```
                  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

```
                SspI
                ------
401  CGCAAATATT AGCAAAAATA TATTAGACAA TACTACAATT AACGATGAGT GTAGATGCTG TTATTTTGAA CCACAGATTA GGATTCTTGA TAGAGATGAG
     >.....MVA164.....<

                                                EcoNI
                                                ----------
                                                BslI
                                                ----------
501  ATGCTCAATG GATCATCGTG TGATATGAAC AGACATTGTA TTATGATGAA TTTACCTGAT GTAGGCGAAT TTGGATCTAG TATGTTGGGG AAATATGAAC
     >.....MVA164.....<

                                                NgoMIV
                                                -----
                                                NaeI     PvuI
                                                -----    -----
                                                FseI     AsiSI      BciVI
                                                -------- --------   -----
601  CTGACATGAT TAAGATTGCT CTTTCGGTGG CTGGTATTTG GAAAGTTTTA TAGGCCGGCC GCGATCGCAT TTAGTATCCT AAAATTGAAT TGTAATTATC
     >.....MVA164.....>>

                                          SalI
                                          -----
                                       XmaI
                                       ------
                                       SmaI
                                       -------
                                 BamHI     HincII
                                 ------    ------
                           TspGWI  AvaI      PstI HindIII
                           ------  --------  ----------------
701  GATAATAAAT GGACGGATCC CGGGTCGACT GCAGAAGCTT TAGTTGATAG AACAAAATAC ATAATTTTGT AAAAATAAAT CACTTTTTAT ACTAATATGA
                                                                                                >>.>
```

FIGURE ONE (cont)

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

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

                                                                                                      RsaI
                                                                                                      ----
