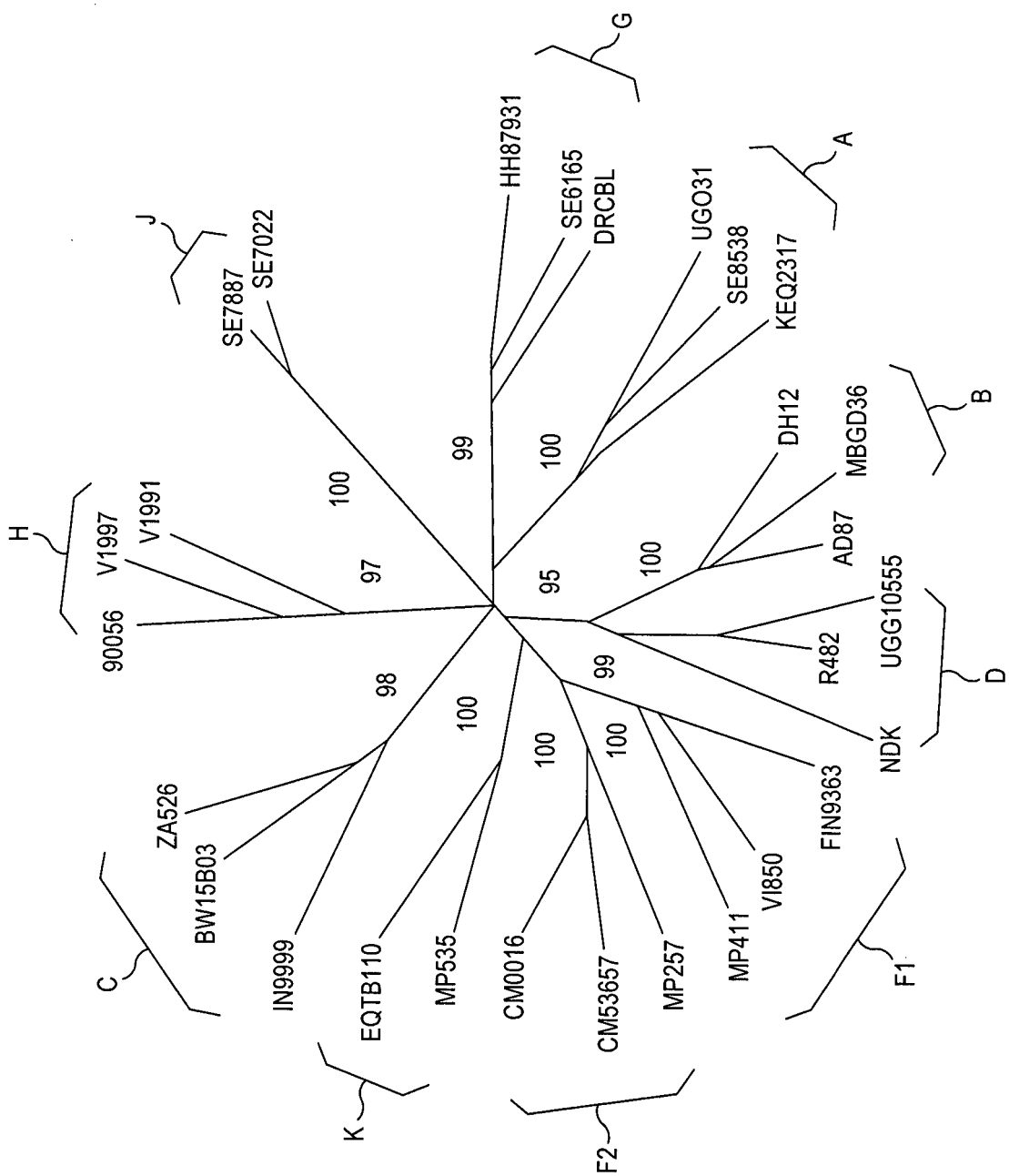

H
V1997
V1991
90056
J
SE7887
SE7022
G
HH87931
SE6165
DRCBL
A
UGO31
SE8538
KEQ2317
B
DH12
MBGD36
AD87
D
UGG10555
R482
NDK
F1
FIN9363
VI850
MP411
MP257
F2
CM53657
CM0016
MP535
EQTB110
K
IN9999
C
BW15B03
ZA526
100
97
99
100
95
100
99
100
100
100
98
100

