGCCCC ACCGAGTCCG AGTCCAGGCT GGTGAACCAG ATCATCGAGG
      >.............................pol.............................>

3421  AGATGATCAA GAAGTCCGAG ATCTACGTGG CCTGGGTGCC CGCCCACAAG GGCATCGGCG
      >.............................pol.............................>

3481  GCAACCAGGA GATCGACCAC CTGGTGTCCC AGGGCATCAG GCAGGTGCTG TTCCTGGAGA
      >.............................pol.............................>

3541  AGATCGAGCC CGCCCAGGAG GAGCACGACA AGTACCACTC CAACGTGAAG GAGCTGGTGT
      >.............................pol.............................>

3601  TCAAGTTCGG CCTGCCCAGG ATCGTGGCCA GGCAGATCGT GGACACCTGC GACAAGTGCC
      >.............................pol.............................>

3661  ACCAGAAGGG CGAGGCCATC CACGGCCAGG CCAACTCCGA CCTGGGCACC TGGCAGATGG
      >.............................pol.............................>

3721  ACTGCACCCA CCTGGAGGGC AAGATCATCA TCGTGGCCGT GCACGTGGCC TCCGGCTTCA
      >.............................pol.............................>

3781  TCGAGGCCGA GGTGATCCCC CAGGAGACCG GCAGGCAGAC CGCCCTGTTC CTGCTGAAGC
      >.............................pol.............................>

3841  TGGCCGGCAG GTGGCCCATC ACCCACCTGC ACACCGACAA CGGCGCCAAC TTCGCCTCCC
      >.............................pol.............................>

                            SfiI
                            -------------
3901  AGGAGGTGAA GATGGTGGCC TGGTGGGCCG GCATCGAGCA CACCTTCGGC GTGCCCTACA
      >.............................pol.............................>
```

FIGURE 3 (cont)

```
3961  ACCCCCAGTC CCAGGGCGTG GTGGAGGCCA TGAACCACCA CCTGAAGAAC CAGATCGACA
      >.............................pol.............................>

4021  GGATCAGGGA GCAGGCCAAC TCCGTGGAGA CCATCGTGCT GATGGCCGTG CACTGCATGA
      >.............................pol.............................>

4081  ACTTCAAGAG GAGGGGCGGC ATCGGCGACA TGACCCCCGC CGAGAGGCTG ATCAACATGA
      >.............................pol.............................>

4141  TCACCACCGA GCAGGAGATC CAGTTCCAGC AGTCCAAGAA CTCCAAGTTC AAGAACTTCA
      >.............................pol.............................>

4201  GGGTGTACTA CAGGGAGGGC AGGGACCAGC TGTGGAAGGG CCCCGGCGAG CTGCTGTGGA
      >.............................pol.............................>

4261  AGGGCGAGGG CGCCGTGATC CTGAAGGTGG GCACCGACAT CAAGGTGGTG CCCAGGAGGA
      >.............................pol.............................>

4321  AGGCCAAGAT CATCAAGGAC TACGGCGGCG GCAAGGAGGT GGACTCCTCC TCCCACATGG
      >.............................pol.............................>