                                                                                                      CviQI
                                                                                                      -----
                                  PleI
                                  ------
                                  MlyI
                                  ------
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
EciI HincII
MunI
SfcI
TaqII
BceAI
TatI
ScaI
AclI PacI
TseI
BbvI
NruI DrdI
SmlI
AflII
1 GCGGCCGCGG CGCGCCCGGT ATCCAAGCTA GAAAAGAACT GTAATGCGTA TGCGGAGGTT AATAATATTA TAGATATACA GAAATTGGAT ATCGGAGAAT
101 GTTCGGCTCC GCCCGGTCBA CATATGCTTT TACAGATAGT TAATACAGGA TCCGCGGAAG CAAATTGTGG TTTACAGACA ATTGTTAAGT CCTTAAATAA
201 AATATACGTT CCACCTATTA TCGAAAACCG ATTGCCGTAT TACGATCCGT GGTTTCTAGT GGGTGTAGCA ATTATTCTAG TTATTTTTAC TGTAGCTATT
301 TGTTCTATTA GACGAAATCT GGCTCTTAAA TACAGATACG GAACGTTTTT ATACGTTTAA TTAATAAAAA AATTTAATTA CAAGGTATAA AATAGTACTC
401 CATCTACGCA ATCGCGATAA TGGAGGGATC TAAACGGCAG CACGACAGTC GGCGACTACA ACAAGAACAG GAGCAGCCTC GTCCACGTAC ACCGCCATCA

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.....>