FIG. 1

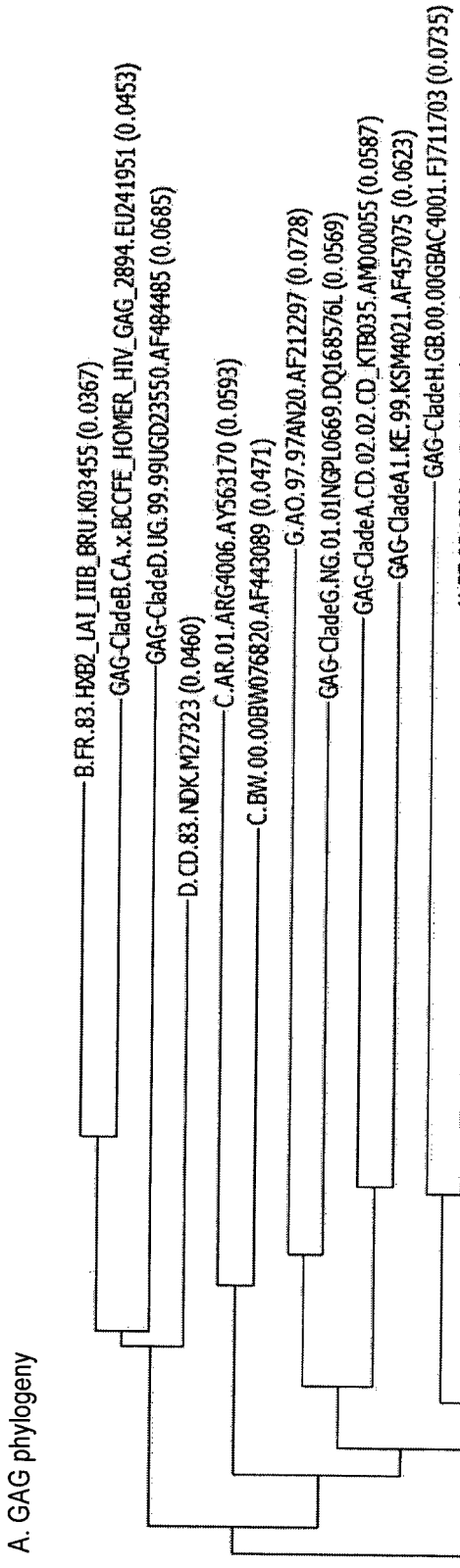

A. GAG phylogeny
B.FR.83.HXB2_LAI_IIIB_BRU.K03455 (0.0367)
GAG-CladeB.CA.x.BCCFE_HOMER_HIV_GAG_2894.EU241951 (0.0453)
GAG-CladeD.UG.99.99UGD23550.AF484485 (0.0685)
D.CD.83.NDK.M27323 (0.0460)
C.AR.01.ARG4006.AY563170 (0.0593)
C.BW.00.00BW076820.AF443089 (0.0471)
G.AO.97.97AN20.AF212297 (0.0728)
GAG-CladeG.NG.01.01NGPL0669.DQ168576L (0.0569)
GAG-CladeA.CD.02.02.CD_KTB035.AM000055 (0.0587)
GAG-CladeA1.KE.99.KSM4021.AF457075 (0.0623)
GAG-CladeH.GB.00.00GBAC4001.FJ711703 (0.0735)
H.BE.93.VI991.AF190127 (0.0605)
J.SE.94.SE9173_7022.AF082395 (0.0722)
F1.AO.06.AO_06_ANG32.FJ900266 (0.0676)
GAG-F1.RW.x.VI69.111796 (0.0577)
GAG-CladeK.CM.96.96CM_MP535.AJ249239 (0.0402)
K.BE.x.VI325.111789 (0.0543)