                                                    PvuI
                                                   ------
                                                   BsiEI
                                                   ------
                                                    SgfI
                                                  --------
                                    BfaI           AsiSI  HindIII
                                    -----         ---------------
4381  AGGACACCGG CGAGGCCAGG GAGGTGGCCT AGTTTTTTTT GCGATCGCAA GCTT
      >..............pol...............>>
```

FIGURE 3 (cont)

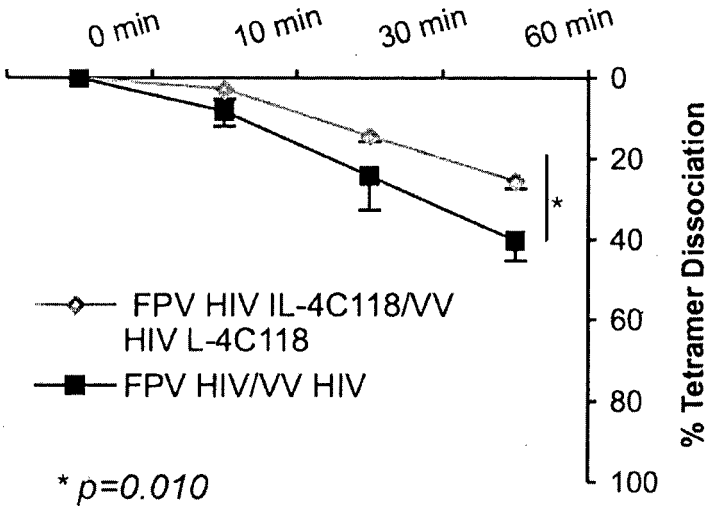


FIGURE FOUR

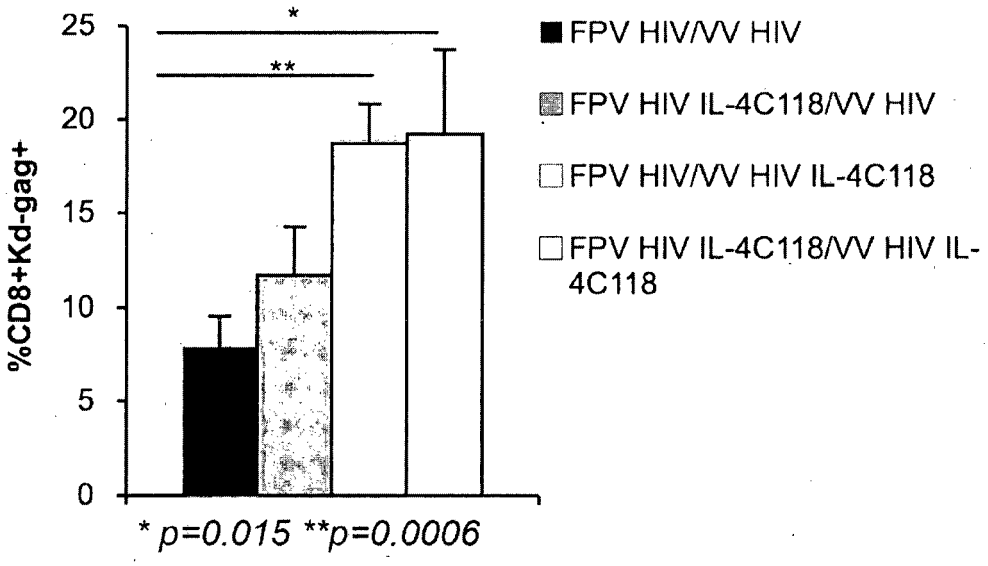


FIGURE FIVE