                                                BsaWI       SphI
                                                ------      -----
                                                AgeI        NspI  TsoI
                                                ------      ----------
                  XbaI
                  -----
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)

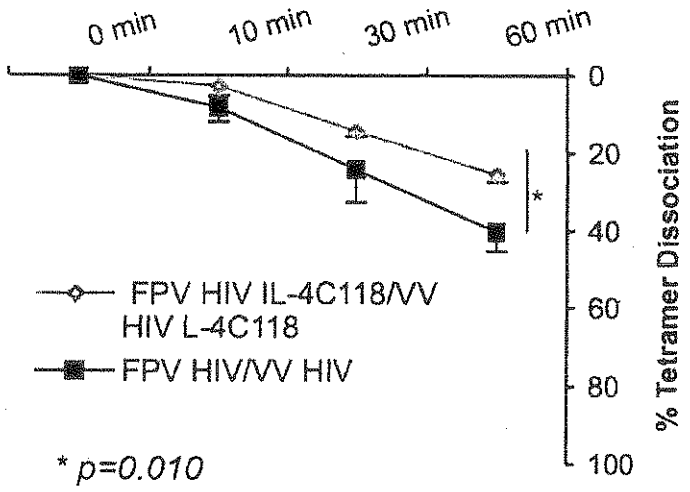


FIGURE FOUR

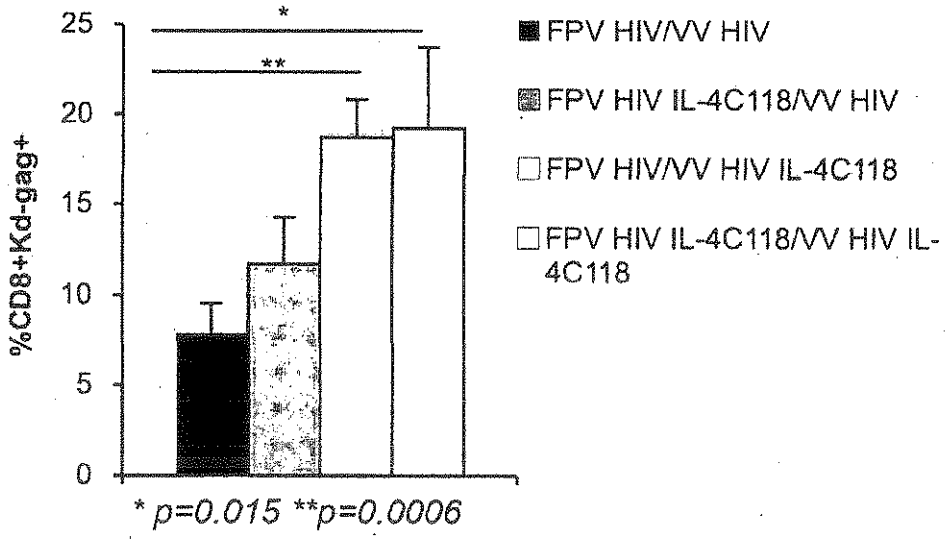


FIGURE FIVE

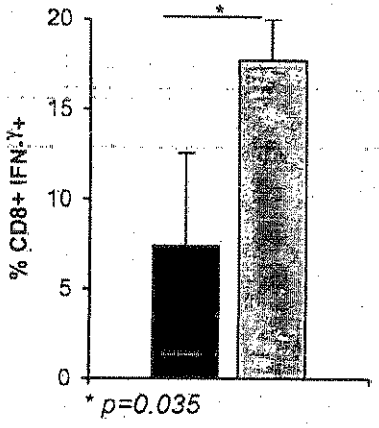


FIGURE SIX

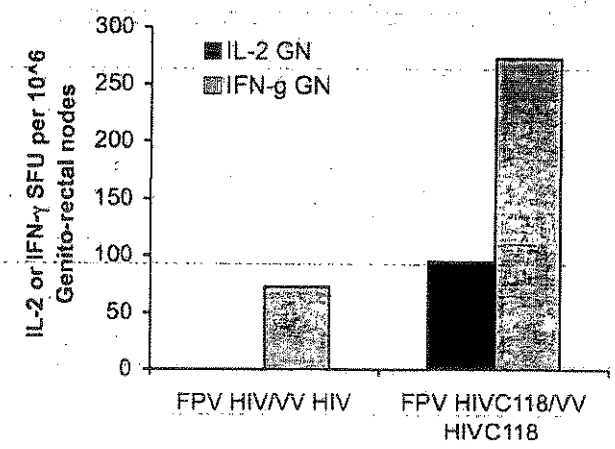
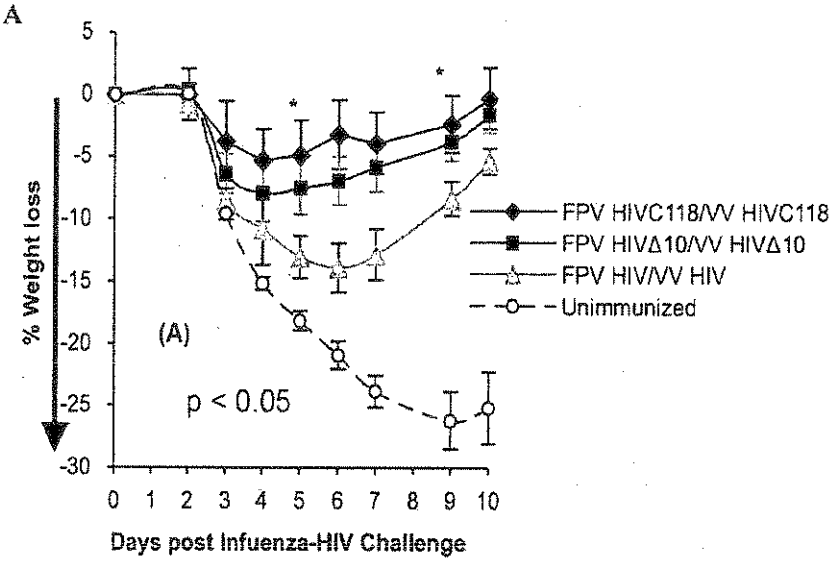


FIGURE SEVEN

A



B

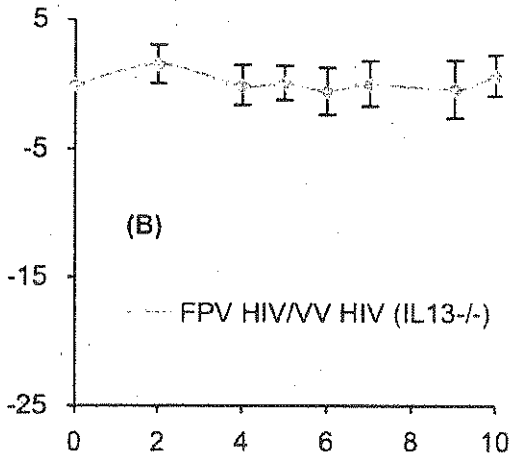


FIGURE EIGHT

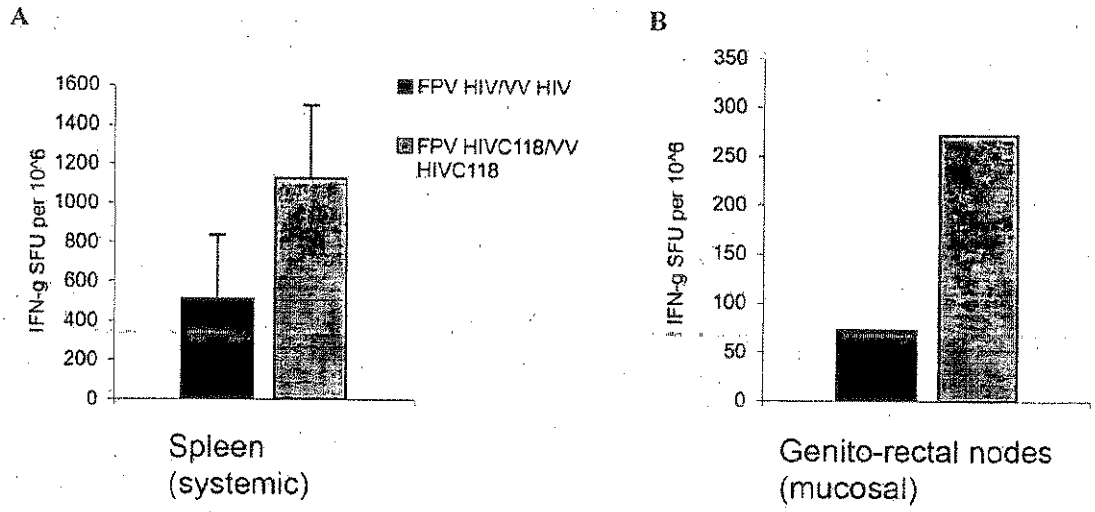

A
1600
1400
1200
1000
800
600
400
200
0
IFN-g SFU per 10^6
FPV HIV/VV HIV
FPV HIVC118/VV HIVC118
Spleen (systemic)
B
350
300
250
200
150
100
50
0
IFN-g SFU per 10^6
Genito-rectal nodes (mucosal)

FIGURE NINE

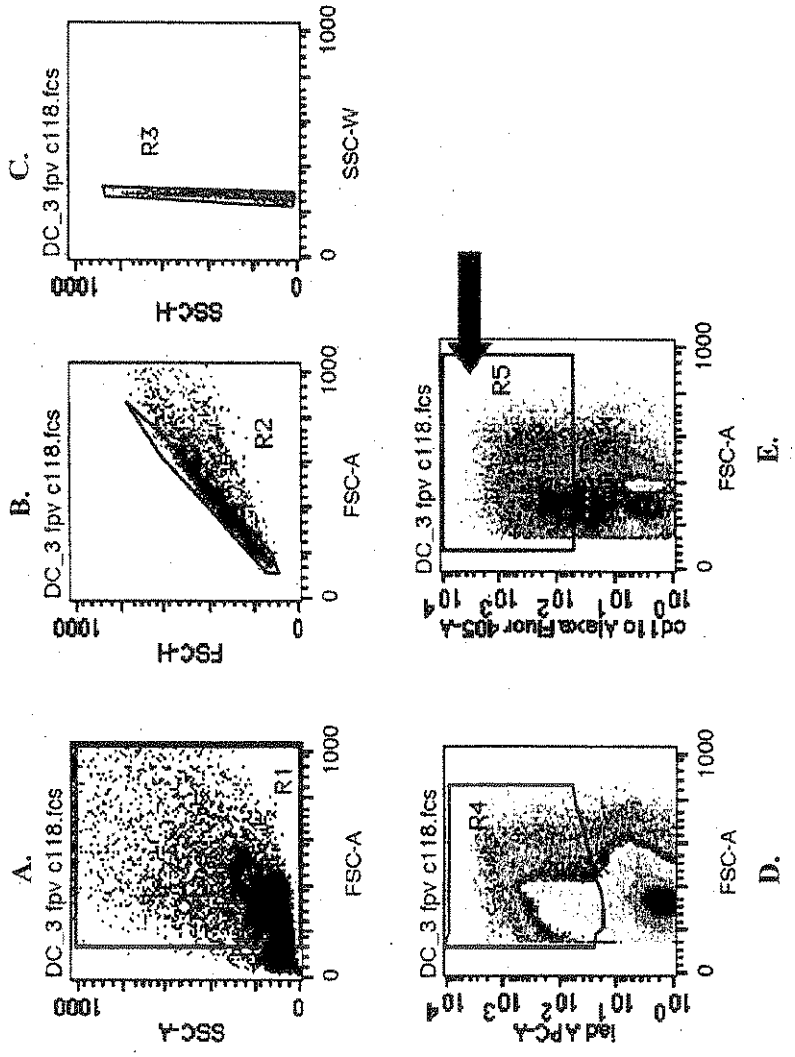

A.
DC_3 fpv c118.fcs
R1
SSC-A
FSC-A
B.
DC_3 fpv c118.fcs
R2
FSC-H
FSC-A
C.
DC_3 fpv c118.fcs
R3
SSC-H
SSC-W
D.
DC_3 fpv c118.fcs
R4
FSC-A
E.