FIG. 2

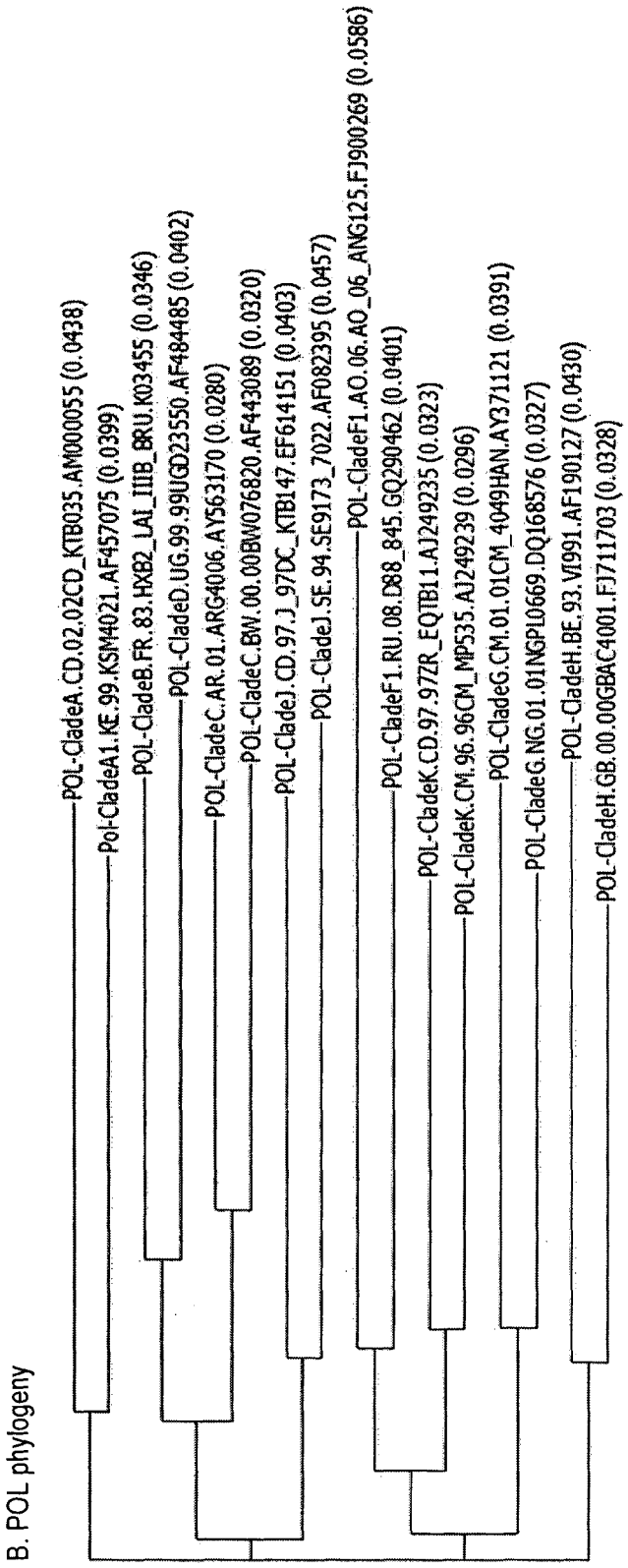

B. POL phylogeny
POL-CladeA.CD.02.02CD_KTB035.AM000055 (0.0438)
Pol-CladeA1.KE.99.KSM4021.AF457075 (0.0399)
POL-CladeB.FR.83.HXB2_LAI_IIIB_BRU.K03455 (0.0346)
POL-CladeD.UG.99.99UGD23550.AF484485 (0.0402)
POL-CladeC.AR.01.ARG4006.AY563170 (0.0280)
POL-CladeC.BW.00.00BW076820.AF443089 (0.0320)
POL-CladeJ.CD.97.J_97DC_KTB147.EF614151 (0.0403)
POL-CladeJ.SE.94.SE9173_7022.AF082395 (0.0457)
POL-CladeF1.AO.06.AO_06_ANG125.FJ900269 (0.0586)
POL-CladeF1.RU.08.D88_845.GQ290462 (0.0401)
POL-CladeK.CD.97.97ZR_EQTB11.AJ249235 (0.0323)
POL-CladeK.CM.96.96CM_MP535.AJ249239 (0.0296)
POL-CladeG.CM.01.01CM_4049HAN.AY371121 (0.0391)
POL-CladeG.NG.01.01NGPL0669.DQ168576 (0.0327)
POL-CladeH.BE.93.VI991.AF190127 (0.0430)
POL-CladeH.GB.00.00GBAC4001.FJ711703 (0.0328)

*FIG. 2 Cont'd*

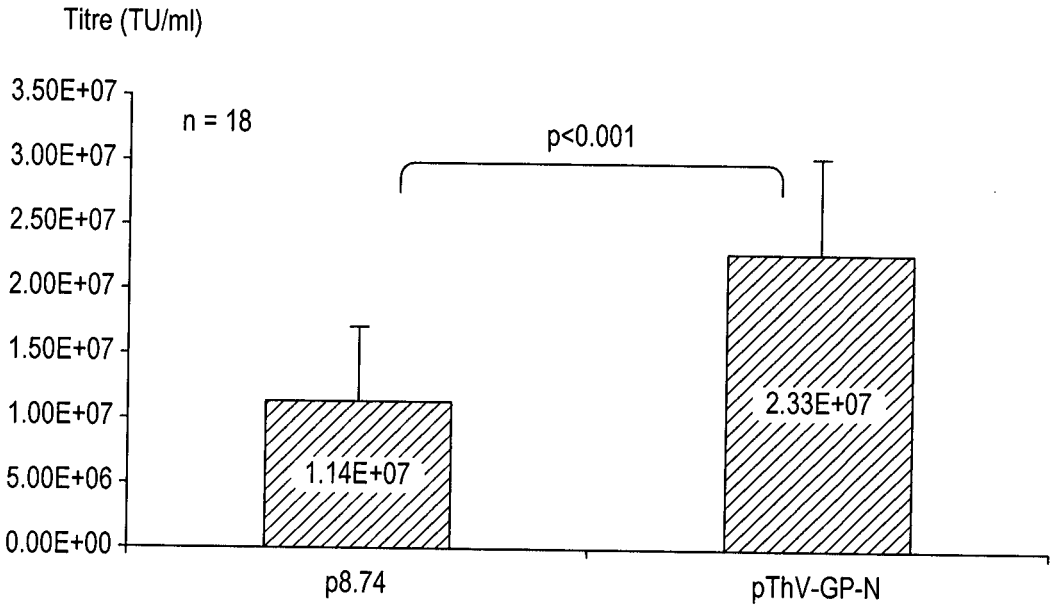

Titre (TU/ml)
3.50E+07
3.00E+07
2.50E+07
2.00E+07
1.50E+07
1.00E+07
5.00E+06
0.00E+00
n = 18
p<0.001
1.14E+07
2.33E+07
p8.74
pThV-GP-N