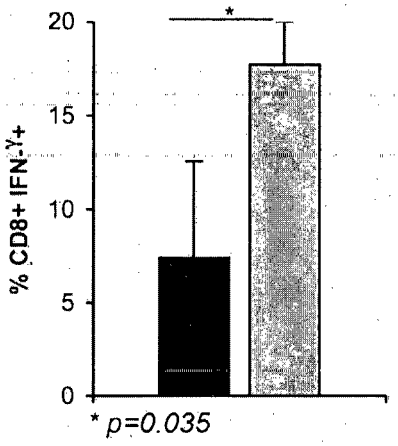


FIGURE SIX

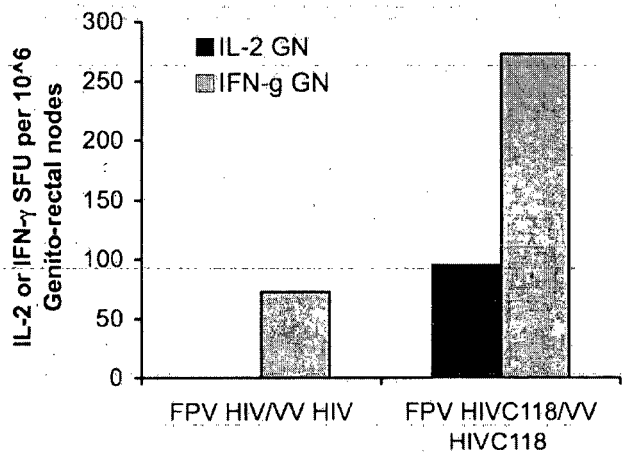
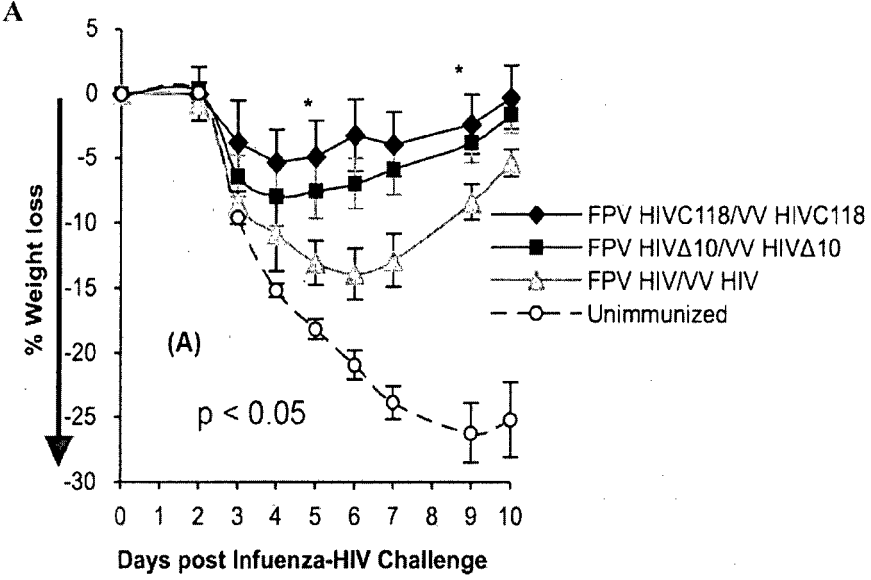


FIGURE SEVEN

A



B

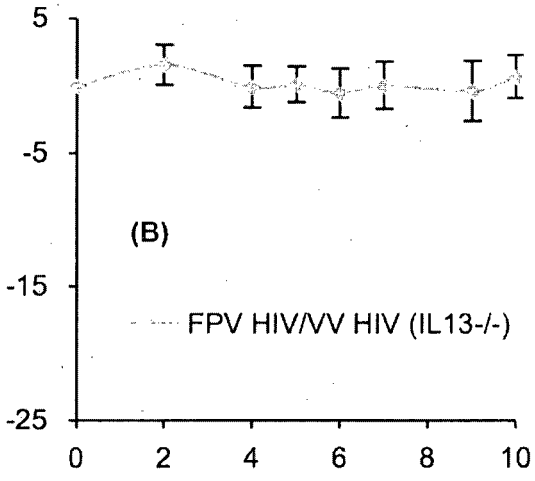


FIGURE EIGHT

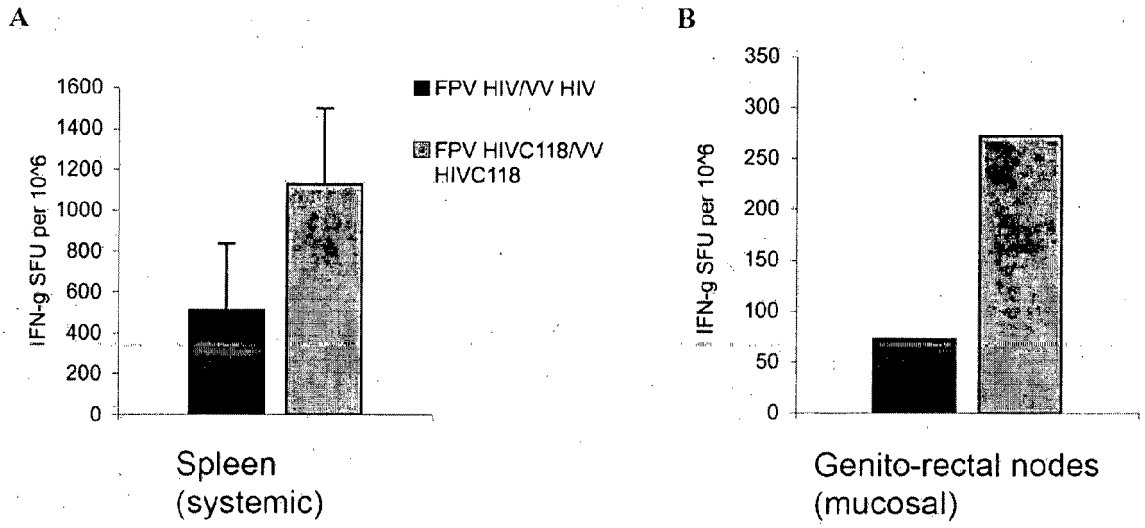