DC_3 fpv c118.fcs
R5
FSC-A

FIGURE TEN

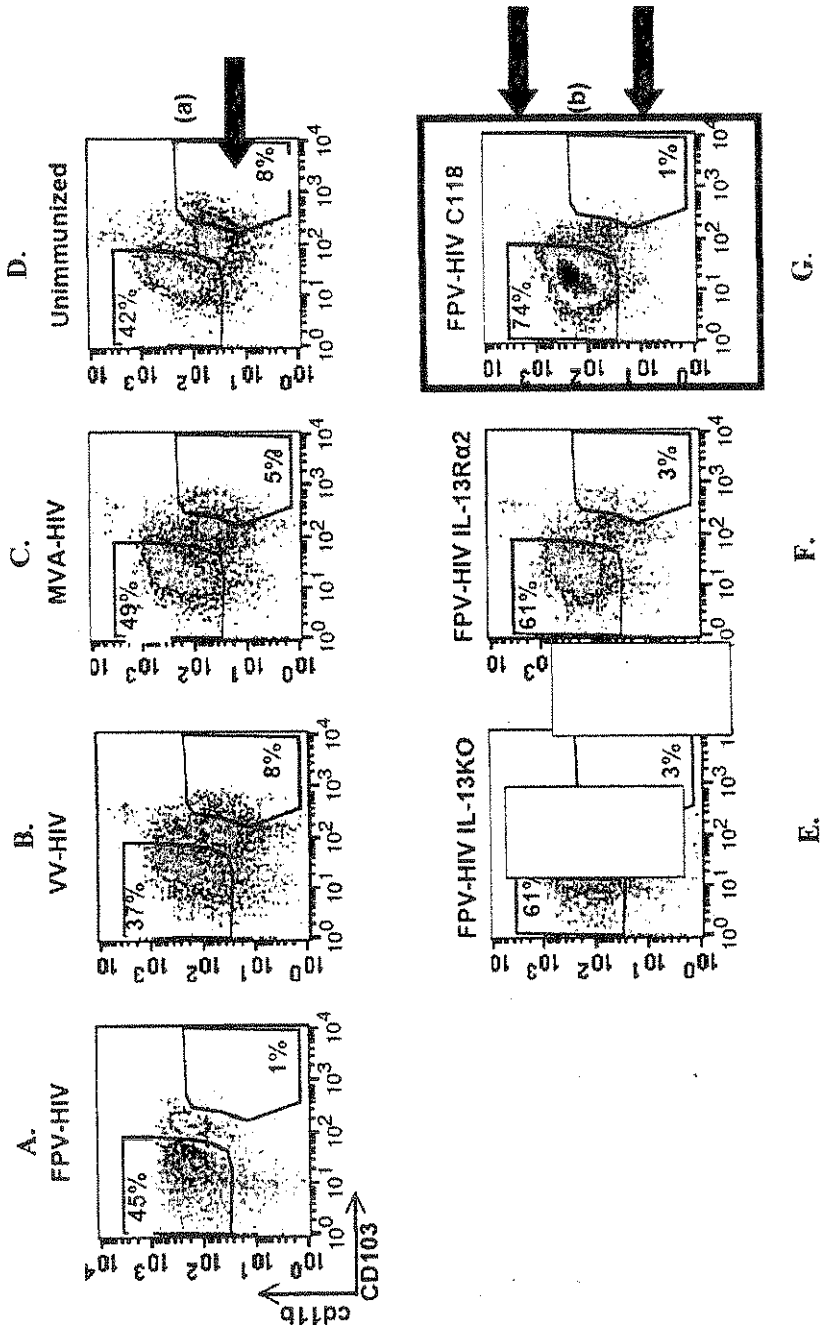


FIGURE ELEVEN