FIG. 3

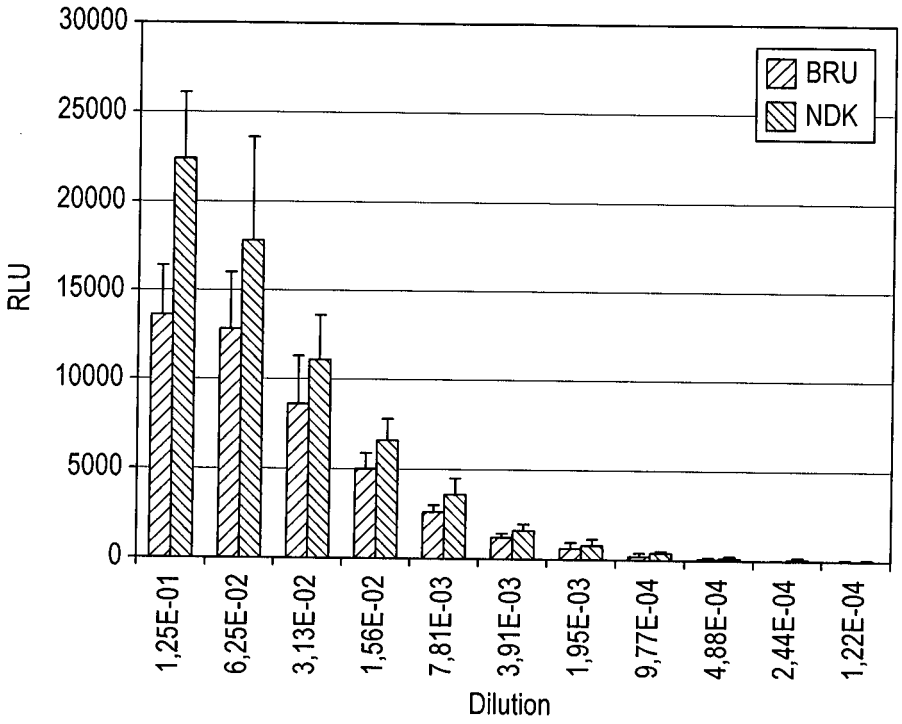

30000
25000
20000
15000
10000
5000
0
RLU
BRU
NDK
1,25E-01
6,25E-02
3,13E-02
1,56E-02
7,81E-03
3,91E-03
1,95E-03
9,77E-04
4,88E-04
2,44E-04
1,22E-04
Dilution

FIG. 4A

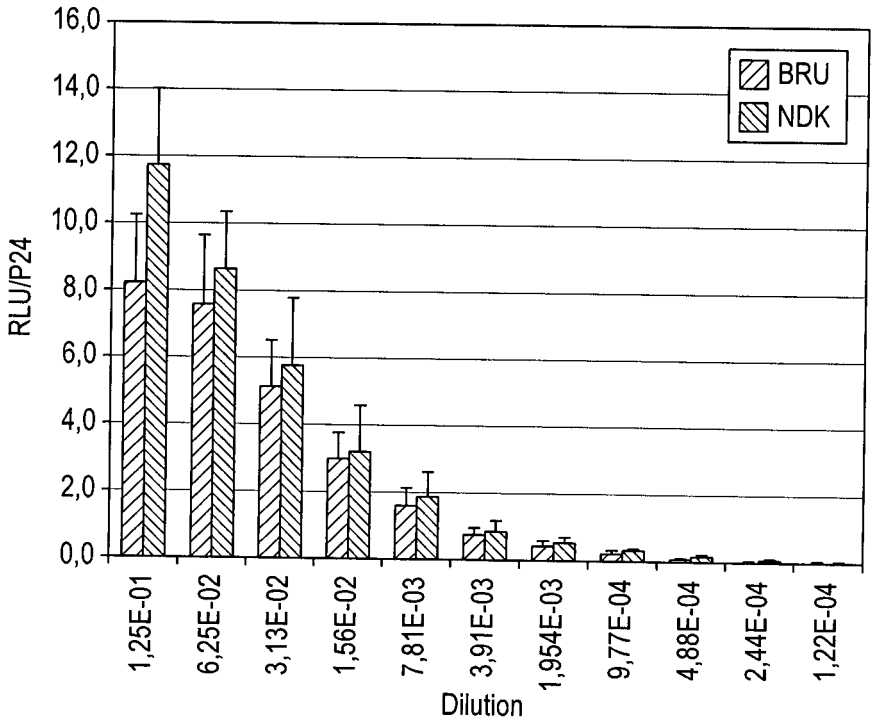

16,0
14,0
12,0
10,0
8,0
6,0
4,0
2,0
0,0
RLU/P24
BRU
NDK
1,25E-01
6,25E-02
3,13E-02
1,56E-02
7,81E-03
3,91E-03
1,954E-03
9,77E-04
4,88E-04
2,44E-04
1,22E-04
Dilution