A
1600
1400
1200
1000
800
600
400
200
0
IFN-g SFU per 10^6
FPV HIV/VV HIV
FPV HIVC118/VV HIVC118
Spleen (systemic)
B
350
300
250
200
150
100
50
0
IFN-g SFU per 10^6
Genito-rectal nodes (mucosal)

FIGURE NINE

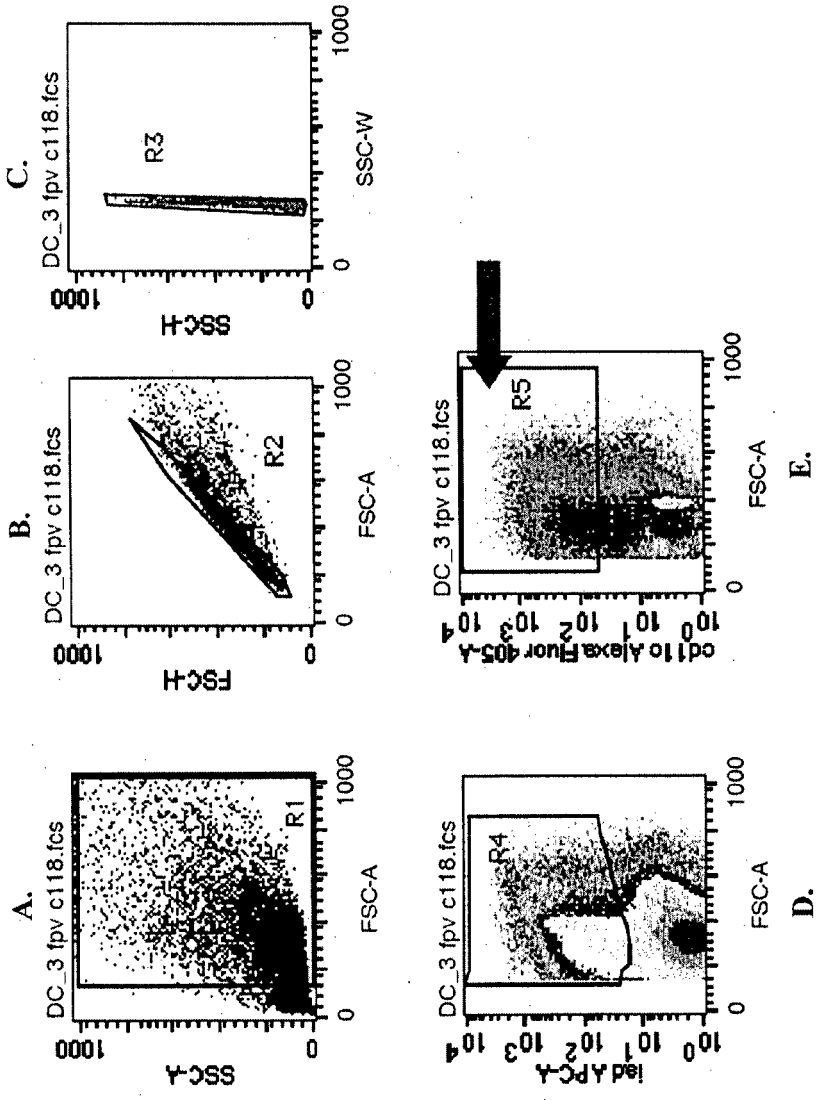