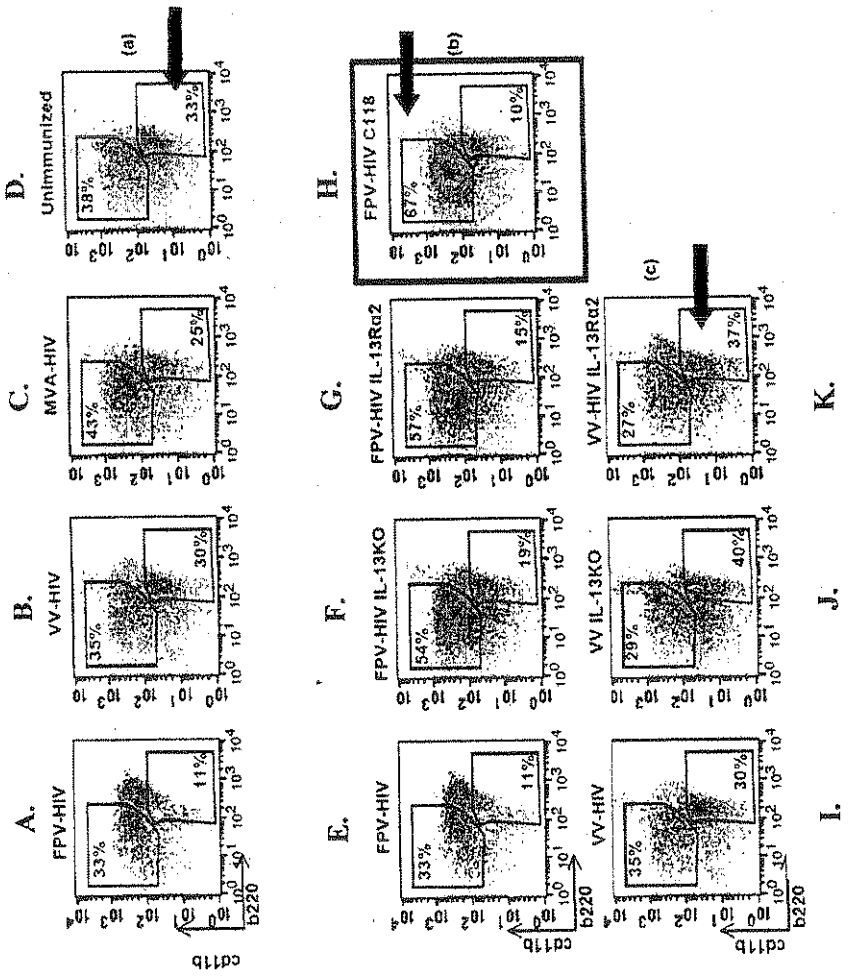


FIGURE TWELVE

Substitute Sheet
(Rule 26) RO/AU