FIG. 4B

| | A3 | B3 | C3 | D3 | E3 | F3 | G3 | H3 | I3 | J3 | K3 |
|---|---|---|---|---|---|---|---|---|---|---|---|
| pThV GP-N | 0µl | 1µl | 2µl | 3µl | 4µl | 5µl | 6µl | 7µl | 8µl | 9µl | 10µl |
| P8,74 | 10µl | 9µl | 8µl | 7µl | 6µl | 5µl | 4µl | 3µl | 2µl | 1µl | 0µl |
| Titre | 6,39E+06 | 8,68E+06 | 1,16E+07 | 3,67E+07 | 5,00E+07 | 4,31E+07 | 4,40E+07 | 2,75E+07 | 3,32E+07 | 3,80E+07 | 3,50E+07 |
| P24 | 430 | 400 | 361 | 521 | 958 | 800 | 1075 | 742 | 600 | 620 | 790 |

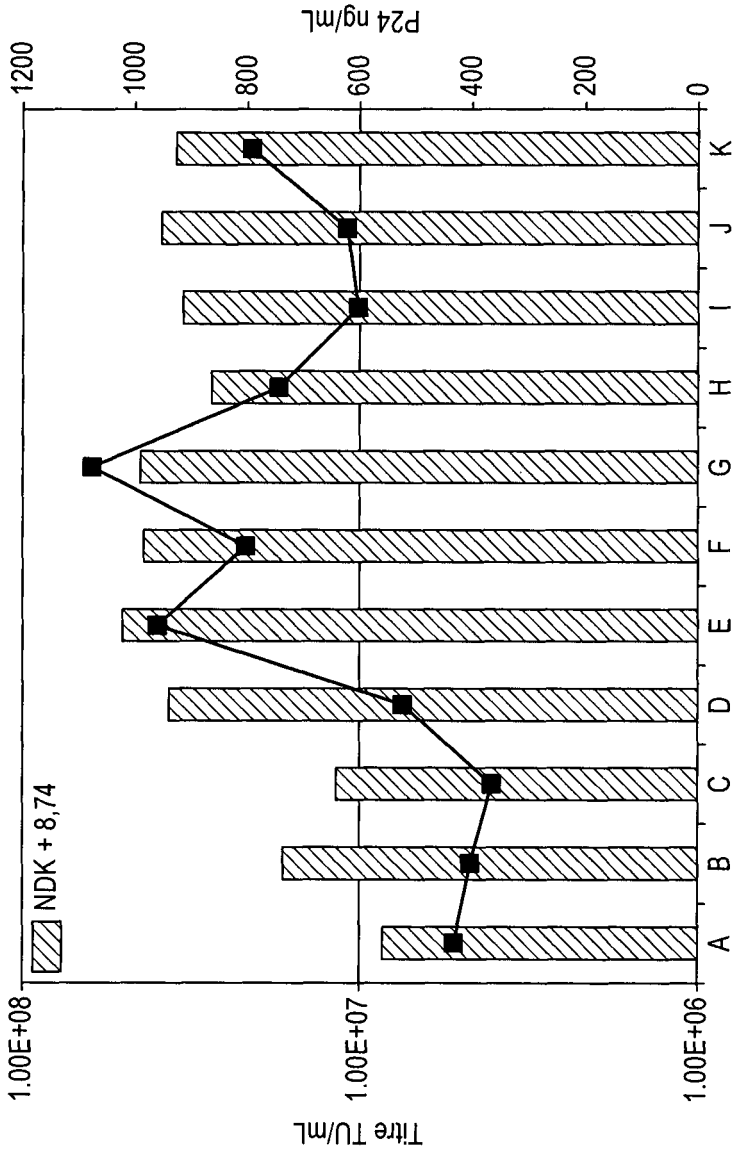



FIG. 5

| KDa | POL |
|---|---|
| 10 | Protéase |
| 66/51 | RT |
| 32 | Intégrase |

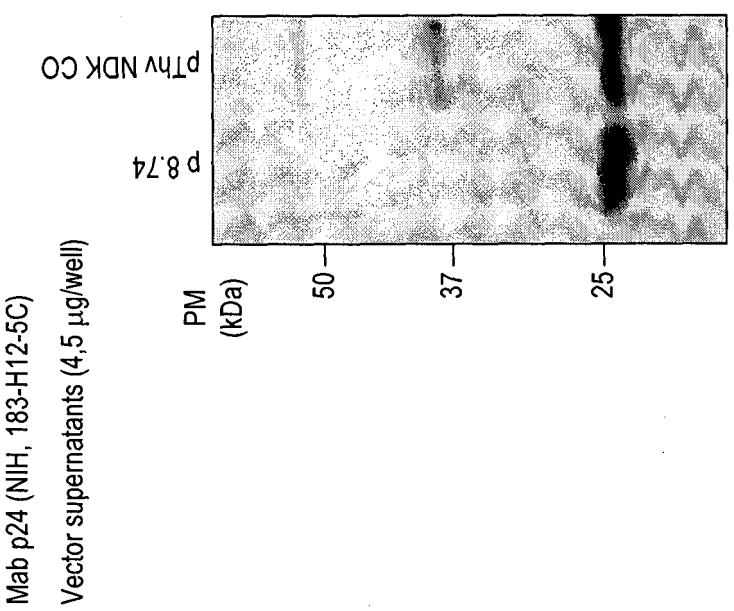



FIG. 6

```
                                    1                                   *   *   *                                       *                                                  **  50
P17-CladeB.FR.83.HXB2_LAI_IIIB_BRU.K03455   (1)  MGARASVLSGGELDRWEKIRLRPGGKKYKLKHIVWASRELERFAVNPGL
                P17-CladeD.CD.83.NDK.M27323 (1)  MGARASVLSGGKLDTWERIRLRPGGKKYALKHLIWASRELERFTLNPGL

                                   51       *   *       *   *                                                  100
P17-CladeB.FR.83.HXB2_LAI_IIIB_BRU.K03455   (51) LETSEGCRQILGQLQPSLQTGSEELRSLYNTVATLYCVHQRIEIKDTKEA
                P17-CladeD.CD.83.NDK.M27323 (51) LETSEGCKQIIGQLQPSIQTGSEEIRSLYNTVATLYCVHERIEVKDTKEA

                                   101                                 132
P17-CladeB.FR.83.HXB2_LAI_IIIB_BRU.K03455   (101) LDKIEEEQNKSKKKAQQAAADTGHSNQVSQNY
                P17-CladeD.CD.83.NDK.M27323 (101) VEKMEEEQNKSKKKTQQAAADS--S-QVSQNY
```

FIG. 7

```
                                                1
                                      *  *  *                **                  *  *  *        *
P17-CladeB.FR.83.HXB2_LAI_IIIB_BRU.K03455  (1) MGARASVLSGGELDRWEKIRLRPGGKKKYKLKHIVWASRELERFAVNPGLLETSEGCRQILGQLQPSLQTGSEEL
P17-B.UY.01.01UYTRA1092.AY781126           (1) --ARASVLSGGELDRWEKIRLRPGGKKKYRLKHIVWASRELERFAVNPGLLETTEGCRQILGQLQPSLQTGSEEL
P17-CladeB.CN.05.05CNHB_dw107.DQ833416     (1) MGARASVLSGGQLDRWEKIRLRPGGKKKYRLKHLVWASRELERFAVNPGLLETSEGCRQILEQLQPSLQTGSEEL