A.
DC_3 fpv c118.fcs
R1
SSC-A
FSC-A
B.
DC_3 fpv c118.fcs
R2
FSC-H
FSC-A
C.
DC_3 fpv c118.fcs
R3
SSC-H
SSC-W
D.
DC_3 fpv c118.fcs
R4
Dead APC-A
FSC-A
E.
DC_3 fpv c118.fcs
R5
cd11c AlexaFluor 405-A
FSC-A

FIGURE TEN

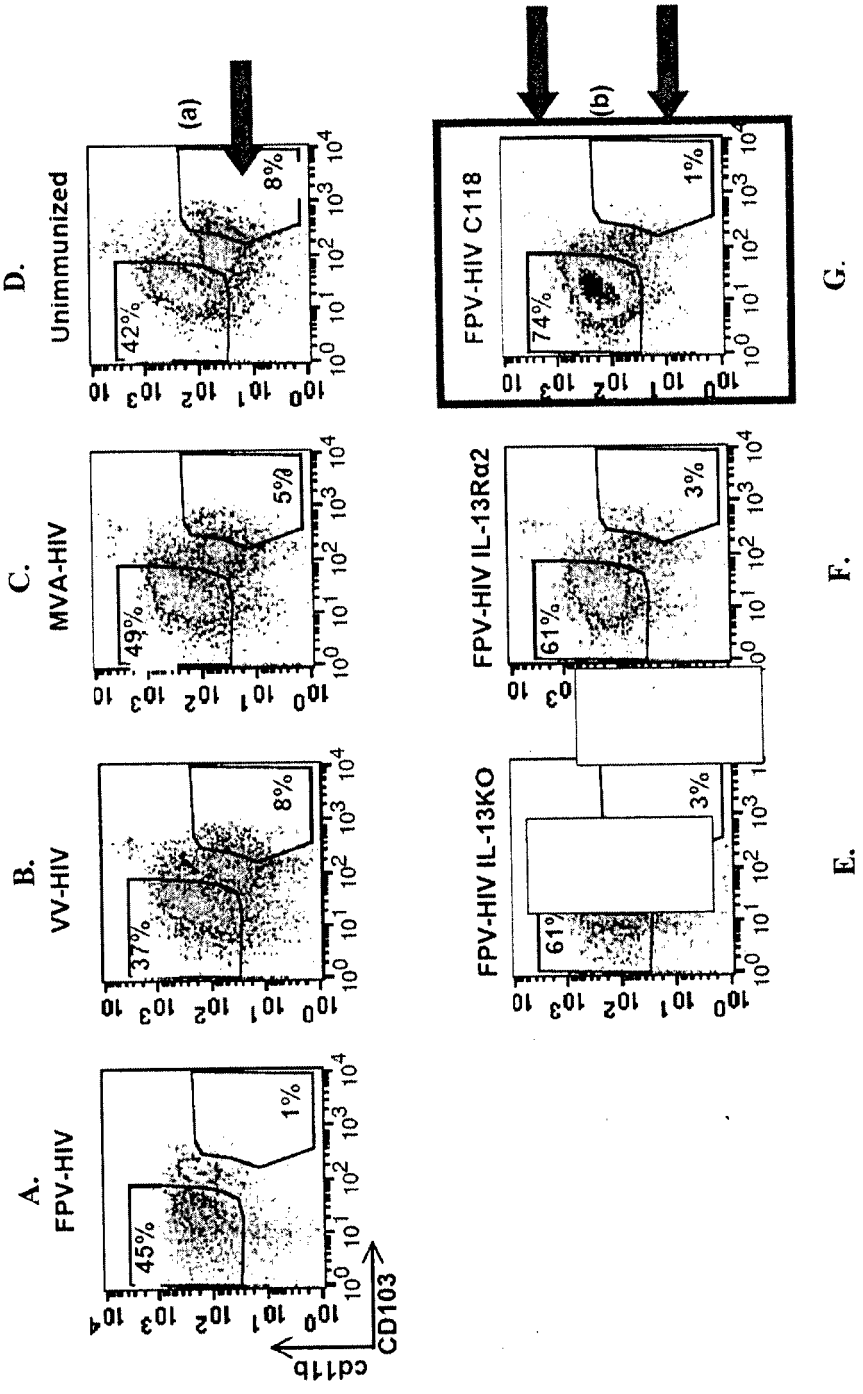