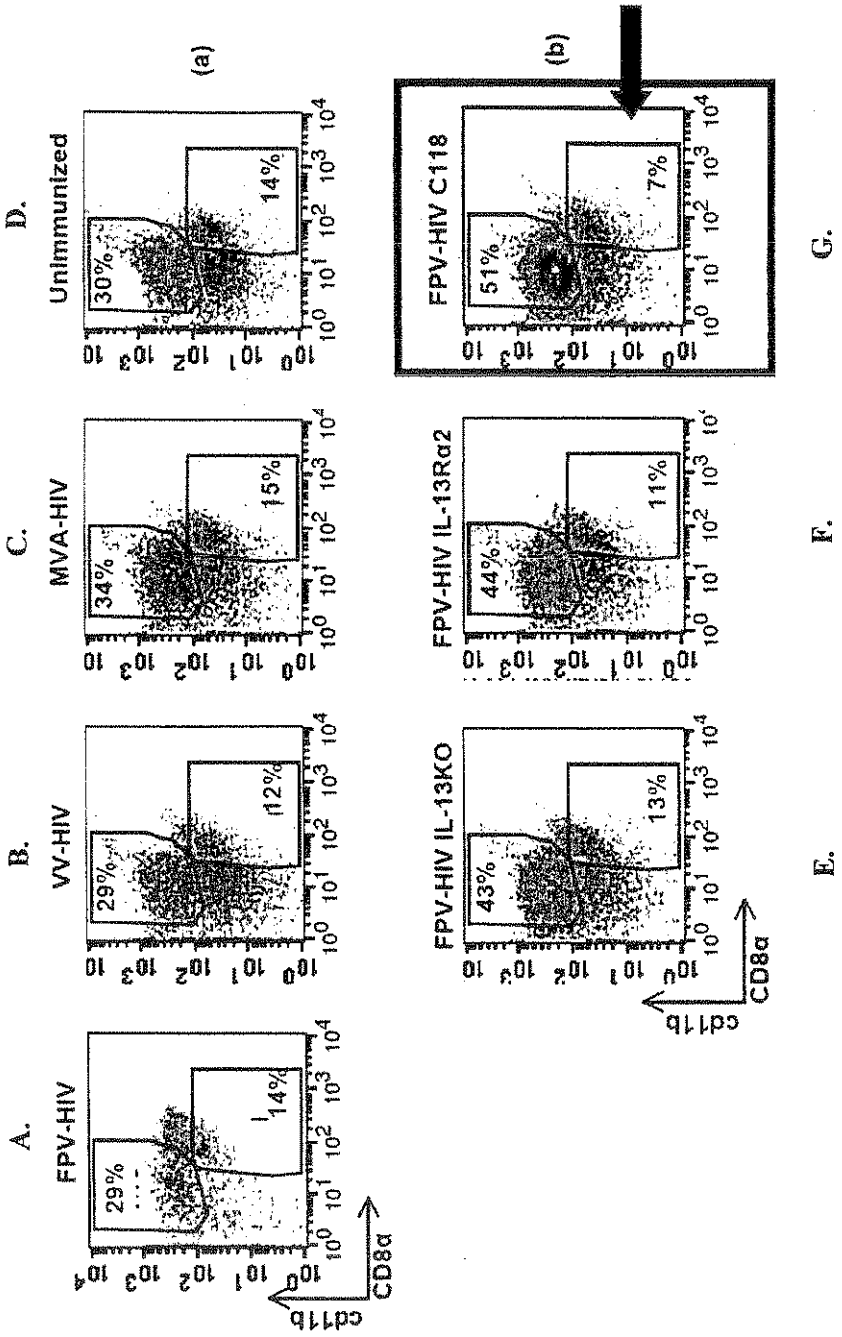


FIGURE THIRTEEN

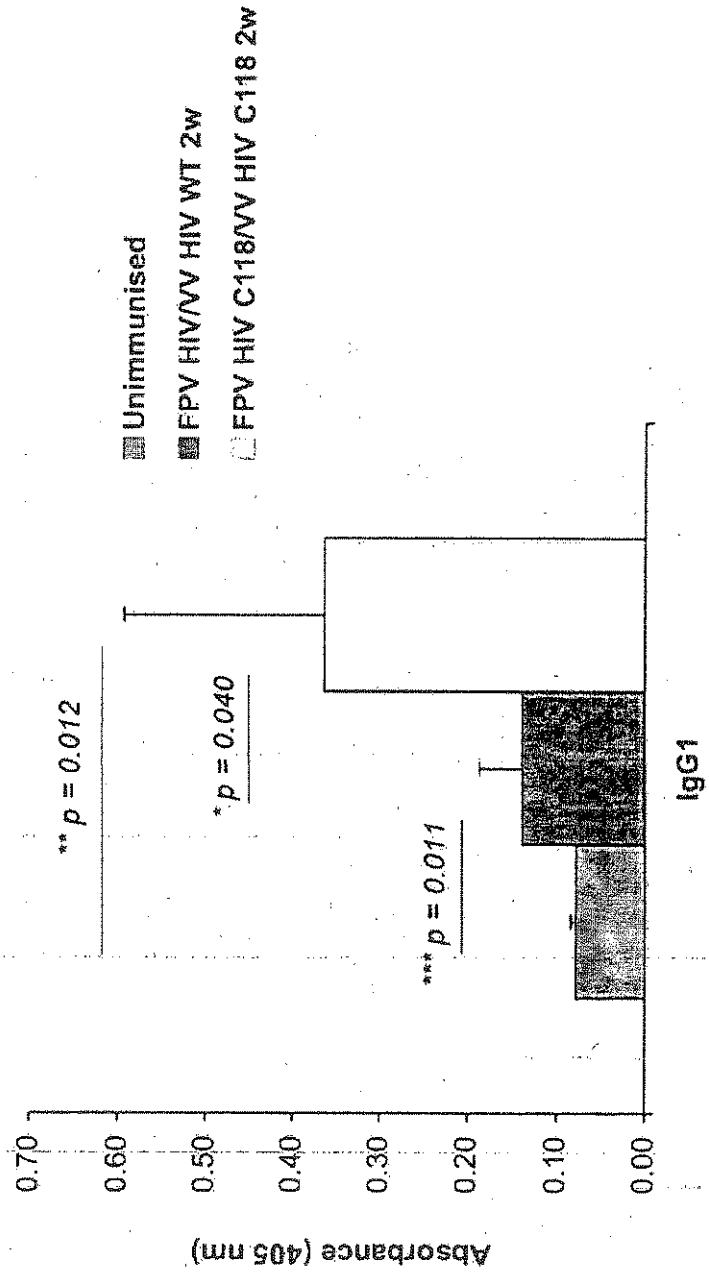


FIGURE FOURTEEN