P17-CladeB.US.x.B4522TOB8U.GQ371250        (1) MGARASVLSGGELDRWEKIRLRPGGKKKYKLKHIVWASRELERFAVNPGLLETSGGCRQILEQLQPSLQTGSEEL
P17-CladeB.ZA.03.03ZAPS045MB2.DQ396398      (1) MGARASVLSGGELDRWEKIRLRPGGKKKYRLKHIVWASRELERFAINPGLLETSAGCRQILGQLHPSLQTGSEEL
P17-CladeB.CO.01.PCM074.AY561240           (1)  -ARASVLSGGELDKWEKIRLRPGGKKKYRLKHIVWASRELERFAVNPGLLETSEGCRQILAQLQPSLPTGSEEL
P17-CladeB.CY.05.CY075.FJ388916            (1) MGARASVLSGGELDRWEKIRLRPGGKKKYKLKHIVWASRELERFAVNPGLLETSEGCRQILGQLQPSLQTGSEEL
P17-CladeB.YE.02.02YE508.AY795905          (1) --ARASILSGGELDRWEKIRLRPGGKKKYKLKHIVWASRELERFAVNPGLLETSEGCIQILGQLQPSLQTGSEEL
P17-CladeB.US.x.X1537TOB8U.GQ371695        (1) MGARASVLSGGELDRWEKIRLRPGGKKKYKLKHVVWASRELERFAVNPGLLETSEGCRKILGQLQPSLQTGSEEL
P17-CladeB.US.02.L8124P.FJ469741           (1) MGARASVLSGGELDRWEKIRLRPGGKKQYKLKHIVWASRELERFALNPGLLETSEGCRQILEQLQPSLQTGSEEI
P17-CladeB.CY.03.CY005.EU673412            (1) MGARASILSGGELDRWEKIRLRPGGKKQYRLKHIVWASRELERFAVNPGLLETSGGCKQILAQLHPSLQTGSEEL
P17-CladeB.AR.04.04AR143170.DQ383750       (1)  -ARASILSGGELDRWEKIRLRPGGKKRYRLKHIVWASRELERFAVNPGLLETSEGCKQIIRQLQPSLQTGSEEL
P17-CladeB.AU.87.MBC925.AF042101           (1) MGARASVLSGGELDRWERIRLRPRGKKKYQLKHIVWASRELERFSVNPGLLETSEGCRQIIRQLQPALQTGSEDF
P17-CladeB.US.x.AC160T9Day1034Dom.EU616649 (1) MGARASVLSGGELDRWEKIRLRPGGKKKYRLKHLVWASRELERFAVNPGLLETSEGCRQILGQLQPSLQTGSEEL
P17-CladeB.US.x.X5597TOB8U.GQ371704        (1) MGARASVLSGGELDRWERIRLRPGGSKKYKLKHIVWASRELERFAVNPSLLETSEGCKQILGQLQPSLQTGSEEL
P17-CladeB.AR.05.2005_03.FJ155192          (1) MGARASVLSGGELDRWEKIRLRPGGKKKYQLKHIVWASRELERFAVNPSLLETSEGCRQIIGQLQPSLQTGSEEL
P17-CladeB.CA.x.BCCFEHOMERHIVGAG2991.EU242048 (1) MGARASVLSGGELDKWERIRLRPGGKKKYKLKHIVWASRELERFAVNPGLLETSEGCRQIIGQLQPSLQTGSEEL
P17-CladeB.AR.05.2005_11.FJ155200          (1) MGARASVLSGGELDRWEKIRLRPGGKKKYRLKHVVWASRELERFAVNPGLLETAEGCKQILAQLHPSLQTGSEEL
P17-CladeB.AU.x.492214Z.AY857059           (1) ---RASVLSGGELDRWEKIRXRQGGKKKYKLKHIVWASRELERFAVNPGLLETXEGCRQILEQLQPALQTGSEEL
P17-CladeB.US.04.ES8_43.EF363126           (1) MGARASVLSGGELDRWEKIRLRPGGKKKYKLKHIVWASRELERFAVNPGLLETSGGCRQILGQLQPSLQTGSEEL
P17-CladeD.CD.83.NDK.M27323                (1) MGARASVLSGGKLDTWERIRLRPGGKKKYALKHLIWASRELERFTLNPGLLETSEGCKQIIGQLQPSIQTGSEEI
```