FIGURE ELEVEN

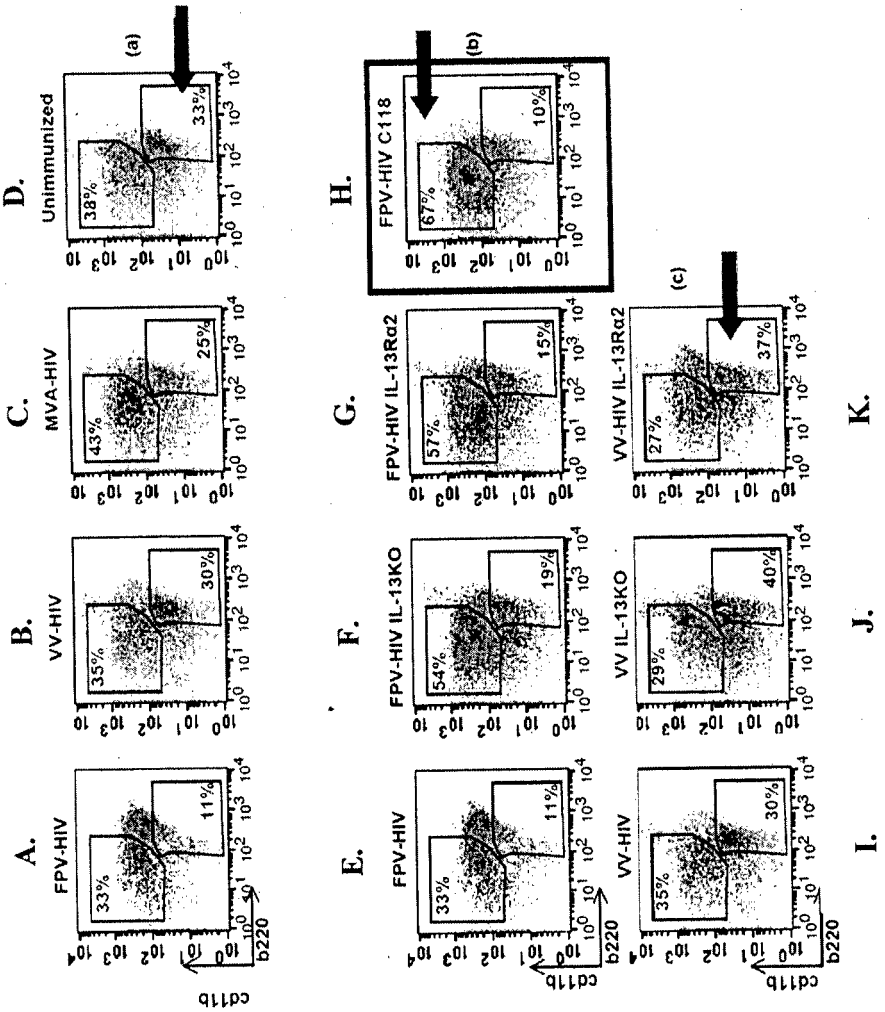


FIGURE TWELVE

Substitute Sheet
(Rule 26) RO/AU

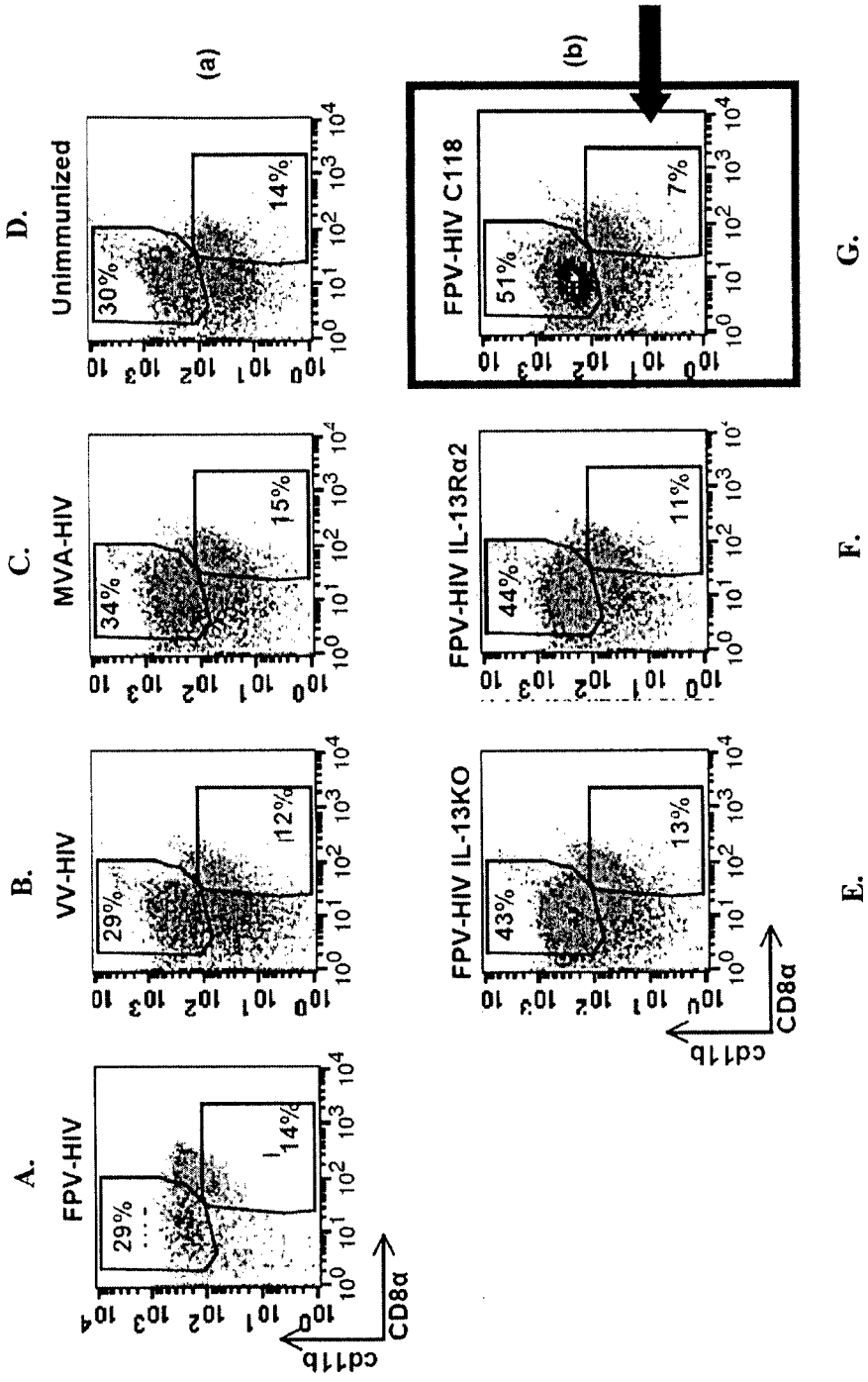


FIGURE THIRTEEN

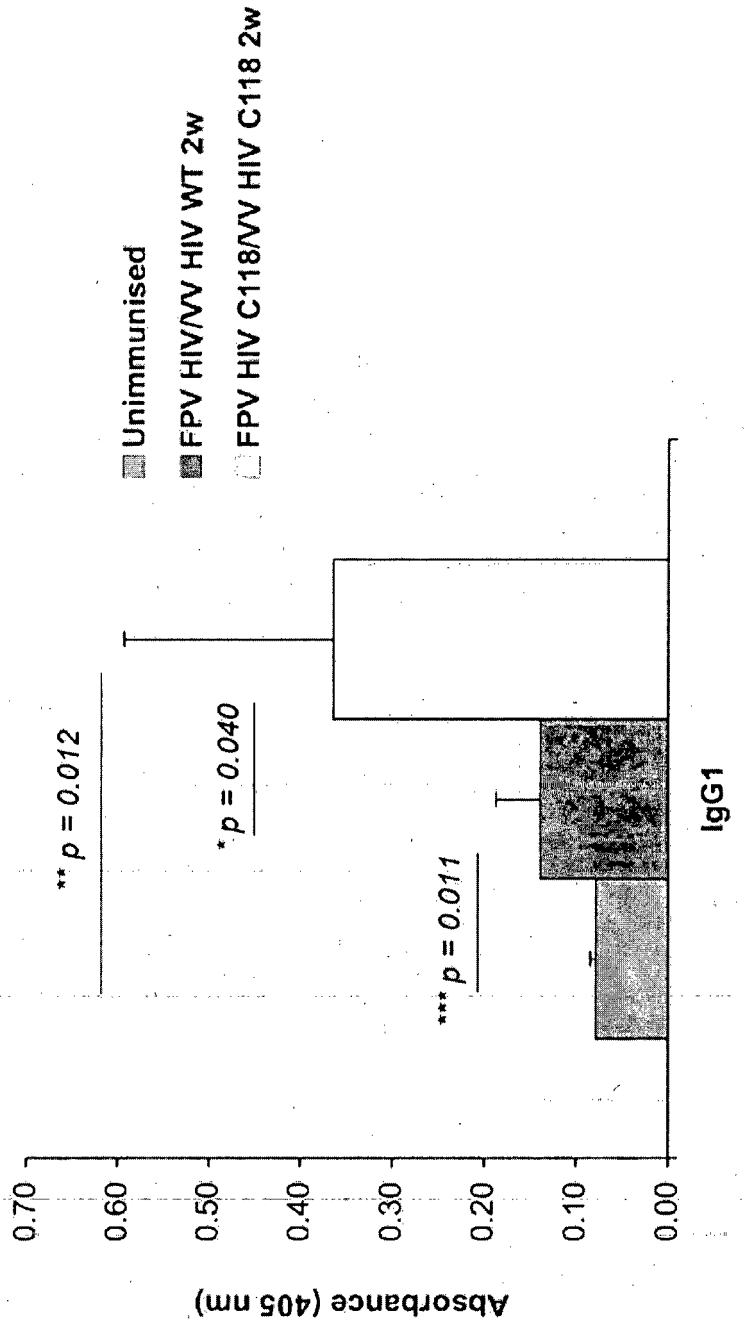


FIGURE FOURTEEN