FIG. 8

```
                                                1         *   *                                    **                    *     *     *
P17-CladeB.FR.83.HXB2_LAI_IIIB_BRU.K03455 (1) MGARASVLSGGELDRWEKIRLRPGGKKKYKLKHIVWASRELERFAVNPGLLETSEGCRQILGQLQPSLQTGSEEL
P17-CladeD.CD.83.NDK.M27323               (1) MGARASVLSGGKLDTWERIRLRPGGKKKYALKHLIWASRELERFTLNPGLLETSEGCKQIIGQLQPSIQTGSEEI
P17-CladeD.FR.x.Vis20.FJ649608            (1) MGARASVLSGGKLDAWEKIRLRPGGKKKYKLKHIVWASRELERFALNPGLLETSEGCRQIISQLQPSLKTGSEEL
P17-CladeD.UG.02.TC025704.AY803405        (1) MGARASVLSGGKLDEWEKIRLRPGGRKTYKLKHIVWASRELERFALNPGLLETSEGCKQIIAQLQSSIQTGSEEI
P17-CladeD.UG.99.99UGD23550.AF484485      (1)  -ARASVLSGGKLDEWEKIQLRPGGHKRYKLKHIVWASRELERFAINPGLLETSGGCRQIMGQLQPAIQTGSEEL
P17-CladeD.CM.01.01CM_0009BBY.AY371155    (1) --ARASVLSGGKLDAWEKIRLRPGGRKRYRLKHIVWASRELERFALNPGLLETSEGCKQIISQLQPSLKTGSEEL
```

*FIG. 9*

```
                                                                1               *   *                                    *           *
P17-CladeB.FR.83.HXB2_LAI_IIIB_BRU.K03455     (1) MGARASVLSGGELDRWEKIRLRPGGKKKYKLKHIVWASRELERFAVNPGLLETSEGCRQIL
P17-CladeD.CD.83.NDK.M27323                   (1) MGARASVLSGGKLDTWERIRLRPGGKKKYALKHLIWASRELERFTLNPGLLETSEGCKQII
P17-CladeD.FR.x.Vis20.FJ649608                (1) MGARASVLSGGKLDAWEKIRLRPGGKKKYKLKHIVWASRELERFALNPGLLETSEGCRQII
P17-CladeD.UG.02.TC025704.AY803405            (1) MGARASVLSGGKLDEWEKIRLRPGGRKTYKLKHIVWASRELERFALNPGLLETSEGCKQII
P17-CladeD.UG.99.99UGD23550.AF484485          (1) --ARASVLSGGKLDEWEKIQLRPGGHKRYKLKHIVWASRELERFAINPGLLETSGGCRQIM
P17-CladeD.CM.01.01CM_0009BBY.AY371155        (1) --ARASVLSGGKLDAWEKIRLRPGGRKRYRLKHIVWASRELERFALNPGLLETSEGCKQII
P17-CladeG.CU.99.Cu87.AY586549                (1) MGARASVLSGGRLDAWEKIRLRPGGKKKYRMKHLVWASRELERFALNPGLLETAEGCKQLM
P17-CladeG.CM.04.944_5.FJ389366               (1) MGARASVLSGGKLDSWEKIRLRPGGKKKYRMKHLVWASREMERFALNPDLLETXEGCQQIX
P17-CladeG.NG.01.01NGPL0669.DQ168576L         (1) --ARASVLSGGKLDAWEKIRLRPGGKKKYRIKHLVWASRELERFALNPGLLETAEGCQQIM
P17-CladeG.BE.96.DRCBL.AF084936               (1) MGARASVLSGGKLDAWEKIRLRPGGKKRYRMKHLVWASRELDRFALNPGLLETAEGCQKIM
P17-CladeG.SE.93.SE6165.AF061642              (1) MGARASVLTGGKLDAWEKIRLRPGGRKSYKIKHLVWASRELERFALNPDLLETAEGCQQIM
P17-CladeA.CD.02.02.CD_KTB035.AM000055        (1) MGARASVLSGGKLDAWEKIRLRPGGKKKYRLKHLVWASRELDRFALNPSLLETSEGCQQII
P17-CladeA.RW.x.VI415.L11791                  (1) MGARASVLSGGKLDAWEKIRLRPGGRKKYRMKHLVWASRELDRFALNPGLLETAEGCQQIL
P17-CladeA1.AU.04.PS1044_Day177.DQ676873      (1) MGARASILSGGRLDAWEKIRLRPGGKKKYRLKHLVWASRELXRFALNPXLLESAEGCQQIM
P17-CladeA1.KE.00.MSA4070.AF457081            (1) --ARASVLSGGKLDAWEKIQLRPGGKKKYRLKHLVWASRELERFALNPDLLETSEGCQQII
P17-CladeA1.KE.99.KSM4021.AF457075            (1)  -ARASVLSGGKLDSWEKIRLRPGGKKKYRLKHLVWASRELERFALNPSLLETAEGCQQIM
P17-CladeC.BR.04.04BR013.AY727522             (1) MGARASVLRGEKLDTWERIRLRPGGKKKYMMKHLVWASRELERFALAPGLLETAEGCRQII
P17-CladeC.ZM.05.ZM1223M.FJ606168             (1) MGARASILRGGKLDAWEKIQLRPGGKKRYMLKHLVWASRELERFALNPGLLETAEGCRQII
P17-CladeC.BR.04.04BR013.AY727522#2           (1) MGARASVLRGEKLDTWERIRLRPGGKKKYMMKHLVWASRELERFALAPGLLETAEGCRQII
P17-CladeC.ZM.05.ZM1223M.FJ606168#2           (1) MGARASILRGGKLDAWEKIQLRPGGKKRYMLKHLVWASRELERFALNPGLLETAEGCRQII
P17-CladeC.IL.99.99ET7.AY255824               (1) --ARASILRGGQLDRWEKIRLRPGGKKHYMLKHLVWASRELERFVLNPGLLETAEGCKQIM
P17-CladeAE.HK.2004.HK001                     (1) MGARASILTGEKLDAWEKIRLRPGGKKKYMIKHLVWASRELERFALNPGLLETAEGCQQII
P17-01_AE.TH.1995.95TNIH022                   (1) MGARASILSGGKLDAWEKIRLRPGGRKKYRMKHLVWASRELERFALNPGLLETAEGCQQLI
P17-01_AE.TH.1993.93TH062                     (1) MGARASVLSGGKLDAWEKIRLRPGGKKKYQLKHVVWASRELERFALNPGLLETAEGCQQII
P17-01_AE.HK.2004.HK001                       (1) MGARASILTGEKLDAWEKIRLRPGGKKKYMIKHLVWASRELERFALNPGLLETAEGCQQII
P17-CladeF1.AO.06.AO_06_ANG32.FJ900266        (1) MGARASVLSGGKLDDWEKIRLRPGGKKQYKLKHLVWASRELERFALNPGLLETSEGCRKII
P17-CladeF1.AR.06.2006_03.FJ155204            (1) MGARASVLSGGKLDAWERIRLRPGGKKKYRMKHLIWAGRELDRFALDPGLLETSEGCRKII
P17-CladeF1.BR.02.02BRI70.FJ771007            (1) MGARASVLSGGKLDAWEKIRLRPGGKKKYRMKHLIWASRELERFALDSGLLETTEGCRKII
P17-CladeF1.RW.x.VI69.L11796                  (1) MGARASVLSGGKLDAWEKIRLRPGGRKKYKMKHLIWASRELERFALDPGLLETSEGCRKII
P17-CladeF2.CM.x.CA16.AF247520                (1) ----------------------GGKKKYRLKHLVWASRELERFALNPGLLETTEGCKQII
P17-CladeH.BE.93.VI991.AF190127               (1) MGARASVLSGGKLDAWEKIRLRPGGRKKYRLKHLVWASRELERFALNPDLLETADGCQQIL
P17-CladeH.CD.91.VI557.L11793                 (1) MGARASVLSGGKLDAWEKIRLRPGGKKKYRLKHLVWASRELERFALNPDLLDTAEGCLQLI
P17-CladeH.CF.90.056.AF005496                 (1) MGARASVLSGGKLDAWEKIRLRPGGKKKYRLKHLVWASRELERFALNPGLLETPEGCLQII
P17-CladeH.GB.00.00GBAC4001.FJ711703          (1) MGARASVLSGGKLDAWEKIRLRPGGKKKYRLKHLVWASRELDRFALNPDLLETADGCLKIX
P17-CladeJ.SE.94.SE9173_7022.AF082395         (1) MGARASILSGGKLDDWEKIRLRPGGKKQYRIKHLVWASRELDRFALNPGLLESAKGCQQIL
```

FIG. 10